UC Riverside UC Riverside Electronic Theses and Dissertations

Title

Computational Analysis of Receptor-Odor Interactions and Prediction of Behavior-Modifying Chemical Space

Permalink https://escholarship.org/uc/item/5j67m8w8

Author Boyle, Sean Michael

Publication Date 2012

Peer reviewed|Thesis/dissertation

UNIVERSITY OF CALIFORNIA RIVERSIDE

Computational Analysis of Receptor-Odor Interactions and Prediction of Behavior-Modifying Chemical Space

A Dissertation submitted in partial satisfaction of the requirements for the degree of

Doctor of Philosophy

in

Genetics, Genomics, and Bioinformatics

by

Sean Michael Boyle

March 2012

Dissertation Committee: Dr. Anandasankar Ray, Chairperson Dr. Anupama Dahanukar Dr. Thomas Girke

Copyright by Sean Michael Boyle 2012 The Dissertation of Sean Michel Boyle is approved:

Committee Chairperson

University of California, Riverside

Acknowledgments

Personal Acknowledgements

I would like to acknowledge my parents Laura and Mike Boyle for their constant support and encouragement throughout both my education and life. They have always been a wonderful source of guidance and support while traversing the endeavors of the journey we call life. I would also like to acknowledge the daily guidance, humor, and inspiration provided by my advisor Dr. Anandasankar Ray. He has always been a constant source of wonderful ideas, almost tangible intensity toward science, and at times very needed off topic tangents. I would also like to acknowledge all past and present members of both the Ray and Dahanukar labs for their endless inquisitiveness, humor, and good nature. Without all of you this work would not be so complete and would certainly not have been so enjoyable.

Professional Acknowledgements

- Anandasankar Ray, Anupama Dahanukar, and Thomas Girke for providing research guidance.
- Shane McInally for validating *Drosophila* receptor-odor predictions using electrophysiology.
- Chih-Ying Su, Eliza Kelly-Swift, and John Carlson for validating *Anopheles* receptorodor predictions using electrophysiology.
- Sana Tharadra for performing *Drosophila* larvae behavior experiments.
- Christine Pham for performing *Drosophila* larvae behavior experiments.
- Dyan MacWilliam for performing CO₂ receptor and repellency validations using electrophysiology.
- Tom Guda for performing Mosquito behavior experiments.
- Will Pitt and Tom Blundell for assisting with structure-based virtual screening.
- Sachin Suardre for validating predicted EthR inhibitors.

ABSTRACT OF THE DISSERTATION

Computational Analysis of Receptor-Odor Interactions and Prediction of Behavior-Modifying Chemical Space

by

Sean Michael Boyle

Doctor of Philosophy, Graduate Program in Genetics, Genomics, and Bioinformatics University of California, Riverside, March 2012 Dr. Anandasankar Ray, Chairperson

Coding of information in the peripheral olfactory system and resulting olfactory dependent behavior is thought to depend primarily on two fundamental factors: the interaction of individual odors with different subsets of the odor receptor (Or) repertoire, and the mode of signaling that an individual receptor-odor interaction elicits, activation or inhibition. In order to better understand these processes, we design and implement a structure-based virtual screening approach that identifies common structural features that are highly correlated with odor activity for individual receptors. We then apply these features to rapidly screen for putative ligands in silico from a large untested odor space (>240,000 putative volatiles) for the majority of odor receptors in the Drosophila antenna, allowing for analysis of odor coding for the majority of receptors for the first time. Functional experiments support a high success rate (~71%) for the screen and we validate numerous new activators and inhibitors for the receptors. Following our initial application in *Drosophila*, we extend our approach to predict activating and inhibiting odors for a large number of important pest and disease vector species including 50 Anopheles gambiae Ors (65% validated accuracy), the CO2 receptors of multiple species (48% validated accuracy), 9 newly identified Citrus Psyllid ORNs, and a large number of functionally distinct mammalian receptors. We next extended our in silico

vi

screening approach to identify shared structural features important for a behavioral response to DEET-like repellents for which the molecular target has not yet been identified, identifying ~150 natural compounds as candidate repellents. We select 4 candidates, 3 approved as safe for human food use, and demonstrate that they are strong olfactory and gustatory repellents to both mosquitoes and *Drosophila*. As only a small region of odor space has been explored, there remains potential to uncover previously unidentified patterns of odor coding. Through a combination of *in silico* and electrophysiology screens, we identify odors with ultra-prolonged termination kinetics that are delayed for several minutes, resulting in a memory trace that affects subsequent odor detection. Finally, we successfully perform structure-based virtual screen, identifying potential inhibitors of an important Tuberculosis drug target EthR.

Table of Contents

CHAPTER I: Introduction

p1
p6
р8
p12
p16
p18

CHAPTER II: Designing a Ligand-Based Virtual Screening Approach to Decode *Drosophila* Odor Receptor Chemical Space *In Silico*

 Introduction Results Discussion Figures Tables 	p25 p27 p37 p42 p60
	•

CHAPTER III: Applying Chemical Informatics to Decode Odor Receptors of Several Important Disease Vector and Pest Insect Species as Well as Mammals

 Introduction Results Discussion Figures Tables 	p71 p76 p95 p99 p141
- Tables	p141

CHAPTER IV: A New Generation of Safe DEET Substitutes that are Strong Olfactory and Gustatory Repellents of Mosquitoes and Flies

- Introduction	p201
- Results and Discussion	p204
- Figures	p214

CHAPTER V: Analyzing Termination Dynamics of Prolonged Activating Odors and their Effects on Receptor-Mediated Olfactory Behavior

- Introduction	p227
- Results	p230
- Discussion	p241
- Figures	p245
- Tables	p265

CHAPTER VI: Applying Structure-Based Virtual Screening to Identify Potent Inhibitors of the Tuberculosis Target EthR

- Introduction	p266
- Results and Discussion	p268
- Figures	p281
- Tables	p301

CHAPTER VII: Methods

- Chemical informatics	p302
- Electrophysiology	p302
- Natural odor compound library	p303
- Pubchem compound library	p303
- eMolecules compound library	p303
- Calculation of 3D conformations	, p303
- Calculation of molecular descriptors	p304
- Classification of active compounds	, p304
- Calculation of Accumulative Percentage of Actives (APoA)	, p305
- Determination of optimized descriptor subsets	, p305
- Clustering Ors by most common descriptors	, p306
- Clustering compounds by activity of Or	, p306
- Clustering Ors by predicted ligand space	, p307
- Calculation of Or prediction distribution frequencies	p307
- Or-ligand interaction map	p307
- Computational validation of ligand-based virtual screening (Non-SVM)	p308
- Calculation of LogP and vapor pressure values	p309
- Repellency behavior testing	p309
- Classification of repellent compounds	p311
- Support Vecotor Machine (SVM) predictions	p311
- Computational validation of ligand-based virtual-screening (SVM)	p311
- Vinyl solubility assay	p312
- Olfactory avoidance assay trap assay for Drosophila	p312
- T-maze Assay Methods	p313
- Modified hand in-glove olfactory repellency assay for mosquitoes	p313
- Humidity and warmth attraction assay	p315
- Larval behavior assays	, p315
- Assembly of EthR screening library	p316
- Calculating molecular descriptors for EthR analysis	p316

 Applying machine learning with Pipeline Pilot Performing structure-based virtual screening with Gold 	p317 p317
REFERENCES	p319

List of Figures

CHAPTER I:

1.1: Overview schematic describing neuronal wiring of the insect olfactory system p24

CHAPTER II:

2.1: Comparing efficacy of various structure analysis methods to analyze odor receptor ligands	p42
2.2: A receptor-optimized molecular descriptor approach has strong predictive	
power to find new ligands	p44
2.3: Accumulated percentage of actives analysis	p46
2.4: Electrophysiology validates that odorant receptor-optimized molecular	
descriptors can successfully identify new ligands for Drosophila	p48
2.5: Predicted receptor-odor interactions are highly specific	p50
2.6: High-ranking odors are more likely to be active than distantly ranked odors	p52
2.7: Analysis of receptor-odor relationships and breadth of tuning	p54
2.8: Analysis of receptor-natural odor interactions	p56
2.9: Predicted odor space and network view of odor coding	p58

CHAPTER III:

3.1: A molecular descriptor optimized approach is able to explain odor activity for individual <i>Anopheles</i> Ors	p99
3.2: Optimized molecular descriptor sets are able to cluster either active or inhibitory odors	p101
3.3: Structural relationships between the 75 most diverse aromatic odors	p107
3.4: Newly optimized molecular descriptor sets are able to cluster odors for aromatically tuned Ors	p109
3.5: Optimized descriptors for AgOrs 2, 6, and 10 effectively describe training set activity	p111
3.6: A Support Vector Machine (SVM) integrated approach is highly effective at explaining odor activity for individual Ors	p113
3.7: SVMs trained using optimized descriptors for AgOrs 2, 6, and 10	•
effectively describe training set activity	p115
3.8: A molecular descriptor optimized approach is able to explain odor activity for CO2 receptors	p117
3.9: Optimized molecular descriptor sets are able to cluster odors by CO2	P
receptor response	p119
3.10: Active compounds cluster into three distinct structural classes	p121
3.11: Chemical structures of validated activators and inhibitors	p123
3.12: A SVM integrated molecular descriptor optimized approach is able to	
explain odor activity for individual Citrus Psyllid ORNs	p125
3.13: Optimized molecular descriptor sets are able to cluster ORN activators	p127
3.14: SVMs trained using descriptor sets that were optimized for individual	
ORNs effectively describe training set activity	p129
3.15: A molecular descriptor optimized approach is able to explain odor activity	

for individual mammalian ORs	p131
3.16: Mammalian Odorant receptor-optimized molecular descriptors can	100
successfully cluster known ligands	p133
3.17: Optimized descriptors for mammalian ORs effectively describe training	
set activity	p135
3.18: Analyzing relationships between important features for mammalian ORs	p137
3.19: Analysis of mammalian OR tuning breadth	p139

CHAPTER IV:

4.1: Contribution of olfaction and gustation in DEET avoidance	p214
4.2: Mosquito behavioral assay glove setup	p216
4.3: A chemical informatics method to predict repellency	p218
4.4: Identification of repellents using in-silico screening of a large chemical	
space	p220
4.5: A new class of mosquito repellents with desirable safety profiles	p222
4.6: Mosquito escape index	p224
4.7: Natural compounds are effective at repelling aedes aegypti in the	
hand in glove assay	p226

CHAPTER V:

5.1: Activity of a behaviorally important neuron, Ab1A, can be described by an	
odor receptor neuron-optimized chemical inormatics approach	p245
5.2: Electrophysiology validates that ORN-optimized molecular descriptors can	
successfully identify new ligands for ab1A	p247
5.3: Functional identification of Ultra-Prolonged activators and analysis of their	
long-term effects on ab1A using electrophysiology	p249
5.4: Ectopic expression confers Or42b UP activation	p251
5.5: Behavioral effects of Ultra-Prolonged activators on odor detection in ab1A	p253
5.6: Behavioral effects of inhibitory odor on odor detection in ab1A	p255
5.7: Functional identification of Ultra-Prolonged activators of additional odor	
receptors using electrophysiology	p257
5.8: Identification of ultra-prolonged activating odors for additional Ors	p259
5.9: Long-term effects of Ultra-Prolonged activators on odor detection	p261
5.10: Modes of signaling and their behavioral responses	p263

CHAPTER VI:

6.1: Schematics of Ethionamide Activation Pathway	p281
6.2: Solved EthR structures	p283
6.3: The shape of the EthR cavity	p285
6.4: Previously identified EthR ligands bind within the proposed cavity	p287
6.5: Visualizing previously identified EthR ligands	p289
6.6: Single example of successful EthR self-docking	p291
6.7: The results of many EthR site 1 self-docking runs	p293
6.8: The predicted orientation of our strongest identified inhibitors in EthR	p295
6.9: The predicted orientations of 4 modest inhibitors of EthR	p297
6.10: The predicted orientations of the poor inhibitors of EthR	p299

List of Tables

CHAPTER II:

2.1: Optimized descriptor sets for each <i>Drosophila</i> Or2.2: Top 100 predicted compounds for each <i>Drosophila</i> Or	р60 р68
CHAPTER III:	
3.1: Optimized descriptor sets for each <i>Anopheles</i> Or	p141
3.2: Natural odor library predictions found in the top 500 predictions for each	
Anopheles Or	p152
3.3: Predicted odors validated as effective activators for several <i>Anopheles</i> Ors3.4: Activity of a large panel of aromatic odors was tested against three	p160
aromatically tuned Ors	p162
3.5: Optimized descriptor sets for Or2, Or6, and Or10	p164
3.6: Top 75 predicted compounds for each Drosophila Or	p166
3.7: Dividing training odors into three distinct sets based upon odor structure	-
and receptor response	p168
3.8: Optimized descriptors selected for the Aromatic Activator Screen	p170
3.9: Optimized descriptors selected for the Broad Activator	p172
3.10: Optimized descriptors selected for the Inhibitor Screen	p174
3.11: Top predicted natural library compounds for the aromatic activator,	-
broad activator, and inhibitor screens	p176
3.12: Predicted odors validated as activators and inhibitors of the CO2 receptor	p178
3.13: Optimized descriptor sets for each Citrus Psyllid ORN	p180
3.14: Top predicted natural library compounds for Citrus Psyllid ORNs	p184
3.15: Optimized descriptor sets for each mammalian OR	p188
3.16: Top 100 predicted compounds for each mammalian OR	р195

CHAPTER V:

5.1: Optimized descriptor sets for ab1A (Or42b)	p265

CHAPTER VI:

6.1: A breakdown of our structure-based virtual screening accuracy for EthR	p301
---	------

CHAPTER I:

INTRODUCTION

Complexity in the olfactory system

The olfactory system of insects is a very large and intricate neural network, consisting of a peripheral input layer, a middle processing layer, and high level wiring into the brain (Figure 1.1). Odors are detected at the periphery and contextual information about the odors are aggregated and organized in the middle layer. Here additional stages of processing are performed and the information is then provided to the brain for interpretation and decision-making.

The periphery olfactory system in *Drosophila* is housed in two olfactory organs: the antennae and maxillary palps. Both of these organs are covered with many tiny hairs called sensilla, which house between 1 and 4 distinct Olfactory Receptor Neurons (ORNs), however the predominant number of sensilla house 2 (de Bruyne et al., 2001). Interestingly, ORNs generally express only a single odor selective Odor receptor (Or) along with an obligate co-receptor Orco, which is essential for olfaction (Couto et al., 2005; Larsson et al., 2004; Vosshall and Hansson, 2011). *Drosophila* express 60 Or genes, which are translated into 62 proteins, that are housed in ORNs (Robertson et al., 2003). Both Or gene expression by ORNs and housing of ORNs in the antenna and maxillary palps is highly conserved, allowing for sensilla types to be classified according to what ORNs they house and ORNs to be classified by the Or genes they express (Couto et al., 2005; Dobritsa et al., 2003). While the peripheral olfactory system is highly structured and conserved, it also represents a very complex network of gene expression. It is the response of the Or to environmental odors that determines whether an ORN sends information, in the form of either neuronal activation or inhibition, to the higher centers in the brain (Dobritsa et al., 2003; Hallem et al., 2004). Or responses to odors have been demonstrated to range from total inhibition of the ORN to strong activation (>250 spikes/sec) and each Or is uniquely tuned to odors (Hallem and Carlson, 2006). While some Ors are narrowly tuned and respond to only 1 or a few known ligands, such as DmOr67d to the pheromone cVa, others are more widely tuned and respond to a broad array of both functional groups and molecule sizes (Hallem and Carlson, 2006; van Naters and Carlson, 2007). Interestingly, an individual odor may activate multiple receptors, with each receptor being tuned to a different range of odor concentration (Hallem and Carlson, 2006).

While originally identified in mammals, Ors of insects are unique. Mammalian ORs were first discovered in 1991, resulting in award of the prestigious Nobel prize (Buck and Axel, 1991). Insect Ors were discovered for the important model organism *Drosophila* nearly a decade later in 1999 (Clyne et al., 1999; Vosshall et al., 1999). Being extremely divergent from mammalian ORs, the signaling pathway of insect Ors is currently a hotly contested topic. While mammalian ORs function as true GPCRs, Insect receptors have several unique characteristics, including an inverse orientation in the neuronal membrane and the previously mentioned obligate co-receptor Orco (Belluscio et al., 1998; Benton et al., 2006). Even the phyolgenetic similarities between insect Ors are far more divergent than for mammalian ORs (Robertson et al., 2003). It was this dissimilarity between insect Ors and mammalian ORs that was responsible for the 8 additional years that were required for the identification of the first insect Ors, as traditional wet lab techniques attempting to identify genes using mammalian OR

sequence knowledge were highly ineffective and computational approaches designed on the hypothesis of extreme divergence were required (Clyne et al., 1999). Recently two groups have proposed two alternative, albeit slightly overlapping, hypotheses on insect Or function. While one group proposes they function as ligand gated ion channels, another contests that they are both ligand gated and G-protein mediated cyclicnucleotide-activated cation channels (Kain et al., 2008; Sato et al., 2008; Wicher et al., 2008). It is possible their function is an aggregate of both, as there is compelling evidence supporting each hypothesis.

Chemosensation is not limited to Ors. Identification of the Ors in *Drosophila* paved the way for identification of the Gustatory receptor (Gr) family, which was discovered only one year following Or discovery (Clyne et al., 2000). While gustatory receptors are predominately involved in the chemosensation of chemicals in liquid medium, a pair of Gr receptors (Gr21a and G63a) expressed in *Drosophila* is interestingly responsible for detection of CO₂, which is a highly volatile odor (Dahanukar et al., 2001; Kwon et al., 2007). Even more intriguingly, both Gr21a and Gr63a are amongst the rare Grs expressed in the antenna, which almost exclusively houses Or expressing ORNs. As in *Drosophila*, the function of Grs is currently a debated topic including evidence for both GPCR like function and cation channel activity (Ishimoto et al., 2005; Sato et al., 2011; Yao and Carlson, 2010).

Several years after identification of the Or and Gr gene family, a third, more divergent, chemosensory family of Ionotropic Glutamate Receptors (iGluRs) was discovered in *Drosophila* (Benton et al., 2009). While these receptors are related to previously identified known families of glutamate receptors, they appear to be highly

divergent. IRs are expressed in coeloconic sensilla and appear to be tuned to acids, ammonia, and humidity (Abuin et al., 2011; Yao et al., 2005). IRs are believed to function in a heteromeric complex and conduct signals as ion channels (Abuin et al., 2011).

Neuronal wiring of the olfactory system in *Drosophila* is highly complex, containing multiple levels of processing. As discussed above, the peripheral system contains many chemosensory inputs, consisting of three unique classes of receptors, each with their own chemsensory detection spectrum and possibly unique function. The axonal extensions of ORNs project into the antennal lobe, with each ORN class projecting to a unique glomerular location (Fishilevich et al. 2005, Couto et al., 2005). Information processing in the antennal lobe has also been a contested topic, as research groups have debated over the role of local interneurons (LNs). While it was originally claimed that information was faithfully transmitted to higher brain centers without manipulation, it has since been demonstrated that both excitatory and inhibitory local interneuron's play an important role in signal processing prior to transmission (Olsen et al., 2007; Olsen and Wilson, 2008; Root et al., 2007; Shang et al., 2007; Wang et al., 2003; Wilson and Laurent, 2005; Wilson et al., 2004). The main reason for the discrepancy of the two differing claims lies in experimental technique. The Wang research group attempted to tease apart the biological question using calcium imaging, which was not as effective in identifying interneuron communication as Rachel Willson's electrophysiological approach. These different experiments provide a wonderful basis for the importance of teasing apart a biological question from multiple angles to obtain insight that may otherwise be missed. After processing in the antennal lobe, olfactory information is sent to higher brain regions by Projection Neurons (PNs), where it is finally

processed in the mushroom body and lateral horn (Jefferis et al., 2007). It is important to note there are both narrowly and broadly wired neuronal systems. While the majority of ORNs appear to provide information to highly interconnected networks of LNs, a few specialized ORNs form direct channels to PNs (Jefferis et al., 2007). These direct line systems have been termed labeled line and are often observed with pheromone detecting ORNs. The entire 11-cis-vaccenly acetate (cVA) pheromone circuit was beautifully traced from sensory input all of the way to descending output in what is perhaps the best single analysis of olfactory neuronal wiring in *Drosophila* to date, providing an illustrative example for labeled line systems (Ruta et al., 2010). However, these systems appear to be the exception rather than the rule, as processing for the vast majority of ORN input is far to complex for current experimental approaches to have teased apart.

To summarize the system as a whole, the olfactory system is a massive, highly interconnected, and complex neuronal network. It contains inputs from many periphery Ors/ORNs, processes the information in the antennal lobe, and projects processed information into higher brain regions. Luckily for olfactory investigation, the system also has characteristics lending itself to analysis, including the general expression of only a single odor sensitive Or in each ORN, glomerular aggregation of ORN input, and neuronal activity from different ORNs housed in the same sensilla being distinguishable by spike amplitude. While these challenges are considerable, major advances have been made in the field, many of which have been aided by computational approaches.

Only a very small portion of the vast odor space has been tested for activity

It has been estimated that the number of possible carbon based chemical configurations with similar molecular masses to biologically relevant chemicals could exceed 10^{60} unique structures (Bohacek et al., 1996; Dobson, 2004). To put this number into context, it is roughly twice the number of stars than are believed to exist in the universe. Considering that the number of unique chemical structures found in the human body is likely in the hundreds of thousands, this number of potential compounds is staggering (Goto et al., 2002). While volatile chemical space is undoubtedly considerably smaller that 10^{60} , it still likely contains hundreds of thousands of unique compounds, each of which have the potential to activate or inhibit Ors, IRs, or Grs.

Take into consideration that the number of unique Ors expressed by each species has thus far varied from XX on the small end of the scale to over a thousand in mice and each receptor responds independently to a given odor. Clearly, the number of possible Or-odor combinations is staggering. Furthermore, positive classification of a particular odor or blend, such as one produced by a piece of ripe fruit, by the brain requires the integrated response of all expressed Ors to each individual odor in the blend. As one principle goal of olfactory research is to understand how organisms perceive their chemical environment, the aim of understanding the responses of each Or expressed in a particular species to all odors from a large number of behaviorally important source is incredibly challenging, yet still important.

In the 12 years of olfactory research since the discovery of *Drosophila* Ors, 251 unique odors have been experimentally tested for activity in the *Drosophila* olfactory system (de Bruyne et al., 1999; de Bruyne et al., 2001; Dobritsa et al., 2003; Goldman et

al., 2005; Hallem and Carlson, 2006; Hallem et al., 2004; Kreher et al., 2005; Kreher et al., 2008; Kwon et al., 2007; Pelz et al., 2006; Schmuker et al., 2007; Stensmyr et al., 2003; Turner and Ray, 2009; van Naters and Carlson, 2007; Yao et al., 2005). Responses to these screens have recently been assembled and integrated into a single database (Galizia et al., 2010). While some screens have been narrow and focused on testing a small number of odors against a specific Or, others have involved testing a panel of odors across multiple Ors. For example, In 2001 47 odors were tested for activity against 16 ORN classes (de Bruyne et al., 2001). In the largest screen to date 109 odors were tested for activity against 24 Ors expressed in the antenna of *Drosophila* adults using single unit electrophysiology (Hallem and Carlson, 2006). Additionally, 21 Ors expressed in *Drosophila* larvae were tested for activity against 27 odors in 2008 (Kreher et al., 2008). While these three analyses certainly do not represent all of the analyses performed in *Drosophila*, they do represent the largest bodies of work.

Smaller scale olfactory experimentation has also been performed in other insect and mammalian species. While there is great need for an increased understanding of host or food preference in the many important disease vector and pest species, relatively few experiments have tested a sizeable set of odors for activity against multiple receptors. In the largest screen of any insect species outside of *Drosophila*, 110 odors were recently individually tested for activity against 50 *Anopheles* Ors using single unit electrophysiology (Carey et al., 2010). In the largest single mammalian screen a combination of 62 mouse and human ORs were individually exposed to 63 odors and measured for activity using calcium imaging (Saito et al., 2009). The limited number of screened odors tested on a very narrow set of species makes it difficult to tease apart important olfactory cues and pathways that are responsible for attraction, mating, etc.

The odors tested in many screens are meticulously selected, both to cover a broad range of chemical space and for ecological importance. For example, many odors tested in *Drosophila* were selected due to their previous identification in rotting and ripe fruit, an important food source, and a number of odors tested in the *Anopheles* screen performed by Allison Carey were selected for their previously recognized importance as human host volatiles (Carey et al., 2010; Hallem and Carlson, 2006). Odors that were not selected for ecological significance were chosen to cover a broad area of chemical space. These odors cover an expansive range of carbon chain lengths and contain a broad assortment of functional groups including ketones, aldehydes, carboxylic acids, alcohols, and esters. While the majority of screened odors are aliphatic, a number of aromatic odors are usually included as well. These analyses provide the groundwork from which to further expand upon explored odor space, with the ultimate goal of finding effective and species specific behavior modifying chemicals.

Or gene identification in insects was largely aided by computational approaches

Linda Buck correctly made three very important hypotheses in her identification of the OR gene family (Buck and Axel, 1991). Firstly, ORs were likely to belong to a superfamily of proteins involved in GPCR cellular communication. Secondly, the *OR* gene family should be very large and diverse to recognize so many odors. Thirdly, *OR* expression should be restricted to the olfactory epithelium. Guided by these hypothesis, Linda used degenerate primers of known GPCRs to amplify olfactory epithelium cDNA, resulting in the historic identification of band 13 and subsequently the first *OR* gene family (Buck and Axel, 1991).

As previously stated, the Or gene families of Insects are highly divergent from mammalian Ors. While the same approach was applied to identify the *Drosophila* Or gene family, they were unsuccessful. By 1999 bioinformatics approaches were emerging as successful and important tools for biological analysis. Additionally, the first draft of the *Drosophila* genome was underway, providing a ripe time for a computationally guided approach to Or gene family identification (Adams et al., 2000). As conditions were now suitable, two research groups independently identified the *Drosophila* Or gene family in tandem.

Peter Clyne and Coral Warr from John Carlson's lab teamed up with Junhyong Kim and applied bioinformatics approaches to identify 7-transmembrane proteins from the incomplete 1998 Drosophila genome build (Clyne et al., 1999; Kim and Carlson, 2002). Recent evidence had shed light that insect Ors would likely share structural features to GPCRs, yet as previous wet lab attempts had been unsuccessful in identification, it was likely these genes were highly divergent from mammalian ORs. Guided by this insight the team created an algorithm to identify potential members of a large 7TM gene family from the roughly 10% completed *Drosophila* genome build. The algorithm began by identifying Open Reading Frames (ORFs) that were > 300 bases. They then identified important sequence descriptors for 7TM GPCRs, testing 70 parameters for the ability to separate 750 training GPCRs from 1000 non-GPCR proteins by sequence analysis alone. The 5 most important parameters were then applied to screen all predicted ORFs of >300 bases, alternative splicing was considered in order to obtain full length 7TM protein sequences, and the top scoring hits that were not previously known GPCRs were selected. RT-PCR primers were designed for the final list of hits and 2 genes were identified that were only expressed in the antennas. The

well known sequence search tool BLAST was next applied, searching for ORFs with sequence similarity to the two potential Or genes, resulting in identification of 16 Or genes shown to be expressed solely in the antennae and maxillary palps (Altschul et al., 1990). A year later the same approach was applied to identify *Drosophila* Gr genes (Clyne et al., 2000; Kim and Carlson, 2002).

In an independent analysis Leslie Vosshall in Richard Axel's lab identified 10 *Drosophila* Or genes using a combination of wet lab and computational approaches (Vosshall et al., 1999). Vosshall applied difference cloning to identify antennal/maxillary palp specific cDNAs, one of which (dor104) was then applied to scan the *Drosophila* genome for transmembrane proteins using the computational programs Dense Alignment Surface (DAS) and TMAP. 10 of the 12 genes with the highest BLAST determined sequence similarity, albeit very low, to dor104 were demonstrated to be expressed solely in either the antennae or maxillary palps.

Initial insect Or gene discovery has led to an explosion of computationally guided Or identification and analysis. All 60 Or and 68 Gr genes in *Drosophila* had been identified within two years of the initial discovery through iterative application of BLAST on the fully completed *Drosophila* genome (Robertson et al., 2003). Since then, the Or gene families of 12 *Drosophila* species have now been identified, allowing for a comparative analysis identifying both gene conservation prior to subgenera division roughly 40 Mya and providing interesting signs of species specific positive selection (Guo and Kim, 2007). In addition to *Drosophila*, computation has aided in Or family discovery of many other species, including both pest and disease vectors. Examples of species in which Or families have been identified include *Anopheles* gambiae,

Acyrthosiphon pisum (Pea Aphid), *Aedes aegypti, Nasonia vitripennis* (Jewel Wasp), *Rhagoletis pomonella* (Apple Maggot), *Bombyx mori* (Silk Moth), *Danaus plexippus* (Monarch Butterfly) and several others (Bohbot et al., 2007; Fox et al., 2001; Robertson et al., 2003; Schwarz et al., 2009; Smadja et al., 2009; Zhan et al., 2011). In a slightly different direction, computational approaches have also allowed for analysis of Or genes across distantly related species, such as was performed for the CO2 receptors for 12 *Drosophila*, 3 mosquito, the silk moth, and flour beetle species (Robertson and Kent, 2009), providing insight on gene evolution on a very important behavior-regulating receptor.

Or gene family identification for all of these species was made possible by computational advances in genome sequencing, assembly, and search methods able to identify distantly related genes. Without these approaches, identification of the highly divergent Or and Gr families, would certainly have taken far longer to complete, if at all. As sequencing methods continue to improve, the genomes of additional species will begin pouring in, resulting in an increased importance for bioinformatics in Or and Gr gene identification. In turn, the increased volume of Or gene information will further open the door to cross species comparisons. While many of the same tools will likely be applied for Or and Gr gene identification, many new tools will be required for analysis of sequence-activity relationships. Once motifs and protein regions important for odor selectivity are identified, an entirely new field will be available. Traditionally, 3D structures of receptors are required for ligand docking and binding prediction. However, as the Or gene family is highly divergent while likely still retaining core structural features, key motifs or binding regions on Or sequences may be responsible for odor selectivity. As approaches improve it may be possible to computationally predict

receptor-odor interactions from sequence alone. As Or are the largest gene family in several species, this will provide both large challenges and incredible rewards if successful.

Applying ligand-based virtual screening to predict receptor-odor interactions

The field of chemical informatics has been successfully applied to drug discovery by the pharmaceutical industry for years. With the incredible number of chemicals available and the cost required for purchasing and screening, an approach that can computationally identify chemicals with desired features is incredibly useful for initial compound selection (Maldonado et al., 2006). Many distinct chemical informatics approaches have been designed to explain the relationships shared between molecules. Maximum Common Substructure (MCS) determines the largest substructure that is shared between two molecules (Cao et al., 2008). Atom Pairs (AP) identifies atom types with similar distances that are shared between molecules (Carhart et al., 1985). Another approach Molecular Fingerprints (MFs) calculates bit strings, where each 0 or 1 represents the presence or absence of a particular feature, such as a functional group (Nikolova and Jaworska, 2004). Some commercially available programs are available that calculate thousands of individual molecular descriptors for thousands of query compounds, providing quantitative information on many aspects of a compound, such as molecular weight, carbon atom number, predicted vapor pressure, or complex 3dimensional relationships between atoms of a molecule. Large virtual chemical libraries, which can contain hundreds of thousands or millions of chemicals, can be screened for desired characteristics by applying these approaches.

Interestingly, the relatively newly developing field of chemical informatics has only been minimally applied to olfaction. There are several reasons why chemical informatics approaches analyzing receptor-odor interactions from the odor (ligand) side should be of high priority to the olfactory community. As a large portion of drugs currently on the market target GPCRs and insect receptors are hypothesized to have GPCR like function and structure, it is suggestive that these techniques should apply well to olfactory ligand prediction. This is especially true for mammalian ORs, as they are GPCRs. Additionally, the structures of Ors have not been solved. As Odor receptors are membrane bound and in the case of insect receptors pair with an obligate co-receptor, obtaining x-ray crystal structures suitable for computational docking will be challenging. Finally, we currently have all of the tools required for chemical informatics analysis. Diverse subsets of odors have been tested for activity against several species, resulting in large number of decoded receptors in both mammals and several important insect species.

While chemical informatics approaches are promising, additional challenges unique to olfaction must be overcome. Odors are far smaller than chemicals that are traditionally investigated by the pharmaceutical industry (Wishart et al., 2008). While the reduction in size may make some processes, such as 3D structure optimization, more straightforward, it may also make structural feature differentiation more challenging. Olfactory researchers will need to identify chemical informatics approaches that lend themselves well to the smaller number structural features separating odors than would be typically found between larger pharmaceutical chemicals. Additionally, Odors are volatile while the majority of pharmaceutical targets are not. Volatility could effect how well odors reach their receptors targets and should to be taken into account. The few

attempts at chemical informatics application to olfactory research have been fairly successfully and broadly accepted.

In 2000 Jan Kaluza and Heinz Breer demonstrated that carbon chain length of aliphatic aldehydes was an important feature for the prediction of binding (Kaluza and Breer, 2000). Compounds with similar lengths were more likely to bind to the same OR and just as importantly changing the length of a chain by a single carbon could entirely abolish activity. While this may now appear obvious to the community, prior to large panel screens this feature of odor selectivity had not been documented. It was the first support for Olfactory receptors that similar chemical shape may result in similar activity.

Seven years later Michael Schmuker attempted the first prediction of receptorodor activity (Schmuker et al., 2007). Schmuker et al. applied Artificial Neural Networks (ANNs) to predict the responses of 21odors against 7 ORNs. The group calculated ~200 molecular descriptors from MOE (Chemical Computing Group, Montreal) for 47 training odors and 21 test odors. They selected descriptors that were best able to separate the active from inactive molecules and applied them to train the ANN. While the approach was well performed, it unfortunately was only marginally accurate with an accuracy of ~25% (percentage of predicted test odors that activated >50 spikes/sec), which may be due to either molecular descriptor selection, ANN training, or application of ANNs instead of other available approaches.

In 2008 Rafi Haddad from Noam Sobel's laboratory identified molecular descriptors that were correlated among odorants. Haddad et al. calculated 1,664 molecular descriptor values for each odors tested in 7 experimental studies, containing both mammalian and insect receptors (Haddad et al., 2008). The group then selected

which descriptors were the most correlated with activity, resulting in a final set of 32 molecular descriptors that best explained general and non-receptor specific olfactory activity. These 32 descriptors explained activity of the 7 datasets better than carbon atom number or the full set of descriptors. While this approach does not attempt to explain receptor specific selectivity, it was a step in the correct direction.

Most recently in 2010, Sheng Guo and Junhyong Kim applied their own Quantitative Structure Activity Relationship (QSAR) technique to explain the activity of Elissa Hallems analysis where 108 odors were previously tested against 24 *Drosophila* Ors (Guo and Kim, 2010; Hallem and Carlson, 2006). Their model mapped 3D features of each odor and identified which features were most important for receptor activity. Additionally, they performed a sequence analysis for each of the 24 receptors, hypothesizing that the binding pocket of *Drosophila* Ors is on the extracellular halves of it Trans Membrane (TM) domains. The model suggests that the binding pocket is 15 angstroms deep and 6 angstroms wide.

Each of these approaches provides compelling evidence that chemical informatics can be successfully and beneficially applied to olfactory research. However, none of the approaches is successful in explaining receptor specific activity, which should be a major goal of the computational olfaction community. Testing odors using current experimental approaches take a great deal of time and the purchase of a large number of chemicals, many of which may be ineffective. Both of these drawbacks are very expensive. An easy to apply tool that is highly effective at predicting receptor-odor interactions would be immensely beneficial to the olfactory community, allowing for intelligent and quick prioritization of odors for experimental validation. As the number

species for which an initial set of odors has been tested against is currently increasing rapidly, the olfactory field is ripe for such an approach.

Applying structure-based virtual screening to predict receptor-odor interactions

The field of structural-based virtual screening, which involves docking the 3D structure of a chemical into a solved protein structure *in silico*, is regularly used in the field of drug discovery(Kitchen et al., 2004; Nikolova and Jaworska, 2004). Both pharmaceutical companies and academic institutions can have large research groups dedicated to docking libraries of untested chemicals onto the 3D protein structures of potentially drugable targets. The most promising hits are usually selected for experimental validation. The benefits of this system over the ligand-based molecular descriptor prediction techniques are that the resulting dockings can be visually inspected to check that the interaction appears valid, verifying that shape constraints and important polar and non-polar interactions are satisfied. Additionally, manual inspection can reveal important characteristics that can improve structures of current dockings, such as the addition an atom to fully fill a cavity or addition of an oxygen atom to satisfy a structurally important hydrogen bond. Both ligand-based and structure-based and virtual screening can be integrated into a single highly effective pipeline. Molecular descriptors can be applied to select ligands with the most promising characteristics and selected compounds can then be virtually docked into a protein-binding site.

Structure-based virtual screening has been successfully applied for a limited number of mammalian Ors. While structures for insect or mammalian odor receptors have not yet been reported, mammalian receptors are structurally related to rhodopsin,

which has been structurally solved. By applying the structural knowledge from rhodopsin to mammalian Ors research groups have been able to predict a basic structure of mammalian receptors including Rat Or5, Mouse S25, and Rat I7 (Floriano et al., 2000; Singer, 2000; Singer and Shepherd, 1994). The first virtual screening tied to a site directed mutagenesis for functional validation was performed for the mouse mOR-EG in 2005 (Katada et al., 2005). Katada et al. were able to identify the location of an odorant-binding site, as well as how the odor eugenol specifically interacted with it, for the first time, representing a major step forward for the mammalian olfactory community. Since the first successful demonstration of molecular modeling of mammalian ORs, several computational groups have performed similar analyses in additional receptors, including mOR147-9, hOR17-210, and rat OR-I7, without wet lab experimental validation (Khafizov et al., 2007; Kurland et al., 2010; Lai et al., 2008).

In the largest and most complex OR virtual screening attempt to date, 758 compounds from the CAP database were computationally screened for activity against the 5.24 receptor from goldfish, which is activated by all 20 naturally occurring amino acids (Triballeau et al., 2008). Both ligand-based and structure-based virtual screening was applied, reducing the number of potential ligands to 46. Activities of the top 4 predictions were validated using an electro-olfactogram (EOG), each of which produced activation.

Interestingly, structure-based virtual screening has loosely been applied to the human taste receptor TAS2R46 (Brockhoff et al., 2010). Protein chimeras between receptors hTAS2R46 and hTAS2R31 were analyzed to identify important amino acid binding regions, classifying the C-terminus as an important region for ligand selectivity.

Focusing their attention on the extracellular side of trans-membrane spanning alpha helices 6 and 7, they swapped amino acid residues to identify the location of the ligandbinding site. Once a region was identified, a structure-based virtual screen was performed to predict the exact biding site, important interacting residues, and ligand orientation in the membrane bound receptor. This effective blending of wet lab experimental and computational analyses hypothesized the exact orientation of Strychnine on the extracellular side of hTAS2R46.

The field of protein structure determination is rapidly advancing, allowing for determination of structures that were previously untenable. As methodologies continue to advance, our ability to solve membrane bound receptors with heteromeric partners will become possible in the near future, paving the way for structure-based virtual screening of the structurally elusive insect Ors. As the sequences of insect Ors are highly divergent, an additional challenge will be to model the structures of many divergent Ors based upon the few initially solved Insect Ors. As these structures become available, a combined approach involving an initial ligand-based screen of a very large chemical space followed by a focused structure-based virtual screen will likely provide accurate predictions of receptor activations for hundreds of thousands of odors, which would take an unknown number of years to test using wet lab experimentation alone.

High-throughput approaches are effective tools for olfactory analysis

While virtual screening is proving to be an effective tool for identification of receptor-odor interactions, expression analyses are also highly aided by computational approaches. Recent advances in next generation analysis tools, such as microarrays,

RNA-seq, and chip-seq have provided wonderful new ways to understand gene regulation. What would have been impossible just a few years ago is quickly become standard experimental procedure today. Since the initial discovery of the structure and organization of DNA in 1953, a strong charge has been made to understand as much about the genetic makeup of as many species as possible (Watson and Crick, 1953). A major step in this direction was made when Fredrick Sanger and colleagues published the Sanger sequencing method (Sanger and Coulson, 1975). While this method was in no way high throughput by today's standards, it allowed for the sequencing of individual sequences in a straightforward manner that could be performed in a general lab setting. Similar approaches were applied for roughly twenty years until the field-changing introduction of current high throughput techniques. Using today's approaches, such as microarray analysis, RNA-seq, Chip-seq, it is possible to determine the expression of thousands of unique genes of interest or chromatin protein-association in a single experimental protocol. Millions of base pairs can be sequenced. This explosion in sequencing was been greatly aided by computational approaches.

The sheer volume of data produced by a single experiment is astonishing and analysis would simply not be possible without computation. Every aspect from genome assembly to quantification of transcriptional analysis is almost exclusively performed by bioinformatics. For example, transcriptional analysis using Illumina sequencing requires the reading and recording of millions of base pairs. Each read sequence must be checked for quality and aligned to a reference genome. Relative expression profiles must be determined for every gene in the genome prior to promoter sequence, alternative splicing, or SNP analysis is performed. By applying bioinformatics to these approaches a researcher can literally determine SNP placement for every gene in an

individual against a reference genome. As many transcriptional analyses compare gene regulation across experimental conditions, such as time, the entire analysis is performed multiple times and compared, further increasing the complexity. Clearly, computational approaches are advantageous to biological research. High-throughput approaches are increasingly being successfully applied to olfactory research.

Diego Rodriguez-gil from Stuart Firestein's lab recently applied micro-arrays to analyze Or gene expression across mouse development (Rodriguez-Gil et al., 2010). His analysis demonstrated that OR expression is first detectable at embryonic day 9 and that by day 13 expression of nearly all OR genes is detectable. Interestingly, they also noted that gene expression is not constant throughout the course of a mouse life as the "olfactome" expression decreased beyond 3 months of age.

Ewald Grosse-Wilde of Bill Hanson's lab recently identified the Or gene family of *Manduca sexta* using transcriptome analysis by applying 454 sequencing to an antennal cDNA library (Grosse-Wilde et al., 2011). Gene Ontology (GO) annotation using the software Blast2GO was applied to identify olfactory related ontologies. Ors were additionally identified by Blast and HMM profile searches from custom build databases. Predicted amino acid sequences for putative Ors were aligned to previously known *Heliothis* and *Bombyx* sequences, allowing for positive gene identification. Odor Binding Proteins (OBPs) and IR genes were also identified using the same method. In total 54 unique Or gene fragments were identified in a species that contains 73 unique globeruli. If *Manduca* follows the generally applicable one neuron to globerulus map, then roughly 73% of functional Or genes were identified. This approach is considerably significant as it represents application of high throughput transcription analysis in order to identify Or

genes in a species that have not been sequenced by using related species as a reference. As Or identification is traditionally achieved through genome sequencing, this faster and far less expensive transcriptome analysis demonstrates and approach that can be applied to many more species in the future.

R Jason Pitts of Laurence Zwiebel's lab has recently applied transcriptome profiling in *Anopheles gambiae* (Pitts et al., 2011). Both sex specific (male vs female) and olfactory appendage specific (antenna vs whole body) transcriptional regulation was compared using Illumina sequencing (RNA-seq). This approach was able to identify nearly all chemosensory genes from antennal tissue at quantifiable and statistically significant levels. The analysis revealed that expression levels of olfactory genes were present in both sexes, however the levels were much higher in females than males. Additionally, males had a significantly larger number of genes involved in audition. These results were interesting and make sense as it is the female mosquitoes that need to identify hosts for blood feeding and males that need to hear females for mating. This approach demonstrates the sheer volume of information that can be acquired using RNA-seq and its effective application to understand tissue specific regulation in a species and it's broader implications.

Each of the previously highlighted analyses demonstrates how high throughput approaches can be successfully and advantageously applied to answer direct questions or identify targeted genes in the field of olfaction. With the continual reduction in cost as well as increased computational analysis tools available for these methods, more information can be gained at a less expensive price. As computational power has steadily increased, analyses that was once impossible can now be easily performed on a

desktop computer. Large numbers of need-driven computational approaches are being designed to assist in answering biological and chemical questions that can now be asked as the technology that was once considered science-fiction is now simply science.

Figure 1.1: Overview schematic describing neuronal wiring of the insect olfactory system

Odors are detected by Olfactor receptor (Or) expressing neurons in the periphery organs (antennae and maxillary palps). The axons of Olfactory Receptor Neurons (ORNs) expressing the same Or proteins, thus being housed in the same sensilla class, extend into unique glomerular locations within the antennal lobe. Local interneurons (LNs) allow for both excitatory and inhibitory information to be shared between specific sets of glomeruli. Projection Neurons (PNs) then send information from the antennal lobe to higher brain centers in the Mushroom Body (MB) and Lateral Horn (LH), where behavioral decisions occur. The figure was taken from (Carey and Carlson, 2011).

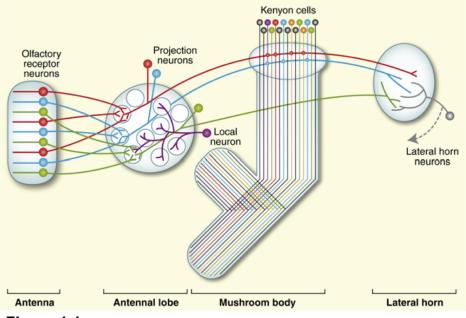


Figure 1.1

CHAPTER II:

Designing a Ligand-Based Virtual Screening Approach to Decode Drosophila Odor Receptor Chemical Space In Silico

INTRODUCTION

The peripheral olfactory system is unparalleled in its ability to detect and discriminate amongst an extremely large number of volatile compounds in the environment. To detect this wide variety of volatiles, most organisms have evolved large families of receptor genes that typically encode 7-transmembrane proteins expressed in the olfactory neurons (Buck and Axel, 1991; Clyne et al., 1999; Dahanukar et al., 2005; de Bruyne and Baker, 2008; Vosshall et al., 1999). Each volatile chemical in the environment is thought to interact with a specific subset of odor receptors depending upon odor structure and binding sites on the receptor. This precise detection and coding of odors by the peripheral olfactory neurons are subsequently processed, transformed and integrated in the central nervous system to generate specific behavioral responses that are critical for survival such as finding food, finding mates, avoiding predators etc (van der Goes van Naters and Carlson, 2006).

Currently there are two major rate-limiting steps in analysis of peripheral coding in olfaction: a very small proportion of chemical space can be systematically tested for its activity on odor receptors, and a very small fraction of the numerous odor receptors have been tested for responses (Araneda et al., 2000; Hallem and Carlson, 2006; Hallem et al., 2004; Kreher et al., 2008; Pelz et al., 2006; Saito et al., 2009). The challenges for overcoming the rate-limiting steps are enormous. First, volatile chemical space is immense, more than 2,000 odors in the environment have been catalogued from a small

fraction of plant sources alone (Knudsen et al., 2006). Second, the complete 3-D structures of the 7-transmembrane odor receptor proteins have not yet been determined and modeling of protein-odor interactions and sophisticated virtual screening methods are not yet possible except in rare instances (Triballeau et al., 2008). In the decade since the first systematic study of 47 odorants on the *Drosophila* antenna in 2001 (de Bruyne et al., 2001), additional studies have only identified a total of 251 novel active odors (de Bruyne et al., 1999; de Bruyne et al., 2001; Dobritsa et al., 2003; Goldman et al., 2005; Hallem and Carlson, 2006; Hallem et al., 2004; Kreher et al., 2005; Kreher et al., 2007; Pelz et al., 2006; Schmuker et al., 2007; Stensmyr et al., 2003; Turner and Ray, 2009; van Naters and Carlson, 2007; Yao et al., 2005), which have been assembled and compared in an online database (Galizia et al., 2010).

Here we overcome this challenge by designing a chemical-informatics platform that is effective and fast. In order to do so we focused our attention on one of the most comprehensive quantitative data sets available, where measurements of responses of 24 *Drosophila* odor receptors to a panel of 109 odorants are known (Hallem and Carlson, 2006). We devised a method to identify molecular structural properties that are shared amongst the activating odorants for each receptor. We then utilize information about these shared molecular features of actives, that are presumably required for binding to a receptor, to perform *in silico* screens on a chemical space of >240,000 chemicals and predict the top 500 hits as new ligands for each of the odorant receptors (Ors). We then use single-unit electrophysiology to validate a subset of predictions *in vivo* and find that our method met with an overall success rate of ~71% in identifying novel ligands, as compared with a low 10% receptor activation rate while using non predicted odors. This approach allows us to create a peripheral coding map of a large

chemical space, which substantially improves our ability to study peripheral olfactory coding and provides a powerful tool for the discovery of novel ligands for Ors.

RESULTS

Analysis of odorant structure

Since the structure of receptor protein complexes is not known, we analyzed receptor-odor interactions by applying the *similarity property principle*, which reasons that structurally similar molecules (e.g. activating odorants) are more likely to have similar properties (Hendrickson, 1991; Martin et al., 2002). Although this general approach has been useful in the area of pharmaceuticals (Keiser et al., 2009; Martin et al., 2002), receptor-odor analysis presents significant additional challenges. Not only are odorant molecules generally smaller in size than pharmaceuticals (average MW of known odors ~3-fold less than FDA approved pharmaceuticals (Wishart et al., 2008)) and therefore offer fewer structural features for differentiation, they are also detected by the receptors with specificity at extremely low concentrations in the volatile phase (Hallem and Carlson, 2006; Kreher et al., 2008). Additionally, odor receptors are differentially tuned and can sometimes appear not to follow distinct structural rules: odors that look structurally different can strongly activate the same receptor, while odors that appear very similar may have very different levels of activity (Hallem and Carlson, 2006)(Figure 2.1A).

General measures of odorant similarity

Similarity in chemical structure can be described and measured quantitatively using multiple approaches, however a single method may not be ideal for every single application (Maldonado et al., 2006). In order to test whether non-optimized approaches would be able to identify similarities in shape of known activators we compared four different approaches: Cerius2 (Accelrys Software Inc), Dragon (Talete), Maximum-Common-Substructure (MCS) (Cao et al., 2008b), and Atom-Pair (AP) (Cao et al., 2008a; Carhart et al., 1985). Cerius2 and Dragon represent collections of 200 and 3,224 molecular descriptors, respectively, that calculate values for a broad range of chemical properties such as molecular weight, functional group counts, and in the case of Dragon, 3 dimensional relationships within molecules. The AP method compares shortest path distances between all atom pairs in a molecule. Lastly, MCS identifies the largest 2 dimensional substructure that exists between two compounds. Using each of these approaches, we computed distances between 109 odors that had previously been tested against 24 Ors from Drosophila melanogaster (Hallem and Carlson, 2006) (Figure 2.1B). These represent most of the Or genes expressed in the Drosophila antenna (Hallem and Carlson, 2006). Upon comparison, we find that none of the four methods were vastly superior and that each method varied in the ability to group known activating odorants "actives" close together in distance as measured for each Or using a method called Accumulative-Percentage-of-Actives (APoA)(Chen and Reynolds, 2002) (Figure 2.3A, See Methods), and value of the Area-Under-the-Curve (AUC). Ultimately, Dragon and Cerius2, which utilize a large number of diverse molecular descriptor values to describe each odor structure, performed better than AP or MCS, suggesting that a more diverse

set of descriptors is better at explaining Or activity than 2D measures alone (Figures 2.2B, 2.3B). Atom-Pair and MCS were subsequently ignored from further development.

Identification of unique subsets of optimized descriptors for each *Drosophila* Or

Individual Ors respond to distinct subsets of ligands with some degree of overlap (Hallem and Carlson, 2006; Kreher et al., 2008). We reasoned that rather than using entire Dragon or Cerius2 descriptor sets, which likely includes a number of measurements for features irrelevant for ligand-binding to an individual Or, judiciously selecting subsets of molecular descriptors suited to cluster actives for an individual receptor may be more effective at defining an Or-specific chemical space. To test this hypothesis, we used a Sequential-Forward-Selection (SFS) method to incrementally create unique optimized descriptor subsets for each Or from an initial combined set of 3,424 descriptors from Dragon and Cerius2 (Whitney, 1971) (See Methods, Figure 2.2A). This optimization-based analysis was performed on the 19 Ors from the dataset with known activating odors, excluding Or82a, since it has but a single known strong active (Hallem and Carlson, 2006).

Not surprisingly, the composition of the optimized descriptor sets varied greatly between Ors (Table 2.1). Molecular descriptors can be categorized from 0 to 3 dimensions. 0-Dimensional (0-D) descriptors define features that can be viewed as not directly being shape dependent, such as molecular weight or vapor pressure. On the other end of the scale, 3-Dimensional (3-D) descriptors define features of molecules in three-dimensional space, such as the distance between two atoms of an odor molecule. We find an overwhelming preference for 3-D and 2-D descriptors compared to 1-D and 0-D descriptors, suggesting that structural shape features are more important for

receptor-odor interactions. The Or-optimized descriptor sets were far superior at grouping together activating odors from the training set (Figure 2.2B) when compared to the non-optimized methods (Dragon, Cerius2, MCS, AP) and a previously identified collection of descriptors that were identified without receptor-specific optimization (Haddad et al., 2008).

Computational validation of optimized descriptor sets

In order to validate the predictive ability of the *Or*-optimized method, we performed 5 independent trials of 5-fold cross-validations followed by a Receiver-Operating-Characteristic (ROC) analysis, an established computational approach (Hastie et al., 2001; Tan et al., 2006) (see methods). Briefly, this involved withholding 20% of the 109 previously tested odors for a receptor. Descriptors were optimized using the remaining 80% odors for training, and ligand-predictions were subsequently performed on the 20% of odors that were withheld. This operation was repeated 5 times for each receptor, each time selecting a different 20% as withheld from the training set. The entire 5-fold operation was repeated 5 times for each receptor and a mean ROC curve representing the prediction accuracy determined. This analysis was possible for 12 *Ors* which had >6 known ligands that activated >100 spikes/sec. The Area-Under-Curve (AUC) value (0.815) is very promising and suggests that the *Or*-optimized descriptor sets are effective at predicting novel ligands (Figure 2.2C).

In addition to performing the 5-fold cross-validation, we also clustered the 109 training odors independently for each Or using distances calculated from the previously determined receptor specific descriptor sets (Figure 2.2D). As expected, we find that active odors cluster tightly together for each Or (Figure 2.2D). In a few cases, such as

for Or35a and Or98a, not all the highly active compounds are clustered, suggesting the possibility of multiple or flexible binding sites, or imperfect selection of descriptors. Four of the Ors (Or2a, Or23a, Or43a and Or85f) have few known activators, none of which activate the receptors at greater than 150 spikes/sec, however our descriptor optimization approach is still able to cluster each the few weak activators together (Figure 2.2D).

High-throughput in silico screening of odor receptors

Since Or-optimized descriptor sets can efficiently group highly active compounds in chemical space, we used them to rank untested compounds according to their distance from known actives for specific Ors. We assembled a natural odor library, which contains 3,197 naturally occurring odors, and a library derived from Pubchem (Bolton et al., 2008), which contains >240,000 compounds with similar molecular weights and atom type compositions to known volatiles (See Methods). We then systematically screened both libraries using the optimized descriptor sets of 19 *D. melanogaster* Ors representing ~5,000,000 receptor-odor interactions *in silico*. We identify the top 500 (0.2%) hits from this vast chemical library for each Or, the top ~100 of which are reported in Table 2.2.

Electrophysiological validation of in silico screen and identification of agonists

To validate our *in silico* screen, we obtained several untested odorants (141 total; ~11-23/Or) belonging to the top 500 predicted ligands for 9 different Ors that were available from commercial sources at high purity and reasonable prices. The 9 receptors were selected on the basis of previous functional mapping studies that enable us to

unambiguously identify the antennal olfactory receptor neurons (ORNs) they are housed in (Couto et al., 2005; Hallem et al., 2004). We systematically tested each predicted receptor-odor combination using single-unit electrophysiology to record from the ORNs to which these 9 Ors have been previously mapped (Couto et al., 2005; Hallem et al., 2004). We find that a majority of the predicted ligands evoked responses from the target ORNs; ~71% evoked either activation (>50 spikes/sec above the spontaneous activity) or inhibition (>50% reduction in spontaneous activity) (Fig. 2.6A). These cutoffs were selected based on study from which the training set was obtained and has been used in other studies in the past that use this type of recordings (Hallem and Carlson, 2006; Kreher et al., 2008). Interestingly, the mean vapor pressure of activating odors (11.84 Torr) is 7.5 times higher than of inactive odors (1.58 Torr), raising the possibility that some inactive odors may not be volatilized and delivered at adequate levels to the ORNs. Additionally, we find that ~13% of the predicted compounds we tested showed an inhibitory effect on baseline activity of the respective neuron (Fig. 2.6A). These inhibitors were identified by virtue of structural similarity to known activators suggesting that they may bind to similar sites on the receptor. Thus as an additional benefit our approach may provide a method to identify inhibitors as well. Such inhibitors would not only provide important tools to investigate mechanisms of odor receptor inhibition but could also be used in blocking specific odor-mediated behaviors. Consistent with our observations three of the receptor-odor interactions had been previously identified independently as well, Or22a (Pelz et al., 2006), and Or49b (Hallem et al., 2004). The electrophysiological analysis provides the most important validation of our Or-optimized descriptor-based in silico screen.

Odor response spectra of individual Ors

Since we systematically analyzed responses of a large number of new odorants individually, we were able to characterize the odor-response spectra of several antennal ORN classes to these new ligands (Figure 2.4B). New activators are reported for every receptor, and inhibitors are identified for several. Ligand predictions for 2 of the 3 receptors that do not perform as well are Or10a and Or49b that detect aromatic compounds. Their poor performance is explained by the lack of aromatic ligands in the initial training set (13/109) odorants. We find that a >85% of the predicted ligands activate odor receptors Or7a, Or22a, Or59b, Or85a, Or85b, and Or98a (Figure 2.4B).

Specificity of in silico predicted ligands

We rigorously examined the rate of false negative predictions for each Or by systematically testing newly identified ligands of each Or against the other non-target receptors using electrophysiology. Of 504 non-target receptor-odor interactions tested, we found that only 10% evoked a response >50 spikes/sec and 3.7% evoked a response >100 spikes/sec (Figure 2.5A). This represents a high degree of specificity, especially considering that the Or-optimized descriptor method did not incorporate any additional computational screening to rule out non-target activators. Additionally, when we plot the percentage of odors that validated as activators when tested using electrophysiology (considering both predicted and non-target receptor-odor interactions), we find that activity is strongly related to predicted odor ranking (Figure 2.5B). Odors which rank closest to known actives for each Or, particularly within the top 500 hits, are far more likely to be activators than odors further away, and there is a drastic drop-off in activating odors present beyond the 1,000 rank. We see the same trend if we plot mean

activity of odors for the same ranking divisions (Figure 2.6). Highly ranked odors have a far higher mean activity than distantly ranked odors.

Relationship between descriptor sets and Or sequence and activity

Since receptor-optimized descriptor sets and the predicted ligand space they define are a function of shared molecular features that a receptor may employ to recognize ligands, we were now in a position to determine how these characteristics correlate with receptor properties such as their known-activity profiles and amino acid sequences. We used hierarchical cluster analysis to create trees that represent the various receptors based on: shared descriptors selected; known activity-based relationships (Hallem and Carlson, 2006); degree of overlap of predicted ligands; and amino acid sequence (Figure 2.7A, See Methods). We found that the maximum overlap in Or relationships is retained between the descriptor and the activity trees, and the descriptor and the cross activity trees with 11 out of 24 Ors present in subgroups that are common in both cases. However, only two subgroups (vellow and grey) are conserved across the 3 trees. The largest shared overlap existing in the descriptor tree suggests that the Or-optimized descriptors link the known and the predicted receptorodor interactions and that our analysis may expand upon odor receptor activity relationships beyond those previously known from the training data. We also found that the phylogenetic tree has fewer relationships conserved with each of the trees, consistent with previous observations (Hallem et al., 2004) supporting the idea that, while the most conserved amino acid residues in the Ors provide the structure of the tree, they do not correlate strongly with ligand specificity.

Analysis of breadth of predictions for each Or in chemical space

Coding of odors in a large volatile space (>240,000) by a receptor repertoire is virtually impossible to determine experimentally. However, based on the Or-optimized descriptor sets we computationally derived prediction frequency distributions for each of the *Drosophila* Ors in this large chemical space (Figure 2.7B). As expected, we find substantial variation in the distribution frequency of predicted ligands across different receptors. The predicted response profiles support previous observations made with smaller odor panels that the olfactory system can potentially detect thousands of volatile chemicals, many of which the organism may never have encountered in its chemical environment. We computed similar predicted ligand frequency distribution curves to an assembled set of 3,197 known "natural" volatile compounds from plants, humans, and a fragrance collection (Figure 2.8). Plant volatiles constituted a large portion of compounds that are predicted to be ligands for *Drosophila* Ors. To further analyze odor source representation, we classified odors that belong to top 500 prediction lists according to their source, if known, and find that Ors are not specialized for odors from a single source (Figure 2.7C).

Across-receptor activation patterns in Drosophila

To study the ensemble activation patterns of odors predicted across all Ors, we analyzed the across-receptor activation patterns of the 3,197 known compounds for 9 receptors (Or7a, 10a, 22a, 47a, 49b, 59b, 85a, 85b, 98a). Surprisingly, we find that only 25% of compounds from the "natural" odor library found in the top 500 predictions for each Or are predicted to activate multiple Ors (Figure 2.7D, lower left panel). If we consider compounds from the Pubchem library in the top 500 predicted actives for each

receptor, we observe further reduction in the proportion of across-receptor activating compounds (Figure 2.7D, upper right). Consistent with this prediction we find that cross-activation by ligands functionally evaluated in this study for 9 receptors is lower than that reported previously using ligands of comparable strength for the same 9 receptors (Hallem and Carlson, 2006) (Figure 2.7D, lower right panel). These data suggest that a number of natural odors may be detected by only a few receptors, particularly at low concentrations.

Producing a systems level view of receptor activity for the Drosophila antenna

One of the ultimate challenges of understanding peripheral coding of olfactory information is to be able to map responses of large number of receptors to their ligands. Following the *in silico* analysis, we were able to create such a network-view of peripheral odor coding in the *Drosophila* antenna by mapping all predicted and tested receptor-odor combinations (Figure 2.9A) as has been done previously for mapping drug-target networks (Keiser et al., 2009). Using our chemical informatics pipeline, it becomes possible to infer the network of odor receptors that are activated from complex odor sources without the expensive and time consuming process of purchasing and testing all possible odors.

DISCUSSION

A primary element of the olfactory code is information about odor identity, represented by the characteristic interaction of an odor with the ensemble of olfactory receptors in the nose. Here we report an *in silico* approach to systematically identify ligands from a vast chemical space for a majority of Ors in the antenna of *Drosophila*. We demonstrate that our predictions are accurate using two different validation approaches- computational validations and functional validation using electrophysiology. There is a strong correlation between ranks of predicted ligands to electrophysiological activity.

Obtaining and testing odors using traditional methods is time and cost intensive. Electrophysiology and calcium imaging are consuming processes that require not only a great deal of time to perform, but also the purchase of each odor to be physically tested. Moreover, large plate-based combinatorial chemical libraries, which are commonly implemented in drug discovery in the pharmaceutical industry, are not available for volatile odor libraries for reasonable costs. Since *Drosophila* is a premier model for understanding neurobiology of olfaction, several laboratories over the last 12 years have together screened ~250 odors, activities of which have been and compiled into a valuable database that standardizes across studies (Galizia et al., 2010). In this study we screen >240,000 chemicals and predict >10,000 new ligands which represents a substantial expansion of the known peripheral olfactory code for this important model organism and provides a system-level view of odor detection (Figure 2.9B).

A similar, yet much smaller, analysis applied chemical informatics on *Drosophila* olfactory neuron activities to 47 odorants and screened ligands from 21 untested compounds in *Drosophila* (Schmuker et al., 2007). Although this study had a relatively

modest success rate of ~25% at predicting untested odorants as activators (by applying the same 50 spikes/sec threshold for comparison), it also highlighted that structurebased ligand prediction is a viable method for further development. In another interesting analysis a Quantitative Structure Activity Relationship (QSAR) model was applied to describe odor-activity for Drosophila Ors. Important amino acid residues were identified using information from orthologous Or sequences identifying potential odor-binding regions, which was postulated to be 15 angstroms deep and 6 angstroms wide (Guo and Kim, 2010). Our approach is conservative and designed to search for novel odors that share structural features from a previously tested odor panel. Odor molecules are limited in size as well, and may offer a limited scaffold such that novel isofunctional chemotype identification may not be as prevalent as has been seen in other examples of scaffoldhopping (Schneider et al., 2006). However while compounds that share similar values for the optimized descriptors do have structural similarity for selected parts of the molecule, it does not mean that they are not structurally different in other parts of the molecule. In the future, application of machine learning approaches, such as Support Vector Machines (SVMs) to the receptor-optimized molecular descriptor sets, may be useful to further increase the predictive ability. Additionally, we could replace our SFS approach with sequential floating search techniques, which allows for removal, as well as addition, of descriptors in the growing optimized list.

We predict that a number of odorants at low concentrations may be detected by only one or a few receptors. This contrasts a current model of combinatorial coding in which emphasis is placed on the notion that a majority of volatile chemicals, with the exception of pheromones and CO₂, are detected by combinations of several odor receptors. One possible explanation for this disparity could be that our predictions are

fundamentally conservative in nature because we focus only on structurally similar ligands and 7-transmembrane heteromeric receptors may also contain additional unexplored binding sites. Moreover, receptors may respond to compounds ranked beyond the top 500 hits. Another possibility is that previously tested subsets of odors were potentially selected on the basis of strong responses in electroantennograms and behavior assays, which could bias selection of cross-activating odors. In fact it is known that complex fruit odors activate fewer Ors than the number activated by individual odorants at comparable concentrations (Hallem and Carlson, 2006, Semmelhack and Wang, 2009). The architecture of the olfactory code therefore appears to integrate two different models. On the one hand, most odors are detected by a few Ors from the repertoire, which may enhance the specificity of the olfactory system for detection of a large number of odors. On the other hand, 15-20% of odors are predicted to activate several Ors (up to 50%) at the same time, which may serve to aid the olfactory of the system in discriminating between fine concentration changes of important stimuli by having Ors tuned to low and high concentrations such as shown for Or42a and Or42b (Kreher et al., 2008).

By identifying a large number of new ligands for each odor receptor, we can also begin to systematically compare the ligand tuning profiles for each in the endogenous neurons versus the "empty neuron" decoder system. If clear differences were identified, it could enable the identification of underlying reasons such as differences in levels of receptor expression in the neurons, or presence of different Odorant Binding Proteins (OBPs) in the sensillum lymph.

This cheminformatics pipeline can also be applied for system-level analysis of other insects whose receptors and ORNs have been decoded such as mosquitoes

(Carey et al., 2010), and vertebrates such as mice and humans (Saito et al., 2009). The search for novel insect repellents and attractants for species that transmit disease and destroy crops can be greatly assisted by a rational prioritization using such a cheminformatics approach.

Figure 2.1: Comparing efficacy of various structure analysis methods to analyze odor receptor ligands

(A) Comparison of odor structures for known actives and inactive odorants for Or85b and Or98a from(Hallem and Carlson, 2006) (activity shown in parenthesis). (B)
 Overview of the process by which 4 molecular descriptor methods were compared to determine which one best clusters known actives close together in descriptor space.

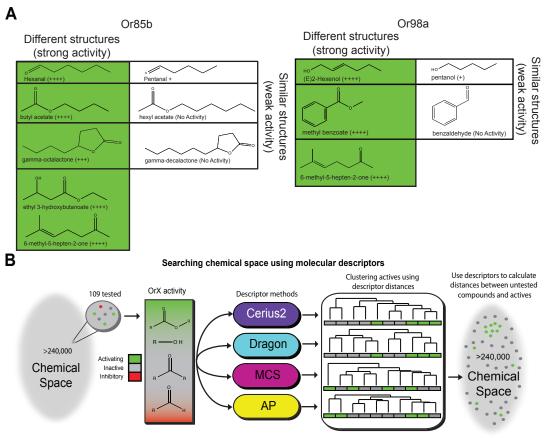


Figure 2.1

Figure 2.2: A receptor-optimized molecular descriptor approach has strong predictive power to find new ligands

(A) Schematic of the cheminfomatics pipeline used to identify novel ligands from a larger chemical space. (B) Plot of mean APoA values for 19 *Drosophila* Ors calculated using various methods including a previously identified set (Haddad et al., 2008). (C) Receiver-operating-characteristic curve (ROC) representing computational validation of ligand predictive ability of the Or-optimization approach. (D) Hierarchical cluster analysis of the 109 odorants of the training set (Hallem and Carlson, 2006) using Or-specific optimized descriptor sets to calculate distances in chemical space for odorant receptors with strong activators (green), and odorant receptors with no strong activators (yellow).

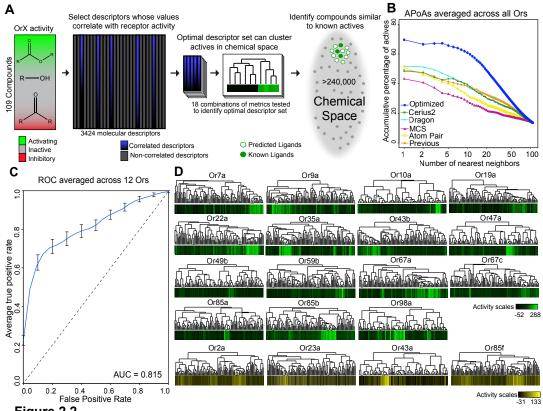


Figure 2.2

Figure 2.3: Accumulated percentage of actives analysis

(A) Representative example for Accumulated Percentage of Actives (APoA) calculation. Green box=active, grey box=inactive. To calculate APoA each active compound was iteratively used as a reference active. Compounds are sorted based upon their increasing descriptor based distance from reference active, and the APoA calculated for each of the other compounds as a ratio of the number of actives over the total number of compounds considered from the reference compound. This process was repeated using each active odorant as a reference active. Reference compound APoAs were averaged to a single mean APoA value. The higher the APoA value while considering a fixed number of nearest neighboring compounds, the greater the proportion of active compounds clustered together. (B) Coloured cells mark the method that clusters active ligands best as determined by the highest Area-Under-Curve (AUC) for APoA values.

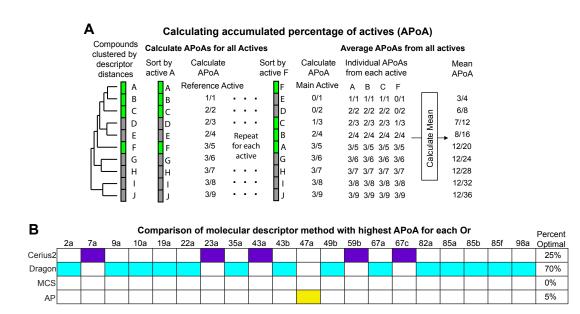




Figure 2.4: Electrophysiology validates that odorant receptor-optimized molecular descriptors can successfully identify new ligands for *Drosophila*

(A) Summary of prediction accuracy percentages obtained by electrophysiology validation. Ligands = Agonists (>=50 spikes/s) + Inhibitors (>50% reduction from baseline activity). (B) Mean increase in response of neurons to 0.5-sec stimulus of indicated odors (10^{-2} dilution) predicted for each associated Or. Dashed lines indicate the activator threshold (50 spikes/second). Δ H: Or85b (ab3B) = flies lack expression of Or22a in neighboring neuron, thus all observed neuron activation is unambiguously caused by Or85b. N=3, error bars=s.e.m.

A	

Classification	Or7a	Or10a	Or22a	Or47a	Or49b	Or59b	Or85a	Or85b	Or98a	Total
Ligands	88%	31%	86%	39%	27%	91%	92%	87%	100%	71%
Agonists (>50 spikes/sec)	63%	31%	81%	33%	18%	64%	69%	70%	92%	58%
Agonists (>100 spikes/sec)	31%	13%	62%	11%	9%	45%	54%	48%	67%	37%
Inhibitors	25%	0%	5%	6%	9%	27%	23%	17%	8%	13%

	-													
В											propionate			-
										Pentyl p Eth	oropionate			-
5-Hexen-1-ol)				Butyl L-lactate	_				Ethyl h	eptanoate			
trans-2-Pentenal				1	Methyl nicotinate Furfurvl acetate	-				Methyl is	ocaproate	-		
Prenal					Propyl butyrate						yl valerate enanthate	1		-
cis-2-Penten-1-ol Tiglic aldehyde					Propiophenone					Propylin	propionate			-
Isobutanol			Met	hvl cvclohe	xanecarboxylate					Propy	I caproate	-		-
3-Furaldehvde		-			ofurfuryl acetate				Moth	But But trans 2	yl butyrate octenoate			
lsovaleraldehyde		4			hylbenzaldehyde				weu	Prop	vl butyrate		_	
2-Methyl-2-pentenal		H		N-P	henyl formamide	 .				Isoprop	yl butyrate 🕯		-	
Nicotinaldehyde		-			o-Tolualdehyde						yl butyrate propionate	-		
4-Hexen-1-ol				4-Hydro	bxybenzaldehyde Butyrophenone					l e l e	af acetate			
Furfuryl alcohol H 3-Methyl-1-pentanol H					Benzalacetone					Isoprop	yl acetate	-		
2-Methyl-1-butanol				Hv	dratropaldehyde					2-Ethylbu	tyl acetate		-	
2-Methyl-3-buten-1-ol					Butyl propionate						yl valerate	a		
Furfuryl mercaptan		Or7a	(ab4A)		obutyl crotonate		Or1	0a (ab'	1D)		maleate		Or22a	i (ab3A
-50	0 50	100 150 Spikes/sec	200 25	D	-50	0 5	0 100 15 Spikes/sec	50 200	250		-50 0	50) 100 150 Spikes/sec	200 2
Methyl pentanoate					2-Bromophenol	-				Isoprope	nyl acetate			-4
Pentyl propionate 2-Hexanone							_			Methyl	propionate			
Methyl-3-methylpentanoate		-			2-Chlorophenol									
4-Methylthio-2-butanone		-			4-Methylphenol	-					hyl ketone		_	
2-Methylbutyl acetate 2-Octanone		4			3-Methylphenol					Ethyl t	hioacetate		-	
Methyl enanthate					Phenol	•			Methy	l (methylt	hio)acetate	-	-	
Methyl isocaproate 1-Octen-3-one					2,4-Xylenol	H-			3-1	Aercapto-	2-butanone			
-(Methylthio)-propyl isothiocyanate 5-Methyl-2-hexanone					Resorcinol					2	-Hexenone			
Acetyl valery				Ben	zyl methyl ether H	-				Methyl tl	niobutyrate	•		
2-Ethylbutyl acetate Ethyl(methylthio)acetate					4-Vinylphenol	-				Dimethyl	sulfoxide (
Propyl disulfide	н i			sy	n-Benzaldoxime 🕯				4-Me	thylthio-2-	butanone			
Butyl isothiocyanate Ethyl-2-mercaptopropionate		Or47	a (ab5B)		o-Toluenethiol H		Or4	9b (ab6	6B)	N-Methyl a	acetamide		Or59ł	(ab2A
-50	0 50		200 25	0	-50 () 5	0 100 15	50 200		(moury) (-50 0	50	100 150 200	
		Spikes/sec			2-Heptanol		Spikes/see	C			-00 0	50	Spikes/sec	200 0
2-Heptanol				Methyl tra	ans-3-hexenoate	—			-	Pre	nyl acetate			
4-Hexen-1-ol	-		4		3-Octanone 3-Octanol			_		Propyl	propionate	i i i		-
Hexylamine		_			Heptanal						Propionate	1		
cis-3-Hepten-1-ol	1	_			Butyl propionate 2-Octanone									н
1-Heptanol					1-Heptanol				Ethyl	(methylth	io) acetate		-	
				Et	4-Hexen-1-ol					Ethyl ac	etoacetate		-	
Ethyl acetoacetate	-			tran	s-3-Octen-2-one					Dietho	kymethane	i.	-	
Ethyl tiglate	-				Amyl formate						vl butyrate	1		
5-Hexen-1-ol					Butyl acrylate 5-Hexen-1-ol								-	
Propyl isobutyrate	<u> </u>			2,4	I-Hexandien-1-ol					Eth	nyl valerate	_	-	
Ethyl 2-methylbutanoate					Hexyl formate cis-3-Hepten-1-ol					2-But	oxyethanol	_		
Diethoxymethane					Propyl butyrate	1				cis-3-H	lepten-1-ol	i i i		
Butyrone	-				nylbutýl acetate				2		heptanone			
· · ·		0-05	a (ab2D)	C	is-5-Octen-1-ol 🛏				2		· · ·		0.00	(-1-7-
3-(Methylthio)-1-hexanol			a (ab2B)	tran	apryl alcohol		∆H: Or	85b (a	b3B)	2-	Heptanol H			i (ab7A
	0 50	100 150 Spikes/sec	200 250)		0 5	0 100 1 Spikes	50 200	0 250	300	-50 0	50	100 150 20 Spikes/sec	0 250 3
Figure 2.4														
0.0														

Figure 2.5: Predicted receptor-odor interactions are highly specific

(A) Plot of activity (Top) for electrophysiologically tested receptor-odor interactions. (Bottom) Plot indicating locations of predicted receptor-odor combinations (green) and same odorants tested in non-target receptor-odor combinations (gray). (B) Plot of percentage of activating odors (>50 spikes/sec) considering all activating or inactive odors (>0 spikes/sec) across ranking bins for all odors tested using electrophysiology.

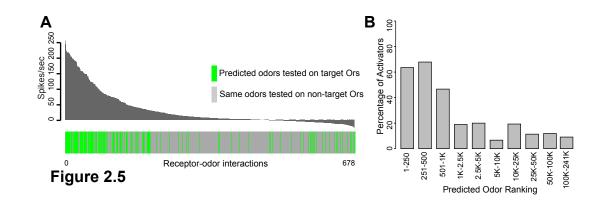


Figure 2.6: High-ranking odors are more likely to be active than distantly ranked odors

Bar plot of the mean electrophysiological activity (in spikes/sec) of all activating or inactive odors (>0 spikes/sec), considering both predicted receptor-odor combinations and same odorants tested in non-target receptor-odor combinations, grouped by predicted rankings.

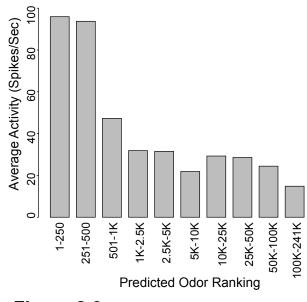


Figure 2.6

Figure 2.7: Analysis of receptor-odor relationships and breadth of tuning

(A) Hierarchical clusters created from Euclidean distance values between Drosophila Ors calculated using: (left to right) shared optimized descriptors; known activity to training set odors (Hallem and Carlson, 2006); overlap across top 500 predicted ligands; and Phylogenic tree of receptors (Hallem and Carlson, 2006). Sub clusters shaded with colors or bars. (B) Frequency distribution of compounds from the >240K library within the top 15% distance from highest active plotted to generate predicted breadth of tuning curves. Green arrows indicate relative distance of the furthest known activating compound determined by electrophysiology. (C) (Left) The numbers of compounds present in the collected volatile library according to source. (Right) The numbers and sources of predicted ligands for the 19 Drosophila odor receptors/neurons within the top 500 predicted compounds (D) Comparison of plots for percentage of receptors that are: (top left) activated by percentage of known odors from training set (Hallem and Carlson, 2006); (bottom left) predicted to be activated by collected compounds; (top right) predicted to be activated from >240K library; and (bottom right) activated by ligands for 10 shared Ors in this study versus activated by comparable actives previously tested (Hallem and Carlson, 2006).

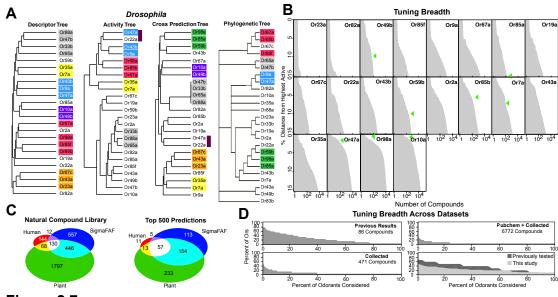


Figure 2.7

Figure 2.8: Analysis of receptor-natural odor interactions

Compounds from the collected compound library that have been cataloged as plant, human and total collected volatiles were ranked according to their relative distance from the compound with highest activity. Frequency distribution of compounds within the top 15% is plotted to generate predicted breadth of tuning curves.

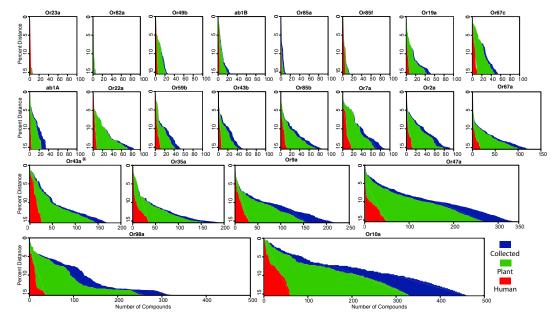


Figure 2.8

Figure 2.9: Predicted odor space and network view of odor coding

(A) *Drosophila* receptor-odor network. Each known interaction (>50 spikes/sec) from this and previous studies(Hallem and Carlson, 2006) is linked by a purple edge. Predicted receptor-odor network (top 500 hits) are linked by light-grey edges. All compounds are represented as small black circles and Ors are represented as large colored circles matching the colors used in (Fig. 4A and SI). (B) Expansion of the peripheral olfactory code in this study: large increase in numbers of identified activators and inhibitors. The different sized circles represent the approximate ratio of numbers of previously known ligands (top circles), predicted ligands based on a cutoff of the top 500 predicted compounds per receptor and corrected to the validation success rate (lower, diffuse circles).

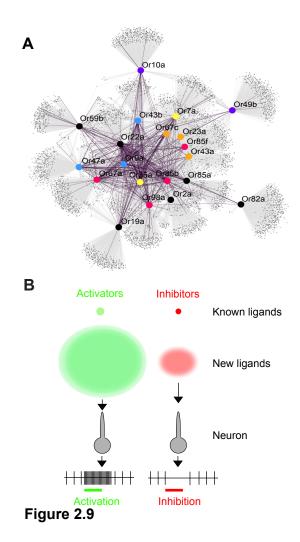


Table 2.1: Optimized descriptor sets for each Drosophila Or

Optimized descriptors occurrences, symbol, brief description, class, and dimensionality are listed. A summary of the total number of descriptors selected for the receptor repertoire is provided at the beginning. Descriptors are listed in ascending order of when they were selected into the optimized set. Weights indicate the number of times a descriptor was selected in an optimized descriptor set.

Supplementary Table 1

Descriptor #	Weight Eughel	Description	Class	Dimensional
Or2a (18 Unique)	Weight Symbol	Description	Class	Dimensional
	1 Mor18p	3D-MoRSE - signal 18 / weighted by atomic polarizabilities	3D-MoRSE descriptors	
	1 Mor17e	3D-MoRSE - signal 17 / weighted by atomic Sanderson electronegativities	3D-MoRSE descriptors	
	1 Mor28u 1 J3D	3D-MoRSE - signal 28 / unweighted 3D-Balaban index	3D-MoRSE descriptors geometrical descriptors	
	2 0-057	phenol / enol / carboxyl OH	atom-centred fragments	
	1 SIC2	structural information content (neighborhood symmetry of 2-order)	information indices	
	1 EEig10x	Eigenvalue 10 from edge adj. matrix weighted by edge degrees	edge adjacency indices	
	1 MATS5e	Moran autocorrelation - lag 5 / weighted by atomic Sanderson electronegativities frequency of C - O at topological distance 05	2D autocorrelations 2D frequency fingerprints	
	1 F05[C-O] 1 HNar	frequency of C = O at topological distance 05 Narumi harmonic topological index	2D frequency fingerprints topological descriptors	
	1 MATS8m	Moran autocorrelation - lao 8 / weighted by atomic masses	2D autocorrelations	
	1 G3s	Moran autocorrelation - lag 8 / weighted by atomic masses 3st component symmetry directional WHIM index / weighted by atomic electrotopological states	WHIM descriptors	
	1 Mor27m	3D-MoRSE - signal 27 / weighted by atomic masses presence/absence of C - O at topological distance 04	3D-MoRSE descriptors	
	1 B04[C-O]		2D binary fingerprints	
	1 H8v 1 Mor10v	H autocorrelation of lag 8 / weighted by atomic van der Waals volumes 3D-MoRSE - signal 10 / weighted by atomic van der Waals volumes	GETAWAY descriptors 3D-MoRSE descriptors	
	1 Mor18v	3D-MoRSE - signal 10 / weighted by atomic van der Waals volumes	3D-MoRSE descriptors	
	2 R8p+	R maximal autocorrelation of lag 8 / weighted by atomic polarizabilities	GETAWAY descriptors	
	1			
Dr7a (31 Unique)	1 (1111)00	and the design of a start of a Marco constraints	have the start down to have	
	1 MAXDP 1 MAXDN	maximal electrotopological positive variation maximal electrotopological negative variation	topological descriptors topological descriptors	
	1 B06[C-C]	presence/absence of C - C at topological distance 06	2D binary fingerprints	
	2 HATS1v	leverage-weighted autocorrelation of lag 1 / weighted by atomic van der Waals volumes	GETAWAY descriptors	
	3 Hy	hydrophilic factor	molecular properties	
	1 S_ssO 1 JGT	S_ssO global topological charge index	atomtypes (Cerius2) topological charge indices	
	2 H-051	H attached to alpha-C	atom-centred fragments	
	2 EEig10d	Eigenvalue 10 from edge adj. matrix weighted by dipole moments	edge adjacency indices	
	1 0-057	phenol / enol / carboxyl OH	atom-centred fragments	
	5 HATS8u	leverage-weighted autocorrelation of lag 8 / unweighted	GETAWAY descriptors	
	1 G2s 2 Mor16u	2st component symmetry directional WHIM index / weighted by atomic electrotopological states 3D-MoRSE - signal 16 / unweighted	WHIM descriptors 3D-MoRSE descriptors	
	2 Mor16u 4 B02[O-O]	3D-MoRSE - signal 16 / unweighted presence/absence of O - O at topological distance 02	3D-MoRSE descriptors 2D binary fingerprints	
	1 R5p+	R maximal autocorrelation of lag 5 / weighted by atomic polarizabilities	GETAWAY descriptors	
	1 EEig08d	Eigenvalue 08 from edge adj. matrix weighted by dipole moments	edge adjacency indices	
	1 DISPp	d COMMA2 value / weighted by atomic polarizabilities	geometrical descriptors	
	2 C-008	CHR2X	atom-centred fragments	
	1 R4e+ 1 EEig09d	R maximal autocorrelation of lag 4 / weighted by atomic Sanderson electronegativities Eigenvalue 09 from edge adj. matrix weighted by dipole moments	GETAWAY descriptors edge adjacency indices	
	1 nArOH	number of aromatic hydroxyls	functional group counts	
	1 R2m+	R maximal autocorrelation of lag 2 / weighted by atomic masses	GETAWAY descriptors	
	1 nRCOOR	number of esters (aliphatic)	functional group counts	
	1 B02[C-O]	presence/absence of C - O at topological distance 02	2D binary fingerprints	
	1 GATS7m 1 E2s	Geary autocorrelation - lag 7 / weighted by atomic masses 2nd component accessibility directional WHIM index / weighted by atomic electrotopological states	2D autocorrelations WHIM descriptors	
	1 nRCO	number of ketones (aliphatic)	functional group counts	
	1 Mor03m	3D-MoRSE - signal 03 / weighted by atomic masses	3D-MoRSE descriptors	
	1 MATS8m	Moran autocorrelation - lag 8 / weighted by atomic masses	2D autocorrelations	
	1 CIC5	complementary information content (neighborhood symmetry of 5-order)	information indices	
	1 D/Dr06	distance/detour ring index of order 6	topological descriptors	
Dr9a (29 Unique)	1 1			
	1 BEHp8	highest eigenvalue n. 8 of Burden matrix / weighted by atomic polarizabilities	Burden eigenvalues	
	1 BELv1	lowest eigenvalue n. 1 of Burden matrix / weighted by atomic van der Waals volumes	Burden eigenvalues	
	1 DISPe	d COMMA2 value / weighted by atomic Sanderson electronegativities	geometrical descriptors	
	2 EEig09d	Eigenvalue 09 from edge adj. matrix weighted by dipole moments highest eigenvalue n. 5 of Burden matrix / weighted by atomic polarizabilities	edge adjacency indices Burden eigenvalues	
	2 BEHp5 1 E2e	2nd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities	WHIM descriptors	
	1 Mor25m	3D-MoRSE - signal 25 / weighted by atomic masses	3D-MoRSE descriptors	
	1 B03[C-C]	presence/absence of C - C at topological distance 03	2D binary fingerprints	
	3 B07[C-C]	presence/absence of C - C at topological distance 07	2D binary fingerprints	
	1 B01[C-O] 1 Atype_H_49	presence/absence of C - O at topological distance 01 Number of Hydrogen Type 49	2D binary fingerprints atomtypes (Cerius2)	
	1 Infective-80	Ghose-Viswanadhan-Wendoloski antiinfective-like index at 80%	molecular properties	
	3 0-057	phenol / enol / carboxyl OH	atom-centred fragments	
	1 Mor22m	3D-MoRSE - signal 22 / weighted by atomic masses	3D-MoRSE descriptors	
	1 EEig10d	Eigenvalue 10 from edge adj. matrix weighted by dipole moments	edge adjacency indices	
	1 R1u+ 1 GATS7m	R maximal autocorrelation of lag 1 / unweighted Geary autocorrelation - lag 7 / weighted by atomic masses	GETAWAY descriptors 2D autocorrelations	
	1 MATS4v	Moran autocorrelation - lag 4 / weighted by atomic van der Waals volumes	2D autocorrelations	
	1 R4e+	R maximal autocorrelation of lag 4 / weighted by atomic Sanderson electronegativities 3st component symmetry directional WHIM index / weighted by atomic polarizabilities	GETAWAY descriptors	
	1 G3p	3st component symmetry directional WHIM index / weighted by atomic polarizabilities	WHIM descriptors	1
	· 1160	hydrophilic factor		
	1 Hy		molecular properties	
	1 S_dssC	S_dssC	atomtypes (Cerius2)	
	1 S_dssC 1 nRCHO	S_dssC number of aldehydes (aliphatic)	atomtypes (Cerius2) functional group counts	
	1 S_dssC	S_dssC number of aldehydes (aliphatic) presence/absence of C - C at topological distance 08	atomtypes (Cerius2) functional group counts 2D binary fingerprints	
	1 S_dssC 1 nRCHO 1 B08[C-C] 1 R2m 1 HATS5e	S_dssC number of aldehydes (aliphatic) presence/absence of C - C at topological distance 08 R autocorrelation of lag 2 / weighted by atomic masses leverage-weighted autocorrelation of lag 5 / weighted by atomic Sanderson electronegativities	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors GETAWAY descriptors	
	1 S_dssC 1 nRCHO 1 B08[C-C] 1 R2m 1 HATS5e 1 D/Dr06	S. dssC mumber of aldehydes (aliphatic) presence/absence of C - C at topological distance 08 R autocorrelation of lag 2 / weighted by atomic masses leverage-weighted autocorrelation of lag 5 / weighted by atomic Sanderson electronegativities distance/detour ing index of order 6	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors GETAWAY descriptors topological descriptors	
	1 S_dssC 1 nRCHO 1 B08[C-C] 1 R2m 1 HATS5e 1 D/Dr06 1 RDF030m	S_dssC number of aldehydes (aliphatic) presence/absence of C - C at topological distance 08 R autocorrelation of lag 2 / weighted by atomic masses leverage-weighted autocorrelation of lag 5 / weighted by atomic Sanderson electronegativities distance/detour ring index of order 6 Radial Distribution Function - 3.0 / weighted by atomic masses	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors GETAWAY descriptors topological descriptors RDF descriptors	
	1 S_dssC 1 nRCHO 1 B08[C-C] 1 R2m 1 HATS5e 1 D/Dr06	S. dssC mumber of aldehydes (aliphatic) presence/absence of C - C at topological distance 08 R autocorrelation of lag 2 / weighted by atomic masses leverage-weighted autocorrelation of lag 5 / weighted by atomic Sanderson electronegativities distance/detour ing index of order 6	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors GETAWAY descriptors topological descriptors	
Dr10a (11 Unique)	1 S_dssC 1 nRCHO 1 B08[C-C] 1 R2m 1 HATS5e 1 D/Dr06 1 RDF030m	S_dssC number of aldehydes (aliphatic) presence/absence of C - C at topological distance 08 R autocorrelation of lag 2 / weighted by atomic masses leverage-weighted autocorrelation of lag 5 / weighted by atomic Sanderson electronegativities distance/detour ring index of order 6 Radial Distribution Function - 3.0 / weighted by atomic masses	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors GETAWAY descriptors topological descriptors RDF descriptors	
Dr10a (11 Unique)	1 S_dssC 1 nRCHO 1 808[C-C] 1 R2m 1 HATS5E 1 D/Dr06 1 RDF030m 2 Jhetv 3 S_d0	S_dss ² presence/absence of C - C at topological distance 08 R autocorrelation of Isg 2 / weighted by atomic masses leverage-weighted autocorrelation of Isg 5 / weighted by atomic Sanderson electronegativities distance/detour min index of order 6 Radial Distribution Function - 3.0 / weighted by atomic masses Salaban+type index from van der Waals weighted distance matrix S_dd	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors GETAWAY descriptors topological descriptors topological descriptors atomtypes (Cerius2)	
Or10a (11 Unique)	1 S_dssC 1 nRCH0 1 B08[C-C] 1 R2m 1 HATS5E 1 D/Dr06 1 RDF030m 2 Jhetv 3 S_d0 1 BEHm7	S, dosC presence/absence of C - C at topological distance 08 R autocorrelation of lag 2 / weighted by atomic masses leverage-weighted autocorrelation of lag 5 / weighted by atomic Sanderson electronegativities distance/detour ring index of order 6 Radial Distribution Function - 3.0 / weighted by atomic masses Balaban-type index from van der Waals weighted distance matrix S, dO highest eigenvalue n. 7 of Burden matrix / weighted by atomic masses	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors topological descriptors topological descriptors atomtypes (Cerius2) Burden eigenvalues	
Dr10a (11 Unique)	1 S_dssC 1 nRCH0 1 B08[c-c] 1 R2m 1 HATS5e 1 D/Dr06 1 RDF030m 2 Jhetv 3 S_dO 1 BEHm7 1 E2u	S, dos ² presence/absence of C - C at topological distance 08 R autocorrelation of Isg 2 / weighted by atomic masses leverage-weighted autocorrelation of Isg 5 / weighted by atomic Sanderson electronegativities distance/detour ning index of order 6 Radial Distribution Function - 3.0 / weighted by atomic masses Balaban-type index from van der Waals weighted distance matrix S, d0 highest eigenvalue n. 7 of Burden matrix / weighted by atomic masses Znd component accessibility directional WHIM Munex / unweidited	atomtypes (Cerius2) functional group counts ZD binary fingerprints GETAWIA descriptors GETAWIA vescriptors RDF descriptors topological descriptors topological descriptors atomtypes (Cerius2) Burden eigenvalues WHIM descriptors	
Dr10a (11 Unique)	1 S_dssC 1 nRCHO 1 B08[C-C] 1 R2m 1 HATSSe 1 D/Dr06 1 RDF030m 2 Jhetv 3 S_dO 1 BEHm7 1 E2u 1 HATS8m	S, dos ^C presence/absence of C - C at topological distance 08 R autocorrelation of lag 2 / weighted by atomic masses leverage-weighted autocorrelation of lag 5 / weighted by atomic Sanderson electronegativities distance/detour ring index of order 6 Radial Distribution Function - 3.0 / weighted by atomic masses Balaban-type index from van der Waals weighted distance matrix S, d0 highest eigenvalue n. 7 of Burden matrix / weighted by atomic masses 2nd component accessibility directional WHIM Index / unweighted leverage-weighted autocorrelation of lag Ø / weighted by atomic masses	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors GETAWAY descriptors topological descriptors topological descriptors topological descriptors atomtypes (Cerius2) Burden eigenvalues WHIM descriptors GETAWAY descriptors	
)r10a (11 Unique)	1 S_dssC 1 nRCHO 1 B08[C-C] 1 R2m 1 HATS5e 1 D/Dr06 1 RDP030m 2 Jhetv 3 S_dO 1 BEHm7 1 E2u 1 HATS8m 1 BELe4	S, dos ² presence/absence of C - C at topological distance 08 R autocorrelation of Isg 2 / weighted by atomic masses leverage-weighted autocorrelation of Isg 5 / weighted by atomic Sanderson electronegativities distance/detour ning index of order 6 Radial Distribution Function - 3.0 / weighted by atomic masses Balaban-type index from van der Waals weighted distance matrix S, d0 highest eigenvalue n. 7 of Burden matrix / weighted by atomic masses Znd component accessibility directional WHIM Munex / unweidited	atomtypes (Cerius2) functional group counts ZD binary fingerprints GETAWIA descriptors GETAWIA vescriptors RDF descriptors topological descriptors topological descriptors atomtypes (Cerius2) Burden eigenvalues WHIM descriptors	
Dr10a (11 Unique)	1 SdssC 1 nRCHO 1 B08(C-C) 1 RZm 1 HATS56 1 D/D/050 1 RDF0300 2 Jhetv 3 SdO 1 BEHm7 1 EZu 1 HATS8m 1 BELe4 1 Mor25e 1 B08(C-C)	S, dss ² S, dss ² presence/absence of C - C at topological distance 08 R autocorrelation of lsg 2 / weighted by atomic masses leverage-weighted autocorrelation of lsg 5 / weighted by atomic Sanderson electronegativities distance/detour ning index of order 6 Radial Distribution Function - 3.0 / weighted by atomic masses Balaban-type index from van der Waals weighted distance matrix S, d0 highest eigenvalue n. 7 of Burden matrix / weighted by atomic masses 2nd component caressibility directional WHIM Index / unweighted leverage-weighted autocorrelation of lsg 8 / weighted by atomic masses 2nd component en. 4 of Burden matrix / weighted by atomic masses 100-weighted autocorrelation of lsg 8 / weighted by atomic masses 3D-MoRSE - signal 25 / weighted by atomic Sanderson electronegativities presence/absence of C - C at topological distance 08	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors GETAWAY descriptors topological descriptors topological descriptors topological descriptors Burden eigenvalues WHIM descriptors GETAWAY descriptors Burden eigenvalues 3D-MGRSE descriptors 2D binary fingerprints	
Dr10a (11 Unique)	1 SdesC 1 RCR-O 1 BOB(C-C) 1 R2m 1 BOB(C-C) 1 R2m 1 D/Dr06 1 R/P630m 2 Jhetv 3 SdO 1 BEHm7 1 E2u 1 HATSonn 1 HATSonn 1 HATSon 1 BOB(C-C) 1 JGI3	S_dss'c mumber of aldehydes (aliphatic) presence/absence of C - C at topological distance 08 R autocorrelation of lag 2 / weighted by atomic masses leverage-weighted autocorrelation of lag 5 / weighted by atomic masses Balaban-type index of order olymical by atomic masses Balaban-type index from van der Waals weighted distance matrix S_d0 highest eigenvalue n. 7 of Burden matrix / weighted by atomic masses Znd component accessibility directional WHIM index / unweighted leverage-weighted autocorrelation of lag 8 / weighted by atomic masses presence/absence of C - C at topological distance 08 mean topological charge index of order3	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors GETAWAY descriptors topological descriptors topological descriptors topological descriptors WITM descriptors WITM descriptors Generation eigenvalues Burden eigenvalues Burden eigenvalues 3D-MORSE descriptors 2D binary fingerprints topological charge indices	
Dr10a (11 Unique)	1 SdssC 1 RCHO 1 B08(C-C) 1 RZm 1 HATS5e 1 D/Dr060 1 RDF030M 2 Jhetv 3 SdO 1 BEHm7 1 EZu 1 HATS8m 1 BELe4 1 Mor25e 1 B08(C-C) 1 JGI3 1 ESpm03u	S, dos ² presence/absence of C - C at topological distance 08 Rautocorrelation of Iag 2 / weighted by atomic masses leverage-weighted autocorrelation of Iag 5 / weighted by atomic Sanderson electronegativities distance/detour ring index of order 6 Radial Distribution Function - 3.0 / weighted by atomic masses Balaban-type index from van der Waals weighted distance matrix S_d0 highest eigenvalue n. 7 of Burden matrix / weighted by atomic masses functional weighted atomic masses breat eigenvalue n. 7 of Burden matrix / weighted by atomic masses breat eigenvalue n. 4 of Burden matrix / weighted by atomic masses breat eigenvalue n. 4 of Burden matrix / weighted by atomic masses breat eigenvalue n. 4 of Burden matrix / weighted by atomic masses breat eigenvalue n. 4 of Burden matrix / weighted by atomic masses breat eigenvalue n. 4 of Burden matrix / weighted by atomic masses breat eigenvalue n. 4 of Burden matrix / weighted by atomic masses breat eigenvalue n. 4 of Burden eigenvalue for a f	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors GETAWAY descriptors topological descriptors topological descriptors atomtypes (Cerius2) Burden eigenvalues WHM descriptors GETAWAY descriptors GETAWAY descriptors Burden eigenvalues 3D-MORSE descriptors 2D binary fingerprints topological charge indices edge adjacency indices	
Dr10a (11 Unique)	1 SdssC 1 RCRCH 1 BOB(C-C) 1 R2m 1 D/Dr06 1 D/Dr06 1 D/Dr06 1 D/Dr07 2 Jhetv 3 SdO 1 BEHm7 1 HATSANN 1 HATSANN 1 HATSANN 1 BOB(C-C) 1 JAG3 1 ESpm03U 1 RG4 1 BOB(C-C) 1 JAG3 1 RG4 1 R	S, dss ² presence/absence of C - C at topological distance 08 R autocorrelation of lsg 2 / weighted by atomic masses leverage-weighted autocorrelation of lsg 5 / weighted by atomic Sanderson electronegativities distance/document of lsg 2 / weighted by atomic masses Baldaban type index from van der Wals weighted by atomic masses Saldaban type index from van der Wals weighted distance matrix S, dO highest eigenvalue n. 7 of Burden matrix / weighted by atomic masses Znd component accessibility directional WHIM index / unweighted leverage-weighted autocorrelation of lsg 8 / weighted by atomic masses Znd component accessibility of the matrix / weighted by atomic masses Znd component accessibility of the matrix / weighted by atomic masses Znd component accessibility of the distance of leverage-weighted autocorrelation of lsg 8 / weighted by atomic masses Znd Moster signal 25 / weighted by atomic Sanderson electronegativities ZD-MotSE - signal 25 / weighted by atomic Sanderson electronegativities Spectral moment 03 from edge adj, matrix number of alightatic tertiary (Csp2)	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors GETAWAY descriptors topological descriptors topological descriptors topological descriptors burden eigenvalues WHIM descriptors GETAWAY descrip	
Dr10a (11 Unique)	1 SdssC 1 RCHO 1 B08(C-C) 1 RZm 1 HATS5e 1 D/Dr060 1 RDF030M 2 Jhetv 3 SdO 1 BEHm7 1 EZu 1 HATS8m 1 BELe4 1 Mor25e 1 B08(C-C) 1 JGI3 1 ESpm03u	S, dos ² presence/absence of C - C at topological distance 08 Rautocorrelation of Iag 2 / weighted by atomic masses leverage-weighted autocorrelation of Iag 5 / weighted by atomic Sanderson electronegativities distance/detour ring index of order 6 Radial Distribution Function - 3.0 / weighted by atomic masses Balaban-type index from van der Waals weighted distance matrix S_d0 highest eigenvalue n. 7 of Burden matrix / weighted by atomic masses functional weighted atomic masses biever eigenvalue n. 4 of Burden matrix / weighted by atomic masses Invest eigenvalue n. 4 of Burden matrix / weighted by atomic masses Invest eigenvalue n. 4 of Burden matrix / weighted by atomic masses Invest eigenvalue n. 4 of Burden matrix / weighted by atomic masses Invest eigenvalue n. 4 of Burden matrix / weighted by atomic masses Invest eigenvalue n. 4 of Burden matrix / weighted by atomic masses Invest eigenvalue n. 4 of Burden matrix / weighted by atomic masses Invest eigenvalue n. 4 of Burden eigen bier is Sanderson electronegativities Invest eigenvalue n. 4 of Burden eigen	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors GETAWAY descriptors topological descriptors topological descriptors atomtypes (Cerius2) Burden eigenvalues WHM descriptors GETAWAY descriptors GETAWAY descriptors Burden eigenvalues 3D-MORSE descriptors 2D binary fingerprints topological charge indices edge adjacency indices	
	1 S. desC 1 RCR-0 1 BOR(-C-0 1 BOR(-C-1) 1 BOR(-C-1) 1 BOR(-C-1) 1 D/Dr06 1 D/Dr06 1 D/Dr06 1 D/Dr030m 2 Jnetv 3 S. d0 3 S. d0	S, dss ² presence/absence of C - C at topological distance 08 R autocorrelation of Iag 2 / weighted by atomic masses leverage-weighted autocorrelation of Iag 5 / weighted by atomic Sanderson electronegativities distance/detour ring index of order 6 Radial Distribution Function - 3.0 / weighted by atomic masses Balaban-type index from van der Waals weighted distance matrix S_d0 highest eigenvalue n. 7 of Burden matrix / weighted by atomic masses Balaban-type index from van der Waals weighted by atomic masses S_d0 highest eigenvalue n. 7 of Burden matrix / weighted by atomic masses 2nd component accessibility directional WHIM index / unweighted Biwest eigenvalue a. 4 of Burden matrix / weighted by atomic Sanderson electronegativities 100-MOSE - signal 25 / weighted by atomic Sanderson electronegativities Biwest eigenvalue of C - C at topological distance mean topological charge index of order3 Spectral moment 03 from edge adj., matrix number of aliphatic tertiary C(sp2) 2nd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors GETAWAY descriptors topological descriptors topological descriptors bropological descriptors burden eigenvalues Burden eigenvalues Burden eigenvalues 3D-MORSE descriptors 2D binary fingerprints topological charge indices edge adjacency indices functional group counts WHIM descriptors	
	1 SdssC 1 RCR-0 1 BOB(C-C) 1 R276 1 HAT266 1 HAT266 1 R07030m 2 Jhetv 3 SdO 1 BEHm7 1 E20 1 HAT286 1	S, dss ² mumber of aldehydes (aliphatic) presence/absence of C - C at topological distance 08 R autocarrelation of Isg 2 / weighted by atomic masses leverage-weighted autocorrelation of Isg 5 / weighted by atomic Sanderson electronegativities distance/detour ing index of order 6 Radial Distribution Function - 3.0 / weighted by atomic masses Balaban-type index from van der Waals weighted distance matrix S, dO highest eigenvalue n. 7 of Burden matrix / weighted by atomic masses Znd component cacessibility directional WHIM Index / unweighted leverage-weighted autocorrelation of Isg 8 / weighted by atomic masses Znd component en A of Burden matrix / weighted by atomic masses SD-MoRSE - signal 25 / weighted by atomic Sanderson electronegativities presence/absence 0f C - C at topological distance 08 mean topological charge index of order3 Znd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities Journe of C - C at topological distance 08 mean topological charge index of order3 Znd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities Journe Accessibility directional WHIM index / weighted by atomic Sanderson electronegativities Journe Accessibility directional WHIM index / weighted by atomic Sanderson electronegativities Journe Accessibility directional WHIM index / weighted by atomic Sanderson electronegativities	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors topological descriptors topological descriptors topological descriptors atomtypes (Cerius2) Burden eigenvalues WHIM descriptors GETAWAY descriptors GETAWAY descriptors Burden eigenvalues 3D-MGRSE descriptors 3D-MGRSE descriptors 3D-MGRSE descriptors 3D-MGRSE descriptors	
	1 S. desC 1 RCR-O 1 BOB(C-C) 1 BOB(C-C) 1 BOB(C-C) 1 D/Dr06 1 D/Dr06 1 D/Dr06 1 D/Dr07 3 S. d0 3 S. d	S, dss ² s, dss ² presence/absence of C - C at topological distance 08 Rautocorrelation of lag 2 / weighted by atomic masses leverage-weighted autocorrelation of lag 5 / weighted by atomic masses Balaban-type index from van der Waals weighted distance matrix S, d0 Nightest eigenvalue n. 7 of Burden matrix / weighted by atomic masses Balaban-type index from van der Waals weighted distance matrix S, d0 Nightest eigenvalue n. 7 of Burden matrix / weighted by atomic masses Balaban-type index from van der Waals weighted by atomic masses S, d0 Nightest eigenvalue n. 7 of Burden matrix / weighted by atomic masses Bowest eigenvalue n. 4 of Burden matrix / weighted by atomic Sanderson electronegativities 10 - MoSE - signal 25 / weighted by atomic Sanderson electronegativities 30 - MoSE - signal 25 / weighted by atomic son decornegativities 30 - MoSE - signal 25 / weighted by atomic son electronegativities 30 - MoSE - signal 31 / weighted by atomic masses 30 - MoSE - signal 31 / weighted by atomic palarizabilities	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors GETAWAY descriptors topological descriptors topological descriptors topological descriptors Burden eigenvalues WHIM descriptors 2D binary fingerprints topological descriptors 2D binary fingerprints topological darge indices edge adjacency indices functional group counts WHIM descriptors 3D-MoRSE descriptors GETAWAY descriptors	
	1 SdssC 1 RCR-07 1 B08[C-C] 1 R2750 1 I/1ATS50 1 RDF030m 2 Jhetv 3 SdO 1 BEFM7 1 EZ0 1 HATS5m 1 BELe4 1 Mor256 1 B08[C-C] 1 JG13 1 RDF0310 1 RDF02 2 EZ6 1 Mor310 1 H2m 1 Lm	S, dss ² s, dss ² presence/absence of C - C at topological distance 08 R autocorrelation of Isg 2 / weighted by atomic masses leverage-weighted autocorrelation of Isg 5 / weighted by atomic Sanderson electronegativities distance/ideour ning index of order 6 Radial Distribution Function - 3.0 / weighted by atomic masses Bababan-type index from van der Waals weighted distance matrix S, d0 highest eigenvalue n. 7 of Burden matrix / weighted by atomic masses Data Component cascsbiblity diroctional WHIM index / unweighted leverage-weighted autocorrelation of Isg 8 / weighted by atomic masses Dato component en. 4 of Burden matrix / weighted by atomic masses Dato component en. 4 of Burden matrix / weighted by atomic masses Subset eigenvalue n. 4 of Burden matrix / weighted by atomic masses Source eigenvalue n. 4 of Burden matrix / weighted by atomic masses Dato component to 3.1 of the distance of 6.2 at pological charge index of order3 Spectral moment D3 from edge ad, matrix number of alighatic tertiary (Csp2) ato component cascsbiblity directional WHIM index / weighted by atomic Sanderson electronegativities 3D-MoRSE - signal 31 / weighted by atomic polarizabilities H autocorrelation of Isg 3 / weighted by atomic masses 13D-MoRSE - signal 31 / weighted by atomic polarizabilities H autocorrelation of Isg 3 / weighted by atomic masses	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors topological descriptors topological descriptors topological descriptors atomtypes (Cerius2) Burden eigenvalues WHIM descriptors GETAWAY descriptors Burden eigenvalues 3D-MGRSE descriptors 2D binary fingerprints topological charge indices edge adjacency indices functional group counts WHIM descriptors 3D-MGRSE descriptors GETAWAY descriptors BURDEN descriptors 3D-MGRSE descriptors GETAWAY descriptors MHIM descriptors	
	1 SdssC 1 RCRO 1 BOB(C-C) 1 R2m 1 BOB(C-C) 1 R2m 1 D/Dr06 1 D/Dr06 1 RDF030m 2 Jhetv 3 SdO 1 BEHm7 1 E21 3 SdO 1 BEHm7 1 E21 1 Ar25e 1 BOB(C-C) 1 JG13 1 E5pm030 1 RC731p 1 K2m 1 L2m 1 R2m 1	S, dss ² S, dss ² presence/absence of C - C at topological distance 08 R autocorrelation of lsg 2 / weighted by atomic masses leverage-weighted autocorrelation of lag 5 / weighted by atomic Sanderson electronegativities distance/deturn of mices or 0 of weighted by atomic masses Balaban-type index from van der Waals weighted distance matrix S, d0 highest eigenvalue n. 7 of Burden matrix / weighted by atomic masses Znd component accessibility directional WHIM index / unweighted leverage-weighted autocorrelation of lag 6 / weighted by atomic masses D-MoSE - signal 25 / weighted by atomic Sanderson electronegativities D-MoSE - signal 25 / weighted by atomic sons electronegativities Spectral moment 03 from edge adj, matrix number of alighteit tertiary (Csp2) Znd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities 3D-MoSE - signal 31 / weighted by atomic sons electronegativities 3D-MoSE - signal 31 / weighted by atomic sons electronegativities 1D-MoSE - signal 31 / weighted by atomic polarizabilities H autocorrelation of lag 2 / weighted by atomic masses 1st component size directional WHIM index / weighted by atomic masses 1st component size directional WHIM index / weighted by atomic masses	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors GETAWAY descriptors topological descriptors atomtypes (Cerius2) Burden eigenvalues WHIM descriptors GETAWAY descriptors GETAWAY descriptors 2D binary fingerprints topological thrage indices edge adjacency indices functional group counts WHIM descriptors 3D-MoRSE descriptors GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors	
	1 SdssC 1 RCHO 1 B08[C-C] 1 R275 1 HATS56 1 HATS6 1 R07030m 2 Jnetv 3 SdO 1 BEHm7 1 E2u 1 HATS8m 1 BELe4 1 Mor256 1 B08[C-C] 1 JGI3 1 R5m030 1 nK=C 2 E2e 1 Mor21p 1 H2m 1 R1m+ 1 R1m+	 Ś. dość momber of aldehydes (aliphatic) presence/absence of C - C at topological distance 08 Rautocretalion of Isg 2 / weighted by atomic masses leverage-weighted autocorrelation of Isg 5 / weighted by atomic Sanderson electronegativities distance/detour ning index of order 6 Radia Distribution Function - 3.0 / weighted by atomic masses Balaban-type index from van der Waals weighted by atomic masses Diababan-type index from van der Waals weighted by atomic masses S, d0 highest eigenvalue n. 7 of Burden matrix / weighted by atomic masses Diadocrelation of Isg 3 / weighted by atomic masses Subcorrelation of Isg 3 / weighted by atomic masses source accessibility directional WHIM index / unweighted west eigenvalue n. 4 of Burden matrix / weighted by atomic masses DiadocsE - signal 25 / weighted by atomic Sanderson electronegativities presence/absence of C - C at topological distance 08 mean topological charge index of order3 Spectral moment 03 from dega ed, matrix number of aliphatic tertiary C(sp2) Zho component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities atocorrelation of Isg 2 / weighted by atomic masses to component accessibility directional WHIM index / weighted by atomic masses to component accessibility directional WHIM index / weighted by atomic masses to component accessibility directional weight moment masses to component accessibility directide by atomic masses to component accessi	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors GETAWAY descriptors topological descriptors topological descriptors topological descriptors Burden eigenvalues WHIM descriptors GETAWAY descriptors Burden eigenvalues 3D-MoRSE descriptors 2D binary fingerprints topological charge indices edge adjacency indices functional group counts WHIM descriptors 3D-MoRSE descriptors GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors SD-MoRSE descriptors GETAWAY descriptors GETAWAY descriptors	
	1 SdssC 1 RCHO 1 B08[C-C] 1 RZm 1 HATSS6 1 RDF0306m 2 Jhetv 3 SdO 1 BEHm7 1 EZu 1 HATS8m 1 BELe4 1 Mor25e 1 B08[C-C] 1 JG13 1 RF=C2 2 EZe 1 Mor21p 1 H2m 1 R1m+ 1 R1m+ 1 R1m+ 1 MaTS4m 2 GG17	 Ś. dość mumber of aldehydes (aliphatic) presence/absence of C - C at topological distance 08 R autocorrelation of Isg 2 / weighted by atomic masses leverage-weighted autocorrelation of a for 6 Radia Distribution Function - 3.0 / weighted by atomic masses Balaban-type index from van der Waals weighted by atomic masses Balaban-type index from van der Waals weighted by atomic masses Composition Function - 3.0 / weighted by atomic masses Balaban-type index from van der Waals weighted by atomic masses Dator and the state of the state of	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors GETAWAY descriptors topological descriptors topological descriptors atomtypes (Carius2) Burden eigenvalues WHIM descriptors GETAWAY descriptors Burden eigenvalues 3D-MORSE descriptors 2D binary fingerprints topological charge indices edge adjacency indices functional group counts WHIM descriptors GETAWAY descriptors	
	1 SdssC 1 RCR-O 1 BOS(C-C) 1 R2m 1 D/0706 1 D/0706 2 Jhetv 3 SdO 1 BEHm7 2 Jhetv 3 SdO 1 BEHm7 1 E2m 1 HATS8m 1 BEL-OFs 1 BOS(C-C) 1 BOS(C-C) 1 BOS(C-C) 1 BOS(C-C) 1 BOS(C-C) 1 BEHm7 1 E2m 1 HATS8m 1 Re-Ct 2 E2e 1 Mor31p 1 H2m 1 H756u 1 Mor31p 1 H756u 1 GGI7 1 Gs	 S, dss² S, dss² mumber of aldehydes (aliphatic) presence/absence of C - C at topological distance 08 R autocorrelation of Isg 2 / weighted by atomic masses Ileverage-weighted autocorrelation of a 5 / weighted by atomic Sanderson electronegativities distance/document of a 20 / weighted by atomic masses Saddan Distribution Function - 3.0 / weighted by atomic masses Saddan Userbaution Function - 3.0 / weighted by atomic masses S, dO highest eigenvalue n. 7 of Burden matrix / weighted by atomic masses Tod component accessibility directional WHII mark / unweighted Ieverage-weighted autocorrelation of Isg 3 / weighted by atomic masses Subsci - signal 25 / weighted by atomic sanderson electronegativities Subsci - signal 25 / weighted by atomic Ganderson electronegativities Subsci - signal 25 / weighted by atomic Sanderson electronegativities Subsci - signal 25 / weighted by atomic Sanderson electronegativities matrix / weighted by atomic compactivities Subsci - signal 25 / weighted by atomic masses Subsci - signal 31 / weighted by atomic compactivities Subsci - signal 31 / weighted by atomic participation atomic masses Subsci - signal 31 / weighted by atomic participation atomic masses Subsci - signal 31 / weighted by atomic participation atomic masses Subsci - signal 31 / weighted by atomic participation atomic masses Subsci - signal 31 / weighted by atomic participation atomic masses Subsci - signal 31 / weighted by atomic masses Subsci - signal 31 / weighted by atomic masses Ricomponent accessibility directional WHII index / weighted by atomic masses Ricomponent accessibility atomic masses Ricomponent size directional WHII index / weighted by atomic mass	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors topological descriptors topological descriptors topological descriptors atomtypes (Cerius2) Burden eigenvalues WHIM descriptors GETAWAY descriptors GETAWAY descriptors Burden eigenvalues 3D-MoRSE descriptors GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors D-MoRSE descriptors GETAWAY descriptors D-MoRSE descriptors GETAWAY descriptors D-MoRSE descriptors GETAWAY descriptors D-MoRSE descrip	
	1 S. desC 1 RCR-O 1 BOB(C-C) 1 BOB(C-C) 1 BOB(C-C) 1 BOB(C-C) 1 D/Dr06 1 D/Dr06 1 D/Dr06 1 D/Dr07 1 BEH 3 S.d0 3 S	S, dss ² S, dss ² presence/absence of C - C at topological distance 08 Rautocorrelation of lag 2 / weighted by atomic masses leverage-weighted autocorrelation of lag 5 / weighted by atomic masses Rautocorrelation fruiton - 3:0 / weighted by atomic masses Balaban-type index from van der Waals weighted distance matrix S, d0 Nightest eigenvalue n. 7 of Burden matrix / weighted by atomic masses Balaban-type index from van der Waals weighted by atomic masses Balaban-type index from van der Waals weighted by atomic masses Balaban-type index from van der Waals weighted by atomic masses Balaban-type index from van der Waals weighted by atomic masses Balaban-type index from van der Waals weighted by atomic masses Balaban-type index from van der Waals weighted by atomic masses Bowest eigenvalue n. 4 of Burden matrix / weighted by atomic Sanderson electronegativities Jo-MoSSE - signal 25 / weighted by atomic sanderson electronegativities Boetaf unomert 03 from edge adj, matrix number of alighteit ctertizyr (2gz) 2nd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities 3D-MoSSE - signal 31 / weighted by atomic masses 1st component of lag 2 / weighted by atomic masses 1st component size directional WHIM index / weighted by atomic masses 1st component size directional WHIM index / weighted by atomic masses 1st component size directional WHIM index / weighted by atomic masses 1st component size directional WHIM index / weighted by atomic masses 1st component gen (edv) of order 7 10 ktolst - signal 27 / unweighted Divertifiest - signal 27 / unweighted Divertifiest - signal 27 / weighted by atomic masses 1st component size directional WHIM index / weighted by atomic masses 1st component size directional WHIM index / weighted by atomic masses 1st component size directional WHIM index / weighted by atomic masses 1st component size directional WHIM index / weighted by atomic masses 1st component size directional WHIM index / weighted by atomic masses	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors topological descriptors topological descriptors topological descriptors Burden eigenvalues 3D-MORSE descriptors 2D binary fingerprints topological harge indices functional group counts WHIM descriptors 3D-MORSE descriptors 3D-MORSE descriptors GETAWAY descriptors 3D-MORSE descriptors GETAWAY GENAWAY GE	
	1 SdssC 1 RCR-O 1 RCR-O 1 RDM 1 DATA06 1 DATA06 2 Jhetv 3 SdO 1 BEHm7 2 Jhetv 3 SdO 1 BEHm7 1 E23 1 HATS8m 1 BEL46 1 Mor25e1 2 E2e 1 Mor31p 1 H2m 1 RI-R-O 2 E2e 1 Mor31p 1 H2m 1 RI-M540 1 RI-M540 1 RI-M540 1 GGI7 1 Ga 1 O-057 1 H-049	 S, dss² S, dss² mumber of aldehydes (aliphatic) presence/absence of C - C at topological distance 08 R autocorrelation of Isg 2 / weighted by atomic masses Ileverage-weighted autocorrelation of Isg 5 / weighted by atomic Sanderson electronegativities distance/detour ning index of order 6 Radia Distribution Function - 3.0 / weighted by atomic masses Balaban-type index from van der Waals weighted distance matrix S, dO highest eigenvalue n. 7 of Burden matrix / weighted by atomic masses Datomatical concentration of Isg 3 / weighted by atomic masses S, dO highest eigenvalue n. 4 of Burden matrix / weighted by atomic masses Subcorrelation of Isg 3 / weighted by atomic masses Subcorrelation of Isg 3 / weighted by atomic masses Datomost eigenvalue n. 4 of Burden matrix / weighted by atomic masses Datomost eigenvalue n. 4 of Burden matrix / weighted by atomic masses Datomost eigenveighted autocorrelation of Isg 3 / weighted by atomic masses Datomost eigenveighted autocorrelation of Isg 3 / weighted by atomic masses Datomost eigenveighted by atomic Sanderson electronegativities mean topological dispendents of order3 mather of aliphatic tertiavy (Cga) contract atocorrelation of Isg 2 / weighted by atomic palarizabilities H autocorrelation of Isg 2 / weighted by atomic masses 3D-MoRSE - signal 31 / weighted by atomic polarizabilities H autocorrelation of Isg 2 / weighted by atomic masses Bounderson electronegativities 3D-MoRSE - alignal 27 / weighted by atomic masses And complexity atomic masses And complexity at directional WHI index / weighted by atomic masses Bounderson electronegativities 	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWX descriptors topological descriptors topological descriptors topological descriptors atomtypes (Cerius2) Burden eigenvalues Burden eigenvalues Burden eigenvalues 3D-MoRSE descriptors GETAWX descriptors GETAWAY descriptors 3D-MoRSE descriptors GETAWAY descriptors AD-MORSE descriptors GETAWAY descriptors AD-MORSE descriptors GETAWAY descriptors AD-MORSE descriptors GETAWAY descriptors AD-MORSE AD-MO	
	1 SdssC 1 RCR-O 1 BD08[C-C] 1 RD7 1 RD7556 1 D/Dr06 1 RD7030m 2 Jhetv 3 SdO 1 BEHm7 1 HATS8m 8 RE44 1 Mor25e 1 B08[C-C] 1 JG13 1 ESpm030 1 RF-C2 2 E2e 1 Mor21p 1 H2m 1 LIm 1 RIm+ 1 Mor270 1 H7560 3 GG17 1 - 0-057 1 + 0-49 1 PC08	S, dss ² S, dss ² presence/absence of C - C at topological distance 08 R autocorrelation of lag 2 / weighted by atomic masses leverage-weighted autocorrelation of lag 5 / weighted by atomic Sanderson electronegativities Balaban-type index from van der Waals weighted distance matrix S, d0 highest eigenvalue n. 7 of Burden matrix / weighted by atomic masses Balaban-type index from van der Waals weighted by atomic masses Balaban-type index from van der Waals weighted by atomic masses Balaban-type index from van der Waals weighted by atomic masses Balaban-type index from van der Waals weighted by atomic masses Balaban-type index from van der Waals weighted by atomic masses D wagen bagen b	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors GETAWAY descriptors topological descriptors topological descriptors topological descriptors descriptors Burden eigenvalues WHIM descriptors 2D binary fingerprints topological charge indices diructional group counts WHIM descriptors 3D-MoRSE descriptors GETAWAY descriptors GETAWAY descriptors 3D-MoRSE descriptors GETAWAY d	
0r10a (11 Unique) 0r19a (25 Unique)	1 SdssC 1 RCR-O 1 RCR-O 1 RDS1C-O 1 RDS1C-O 1 RDS1C-O 1 RDS1D 2 DRS1C 3 SdO 1 BEFW7 3 SdO 1 BEFW7 1 E2u 1 HATS8m 1 BEL44 1 Mor31p 1 R2m031u 1 RAR-OC 2 E2e 1 Mor31p 1 HZm 1 R1m+ 1 R1m+ 1 R1m+ 1 R1m+ 1 R1m+ 1 R2m0 1 R1m+ 1 R2m0 1	 S, dss² S, dss² mumber of aldehydes (aliphatic) presence/absence of C - C at topological distance 08 R autocarrelation of Isg 2 / weighted by atomic masses leverage-weighted autocorrelation of a feed of the standard stance of the standard stance of the standard s	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors topological descriptors topological descriptors topological descriptors atomtypes (Cerius2) Burden eigenvalues WHIM descriptors GETAWAY descriptors GETAWAY descriptors Burden eigenvalues 3D-MoRSE descriptors GETAWAY descriptors Moments Atom-centred fragments walk and path counts WETAWAENT	
	1 S. desC 1 RCR-O 1 BOR[C-O 1 BOR[C-O 1 BOR[C-O 1 BOR[C-O 1 BOR[C-O 1 D/Dr06 1 D/Dr06 1 D/Dr06 1 D/Dr030m 2 Jnetv 3 S. d0 3 S	S, dsi ^C number of aldehydes (aliphatic) presence/absence of C - C at topological distance 08 R autocorrelation of lag 2 / weighted by atomic masses leverage-weighted autocorrelation of lag 5 / weighted by atomic sanderson electronegativities distance/deturn mg index of action of gamma and the same and	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors topological descriptors topological descriptors topological descriptors atomtypes (Cerius2) Burden eigenvalues WHIM descriptors GETAWAY descriptors GETAWAY descriptors Burden eigenvalues 3D-MoRSE descriptors 2D binary fingerprints topological charge indices edge adjacenty indices topological charge indices edge adjacenty indices GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors Burden eigenvalues 3D-MoRSE descriptors GETAWAY descriptors GETAWAY descriptors WHIM descriptors MIM descriptors Burden eigenvalues Burden eigenvalues Burden eigenvalues Sub-MoRSE descriptors GETAWAY descriptors Burden eigenvalues Burden eigenvalues	
	1 SdssC 1 RCR-O 1 RD8(C-C) 1 RD8 1 D/Dr06 1 D/Dr06 1 D/Dr06 1 BEHm7 1 E21 1 E21 1 E21 1 E25 1 B612-61 1 B612-61 1 B612-61 1 JG13 1 E5pm03u 1 RC72e 1 B08(C-C) 1 JG13 1 E5pm03u 1 RC72e 1 Mor21p 1 H2m 1 L1m 1 R1m+ 1 Mor21p 1 Km 1 Km 1 Km 1 Km 1 GG7 1 GG7 1 GG7 1 GG7 1 GG7 1 GG7 2 R7u+ 2 G3s	 S, dss² S, dss² mumber of aldehydes (aliphatic) presence/absence of C - C at topological distance 08 R autocarrelation of Isg 2 / weighted by atomic masses leverage-weighted autocorrelation of a feed of the standard stance of the standard stance of the standard s	atomtypes (Cerius2) functional group counts 2D binary fingerprints GETAWAY descriptors GETAWAY descriptors topological descriptors topological descriptors atomtypes (Cerius2) Burden eigenvalues WHIM descriptors GETAWAY descriptors GETAWAY descriptors 2D binary fingerprints topological charge indices edge adjacency indices functional group counts WHIM descriptors 3D-MoRSE descriptors GETAWAY descriptors Atom-centred fragments atom-centred fragments MIIM descriptors GETAWAY descriptors GETAWAY descriptors	

Table 2.1

		here and a		
	1 Hy 1 ARR	hydrophilic factor aromatic ratio	molecular properties constitutional descriptors	1
	1 BEHp7	highest eigenvalue n. 7 of Burden matrix / weighted by atomic polarizabilities	Burden eigenvalues	2
	1 RDF050v 1 C-005	Radial Distribution Function - 5.0 / weighted by atomic van der Waals volumes CH3X	RDF descriptors atom-centred fragments	3
	1 nRCHO	number of aldehydes (aliphatic)	functional group counts	1
	1 nRCOOH 1 R5m+	number of carboxylic acids (aliphatic)	functional group counts GETAWAY descriptors	1
	2 C-002	R maximal autocorrelation of lag 5 / weighted by atomic masses CH2R2	atom-centred fragments	3 1
Dr22a (43 Unique)				
	1 Mor29v 1 MAXDN	3D-MoRSE - signal 29 / weighted by atomic van der Waals volumes maximal electrotopological negative variation	3D-MoRSE descriptors topological descriptors	3 2
	1 piPC04	molecular multiple path count of order 04	walk and path counts	2
	1 Mor10e 1 Mor27m	3D-MoRSE - signal 10 / weighted by atomic Sanderson electronegativities 3D-MoRSE - signal 27 / weighted by atomic masses	3D-MoRSE descriptors 3D-MoRSE descriptors	3
	1 R7p+	R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities	GETAWAY descriptors	3
	1 S_sCH3 2 EEig12r	S_sCH3 Eigenvalue 12 from edge adj. matrix weighted by resonance integrals	atomtypes (Cerius2) edge adjacency indices	1
	1 nRCOOR	number of esters (aliphatic)	functional group counts	1
	4 R6u+ 1 Mor32p	R maximal autocorrelation of lag 6 / unweighted 3D-MoRSE - signal 32 / weighted by atomic polarizabilities	GETAWAY descriptors 3D-MoRSE descriptors	3
	1 AlogP98	AlogP98 value	structural (Cerius2)	3 3 0
	4 0-057	phenol / enol / carboxyl OH	atom-centred fragments	
	1 L3s 1 R1v+	3rd component size directional WHIM index / weighted by atomic electrotopological states R maximal autocorrelation of lag 1 / weighted by atomic van der Waals volumes	WHIM descriptors GETAWAY descriptors	1 3 1 2
	2 nHDon	number of donor atoms for H-bonds (N and O)	functional group counts	1
	2 B10[C-C] 1 Mor18m	presence/absence of C - C at topological distance 10 3D-MoRSE - signal 18 / weighted by atomic masses	2D binary fingerprints 3D-MoRSE descriptors	2
	1 B04[C-O]	presence/absence of C - O at topological distance 04	2D binary fingerprints	2
	2 Jhetp 1 STN	Balaban-type index from polarizability weighted distance matrix spanning tree number (log)	topological descriptors topological descriptors	2
	2 ESpm15u	Spectral moment 15 from edge adj. matrix	edge adjacency indices	2 2 2
	1 GATS1v 1 F03[O-O]	Geary autocorrelation - lag 1 / weighted by atomic van der Waals volumes frequency of O - O at topological distance 03	2D autocorrelations 2D frequency fingerprints	2
	1 GATS8m	Geary autocorrelation - lag 8 / weighted by atomic masses	2D autocorrelations	2 2
	2 HATS5e	leverage-weighted autocorrelation of lag 5 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors	3 3
	1 DISPv 1 R3v+	d COMMA2 value / weighted by atomic van der Waals volumes R maximal autocorrelation of lag 3 / weighted by atomic van der Waals volumes	geometrical descriptors GETAWAY descriptors	3
	1 E2e	2nd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities	WHIM descriptors	3
	1 Mor32u 2 B02[0-0]	3D-MoRSE - signal 32 / unweighted presence/absence of O - O at topological distance 02	3D-MoRSE descriptors 2D binary fingerprints	3 3 2
	1 G3e	3st component symmetry directional WHIM index / weighted by atomic Sanderson electronegativities	WHIM descriptors	3
	1 nCrs 2 HOMT	number of ring secondary C(sp3) HOMA total	functional group counts geometrical descriptors	1
	1 B05[C-C]	presence/absence of C - C at topological distance 05	2D binary fingerprints	2
	1 MATS7m 1 RDF030m	Moran autocorrelation - lag 7 / weighted by atomic masses Radial Distribution Function - 3.0 / weighted by atomic masses	2D autocorrelations RDF descriptors	3 2 2 3 2 2 3 2 2
	1 EEig12x	Eigenvalue 12 from edge adi, matrix weighted by edge degrees	edge adjacency indices	2
	1 R1m+ 1 MATS4n	R maximal autocorrelation of lag 1 / weighted by atomic masses Moran autocorrelation - lag 4 / weighted by atomic polarizabilities	GETAWAY descriptors 2D autocorrelations	3
	1 B09[C-O]	presence/absence of C - O at topological distance 09	2D binary fingerprints	2
	1 Mor15p 2 S_sOH	3D-MoRSE - signal 15 / weighted by atomic polarizabilities S_sOH	3D-MoRSE descriptors atomtypes (Cerius2)	3
	2 0_0011	5_561	domypes (cenusz)	-
Dr23a (37 Unique)	1 ATS3p	Broto-Moreau autocorrelation of a topological structure - lag 3 / weighted by atomic polarizabilities	2D autocorrelations	2
	2 O-056	alcohol	atom-centred fragments geometrical descriptors	1
	1 J3D 1 BELm5	3D-Balaban index lowest eigenvalue n. 5 of Burden matrix / weighted by atomic masses	Burden eigenvalues	3 2
	1 TPSA(Tot)	topological polar surface area using N,O,S,P polar contributions	molecular properties	1
	1 B08[C-O] 2 Mor27v	presence/absence of C - O at topological distance 08 3D-MoRSE - signal 27 / weighted by atomic van der Waals volumes	2D binary fingerprints 3D-MoRSE descriptors	2
	2 R6u+	R maximal autocorrelation of lag 6 / unweighted	GETAWAY descriptors	3 3 3 2
	1 DISPe 1 ESpm12d	d COMMA2 value / weighted by atomic Sanderson electronegativities Spectral moment 12 from edge adj. matrix weighted by dipole moments	geometrical descriptors edge adjacency indices	3
	1 Mor17m	3D-MoRSE - signal 17 / weighted by atomic masses	3D-MoRSE descriptors	3
	2 EEig09d 1 Hy	Eigenvalue 09 from edge adj. matrix weighted by dipole moments hydrophilic factor	edge adjacency indices molecular properties	
	2 GATS3e	Geary autocorrelation - lag 3 / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 8 / weighted by atomic masses	2D autocorrelations	1 2 2 3 3
	1 GATS8m 1 R4e+	Geary autocorrelation - lag 8 / weighted by atomic masses R maximal autocorrelation of lag 4 / weighted by atomic Sanderson electronegativities	2D autocorrelations GETAWAY descriptors	2
	1 Mor18m	3D-MoRSE - signal 18 / weighted by atomic masses	3D-MoRSE descriptors	3
	2 nRCOOH 1 S_sOH	number of carboxylic acids (aliphatic) S_SOH	functional group counts	1
	1 E3m	3rd component accessibility directional WHIM index / weighted by atomic masses	atomtypes (Cerius2) WHIM descriptors	1 3
	1 G3s	3st component symmetry directional WHIM index / weighted by atomic electrotopological states	WHIM descriptors	3
	2 BELm6 1 GATS1m	lowest eigenvalue n. 6 of Burden matrix / weighted by atomic masses Geary autocorrelation - lag 1 / weighted by atomic masses	Burden eigenvalues 2D autocorrelations	2 2
	2 EEig08d	Eigenvalue 08 from edge adj. matrix weighted by dipole moments	edge adjacency indices	2
	1 F05[C-O] 2 nHDon	frequency of C - O at topological distance 05 number of donor atoms for H-bonds (N and O)	2D frequency fingerprints functional group counts	2 1
	1 EEig10d	Eigenvalue 10 from edge adj. matrix weighted by dipole moments	edge adjacency indices	2
	1 R5p+ 1 BIC	R maximal autocorrelation of lag 5 / weighted by atomic polarizabilities BIC	GETAWAY descriptors topological (Cerius2)	3 2
	2 Infective-80	Ghose-Viswanadhan-Wendoloski antiinfective-like index at 80%	molecular properties	1
	1 GATS4p 1 DISPp	Geary autocorrelation - lag 4 / weighted by atomic polarizabilities d COMMA2 value / weighted by atomic polarizabilities	2D autocorrelations geometrical descriptors	2 3
	1 0-057	phenol / enol / carboxyl OH	atom-centred fragments	1
	1 Atype_H_49 1 GATS5m	Number of Hydrogen Type 49 Geary autocorrelation - lag 5 / weighted by atomic masses	atomtypes (Cerius2) 2D autocorrelations	1
	1 B02[O-O]	presence/absence of 0 - 0 at topological distance 02	2D binary fingerprints	2 2 2
	2 JGI5	mean topological charge index of order5	topological charge indices	2
Dr33b (32 Unique)				
	6 O-057 2 EEig08x	phenol / enol / carboxyl OH Eigenvalue 08 from edge adj. matrix weighted by edge degrees	atom-centred fragments edge adjacency indices	1 2
	1 DISPv	d COMMA2 value / weighted by atomic van der Waals volumes	geometrical descriptors	3
	1 TPSA(NO)	topological polar surface area using N,O polar contributions presence/absence of C - C at topological distance 06	molecular properties 2D binary fingerprints	1
	5 B06[C-C] 4 Atype_H_49	Number of Hydrogen Type 49	atomtypes (Cerius2)	2
	2 R3v+	R maximal autocorrelation of lag 3 / weighted by atomic van der Waals volumes	GETAWAY descriptors	3
	1 G1e 1 R2m+	1st component symmetry directional WHIM index / weighted by atomic Sanderson electronegativities R maximal autocorrelation of lag 2 / weighted by atomic masses	WHIM descriptors GETAWAY descriptors	3
	4 B05[C-O]	presence/absence of C - O at topological distance 05	2D binary fingerprints	3
	1 C-006 2 TPSA(Tot)	CH2RX topological polar surface area using N,O,S,P polar contributions	atom-centred fragments molecular properties	1
	1 L/Bw	length-to-breadth ratio by WHIM	geometrical descriptors	3
	1 EEig08d 3 F04[C-O]	Eigenvalue 08 from edge adj. matrix weighted by dipole moments frequency of C - O at topological distance 04	edge adjacency indices 2D frequency fingerprints	2
	1 BEHv5	highest eigenvalue n. 5 of Burden matrix / weighted by atomic van der Waals volumes	Burden eigenvalues	2 2 3
	1 Mor30p	3D-MoRSE - signal 30 / weighted by atomic polarizabilities	3D-MoRSE descriptors	3
	1 nArCO 1 nRCO	number of ketones (aromatic) number of ketones (aliphatic)	functional group counts functional group counts	1
	1 R1p+	R maximal autocorrelation of lag 1 / weighted by atomic polarizabilities	GETAWAY descriptors	1 3 2 0 2
	1 MATS4p 1 nN	Moran autocorrelation - lag 4 / weighted by atomic polarizabilities number of Nitrogen atoms	2D autocorrelations constitutional descriptors	2
		presence/absence of C - C at topological distance 07	2D binary fingerprints	2
Table 2.1 Co		······	, Serkenne	-

Table 2.1 Continued

1			
	2 JGI4	mean topological charge index of order4	topological charge indices
	1 nRCOOH	number of carboxylic acids (aliphatic)	functional group counts
	1 nCconj 1 C-005	number of non-aromatic conjugated C(sp2) CH3X	functional group counts atom-centred fragments
	1 JGI3	mean topological charge index of order3	topological charge indices
	1 HATS3p	leverage-weighted autocorrelation of lag 3 / weighted by atomic polarizabilities	GETAWAY descriptors
	1 HATS8u 1 E2u	leverage-weighted autocorrelation of lag 8 / unweighted 2nd component accessibility directional WHIM index / unweighted	GETAWAY descriptors WHIM descriptors
	2 H-051	H attached to alpha-C	atom-centred fragments
r35a (51 Unique)			
	1 ATS4e	Broto-Moreau autocorrelation of a topological structure - lag 4 / weighted by atomic Sanderson electroneg	
	2 TPSA(NO) 1 Mor27p	topological polar surface area using N,O polar contributions 3D-MoRSE - signal 27 / weighted by atomic polarizabilities	molecular properties 3D-MoRSE descriptors
	8 R6p+	R maximal autocorrelation of lag 6 / weighted by atomic polarizabilities	GETAWAY descriptors
	6 nRCOOH	number of carboxylic acids (aliphatic)	functional group counts
	3 EEig10d 2 Gs	Eigenvalue 10 from edge adj. matrix weighted by dipole moments G total symmetry index / weighted by atomic electrotopological states	edge adjacency indices WHIM descriptors
	9 JGI2	mean topological charge index of order2	topological charge indices
	3 EEig12r	Eigenvalue 12 from edge adj. matrix weighted by resonance integrals	edge adjacency indices
	7 R4e+ 7 Mor28e	R maximal autocorrelation of lag 4 / weighted by atomic Sanderson electronegativities 3D-MoRSE - signal 28 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors 3D-MoRSE descriptors
	5 MATS7p	Moran autocorrelation - lag 7 / weighted by atomic polarizabilities	2D autocorrelations
	2 L3s	3rd component size directional WHIM index / weighted by atomic electrotopological states	WHIM descriptors
	6 Mor25v 4 Mor30e	3D-MoRSE - signal 25 / weighted by atomic van der Waals volumes	3D-MoRSE descriptors 3D-MoRSE descriptors
	5 HATS8u	3D-MoRSE - signal 30 / weighted by atomic Sanderson electronegativities leverage-weighted autocorrelation of lag 8 / unweighted	GETAWAY descriptors
	7 0-057	phenol / enol / carboxyl OH	atom-centred fragments
	3 HATS5m	leverage-weighted autocorrelation of lag 5 / weighted by atomic masses	GETAWAY descriptors
	3 Jhetp 4 JGI8	Balaban-type index from polarizability weighted distance matrix mean topological charge index of order8	topological descriptors topological charge indices
	3 Mor04m	3D-MoRSE - signal 04 / weighted by atomic masses	3D-MoRSE descriptors
	1 S_dssC	S_dssC	atomtypes (Cerius2)
	2 E1m 2 nHDon	1st component accessibility directional WHIM index / weighted by atomic masses number of donor atoms for H-bonds (N and O)	WHIM descriptors functional group counts
	2 RDF135u	Radial Distribution Function - 13.5 / unweighted	RDF descriptors
	2 D/Dr06	distance/detour ring index of order 6	topological descriptors
	3 E2s 2 EEig10r	2nd component accessibility directional WHIM index / weighted by atomic electrotopological states Eigenvalue 10 from edge adj. matrix weighted by resonance integrals	WHIM descriptors edge adjacency indices
	1 G2s	2st component symmetry directional WHIM index / weighted by atomic electrotopological states	WHIM descriptors
	3 GATS3p	Geary autocorrelation - lag 3 / weighted by atomic polarizabilities	2D autocorrelations
	2 GGI1 2 Atype_C_18	topological charge index of order 1 Number of Carbon Type 18	topological charge indices atomtypes (Cerius2)
	1 nRCO	number of Carbon Type 18 number of ketones (aliphatic)	functional group counts
	1 C-005	CH3X	atom-centred fragments
	1 Mor27u 2 F08[C-O]	3D-MoRSE - signal 27 / unweighted	3D-MoRSE descriptors
	3 G3s	frequency of C - O at topological distance 08 3st component symmetry directional WHIM index / weighted by atomic electrotopological states	2D frequency fingerprints WHIM descriptors
	3 SIC5	structural information content (neighborhood symmetry of 5-order)	information indices
	1 G(NN)	sum of geometrical distances between NN	geometrical descriptors
	2 nR=Ct 2 E3m	number of aliphatic tertiary C(sp2) 3rd component accessibility directional WHIM index / weighted by atomic masses	functional group counts WHIM descriptors
	1 nArCOOR	number of esters (aromatic)	functional group counts
	1 HATS6m 1 nArCO	leverage-weighted autocorrelation of lag 6 / weighted by atomic masses	GETAWAY descriptors
	1 nArCO 1 Jhete	number of ketones (aromatic) Balaban-type index from electronegativity weighted distance matrix	functional group counts topological descriptors
	1 G(00)	sum of geometrical distances between Q.,Q	geometrical descriptors
	1 nCt	number of total tertiary C(sp3)	functional group counts
	1 H-051 1 nN	H attached to alpha-C number of Nitrogen atoms	atom-centred fragments constitutional descriptors
	1 P2s	2nd component shape directional WHIM index / weighted by atomic electrotopological states	WHIM descriptors
	1 C-025	RCRR	atom-centred fragments
r43a (27 Unique)			
r45a (27 ollique)	2 0-056	alcohol	atom-centred fragments
	1 BELm5	lowest eigenvalue n. 5 of Burden matrix / weighted by atomic masses	Burden eigenvalues
	1 B07[C-O] 1 R5e	presence/absence of C - O at topological distance 07	2D binary fingerprints GETAWAY descriptors
	1 TPSA(Tot)	R autocorrelation of lag 5 / weighted by atomic Sanderson electronegativities topological polar surface area using N,O,S,P polar contributions	molecular properties
	1 R6e+	R maximal autocorrelation of lag 6 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors
	2 JGI7	mean topological charge index of order7	topological charge indices
	3 B04[C-C] 1 EEig10d	presence/absence of C - C at topological distance 04 Eigenvalue 10 from edge adj. matrix weighted by dipole moments	2D binary fingerprints edge adjacency indices
		presence/absence of O - O at topological distance 02	2D binary fingerprints
	5 B02[O-O]		2D binary migerprints
	3 Mor13m	3D-MoRSE - signal 13 / weighted by atomic masses	3D-MoRSE descriptors
	3 Mor13m 3 nHDon	number of donor atoms for H-bonds (N and O)	3D-MoRSE descriptors functional group counts
	3 Mor13m 3 nHDon 1 Mor21m 1 JX	number of donor atoms for H-bonds (N and O) 3D-MoRSE - signal 21 / weighted by atomic masses JX	3D-MoRSE descriptors functional group counts 3D-MoRSE descriptors topological (Cerius2)
	3 Mor13m 3 nHDon 1 Mor21m 1 JX 1 R1m+	Inumber of donor atoms for H-bonds (N and O) 30-M6RSE - signal 21 / weighted by atomic masses JX R maximal autocorrelation of lag 1 / weighted by atomic masses	3D-MoRSE descriptors functional group counts 3D-MoRSE descriptors topological (Cerius2) GETAWAY descriptors
	3 Mor13m 3 nHDon 1 Mor21m 1 JX 1 R1m+ 2 GATS7m	number of donor atoms for H-bonds (N and O) 30-MRSE - signal 21 / weighted by atomic masses JX R maximal autocorrelation - lag 7 / weighted by atomic masses Geary autocorrelation - lag 7 / weighted by atomic masses	3D-MoRSE descriptors functional group counts 3D-MoRSE descriptors topological (Cerius2) GETAWAY descriptors 2D autocorrelations
	3 Mor13m 3 nHDon 1 Mor21m 1 JX 1 R1m+ 2 GATS7m 1 BELm6 1 E3m	number of donor atoms for H-bonds (N and O) 3D-MoRSE - gival 21 / weighted by atomic masses X Compared to the second second second second second second Geary autocorrelation - lag 7 / weighted by atomic masses flowest eigenvalue n. 6 of Burden matrix / weighted by atomic masses 3d component accessibility directional WHIM index / weighted by atomic masses	3D-MoRSE descriptors functional group counts 3D-MoRSE descriptors topological (Cerius2) GETAWAY descriptors 2D autocorrelations Burden eigenvalues WHIM descriptors
	3 Mor13m 3 nHDon 1 Mor21m 1 JX 1 R1m+ 2 GAT57m 1 BELm6 1 E3m 2 MAT53e	Inumber of donor atoms for H-bonds (N and O) 30-MRSES - signal 21 / weighted by atomic masses JX R maximal autocorrelation of lag 1 / weighted by atomic masses Geary autocorrelation - lag 7 / weighted by atomic masses Jowest eigenvalue n. 6 of Burden matrix / weighted by atomic masses 3rd component accessibility directional WHIN index / weighted by atomic masses JArona autocorrelation - lag 3 / weighted by atomic Sanderson electronegativities	3D-MoRSE descriptors functional group counts 3D-MoRSE descriptors topological (Cerius2) GETAWAY descriptors 2D autocorrelations Burden eigenvalues WHIM descriptors 2D autocorrelations
	3 Mor13m 3 nHDon 1 Mor21m 1 JX 1 R1m+ 2 GAT57m 1 BELm6 1 E3m 2 MAT53e 1 F04[C-0]	number of donor atoms for H-bonds (N and O) 30-HoRSE - signal 21 / weighted by atomic masses IX Registral autocorrelation of lag 1 / weighted by atomic masses Carbon subcorrelation - lag 7 / weighted by atomic masses Sid component accessibility directional WHIB in mark / weighted by atomic masses Sid component accessibility directional WHIB in mark / weighted by atomic masses Moran autocorrelation - lag 3 / weighted by atomic Sanderson electronegativities frequency of C - 0 at topological distance 04	3D-MoRSE descriptors functional group counts 3D-MoRSE descriptors topological (Cerius2) GETAWAY descriptors 2D autocorrelations Burden ejequenvalues WHIM descriptors 2D autocorrelations 2D frequency fingerprints
	3 Mor13m 3 nHDon 1 Mor21m 1 JX 1 R1m+ 2 GAT57m 1 BELm6 1 E3m 2 MAT53e	Inumber of donor atoms for H-bonds (N and O) 30-HoRSE - signal 21 / weighted by atomic masses JX R maximal autocorrelation of lag 1 / weighted by atomic masses Geary autocorrelation - Ilag 7 / weighted by atomic masses 32 d component accessibility directional WHII moder / weighted by atomic masses 32 d component accessibility directional WHII moder / weighted by atomic masses Moran autocorrelation - Ilag 3 / weighted by atomic Sanderson electronegativities frequency of C - 0 at topological distance 04 number of aldehydes (aliphatic) Ghose-Viswanadhan-Wenddoaki antimfective-like index at 80%	3D-MoRSE descriptors functional group counts 3D-MoRSE descriptors topological (Cerius2) GET&WAY descriptors 2D autocorrelations Burden eigenvalues WHIM descriptors 2D frequency fingerprints functional group counts molecular properties
	3 Mor13m 3 nHDon 1 Mor21m 1 JX 2 GATS7m 1 BELm6 1 E3m 2 MATS3e 1 F04[C-0] 1 nRCHO 1 Infective-80 1 E1g09x	Inumber of donor atoms for H-bonds (N and O) 30-MRSES - signal 21 / weighted by atomic masses JX R maximal autocorrelation of lag 1 / weighted by atomic masses Geary autocorrelation - lag 7 / weighted by atomic masses Givest eigenvalue n. 6 of Burden matrix / weighted by atomic masses 3rd component accessibility directional WHIN index / weighted by atomic masses 3rd component accessibility directional WHIN index / weighted by atomic masses Greany autocorrelation - lag 3 / weighted by atomic Sanderson electronegativities frequency of C - O at topological distance 04 number of aldehydes (aliphatic) Ghose-Visvanadhan-Wendolski antiinfecture-like index at 80% Eigenvalue 09 form edge adj. matrix weighted by edge degrees	3D-MoRSE descriptors functional group counts 3D-MoRSE descriptors topological (Certiac2) GETAWAY descriptors 2D autocorrelations 2D autocorrelations 2D requency fingerprints functional group counts molecular properties edge adjacency indices
	3 Mor13m 3 nHDon 1 Mor21m 1 JX 1 RIm+ 2 GATS7m 1 BELm6 1 E3m 2 MATS3e 1 F04[C-0] 1 nRCH0 1 Infective-80 1 EEig09x 1 GATS1m	number of donor atoms for H-bonds (N and O) 30-HoRSE - signal 21 / weighted by atomic masses JX R maximal autocorrelation of lag 1 / weighted by atomic masses Geary autocorrelation - lag 7 / weighted by atomic masses Movest eigenvalue n. 6 of Burden matrix / weighted by atomic masses Strong autocorrelation - lag 3 / weighted by atomic masses frequency of C - 0 at topological distance 04 number of aldehydes (aliphatic) Giose-Viswanahan-Wendoloski antimfective-like index at 80% Eigenvalue 09 from edge adj. matrix weighted by edge degrees Geary autocorrelation - lag 1.	3D-MoRSE descriptors functional group counts 3D-MoRSE descriptors topological (Cerius2) GET&WAY descriptors 2D autocorrelations Burden eigenvalues WHIM descriptors 2D frequency fingerprints functional group counts molecular properties
	3 Mor13m 3 nHDon 1 Mor21m 1 JX 2 GATS7m 1 BELm6 1 E3m 2 MATS3e 1 F04(C-O) 1 nRCHO 1 Infective=80 1 EEig09x 1 GATS1m 1 CIC2 2 EEig01d	number of donor atoms for H-bonds (N and O) 30-HoRSE - signal 21 / weighted by atomic masses JX R maximal autocorrelation of lag 1 / weighted by atomic masses Geary autocorrelation - 8 of Burden matrix / weighted by atomic masses Sard component accessibility directional WHIM index / weighted by atomic masses Sard component accessibility directional WHIM index / weighted by atomic masses For a strand and the strand strand strand strand strand strand strand forgunery of C - 0 at trandogical distance of a number of aldehydes (aliphatic) Ghose-Viswamadhan-Wendolexki antimfective-like index at 80% Eigenvalue 09 from edge adj. matrix weighted by dople mometrs complementary information content (neighborhood symmetry of 2-order) Eigenvalue 51 from edge adj.	3D-MoRSE descriptors functional group counts 3D-MoRSE descriptors 3D-MoRSE descriptors 2D autocorrelations Burden eigenvalues WHIM descriptors 2D autocorrelations 2D descriptors 2D autocorrelations 2D frequency fingerprints functional group counts metericals properties and and an another and an another and an another and an another and an another and an another and an another and an another 2D autocorrelations information indices edge adjacency indices
	3 Mor13m 3 nHDon 1 Mor21m 1 JX 2 GATS7m 1 BELm6 1 E3m 2 MATS3e 1 F04[C-0] 1 nRCH0 1 Infective-80 1 EEig09x 1 GATS1m 1 GATS1m	number of donor atoms for H-bonds (N and O) 3D-MoRSE - gival 21 / weighted by atomic masses X Carry autocorrelation of lag 1 / weighted by atomic masses Gavary autocorrelation - lag 7 / weighted by atomic masses for early autocorrelation - lag 7 / weighted by atomic masses Gavary autocorrelation - lag 3 / weighted by atomic masses Moran autocorrelation - lag 3 / weighted by atomic stands Moran autocorrelation - lag 3 / weighted by atomic stands Moran autocorrelation - lag 3 / weighted by atomic Sanderson electronegativities frequency of C - 0 at topological distance 04 number of aldehydes (alightatic) Ghose-Viswanachan-Wenddoski antifinetcive-like indsx at 80% Gavary autocorrelation - lag 1 / weighted by atomic masses Gavary autocorrelation - lag 1 / weighted by atomic masses	3D-MoRSE descriptors functional group counts 3D-MoRSE descriptors topological (Certus2) GETAWAY descriptors 2D autocorrelations Burden eigenvalues WHIM descriptors 2D frequency fingerprints functional group counts molecular properties edge adjacency indices 2D autocorrelations information indices
r43b (29 Unique)	3 Mor13m 3 nHDon 1 Mor21m 1 JX 2 GATS7m 1 BELm6 1 E3m 2 MATS3e 1 F04(C-O) 1 nRCHO 1 Infective=80 1 EEig09x 1 GATS1m 1 CIC2 2 EEig01d	number of donor atoms for H-bonds (N and O) 30-HoRSE - signal 21 / weighted by atomic masses JX R maximal autocorrelation of lag 1 / weighted by atomic masses Geary autocorrelation - 8 of Burden matrix / weighted by atomic masses Sard component accessibility directional WHIM index / weighted by atomic masses Sard component accessibility directional WHIM index / weighted by atomic masses For a strain a strain forgunery of C - 0 a tropological distance to 4 number of aldehydes (aliphatic) Giose-Visuranadhan-Wendolexki antimfective-like index at 80% Eigenvalue 09 from edge adj. matrix weighted by dople mometrs complementary information content (neighborhood symmetry of 2-order) Eigenvalue 51 from edge adj.	3D-MoRSE descriptors functional group counts 3D-MoRSE descriptors 3D-MoRSE descriptors 2D autocorrelations Burden eigenvalues WHIM descriptors 2D autocorrelations 2D descriptors 2D autocorrelations 2D frequency fingerprints functional group counts metericals properties and and an another and an another and an another and an another and an another and an another and an another and an another 2D autocorrelations information indices edge adjacency indices
*43b (29 Unique)	3 Mor13m 3 nHDon 1 Mor21m 1 JX 2 RATS7m 2 RATS7m 2 RATS7m 2 RATS7m 1 RATS7m 1 RATS7m 1 RATS7m 1 RATS7m 1 RATS7m 1 RATS1m 1 CEC_01d 1 HATS6u 4 EEig04x	number of donor atoms for H-bonds (N and O) 30-MoSE - signal 21 / weighted by atomic masses JX R maximal autocorrelation of lag 1 / weighted by atomic masses Geary autocorrelation - lag 7 / weighted by atomic masses Geary autocorrelation - lag 7 / weighted by atomic masses Srd component accessibility directional WHIN index / weighted by atomic masses Gran autocorrelation - lag 3 / weighted by atomic Sanderson electronegativities (frequency of C - O at topological distance 04 number of adderbydes (alphatic) Geary autocorrelation - lag 3 / weighted by atomic masses complementary information content (neighted by dogs degrees Geary autocorrelation - lag 1 / weighted by atomic masses complementary information content (neightborhood symmetry of 2-order) Eleverage-weighted autocorrelation of lag 6 / unweighted Figenvalue 04 from edge adj. matrix weighted by dege degrees	3D-MoRSE descriptors functional group counts 3D-MoRSE descriptors topological (Certia 22) GD DMRA descriptors DD Burden eigenvalues WHIM descriptors 2D autocorrelations 2D requency fingerprints functional group counts molecular properties edge adjacency indices edGTAWAY descriptors edge adjacency indices
*43b (29 Unique)	3 Mor13m 3 MHDon 1 MJO21m 1 JX 2 GATS7m 2 GATS7m 1 BELm6 2 MATS3a 1 F04(C-0) 1 MAC400- 8 I EF6024 1 EF6024 1 EF6024 1 EF6044 1 BEFM4	number of donor atoms for H-bonds (N and O) 30-HoRSE - signal 21 / weighted by atomic masses JX R maximal autocorrelation of lag 1 / weighted by atomic masses JX R maximal autocorrelation = JBg 7 / weighted by atomic masses autocorrelation = JBg 7 / weighted by atomic masses Moran autocorrelation = JBg 3 / weighted by atomic Sanderson electronegativities frequency of C = 0 at topological distance 04 number of aldehydes (aliphatic) Gnose-Viswanadhan-Wendoloski antimetrive-like index at 80% Eigenvalue 09 from edge adj. matrix weighted by edge degrees Geary autocorrelation = lag 1 / weighted by atomic masses complementary information content (neiphochood symmetry of 2-order) Eigenvalue 09 from edge adj. matrix weighted by dipole moments leverage-weighted autocorrelation of lag 6 / unweighted Eigenvalue 04 from edge adj. matrix weighted by dege degrees Gearvalue 04 from edge adj. matrix weighted by dege degrees Eigenvalue 04 from edge adj. matrix weighted by dege degrees Eigenvalue 04 from edge adj. matrix weighted by dege degrees Eigenvalue 04 from edge adj. matrix weighted by dege degrees Eigenvalue 04 from edge adj. matrix weighted by dege degrees Eigenvalue 04 from edge adj. matrix weighted by dege degrees Eigenvalue 04 from edge adj. matrix weighted by atomic van der Waals volumes	3D-MoRSE descriptors functional group counts 3D-MoRSE descriptors topological (Certis22) GETAWAY descriptors 2D autocorrelations Burden eigenvalues WHIM descriptors 2D frequency functors 2D frequency functors 2D autocorrelations information indices edge adjacency indices GETAWAY descriptors GETAWAY descriptors edge adjacency indices Burden eigenvalues
436 (29 Unique)	3 Mor13m 3 nHDon 1 MJC1m 1 X 1 RLm+ 2 GELM6 1 ELM6 1 ELM6 1 ELM6 1 RFCH0 1 nRFCH0 1 nRFCH0 1 Infectiv=00 1 EEig09x 1 GATS1m 1 CEC2 1 EEig04x 1 EEig04x 1 EEig04x	number of donor atoms for H-bonds (N and O) 30-MRSE - 3ignal 21 / weighted by atomic masses JX R maximal autocorrelation of lag 1 / weighted by atomic masses Geary autocorrelation - lag 7 / weighted by atomic masses Sard component accessibility directional WHIN index / weighted by atomic masses 3rd component accessibility directional WHIN index / weighted by atomic masses 3rd component accessibility directional WHIN index / weighted by atomic masses 3rd component accessibility directional WHIN index / weighted by atomic masses 3rd component accessibility directional WHIN index / weighted by atomic masses 3rd component accessibility directional WHIN index / weighted by atomic frequency of C - 0 at by topological distance 04 number of addehydes (alphatic) Eigenvalue D1 from edge adj, matrix weighted by adoge degrees Geary autocorrelation - lag 1 / weighted by atomic masses complementary information content (neighborhood symmetry of 2-order) Eigenvalue D1 from edge adj, matrix weighted by dople moments leverage- weighted autocorrelation of lag 6 / unweighted Figenvalue D4 from edge adj, matrix weighted by adomic van der Waals volumes 3D-MRSE - signal 25 / weighted by atomic van der Waals volumes 3D-MRSE - signal 25 / weighted by atomic van der Waals volumes	3D-MoSE descriptors [functional group counts 3D-MoSE descriptors topological (Certia 22) GET NMAY descriptors Darden eigenvalues WHIM descriptors 2D autocorrelations 2D frequency fingerprints functional group counts molecular properties edge adjacency indices edge adjacency indices edge adjacency indices Burden eigenvalues Burden eigenvalues 3D-MoSE descriptors
43b (29 Unique)	3 Mor13m 3 nHDon 1 Mor21m 1 JX 4 GATS/n 1 E3m 2 GATS/n 1 E3m 2 MATS2a 2 MATS2a 1 FAQ(C-0) 1 nRCH0 1 Infectiv-80 1 EEig094 1 EEig014 1 EEig04x 1 EEig0	number of donor atoms for H-bonds (N and O) 3D-MoRSE - givall 21 / weighted by atomic masses X Bond Start -	30-MoSE descriptors functional group counts 30-MoSE descriptors topological (Certiac2) GETAWAY descriptors 20 advaccorrelations 20 advaccorrelations 20 requency fingerprints functional group counts molecular properties edge adjacency indices 20 advaccorrelations 20 advaccorrelations adjacency indices edge adjacency indices Burden eigenvalues 30-MoSE descriptors edge adjacency indices Burden eigenvalues 30-MoSE descriptors
*43b (29 Unique)	3 Mor13m 3 MHDon 1 MGr21m 1 JX 3 MHDon 1 JX 1 Galf57m 1 BELm6 1 EELm6 1 EELm6 1 EELm6 1 RECH0 1 Infective 80 1 Infective 80 1 Infective 80 1 EELm0 1 Infective 80 1 EELm0 1 EE	number of donor atoms for H-bonds (N and O) 30-HRSE - signal 21 / weighted by atomic masses JX R maximal autocorrelation of lag 1 / weighted by atomic masses Geary autocorrelation - Iag 7 / weighted by atomic masses (Seary autocorrelation - Iag 7 / weighted by atomic masses more autocorrelation - Iag 3 / weighted by atomic masses Moran autocorrelation - Iag 3 / weighted by atomic Sanderson electronegativities frequency of C - 0 at topological distance 04 Moran autocorrelation - Iag 3 / weighted by atomic Sanderson electronegativities frequency of C - 0 at topological distance 04 Gonse-Viswanadhan-Wendoloski antiinfective-like index at 80% Eigenvalue 09 from edge adj. matrix weighted by dople moments leverage-weighted autocorrelation of Iag 6 / unweighted Hearts - Iagenvalue 04 from edge adj. matrix weighted by dople moments leverage-weighted autocorrelation of Iag 6 / unweighted Signavalue 04 from edge adj. matrix weighted by dople diperes Gearvalue 04 from edge adj. matrix weighted by dople diperes Signavalue 05 from edge adj. matrix weighted by dople diperes Eigenvalue 04 from edge adj. matrix weighted by dople diperes Signavalue 05 from edge adj. matrix weighted by dople moments leverage-weighted autocorrelation arbits / weighted by atomic van der Waals volumes 3D-MoSE - signal 25 / weighted by atomic Sanderson electronegativities Signavalue 05 from edge adj. matrix weighted by dople moments Ist component accessibility directional WHI index / weighted by atomic polarizabilities highest eigenvalue n. 8 of Burder ded by atomic Sanderson electronegativities Signavalue 05 from edge adj. matrix weighted by dople moments Ist component accessibility directional WHI index / weighted by atomic copalerizabilities highest eigenvalue n. 8 of Burder ded by atomic Sanderson electronegativities Signavalue 05 form edge adj. matrix weighted by atomic sanderson electronegativities Signavalue 05 form edge adj. matrix weighted by atomic sanderson electronegativities Signavalue 05 form edge adj. ma	3D-MoRSE descriptors functional group counts 3D-MoRSE descriptors Itopological (Certaics) 2D autocorrelations Burden eigenvalues WHIM descriptors 2D autocorrelations 2D requency fingerprints functional group counts molecular properties dega adjacency indices GETAWAY descriptors GETAWAY descriptors edge adjacency indices Burden eigenvalues Burden eigenvalues Burden eigenvalues Burden eigenvalues Burden eigenvalues Burden eigenvalues
*43b (29 Unique)	3 Mor13m 3 nHDon 1 Mor21m 1 JX 2 GATS7m 1 BELm6 2 GATS7m 1 BELm6 2 MATS2a 2 M	Inumber of donor atoms for H-bonds (N and O) 3D-MRSE - signal 21 / weighted by atomic masses X Bany subcorrelation of lag 1 / weighted by atomic masses and autocorrelation of lag 1 / weighted by atomic masses and component accessibility directional WHI M index / weighted by atomic masses direction autocorrelation of lag 3 / weighted by atomic masses atocorrelation - lag 3 / weighted by atomic sanderson electronegativities frequency of C - 0 at topological distance 04 number of aldehydes (aliphatic) Gnose-Viswamadhan-Wendolaski antimfective-like index at 80% Gnose-Viswamadhan-Wendolaski antimiketive-like by atomic van der Waals volumes 3D-MoßES - signal 25 / weighted by atomic Sanderson electronegativities Highest eigenvalue n. 8 of Burden matrix / weighted by atomic sanderson electronegativities Maxima autocorrelation of lag 1 / weighted by atomic sanderson electronegativities R maximal autocorrelation of lag 1 / weight	30-MoSE descriptors functional group counts 30-MoSE descriptors topological (Certiac2) GETAWAY descriptors 20 autocorrelations 20 autocorrelations 20 requency fingerprints functional group counts molecular properties edge adjacency indices 20 autocorrelations information indices edge adjacency indices GETAWAY descriptors edge adjacency indices Burden eigenvalues 30-MoSE descriptors edge adjacency indices Burden eigenvalues 30-MoSE descriptors Burden eigenvalues 30-MoSE descriptors Burden eigenvalues GETAWAY descriptors
:436 (29 Unique)	3 MAr13m 3 MHDon 1 MAr21m 1 JX 1 A 2 MAr53e 2 MAr53e 2 MAr53e 2 MAr53e 2 MAr53e 1 F64(C-0) 1 nRCH0 1 nRCH0 1 nRCH0 1 nRCH0 1 nRCH0 1 nRCH0 1 NAT54e 2 EEg004 1 EEg004 1 EEg04 1 EEg04	number of donor atoms for H-bonds (N and O) 30-HRSE - Signal 21 / weighted by atomic masses JX R maximal autocorrelation of lag 1 / weighted by atomic masses Geary autocorrelation - Bag 7 / weighted by atomic masses Shorts algovalue 0.6 of Burden matrix / weighted by atomic masses Shorts algovalue 0.6 of Burden matrix / weighted by atomic masses Shorts algovalue 0.6 of Burden matrix / weighted by atomic masses Shorts algovalue 0.6 of Burden matrix / weighted by atomic masses Shorts algovalue 0.6 of Burden matrix / weighted by atomic masses Shorts algovalue 0.6 of Burden matrix / weighted by atomic masses Complementary Information content (neighted by atomic masses complementary information content (neightborhood symmetry of 2-order) Eigenvalue 0.9 from edge adj. matrix weighted by dople moments leverage-weighted autocorrelation of lag 6 / unweighted Eigenvalue 0.9 from edge adj. matrix weighted by atomic van der Waals volumes 3D-MRSE - signal 2.5 / weighted by atomic van der Waals volumes 2D-MRSE - signal 2.5 / weighted by atomic van der Waals volumes 12D-MRSE - signal 2.5 / weighted by atomic van der Waals volumes 12D-MRSE - signal 2.5 / weighted by atomic van der Waals volumes 12D-MRSE - signal 2.5 / weighted by atomic van der Waals volumes 12D-MRSE - signal 2.5 / weighted by atomic van der Waals volumes 12D-MRSE - signal 2.5 / weighted by atomic van der Waals volumes 12D-MRSE - signal 2.5 / weighted by atomic van der Waals volumes 12D-MRSE - signal 2.5 / weighted by atomic van der Waals volumes 12D-MRSE - signal 2.5 / weighted by atomic van der Waals volumes 12D-MRSE - signal 2.5 / weighted by atomic van der Waals volumes 12D-MRSE - signal 2.5 / weighted by atomic van der Waals volumes 12D-MRSE - signal 2.5 / weighted by atomic van der Waals volumes 12D-MRSE - signal 2.5 / weighted by atomic van der Waals volumes 12D-MRSE - signal 2.5 / weighted by atomic van der Waals volumes 12D-MRSE - signal 2.5 / weighted by atomic van der Waals volumes 12D-MRSE - signal 2.5 / weighted by	3D-MoSE descriptors (Iunctional group counts 3D-MoSE descriptors Iunotional group counts 3D-MoSE descriptors 2D autocorrelations Burden eigenvalues WHIM descriptors 2D autocorrelations 2D requency fingerprints functional group counts molecular properties degle adjacency indices Burden eigenvalues Burden eigenvalues GETWWY descriptors ED binary fingerprints
*43b (29 Unique)	3 Mor13m 3 nHDon 1 Mor21m 1 JX 1 R4 1 EX1+ 1 EX1	number of donor atoms for H-bonds (N and O) 30-HoRSE - signal 21 / weighted by atomic masses JX R maximal autocorrelation of lag 1 / weighted by atomic masses Geary autocorrelation = 0.6 of Burden matrix / weighted by atomic masses Sard component accessibility directional WHIM index / weighted by atomic masses Sard component accessibility directional WHIM index / weighted by atomic masses Sard component accessibility directional WHIM index / weighted by atomic masses Sard component accessibility directional WHIM index / weighted by atomic masses Sard component accessibility directional WHIM index / weighted by atomic masses Component accessibility directional WHIM index / weighted by atomic masses for a same accessibility directional WHIM index / weighted by atomic masses Component accessibility directional WHIM index at 80% Eigenvalue 09 from edge adj. matrix weighted by edge degrees Geary autocorrelation - lag 1 / weighted by atomic masses complementary information content (neighborhood symmetry of 2-order) Eigenvalue 04 from edge adj. matrix weighted by dople moments leverage-weighted autocorrelation of lag 6 / unweighted Eigenvalue 04 from edge adj. matrix weighted by dople moments 10-MoSSC = aginal 25 / weighted by atomic Sanderson electronegativities Eigenvalue 03 from edge adj. matrix weighted by dipole moments Highest eigenvalue n. 8 of Burden matrix / weighted by atomic sanderson electronegativities Eigenvalue 0.8 from edge adj. matrix weighted by dipole sameres and comparison electronegativities R maximal autocorrelation of lag 1 / weighted by atomic sameses R maximal autocorrelation of lag 1 / weighted by atomic sameses presence/absence of C - C at topological distance 07 maximal electrotopological negative variation phenol / enol / carboxyl OH	3D-MoSE descriptors [unctional group counts 3D-MoSE descriptors topological (Certis 22) 2D autocorrelations 2D autocorrelations 2D autocorrelations 2D autocorrelations 2D autocorrelations 2D autocorrelations 2D autocorrelations 2D autocorrelations molecular properties edge adjacency indices 2D autocorrelations molecular properties edge adjacency indices Burden eigenvalues 3D-MoSE descriptors edge adjacency indices Burden eigenvalues 3D-MoSE descriptors edge adjacency indices Burden eigenvalues 3D-MoSE descriptors edge adjacency indices Burden eigenvalues 3D-MoSE descriptors EEWAW descriptors EEWAW descriptors EEWAW descriptors EEWAW descriptors EEWAW descriptors 2D binary fingerprints topological descriptors
43b (29 Unique)	3 Mor13m 3 MHDon 1 MG/21m 1 MG 1 MG/21m 1 MG/21m 1 MG/21m 1 MG/21m 2 MATS3 2 MATS3e 2 MATS3e 1 MG/20 1 MG/20	number of donor atoms for H-bonds (N and O) 30-HoRSE - signal 21 / weighted by atomic masses JX R maximal autocorrelation of lag 1 / weighted by atomic masses Gears autocorrelation of lag 1 / weighted by atomic masses S4 component accessibility directional WHII micel wy stomic masses S6 component accessibility directional WHII micel wy stome masses S6 component accessibility directional WHII micel wy stome masses S6 component accessibility directional WHII micel wy stome masses Complementary information content (neiphborhood symmetry of 2-order) Eigenvalue 03 from edge adj. matrix weiphted by edge degrees S6 complementary information content (neiphborhood symmetry of 2-order) Eigenvalue 04 from edge adj. matrix weiphted by atomic van der Waals volumes 3D-MoSE - signal 25 / weighted by atomic sanderson electronegativities Eigenvalue 04 from edge adj. matrix weighted by atomic van der Waals volumes 3D-MoSE - signal 25 / weighted by atomic sanderson electronegativities Eigenvalue 04 from edge adj. matrix weighted by dople moments 1st component accessibility directional WHII Micel / weighted by atomic parizabilities highest eigenvalue 0.8 of medge adj. matrix weighted by atomic sanderson electronegativities R maximal autocor of the 1 / weighted by atomic masses R maximal autocor of the 1 / weighted by atomic masses Mossimal autocor of the 1 / weighted by atomic masses Mercenary autocor of the 1 / weighted by atomic masses R maximal autocor of the 1 / weighted by atomic masses Mercenary autocor of the 1 / weighted by atomic masses Mercenary autocor of the 1 / weighted by atomic masses Mercenary autocor of the 1 / weighted by atomic sanderson electronegativi	3D-MoRSE descriptors functional group counts 3D-MoRSE descriptors 3D-MoRSE descriptors 2D autocorrelations Burden eigenvalues WHIM descriptors 2D autocorrelations 2D dructoral group counts Indictional group counts and group counts adge adjacency indices 2D autocorrelations information indices edge adjacency indices GETAWAY descriptors Burden eigenvalues 3D-MoRSE descriptors Burden eigenvalues 3D-MoRSE descriptors Burden eigenvalues GETAWAY descriptors burden eigenvalues Burden eigenvalues Burden eigenvalues GETAWAY descriptors burden eigenvalues Burden eigenvalues Burden eigenvalues Burden eigenvalues GETAWAY descriptors burden eigenvalues Burden eigenvalue
r43b (29 Unique)	3 Mor13m 3 nHDon 1 M721m 1 JX 1 RLms+ 1 RLms+ 1 ELm6 1 ELm6 1 ELm6 1 RLms+ 1 RLms+ 1 RLms+ 1 ELm7 1 nRctN-0 1 nRctN-0 1 nRctN-0 1 nRctN-0 1 EEig09x 1 GRTSIm 1 CIC2 2 Eig094x 1 EEig04x 1 E	number of donor atoms for H-bonds (N and O) 3D-MoRSE - 3gran 21 / weighted by atomic masses X Bondrage - 3gran 21 / weighted by atomic masses (any autocorrelation - 1bg 7 / weighted by atomic masses forwast eigenvalue n. 6 of burden matrix / weighted by atomic masses forwast eigenvalue n. 6 of burden matrix / weighted by atomic masses atocorrelation - 1bg 3 / weighted by atomic sanderson electronegativities frequency of C - 0 at topological distance 04 number of aldehydes (aliphatic) Ghose-Viswanadhan-Wendolaski antiinfective-like indsx at 80% Ghose-Viswanadhan-Wendolaski antiinfective-like indsx at 80% fregenvalue 01 from edge adj. matrix weighted by dipole moments 15 component accessibility directional WHI Minderson electronegativities Figenvalue 09 from edge adj. matrix weighted by dipole moments 15 component accessibility directional WHI Minderson electronegativities Figenvalue 09 from edge adj. matrix weighted by atomic sanderson electronegativities Figenvalue 09 form edge adj. matrix weighted by atomic sanderson electronegativities Figenvalue 09 form edge adj. tartix weighted by atomic sanderson electronegativities Figenvalue 07 form edge adj. I weighted by atomic sanderson electronegativities Figenvalue 07 form edge adj. Tweliphet by atomic masses presence/absence of C - C at topological distance 07 maximal diecto	30-MoSE descriptors functional group counts 30-MoSE descriptors topological (Certiac2) GET NMAY descriptors GET MMAY descriptors 20 autocorrelations 20 autocorrelations 20 autocorrelations 20 autocorrelations 20 autocorrelations 20 autocorrelations adjacency indices edge adjacency indices edge adjacency indices Burden eigenvalues 30-MoSE descriptors edge adjacency indices Burden eigenvalues 30-MoSE descriptors edge adjacency indices Burden eigenvalues 30-MoSE descriptors Burden eigenvalues 30-MoSE descriptors Burden eigenvalues 30-MoSE descriptors Burden fragments atom-centred fragments molecular properties 20 binary fingerprints
r43b (29 Unique)	3 Mor13m 3 MHDon 1 MG/21m 1 MG 1 MG/21m 1 MG/21m 1 MG/21m 1 MG/21m 2 MATS3 2 MATS3e 2 MATS3e 1 MG/20 1 MG/20	number of donor atoms for H-bonds (N and O) 30-HoRSE - signal 21 / weighted by atomic masses JX R maximal autocorrelation of lag 1 / weighted by atomic masses Gears autocorrelation of lag 1 / weighted by atomic masses S4 component accessibility directional WHII micel wy stomic masses S6 component accessibility directional WHII micel wy stome masses S6 component accessibility directional WHII micel wy stome masses S6 component accessibility directional WHII micel wy stome masses Complementary information content (neiphborhood symmetry of 2-order) Eigenvalue 03 from edge adj. matrix weiphted by edge degrees S6 complementary information content (neiphborhood symmetry of 2-order) Eigenvalue 04 from edge adj. matrix weiphted by atomic van der Waals volumes 3D-MoSE - signal 25 / weighted by atomic sanderson electronegativities Eigenvalue 04 from edge adj. matrix weighted by atomic van der Waals volumes 3D-MoSE - signal 25 / weighted by atomic sanderson electronegativities Eigenvalue 04 from edge adj. matrix weighted by dople moments 1st component accessibility directional WHII Micel / weighted by atomic parizabilities highest eigenvalue 0.8 of medge adj. matrix weighted by atomic sanderson electronegativities R maximal autocor of the 1 / weighted by atomic masses R maximal autocor of the 1 / weighted by atomic masses Mossimal autocor of the 1 / weighted by atomic masses Mercenary autocor of the 1 / weighted by atomic masses R maximal autocor of the 1 / weighted by atomic masses Mercenary autocor of the 1 / weighted by atomic masses Mercenary autocor of the 1 / weighted by atomic masses Mercenary autocor of the 1 / weighted by atomic sanderson electronegativi	3D-MoRSE descriptors functional group counts 3D-MoRSE descriptors 3D-MoRSE descriptors 2D autocorrelations Burden eigenvalues WHIM descriptors 2D autocorrelations 2D dructoral group counts Indictional group counts and group counts adge adjacency indices 2D autocorrelations information indices edge adjacency indices GETAWAY descriptors Burden eigenvalues 3D-MoRSE descriptors Burden eigenvalues 3D-MoRSE descriptors Burden eigenvalues GETAWAY descriptors burden eigenvalues Burden eigenvalues Burden eigenvalues GETAWAY descriptors burden eigenvalues Burden eigenvalues Burden eigenvalues Burden eigenvalues GETAWAY descriptors burden eigenvalues Burden eigenvalue
r 43b (29 Umque)	3 Mor13m 3 MHDon 1 MG21m 1 JX 1 JX 1 CATS7m 1 EELm6 1 EELm6	number of donor atoms for H-bonds (N and O) 30-HoRSE - signal 21 / weighted by atomic masses JX R maximal autocorrelation of lag 1 / weighted by atomic masses JX R maximal autocorrelation of lag 1 / weighted by atomic masses autocorrelation - lag 7 / weighted by atomic masses Autocorrelation - lag 3 / weighted by atomic Sanderson electronegativities frequency of C - 0 at topological distance 04 Noran autocorrelation - lag 1 / weighted by atomic Sanderson electronegativities frequency of C - 0 at topological distance 04 Conse-Viswanadhan-Wendoloski antimfective-like index at 80% Eigenvalue 09 from edge adj. matrix weighted by dogle dogrees Geary autocorrelation - lag 1 / weighted by atomic masses complementary information content (neightborhood symmetry of 2-order) Eigenvalue 01 from edge adj. matrix weighted by dogle moments leverage-weighted autocorrelation of lag 6 / unweighted Signavalue 04 from edge adj. matrix weighted by dogle moments Eigenvalue 05 from edge adj. matrix weighted by dogle moments leverage-weighted autocorrelation of lag 1 / uweighted by atomic van der Waals volumes 3D-MoSE - signal 25 / weighted by atomic Sanderson electronegativities Figenvalue 01 from edge adj. matrix weighted by atomic van der Waals volumes 3D-MoSE - signal 25 / weighted by atomic Sanderson electronegativities R maximal autocorrelation of lag 1 / weighted by atomic masses presence/absence of C - C at topological distance 04 Moran autocorrelation of lag 1 / weighted by atomic masses presence/absence of C - C at topological distance 04 Moran autocorrelation - lag 5 / weighted by atomic Sanderson electronegativities 3D-MoSE - signal 24 / weighted by atomic Sanderson electronegativities 3D-MoSE - signal 24 / weighted by atomic Sanderson electronegativities 3D-MoSE - signal 24 / weighted by atomic Sanderson electronegativities 3D-MoSE - signal 24 / weighted by atomic van der Waals volumes 3D-MoSE - signal 25 / weighted by atomic van der Waals volumes	30-MoSE descriptors Iunctional group counts 30-MoSE descriptors Iunctional group counts 30-MoSE descriptors 20 autocorrelations Burden eigenvalues WHIM descriptors 20 autocorrelations 20 requency fingerprints Iunctional group counts molecular properties 50 autocorrelations 20 autocorrelations 20 autocorrelations GETAWAY descriptors Burden eigenvalues Burden eigenvalues Burden eigenvalues Burden eigenvalues Burden eigenvalues Burden eigenvalues Burden eigenvalues Burden eigenvalues GETAWAY descriptors Burden eigenvalues GETAWAY descriptors Burden eigenvalues GETAWAY descriptors Burden eigenvalues GETAWAY descriptors Burden eigenvalues GETAWAY descriptors 20 binary fingerprints topological descriptors 20 binary fingerprints 10 binary fingerprints 20 bin
r 43b (29 Unique)	3 MAr13m 3 MHDon 1 M721m 1 JX 4 GATSA 2 GATSA 2 GATSA 2 GATSA 2 GATSA 2 GATSA 2 GATSA 2 GATSA 2 GATSA 1 FAG(C-0) 1 nRCHO 1 Infectiv-80 1 CIC2 2 EEig094 1 EEig014 1 EEig014 1 EEig04 2 EEig044 1 EEIg0	number of donor atoms for H-bonds (N and O) 3D-MoRSE - aignal 21 / weighted by atomic masses X Bany subcorrelation - 16 g7 / weighted by atomic masses and component accessibility directional WHIB index / weighted by atomic masses direction - 16 g7 / weighted by atomic sanderson electronegativities frequency of C - 0 at topological distance 04 number of aldehydes (aliphatic) Ginose-Viswamadhan-Wendolaski antimetrive-like index at 80% Ginose-Viswamadhan-Wendolaski antimetrive-like index at 80% Bigenvalue 03 from edge adj, matrix weighted by dege degrees Highest eigenvalue 0.4 of Burden matrix / weighted by atomic van der Waals volumes 10-MoRSE - asgnal 25 / weighted by atomic Sanderson electronegativities highest eigenvalue n. 4 of Burden matrix / weighted by atomic sanderson electronegativities presence/absence of C - C at topological distance 07 maximal electrotopological negative variation phenol / enol / carboxyi OH Ginse-Viswamadhan-Wendolaski antimfective-like index at 80% promaximachiestichesti antimfective-like index at 80% DPMORSE - signal 24 / weighted by atomic Sanderson electronegativities 3D-MoRSE - signal 24 / weighted by atomic Yanose 3D-MoRSE - signal 24 / weighted by atomic	30-MoSE descriptors [unctional group counts 30-MoSE descriptors borpological (Certiac2) GETAWAY descriptors 20 addocrentations WHIM descriptors 20 addocrentations 20 frequency fingerprints functional group counts molecular properties edge adjacency indices 20 addocrentations adjacency indices edge adjacency indices Burden eigenvalues 30-MoSE descriptors Burden eigenvalues 30-MoSE descriptors 20 binary fingerprints tabomics 20 binary fingerprints 20 binary fing
r 43b (29 Unique)	3 MAr13m 3 MHDon 1 MGr21m 1 JX 1 LX 1	number of donor atoms for H-bonds (N and O) 30-HoRSE - signal 21 / weighted by atomic masses JX R maximal autocorrelation of lag 1 / weighted by atomic masses Geary autocorrelation - 18g 7 / weighted by atomic masses Geary autocorrelation - 18g 7 / weighted by atomic masses Moran autocorrelation - 18g 3 / weighted by atomic Sanderson electronegativities frequency of C - 0 at topological distance 04 number of aldehydes (aliphatic) Giose-Viswanadhan-Wendoloski antimfective-like index at 80% Eigenvalue 09 from edge adj. matrix weighted by dogle degrees Geary autocorrelation - 18g 1 / weighted by atomic masses complementary information content (neighborhood symmetry of 2-order) Eigenvalue 09 from edge adj. matrix weighted by dogle degrees Geary autocorrelation - 18g 1 / weighted by atomic Sanderson electronegativities Figenvalue 09 from edge adj. matrix weighted by dogle degrees Geary autocorrelation - 18g 1 / weighted by atomic masses complementary information content (neighborhood symmetry of 2-order) Eigenvalue 04 from edge adj. matrix weighted by dogle degrees Highest eigenvalue 04 from edge adj. matrix weighted by atomic van der Waals volumes 3D-MoSE - signal 25 / weighted by atomic Sanderson electronegativities Tist component accessibility directional WHIN index / weighted by atomic polarizabilities highest eigenvalue 0.8 of Durden matrix / weighted by atomic masses presence/absence of C - C at topological distance 04 maximal autocorrelation of lag 1 / weighted by atomic Sanderson electronegativities Chose-Viswanadhan-Wendoski antimfective-like index at 80% Ghose-Viswanadhan-Wendoski antimfective-like index at 80% Ghose-Liswanadhan-Wendoski by atomic conder Waals volumes 3D-MoSE - signal 25 / weighted by atomic Yaaderson electronegativities 3D-MoSE - signal 25 / weighted by atomic van der Waals volumes highest eigenvalue n. 4 of Burden matrix / weighted by atomic polarizabilities highest eigenvalue n. 4 of Burden matrix / weighted by atomic polarizabilities highest eigenvalue n	30-MoSE descriptors [unctional group counts 30-MoSE descriptors bordiogical (Certis 2) 20 autocorrelations 20 autocorrelations 20 autocorrelations 20 autocorrelations 20 frequency fingerprints functional group counts molecular properties dege adjacency indices 20 frequency fingerprints adjacency indices Burden eigenvalues Burden eigenvalues 30-MoSE descriptors dege adjacency indices Burden eigenvalues 30-MoSE descriptors dege adjacency indices Burden eigenvalues 30-MoSE descriptors 20 binary fingerprints topological descriptors 20 binary fingerprints topological descriptors 20 binary fingerprints 20 binary fingerprints
r43b (29 Unique)	3 MAr13m 3 MHDon 1 M721m 1 JX 4 GATSA 2 GATSA 2 GATSA 2 GATSA 2 GATSA 2 GATSA 2 GATSA 2 GATSA 2 GATSA 1 FAG(C-0) 1 nRCHO 1 Infectiv-80 1 CIC2 2 EEig094 1 EEig014 1 EEig014 1 EEig04 2 EEig044 1 EEIg0	number of donor atoms for H-bonds (N and O) 3D-MoRSE - aignal 21 / weighted by atomic masses X Bany subcorrelation - 16 g7 / weighted by atomic masses and component accessibility directional WHIB index / weighted by atomic masses direction - 16 g7 / weighted by atomic sanderson electronegativities frequency of C - 0 at topological distance 04 number of aldehydes (aliphatic) Ginose-Viswamadhan-Wendolaski antimetrive-like index at 80% Ginose-Viswamadhan-Wendolaski antimetrive-like index at 80% Bigenvalue 03 from edge adj, matrix weighted by dege degrees Highest eigenvalue 0.4 of Burden matrix / weighted by atomic van der Waals volumes 10-MoRSE - asgnal 25 / weighted by atomic Sanderson electronegativities highest eigenvalue n. 4 of Burden matrix / weighted by atomic sanderson electronegativities presence/absence of C - C at topological distance 07 maximal electrotopological negative variation phenol / enol / carboxyi OH Ginse-Viswamadhan-Wendolaski antimfective-like index at 80% promaximachiestichesti antimfective-like index at 80% DPMORSE - signal 24 / weighted by atomic Sanderson electronegativities 3D-MoRSE - signal 24 / weighted by atomic Yanose 3D-MoRSE - signal 24 / weighted by atomic	30-MoSE descriptors [unctional group counts 30-MoSE descriptors borpological (Certiac2) GETAWAY descriptors 20 addocrentations WHIM descriptors 20 addocrentations 20 frequency fingerprints functional group counts molecular properties edge adjacency indices 20 addocrentations adjacency indices edge adjacency indices Burden eigenvalues 30-MoSE descriptors Burden eigenvalues 30-MoSE descriptors 20 binary fingerprints tabomics 20 binary fingerprints 20 binary fing
r43b (29 Unique)	3 Mor13m 3 MHDon 1 MG/21m 1 MG 1 MG/21m 1 MG/21m 1 MG/21m 2 GATS/m 1 BELm6 1 EEm 2 MATS3e 1 GATS/m 1 GATS4 1 GATS5 1 GATS4	number of donor atoms for H-bonds (N and O) 30-HoRSE - signal 21 / weighted by atomic masses JX R makinal autocorrelation of lag 1 / weighted by atomic masses Genet autocorrelation of lag 1 / weighted by atomic masses Genet autocorrelation of lag 1 / weighted by atomic masses at component accessibility directional WHIB index / weighted by atomic masses do component accessibility directional WHIB index / weighted by atomic masses for autocorrelation - lag 3 / weighted by atomic Sanderson electronegativities frequency of C - 0 at topological distance 04 number of aldehydes (aliphatic) Ginose-Viswanadhan-Wendoloski antimfective-like index at 80% Eigenvalue 03 from edge adj. matrix weighted by dege degrees Geary autocorrelation - lag 1 / weighted by atomic masses complementary information content (neighborhood symmetry of 2-order) Eigenvalue 03 from edge adj. matrix weighted by dege degrees Genevalue 04 from edge adj. matrix weighted by dege degrees Genevalue 04 from edge adj. matrix weighted by atomic van der Waals volumes 30-MoSE - signal 25 / weighted by atomic Sanderson electronegativities Eigenvalue 04 from edge adj. matrix weighted by atomic van der Waals volumes 30-MoSE - signal 25 / weighted by atomic Sanderson electronegativities Eigenvalue 04 from edge adj. matrix weighted by atomic van der Waals volumes 30-MoSE - signal 25 / weighted by atomic Sanderson electronegativities Eigenvalue 04 from edge adj. matrix weighted by atomic sanderson electronegativities presence/absence of C - C at topological distance 07 maximal electrotopological negative variation phenol / enol / carboxyl OH Ghose-Viswanadhan-Wendoloski antimfective-like index at 80% presence/absence of C - C at topological distance 04 Moran autocorrelation - lag 5 / weighted by atomic conder weighted by atomic 30-MoSE - signal 24 / weighted by atomic conder walas volumes 30-MoSE - signal 24 / weighted by atomic conder walas volumes 30-MoSE - signal 24 / weighted by atomic conder walas volumes 30-MoSE - signal 24 / weighted by atomic conder walas v	30-MoSE descriptors Iunctional group counts 30-MoSE descriptors 20-autocorrelations 20-autocorrelations Burden eigenvalues WHIM descriptors 20 autocorrelations 20 frequency fingerprints functional group counts midge adjacency indices 20 autocorrelations Information indices edge adjacency indices Burden eigenvalues 30-MoSE descriptors Burden eigenvalues 30-MoSE descriptors Burden eigenvalues 30-MoSE descriptors Burden eigenvalues 30-MoSE descriptors 20 binary fingerprints atom-centred fragments atom-centred fragments 30-MoSE descriptors 30-MoSE descriptors 30-MoSE descriptors 30-MoSE descriptors 30-MoSE descriptors 30-MoSE descriptors 30-MoSE descriptors Burden eigenvalues 30-MoSE descriptors Burden eigenvalues 30-MoSE descriptors Burden eigenvalues 30-MoSE descriptors Burden eigenvalues 30-MoSE descriptors Burden eigenvalues 30-MoSE descriptors Burden eigenvalues 30-MoSE descriptors Burden eigenvalues Burden eigenvalues 30-MoSE descriptors Burden eigenvalues 30-MoSE descriptors Burden eigenvalues 30-MoSE descriptors Burden eigenvalues 30-MoSE descriptors Burden eigenvalues 30-MoSE descriptors Burden eigenvalues 30-MoSE descriptors Burden eigenvalues 30-MoSE descriptors
r43b (29 Unique)	3 MAr13m 3 MHDon 1 MGr21m 1 JX 1 R1H 1 R2H 1	number of donor atoms for H-bonds (N and O) 3D-MoRSE - signal 21 / weighted by atomic masses 2X Bond Start - Signal 21 / weighted by atomic masses Carary autocorrelation - lag 7 / weighted by atomic masses 37 37 37 37 37 37 37 37 37 37	30-MoSE descriptors [unctional group counts 30-MoSE descriptors bopological (Certia 22) Control (Certia 22) Certia 22) Cert
r436 (29 Unique)	3 Mor13m 3 MHDon 1 MG/21m 1 MG 1 MG/21m 1 MG/21m 1 MG/21m 2 GATS/m 1 BELm6 1 EEm 2 MATS3e 1 GATS/m 1 GATS4 1 GATS5 1 GATS4 1 GATS4 1 GATS4 1 GATS5 1 GATS4	number of donor atoms for H-bonds (N and O) 30-HoRSE - signal 21 / weighted by atomic masses JX R maximal autocorrelation of lag 1 / weighted by atomic masses JX R maximal autocorrelation of lag 1 / weighted by atomic masses and component accessibility directional WHII micel / weighted by atomic masses Moran autocorrelation - lag 3 / weighted by atomic Sanderson electronegativities frequency of C - 0 at topological distance 04 number of aldehydes (aliphatic) Geary autocorrelation - lag 3 / weighted by atomic masses Complementary Information content (neiphborhood symmetry of 2-order) Eigenvalue 03 from edge adj. matrix weighted by dogle argenes Geary autocorrelation - lag 1 / weighted by atomic masses Complementary Information content (neiphborhood symmetry of 2-order) Eigenvalue 03 from edge adj. matrix weighted by dipole moments leverage-weighted autocorrelation of lag 6 / unweighted 30-MoRSE - signal 25 / weighted by atomic Sanderson electronegativities Fegenvalue 04 from edge adj. matrix weighted by dipole moments leverage-weighted autocorrelation of lag 1 / uweighted by atomic van der Waals volumes 30-MoRSE - signal 25 / weighted by atomic Sanderson electronegativities Rigenvalue 04 from edge adj. matrix weighted by dipole moments 1st component accessibility directional WHII Mick / weighted by atomic Sanderson electronegativities R maximal autocorrelation of lag 1 / weighted by atomic Sanderson electronegativities Armatima autocorrelation of lag 1 / weighted by atomic Sanderson electronegativities Armatima autocorrelation of lag 1 / weighted by atomic Sanderson electronegativities 30-MoRSE - signal 25 / weighted by atomic Sanderson electronegativities 30-MoRSE - signal 24 / weighted by atomic Sanderson electronegativities 30-MoRSE - signal 24 / weighted by atomic van der Waals volumes 30-MoRSE - signal 24 / weighted by atomic van der Waals volumes 30-MoRSE - signal 24 / weighted by atomic van der Waals volumes 30-MoRSE - signal 24 / weighted by atomic van der Waals volumes 30-MoRSE - signal 25 / weighted by	30-MoRSE descriptors Innctional group counts 30-MoRSE descriptors Intorious group counts 30-MoRSE descriptors 20 autocorrelations Burden eigenvalues WHIM descriptors 20 autocorrelations 20 requency fingerprints Innctional group counts molecular properties and and an another and another and and another another and another another and another another GETAWAY descriptors Burden eigenvalues Burden eigenvalues Burden eigenvalues Burden eigenvalues GETAWAY descriptors Burden eigenvalues GETAWAY descriptors Burden eigenvalues 20 binary fingerprints topological descriptors Burden eigenvalues 30-MoRSE descriptors 30-MoRSE descriptors 30-MoRS
43b (29 Unique)	3 MAr13m 3 MHDon 1 MG21m 1 JX 1 A 2 MF1 2 MATS3e 2 MATS3e 2 MATS4 2 MATS4	number of donor atoms for H-bonds (N and O) 30-HoRSE - signal 21 / weighted by atomic masses JX R maximal autocorrelation of lag 1 / weighted by atomic masses Geary autocorrelation = 10g 7 / weighted by atomic masses atocorrelation = 10g 7 / weighted by atomic masses atocorrelation = 10g 7 / weighted by atomic masses atocorrelation = 10g 3 / weighted by atomic Sanderson electronegativities frequency of C = 0 at topological distance 04 Noran autocorrelation = 10g 1 / weighted by atomic masses Complementary information content (neighborhood symmetry of 2-order) Eigenvalue 09 from edge adj. matrix weighted by dogle engrees Geary autocorrelation = 10g 1 / weighted by atomic masses complementary information content (neighborhood symmetry of 2-order) Eigenvalue 09 from edge adj. matrix weighted by dipole moments leverage-weighted autocorrelation of lag 6 / unweighted Eigenvalue 04 from edge adj. matrix weighted by dipole moments leverage-weighted autocorrelation atom size Signal 25 / weighted by atomic Sanderson electronegativities Eigenvalue 04 from edge adj. matrix weighted by dipole moments leverage-weighted autocorrelation atom size (sanderson electronegativities Eigenvalue 04 from edge adj. matrix weighted by dipole moments 1st component accessibility directional WHI index / weighted by atomic conderson electronegativities R maximal autocorrelation of lag 1 / weighted by atomic masses presence/absence of C - C at topological distance 04 Moran autocorrelation of lag 1 / weighted by atomic sanderson electronegativities 3D-MoRSE - signal 25 / weighted by atomic sanderson electronegativities 3D-MoRSE - signal 25 / weighted by atomic sanderson electronegativities 3D-MoRSE - signal 24 / weighted by atomic sanderson electronegativities 3D-MoRSE - signal 24 / weighted by atomic van der Waals volumes highest eigenvalue n. 4 of Burden matrix / weighted by atomic polarizabilities highest eigenvalue n. 4 of Burden matrix / weighted by atomic polarizabilities highest eigenvalue n. 4 of Burden	30-MoSE descriptors [unctional group counts 30-MoSE descriptors bopological (Certia 22) Control (Certia 22) Certia 22) Cert

Table 2.1 Continued

		Number of Hydrogen Type 49	atomtypes (Cerius2)
	1 EEig08d 1 nCrs	Eigenvalue 08 from edge adj. matrix weighted by dipole moments number of ring secondary C(sp3)	edge adjacency indices functional group counts
	2 H-047	H attached to C1(sp3)/C0(sp2)	atom-centred fragments
Or47a (21 Unique)			
	1 piPC04 2 DISPm	molecular multiple path count of order 04 d COMMA2 value / weighted by atomic masses	walk and path counts geometrical descriptors
	1 R7e+	R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors
	1 Mor10p 1 Mor20u	3D-MoRSE - signal 10 / weighted by atomic polarizabilities 3D-MoRSE - signal 20 / unweighted	3D-MoRSE descriptors 3D-MoRSE descriptors
	1 IC1	information content index (neighborhood symmetry of 1-order)	information indices
	1 nRCOOH 1 EEig01d	number of carboxylic acids (aliphatic) Eigenvalue 01 from edge adj. matrix weighted by dipole moments	functional group counts edge adjacency indices
	2 Infective-80 1 MATS4m	Ghose-Viswanadhan-Wendoloski antiinfective-like index at 80% Moran autocorrelation - lag 4 / weighted by atomic masses	molecular properties 2D autocorrelations
	1 GATS5p	Geary autocorrelation - lag 5 / weighted by atomic polarizabilities	2D autocorrelations
	1 PW4 1 Mor32p	path/walk 4 - Randic shape index 3D-MoRSE - signal 32 / weighted by atomic polarizabilities	topological descriptors 3D-MoRSE descriptors
	1 Mor09e	3D-MoRSE - signal 09 / weighted by atomic Sanderson electronegativities	3D-MoRSE descriptors
	1 TPSA(NO) 1 B04[C-C]	topological polar surface area using N,O polar contributions presence/absence of C - C at topological distance 04	molecular properties 2D binary fingerprints
	1 O-057 1 Atype H 49	phenol / enol / carboxyl OH Number of Hydrogen Type 49	atom-centred fragments atomtypes (Cerius2)
	1 ESpm01d	Spectral moment 01 from edge adj. matrix weighted by dipole moments	edge adjacency indices
	1 EEig10d 1 P2m	Eigenvalue 10 from edge adj. matrix weighted by dipole moments 2nd component shape directional WHIM index / weighted by atomic masses	edge adjacency indices WHIM descriptors
	2 Mor06e	3D-MoRSE - signal 06 / weighted by atomic Sanderson electronegativities	3D-MoRSE descriptors
Or47b (14 Unique)			
	3 EEig02d 5 ESpm03d	Eigenvalue 02 from edge adj. matrix weighted by dipole moments	edge adjacency indices
	1 nHBonds	Spectral moment 03 from edge adj. matrix weighted by dipole moments number of intramolecular H-bonds (with N,O,F)	edge adjacency indices functional group counts
	4 X5A 1 EEig08x	average connectivity index chi-5 Eigenvalue 08 from edge adj. matrix weighted by edge degrees	connectivity indices edge adjacency indices
	1 C-006	CH2RX	atom-centred fragments
	1 nRCHO 2 nRCOOR	number of aldehydes (aliphatic) number of esters (aliphatic)	functional group counts functional group counts
	1 nRCOOH	number of carboxylic acids (aliphatic)	functional group counts
	1 EEig08d 1 X4Av	Eigenvalue 08 from edge adj. matrix weighted by dipole moments average valence connectivity index chi-4	edge adjacency indices connectivity indices
	1 GATS6m 1 EEig07r	Geary autocorrelation - lag 6 / weighted by atomic masses	2D autocorrelations
	1 EEigU/r 1 R2m	Eigenvalue 07 from edge adj. matrix weighted by resonance integrals R autocorrelation of lag 2 / weighted by atomic masses	edge adjacency indices GETAWAY descriptors
0r49b (37 Unique)			
(S) olique)	2 nCb-	number of substituted benzene C(sp2)	functional group counts
	1 BEHm6 2 F04[C-O]	highest eigenvalue n. 6 of Burden matrix / weighted by atomic masses frequency of C - O at topological distance 04	Burden eigenvalues 2D frequency fingerprint
	1 D/Dr06	distance/detour ring index of order 6	topological descriptors
	1 BEHp6 3 H-047	highest eigenvalue n. 6 of Burden matrix / weighted by atomic polarizabilities H attached to C1(sp3)/C0(sp2)	Burden eigenvalues atom-centred fragments
	1 GATS1m 3 HATS8p	Geary autocorrelation - lag 1 / weighted by atomic masses	2D autocorrelations GETAWAY descriptors
	2 ISH	leverage-weighted autocorrelation of lag 8 / weighted by atomic polarizabilities standardized information content on the leverage equality	GETAWAY descriptors
	1 Mor16e 1 JGI5	3D-MoRSE - signal 16 / weighted by atomic Sanderson electronegativities mean topological charge index of order5	3D-MoRSE descriptors topological charge indice
	1 R8e+	R maximal autocorrelation of lag 8 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors
	1 Mor25e 2 EEig10d	3D-MoRSE - signal 25 / weighted by atomic Sanderson electronegativities Eigenvalue 10 from edge adj. matrix weighted by dipole moments	3D-MoRSE descriptors edge adjacency indices
	1 Mor16p	3D-MoRSE - signal 16 / weighted by atomic polarizabilities	3D-MoRSE descriptors
	1 JGI4 1 MATS3p	mean topological charge index of order4 Moran autocorrelation - lag 3 / weighted by atomic polarizabilities	topological charge indice 2D autocorrelations
	3 CIC 1 P2m	CIC 2nd component shape directional WHIM index / weighted by atomic masses	topological (Cerius2) WHIM descriptors
	1 nHDon	number of donor atoms for H-bonds (N and O)	functional group counts
	1 Mor03m 2 JGI7	3D-MoRSE - signal 03 / weighted by atomic masses mean topological charge index of order7	3D-MoRSE descriptors topological charge indice
	1 Mor23v	3D-MoRSE - signal 23 / weighted by atomic van der Waals volumes	3D-MoRSE descriptors
	1 Mor30e 1 IC	3D-MoRSE - signal 30 / weighted by atomic Sanderson electronegativities	3D-MoRSE descriptors topological (Cerius2)
	1 Mor21m	3D-MoRSE - signal 21 / weighted by atomic masses 3D-MoRSE - signal 13 / weighted by atomic masses	3D-MoRSE descriptors
	1 Mor13m 1 R7v+	SD-MORSE - signal 13 / weighted by atomic masses R maximal autocorrelation of lag 7 / weighted by atomic van der Waals volumes	3D-MoRSE descriptors GETAWAY descriptors
	1 piPC07	molecular multiple path count of order 07	walk and path counts
	1 nArOH 1 Mor25v	number of aromatic hydroxyls 3D-MoRSE - signal 25 / weighted by atomic van der Waals volumes	functional group counts 3D-MoRSE descriptors
	1 Mor08v 1 R6e+	3D-MoRSE - signal 08 / weighted by atomic van der Waals volumes R maximal autocorrelation of lag 6 / weighted by atomic Sanderson electronegativities	3D-MoRSE descriptors GETAWAY descriptors
	1 EEig06x	Eigenvalue 06 from edge adj. matrix weighted by edge degrees	edge adjacency indices
	1 C-001 1 Mor07m	CH3R / CH4 3D-MoRSE - signal 07 / weighted by atomic masses	atom-centred fragments 3D-MoRSE descriptors
	1 DISPe	d COMMA2 value / weighted by atomic Sanderson electronegativities	geometrical descriptors
	1 nR05 1 Mor07e	number of 5-membered rings 3D-MoRSE - signal 07 / weighted by atomic Sanderson electronegativities	constitutional descriptor 3D-MoRSE descriptors
	1 EEig09x	Eigenvalue 09 from edge adj. matrix weighted by edge degrees	edge adjacency indices
	1 B05[C-O] 1 X5Av	presence/absence of C - O at topological distance 05 average valence connectivity index chi-5	2D binary fingerprints connectivity indices
	1 HATS3p	leverage-weighted autocorrelation of lag 3 / weighted by atomic polarizabilities	GETAWAY descriptors
	1 R8u+ 1 O-060	R maximal autocorrelation of lag 8 / unweighted Al-O-Ar / Ar-O-Ar / ROR / R-O-C=X	GETAWAY descriptors atom-centred fragments
	2 B04[C-O]	presence/absence of C - O at topological distance 04	2D binary fingerprints
0r59b (23 Unique)			
	1 piPC06 1 R3u	molecular multiple path count of order 06 R autocorrelation of lag 3 / unweighted	walk and path counts GETAWAY descriptors
	1 S_sCH3	S_SCH3	atomtypes (Cerius2)
	4 B06[C-C] 1 R1e+	presence/absence of C - C at topological distance 06 R maximal autocorrelation of lag 1 / weighted by atomic Sanderson electronegativities	2D binary fingerprints GETAWAY descriptors
	1 ESpm03u	Spectral moment 03 from edge adj. matrix	edge adjacency indices
	1 EEig08d	Eigenvalue 10 from edge adj. matrix weighted by resonance integrals Eigenvalue 08 from edge adj. matrix weighted by dipole moments	edge adjacency indices edge adjacency indices
	1 E1u	1st component accessibility directional WHIM index / unweighted number of non-aromatic conjugated C(sp2)	WHIM descriptors functional group counts
	1 nCconj 1 SP13	shape profile no. 13	Randic molecular profile
	2 S_dO	S_dO Number of Hydrogen Type 49	atomtypes (Cerius2) atomtypes (Cerius2)
	1 EEig10d	Eigenvalue 10 from edge adj. matrix weighted by dipole moments	edge adjacency indices
	1 nHDon 1 R8u+	number of donor atoms for H-bonds (N and O) R maximal autocorrelation of lag 8 / unweighted	functional group counts GETAWAY descriptors
	2 0-057	phenol / enol / carboxyl OH	atom-centred fragments
	1 Mor10v 1 R5m+	3D-MoRSE - signal 10 / weighted by atomic van der Waals volumes R maximal autocorrelation of lag 5 / weighted by atomic masses	3D-MoRSE descriptors GETAWAY descriptors
	1 Mor09e	3D-MoRSE - signal 09 / weighted by atomic Sanderson electronegativities	3D-MoRSE descriptors
	1 nOHp 1 EEig09d	number of primary alcohols Eigenvalue 09 from edge adj. matrix weighted by dipole moments	functional group counts edge adjacency indices
	1 nCrs	number of ring secondary C(sp3) Spectral moment 01 from edge adj. matrix weighted by dipole moments	functional group counts edge adjacency indices

Table 2.1 Continued

Or65a (14 Unique)			
	1 F04[O-O] 2 Mor30m	frequency of O - O at topological distance 04 3D-MoRSE - signal 30 / weighted by atomic masses	2D frequency fingers 3D-MoRSE descripto
	4 Atype_H_51	Number of Hydrogen Type 51	atomtypes (Cerius2)
	1 EEig08d 2 nArOH	Eigenvalue 08 from edge adj. matrix weighted by dipole moments number of aromatic hydroxyls	edge adjacency indic functional group cou
	2 JGI7	mean topological charge index of order7	topological charge in
	1 Mor13p	number of intramolecular H-bonds (with N,O,F) 3D-MoRSE - signal 13 / weighted by atomic polarizabilities	functional group cou 3D-MoRSE descripto
	1 EEiq07d	Eigenvalue 07 from edge adj. matrix weighted by dipole moments	edge adjacency indic
		presence/absence of C - O at topological distance 06 CHR2X	2D binary fingerprint atom-centred fragme
		Eigenvalue 08 from edge adj. matrix weighted by resonance integrals presence/absence of C - O at topological distance 01	edge adjacency indic
	1 B01[C-O] 2 Mor32e	presence/absence of C - O at topological distance 01 3D-MoRSE - signal 32 / weighted by atomic Sanderson electronegativities	2D binary fingerprint 3D-MoRSE descripto
Dr67a (37 Unique)			
(i) onque)	2 AlogP98	AlogP98 value	structural (Cerius2)
	8 B04[C-O] 6 F08[C-O]	presence/absence of C - O at topological distance 04 frequency of C - O at topological distance 08	2D binary fingerprint 2D frequency fingerp
	1 GGI4	topological charge index of order 4 2nd component accessibility directional WHIM index / unweighted	topological charge in
		phenol / enol / carboxyl OH	WHIM descriptors atom-centred fragme
	1 Mor03v	3D-MoRSE - signal 03 / weighted by atomic van der Waals volumes average connectivity index chi-5	3D-MoRSE descripto
	3 Mor10v	3D-MoRSE - signal 10 / weighted by atomic van der Waals volumes	connectivity indices 3D-MoRSE descripto
		presence/absence of C - O at topological distance 03 average connectivity index chi-4	2D binary fingerprint connectivity indices
	3 nCt	number of total tertiary C(sp3)	functional group cou
	1 C-026 3 RDF075m	RCXR Radial Distribution Function - 7.5 / weighted by atomic masses	atom-centred fragm RDF descriptors
	2 C-008	CHR2X	atom-centred fragm
	2 B03[C-C] 1 B01[C-O]	presence/absence of C - C at topological distance 03 presence/absence of C - O at topological distance 01	2D binary fingerprint
	1 nRCHO	number of aldehydes (aliphatic)	2D binary fingerprin functional group cou
	1 Jhetv	Balaban-type index from van der Waals weighted distance matrix 1st component size directional WHIM index / weighted by atomic electrotopological states	topological descripto WHIM descriptors
	1 Hy	hydrophilic factor	molecular properties
		CHR3	atom-centred fragm
	1 Mor16e	Geary autocorrelation - lag 7 / weighted by atomic masses 3D-MoRSE - signal 16 / weighted by atomic Sanderson electronegativities	2D autocorrelations 3D-MoRSE descripto
	1 Mor06u	3D-MoRSE - signal 06 / unweighted Radial Distribution Function - 3.0 / weighted by atomic masses	3D-MoRSE descripto RDF descriptors
	1 Atype_C_18	Number of Carbon Type 18	atomtypes (Cerius2)
	1 F03[O-O] 1 nCrs	frequency of O - O at topological distance 03 number of ring secondary C(sp3)	2D frequency finger functional group cou
	2 nArOH	number of aromatic hydroxyls	functional group cou
	1 GATS8m 1 Jhete	Geary autocorrelation - lag 8 / weighted by atomic masses Balaban-type index from electronegativity weighted distance matrix	2D autocorrelations topological descripto
	1 EEig13x	Eigenvalue 13 from edge adj. matrix weighted by edge degrees	edge adjacency indi
		d COMMA2 value / weighted by atomic masses average connectivity index chi-3	geometrical descript connectivity indices
	1 G(NN)	sum of geometrical distances between NN 3D-MoRSE - signal 32 / unweighted	geometrical descript 3D-MoRSE descripto
	1 100 520	SC-MORSE - Signal 52 / unweighted	50-HokSE descripte
Dr67c (24 Unique)		highest eigenvalue n. 8 of Burden matrix / weighted by atomic Sanderson electronegativities	Burden eigenvalues
		alcohol 3D-MoRSE - signal 25 / weighted by atomic masses	atom-centred fragm 3D-MoRSE descripto
	1 BELv4	lowest eigenvalue n. 4 of Burden matrix / weighted by atomic van der Waals volumes	Burden eigenvalues
	3 B07[C-C]	presence/absence of C - C at topological distance 07	2D binary fingerprin
	1 TPSA(Tot) 1 DISPm	topological polar surface area using N,O,S,P polar contributions d COMMA2 value / weighted by atomic masses	molecular properties geometrical descript
	4 HATS6u	leverage-weighted autocorrelation of lag 6 / unweighted	GETAWAY descriptor
	2 EEig08d 2 EEig10d	Eigenvalue 08 from edge adj. matrix weighted by dipole moments Eigenvalue 10 from edge adj. matrix weighted by dipole moments	edge adjacency indic edge adjacency indic
	1 Gs	G total symmetry index / weighted by atomic electrotopological states	WHIM descriptors
	1 B08[C-C]	phenol / enol / carboxyl OH presence/absence of C - C at topological distance 08	atom-centred fragm 2D binary fingerprin
	1 R1m+	R maximal autocorrelation of lag 1 / weighted by atomic masses	GETAWAY descriptor
		lowest eigenvalue n. 5 of Burden matrix / weighted by atomic masses frequency of O - O at topological distance 03	Burden eigenvalues 2D frequency finger
	1 STN	spanning tree number (log)	topological descripto
	1 Atype_H_49 1 H-051	Number of Hydrogen Type 49 H attached to alpha-C	atomtypes (Cerius2) atom-centred fragm
	1 B01[C-O]	presence/absence of C - O at topological distance 01	2D binary fingerprin
	1 Infective-80 1 Hy	Ghose-Viswanadhan-Wendoloski antiinfective-like index at 80% hydrophilic factor	molecular properties molecular properties
		3D-MoRSE - signal 22 / weighted by atomic masses mean topological charge index of order7	3D-MoRSE descripto topological charge in
	1,5017		topological charge in
Dr82a (31 Unique)	1 GGI9	topological charge index of order 9	topological charge in
	1 Mor02e	3D-MoRSE - signal 02 / weighted by atomic Sanderson electronegativities	3D-MoRSE descripto
		3D-MoRSE - signal 30 / weighted by atomic van der Waals volumes 3D-MoRSE - signal 02 / weighted by atomic van der Waals volumes	3D-MoRSE descripto 3D-MoRSE descripto
	1 Mor30u	3D-MoRSE - signal 30 / unweighted	3D-MoRSE descripto
		Verhaar model of Daphnia base-line toxicity from MLOGP (mmol/l) 3D-MoRSE - signal 10 / weighted by atomic van der Waals volumes	molecular properties 3D-MoRSE descripto
	2 Atype_H_53	Number of Hydrogen Type 53	atomtypes (Cerius2)
	1 O-058 1 B02[C-O]	=0 presence/absence of C - O at topological distance 02	atom-centred fragm 2D binary fingerprin
	2 R5u+	R maximal autocorrelation of lag 5 / unweighted H autocorrelation of lag 6 / weighted by atomic Sanderson electronegativities	GETAWAY descriptor GETAWAY descriptor
	1 MATS7p	Moran autocorrelation - lag 7 / weighted by atomic polarizabilities	2D autocorrelations
	1 GATS3p	Geary autocorrelation - lag 3 / weighted by atomic polarizabilities 3D-MoRSE - signal 18 / weighted by atomic masses	2D autocorrelations 3D-MoRSE descripto
	1 H-051	H attached to alpha-C	atom-centred fragm
	2 Mor13p	3D-MoRSE - signal 13 / weighted by atomic polarizabilities structural information content (neighborhood symmetry of 2-order)	3D-MoRSE descripto information indices
	1 Mor32u	3D-MoRSE - signal 32 / unweighted	3D-MoRSE descripto
	1 Mor10m	3D-MoRSE - signal 10 / weighted by atomic masses	3D-MoRSE descripto
	1 Mor25p	number of terminal primary C(sp2) 3D-MoRSE - signal 25 / weighted by atomic polarizabilities	functional group cou 3D-MoRSE descripto
	1 GATS8m	Geary autocorrelation - lag 8 / weighted by atomic masses	2D autocorrelations
		mean topological charge index of order1 E-ADJ-mag	topological charge in topological (cerius2)
	1 EEig11x	Eigenvalue 11 from edge adj. matrix weighted by edge degrees	edge adjacency indic
	1 B03[O-O] 1 Mor30e	presence/absence of O - O at topological distance 03 3D-MoRSE - signal 30 / weighted by atomic Sanderson electronegativities	2D binary fingerprint 3D-MoRSE descripto
	1 Rotlbonds	Number of rotatable bonds	structural (Cerius2) edge adjacency indig
	1 EEig09d 2 GATS7m	Eigenvalue 09 from edge adj. matrix weighted by dipole moments Geary autocorrelation - lag 7 / weighted by atomic masses	2D autocorrelations
Dr85a (15 Unique)			
	1 EEig04r	Eigenvalue 04 from edge adj. matrix weighted by resonance integrals	edge adjacency indi

 $\begin{smallmatrix} 2 & 1 & 3 \\ 1 & 3 & 2 & 2 \\ 1 & 3 & 3 & 2 & 2 \\ 3 & 1 & 2 & 3 & 2 & 2 \\ 1 & 2 & 1 & 1 & 2 & 1 \\ 1 & 3 & 2 & 2 \\ 1 & 1 & 2 & 1 & 1 \\ 1 & 3 & 2 & 2 \\ 1 & 1 & 2 & 1 & 1 \\ 1 & 2 & 1 & 1 & 2 \\ 1 & 1 & 2 & 1 & 1 \\ 1 & 2 & 1 \\ 1 & 2 & 1 & 1$

Table 2.1 Continued

	3 ATS6e 3 JGI5	Broto-Moreau autocorrelation of a topological structure - lag 6 / weighted by atomic Sanderson electrone mean topological charge index of order5	g 2D autocorrelations topological charge indices
	2 B07[C-C]	presence/absence of C - C at topological distance 07	2D binary fingerprints
	1 nCp	number of terminal primary C(sp3)	functional group counts geometrical descriptors
	2 DISPm 2 GATS4m	d COMMA2 value / weighted by atomic masses Geary autocorrelation - lag 4 / weighted by atomic masses	2D autocorrelations
	1 Mor25p	3D-MoRSE - signal 25 / weighted by atomic polarizabilities	3D-MoRSE descriptors
	1 nHDon 1 EEig09d	number of donor atoms for H-bonds (N and O) Eigenvalue 09 from edge adj. matrix weighted by dipole moments	functional group counts edge adjacency indices
	1 R2m+	R maximal autocorrelation of lag 2 / weighted by atomic masses	GETAWAY descriptors
	1 JGI4 1 Mor11e	mean topological charge index of order4 3D-MoRSE - signal 11 / weighted by atomic Sanderson electronegativities	topological charge indices 3D-MoRSE descriptors
	2 HATS7m	leverage-weighted autocorrelation of lag 7 / weighted by atomic masses	GETAWAY descriptors
r85b (26 Unique)	1 piPC05	molecular multiple path count of order 05	walk and path counts
	1 BLTF96	Verhaar model of Fish base-line toxicity from MLOGP (mmol/I)	molecular properties
	2 GATS4p 1 GGI7	Geary autocorrelation - lag 4 / weighted by atomic polarizabilities topological charge index of order 7	2D autocorrelations topological charge indices
	3 B05[C-O]	presence/absence of C - O at topological distance 05	2D binary fingerprints
	2 O-057 1 Mor27v	phenol / enol / carboxyl OH 3D-MoRSE - signal 27 / weighted by atomic van der Waals volumes	atom-centred fragments 3D-MoRSE descriptors
	1 HATS4v	leverage-weighted autocorrelation of lag 4 / weighted by atomic van der Waals volumes	GETAWAY descriptors
	1 Gs	G total symmetry index / weighted by atomic electrotopological states	WHIM descriptors
	2 Infective-80 2 R7u+	Ghose-Viswanadhan-Wendoloski antiinfective-like index at 80% R maximal autocorrelation of lag 7 / unweighted	molecular properties GETAWAY descriptors
	2 nCbH	number of unsubstituted benzene C(sp2)	functional group counts
	1 B04[C-O] 2 JGI7	presence/absence of C - O at topological distance 04 mean topological charge index of order7	2D binary fingerprints topological charge indices
	2 DISPe	d COMMA2 value / weighted by atomic Sanderson electronegativities	geometrical descriptors
	1 R4p+	R maximal autocorrelation of lag 4 / weighted by atomic polarizabilities	GETAWAY descriptors
	1 EEig12x 1 B06[C-O]	Eigenvalue 12 from edge adj. matrix weighted by edge degrees presence/absence of C - O at topological distance 06	edge adjacency indices 2D binary fingerprints
	1 MATS5e	Moran autocorrelation - lag 5 / weighted by atomic Sanderson electronegativities	2D autocorrelations
	1 HATS4m 1 HATS6u	leverage-weighted autocorrelation of lag 4 / weighted by atomic masses leverage-weighted autocorrelation of lag 6 / unweighted	GETAWAY descriptors GETAWAY descriptors
	1 GATS4m	Geary autocorrelation - lag 4 / weighted by atomic masses	2D autocorrelations
	1 F03[O-O] 1 H8v	frequency of O - O at topological distance 03 H autocorrelation of lag 8 / weighted by atomic van der Waals volumes	2D frequency fingerprints GETAWAY descriptors
	1 EEig09d	Eigenvalue 09 from edge adj. matrix weighted by dipole moments	edge adjacency indices
	2 Mor16e	3D-MoRSE - signal 16 / weighted by atomic Sanderson electronegativities	3D-MoRSE descriptors
r85f (53 Unique)	1 BEHp8	highest eigenvalue n. 8 of Burden matrix / weighted by atomic polarizabilities	Burden eigenvalues
	5 F05[C-0]	frequency of C - O at topological distance 05	2D frequency fingerprints
	4 BELm4 1 HATS8m	lowest eigenvalue n. 4 of Burden matrix / weighted by atomic masses leverage-weighted autocorrelation of lag 8 / weighted by atomic masses	Burden eigenvalues GETAWAY descriptors
	2 B04[C-O]	presence/absence of C - O at topological distance 04	2D binary fingerprints
	6 O-057 1 RDF030v	phenol / enol / carboxyl OH Radial Distribution Function - 3.0 / weighted by atomic van der Waals volumes	atom-centred fragments RDF descriptors
	1 GGI7	topological charge index of order 7	topological charge indices
	1 Gs	G total symmetry index / weighted by atomic electrotopological states presence/absence of C - C at topological distance 07	WHIM descriptors 2D binary fingerprints
	4 B07[C-C] 1 E2e	2nd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities	WHIM descriptors
	1 MATS2m	Moran autocorrelation - lag 2 / weighted by atomic masses	2D autocorrelations
	2 Mor28u 3 BEHp5	3D-MoRSE - signal 28 / unweighted highest eigenvalue n. 5 of Burden matrix / weighted by atomic polarizabilities	3D-MoRSE descriptors Burden eigenvalues
	2 Infective-80	Ghose-Viswanadhan-Wendoloski antiinfective-like index at 80%	molecular properties
	1 HATS4e 3 JGI6	leverage-weighted autocorrelation of lag 4 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors topological charge indices
	6 B05[C-O]	mean topological charge index of order6 presence/absence of C - O at topological distance 05	2D binary fingerprints
	2 JGI7	mean topological charge index of order7	topological charge indices
	2 DISPm 5 RDF030m	d COMMA2 value / weighted by atomic masses Radial Distribution Function - 3.0 / weighted by atomic masses	geometrical descriptors RDF descriptors
	1 R1e+	R maximal autocorrelation of lag 1 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors
	1 HATS8p	leverage-weighted autocorrelation of lag 8 / weighted by atomic polarizabilities	GETAWAY descriptors
	1 Atype_H_49 2 Hy	Number of Hydrogen Type 49 hydrophilic factor	atomtypes (Cerius2) molecular properties
	1 Jhetp	Balaban-type index from polarizability weighted distance matrix	topological descriptors
	1 H8v 2 EEig11d	H autocorrelation of lag 8 / weighted by atomic van der Waals volumes Eigenvalue 11 from edge adj. matrix weighted by dipole moments	GETAWAY descriptors edge adjacency indices
	1 MATS8m	Moran autocorrelation - lag 8 / weighted by atomic masses	2D autocorrelations
	1 MATS2p 4 B08[C-C]	Moran autocorrelation - lag 2 / weighted by atomic polarizabilities presence/absence of C - C at topological distance 08	2D autocorrelations 2D binary fingerprints
	1 S_sCH3	S_sCH3	atomtypes (Cerius2)
	2 HATS1e	leverage-weighted autocorrelation of lag 1 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors
	1 nCconj 1 B04[C-C]	number of non-aromatic conjugated C(sp2) presence/absence of C - C at topological distance 04	functional group counts 2D binary fingerprints
	1 S_aasC	S_aasC	atomtypes (cerius2)
	1 R8m+ 1 nRCOOH	R maximal autocorrelation of lag 8 / weighted by atomic masses number of carboxylic acids (aliphatic)	GETAWAY descriptors functional group counts
	1 S_sOH	S_SOH	atomtypes (Cerius2)
	1 BELe3 1 GATS8m	lowest eigenvalue n. 3 of Burden matrix / weighted by atomic Sanderson electronegativities	Burden eigenvalues
	1 GATS8m 1 BEHp4	Geary autocorrelation - lag 8 / weighted by atomic masses highest eigenvalue n. 4 of Burden matrix / weighted by atomic polarizabilities	2D autocorrelations Burden eigenvalues
	2 MATS5e	Moran autocorrelation - lag 5 / weighted by atomic Sanderson electronegativities	2D autocorrelations
	1 E3s 2 Jhetv	3rd component accessibility directional WHIM index / weighted by atomic electrotopological states Balaban-type index from van der Waals weighted distance matrix	WHIM descriptors topological descriptors
	1 nR=Ct	number of aliphatic tertiary C(sp2)	functional group counts
	1 nRCHO 1 HATS8v	number of aldehydes (aliphatic)	functional group counts GETAWAY descriptors
	1 Mor28p	leverage-weighted autocorrelation of lag 8 / weighted by atomic van der Waals volumes 3D-MoRSE - signal 28 / weighted by atomic polarizabilities	3D-MoRSE descriptors
	1 C-003	CHR3	atom-centred fragments
	1 GATS7m 1 JGI9	Geary autocorrelation - lag 7 / weighted by atomic masses mean topological charge index of order9	2D autocorrelations topological charge indices
	1 B03[C-C]	presence/absence of C - C at topological distance 03	2D binary fingerprints
9r88a (19 Unique)	3 nHBonds	number of intramolecular H-bonds (with N,O,F)	functional group counts
	2 nRCO	number of ketones (aliphatic)	functional group counts
	3 GATS6m 2 EEig08x	Geary autocorrelation - lag 6 / weighted by atomic masses Eigenvalue 08 from edge adj. matrix weighted by edge degrees	2D autocorrelations edge adjacency indices
	1 nFuranes	number of Furanes	functional group counts
	1 nArCO 1 ESpm15d	number of ketones (aromatic) Spectral moment 15 from edge adj. matrix weighted by dipole moments	functional group counts edge adjacency indices
1	1 C-005	СНЗХ	edge adjacency indices atom-centred fragments
	1 0-057	phenol / enol / carboxyl OH	atom-centred fragments
	1 L/Bw 1 nArCOOR	length-to-breadth ratio by WHIM number of esters (aromatic)	geometrical descriptors functional group counts
		Spectral moment 15 from edge adj. matrix	edge adjacency indices
	1 ESpm15u 1 E2u	2nd component accessibility directional WHIM index / unweighted	WHIM descriptors
	1 ESpm15u 1 E2u 1 EEig08d	2nd component accessibility directional WHIM index / unweighted Eigenvalue 08 from edge adj. matrix weighted by dipole moments	WHIM descriptors edge adjacency indices
	1 ESpm15u 1 E2u 1 EEig08d 1 H-051 1 ESpm14d	2nd component accessibility directional WHIM index / unweighted Eigenvalue 08 from dega adj. matrix weighted by dipole moments H attached to alpha-C Spectral moment 14 from edge adj. matrix weighted by dipole moments	WHIM descriptors edge adjacency indices atom-centred fragments edge adjacency indices
	1 ESpm15u 1 E2u 1 EEig08d 1 H-051	2nd component accessibility directional WHIM index / unweighted Eigenvalue 08 from edge adj. matrix weighted by dipole moments H attached to alpha-C	WHIM descriptors edge adjacency indices atom-centred fragments

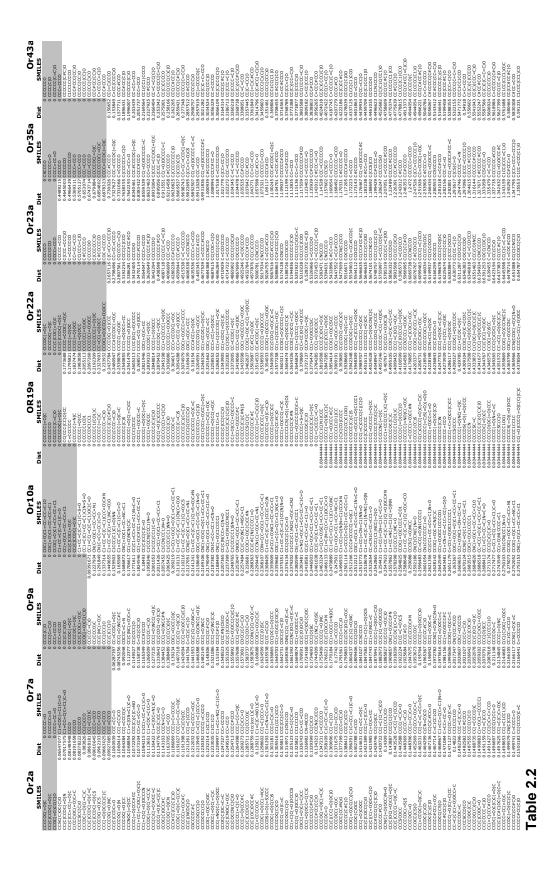
Table 2.1 Continued

Or98a (20 Unique)				I I
	1 Lop	Lopping centric index	topological descriptors	2
	4 0-057	phenol / enol / carboxyl OH	atom-centred fragments	1
	2 B04[C-0]	presence/absence of C - O at topological distance 04	2D binary fingerprints	2
	1 GVWAI-80	Ghose-Viswanadhan-Wendoloski drug-like index at 80%	molecular properties	1
	1 HATS7p	leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities	GETAWAY descriptors	3
	1 HATS5v	leverage-weighted autocorrelation of lag 5 / weighted by atomic van der Waals volumes	GETAWAY descriptors	3
	1 MLOGP2	Squared Moriguchi octanol-water partition coeff. (logP^2)	molecular properties	1
	2 GATS5e	Geary autocorrelation - lag 5 / weighted by atomic Sanderson electronegativities	2D autocorrelations	2
	1 H-049	H attached to C3(sp3)/C2(sp2)/C3(sp2)/C3(sp)	atom-centred fragments	1
	1 MATS8m	Moran autocorrelation - lag 8 / weighted by atomic masses	2D autocorrelations	2
	1 nCrs	number of ring secondary C(sp3)	functional group counts	1
	3 HATS3p	leverage-weighted autocorrelation of lag 3 / weighted by atomic polarizabilities	GETAWAY descriptors	3
	1 G1s	1st component symmetry directional WHIM index / weighted by atomic electrotopological states	WHIM descriptors	3
	1 S_aasC	S_aasC	atomtypes (Cerius2)	1
	1 SP18	shape profile no. 18	Randic molecular profiles	3
	1 B05[C-C]	presence/absence of C - C at topological distance 05	2D binary fingerprints	2
	1 JGI2	mean topological charge index of order2	topological charge indices	2
	1 JGI8	mean topological charge index of order8	topological charge indices	2
	1 X4A	average connectivity index chi-4	connectivity indices	2
	1 H5e	H autocorrelation of lag 5 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors	3

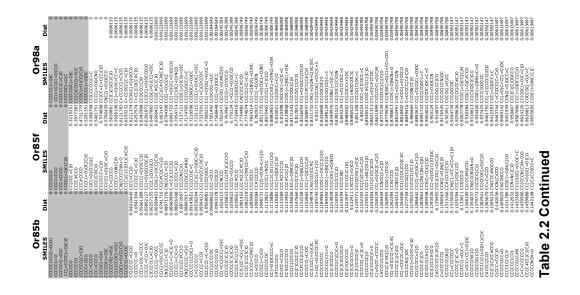
Table 2.1 Continued

Table 2.2: Top 100 predicted compounds for each Drosophila Or

Chemical name or Pubchem compound ID (CIDs), SMILES strings, and distances, of the top ~100 predicted compounds for each Or. All distances represent the minimum distance based on optimized descriptors to the previously known strongest active compound listed in the gray cells for that particular Or.



Dist D
Dist Status Control of
 Dist Bart Bart Bart Bart Bart Bart Bart Bar
Dist Structure of the second s
Dist Barbandi Barband
Dist Description of the second
OFAGE CHAGE 1011 SMILES 2012 SMILES 2013 SMILES 2014 SMILES 2015 SMILES 2016 SMILES 2017 SMILES 2018 SMILES 2019 SMILES 2010 SMILES 2010 SMILES 2011 SMILES 2011 SMILES 2012 SMILES 2013 SMILES 2014 SMILES 2015 SMILES 2015 SMILES 2016 SMILES 2017 SMILES 2018 SMILES 2018 SMILES 2018 SMILES 2018 SMILES 2019
bit shures and a straight and a stra
Dist State of the second secon
Or43a



CHAPTER III:

Applying Chemical Informatics to Decode Odor Receptors of Several Important Disease Vector and Pest Insect Species as Well as Mammals

INTRODUCTION

Olfaction is exceedingly important for a broad array of species living in all ecological regions of this planet (van Naters and Carlson, 2006). While a major effort has been made by the scientific community to decode and analyze Olfactory receptors (Ors) in *Drosophila* over the last decade, there remains a vast number of important pest and disease vector species for which very little is known. Very recently, odor receptors of several high priority pest and disease vector species have been the focus of investigation (Carey et al., 2010; Ditzen et al., 2008; Ghaninia et al., 2007; Hill et al., 2009; Stanczyk et al., 2010; Syed and Leal, 2008; Turner et al., 2011). Olfactory receptors (Ors) or Odor Receptor Neurons (ORNs) in these species are being tested against relatively small panels of odors in an attempt to decode their response profiles. While these panels are limited in size and scope, they do generally consist of multiple functional groups and carbon chain lengths and often a number of odors in the panels were selected for their ecological significance. Humanity could greatly benefit from the identification of highly effective, safe, and receptor-specific odors for these species, ideally a number of which will prove to be behavior modifiers. We demonstrate that our chemical informatics pipeline can be applied to predict active odors for 5 important species.

Anopheles gambiae is the principle disease vector for malaria, which is a devastating disease in many parts of the world, including South America, Africa, India,

and Asia (World Health Organization., 2011). Malaria symptoms include vomiting, retinal damage, anemia, joint pain, convulsions and in some cases coma and death. The World Health Organization (WHO) estimated 216 million episodes of malaria in 2010, resulting in over 655,000 deaths (World Health Organization., 2011). While these numbers do represent a reduction in the incidence of malaria from previous years. growing resistances to current treatments and repellents have been identified. It is estimated that over 2 billion dollars were spent on financing malaria control in 2011, with higher predictions for future years if global control targets are to be achieved. To further complicate matters, current preventative medications are too expensive for widespread use in developing countries. Identification of safer odors with better organoleptic properties that activate or inhibit behaviorally important Ors, such as those used for detection of human hosts, could greatly aid in the global fight against vector-borne diseases, such as malaria. Recently, 110 odors were tested against 50 Anopheles gambiae Ors using the "empty neuron" expression system, resulting in newly identified activators and inhibitors (Carey et al., 2010). The 110 compound set consisted of an array of functional groups and sizes, providing a wonderful training set for our computational pipeline.

In addition to *Anopheles* Or responses, we are also interested in predicting odors for the CO₂ receptors of several important species. CO₂ is a primary long-range detection cue that mosquitoes use to identify and navigate towards their blood meal (Gillies, 1980; Grant and Oconnell, 1996). By navigating upstream in CO₂ plumes, mosquitoes are able to identify hosts at long ranges with high effectiveness (Carde and Gibson, 2010; Zwiebel and Takken, 2004). It is believed that other important attractive odors play additional roles in more specific host preference once the mosquito is in close

range (Gillies, 1980; Takken, 1996). As the CO_2 receptor is behaviorally very important, it is not surprising that the genes are conserved across mosquito species including *Anopheles gambiae*, *Aedes aegypti*, and *Culex pipiens*, all of which express a CO_2 receptor in the cpA neuron on the antenna. Interestingly, CO_2 detection is even important in *Drosophila*, which are able to detect CO_2 through gustatory receptors in their ab1C ORN (Turner and Ray, 2009). While no large unified panel of odors has been tested on the CO_2 neuron of the previously mentioned 3 species of mosquito and *Drosophila*, a number of smaller panels have been tested across each and a small panel was tested across all 4 (Turner et al., 2011; Turner and Ray, 2009). As the response profiles for the receptor across species appears to be at least moderately conserved, we integrate the responses of all species into a single unified odor response set, which we use to train our prediction pipeline.

The Asian Citrus Psyllid (ACP), *Diaphorina citri* Kuwayama, is posing a major challenge to the global citrus industry. While originally present only in Asia, this insect has recently invaded North America, including both Florida and Southern California (Halbert and Manjunath, 2004)(http://www.californiacitrusthreat.com/). While the insect itself does not cause major damage to citrus trees, the ACP is a vector for the bacterial disease Huanglongbing (HLB), also known as the Citrus Greening Disease, caused by *Candidatus* Liberobacter (Bove, 2006; Dagraca, 1991). If infected, the resulting HLB causes a chronic decline in fruit production. The limited fruit that is produced is often small, misshapen and bitter (Baldwin et al., 2010; Bove, 2006). Unfortunately, there is currently no cure for a tree once it is infected. Several attempts have been made to repel the insect, with limited success, or to super nutrient infected orange trees, which is ultimately not cost effective as a long-term solution (Onagbola et al., 2011). Recently,

our lab has decoded ORNs in the ACP antenna against a panel of 62 odors, several of which are known citrus vegetative volatiles (unpublished data). Each of these odors in the rhinarial plates on each segment of the antenna, identifying ORNs on rhinarial plates 2, 4, 6, and 7. Each rhinarial plate appears to house 3 ORNs, which have been labeled A, B, and C in decreasing order of spike amplitude. While very few ligands for the A neurons have been identified, a number of activators for the B and C neurons in each plate have been classified. If we can identify inexpensive, safe, and effective activators and inhibitors of these ORNs, a number of which will hopefully be attractants and repellents, the citrus industry can apply them as lures for surveillance and repellents to curtail the progressing ACP population, thus stopping the spread of HLB. We use these odors as our training set to predict additional ACP Or activating odors.

Insect and mammalian Ors are functionally distinct from one another. Insect Or proteins are considered to be 7-transmembrane proteins that have a non-traditional inside-out membrane orientation. They are believed to function as ligand-gated ion channels and form a heteromer with an obligate partner Orco, which is required for function (Benton et al., 2006; Sato et al., 2008). Mammalian odor receptors on the other hand are G-protein coupled receptors with a traditional outside-in 7-transmembrane orientation (Zhang and Firestein, 2002). Additionally, Mammals have far larger families of odor receptors (~1000 in mice, ~350 in humans) and thus pose an even greater challenge to examine odor coding (Saito et al., 2009; Saito et al., 2004). These distinctions provide an additional challenge for our ligand discovery pipeline. While our method is highly effective for insect Ors, we now have the opportunity to predict odors for functionally distinct mammalian receptors. 52 mouse and 10 human ORs were recently decoded using panel of 63 odorants. Unlike the previous analyses, these

receptors were decoded using calcium imaging and are reported as concentration required for 50 percent effectiveness (EC50). If successful, predictions for these receptors both demonstrate the breadth of our pipline and provide a tool that would allow the fragrance industry to identify natural and pre-approved odors that activate specific human odor receptors, providing the possibility of truly tailor made fragrances.

In this chapter we apply our cheminformatics platform to predict activators and inhibitors for *Anopheles* Ors, the mosquito CO₂ receptor, Asian Citrus Psyllid ORNs, Mouse ORs, and Human ORs. Computational validations are performed in all instances, and electrophysiological validations are performed for both the *Anopheles* Ors and CO₂ receptor predictions, demonstrating that our chemical informatics approach can be successfully applied in each of the 5 species. A comparative analysis of predicted receptor-odor relationships between *Drosophila* and mammals is also performed, where interesting properties are uncovered. Most importantly, thousands of new odors are identified for over a hundred odor receptors.

RESULTS

Predictions for Anopheles gambiae Odor Receptors

Or tuning of previously identified Anpheles receptor-odor interactions

The tuning of the 50 previously tested *Anopheles gambiae* Ors is distinctly different from what was observed in Drosophila (Allison 2011, Hallem 2006). Activating odors (>50 spikes/sec) for 21 out of 24 Drosophila Ors expressed in the antenna were identified. By contrast, activators for only 35 out of 50 were identified for Anopheles. For the 15 Ors that remained, an average of 64% of tested odors were inhibitors. This differs sharply from the other Ors of both Anopheles and Drosophila, where on average only 30% and 28% of tested odors reduced the activity of Ors below spontaneous respectively. Based on the limited training set there are two hypotheses that can explain this distinction. While it is possibly that the true odors for these receptors have not yet been identified, an alternative explanation could be that these receptors are specifically tuned for inhibition. As a result, we have divided the Anopheles Ors into 3 different classes, each of which we individually apply the chemical informatics platform to, predicting receptor-odor interactions for the following three classes: Activating (Or57, Or12, Or50 ,Or38 ,Or56 ,Or21 ,Or20 ,Or18 ,Or4 ,Or75 ,Or11 ,Or15 ,Or39 ,Or48, Or46, Or30, Or9, Or13, Or1, Or10, Or6, Or2, and Or8), no strong activators (Or32, Or26, Or53, Or16, Or64, Or31, Or27, Or65, Or59, Or63, and Or61), and Inhibitory receptors (Or35, Or25, Or3, Or76, Or44, Or66, Or43, Or54, OR67, Or42, Or41, Or33, and Or45).

Chemical Informatics can successfully explain Anopheles receptor-odor activity

It is the molecular structures and properties of odors that determine their activity against an Or. As a result, we have designed a chemical informatics pipeline to identify which structural features are important for the activity of odors for individual Ors and have applied these features to predict the activity of the Or to a large set of untested chemicals, as we have previously done for Drosophila (Figure 3.1). A single 3D structure was calculated for each of the odors using the Omega software package (See Methods)(Hawkins et al., 2010). We calculated molecular descriptors, which are mathematical values that describe the structure and features of a molecule, from the 3D conformations to quantitatively explain the odor structures. Dragon (Talete) and Cerius2 (Accelrys), which are commercially available software suites, was applied to calculate 3,424 molecular descriptors for each compound tested against an Anopheles Or. We then applied a Sequential Forward Selection (SFS) approach to identify which of the molecular descriptors were most highly correlated with activity, resulting in a single subset of descriptors that describe the activity of the training odors against a single Or (See Methods) (Whitney, 1971). While descriptors for Ors classified as activating or fishing "no strong activators" were selected for their ability to describe activation, descriptors for Ors classified as inhibitory were selected for their ability to describe inhibition.

As observed in *Drosophila*, our approach was able to successfully identify molecular descriptors for each *Anopheles* Or that were highly correlated with activity (Table 3.1). We then applied each Ors optimized descriptors to cluster the training odors in order to visualize how well these descriptors grouped the activating or inhibitory odors (Figure 3.2). We find that our approach is able to successfully cluster together odors

tested against Ors for all three classes. While we had observed similar results in our *Drosophila* predictions, this was the first application of our approach to structurally classify inhibition. Inhibitory odors for the majority of Ors were successfully clustered together using optimized structural features. As inhibition can happen both allostericly and competitively, these results pose two interesting hypothesies. Firstly, the very tight clustering for all inhibitory odors observed for several of the Ors could signify competitive or allosteric inhibition in a single pocket. Secondly, the broader clustering of inhibitory odors observed for several of the Ors could signify an imperfect selection of descriptors.

Predicting receptor-odor interactions

We next applied our approach to predict the activity of the Ors to a large untested odor panel. Our panel consisted of two odor libraries (See Methods). One panel was a natural odor library containing 3,197 odors emitted by plants, flowers, insects, and mammals. The second was large library of Pubchem odors containing over 240,000 compounds with similar molecular weight (<200) and atom type compositions to those found in nature. We ranked the activity of each compound from both libraries using each of the receptor-optimized descriptor sets, resulting in individual rankings for each Or (See Methods). We list odors from the natural odor library that were ranked in the top 500 predictions for each Or (Table 3.2)

Validating predicted receptor-odor interactions using single unit

electrophysiology

Several inexpensive and easily obtainable odors were selected from the natural odor prediction lists of 12 Anopheles Ors for experimental validation. Members of Dr. John Carlson's lab at Yale performed the experimental validations using single unit electrophysiology. Each Anopheles Or gene to be validated along with the obligate coreceptor was heterologously expressed in the empty neuron system in Drosophila (Carey et al., 2010; Dobritsa et al., 2003). As this was the same group that created the initial training set using the same experimental procedure, the validations are expected to be highly accurate. A total of 129 receptor-odor interactions were tested across 12 Ors. On average 65 percent of predicted odors activated the Ors (>50 spikes/sec) (Table 3.3). While this is lower than the 71% we had observed for our Drosophila predictions, it is still far better than the average activation rate of 16% that was observed across the Ors from our training set. In Drosophila, we had observed that our computational pipeline was more accurate at predicting odors for Ors that respond primarily to aliphatic rather than aromatic compounds. We again see this trend for Anopheles, with primarily aliphatic responsive Ors having a high accuracy of 84%, whereas aromatic responsive Ors have a relatively low accuracy of 38%.

Increasing the number of aromatic odors in the training set

In *Drosophila* we had hypothesized that our low aromatic prediction accuracy could be due to a lack of aromatic odors in the training set (Hallem and Carlson, 2006). In order to test this hypothesis in *Anopheles*, we increased the size of our aromatic training set by testing a broad panel of aromatic odors. Ideally, we wanted to test as

broad a set of aromatic compounds as possible, providing the largest amount of information on what aromatic structures are or are not active to our computational pipeline for training. As testing odors for activity is a time intensive and expensive process, we applied chemical informatics to select the most structurally diverse set of aromatic odors for testing. Beginning with all 306 aromatic compounds available in the laboratory of Dr. John Carlson, we applied all 3,224 Dragon descriptors to cluster the 306 odors, producing a cluster derived from non-optimized and broad features. We used the dendrogram to select the 75 most diverse aromatic odors (Figure 3.3). Interestingly, the tree is divided into two main branches with small single ring aromatics being in the left subcluster and large multi ring aromatics residing in the right. The Carlson lab then tested 37 of these diverse odors on the primarily aromatic responsive Or2, Or6, and Or10 using electrophysiology. As expected, only a small percentage (9%) of this structurally broad array of 37 aromatic odors activated the Ors (Table 3.4). Interestingly, this number is similar to the random activation chance observed both for *Drosophila* (10%) and in *Anopheles* (16%).

Predicting receptor-odor interactions using our expanded aromatic training set

We applied our ligand prediction pipeline for Or2, Or6, and Or10, using the original 109 odors, odors validated during the initial round of testing, and the newly tested 37 aromatic odors for training, and optimizing descriptor sets for each of the three receptors. (Table 3.5). Since only 29 of the 109 odors in the original training set were aromatics, the inclusion of the additional 37 odors more than doubled the number of aromatics. This large expansion in size, combined with being a very broad array of structural features, increased the challenge of descriptor selection for our pipeline, as

descriptors that once completely separated active from inactive aromatics now resulted in imperfect classification. Additionally, only 22% of the original molecular descriptors are present in the newly optimized sets and the mean number of descriptors per Or has increased from 21 to 30 for these three receptors, further indicating inclusion of the new aromatics into the training set has increased the complexity of the system.

When we cluster the training odors using the optimized descriptors we find that the descriptor sets are successful in clustering training odors (Figure 3.4). Nearly all activating odors are clustered tightly together for Or2, Or6, and Or10. In order to further validate the predictive ability for these three receptors we performed a 5-fold cross validation as was performed for *Drosophila* (See Methods) (Hastie et al., 2001; Tan et al., 2006). The training sets for each Or were divided into 5 equal partitions. One partition was withheld as a test set while the remaining 4 were used to optimize descriptors. The predictive ability of the system was assessed by performing a Receiver Operating Characteristic (ROC) analysis on the withheld test set. This process was repeated 5 times where each of the 5 partitions was used as the test set once. The whole process was repeated 5 times to improve accuracy. A single mean ROC curve was plotted for each Or and an Area Under the Curve (AUC) was calculated (Figure Figure 3.5). We find that the average AUC value across the three receptors was 0.832, which is very close to the value of 0.815 that we observed in *Drosophila*, suggesting that our approach should show similar effectiveness to what we saw in that species.

We applied the newly determined optimized descriptor sets to rank both the Pubchem and Natural odor libraries (Table 3.6). The three prediction lists are quite different from those previously calculated. The next stage will be to validate these predictions using single-unit electrophysiology.

Predicting receptor-odor interactions using machine learning

In order to improve predictive ability we integrated a Support Vector Machine (SVM), which is a well-known and widely applied machine learning approach (Cortes and Vapnik, 1995), into our prediction pipeline (Figure 3.6). We train the SVM using previously determined optimized descriptor set values for Or2, Or6, and Or10 (See Methods Chapter). The trained SVM is then applied to predict the activity of odors from both the Pubchem and Natural Odor libraries. While we have not yet performed electrophysiological validation of our predictions, we have performed a 5-fold cross validation with the SVM, observing far higher AUC values (Figure 3.7). The mean AUC value of 0.988 is far higher than that of the previous value of 0.832 when SVMs were not applied, suggesting that the approach may be highly successful in predicting activating aromatic compounds for these three receptors.

Identifying safer alternative activators with better organoleptic profiles

One target of our approach is to predict odors from a large library of natural odors, many of which are already approved for use in food and/or fragrances. We compare the organoleptic properties of our newly identified activating odors vs those previously identified and discover that odors from our natural odor library have more favorable profiles for several receptors. For example, we have identified new activators for AgOr8, which is believed to be important for host identification through activation by 1-octen-3-ol, that smell more pleasant to the human nose than those previously known. Previously known activators included 3-octanone, 1-octen-3-ol, and 2-heptanone, the first two of which have been described as smelling either moldy or fungal at high

concentrations (www.thegoodscentscompany.com). 2-heptanone is described as fruity, spicy, or woody, however it is also listed as having a high odor strength resulting in a suggested smelling concentration of 10% or less. Our identified compound 2-Heptanol activates the receptor equally as strongly, is described as smelling like fresh lemon grass, and only has a medium odor strength allowing for a pleasant odor experience even at concentrations as high as 100%. Using our approach it becomes possible to easily explore the organoleptic properties of predicted odors, providing a way to select lures and repellent odors based upon their safety profiles and pleasant aroma.

Predictions for CO₂ receptors in a broad range of species

Integrating response profiles to CO₂ from multiple insect species

The olfactory receptors of insects are highly divergent and very little information can be gained from comparing the full-length sequences of Ors between species. As a result of this divergence, we are very rarely able to compare the response profiles of Ors across species. However, the CO₂ receptor is extremely important in many insect species for host detection or predator avoidance, providing a rare case where receptor response profiles are moderately retained across species. The CO₂ receptor of 3 mosquito species as well as *Drosophila* have recently been identified and exposed to panels of odors (Jones et al., 2007; Kwon et al., 2007; Lu et al., 2007; Turner et al., 2011; Turner and Ray, 2009). While several odors were unique to testing in a single species, a panel of 29 odors was tested across all four species. The response profiles of overlapping odors appear in general similar, suggesting the possibility for pooling the responses of the 4 species into a single metric of CO₂ receptor activity.

We wanted our metric to consider the responses of multiple species for odors where more than one species had been tested, however since responses to some odors were significantly lower in one species than the others, we decided upon selection based on customized criteria. We averaged the two highest activity values for each odor that had been tested on more than 1 species, resulting in a metric that was influenced by multiple species, yet not unfavorably reduced by low activity outliers. The resulting activity values were used as our training set for the remainder of our CO_2 analysis.

The resulting training set contained a large variety of odor structures including both aromatic and aliphatic activators. Visual inspection revealed there were two distinct structural classes of known activating odors (aromatic and aliphatic) and one for inhibiting odors. As we have both recognized the challenges posed in describing aromatic compounds in our analyses of *Drosophila* and *Anopheles* Ors and considered that these two structurally distinct classes of odors may bind in distinct pockets on the receptor, we decided to separate our training odors into three groups with different predictive aims: aromatic ligands, structurally diverse ligands, and aliphatic ligands (Table 3.7). Our aromatic set focused on screening for highly active and aromatic structures and did not consider inhibitors. Our Broad activator screen focused on structurally diverse ligands and tested all previously tested odors including both activators and inhibitors. Finally, we performed an inhibition screen to identify CO₂ receptor inhibitors, where we only considered inhibitory or inactive odors and did not include activators.

Chemical Informatics can successfully explain CO₂ receptor-odor activity

We once again applied our chemical informatics pipeline to predict active odors, in this instance predicting activators and inhibitors for the CO₂ receptor (Figure 3.8). We again calculated a single 3D structure using Omega software (Hawkins et al., 2010) and calculated 3,224 molecular descriptors using Dragon (Talete) for each odor from all three training sets. We then implement our computational pipeline to identify a subset of the 3,224 molecular descriptors that are most important for activity in each of the training sets through application of a Sequential Forward Selection (SFS) method (Whitney, 1971). This method identifies molecular descriptors that are the most highly correlated with odor activity by incrementally building a best descriptor set, which involves adding a single molecular descriptor at a time until the correlation ceases to increase (See Methods Chapter VII). We applied this process independently for each of the training sets, resulting in three uniquely optimized molecular descriptor sets (Tables 3.8, 3.9, 3.10).

While there were many important 2D and 3D descriptors selected for all three of the training sets, several more intuitive 0D and 1D descriptors were selected as well. Chiefly, the number of non-terminal nitrogen atoms and number of aldehydes were important for the aromatic activator training set, the number of aldehydes, presence of a carbon-oxygen bond 6 atoms apart and number of donor atoms for H-bonds were important for the broad activator training set, and the presence of a carbon and oxygen atoms 3 atoms apart, number of aliphatic secondary carbons, presence of carbon and carbon atoms 6 atoms apart, and absence of ring secondary carbons were important for the broad activator set was the smallest, containing 11 descriptors, and the broad activator set was the largest with 27.

We clustered each of the training odors by the values of their previously determined optimized descriptor sets in order to visualize how well each descriptor set groups activating or inhibiting odors (Figure 3.9). We observed odors of interest are grouped tightly together for all three training sets, supporting that the optimized descriptors do indeed explain odor activity.

Predicting the response of the CO₂ receptor to a broad panel of untested odors

We next applied the optimized descriptor sets to computationally rank two large libraries of untested odors. We assembled both eMolecules and natural odor libraries containing over 440,000 and 3,197 odors, respectively (See Methods Chater VII). The eMolecules library contains all chemicals from the eMolecules library of similar molecular weight (<350 MW) and atom type compositions (C, O, N, H, I, CI, S, F) of known volatile odors. The Natural Odor library contained 3,197 odors of identified floral, vegetative, insect, or mammalian origins. We ranked each odor from both libraries based on their similarity to known activators using the previously determined optimized descriptor sets, resulting in three independent rankings, one for each training set (See Methods Chater VII). We provide the top 60 predictions for each of the training sets (Table 3.11).

Many predictions validated as either activators or inhibitors of the CO₂ receptor

Electrophysiological tests were conducted by collaborator Dr. Dyan McWilliams for 139 predicted ligands originating from the three prediction lists, that were considered reasonably safe for human use. Each predicted odor was individually tested for activity using single unit electrophysiology on the *Aedes aegypti* CpA neuron, resulting in identification of many new actives for the CO₂ responsive neuron. We observed a broad

range of activity for our validated odors, including both activators and inhibitors (Table 3.12).

In our initial observation we noticed that far fewer (18%) of our predicted CO_2 odors activated the receptor at the threshold (>50 spikes/sec) previously applied for both *Drosophila* (58%) and *Anopheles* (65%) (Table 3.21). As previously described the CO_2 receptor is actually a gustatory receptor, which are believed to function uniquely from Ors. Additionally, the strongest identified activator (143 spikes/sec) for this receptor from either our large screen or any previous screen, which encompasses the responses of over 200 odors, activates significantly lower (~44%) than those observed in either *Drosophila* or *Anopheles* Ors (~250 spikes/sec), leading us to hypothesize that these Gr structured CO_2 receptors may be tuned uniquely from general Ors. As a result we have lowered our activity threshold from 50 spikes/sec to 30 spikes/sec, which loosely relates to the 44% reduction observed from the strongest known activators of other insect species to those observed for the CO_2 receptor. Even with this threshold reduction we observe that only 30% of compounds activated the CO_2 receptor at greater than or equal to 30 spikes/sec.

Interestingly, CO_2 responsive neurons in mosquitoes do not appear to have a spontaneous activity, responding only to the quantity of CO_2 present in the environment, which vary slightly depending on how many people have been in the electrophysiology room that day. As a result, we tested for inhibition by overlaying odors on a 0.15% CO_2 pulse, which on average activates the receptor at 100 spikes/sec, providing a standardized metric by which to compare inhibitory odors. We observed a similar number of tested odors inhibited the CO_2 neruon (18%) as we had observed in *Drosophila*.

In addition to CO₂ receptor structure/function differences, we also must take account of the noise introduced by the multi-species integrated training odor set. As there were no large unified odor panels tested on a single species, we integrated the responses of similarly responding CO₂ receptors for 4 insect species. While this challenge did pose a very interesting intellectual question of whether ligand structural similarity can be compared across species for similarly tuned receptors, it undoubtedly will reduce the accuracy compared to when training is performed on responses of only a single species. Considering these additive challenges, we feel our computational approach was successful in predicting ligands.

Active predicted odors appear to target up to three distinct binding pockets

We next analyzed the structures of our predicted odors that validated as actives. Interestingly, from visual inspection of their structures it appeared the odors could be structurally diverse enough to be acting on distinct binding pockets. In order to identify whether ligands fall into diverse structural classes that could potentially bind to distinct active sites on the receptor, we clustered all activating (>30 spikes/sec) and strongly inhibiting (<-10 spikes/sec) odors. We concatenated all molecular descriptors from each of the three distinct optimized descriptor sets, which we had individually optimized to predict ligands with unique characteristics, creating a single set of optimized descriptors explaining both activation and inhibition of the CO_2 receptor. We then applied hierarchical clustering to organize odor relationships based on the Euclidean distances between odors based on each odors optimized descriptor values (Figures 3.10, 3.11).

The resulting tree had three distinct branches or clusters, each of which contains structurally distinct odor classes. Cluster 1 contains only aliphatic odors that have a

variety of functional groups including aldehydes, ketones, alcohols, and esters. With the exception of the few alcohols, which are H-bond donors, nearly all compounds in this cluster contain an H-bond acceptor group. Cluster 2 contains pyrazine based heterocycles with a variety of small branched side chains. Lastly, cluster 3 contains both small 5 and 6 member non-aromatic cyclic compounds and aromatics.

We hypothesize that each of these three odor classes bind to distinct regions in the CO_2 receptors. As the structures of the CO_2 receptors have not been solved, we can only hypothesize on whether or not they bind to distinct regions, however it is very curious as to whether these distinct structures bind in entirely different protein regions, or to distinct regions in the same binding pocket, or whether the binding pockets of Ors are highly variable, accepting a very wide variety of shapes and sizes.

Interestingly, inhibitory and activating odors are interspersed across sub clusters. While the largest grouping of inhibitors occurs for cluster 2, there are strongly inhibiting odors distinctly residing in both clusters 1 and 3. In the same fashion activating odors exist in all three clusters. If three distinct binding regions do indeed exist within the CO_2 receptors, this would mean that we have identified site selective activators and inhibitors for all three.

It will be interesting to test the proposed three distinct binding region hypothesis by creating odor blends containing odors from each of the clusters. In theory, if these odors do function through distinct binding sites, exposure of a CO₂ receptor to odors from multiple clusters should provide a stronger response than similarly strong odors from within a single cluster, as binding in distinct regions at the same time should further stabilize the active conformation. This can be tested using single unit electrophysiology.

We also plan to test the strongest activating and inhibiting odors from behavioral response. Since we predicted ligands from a large collection of naturally occurring odors, many have safe activity profiles and a few are even approved for use as flavorings, fragrances, or cosmetics. If we can identify safe odors that are highly effective at altering the activity of the CO₂ receptor neuron, we will have made a major step in the crusade for global health.

Citrus Psyllid Odor Receptors

Chemical Informatics can be applied to explain Psyllid receptor-odor activity

Through work performed in our lab, activators for 11 ORNs found on 4 rhinerial plates of Citrus Psyllids have been identified. One activator has been found for PR4_A, two have been found for RP6_A, and one has been found for RP7_A, with none of the actives increasing firing rates more than 70 spikes/sec. As our computational approach requires at least two activating odors in order for optimization, we will focus our efforts on 9 AsCP neurons (RP2_B, RP2_C, RP4_A, RP4_C, RP6_A, RP6_B, RP6_C, RP7_B, RP7_C).

We begin our computational pipeline as performed for *Drosopihla*, calculating 3D structures with Omega (Hawkins et al., 2010) and 3,224 molecular descriptors using Dragon (Talete) for each of the 61 odors tested against the 9 ORNs (Figure 3.12). Molecular descriptors, which are mathematical values attempting to describe the structure of each compound, are then optimized individually for each ORN using a Sequential Forward Selection (SFS) approach, resulting in a single optimized set of descriptors for each ORN (See Methods Chapter VII) (Whitney, 1971)(Table 3.13). When we cluster the training odors based upon their optimized descriptor values, we find

that each optimized descriptor set is successful in grouping together highly active odors (Figure 3.13).

Predicting the response of the Psyllid ORNs to a broad panel of untested odors

We next used each ORN optimized descriptor set to train a Support Vector Machine (SVM), which is a highly applied machine learning approach (Chang and Lin, 2001; Karatzoglou et al., 2006). The SVM was trained to optimally predict the activity of each odor in the training set using only information provided by each ORNs optimized descriptor set, resulting in one trained SVM for each ORN. We next performed a 5-fold cross validation followed by a Receiver Operating Characteristic (ROC) analysis to validate the predictive ability for each ORN (See Methods Chapter VII). The Area Under the Curve (AUC) was calculated and the ROC analysis was plotted for each ORN (Figure 3.14). The extremely high AUC values, with a mean value of 0.99 across all ORNs, indicates that our odor prediction pipeline was extremely efficient at describing the activity of the training sets for all 9 ORNs.

We next assembled both natural odor and eMolecules libraries, representing large collections of previously untested odors (See Methods Chapter VII). We next applied each trained SVM to predict the responses of all odors from both training sets for each ORN. We provide the top 100 predicted natural odors for each ORN (Table 3.14). Predicted ligands can be validated, identifying strong activators and inhibitors for each ACP ORN. Strong actives can then be tested for their ability to modify ACP behavior. Ideally, we will be able to identify strong attractants for trap lures and strong repellents odors to protect citrus trees.

Mammalian Odor Receptors

Identification of unique subsets of optimal descriptors for mammalian receptors

Insect Or proteins are believed to consist of 7-transmembrane regions that are inversely oriented in the membrane. It is believed that they function as ligand-gated ion channels with a possible cyclic-nucleotide-activated cation channel function along with an obligate co-receptor Orco, forming a heteromer (Benton et al., 2006; Sato et al., 2008; Wicher et al., 2008). Alternatively, mammalian Ors function as G-protein coupled receptors with a traditional outside-in 7-transmembrane orientation and do not require an obligate co-receptor such as Orco (Zhang and Firestein, 2002). In order to test whether the chemical informatics platform would be successful at predicting ligands for the functionally distinct mammalian Ors, we performed a similar analysis on 33 ORs from mouse and 4 ORs from humans. The responses of each of these mammalian receptors to a panel of 62 odorants have been determined by functional expression in heterologous cells and >2 actives have been identified for each (Saito et al., 2009).

We applied our chemical informatics pipeline to optimize descriptors for each of the 37 mammalian ORs (Figure 3.15). 3D conformations for each of the training odors were calculated by Omega (See Methods Chapter VII). Dragon and Cerius2, which are commercially available programs for calculating molecular descriptors, were used to calculate 3,224 and 200 molecular descriptors for each of the training odors (See Methods Chapter VII).

We implemented a Sequential Forward Selection (SFS) approach to select a subset of molecular descriptors that best correlated with the activity of the training set odors (Whitney, 1971) (See Methods Chapter VII) (Figure 3.15). The SFS approach iteratively assembles an optimized subset of descriptors, beginning with a single best

descriptor and then incrementally adding additional descriptors one at a time until the correlation between descriptor values and OR activity fails to increase. The SFS approach is applied for each OR, resulting in 37 unique optimized descriptor sets (Table 3.15).

We applied hierarchical clustering on the Euclidean distances calculated between training odors using optmized descriptor set values for each of the 37 ORs in order to visualize how well our approach brought together activating odors (Figure 3.16). Upon visual inspection, clustering of the 62 training odors by each OR's optimized descriptor set indicated that the receptor-optimized descriptor sets were indeed able to effectively cluster activating odors together.

Computational validation of mammalian OR-optimized descriptor sets and *insilico* prediction of ligands

Since functional testing of predictions for mammalian receptors are beyond the scope of this study, we performed the well established computational 5-fold cross-validation to determine the predictive ability of the *in silico* approach. ORs with >15 known ligands were selected and for each OR 20% of the compounds (12/60) were excluded as a test set, while the remaining were used as a training set to generate the optimized descriptors. As before we performed a ROC analysis for each of the withheld test-set odors by classifying activity based on distance in the training set derived Or-optimized chemical space. We repeated this operation five times for each receptor, each trial performed by excluding a different subset of odors.

We generated mean ROC curves for each OR and calculated AUC values (Figure 3.17). Using this method we demonstrate that the OR-optimized-descriptor sets

generated using the training odors could accurately identify actives from the test odorants. Both the ROC and ApoA values were comparable, if not better (data not shown), than for the *Drosophila* Ors suggesting that the descriptors are able to efficiently explain the activity of the mammalian Ors.

Predicting mammalian receptor-odor interactions for a large untested odor space

We then applied the OR-optimized descriptors to systematically screen both the Natrual Odor and Pubchem libraries *in silico*, comprising over ~8,880,000 receptor-odor interactions and representing 33 mouse ORs, 4 human ORs (See Methods Chapter VII). We identify the top 500 (0.2%) hits from this vast chemical library for each Or/ORN, the top ~100 for each are reported in Table 3.16.

Relationship between descriptor sets and Or sequence and activity

We next analyzed the relationship between ORs based upon their shared molecular descriptor sets, training set activity, predicted odor sets, and phylogenetics, as we had previously performed for *Drosophila* (Figure 3.18). In contrast to what was observed in *Drosophila*, the analysis for the mammalian dataset reveals a greater degree of common relationships across the known-activity, predicted cross-activity and descriptor trees (~77% ORs present in common subgroups). Similarly, the *Drosophila* Or-phylogenetic tree has sparser subgroup relationships conserved with each of the other trees (<45%), as opposed to the mammalian ORs where the majority of subgroups in the phylogenetic tree (>56%) are conserved across the different trees. This difference may reflect the much greater amino-acid similarity across the mammalian receptors (47%) as compared to the divergent *Drosophila* receptors (23%).

94

Analysis of breadth of predictions for each mammalian OR in chemical space

Determining the breadth of coding in a large volatile chemical space across many receptors is virtually impossible to determine experimentally. However, if we apply the OR-optimized descriptor sets, it becomes possible to computationally predict frequency distributions for each of the mammalian ORs for the odor space of both libraries (>240,000 odors) (Figure 3.19). As expected, we find a great deal of variation across the ORs. While some ORs are predicted to be very broadly tuned, others are decisively narrower. Analyses such as these allow inferences of OR properties that would be very difficult to assess through wet lab experimentation alone.

DISCUSSION

We have applied our chemical informatics pipeline to predict activating and inhibiting odors for a large number of extremely important species, including several pest and disease vector insects. For *Anopheles* Ors we applied our pipeline to predict activators and inhibitors for a large number of receptors. We validated predictions experimentally for 12 Ors, demonstrating an effectiveness similar to that observed for *Drosophila*. For the CO₂ receptor, we considered the responses of multiple species integrating them into a single metric for molecular descriptor optimization. While validations for this receptor were not as successful as seen in either *Drosophila* or *Anopheles* Ors, it still signifies a major progression in the fight for behavior modification on disease vector species. We predicted activating odors for the very first time in ACP, creating a vast expansion upon the previously tested odor space. Finally, we predicted odors for 33 mouse and 4 human Ors.

95

We have noted challenges involved in predicting aromatic odors in both *Drosophila* and *Anopheles*. In an attempt to improve our accuracy for aromatic responsive Ors we have performed a thorough expansion of aromatic odor space. This is the first time a focused effort has been made to expand upon and explore responses of highly diverse aromatic odors. We applied chemical informatics to select and test 27 aromatic odors that were intelligently selected for their extremely broad composition of molecular features. Further, we integrated SVMs into our prediction pipeline to increase the abilities of our computational approach. Future experimental validation will expose how successful our attempts were.

No computational analyses in olfaction had been previously performed to integrate the responses of multiple species into a single metric for odor prediction. We successfully integrated the responses of 4 divergent species to predict odors for the very important CO_2 receptor. Additionally, while the three mosquito species are attracted to CO_2 , *Drosophila* are repelled, further creating an interesting intellectual challenge by integrating odors causing mixed behavioral responses. All of these differences introduce noise into the training set. As a result, the observed lower accuracy (48%) compared to that previously observed in both *Drosophila* (71%) and *Anopheles* (65%) Or predictions was not unexpected. However, due to these multiple challenges we still consider this to be a significant achievement.

It will be interesting to perform experimental validations for both the ACP and mammalian predictions in the future. There are several ways to further improve our computational approach in the future. Sequential Floating Forward Selection (SFFS) allows for the intermittent removal of previously selected descriptors instead of a steady building of an optimized list. Additionally, other predictive approaches beyond SVMs

96

and other alternative approaches can be considered. Since machine learning has been demonstrated to be highly effective for our pipeline, we plan on applying it for all future analyses.

Figure 3.1: A molecular descriptor optimized approach is able to explain odor activity for individual *Anopheles* Ors

Schematic of our chemical informatics pipeline. Molecular descriptors that are most correlated with activity are selected, resulting in a metric that is able to cluster together highly active odors using important structural features. The optimized descriptor sets can then be applied to predict Or activity against a large panel of odors. This pipeline is applied independently, optimizing descriptors for either activators (Top) or inhibitors (Bottom).

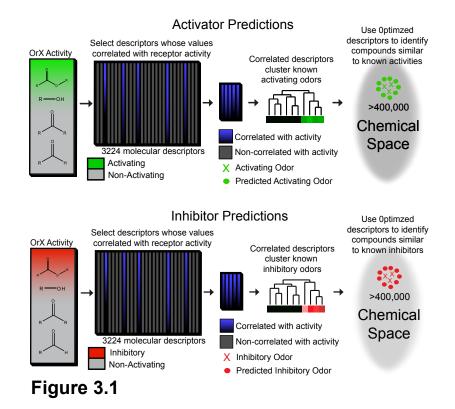


Figure 3.2: Optimized molecular descriptor sets are able to cluster either active or inhibitory odors

Optimized molecular descriptors values were applied to cluster training set odors individually for each Or. Clusters are divided into Activators, Fishing Activators, and Inhibitors. Colors for Activators and Fishing activators range from purple to red for lowest activity to highest activity and are individually applied for each Or. Colors for Inhibitors range from blue to bright for highest activity to most inhibitory.

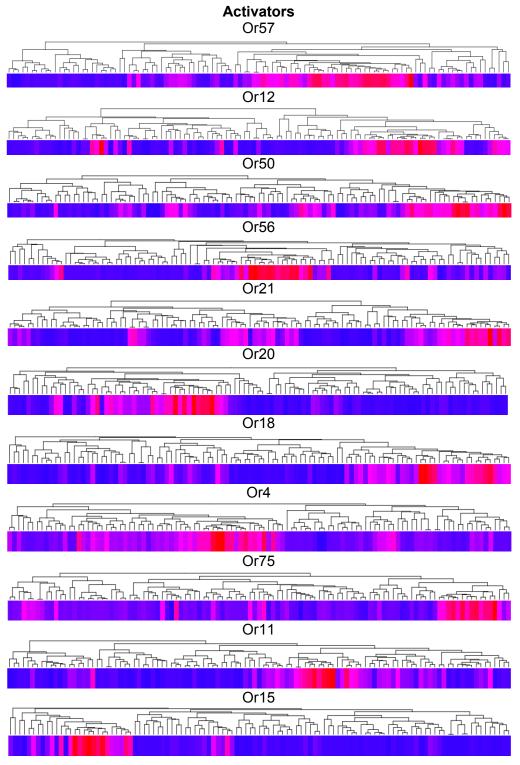


Figure 3.2

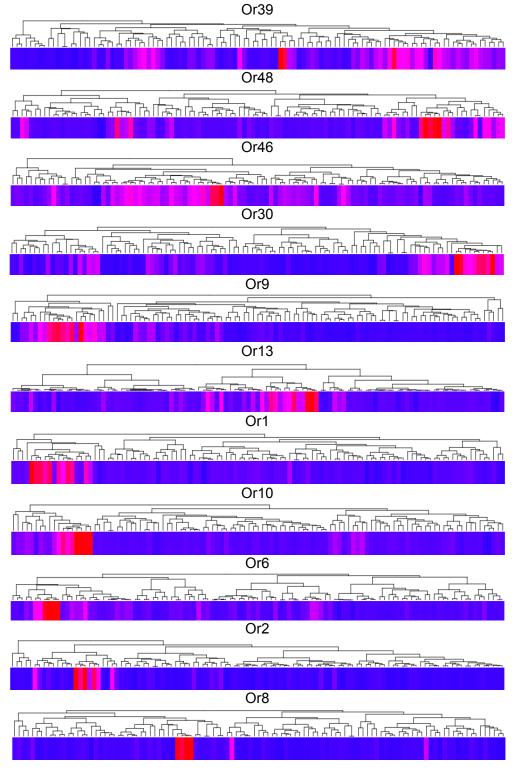


Figure 3.2 Continued

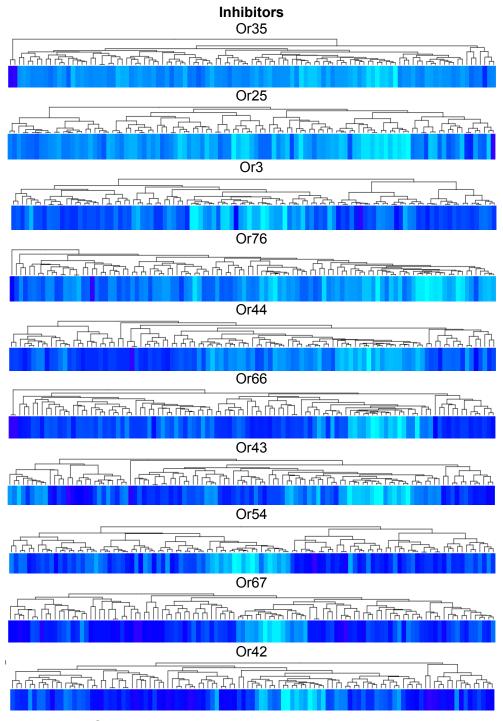


Figure 3.2 Continued

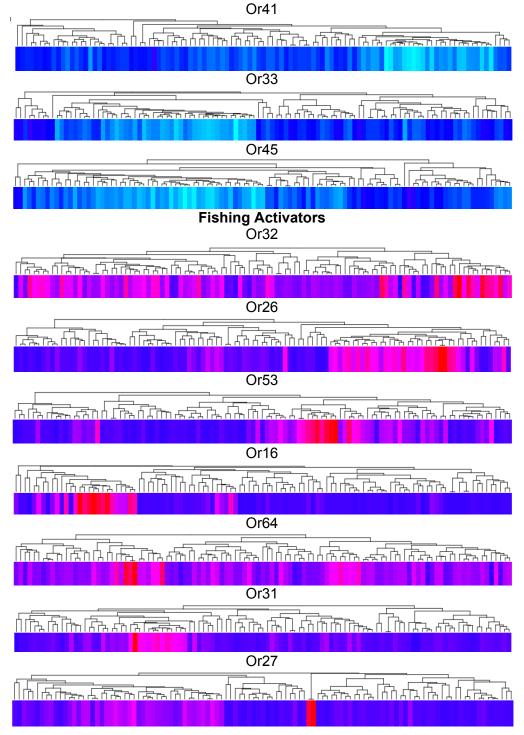


Figure 3.2 Continued

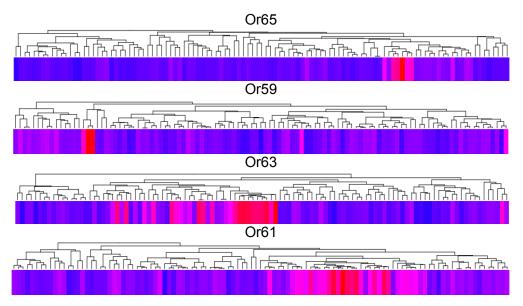


Figure 3.2 Continued

Figure 3.3: Structural relationships between the 75 most diverse aromatic odors Hierarchical clustering for 75 odors using Euclidean distances between odors calculated using all 3,224 molecular descriptors calculated by Dragon. Compound names are provided for each odor.

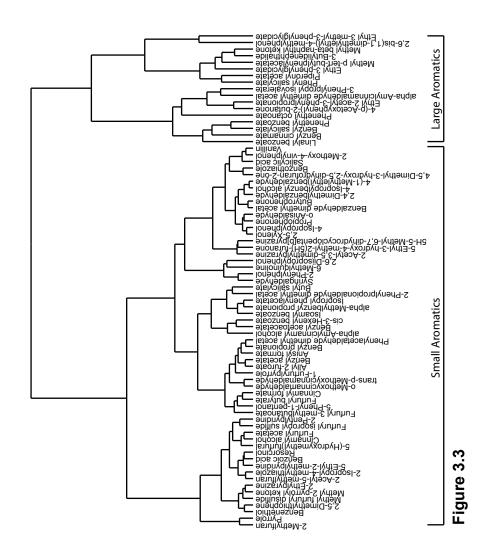


Figure 3.4: Newly optimized molecular descriptor sets are able to cluster odors for aromatically tuned Ors

Optimized molecular descriptors values were applied to cluster training set odors individually for each Or. Colors range from gray to black, representing the lowest to highest activity.

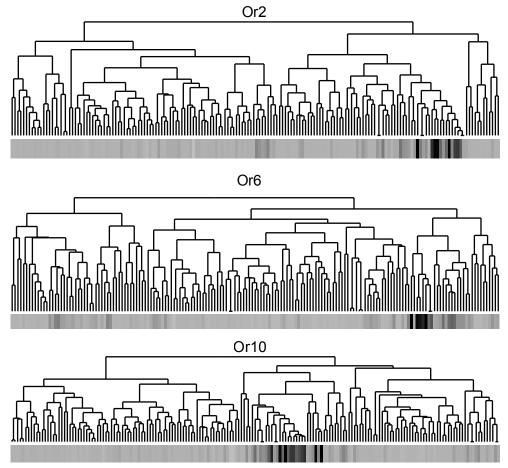
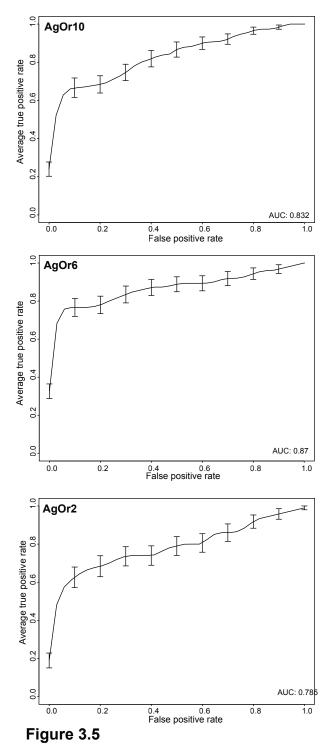


Figure 3.4

Figure 3.5: Optimized descriptors for AgOrs 2, 6, and 10 effectively describe training set activity.

A Receiver-Operating-Characteristic (ROC) curve is plotted for each Or, depicting the computational validation of ligand predictive ability of the Or-optimization approach.



Averaged ROC values for each Or

Figure 3.6: A Support Vector Machine (SVM) integrated approach is highly effective at explaining odor activity for individual Ors

Schematic of our SVM integrated chemical informatics pipeline. Molecular descriptors that are most correlated with activity are selected, resulting in a metric that is able to cluster together highly active odors using important structural features. The optimized descriptor sets are then be applied to train a SVM to predict Or activity, which is then applied to predict the activity of a large untested odor space.

SVM Mosquito Prediction Pipeline

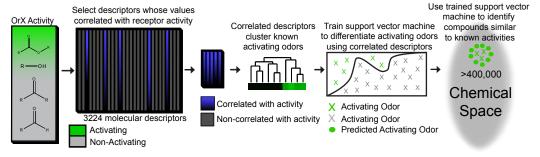
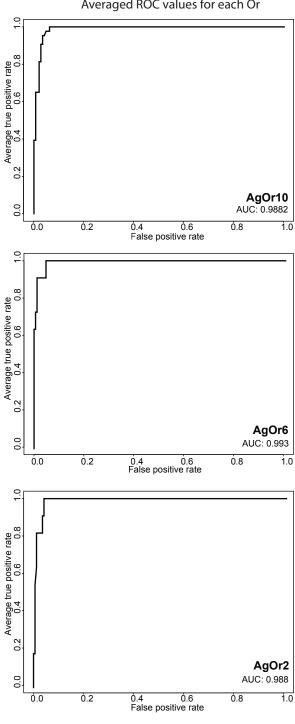


Figure 3.6

Figure 3.7: SVMs trained using optimized descriptors for AgOrs 2, 6, and 10 effectively describe training set activity

A Receiver-Operating-Characteristic (ROC) curve determined from 100 independent iterations of a SVM applied 5-fold cross validation is plotted for each Or, depicting the predictive ability of the Or-optimization approach.

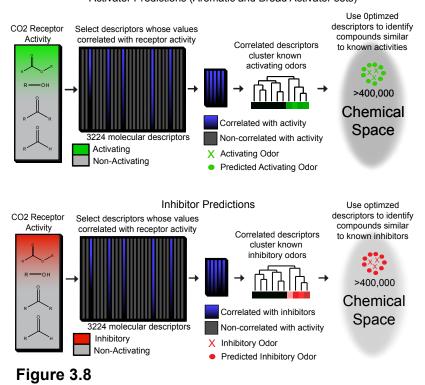


Averaged ROC values for each Or

Figure 3.7

Figure 3.8: A molecular descriptor optimized approach is able to explain odor activity for CO₂ receptors

Schematic of our chemical informatics pipeline. Molecular descriptors that are most correlated with activity are selected, resulting in a metric that is able to cluster together highly active odors using important structural features. The optimized descriptor sets can then be applied to predict CO₂ receptor activity against a large panel of odors. This pipeline is applied independently, optimizing descriptors for either activators (Top) or inhibitors (Bottom).



CO2 Predictions Activator Predictions (Aromatic and Broad Activator sets)

Figure 3.9: Optimized molecular descriptor sets are able to cluster odors by CO₂ receptor response

Optimized molecular descriptors values were applied to cluster training set odors individually for each screening set. Odor activity is represented individually for each screening set, ranging from gray to black in increasing activity.



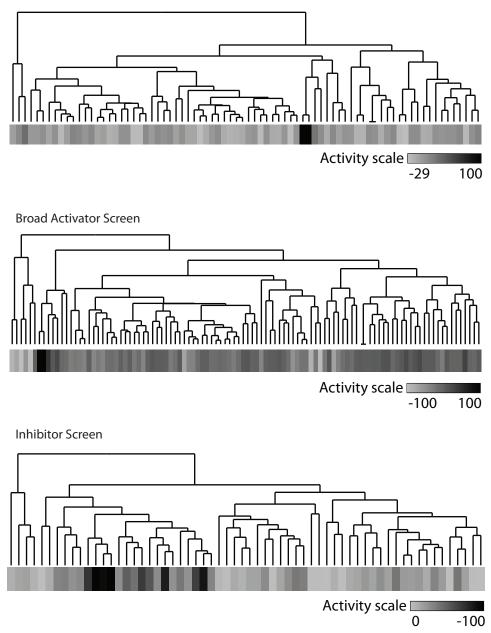




Figure 3.10: Active compounds cluster into three distinct structural classes

Active compounds were clustered by the combined 3 sets of optimized descriptors. Hierarchical clustering was performed on compound optimized molecular descriptor values, dividing the chemical structures into three distinct classes that have been outlined by both label and color. CO2 receptor responses (spikes/sec) have been provided for each compound and green and red boxes label activators or inhibitors, respectively. Representative chemical structures for each class are provided.

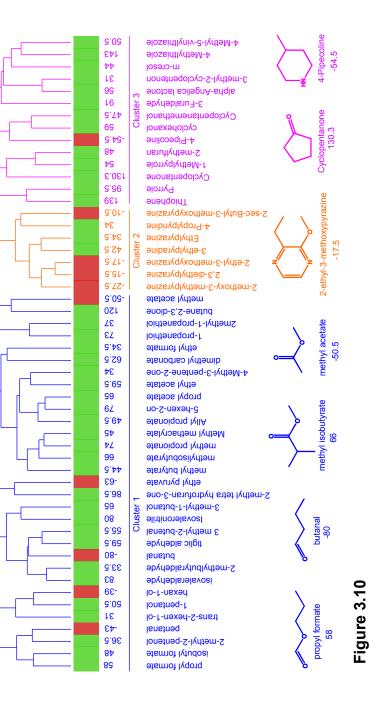


Figure 3.11: Chemical structures of validated activators and inhibitors

The structures for each of the compounds that validated as either activators (>30 spikes/sec) or inhibitors (<0) spikes/sec are provided. Compounds are divided their cluster as described in figure 3.22.

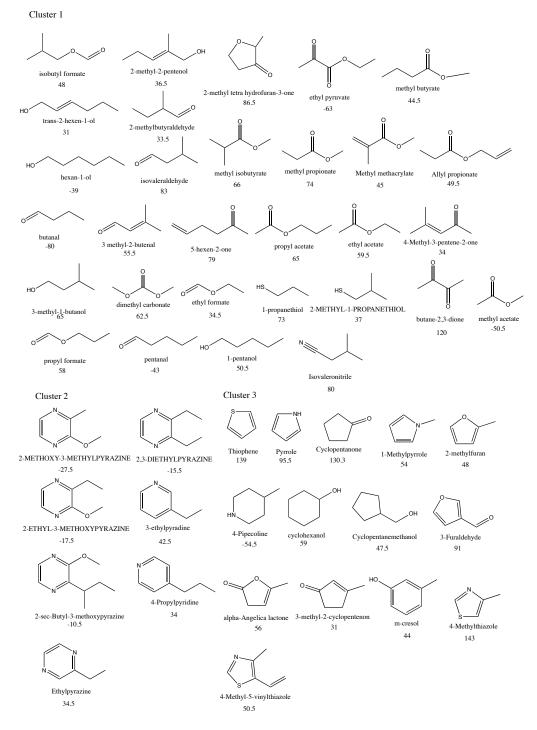


Figure 3.11

Figure 3.12: A SVM integrated molecular descriptor optimized approach is able to explain odor activity for individual Citrus Psyllid ORNs

Schematic of our SVM integrated chemical informatics pipeline. Molecular descriptors that are most correlated with activity are selected, resulting in a metric that is able to cluster together highly active odors using important structural features. The optimized descriptor sets are then be applied to train a SVM to predict Or activity, which is then applied to predict the activity of a large untested odor space.

Psyllid Activator Prediction Pipeline

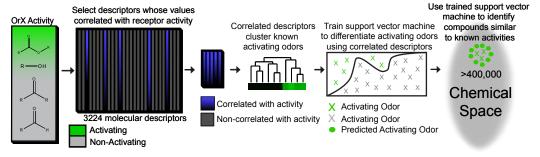


Figure 3.12

Figure 3.13: Optimized molecular descriptor sets are able to cluster ORN

activators

Optimized molecular descriptor values were applied to cluster training set odors individually for each ORN. Odor activity is represented individually for each screening set, ranging from gray to black in increasing activity.

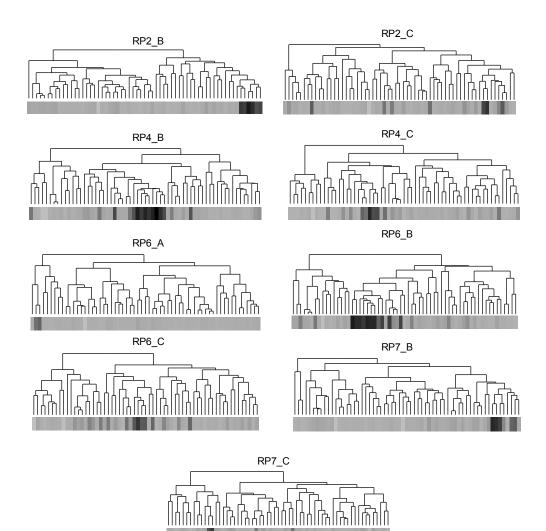
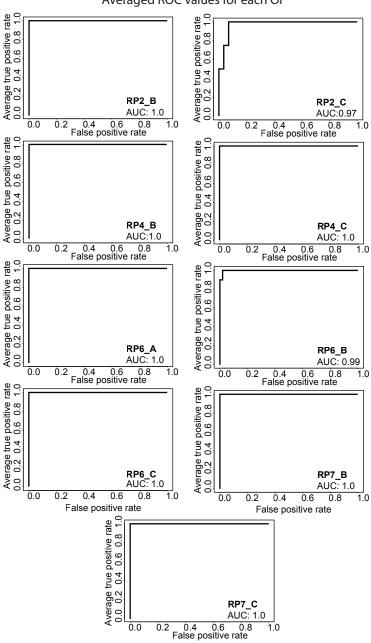




Figure 3.14: SVMs trained using descriptor sets that were optimized for individual ORNs effectively describe training set activity

A Receiver-Operating-Characteristic (ROC) curve determined from a SVM applied 5-fold cross validation is plotted for each ORN, depicting the predictive ability of the ORN-optimization approach.



Averaged ROC values for each Or

Figure 3.14

Figure 3.15: A molecular descriptor optimized approach is able to explain odor activity for individual mammalian ORs

Schematic of our chemical informatics pipeline. Molecular descriptors that are most correlated with activity are selected, resulting in a metric that is able to cluster together highly active odors using important structural features. The optimized descriptor sets can then be applied to predict Or activity against a large panel of odors.

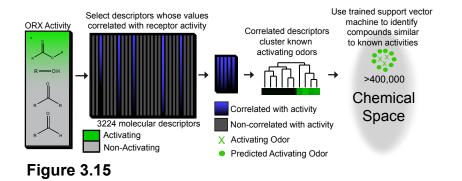


Figure 3.16: Mammalian Odorant receptor-optimized molecular descriptors can

successfully cluster known ligands

Hierarchical cluster for 33 mouse receptors and 4 human receptors using receptoroptimized descriptor sets using data from (Saito et al., 2009). Known odorant activity scale is indicated using independent color gradient scales.

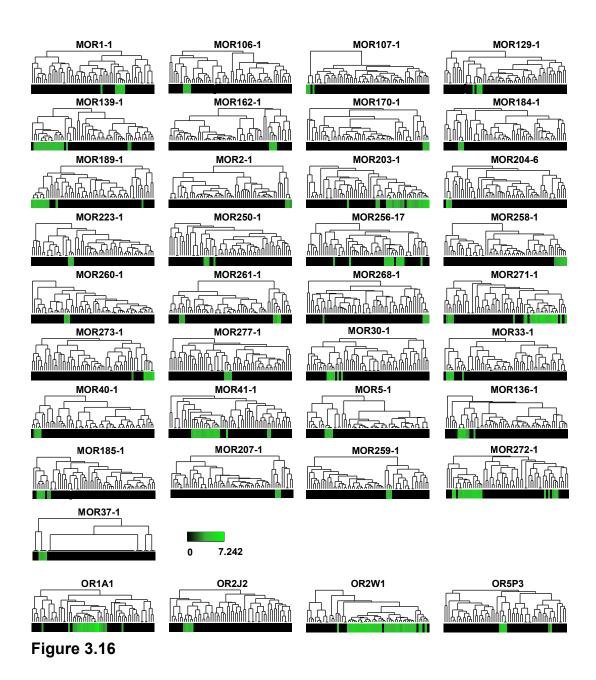


Figure 3.17: Optimized descriptors for mammalian ORs effectively describe

training set activity

Receiver-operating-characteristic (ROC) curve representing computational validation of ligand predictive ability of the Or-optimization approach. The mean true-positive value from 5 independent 5–fold cross validation runs for 5 mouse and 2 human receptors are plotted.

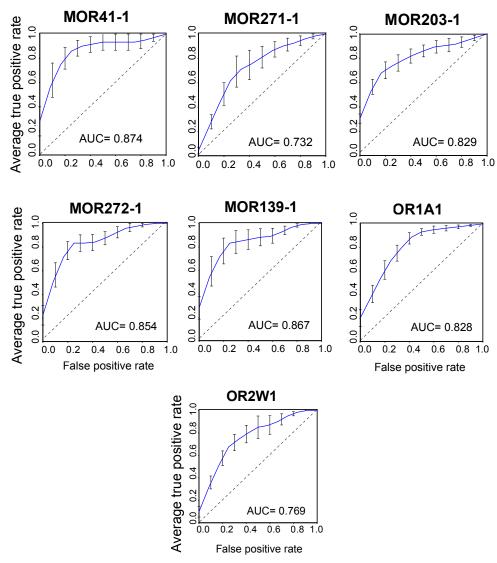


Figure 3.17

Figure 3.18: Analyzing relationships between important features for mammalian ORs

Hierarchical clusters created from Euclidean distance values between mammalian ORs calculated from the following sources: (left to right) shared optimized descriptors; activity to training odor set; similarity across top 500 predicted ligands; and Phylogenic tree of receptors. Phylogenetic tree of Mammalian ORs calculated from protein sequences. Subclusters are shaded with different colors or bars to enhance ease of comparison.

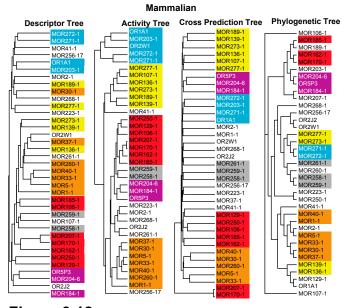


Figure 3.18

Figure 3.19: Analysis of mammalian OR tuning breadth

Frequency distribution of compounds from the >240K library within the top 15% distance from highest active plotted to generate predicted breadth of tuning curves.

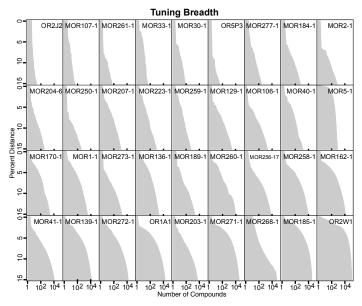


Figure 3.19

Table 3.1: Optimized descriptor sets for each Anopheles Or

Optimized descriptor symbols are listed for each Or. Descriptors are listed in the order in which they were included into the list. The same descriptor can be present multiple times for an Or representing the importance of the descriptor for a particular Or. The final correlation between the optimized descriptor set and odor activity is provided.

Or	Desc. Symbol		Or	Desc. Symbol	Or	Desc. Symbol	Or	Desc. Symbol		
AgOr57 Correlation	AlogP98 0.057	C.043 Mor13p	AgOr12 Correlation	B06.C.C. nRCOOH	AgOr50 Correlation	SP05 0.057	AgOr38 Correlation	AlogP98 DELS	nRCHO Atype_C_40.1	nR.Cp.3
0.933835	EEig10d	0.057.8	0.8635844	BELe2	0.9031393	piPC08	0.8536688	B06.C.C.	R5m.	nRCOOH.7
0.000000	nRCOOH	EEig10d.3	0.0000011	EEig10d	0.0001000	H1p	0.0000000	PW4	C.026	nRCOOR.4
	B07.C.C.	T.NN.		nRCO		R8m.		nRCOOH	nRCO.2	MATS7 v.2
	Hy	nRCOOH.9		nRCHO		nCconj		EEig10d	MATS2e.1	MATS7 v.3
	Ds	B07.C.C6		C.040		E2u		GATS2e	C.008	
	EEig02d	BIC		Hy		Gs		HATS8e	B07.C.C4	
	Mor27p B07.C.O.	GV W AI.80.2 0.057.9		B06.C.C1 BEHp4		JGI6 L2u		O.057 G1u	Atype_C_40.2 RDF035m.1	
	Ms	B06.C.C.		nRCOOH.1		0.057.1		C.040	MATS7 v.1	
	O.057.1	nRCOOH.10		EEig 11d		B07.C.C.		B06.C.C1	MATS4m.1	
	HATS8v	nCbH.1		HATS8u		piPC05		JGI2	J.4	
	MATS2e	nRCHO.3		O.057		De		RDF035m B07.C.C.	Hy.2	
	EEig10d.1 nRCOOH.1	nRCO.2 MATS3m.1		C.001 JGI6		JGI7 H0e		Ms	H.051.1 O.057.7	
	nRCHO	B02.C.C1		Ms		MATS6v		nR.Ct	nR.Ct.1	
	GV WAI.80	nR.Ct.1		Ms.1		C.040		MATS2e	Vindex	
	O.057.2	O.057.10				X5 Av		O.057.1	B06.C.C8	
	F03.C.N.	nR09.1 nRCOOH. 11				nR.Ct RTu.		F03.C.N. B06.C.C2	Atype_C_40.3 MEcc.1	
	BELe2 S_dssC	B07.C.C7				P2u		JGI3	B07.C.C5	
	O.057.3	C.026.2				piPC08.1		nRCOOR	0.057.8	
	MATS3v	nRCOOH.12				O.057.2		nRCO	MATS3m.1	
	B07.C.C1	B07.C.C8				BEHp4		MATS7v	B06.C.C9	
	0.057.4 nRCO	nRCOOH.13 EEig10d.4				B07.C.C1 0.060		0.057.2 GATS2e.1	E2s G2m	
	R3u.	JGI1				Mor25e		Hy	BEHm3	
	EEig09r	JGI1.1				X5 Av.1		B07.C.C1	B06.C.C10	
	nRCOOH.2					C.026		nR.Cp	G.NO1	
	MATS7v					Hy		O.057.3	0.057.9	
	Hy.1 C.026					E2e Ds		MATS4m	nRCOOR.1 nR.Cp.2	
	Infective.80					F04.C.O.		EEig10d.1	Mor10u	
	nRCOOH.3					B07.C.C2		R4e.	nArCOOH	
	B07.C.C2					HNar		G.NO.	nRCOOH.2	
	MATS2e.1					nCconj.1		B07.C.C2	nRNH2	
	BELe2.1 nRCOOH.4					R7m. F03.C.N.		MEcc C.040.1	B07.C.C6 Yindex	
	nR09					X4A		J.1	S aaaC.1	
	nRCHO.1					B08.C.C.		B06.C.C3	B06.C.C 11	
	nR.Ct					B03.C.C.		O.057.4	nRCO.3	
	O.057.5 DISPe					RBF C.026.1		H.051 X4A	B02.C.C. B06.C.C12	
	GV W AI.80.1					MATS2e		B06.C.C4	0.057.10	
	nCbH					R1e		nCb.	GATS8m.1	
	nRCOOH.5					nR.Ct.1		C.040.2	JGI3.2	
	Ну.2					C.040.1		GATS8m	nRCOOR.2	
	S_dCH2 MATS4v					B07.C.C3 B04.C.C.		G1u.1 MATS3m	nRCOOH.3 C.026.1	
	B07.C.C3					piPC08.2		J.2	E2e	
	Ms.1					E2e.1		Atype_C_18	MATS3m.2	
	O.057.6					O.057.3		B06.C.C5	nRCO.4	
	EEig10d.2					O.057.4		nRCOOH.1	B06.C.C13	
	G2m nRCOOH.6							R1u. EEig10d.2	nRCOOH.4 JGI3.3	
	B07.C.C4							nRCO.1	B06.C.C14	
	F03.C.N1							O.057.5	nRCOOR.3	
	C.026.1							nR.Cp.1	G1u.2	
	Atype_C_18 B02.C.C.							Hy.1	nR.Ct.2 nRCOOH.5	
	HATS8e							Atype_C_40 B07.C.C3	GATS2e.3	
	nRCOOH.7							S_aaaC	B06.C.C15	
	MATS3m							JGI1	nRCOOH.6	
	nRCHO.2							B06.C.C6	MEcc.2	
	nRCOOH.8							0.057.6	C.026.2 B07.C.C7	
	EEig12x 0.057.7							GATS2e.2 B06.C.C7	Yindex.1	
	nRCO.1							JGI3.1	J.5	
	B07.C.C5							J.3	MATS4v	

Table 3.1

Or	Desc. Symbo	I		Or	Desc. Symbol	Or	Desc. Symbol	Or	Desc. Symbol	Or
AgOr56	Ss	C.024.2	TIC4	AgOr21	SP02	AgOr20	O.058	AgOr18	Mor20m	AgOr4
Correlation		nRCOOH.3	nRCOOH.8		0.057	Correlation		Correlation		Correlation
0.9312913	B07.C.O.	nRCO Atype_C_18	S_sNH2.1 EEig09d.3	0.9052854	TPSA.NO.	0.8829924	C.040	0.9201605	EEig10d	0.896526
	0.057	nR09.1	O.058.5		B06.C.C.		GATS7m		Gu	
	Hy	nRCOOH.4	MATS2e.7		H1p		X3Av		DISPe	
	EEig09d	B07.C.C5	O.057.16		Yindex		De		nRCHO	
	MATS2m	C.026.2	GVWAI.80.4		ASP		C.040.1		EEig12r	
	S_dssC	MATS3p	nRCHO.6		O.057.1		EEig10r		MATS4p	
	B07.C.C.	BELe2.2	O.057.17		R8m.		BEHm4		J	
	Ms	Atype_C_40	S_ssO.5		nDB H1e		O.058.1		0.057.1	
	nBnz nRCHO	nRCHO.3 nArCHO	Mor04m.1 MATS2e.8		TPSA.NO1		Hy JGI7		JGI7 X3A	
	C.040	GVWAI.80.2	nRCOOH.9		EEig10d		E2e		Mor23m	
	BELe2	nRCOOH.5	EEig09d.4		nRCHO		nCconj		B06.C.C.	
	O.057.1	nR.Ct.3	EEig09d.5		BEHp4		HNar		nHDon	
	EEig05d	nRNH2			O.057.2		JGI6		Mor27p	
	MATS2e	0.057.7			B06.C.C1		Ku		nRCOOH	
	B04.C.N.	CIC5			B04.C.O.		JGI5		GATS3m	
	O.058 O.057.2	S_ssO.1 EEig09d.1			C.040 X4Av		B03.C.C. C.040.2		Mor28e C.026	
	GVWAI.80	RDF150u			0.057.3		nRCHO		X4A	
	MATS8v	nRCOOH.6			R7m.		MATS4v		S_dssC	
	IC2	nRCO.1			Hy		C.040.3		E2e	
	O.057.3	O.057.8			E2u		nRCO		MATS2v	
	nR.Ct	B07.C.C6			0.057.4		R8m.		nRCHO.1	
	C.040.1	nPyrroles			Neoplastic.80		IC1		nRCOOH.1	
	C.024 MATS3v	MATS3p.1 S ssO.2			EEig10d.1 MATS2p		O.057 O.060		Infective.80 nR09	
	Xt	0.057.9			0.057.5		MATS6v		HATS3u	
	B07.C.C1	nRCHO.4			B06.C.C2		R1e		R8e.	
	nRCOOH	X4A.1			BEHp4.1		L2e		nRCOOH.2	
	F03.C.N.	O.057.10			F03.C.N.		piPC09		JGI1	
	O.058.1	B07.C.C7			Ms		nRCOOH		C.026.1	
	C.026	nR.Ct.4			HATS6m		nR.Ct De.1		RARS	
	MATS2e.1 nRCHO.1	O.057.11 C.043.1			B07.C.C. 0.057.6		PW4		MATS4v B06.C.C1	
	C.040.2	S ss0.3			nRCHO.1		O.060.1		nRCO	
	X4A	MATS7v.1			Yindex.1		E2e.1		nRCOOH.3	
	B07.C.C2	MATS2e.4			C.040.1		G2m		Gu.1	
	Hy.1	O.057.12			C.026		nRCOOH.1		nRCHO.2	
	0.057.4	Mor04m			B06.C.C3		nRCHO.1		EEig12x	
	GVWAI.80.1 MATS7v	CIC5.1 B07.C.C8			ESpm05d BEHp4.2		S_aaCH C.040.4		nRCOOH.4 X4A.1	
	C.043	0.057.13			nRCOOH		BEHe3		EEig10d.1	
	C.040.3	S_sNH2			EEig10d.2		nRCO.1		MATS5p	
	nR.Ct.1	EEig09d.2			H1e.1		JGI6.1		PJI2	
	nR09	O.058.3			H1e.2		Ku.1		PJI2.1	
	Ms.1	Mor24e.1					GATS6v			
	C.026.1 MATS2e.2	C.026.3 MATS3p.2					X5Av C.040.5			
	0.058.2	nR.Ct.5					MATS5v			
	Mor24e	Atype_C_40.1					B07.C.O.			
	G1v	Ms.2					R6e.			
	nRCOOH.1	B07.C.C9					R6e1			
	B07.C.C3	nRCHO.5								
	C.024.1	nRCOOH.7								
	C.040.4 BELe2.1	GVWAI.80.3 MATS2e.5								
	EEig10d	S aaNH								
	nRCOOH.2	RDF130m								
	MATS1v	O.057.14								
	nRCHO.2	S_ssO.4								
	nR.Ct.2	X4A.2								
	0.057.5 S_ssO	O.057.15 O.058.4								
	S_SSU 0.057.6	C.026.4								
	Hy.2	MATS2e.6								
	B07.C.C4	nR.Ct.6								
	MATS2e.3	B07.C.C10								

Desc. Symbol BLTF96 F05.C.O. B08.C.O. PW4 nRCOOH B05.C.O. Infective.80 DISPm BEHp1 nRCOOH.1 HATS5v B08.C.O.1 B05.C.C. EEig09d DISPm.1 nR.CC Gs MATS3e nRCOOH.2 Mor10u R5e. B08.C.O.2 G3s EEig10d GATS4p nRCOOH.3 EEig12r F03.C.N. RARS nRCOOH.4 R5e.1 RARS nRCOOH.4 R5e.1 R3m. Mor32v HATS4u HATS4u HATS4u HATS4u	Or AgOr75 Correlation 0.8265765	Or AgOr32 Correlation 0.6823186	Desc. Symbol E1s B06.C.O. Mor10p Atype_H_47 H.049 nRCOOH HNar GATS1v nCconj R7v. GATS7m CIC B06.C.O.1 Mor10u E1s.1 RDF020m R8m. B06.C.O.2 nRCH0 DISPm R7e MATS2m Mor10p.1 P2s P2s.1	AgOr26	O.057	Or AgOr11 Correlation 0.889735	HNar	Or AgOr15 Correlation 0.9092773	BELe3 E2e nAB Mor10u HOMA R7m. SPH E2e.1 F04.C.N. HOMA.1 nOHs GATS6m GATS6m GATS6m B06.C.C. ESpm01d B06.C.C. ESpm01d B06.C.C. HATS4u MATS4v B06.C.C. BIC nRCOOH 22e.2 BIC nRCO E2e.2 BIC nRCO E2e.2 BIC nRCO E2e.2 SIC nRCO E2E.2 SIC NO SIC SIC SIC SIC SIC SIC SIC SIC SIC SIC
									BIC.2

Table 3.1 (Continued)

Or AgOr39	Desc. Symbol ALOGP	Or AgOr53	Desc. Symbol Ss	Or AgOr16	Desc. Symbol BELe3	Or AgOr48	Desc. Symbol F06.C.O.	Or AgOr46	Desc. Symbol Mor25e	Or AgOr30
Correlation	RDF035m	Correlation		Correlation		Correlation		Correlation		Correlation
0.8405153		0.8962904		0.853112		0.8627068		0.8647854		0.8920303
	R5e.		nHAcc		ARR		DISPe		E2u	
	RBF		BELe2		R5v.		R8u.		O.057	
	ALOGP.1		B04.C.N.		Mor10e		ESpm03u		EEig10d	
	HATS6e B09.C.O.		MATS2v HATS6e		nRCOOH EEig10d		F06.C.O1 0.057		HATS7m B04.C.O.	
	MATS8m		0.057.1		R2v.		Mor18m		ESpm15u	
	B05.C.O.		Infective.80		X4A		GATS1v		0.057.1	
	nCconj		O.057.2		nRCHO		R8u		S_dssC	
	Mor10e		R7m.		S_dssC		JGT		S_dssC.1	
	F02.C.O.		R1u.		MATS2v		Atype_C_40			
	nRCOOH.1		Mor25p		B04.C.N.		G3s			
	R6u. Mor27u		BELe2.1		BIC		DISPm piPC04.1			
	B06.C.O.		MATS3e 0.057.3		JGI7 B04.C.C.		ESpm05u			
	Ke		nRCHO		EEig11x		S_dssC			
	nHDon		C.040		IC2		AROM			
	B09.C.O1		EEig08d		nRCOOH.1		nRCOOH			
	R5e1		Infective.80.1		E1p		B06.C.O.			
	MATS8m.1		F04.C.N.		EEig10d.1		EEig12x			
	MATS3v		E2s		X4A.1		E1s			
	RDF035m.1 nRCOOH.2		Mor32p X3Av		Mor10e.1 TPSA.NO.		E1s.1			
	RBF.1		HATS6u		S_dCH2					
	R6u1		0.057.4		EEig09d					
	nR.Ct		B06.C.C.		L2u					
	L3s		HATS4e		F04.C.O.					
	Mor23m		O.057.5		E1s					
	nRCHO		Mor10e		E2e BIC.1					
	S_sOH HATS6u		E2u RTu.		Mor10e.2					
	EEig09x		EEig09d.1		EEig10d.2					
	R5e2		MATS5v		C.027					
	C.008		SRW09		nRCOOH.2					
	SPH		C.040.1		Mor32m					
	DISPe		nR.Ct		B04.C.C1					
	nDB X4A		O.057.6 EEig08d.1		JGI7.1 Mor08p					
	B09.C.C.		MATS2e		MATS3m					
	R6u2		E1p		EEig10d.3					
	RDF035m.2		B04.C.N1		G1p					
	MATS7m		O.057.7		nRCHO.1					
	MATS7m.1		nArCO		nRCOOH.3					
			nRCHO.1		RDF035m BIC2					
			C.040.2 C.026		JGI6					
			BELe2.2		B05.C.O.					
			MATS2v.1		J					
			Infective.80.2		X4A.2					
			nRCOOH		Mor16e					
			G2p		Mor16e.1					
			C.043 X4Av							
			Mor27e							
			C.040.3							
			C.026.1							
			BELe2.3							
			MATS6v							
			E2s.1							
			B06.C.C1 Mor10p							
			Mor10p.1							
	~ / / ~									

Table 3.1 (Continued)

Desc. Symbol		Or	Desc. Symbol	Or	Desc. Symbol		Or	Desc. Symbol		Desc. Symbol
Kappa.3.AM Ks O.057 nR EEig01x EE	s.1 RCOOH.8 Eig11x Eig11x.1	AgOr64 Correlation 0.7699497	Mor14e R3v.	AgOT9 Correlation 0.946032	nAB ESpm01d	nAB.7 MATS3m.2 R7m.2 nArCO.1 nAB.8 E1m nAB.9 GATS6v.1 F04.C.N. BIC.1 Linfective.80 X4A EEig10r nAB.10 BELv4.2 MATS2e.1 nAB.11 R7m.3 S_aaaC.1 RCI.4 nRCOOH.3 X5A.3 AMW X5A.3 AMW ATS3m.3 Mor18m B06.C.0.2 X5A.4 nRCOOH.4 E2e.1 0.056.1 R3m.1 R8p2 BIC.3	Or AgOr13 Correlation 0.8117099	ARR B05.C.C.	AgOr1 Correlation 0.7939964	ESpm01d S_sOH
X5A			B03.C.C.		Gu	MATS3m.3				
nRCOOH.1			JGI5.1		nRCOOH	Mor18m				
EEig12r.1			Mor13v.2		nArCO	X5A.4				
ESpm15u.2					nAB.5	E2e.1				
G3s.2					R8p.	R3m.1				
GATS5e					RCI	BIC.2				
					EEig10d	BIC.3				
C.027					BELv4					
B06.C.O2					S_dCH2					
nR.Ct					R7m1					
nCb. B09.C.O2					BELv4.1 nRCHO					
B06.C.O3					SPH					
S_dCH2 ESpm15u.5					S_aaaC S_dO					
HATS6u nRCOOH.6					RCI.1 nArCHO					
nArOR B03.C.O.					RCI.2 H3m					
L2s 0.057.3					MATS3m.1 R8p1					
PW5.2					G1u					
ESpm15u.6 R8p1					Mp E2e					
EEig12x 0.057.4					BIC JGI7.1					
G3s.3 MATS5p					T.OO. RCI.3					
B09.C.O3 PW5.3					Mor32u EEig12d					
nRCOOH.7					X5A.2					
G3s.4 nCb1					O.056 EEig09d					
ESpm15u.7					nRCOOH.2					

Or AgOr31	Desc. Symbol TI2	AgOr10	nCar	Symbol	AgOr27		Or AgOr6		Or AgOr2		Or AgOr65
	0.057	Correlation	R8e.			MEcc				HATS6v	Correlation
0.8778699	Mor32e	0.9310224	C.025 ZM1V		0.8758972	0.057 R8m	0.9545822	0.057	0.8565036	HATS3V E2e	0.863439
	G3s		H.047			MATS2m		ESpm03u		Gs	
	Mor10v		X5A			nBnz		R7m.		Gs.1	
	S_sOH		RTm			Ms		EEig03x		03.1	
	B06.C.O.		RCI			MATS8v		nDB			
	ESpm15u		MATS	2p		C.006		Mor23m			
	R6u.		R8u.			B09.C.O.		E2e			
	nRCOOH		nBnz			R2e.		Кр			
	E3p		HATS	5m		O.057.1		nCconj			
	nHDon		Кр			nCb.		S_sOH			
	nCrs R5u.		JGI1 0.060			B08.C.C. X3A		ESpm01d nAB			
	GATS6v		nBnz.1			S aasC		F04.C.O.			
	nRCOOH.1		GATS			C.040		B06.C.O.			
	B06.C.O1		JGI6			nCq		GATS3e			
	Mor23m		B04.C	.C.		MATS8v.1		GATS3e.1			
	Mor32e.1		Mor25			MATS5p					
	HATS6u		MATS			C.024					
	IVDE		0.056			nRCOOH					
	O.057.1 nOHp		nRCO Mor25			Neoplastic.80 C.040.1					
	D.Dr05		H.051	v		X3A.1					
	B06.C.O2		E3m			nCb1					
	nRCHO		P2v			nRCHO					
	O.057.2		nOHs			MATS3e					
	B06.C.O3		C.006			B07.C.C.					
	C.008		EEig04	4r		R6u.					
	nRCOOH.2 R6u1		R4v. Mor11	n		C.040.2 MATS6v					
	C.026		GATS			C.024.1					
	E1s		B04.C			REIG					
	MATS5v		JGI6.1			R8m.					
	Mor32e.2		nBnz.2			MEcc.1					
	G3s.1		MATS			0.057.2					
	nCconj		HOMA			C.034					
	nOHp.1 EEig12x		HATS: RBF	DITI. I		0.057.3 MATS1v					
	JGI5		Mor07			nOHp					
	nRCOOH.3		C.027	-		C.040.3					
	G3s.2		JGI7			HATS8v					
	JGI6		ARON			O.057.4					
	Mor10p		JGI1.1			EEig08d					
	R5e.		R8u1 RCI.1			EEig08d.1					
	B09.C.O. HATS6u.1		RCI.1								
	GATS6v.1										
	nRCOOH.4										
	GATS5v										
	nArCO										
	B05.C.O.										
	RDF125u C.026.1										
	C.026.2										

Desc. Symbol		Or	Desc. Symbol	Or	Desc. Symbol	Or	Desc. Symbol	Or	Desc. Symbol	Or	Desc. Symbol
nArOH	R6u.	AgOr8	R6m.	AgOr59	S_dCH2 /	AgOr63	nH .	AgOr61	nHAcc	AgOr35	Hypnotic.80
	Ke.1		GATS2p		nOHs	Correlation		Correlation		Correlation	
	E3s	0.7551107		0.85381		0.8400413		0.8538082		0.8460269	
	nAB.2		J3D		nROH		B04.C.O.		O.057		Ui
	R1m.		B07.C.O.		JGI4		H2m		MATS2e		S_dsCH
E1u	MATS4p.1		B06.C.C.		Hbond.acceptor		H.049		EEig10d		R8v.
	nRCHO.2		nDB		JGI7		R5e.		Gs		S_sOH
	nRCOOH.3		JGI1		JGI5		0.057.1		PW4		GGI9.1
	nArCO.2		Atype_C_40		R1v.		Mor13p		B08.C.O.		nDB
	nAB.3 nArOR		ESpm05u EEig09d		Mor17m ESpm01d		G3s B08.C.O.		O.057.1 O.060		EEig09d GATS4e
	G2u.1		GATS4e		JGI5.1		GATS5v		PW4.1		JGI9
	nAB.4		GATS4e.1		nR.Cs		Vindex		nHDon		DISPv
	JGI5		0A1046.1		nR.Cs.1		nRCOOH		0.057.2		S_dssC
	Mor04m.1				111(.00.1		Ui		Infective.80		JGI7
	nAB.5						B09.C.O.		MATS2v		O.056
	R8m.						B06.C.C.		Mor23m		Mor16p
	Mor16p.3						MATS7v		Mor23m.1		E1u
nArOH.1	R6u1						MATS5e				DISPm
	Atype_C_40						G3s.1				GGI9.2
	F03.C.N.						nCconj				Hypnotic.80.1
	MATS4p.2						B08.C.O1				JGI3
	nCconj.1						PW5				S_dsCH.1
	HATS1p						B06.C.C1				Mor09u
	E1u.3						EEig10d				R8v1
	E1u.4						B09.C.O1				JGI4
F04.C.O.							G3s.2				JGI4.1
H0e Ke							MATS4e 0.057.2				
E1u.1							R8m.				
JGI7							GATS6v				
Mor16p							HATS6u				
Hy							Mor17m				
SPAM.1							Mor17m.1				
nRCOOH.1											
R4m.											
nAB.1											
H.049											
MATS4v											
nR.Ct											
C.040.1											
nR09											
HATS3p MATS7v											
E1u.2											
E2e											
Mor16p.1											
nCconj											
nOHs											
HATS4p											
nHDon											
MATS2e											
nArCO.1											
C.040.2											
B04.C.C1											
nRCHO.1 EEig11d											
JGI7.1											
B04.C.C2											
Mor16p.2											
nArCOOR											
J3D											
HATSp											
nBM											
HATSe											
nRCOOH.2											
C.006											
Mor04m											
MATS2e.1											
Infective.80											

Table 3.1 (Continued)

Or	Desc. Symbo	Or	Desc. Symbol	Or	Desc. Symbo	I	Or	Desc. Symbol	Or	Desc. Symbo	1	Or
AgOr25 Correlation		AgOr3 Correlation		AgOr76 Correlation	EEig10d	X4A.3 Neoplastic 80	AgOr44 Correlation		AgOr66 Correlation	EEig10x	MATS4p.1 BEHp5.1	AgOr43 Correlation
0.7611209			Infective.80	0.7581273		nRCOOH.6		nRCOOH	0.866496		EEig12d.1	0.8854268
	EEig12x		B04.C.O.		MATS8m	EEig10d.13		EEig10r		SPH	JGI4.3	
	HATS3p B09.C.O.		JGI7		nOHt EEig10d.1	EEig09d.1 G2m.1		B03.C.O. B07.C.O.		B05.C.O. B08.C.O.	nRCOOH.3 EEig10d.6	
	nN		nCconj G2v		X4A	MATS7p.1		Mor08m		Mor08p	B05.C.O6	
	nCconj		nRCOOH.1		JGI7	nRCOOH.7		nRCOOH.1		TPSA.NO.	B09.C.O4	
	nOHp.1		F02.C.N.		MATS4v	nR.Ct		EEig12r		EEig10d	SPH.2	
	nRCOOH.1 nThiophenes		B09.C.O. PW5		R1e. B07.C.O.	nOHt.4 B02.C.C2		JGI7 nRCHO		JGI4 F04.C.N.	C.026.1 E1u	
	MATS5v		ATS1p		EEig10d.2	EEig10d.14		MATS3m		EEig12d	E1u.1	
	B09.C.O1		E2s		MATS6v	MATS8m.5		SPH		HATS4u		
	ESpm14d E1m		Infective.80.1 nRCOOH.2		S_dssC nRCOOH.1	nRCOOH.8 EEig10d.15		DISPe Gs		EEig09d DISPe.1		
	HATS8m		EEig04x		EEig10d.3	MATS4v.1		O.057		GATS4v		
	GATS5e		Hy		B02.C.C.	X4A.4		Infective.80		B09.C.O.		
	nOHp.2 0.057		EEig10d nRCOOH.3		G2m MATS8m.1	B06.C.O. EEig10d.16		Mor16e Mor16e.1		MEcc PW5		
	F03.C.N.		B02.C.C.		E2s	E2s.2				EEig10d.1		
	nCrs		B08.C.C.		EEig10d.4	E2s.3				nRCOOH		
	E1s nRCOOH.2		nArCO B04.C.O1		MATS7p nOHt.1					B05.C.O1 Mor10u		
	nOHp.3		nRCHO		EEig10d.5					G2s		
	EEig12d		H.052		MATS4p					MATS8m		
	ESpm15u E1u		nRCOOH.4 PW5.1		RDF085e EEig09d					Mor13p DISPe.2		
	EEig09d		Infective.80.2		X4A.1					B05.C.O2		
	S_dsCH		RDF140m		nRCOOH.2					B09.C.O1		
	X5A DISPe		B04.C.O2		EEig10d.6					Infective.80		
	Ke		nRCOOH.5 JGI7.1		MATS8m.2 nRCO					nHBonds C.026		
	Ke.1		PW5.2		GVWAI.80					MATS5v		
			F02.C.N1		S_aaaC nRCOOH.3					SPH.1 B09.C.O2		
			E2s.1 Mor10e		CIC4					B09.C.O2 B05.C.O3		
			EEig10d.1		nOHp					EEig10d.2		
			nRCOOH.6		MATS8m.3					JGI4.1		
			G2v.1 nCconj.1		MATS4e EEig10d.7					nRCOOH.1 MEcc.1		
			X5A		nOHt.2					EEig09d.1		
			Infective.80.3		nRCOOH.4					F04.C.N1		
			nRCOOH.7 C.043		JGI7.1 EEig10d.8					Mor32e C.008		
			B08.C.C1		nCconj					BEHp5		
			PW5.3		B04.C.N.					EEig10d.3		
			Hy.1 EEig09d		R7m. MATS2e					MATS4p nPyridines		
			nRCOOH.8		X4A.2					B09.C.O3		
			CIC		E2e EEio12r					B05.C.O4		
			MATS8m GATS5e		EEig13r EEig10d.9					MATS8m.1 HATS4p		
			MATS2m		PJI3					nRCOOH.2		
			EEig04x.1 Infective.80.4		MATS8v E2s.1					Infective.80.1 JGI4.2		
			X5A.1		EZS. I EEig10d.10					EEig10d.4		
			X5A.2		MATS4p.1					B05.C.O5		
					B02.C.C1 nRCHO					Mor10e DISPm		
					nRCHO nRCOOH.5					B05.C.C.		
					EEig10d.11					B10.C.O.		
					nOHt.3					EEig10d.5		
					JGI7.2 nRCO.1					nThiophenes MEcc.2		
					JGI6					G2s.1		
					E1u					0.057		
					MATS6v.1 EEig10d.12					F04.C.N2 Mor32p		
					MATS4p.2					Mor13p.1		
					MATS8m.4					GATS8v		

Table 3.1 (Continued)

Desc. Symbol		Desc. Symbo		Or	Desc. Symbo		Desc. Symbol		Desc. Symbo		Desc. Symbol
	AgOr54	TI1	HATS4p	AgOr67	VRv2	AgOr42		AgOr41		AgOr33	EEig06x
nRCOOH	Correlation		MATS5m	Correlation		Correlation		Correlation		Correlation	
EEig10d	0.8997646	nRCOOH	nOHp	0.8871336		0.84541		0.8698281		0.890219	EEig10d
Hy		BAC	EEig11x.5		Ui		Infective.80		RBF		Hy
GNar		BLTD48	nRCOOH.6		EEig09d		TPSA.NO.		DISPe		Mor32v
O.057		JGI4	EEig09d.4		nDB		HNar		H2m		Infective.80
Infective.80		B08.C.O.	JGI4.5		H2m		DISPm		Hy		O.057
PHI		B03.C.O.	MATS8v.1		MATS5e		E2s		Dv		Xindex
MATS3p		EEig11x	G3s		G3v		B08.C.O.		O.057.1		EEig09d
MATS8v		R2m.	MATS2p		S sOH.1		Mor07u		Infective.80		MATS4v
BEHp1		EEig09d	H2m		JGI7		B05.C.O.		EEig09d		B09.C.O.
HATS3p		B05.C.C.	H2m.1		BEHm1		B09.C.O.		JGI4		nRCOOH.1
nRCOOH.1		RDF140e			E2u		Ну		JGI10		Mor10u
EEig09d		GATS8v			B09.C.O.		nRCOOH		E1e		R8m.
G2u		MATS5e			O.057		EEig10d		MATS4e		RARS
nHBonds		HATS5m			ESpm01d		JGI4		JGI7		EEig10d.1
B09.C.O.		Mor30m			EEig12d.1		L3m		0.057.2		F03.O.O.
S_sNH2		nRCOOH.1			IC1		X5Av		BEHm1		Mor30m
BEHp1.1		Infective.80			JGI4		HATS8m		DISPm		MATS5e
		GATS4e					E2s.1		HATS5e		RDF150e
EEig12d		GAT 54e B09.C.O.			EEig09d.1		JGI10		HATS56 B09.C.O.		Infective.80.1
E1u EFictod 1					ESpm15d						
EEig10d.1		R4e			E1u		MATS3e		C.026		nRCOOH.2
E1m		Ui			HATS8m		Mor10e		SPAM		G1u
nRCOOH.2		nRCOOH.2			G3v.1		DISPm.1		nRCOOH		EEig09d.1
nRCHO		EEig10d.1			EEig11d		PW5.1		EEig10x		EEig09d.2
PW5		JGI4.1			nROH		EEig09d		nN		
BEHp1.2		nN			R5p.		MATS6p		PW3		
Mor32v		MATS8v			DISPm		nRCOOH.1		S_dssC		
HATS3p.1		R3u.			Infective.80		Infective.80.1		O.057.3		
Infective.80.1		MATS3p			O.057.1		GATS5e		nCrs		
O.057.1		B09.C.O1			E2e		GATS5e.1		DISPm.1		
Jhetp		EEig11x.1			nN				DISPm.2		
EEig09d.1		Mor28u			B08.C.O.						
E1u.1		nHBonds			Jhetp						
E1u.2		JGI4.2			EEig09d.2						
		EEig10d.2			O.056						
		E1u			RDF125m						
		Ts			nR05						
		EEig09d.1			C.026						
		B05.C.C1			G3v.2						
		nArOR			nRCOOH						
		B09.C.O2			nDB.1						
		MATS8m			HATS8m.1						
		B05.C.C2			HATS8m.2						
		EEig11x.2									
		nRCOOH.3									
		MATS6v									
		R5e.									
		Mor10e									
		JGI4.3									
		EEig09d.2									
		B02.C.C.									
		RDF150v									
		EEig11x.3									
		GATS4e.1									
		nRCOOH.4									
		C.034									
		MATS5p									
		GATS8v.1									
		EEig11x.4									
		B09.C.O3									
		R5m.									
		JGI4.4									
		EEig09d.3									
		R2m1									
		EEig04r									
		nRCOOH.5									
		EEig10d.3									
		GATS4e.2									
		B09.C.O4									

Table 3.1 (Continued)

Or Desc. Sy AgOr45 nRCOOI Correlation 0.8828472 RATS1m Desc. Symbol nRCOOH R2m. Hy B09.C.O. nRCOOH.1 Mor13m nRCOOH.2 nDB Mor10p B03.C.C. GATS5e EEig10d nRCOOH.3 nN nΝ nN EEig12x MATS4p nOHp nRCOOH.4 GGI8 R2m..1 nRCOOH.5 B02.C.C. RDF140e MATS6p Infective.80 R2m..2 F03.C.N. nRCOOH.6 JGI4 nRCOOH.7 JGI8 MATS3m C.006 R2m..3 S_dssC nRCOOH.8 nCOOH.8 nCrs B03.C.C..1 RDF150p Hy.1 HATS4p nRCOOH.9 EEig09d GATS5p nHBonds B09.C.O..1 nOPp.1 nRCOOH.10 R2m..4 R2m..5

Table 3.1 Continued

Table 3.2: Natural odor library predictions found in the top 500 predictions foreach Anopheles Or

The prediction type (Activators, Fishing Activators, or Inhibitors), chemical structure, and predicted distance from the known training activators is listed for each odor. Compounds marked in grey boxes represent odors from the training library.

ors		Dist	000	0 0	0 0.28607																									
Predicted activators	Or20	Structure	CC1(CCC(01)C(C)(C)0)C=C 0 Cc1sq(nc1C)C 0 C=CC(CCC)0 0		CC1CCC(CC1)O CCCC(CCC=C)O																									
/ators		Dist	000	0 0.13836	0.18559 0.23354	0.23747	0.2591	0.29317	0.321/29	0.34758 0.35081	0.35445	0.37682	0.38522	0.39915 0.41159	0.4336	0.45964	0.48283	0.48809	0.48973	0.50695	0.50946	0.51199	0.52976	0.54279						
s Predicted activators	0r21	: Structure	C(=0)(C)c1cccc1 C=CC(CCC)0 CC/C=C\CC0	CC1=CC(CCC1)0 CCC=CCC0	2 CC(CCO)C=C 6 CC(=CCO)C				00	2 CC1CCCCC1=0 3 CC1C(CCC1)C(=0)C	00	00		00	4 C1(CC=CCC1)CO	. 0	2 CCC(=0)CC(C)C	0	9 CCC(C)CC(=0)C		7 CC1=CC(=0)CCC1	.0	1 CCI =CCC(=0)CC1 9 CCI =CCCC(=0)C1	-	1	7	0	10.4	3	5
ctivator	9	Dist	000	00	0.32202 0.32466	0.32615	0.32925	0.34169		0.40662 0.41673	0.42004 0.43056	0.43518	0.45538	0.45797 0.0.46236	0.47274	0.47641	0.47712	0.49792	0.50499		0.52487	0.57069	0.58139	0.60201	0.61211	0.61447	0.6246	0.64035	0.65727	0.77596
Predicted activators	Or56	Structure	s1cncc1 Cc1 ncsc1 C(CCCCC)O	CC(CCO)C	c(cc=cc)o cc(co)cc	CCC=CCO			00	CC(C(C)0)CC	CSCCCO CSCCCO	00	0	00	CC(C=CC)0	0	00	.0	v cc(c)c(c)o			.0				0(0)0(0)0000	CCC(C=C)0	CCCCCC(C)0 CCCCCC(C)0	ccccccs cc(c)ccs	cct (ccc) (cct ccc) (cct ccc1
vators		Dist	000	00	0 0	00	0.131918	0.43901	0.467956	0.469796 0.501183	0.535788	0.575718	0.611034		0.666086	0.739457	0.759834	0.764383	0.783687	0.791385	0.797689	0.806178	0.82486 0.828945							
Predicted activators	0r38	Structure	CCC/C=C/C=0 c1(cccc1)C=0 s1cncc1	C(C)Oc1sccn1 CC(C)CC1=NC=CS1	c(cccc)o c(cccc)o					CCCCCCO	CC(CCCO)C	C(CC=CC)0 0.575718 CC1 - CC - CC1 -	C1 = CC = C(C = C1)CCO	CC1 = CC= CC(=C1)C= 0 CC1 = CC= CC=C1C=0	C1(CC=CCC1)CO	CCSC	cc(ccco)cc	CN1C=CC=C1	C1=CNC=C1	CCC1=CC=C01	0100001	c1(cacc1)C(C)O	C=NCC CC1 NCCS1							
		Dist	000	0.1952 0.27902	0.28733 0.29512	0.29931	0.37874	0.38646	0.39218	0.40798 0.40825	0.41836 0.41886	0.42959	/70004-0																	
Predicted activators	0r50	Structure	0=C1[C@@](C2)(C)CC[C@@]2([H])C1(C)C 0 CC1(CCC(01)C(C)(C)0)C=C 0 CC1sc(nc1C)C 0)C=C 0	CC1(C(=0)C2CCC1C2)C CC(C)C12CCC(=0)C1C2	CC1C2CC2(CC10)C(C)C C(=0)(C)C10C(CC1)(C)C=C		CC(C)C12CCC(C1C2)(C)0		CSC1=NC=CN=C1 C[C@@H]1[C@H]2C[C@]2(CC1=0)C(C)C	cc1cccc(c1=0)(c)c cc12cccc(01)(c02)C	CC(C)C12CCC(01)(CC2)C CCC1=NC(=C31)C																			
ators		Dist				0.00439546	0.04337664	.05512895	0.07779456	0.07845724 0.08242568	0.0903326	0.09366896	0.0993155	0.1063697 0.1119358	0.113021	.1138653														
s Predicted activat	0r12	Structure	C(=0)(C)c1sccc1 0 Cc1ncsc1 0 C(=0)(C)c1sccn1 0	C(C)Oc1sccn1 0 CC/C=C\CC0 0	CCI CCC(CC1)0 0 CCI =CC(CCC1)0 0	CCC=CCC0	01C(C1CC)CC0	CCI = CC = CC = CIS	cc(=0)c1=cc=c01 cc(=0)c1=cc=c01	CCI =C(SC=N1)C=C C(C)CI C(CC1)O	CC1 = C(C= C01)SC CC1 = O(C1 = NC=CN=C1	CCC1=NC=CN=C1		cc=cc=cc0 cc1=cc=c01	CC1 = CC= CC(=C1)C= 0	CC(=0)C1 =CN=CC=C1											_			
ctivators	-	Dist	000	00	0 0	0.04578		0.39271	0.39862	0.42129 0.44045	0.44514	0.46992	0.47871	0.53738 0.54014	0.55011	0.55595	0.60273		0.6465	0.65665	0.65837	0.66895	0.67588		0.69244		0.71214 C 0.71248			3.2
Predicted activators	Or57	Structure	Cc1 ncsc1 C(CCCC)O CC(CCO)C	cc/c=c/co	CC1 CCC(CC1)0 C(CC)0C(=0)C	CCC=CCC0	C1(CC=CCC1)CO		CCC(C)CCO	CC(CC(C)0)C CC1(CCCC1)0	CC(CC)OC(=0)C		c(cc=cc)o	cct =cc=co1 cc(ccco)c	CCI CC(CC1)0	CC=CCCC0	CICC=NC1	C1=COC(=C1)CS	C1CC=CC(C1)0	20(20)22	CCC(CCC)0	CNIC=CC=CI	CCC(C)C(CC)0	CCI CCCC(=0)01		CC1 (CCCC=C1)0	CCCC(C)C(C)O	coc(=o)c=cc		Table 3.

vators		Dist	0 0 0 0 0.04093 0.08321 0.08321 0.08321 0.093717 0.093717 0.093717 0.093717 0.093717 0.014785 0.014850 0.014850 0.014850 0.014850 0.014850 0.014850 0.014850 0.014850 0.014850 0.014850 0.014850 0.014850 0.0148500 0.0148500000000000000000000000000000000000
Predicted activators	0r46	Structure	cc(ccop)c cc(cco
ators		Dist	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Predicted activators	0r48	Structure	Cicti-a)Create Cicti-a)Create Cicti-a)Create Cicti-a)Create Cicti-a)Create Cicti-a)Create Cicti-a)Create Cicti-a)Create Cicti-a)Create Cicti-a)Create Cicti-a)Create Cicti-a)Create Cicti-a)Create Cicti-Cictica)Create Cicti-Cictica)Create Cicti-Cictica)Create Cicti-Cictica)Create Cicti-Cictica)Create Cicti-Cictica)Create Cicti-Cictica)Create Cicti-Cictica)Create Cicti-Cictica)Create Cicti-Cictica)Create Cicti-Cictica)Create Cicti-Cictica)Create Cicti-Cictica)Create Cicti-Cictica)Create CicticaCreate
SI		Dist	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Predicted activators	0r39		
ators		Dist	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Predicted activators	Or 15	Structure	
tors		Dist	0 0.03501 0.055819 0.055819 0.055819 0.055819 0.0558461 0.0584861 0.07812 0.098133 0.098179 0.098179
Predicted activators	Or11	Structure	d(creat)c=0 c(c)d(creat)c=0 c(c)d(c)d(creat)c c(c)d(c)d(creat) c(c)c(c)d(creat)c c(c)c(c)d(creat)c c(c)c(c)d(creat)c c(c)c(c)d(creat)c c(c)c(c)d(creat)c c(c)c(c)d(creat)c c(c)d(creat)c(c) c(c)d(creat)c c(c)d(creat)c c(c)d(creat)c c(c)d(creat)c c(c)d(c)d(creat)c c(c)d(c)d(c)d(c)d(c) c(c)d(c)d(c)d(c)d(c)d(c)d(c) c(c)d(c)d(c)d(c)d(c)d(c)d(c)d(c)d(c)d(c)
ators		Dist	000001010010000000000000000000000000000
Predicted activators	0r75	Structure	CCI = 001CCCCCC CCI = 001CCCCCC CCI = 001CCCC CCI = 001CCC CCI = 001CC CCI = 0
ators		Dist	(1115557) (1115557) (1115557) (1115577) (1115577) (1115577) (1115577) (1115577) (1115577) (11
Predicted activators	Or4	Structure	creations of the construction of the construct
tors		Dist	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Predicted activators	0r18	Structure	

Predicted activators	Predict	tors	Predicted activators	ators	Predicted activators	tors	Predicted activators	tors	Predicted activators	itors	Predicted activators	S
0			0r13		0r1		0r10		0r6		0r2	
Structure Dist		Dist	Structure	Dist	Structure	Dist	Structure	Dist	Structure	Dist	Structure	Dist
CC(CCC=C(C)C)CC=0 0	Cc1c(cccc1)0 Cc1cr(crc1)0	0 0	c1(cccc1)C=0 Cc1ccc(cc1)0	0 0	c1(ccccc1)0 Cc1cc(ccc1)0	00	c1(cccc1)C=0 C(C)c1 c(cccc1)0	0 0	C(=0)(C)c1ccccc1 C(=0)(C)c1sccc1	0 010	c1(ccccc1)0 c1(ccccc1)C=0	0 0
CC(=CCC(=0)C)C = 0	Cc1ccc(cc1)0	0	C(=0)(C)c1sccc1	0	Cclccc(cc1)O	0	C12=C(NC=C2)C=CC=C1	0	C(=0)(C)c1sccn1	0 Cc1	Cc1c(cccc1)0	0
C(CCCC)OC(=0)C 0	C(C)c1c(cccc1)O	0	Cc1scnc1C	0	c(cccc)o	0	CC1=CNC2=C1C=CC=C2	0	C(=0)(C)c1ncccc1		C12=C(NC=C2)C=CC=C1	0
		0 0	c1(cccc1)C#N		cc1ccc(cc1)0	0	CCC1=CC(=CC=C1)0	0.1015	CC(=0)C1=CC=NC=C1		CI=CC(=CC=CIC=0)0	0.010196
	23 CelsenelC				CI(CCCCL)0			0.184/		0.01229 C1(0	c1(ccccc1)c(=0)0	0.017154
Ļ		0 27619	כורדתה(ניד)כו		CCT=C(C=C(C=CT)O)C	77001.0		0 5827				710710 0
· · ·		0.41637	C1 = CC = C(C = C1)CS		2010/12/2010/2010/2010/2010/2010/2010/2		CCC1=CC=CC=C1S	0.6009	CC(=0)C1=CN=CC=C1			0.019241
	98 CCC1=CC=CCS	0.47183	C1 = CC(=CC=C10)0	0	C=CC1=CC=C(C=C1)0	0.20264	CCC1 = CC(= CC(= C1)C)0	0.6019	CC1=CC=C(S1)C=0	0.0597 0=0	0=C1SC2=CC=CC=C2N1	0.020891
0	16 CC1=CC=CC=C1S	0.53176	n1cc(ccc1)C=0	0.02253	CC1=CC(=C(C=C1)C)O	-	CC1=CC=CC=C1C=O	0.6048	olc(cccl)C=0		CC1=CC=C(C=C1)C=0	0.021228
		0.56118	cc1=cc=c(S1)C=0		cc1=c(c(=cc=c1)o)c	-	c1(cccc1)C(C)(C)0	0.6131	CC1=CC=C(01)C=0		nc2c1cccc2	0.022034
		0.63001	CC(=0)C1=CC=CN1	0.0256	c1(ccccc1)C(C)O		c1(cccc1)C(C)N	0.654	CC1=C(SC=N1)C=C		c1(ccccc1)NC=0	0.023269
		0.70917			CCCC=CCO	0.22901	C1CC2=CC=CC=C2NC1	0.6613	CCC(=0)C1=CC=CC=C1		CC1=CC=CC=C1S	0.028825
		0.73839			Oc1ccc(cc1)OC	0.23076	Nc1c(cccc1)C=O	0.6737	C1=COC=C1C=O		C1=CC=C(C=C1)C=NO	0.032971
Ū.		0.74378			CC1=CC(=CC(=C1)0)C	-	CC1=C(C(=CC=C1)0)C	0.6781	CC1=CC=CC(=C1)C=O		C1=CC=C(C(=C1)0)Cl	0.03301
-		0.78212			01c(ccc1)C0		C(C)c1 c(cccc1)C=0	0.6902	nlcc(cccl)C=0	0.09833	Cc1ccc(cc1)C(=0)CC	0.033088
CCCCOC(=0)CC 0.39692		0.89065				0.24619	CC1=CC(=C(C=C1)C)0	0.6948	COC(=0)C1=CN=CC=C1		COCI=CC=C(C=CI)C=0	
ر	9/ CSULIEUCEUU	0.89947				0.24803		01/10/		O.IZIIB CI	0.12116 CI=CC=C(C(=C1)[N+](=O)[O-])O	10054061
	~	14/06/0				0.28043				5		0.034//2
		20806.0				0.28/8/ 0		0.7201				
ç	// LIEUCEU(L(ELI)CU)U	44/06-0				59C0C 0		102/.0				
		0.99202				1002 0						
ç		1.00099				0.32257						
	88 CNc1cccc1	1.00204				0.32611						
	98 CCC1=CN=CC=C1	1.00636				0.33756						
		1.00813			c1(ccccc1)CO	0.34707						
20	85 c1(ccccc1)CO	1.00997			cc1(cccc1)0	0.35191						
	52 CC1=CC=C(01)C	1.01527			c1ccc2cc(ccc2c1)0	0.35659						
		1.02951			ccic(ccci)o	0.35719						
CCCC(=0)OCCC(C)C 0.56128	28 C1=CC=C(C=C1)N	1.04535			cc(c(c) 0)cc	0.35725						
	0.56304 C(CCC)cloccc1	1.05691			ccc(c)o	0.3574						
	0.57665 CC1=CN=CC(=N1)C	1.1009			C1CC(0C1)C0	0.38537						
	0.57963 NC1=CC=CC=CIS	1.10182			C=C(CO)CC	0.38622						
ğ	0.59023 CC1=CC=C(C=C1)OC	1.11908			ccc(c)c(cc)o	0.39381						
	08				cocc(c)o	0.39605						
5	67				cclcc(ccl)o	0.40156						
	02					0.41058						
Ľ	20					1/11+.0						
	53											
0	55											
CCC(=0)OCCC(C)C 0.64353	53											
	70											
	;											

Predicted activators	Predicted Fishing Activators	vators	Predicted Fishing Activators	s	Predicted Fishing Activators	ators	Predicted Fishing Activators	ators	Predicted Fishing Activators	ors
Or8	0r32		0r26		0r53		Or 16		0r64	
Structure Di	Dist Structure	Dist	Structure	Dist	Structure	Dist	Structure	Dist	Structure	
CC(=0)CCCCC 0	CC1(CCC(01)C(C)(C)0)C=C	00	0=c1[C@](C2)(C)cc[C@]2([H])C1(C)C	00	C1(=0)CCCCC1	0 C1(c1(ccccc1)C=0	=0	0=c1[c@](c2)(c)cc[c@]2([H])c1(c)c	
	c(c)oc(=0)ccccc	00	CC1(CCC(01)C(C)(C)0)C=C	00	CclscnclC	0.0	Cc1c(cccc1)0			
0	CCC=CCCO		cc1(c2ccc(c2)(c1=0)c)c	-	c(ccc)o	0 C1(c1(ccccc1)C0		C1(CCCCC1)O	
CCCCC(=0)CC 0.10224	224 CC(C)CCOC(=0)C(C)C	0.3159 0	cc(c)c1ccc(c=c1)(c)0	0.54132 0			CCI=CC=CCS	0.05644 CC	CC1(C2CCC1(C(C2)0)C)C	
			cc1/c)c1zccc(c=c1)(00z)c cc1/c)c1c2()cc3=0		ct(=0)C=CCCC1		0.19305 ct1(mmc1)C(C)0	~	CCCC(C)(C)) CCCC(C)(C)(C) CCCC(C)(C)(C)	
	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC		C12(C(=0)CC(C1(C)C)CC2)C	-	C1(CCCC1)0	0.2259 C1	C1=CC=C(C=C1)CS		CC(=C)C1CCC1(C)CCO	
U	-		ccioc2(occc2)ccci		CCICCCNCI	0.28112 CO	COC1=CC=CC=C1		c[c@]i2c[c@@H]3c1c(c)(c)0[c@@H](03)c2	3)C2
	-		CC(C1OC(C=C)(C)CC1)CO	~	CC(CO)C=C	0.29902 CC:	CC1=CSC(=N1)C	-	OC1C2C(C)=CCC(C2)C1C	
U	766 CCCCCCC(=0)C(C)C		CC1(C2C(=0)C(CC1C2)C)C	0.701 C	cc(c)c(c)o	0.30959 CC:	CC1 = CC = C(C = C1)C = 0		cc1(c2cc=c(c1c2)c0)c	
	-	0.4074		ō	CC1C(CC01)S		CSC1=CC=CC=C1		CC1=CC(C2CC1C2(C)C)0	
		0.41182		Ö	CCICCCCNI		CCI = CC(=C(C=CI)C)		cc(c(c)o)cc	
CC(C(=0)C)CCCC 0.36/22	722 c1(ccccc1)C(0)C(=0)C	0.44233		50		0.33909 CC	cc1=c(c(=cc=c1)c)0 c1=cr(=cr=c1c=o)0	0.13249 CI	CI(CC=CCCI)CO	
L L		0.44000		50						
		0.46148		50			0-1-0000000000000000000000000000000000			
		0.46867		00				0.14		
	100000000000000000000000000000000000000						CC1 = C(C = CC1 = C1)0)Cl	0.14146		
~	524			0				0.14307		
0	115			0	C(C)(CC0)S		CC1=CC=C(01)C	0.14687		
	199			ö	ccc(c)o	-	CNc1 ccccc1	0.14727		
	255			ō	ccc(c=c)o		C=CC1=CC=C(C=C1)O	0.14751		
CCC(C)CC(=0)CC 0.47386	386			Ū	CNICCCCI		CCC1=CC=C01	0.1488		
	679			U	CICCNCCI		c1(ccccc1)COC	0.15768		
-	135			5	nH]1cncc1		CC1=C(C=C(C=C1)0)C	0.1614		
0	664			U	C1=C0C(=C1)CS		c1(ccccc1)C#N			
	194			5	nH]1nccc1	-	C1=CC=C(C=C1)COCC2=CC=CC=C2			
ŭ	218			ō	200(0)00		CC1=CC(=C(C=C1)0)C	0.17198		
	571			0		-	Cclcc(cccl)C	0.17222		
0	221			0	cc(c)(c=c)0		CI =CC=C(C=CI)S	0.17682		
	877			50				0.17892		
	233			50				0.180/8		
	L30 037			50		0.44354 CL.		0.18080		
	02/ 901			00				0.18909		
	754				atronat			0.18008		
	055			÷C	rrccct rrccct			0.19022		
	200			00				0 19127		
	59			00		-		0.19216		
	873			00			C1=CC=C(C=C1)N	0.1945		
CCCCCCCC	375			0.2	s1cccc1					
ccccccccccc(=0)cc 0.5554:	541			Ŭ	Cc1cocc1	0.4798				
g	119			Ö	CC1C(=0)CCS1	0.48568				
	799									
CCCCCC(=0)CCCCC 0.56822	822									

ivators	Dist	000	0 0	0.18488	0.20736	0.23524	0.25102	0.25239	0.2526 0.28055	0.28207	0.28994	0.31016		0 32034	0.32318	0.32654	0.3297	0.34256	0.34589	0.34903	0.35361	0.35646	0.35945	0.36183	0.36369													
Predicted Fishing Activators Or 63	Structure	CCC(=0)CCCCC C=CC(CCCC)0 C=CC(CCCCC)0	c(cccc)oc(=0)c c(cc(c)c)oc(=0)c	ccc(cc)coc(=o)c	<pre>ccc(=0)occ(c)c</pre>	CCCCOC(=0)C(C)0	CCC(C)COC(=0)C OC(C)C(=0)CCCCC	oc(c(=o)c)ccccc	COC(=0)CC(C)CC	COC(=0)C(0)C(C)CC	CC(N(C)CCCC)=0	CC(C)CCNC(=0)C	CCC(C)CNC(=0)C	NLG@@TJ(LC@@TJ(C)CC)=0 CCOC(=0)C(C)CC=C	OC(C(=0)C)CCCC	CC(CNC(=0)CC)CC	oc(c)c(=0)ccc		CC(=CCCC(=0)C	COC(=0)C(0)CC(C)C	CC(C(=0)C)CCCC	CCCCCCC(=0)0C		CCCC=C(CC)CO	ccc(=0)0ccc(c)c													
Ors	Dist	0 0 0.02263	0.04185 0.0791	0.08094	0.49185	0.4922	0.49409 0.49466	0.49729	0.51273		0.51843																											
Predicted Fishing Activators Or59	Structure	c=cc(cccc)0 c=cc(cccc)0 ccccccc(c=c)0	cccccccc(c=c)o			C(CCC=C)O	CC(CC)(C=C) CC(C)(C=C)0	cc(co)c=c		cc(c)cccc(c)cccc(c)cccc(c)(c=c)o	CC(CCCC(C)(C)0)C=C																											
tivators	Dist	000	0.10759 0.25083	0.25956	0.35369	0.37792	0.41393 0.41484	0.4324	0.44034		0.51696	0.86599	0.89011	0.91951	0.94882	0.95335	0.9912	1.03879	01c0.1	1.14164	1.15157	1.15798	1.1648	1.20152	1.20494	1.21477	1.22659	1.23816	1.25784	1.27299								
Predicted Fishing Activators Or65	Structure	Cc1c(cccc1)O Cc1ccc(cc1)O C(C)c1c(cccc1)O	CCC1=CC(=CC=C1)0 CC1=C(C(=CC=C1)0)C	CC1 = CC(=C(C=C1)C)O	CCCC1=CC(=CC=C1)0)	CC1=C(C=CC(=C1)0)Cl	CC1=CC(=CC(=C1)0)C CC1=CC(=C(C=C1)0)C	CC1 = C(C(=CC=C1)C)O	CC(C)C1=CC=CC=CC=C10 CCC1=CC(=CC(=C1)C)0	CC1 = C(C(=C(C=C1)0)C)C	CC1=C(C(=C(C=C1)C)O)C	CCC1=CC(=CC=C1)CO	CCC(C1=CC=CC=C1)0	UCT CCC(CCT)UC	c1(ccccc1)C(C)(C)0	CC(CC1=CC=CC=C1)0	C1=CC=C(C=C1)CCO	CC1=CC(=C(C=C1)0)0C	Colorection Colorection	CC1=CC=C(C=C1)OC	COC1=CC=CC=C1	CC1=CC=CC=C10C	c1(ccccc1)CCOC	CC1=CC(=C(C=C1)OC)C	C=CCI=CC=C(C=CI)0 C(CC)c1occc1	C1C(01)C2=CC=CC=C2	C(CCC)clocccl	c1(ccccc1)CC	CC1=CC=CC=C1S	c1(cccc1)C(C)N C1=CC=C(C=C1)CCN								
	Dist	0 0 0.0046	0.0062 0.0114	0.0114					0.0251 0		0.0283 0													0			0											
Predicted FISHING ACLIVATORS	Structure	0=C1[C@](C2)(C)CC[C@]2([H])C1(C)C 0=C1[C@@](C2)(C)CC[C@@]2([H])C1(C)C CC1(C2CCC(C2)(C10)C)C	cc1(c(=0)c2ccc1c2)c cc1(c2ccc(=0)c1c2)c		CC1(C2CCC(C2)C1(C)O)C	CC(C)C12C(C=C(C)C1C2)=0	CC1(C2CCC1(C(C2)0)C)C CC1CCCC(C1=0)(C)C	cc1(c2c1c(cc(c2)c)0)c	C12(C(=0)CC(C1(C)C)CC2)C CC1=CC(C2CC1C2(C)C)0	CC1=CC(=0)C2CC1C2(C)C	CC1(0)C=CC2CC1C2(C)C																											
	Dist	000	0.14358 0.18468	0.20187	0.2304	0.23787	0.23893 0.24076	0.25091	0.25377	0.25888	0.27203	0.28335	0.29031	0.30144	0.30914	0.31214	0.32292	0.32458	0.33174	0.33793	0.33979	0.34591	0.34683	0.3502	0.366	0.37069	0.37486	0.38056	0.39057	0.3917	0.39703	0.40361	0.40545	0.40586 0.40618	0.41297	0.41736	0.41885 0.42487	0.43247
Or31	Structure	CC(=CC/C(=C/COC(=O)C)/C)C c1(ccccc1)COC(=O)C COC(=O)CCCCCCC	C(C)OC(=0)CCCCCC CC(CCCC(=C)C)CCCCC	cc(=cccc(=ccoc(=o)c)c)c	<pre>cc(ccc=c(c)c)ccoc(=0)c</pre>	CC(=CCCC(=CCCC=0)C)C	CCCCC=CCCC(=0)0CC	CCCCCCCC(=0)CCC	COC(=0)CCC=CCCC CCCCCC(=0)OC	CC(CCCCCC(=0)C)C			CCCC(=0)CC(=0)OCC			C(C)OC(=0)CC=CCCCC	CCCCCC#C(-)C)/CCC=0		CCC=CCCCC(=0)CC	CCC(=0)OCC=C(C)CCC=C(C)C				CC(=CC)COC(=0)C	C(CCC=CC)OC(=0)C	ccc(=0)occ=c(c)cccc(=c)c		0=C(0C)CCCCC(0C)=0	C(C)OC(=O)CCC(C)CC	CCCCCC#CC(=0)0CC U=U(UCUC(=0)U)UUU		COC(=0)CC1=CC=CC=C1	COC(=0)CCC(C)CC	CC(CCOC(=0)C)CC	cccccoc(=0)cc		CCCC=CCOC(=0)[0-])CC	
	Dist	000	0.07571 0.09705	0.11173	0.18487	0.19363	0.19597 0.19624	0.19684	0.19878	0.20029	0.20132																											

ictions		Dist	0000		0.60377 0.60603 0.60621
Inhibitor Predictions	Or66	Structure	0 CC(=0)CCCCC 0 CC(=CCCC)0 0 CC(=CCCC)0 0 CC(=0)C)C		CC(CCCO)CC CCC=CCC(=0)OC CCCC(=0)OCC=C
tions		Dist			
ions Inhibitor Predictions		Dist Structure	0 CCC(=0)CCCCC 0 C(=0)(C)c1sccc1 0 C(=0)(C)c1nccc1 0 C(=0)(C)c1nccc1	0 = = = = = = = = = = = = = = = = = = =	
ons Inhibitor Predictions		Dist Structure [0 slencc1 0 Cclncsc1 0 C=CC(CCCC)0 0 C=CC(CCCC)0	0.13684 CICCC10 0.4339 CICCC0CC=0/C 0.4374 CICCC10 0.4374 CICCC10 0.4374 CICCC10 0.39321 CI-CSCC1 0.39321 CI-CSCC1 0.49392 CICCC10 0.39581 CI-CSCC1 0.49392 CICCC10 0.49392 CICCC10 0.49392 CICCC10 0.55892 CICCC10 0.55895 CICCC10 0.55895 CICCCC00 0.55895 CICCC00 0.55895 CICCCC00 0.55895 CICCC00 0.55895 C	
ions Inhibitor Predictions		Dist Structure	0 cl (ccccc1)0 0 Cc1c(cccc1)0 0 C=CC(CCCCC)0 0 CCC/C=C\C0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
Inhibitor Predictions	0r25	Dist Structure	0 CC(=0)CCCCC 0 c1(cccc1)COC(=0)C 0 C=CC(CCCC)0 0 C(C(C)C)OC(=0)C	0 1111 5 (CCCC)(5)05(7=0)7 0 12845 CCCCCCC = 0)7 0 12845 CCCCCCCC = 0)7 0 12845 CCCCCCCC = 0)7 0 32815 CCCCCCCCC = 0)7 0 32815 CCCCCCCC = 0)7 0 33815 CCCCCCC = 0)7 0 43815 CCCCCCC = 0)7 0 43815 CCCCCCC = 0)7 0 44111 0 48339 0 44124 0 44233 0 44124 0 44233 0 44134 0 44233 0 44134 0 44233 0 44134 0 4423 0 44134 0 4423 0 44134 0 4423 0 44134 0 4413 0 44134 0 4414 0 4414 0 4414 0 44134 0 4414 0 44134 0 4414 0 4414 0 44	
Inhibitor Predictions		Structure	ų	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ued)
ators		Dist		0.0.021 0.0.021 0.0.035 0.0.0453 0.0.0453 0.0.0453 0.0.0453 0.0.0453 0.0.0453 0.0.0453 0.0.0453 0.0.0453 0.0.0453 0.0.0453 0.0.0453 0.0.0453 0.0.0453 0.0.0453 0.0.0453 0.0.0453 0.0.0453 0.0.0453 0.0.0553 0.00530000000000	ntin
Predicted Fishing Activators	Or61	Structure	cc(=0)ccccc c(cccc)o c=cc(cccc)o	CCCCCCCCCC CCCCCCCCCCC CCCCCCCCCCC CCCCC	Table 3.2 (Continued)

ctions		Dist D	
ctions Inhibitor Predictions	0r45	Dist Structure Creation Creation Creat	
ctions Inhibitor Predictions	0r33	Dist Structure 0 <t< th=""><th></th></t<>	
ctions Inhibitor Predictions	0r41	Dist Entructure 0.23123 CCCCCCD 0.23124 CCCCCCCD 0.23124 CCCCCCCD 0.23124 CCCCCCCD 0.23124 CCCCCCCCD 0.23124 CCCCCCCD 0.23242 CCCCCCCCD 0.23242 CCCCCCCCD 0.23242 CCCCCCCCD 0.23243 CCCCCCCCO 0.23243 CCCCCCCCO 0.23243 CCCCCCCCO 0.23243 CCCCCCCCO 0.23343 CCCCCCCCO 0.24234 CCCCCCCCO 0.24234 CCCCCCCCO 0.24234 CCCCCCCCO 0.24234 CCCCCCCCO 0.24234 CCCCCCCCO 0.24244 CCCCCCCCO	
ctions Inhibitor Predictions	0r42	Dist Entructure 0.010123 CCCCONCCONC 0.0101235 CCCCCCCONC 0.0101235 CCCCCCCONC 0.0101235 CCCCCCCCONC 0.011235 CCCCCCCCCONC 0.011235 CCCCCCCCCONC 0.011235 CCCCCCCCCONC 0.011235 CCCCCCCCCCONC 0.011235 CCCCCCCCCCONC 0.011235 CCCCCCCCCCONC 0.011235	
ctions Inhibitor Predictions	Or67	Dist Structure 0.0151 Structure 0.01170 CCCCCCCCCCCC 0.011170 CCCCCCCCCCCC 0.011170 CCCCCCCCCCCCCCCCC 0.011170 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	
ctions Inhibitor Predictions	0r54		
Inhibitor Predictions	0r43	Structure Dist Structure Contraction Contraction Contraction Contraction	

Table 3.3: Predicted odors validated as effective activators for several AnophelesOrs

Subsets of purchasable odors from prediction lists for several Ors were validated using single unit electrophysiology. The Or names, number of activators over the number of odors tested, accuracy percentage, and primary class (aliphatic or aromatic) of responding odors is listed for each validated Or. The total accuracy, as well as accuracies for aliphatic and aromatic responsive Ors, is also provided.

Ors	Active/Tested	Accuracy	Responding Class
AgOr1	5/9	56%	Aliphatic
AgOr2	1/6	17%	Aromatic
AgOr4	12/13	92%	Aliphatic
AgOr6	2/5	40%	Aromatic
AgOr8	7/9	78%	Aliphatic
AgOr10	8/14	57%	Aromatic
AgOr12	8/8	100%	Mix
AgOr20	2/15	13%	Mix
AgOr30	16/16	100%	Aliphatic
AgOr48	7/8	88%	Aliphatic
AgOr53	5/12	42%	Mix
AgOr56	13/14	93%	Aliphatic
Total		65%	

Aliphatic Only	84%
Aromatic Only	38%

Table 3.3

Table 3.4: Activity of a large panel of aromatic odors was tested against three aromaticly tuned Ors

Responses of the previously selected 37 aromatic odors are reported for Or2, Or6, and Or10. The number of odors tested, number activating at greater than 50 spikes/sec, and percentage are listed for each Or. An average activity is provided below.

	General Ar	omatic Assay	
Odor Receptor	Num Tested	Num >50 Spikes/Sec	Percentage
AgOr2	37	4	11%
AgOr6	37	3	8%
AgOr10	37	3	8%
		Average	9%

Table 3.4

Table 3.5: Optimized descriptor sets for Or2, Or6, and Or10

Optimized descriptor symbols and final descriptor-activity correlations are listed for each *Anopheles* Or. Descriptors are listed in ascending order of when they were selected into the optimized set. The number of times a descriptor was selected in an optimized descriptor set represent weights.

Or AgOr6	Descriptors ARR	Or AgOr2	Descriptors ATS6m	Or AgOr10	Descriptors Dv
Correlation	R8e.	Correlation	nCconj	Correlation	ARR
0.7075761	Mor07u	0.7844095	H1v	0.7818453	Infective.80
	BEHm7		ASP		Mor18p
	GATS2v		EEig11r		JGI6
	C.040		X4A		nBnz
	Mor16e		nArCO		HATS6m
	C.024		E3p		X5A
	Infective.80		0.057		B07.C.C.
	nFuranes ARR.1		Gs piPC09		N.075 HOMA
	H.049		GATS3e		Infective.80.1
	Mor30m		B06.C.O.		nROH
	R8e1		ESpm01d		HATS5m
	R3u		Mor23m		C.006
	Mor07e		nROH		Mor28u
	DISPv		Infective.80		RCI
	X4A		E2e		B07.C.C1
	B06.C.O.		B04.C.N.		MATS3e
	C.001		B06.C.O1		JGI6.1
	TPSA.NO.		piPC05		piPC05
			EEig11d		Infective.80.2
			0.057.1		RCI.1
			H1m		nFuranes
			nRCHO R3e.		EEig14r RCI.2
			nRCOOR		GATS6v
			MATS3e		N.075.1
			Gm		EEig11d
			Infective.80.1		ARR.1
			nROH.1		HATSv
			Mor28e		JGI7
			JGI4		PCR
			MATS7v		Infective.80.3
			nR.Cp		Ds
			PJI3		C.043
			C.006		JGI6.2
			0.057.2		Mv
			piPC09.1		EEig13d
			Mor08p nPyridines		HOMA.1 Infective.80.4
			R6e.		X5A.1
			B06.C.O2		G3e
			ESpm01d.1		PCD
			EEig11d.1		B07.C.C2
			0.057.3		Mor32m
			R3e1		nFuranes.1
			G3s		RCI.3
			ESpm05u		nPyridines
Table 0 /	-				

Table 3.5

Table 3.6: Top 75 predicted compounds for each Drosophila Or

The chemical structure and predicted distance from the known training activators is listed for each odor. All distances represent the minimum distance based on optimized descriptors to the previously known strongest active compound listed in the gray cells for that particular Or.

Or2		Or6		Or10	
Structure	Distance	Structure	Distance	Structure	Distance
C(=O)(C)c1ccccc1		C(=O)(C)c1ccccc1		Cc1c(cccc1)O	0
Cc1c(cccc1)O Cc1cc(ccc1)O) C(=O)(C)c1sccc1) C(=O)(C)c1sccn1		Cc1cc(ccc1)O Cc1ccc(cc1)O	0
Cc1ccc(cc1)O) CCC(C1=CC=CC=C1)=O		C(C)c1c(cccc1)O	0
C(C)c1c(cccc1)O) CC1=CC=C(C(C)=O)O1		CC1=CNC2=C1C=CC=C2	0
c12c([nH]cc1)cccc2) CCC(C1=CC=CC=C1)=O		COC1=CC=C(C)C=C1	0
CC1=CNC2=C1C=CC=C2) CC(=0)C1=CC=CO1	2.814136	COC1=CC=CC=C1C	0
N1C=CC=C1 CC1=CC(O)=CC=C1		CC(=O)C1=CC=CN1 CC(=O)C1=CC=CC=C1N	3.024555 3.589921	COC1=CC=C(C)C=C1C COC1=CC=CC=C1	0
SC1=CC=CC=C1) CC1=CC(=C(01)C)C(=O)C	4.542537	Cn1c2c(cc1)cccc2	0.9605277
CCC1=CC(=CC=C1)O	0.51988	CC(=0)C1=CN=CC=C1	4.603079	CCC1=CC=CC=C1S	1.08787
c1(ccccc1)C(C)N	0.7157186	C1=CC=C(C=C1)C(=O)C#N	4.853174	CC1=CC=CC=C1S	1.182823
Cn1c2c(cc1)cccc2	1.037082	CC(=O)C1=CC=CC=C10	5.11137	CC1=C(C(=CC=C1)O)C	1.216329
CCC1=CC=CC=C1S C1=CC=C(C(=C1)O)Cl	1.090404 1.202171	CC(=O)C1=NC=CN=C1 CC1=NC=CN=C1C(=O)C	5.311086 5.32461	CC1=CC(=C(C=C1)C)O CC1=CC(=C(C=C1)O)C	1.239482 1.239482
CC1=CC=CC=C10C	1.261832	C1C(O1)C2=CC=CC=C2	5.368613	CCC1=CC(=CC=C1)O)C	1.324363
CC(=O)C1=CC=CC=C1O	1.263328	CC1=CC=C(O1)C=O	5.706266	c1(ccccc1)C(C)N	1.382239
CC1=CC(=CC(=C1)O)O	1.27613	O=C(C1=CC=CO1)OC	5.861467	CC1=C(C(=C(C=C1)C)O)C	1.445959
CC1=C(C(=CC=C1)C)O	1.279905	CC1=C2C(=O)CCN2C=C1	5.918714	CC1=C(C=CC(=C1)O)O	1.446803
CC1=C(C(=CC=C1)O)C	1.28218	C1=CC=C(C=C1)CS	5.951914	COc1c(cccc1)N	1.465265
NC1=CC=CC=C1S CN1C=CC=C1	1.305137 1.318499	CCOC(=0)C1=CC=C01 CC1=CC=C(C=C1)OC	5.958834 6.049608	CNc1ccccc1 CC1=C(C(=C(C=C1)O)C)C	1.483803 1.627195
CC1=C(C=C(C=C1)O)C	1.346765	COC1=CC=CC=C1	6.09279	CCC1=CC(=CC(=C1)C)O	1.716798
CNc1ccccc1	1.360506	CC1=CC=CC=C1OC	6.180274	C1=CC=C(C(=C1)N)O	1.807295
CC(=O)C1=CC=CC=C1N	1.372227	COC(=O)C1=CN=CC=C1	6.185672	CC(=O)C1=CC=CC=C1N	1.828949
CC1=C(C=CC(=C1)O)O	1.407024	C1=COC(=C1)CS	6.205407	CCC1=C(C=CC(=C1)O)O	1.857206
CC1=CC(=C(C=C1)C)O	1.426872	CC1=CC=C(C=C1)C(=O)C	6.300831	CC1=CC=CC(=C1)C=O	1.860195
CC1=CC(=C(C=C1)O)C CC1=CC(=CC(=C1)O)C	1.426872 1.431107	O=CC1=CC=CC=C1NC CC1=CC=CC(=C1)C=O	6.304842 6.348972	CC(=0)C1=CC=CC=C10 CC(C)C1=CC=CC=C10	1.916893 1.91721
COC1=CC=CC=C1	1.441395	CC1=C(SC(=N1)C)C(=O)C	6.383765	C1C(O1)C2=CC=CC=C2	2.006981
COc1c(cccc1)N	1.526856	n1cc(ccc1)C=O	6.396123	CC1=CC(=CC(=C1)O)O	2.040846
C1=CC(=CC(=C1)O)O	1.547724	CNc1ccccc1	6.452874	CC1=CC(=C(C=C1)O)OC	2.170293
COC1=CC=CC=C1O	1.549906	Nc1c(cccc1)C=O	6.516774	CC1=C(C=C(C=C1)O)C	2.424889
C1=CC=C(C(=C1)CO)O	1.562781	C1=CC=C(C=C1)N	6.516774	CC1=CC=CC=C1C=O	2.456347
C1=CC(=CC=C1O)O CSC1=CC=CC=C1	1.612072 1.635403	CC1=CN=C(C(=N1)C)C CCOC(=O)C1=CC=CC=C1	6.529618 6.54385	Nc1c(cccc1)C=O C1=CC=C(C=C1)N	2.472857 2.472857
c1(c(cccc1)O)O	1.638952	COc1c(cccc1)C=0	6.641815	CC1=CC(0)=C(0)C=C10	2.545385
C1=CC(=C(C(=C1)CI)O)CI	1.665124	COC(=O)C1=CC=CN1	6.65084	CC1=C(C(=CC=C1)C)O	2.54936
CC(C)C1=CC=CC=C1O	1.747473	CCC1=CC=CO1	6.67399	O=CC1=CC=CC=C1NC	2.561711
C1=CSC(=C1)S	1.760378	C(C)c1c(cccc1)C=O	6.678888	COC1=CC=CC=C1O	2.582564
C1=CC=C(C(=C1)N)O	1.773475	CC1=NC=CN=C1	6.69373	NC1=CC=CC=C1S	2.663355
c1(ccccc1)C(C)(C)O CC(=0)C1=CC=CN1	1.77454 1.784645	OCC(=0)c1ccccc1 O=[C]1(C(C)=0)OCCC1	6.706399 6.764351	CC1=C(C(=CC=C1)C)S c1(ccccc1)CO	2.664136 2.713267
CC1=C(C(=CC=C1)C)S	1.865646	CCC1=CC=CC=C1S	6.799576	C1=CC=C(C(=C1)CO)O	2.729375
C1=CC(=C(C=C1CI)O)CI	1.879134	Cc1c(c(ccc1)C)CO	6.824733	c1(ccccc1)C(C)(C)O	2.737525
CC1=CC=NC2=CC=CC=C12	1.881836	C1=CC=C(C=C1)C(C#N)O	6.85846	CSC1=CC=CC=C1	2.753418
C1=CC=C2C(=C1)C=CC=N2	1.925142	CC1C(=CCC1)C(=O)C	6.886481	CC1=CC(=CC(=C1)O)C	2.79423
C1=CC(=C(C=C1CI)CI)O	1.927863 1.96065	CSC1=CC=CC=C1	6.892301	C1=CC=C(C=C1)S	2.800785 2.835645
CC1=CC(=C(C=C1)O)OC C1=CC=C(C(=C1)O)Br	2.024861	COC1=CC=C(C=C1)C=O CC1=CCCC(=O)C1	6.905708 6.941003	CC1=CNC(=C1)C(=O)OC COC1=CC(=CC=C1)OC	2.932035
[C-]#[N+]CC1=CC=CC=C1	2.06791	CCC1C=CC(=0)01	6.988239	COC1=CC=CC=C1OC	2.942067
c1(ccccc1)CO	2.099141	CC(=O)C(=O)C1=CC=CC=C1	6.995212	C(C)c1c(cccc1)C=O	3.022379
CCC1=C(C=CC(=C1)O)O	2.147843	c1(ccccc1)COC	7.014262	CC(=O)C1=CC=CN1	3.047612
C1=CC(=CC(=C1)O)C=O	2.169262	c1(ccccc1)CC(=O)C	7.018756	Cc1c(c(ccc1)C)CO	3.071884
C1=CC=C(C=C1)C(C#N)O s1cccc1	2.171679 2.200401	CC1=CC(=O)CCC1 CC1=NC=CN=C1OC	7.043093 7.0771	CC1=C(C=CC(=C1C)O)O COC(=O)C1=CC=CN1	3.142583 3.199062
C1=CC(=CC=C1C=O)O	2.200401	CC1=CNC(=C1)C(=O)OC	7.116798	CC1=C(SC=N1)C=C	3.232885
C1=CC=C(C=C1)C(=O)C#N	2.228871	Oc1oc(cc1)C=O	7.117114	c1(c(cccc1)O)O	3.240345
COC1=CC=CC=C1OC	2.27902	c1(ccccc1)CO		C1=CC(=CC=C1O)O	3.263079
O=CC1=CC=C(O)C=C1C	2.285233	OCc1oc(cc1)C=O		C1=CC=C(C(=C1)C=O)O	3.287156
C1=CC=C(C(=C1)C=O)O	2.308407	o1c(ccc1)C=O		Oc1c(c(ccc1)C)C=O	3.296966
c1(ccccc1)C#N Oc1c(c(ccc1)C)C=O	2.315736 2.348356	CCC1CCC(=0)01 CC(C)C=CC(=0)C	7.222036 7.232699	CC1=NC=NC2=CC=CC=C12 C1=CC=C(C(=C1)O)Cl	3.301889 3.336167
O=CC1=CC=CC=C1NC	2.357368	CC1CCCC(=0)C1=0	7.235711	C1=CC(=CC(=C1)C)C=O	3.365463
C1=CC=C(C=C1)CS	2.373006	CC(=O)C1=NCCS1	7.239078	0=CC1=CC=C(0)C=C1C	3.3787
CC1=NC=NC2=CC=CC=C12	2.393298	c1(ccccc1)CC#N	7.29472	C1=CC(=CC=C1CO)O	3.382749
[nH]1nccc1	2.398815	CC1=CC(=C(S1)C)C(=O)C	7.298992	C1=CC(=CC(=C1)O)O	3.391496
CCC1=CC(=CC(=C1)C)O	2.429883	Oc1ccc(cc1)C(=O)C	7.307233	C1=CC(=CC=C1C=O)O	3.392312
c1(ccccc1)C(=O)O c1(ccccc1)CC#N	2.440054 2.450592	CC1C(CCC1)C(=O)C CC1=CC=CC=C1C(=O)O	7.312247 7.32185	C1=CC=C(C=C1)CS CC1=CC=C(S1)C=O	3.409539 3.438549
C1C(O1)C2=CC=CC=C2	2.481837	COc1c(cccc1)N	7.336948	n1c[nH]cc1CCN	3.481199
CC1=CC=CC=C1C(=O)O	2.485752	CCC1=NC(=CS1)C	7.352985	C1CC2=CC=CC=C2NC1	3.50207
Nc1c(cccc1)C=O	2.490524	NC1=CC=CC=C1S	7.35831	CC1=C2C(=CC=C1)N=CC=N2	3.505628
C1=CC=C(C=C1)N	2.490524	CCNC1=CNC=N1	7.365535	CC1=CC=NC2=CC=CC=C12	3.53354
CC1=CC=CC=C1C=O	2.533502	C1=C(NC=N1)CCN	7.365535	CC1=C(C=CO1)SC	3.541116
Table 3.6					

Table 3.7: Dividing training odors into three distinct sets based upon odorstructure and receptor response

Odors were divided into three different screening categories (Aromatic Activator Screen, Broad Activator Screen, and Inhibitor Screen). For each odor the name, final activity value, and inclusion in each screening set are listed. Odor activities were normalized normalized to range from -100 (maximum observed inhibition) to 100 (maximum observed activation).

DataSin by NoteYesYesportanal-2 i NosYesYeshyperanal-2 i NosYesYeshyperanal-1 i NosYesYeshyperanal-1 i NosYesYeshyperanal-1 i NosYesYeshyperanal-1 i NosYesYeshyperanal-1 i NosYesYes<	Odor Name	Final Activity	Aromatic Activator Screen	Broad Activator Screen	Inhibition Screen
netanal-22 No1YesYesYesCalara-22 No1YesYesYesCalara-21 YesYesYesYesPartanol-20 NoYesYesYesPartanol-70 NoYesYesYesPartanol-20 NoYesYesYesPartanol-20 NoYesYesYesPartanol-20 NoYesYesYesPartanon-10 YesYesYesYesPartanon-10 YesYesYesYesPartanon-10 YesYesYesYesPartanon-10 YesYesYesYesDayl Scataba-10 YesYesYesYesPartanoc-21 YesYesYesYesPartanoc-21 YesYesYesYesPartanoc-21 YesYesYesYesPartanoc-21 YesYesYesYesPartanoc-21 YesYesYesYesPartanoc-21 YesYesYesY			No		
hephand-27 (Yes)YesYesYesYesbland-26 (Yes)YesYesYesbland-26 (Yes)YesYesYeshepland-38 NoYesYesYeshepland-38 NoYesYesYesbland-38 NoYesYesYeshepland-38 NoYesYesYeshepland-38 NoYesYesYeshepland-38 NoYesYesYeshepland-38 NoYesYesYeshepland-19 YesYesYesYeshepland-12 (YesYesYesYeshepland-16 (YesYesYesYeshepland<			No		
clanal					
batanol					
nearbol	butanol	-25	Yes	Yes	Yes
heptand					
column partamone					
balance					
hexanone -1-8 (Pes Yes Yes Yes Yes Yes Yes Yes Yes Yes Y	butanone	-25	Yes	Yes	Yes
heptance1-2VesVesVesbityl actatac2-8VesVesVesVesbityl actatac2-8VesVesVesVesberyl actatac1-2VesVesVesVesberyl actatac1-5VesVesVesVesberyl actatac2-8VesVesVesVesberylactac2-8VesVesVesVesberylactac2-8VesVesVesVesberylactac2-14VesVesVesVesberylactac2-25VesVesVesVesberylactac2-26VesVesVesVesberylactac2-26VesVesVesVesberylactac2-26VesVesVesVesberylactac2-26VesVesVesVesberylactac2-26VesVesVesVesberylactac2-26VesVesVesVesberylactac2-26VesVesVesVesberylactac2-27VesVesVesVesberylactac2-26VesVesVesVesberylactac2-26VesVesVesVesberylactac2-26VesVesVesVesberylactac2-26VesVesVesVesberylactac2-26VesVesVesVes <td></td> <td></td> <td></td> <td></td> <td></td>					
c.danone 1-8 Yes Yes bytyl actatte 1-8 Yes Yes Yes bytyl actatte 1-8 Yes Yes Yes cxtyl actatte 1-8 Yes Yes Yes cxtyl actatte 1-8 Yes Yes Yes cxtyl actatte 1-8 Yes Yes Yes beptancic acd 1-16 Yes Yes Yes pertaine 2-31 No Yes Yes Yes pertaine 2-31 No Yes Yes Yes pertaine 2-31 No Yes Yes Yes Actasta 2-31 No Yes Yes Yes Sociand 1-45 Yes Yes Yes Yes Sociand 1-46 Yes Yes Yes Yes Yes Yes Yes Yes Yes Yes Yes Yes Yes Yes					
pentyl actable -15 (ves Yes Yes Yes Yes heyd actable -2 (ves Yes Yes Yes Yes heyd actable -3 (ves Yes Yes Yes Yes heyd actable -4 (ves Yes Yes Yes Yes heydanolic acid -4 (ves Yes Yes Yes Yes heptanolic acid -4 (ves Yes					
nexy actaba heyd					
hetp/d actatile-3VesYesYesDutyre add-46No.YesYesDutyre add-46No.YesYespertance-21NosYesYesheptanocic add-47NosYesYescatanoci add-21NosYesYespertance-21NosYesYespertance-22NosYesYesheptane-20NosYesYesheptane-20NosYesYes1-octen >04-27NosYesYes2-balandione-46NosYesYes2-balandione-47NosYesYes2-balandione-16NosYesYes2-balandione-16NosYesYes2-balandione-27NosYesYes2-balandione-27NosYesYesActes Add-7NosYesYes2-balandione-27NosYesYes2-balandione-27NosYesYes2-balandione-27NosYesYes2-balandione-27NosYesYes2-balandione-27NosYesYes2-balandione-27NosYesYes2-balandione-27NosYesYes2-balandione-27NosYesYes2-balandione-27	pentyl acetate				
chylactate1-5YesYesYespertanolc add-2eYesYesYespertanolc add-2eYesYesYeshestanolc add-2YesYesYespertanolc add-2YesYesYespertanol-2YesYesYespertanol-2YesYesYespertanol-2YesYesYespertanol-2YesYesYespertanol-2YesYesYescdano-3NoYesYescdano-4YesYesYescdano-4YesYesYesCaland-14YesYesYesCaland-14YesYesYesCaland-14YesYesYesCaland-14YesYesYesCaland-14YesYesYesCaland-14YesYesYesCaland-14YesYesYesCaland-14YesYesYesCaland-14YesYesYesCaland-14YesYesYesCaland-14YesYesYesCaland-14YesYesYesCaland-14YesYesYesCaland-14YesYesYesCaland-14YesYesYes <td></td> <td></td> <td></td> <td></td> <td></td>					
buyinz add -44 No. Yes Yes Yes Yes haxanoic add -46 No. Yes			Yes		
inclusion add 1-10 Yes Yes Yes cctancia add 2.21 Yes Yes Yes Yes peratine 2.31 No. Yes Yes Yes brazane 2.35 Yes Yes Yes Yes 2.3-butanedione -30 No. Yes Yes Yes 2.3-butanedione -30 No. Yes Yes Yes 2.3-butanedione -30 No. Yes Yes Yes 2.3-butanedione -40 Yes Yes Yes Yes Caten 3-0 -14 Yes Yes Yes Yes Caten 3-0 Yes Yes Yes Yes Yes Caten 3-0 Yes Yes Yes Yes Yes Socand -7<		-94	No		
hepsancic acid 1-4 Yes Yes Yes cataroic acid -21 Yes Yes Yes heptane -30 No Yes Yes heptane -20 Yes Yes Yes heptane -20 Yes Yes Yes 2-3-bulanecione -20 Yes Yes Yes 1-oten-3-ol -27 Yes Yes Yes Sactanol -14 Yes Yes Yes Sactanol -14 Yes Yes Yes Nonand -12 Yes Yes Yes Nonand -12 Yes Yes Yes Sepront Amy Ether -2 Yes Yes Yes Isoamy Acetate -2 Yes Yes Yes Isoamy Acetate -2 Yes Yes Yes Stata Yes Yes Yes Yes Statamote -2 Yes					
octanoic acid pertane-2.1VesVesVeshexane-2.2VesYesYesYeshexane-2.2VesYesYesYescdane-3.4NoYesYesYescdane-3.4NoYesYesYescdane-3.4NoYesYesYescdane-3.4NoYesYesYescdane-3.4NoYesYesYesEhanol-1.4YesYesYesYesActel Acid-1.4YesYesYesYesActel Acid-1.4YesYesYesYesActel Acid-7YesYesYesYesactel Acid-7YesYes<					
hexane -25 %s / Yes / Yes / Yes / Yes / Yes / Yes / Cdane3-M No / Yes /					
heptane					
ciciane-3-3NoYesYes1-cclen-3-d-27YesYesYes1-cclen-3-d-27YesYesYesStandol-14YesYesYesMehand-14YesYesYesMachand-14YesYesYesMachand-14YesYesYesMachand-14YesYesYesMachand-14YesYesYesMachand-14YesYesYesMachand-14YesYesYesMachand-14YesYesYesMachand-16YesYesYesGarant/Actata-2YesYesYesMenthol-2YesYesYesGarant/Actata0YesYesYesGarant/Actata0YesYesYesGarant/Actata0YesYesYesLopopot/Acobal1YesYesNoCaronen4YesYesNoCaronen6YesYesNoCaronella1YesYesNoCaronella1YesYesNoCaronella1YesYesNoCaronella1YesYesNoCaronella1YesYesNoCaronella1YesYesNoCaronella1YesYes<					
2.3-buttendione 99 No Yes Yes Ethanol -16 Yes Yes Yes Ethanol -14 Yes Yes Yes Methanol -14 Yes Yes Yes Methanol -14 Yes Yes Yes Actel Add -7 Yes Yes Yes Stadte Add -7 Yes Yes Yes graderolastore -3 Yes Yes Yes graderolastore -2 Yes Yes Yes Grannyl Acetale -2 Yes Yes Yes Linnone -2 Yes Yes Yes Grannyl Acetale 0 Yes Yes No E2-hexenal 0 Yes Yes No Grannyl Acetale 0 Yes Yes No Elgenol 1 Yes Yes No Eagenol 1 Yes Yes No Elgenol 1 Yes Yes No Carvone 4 Yes Yes No <t< td=""><td></td><td></td><td></td><td></td><td></td></t<>					
1 coten 3-ol 227 Ves Yes Yes Yes Sactanol -14 Yes Yes Yes Yes Methanol -14 Yes Yes Yes Yes Sactanol -14 Yes Yes Yes Yes Subanol -12 Yes Yes Yes Yes Syvaerolactone -2 Yes Yes Yes Yes Syvaerolactone -2 Yes Yes Yes Yes Menthol -2 Yes Yes Yes Yes Menthol -2 Yes Yes Yes Yes Menthol -2 Yes Yes Yes Yes Methonal 0 Yes Yes Yes Yes Caraona 0 Yes Yes No Isoprop/Acobid 3 Yes Yes No Soctanone 4 Yes Yes Yes No Isoprop/Acobid Anole Soctanone 6 Yes Yes Yes No Isoprop/Acobid No I					
3.odanol -1.4 Yes Yes Yes Nonanol -1.2 Yes Yes Yes Supanol Methy Ether -1.2 Yes Yes Yes Yes Acetic Acid -7 Yes Yes Yes Yes Yes Systematic -2 Yes Yes Yes Yes Subarnyi Acetate -2 Yes Yes Yes Yes Linnenie -2 Yes Yes Yes Yes Caranyi Acetate 0 Yes Yes Yes No Caraone 4 Yes Yes No No Isopropi Alcohol 3 Yes Yes No No Phenytehanone 5 Yes Yes No No Benzalehyde 6 Yes Yes No No Caraone 4 Yes Yes No No Socanone 4 Yes Yes	1-octen-3-ol	-27	Yes		
Internand 1-14 Yes Yes Yes Yes Eugenol Methyl Ether -9 Yes Yes Yes Yes Grand Methyl Ether -9 Yes Yes Yes Yes gvaleridactone -5 Yes Yes Yes Yes graderidactone -2 Yes Yes Yes Yes Linomene -2 Yes Yes Yes Yes Methol -2 Yes Yes Yes Yes Methol -2 Yes Yes Yes Yes Methol -2 Yes Yes Yes Yes Garanty Acetate 0 Yes Yes Yes No Augroph Acetate 0 Yes Yes No No Cancone 4 Yes Yes No No Cancone 5 Yes Yes No No Cancone 6 Yes Yes No No Cancone 8 Yes Yes No No Cancone					
Nonand -12 Yes Yes Yes Yes Acetic Add -7 Yes Yes Yes Yes Syalerolactore -2 Yes Yes Yes Yes Fenchone -2 Yes Yes Yes Yes Limonene -2 Yes Yes Yes Yes Carront Acetate -2 Yes Yes Yes Yes E2-hexenal 0 Yes Yes Yes Yes Bernard/Acetate 0 Yes Yes Yes No Limonene 1 Yes Yes No Heinonal E2-hexenal 0 Yes Yes No Heinonal Eagend 1 Yes Yes No Heinonal Eagend Methylophenol 3 Yes Yes No Heinonal Eagend Methylophenol 3 Yes Yes No Heinonal Eagend Methylophenol 4 Yes Yes No Heinonal Eagend Methylophenol 10 No Yes No <td< td=""><td></td><td></td><td></td><td></td><td></td></td<>					
Eugeno Yes Yes Yes Yes gvalerolactone -5 Yes Yes Yes Yes gvalerolactone -2 Yes Yes Yes Yes iscami/Actetite -2 Yes Yes Yes Yes Linonene -2 Yes Yes Yes Yes Menthol -2 Yes Yes Yes Yes Menthol -2 Yes Yes Yes Yes Garant/Actetite 0 Yes Yes Yes No Augropris/Actetal 0 Yes Yes No No Augropris/Actetal 1 Yes Yes No No Caroone 4 Yes Yes No No No Benzaldehyde 6 Yes Yes No No Yes No Chronelial 8 Yes Yes No No Yes No	Nonanol		Yes	Yes	Yes
g-valencialcone - 5 ¹ Yes Yes Yes Yes Yes Isoamy Acetate - 2 ¹ Yes Yes Yes Yes Yes Isoamy Acetate - 2 ¹ Yes Yes Yes Yes Yes Menthol - 2 ¹ Yes Yes Yes Yes Yes Menthol - 2 ¹ Yes Yes Yes Yes Yes Eugenol - 1 ¹ Yes Yes Yes No Armethylactate - 0 ¹ Yes Yes Yes No Isoproy Acetate - 0 ¹ Yes Yes No Benzalehyde - 0 ¹ Yes Yes No Benzalehyde - 0 ¹ Yes Yes No Benzalehyde - 0 ¹ Yes Yes No Chronela - 0 ¹ Yes Yes No Chronela - 0 ¹ Yes Yes No Chronela - 0 ¹ Yes Yes No Herhydelitylate - 0 ¹ No Yes Yes No Chronela - 0 ¹ Yes Yes No Herhydelitylate - 0 ¹ No Yes No Herhydelitylate - 0 ¹ No No Pres No - 0 ¹ Yes Yes No Chronela - 0 ¹ Yes Yes No Herhydelitylate - 0 ¹ No No Pres No - 0 ¹ Yes Yes Yes No - 0 ¹ Yes Yes Yes - 0 ¹ Yes Yes No - 0 ¹ Yes Yes Yes - 0 ¹ Yes Yes No - 0 ¹ Yes Y		-9	Yes		
Penchone -2 Yes Yes Yes Yes Limonene -2 Yes Yes Yes Yes Limonene -2 Yes Yes Yes Yes Carpany Acctate 0 Yes Yes Yes Yes E2-hexenal 0 Yes Yes Yes Yes Eugenol 1 Yes Yes No 4 Laportoyi Acohol 3 Yes Yes No 4 Laportoyi Acohol 3 Yes Yes No A Anisole 6 Yes Yes No A Benzaldehyde 6 Yes Yes No B Cittonella 8 Yes Yes No C Cittonella 8 Yes Yes No C Cittonella 8 Yes <					
Joarny Acetate 2 Yes Yes Yes Linnonen 2 Yes Yes Yes Yes Menthol 2 Yes Yes Yes Yes Geranyl Acetate 0 Yes Yes Yes Yes Menthol 1 Yes Yes Yes No Arenthylphenol 1 Yes Yes No Isopropyl Acetate 6 Yes Yes No Ansole 6 Yes Yes No Denzolehonone 6 Yes Yes No Benzaldehyde 6 Yes Yes No Benzaldehyde 6 Yes Yes No Caraone 8 Yes Yes No Benzaldehyde 8 Yes Yes No Benzaldehyde 13 No Yes No Caraone 4 No Yes No Methystalicytate 13 No Yes No Chronellal 8 Yes Yes No Caraony Acectate					
Menthol -2 Yes Yes Yes Yes Caranyl Actata 0 Yes Yes Yes Yes Methional 0 Yes Yes Yes No Hendinyland 1 Yes Yes No Laperopi Alcohol 3 Yes Yes No Isopropi Alcohol 3 Yes Yes No Ansiole 6 Yes Yes No Phenylethanone 5 Yes Yes No Benzadehyde 6 Yes Yes No Benzadehyde 6 Yes Yes No Citronelal 8 Yes Yes No Ethyl Acetate 8 Yes Yes No Herhysalicylate 13 No Yes No Indide 21 Yes Yes No Indide 21 No Yes	Isoamyl Acetate	-2	Yes	Yes	Yes
12-2-beschall Yes Yes Yes Yes Yes Methional 0 Yes Yes Yes Yes Methional 0 Yes Yes Yes No A-methylphenol 3 Yes Yes No A-methylphenol 3 Yes Yes No Carvorde 4 Yes Yes No Denzophanone 6 Yes Yes No Benzabilshyde 6 Yes Yes No Benzophanone 8 Yes Yes No Chronelial 8 Yes Yes No Chronelia 9 Yes Yes No Chronelia 16 No Yes No Thyprol 16					
Caranyl Acetate O Yes Yes Yes Yes Eugenol 1 Yes Yes No Isopropyl Alcohol 3 Yes Yes No Isopropyl Alcohol 3 Yes Yes No Carvone 4 Yes Yes No Phenylethanone 5 Yes Yes No Berzadplenone 6 Yes Yes No Berzadplenone 8 Yes Yes No Carroni 8 Yes Yes No Carroni 8 Yes Yes No Geraniol 8 Yes Yes No Carroni 13 No Yes No Velatista 3 No Yes No Orycholexanone 48 No Yes No Indide 21 Yes Yes No Orycholexanone 48 No Yes Yes propionyl choride -88 No Yes Yes propionyl choride -73 No Yes Yes					
Methional O Yes Yes Yes Yes No 4-methylphenol 3 Yes Yes No No 1sopropyl Alcohol 3 Yes Yes No Carvone 4 Yes Yes No Phenylethanone 5 Yes Yes No Anisole 6 Yes Yes No Berzaldehyde 6 Yes Yes No Berzaldehyde 8 Yes Yes No Citronelial 8 Yes Yes No Geraniol 8 Yes Yes No Citronelial 8 Yes Yes No Thymol 15 No Yes No Cyclohexanone 48 No Yes Yes Probinnyl Choride -100 No Yes Yes Probinnyl Choride -30 No Yes Yes Probinnyl Choride -30 No Yes Yes 2.pentanotione -50 No Yes Yes 2.pentanotione					
a-metrylphenol 3 Yes Yes Yes Yes No Carvone 4 Yes Yes Yes No Carvone 4 Yes Yes Yes No Phenylethanone 5 Yes Yes No Benzahlenyde 6 Yes Yes No Benzahlenyde 6 Yes Yes No Cittonelal 8 Yes Yes No Caranol 8 Yes Yes No Ethyl Acetate 8 Yes Yes No Cyclohexanone 48 No Yes No Indide 21 Yes Yes No Cyclohexanone 48 No Yes No Indide 21 Yes Yes No propionyl bromide -88 No Yes Yes propionyl bromide -89 No Yes Yes 2.3 pentanecione -55 No Yes Yes 2.4 propylamino) ethanol -16 Yes Yes Yes <td< td=""><td></td><td>0</td><td>Yes</td><td>Yes</td><td>Yes</td></td<>		0	Yes	Yes	Yes
isopropi Alcohol 3 Yes Yes No Phenylethanone 5 Yes Yes No Anisole 6 Yes Yes No Benzaldehyde 6 Yes Yes No Benzaldehyde 6 Yes Yes No Benzaldehyde 6 Yes Yes No Citronellal 8 Yes Yes No Caranon 13 No Yes No Methylsalicylate 13 No Yes No Cycobnexanone 43 No Yes No Indde 21 Yes Yes No Prophony bromide 48 No Yes Yes prophony bromide 78 No <td></td> <td></td> <td></td> <td></td> <td></td>					
Carvone 4 Yes Yes No Anisole 6 Yes Yes No Anisole 6 Yes Yes No Benzaldehyde 6 Yes Yes No Benzaldehyde 8 Yes Yes No Caronald 15 No Yes No Cycohexanone 48 No Yes No India 21 Yes Yes No Cycohexanone 48 No Yes Yes propionid/phranol 24 No Yes Yes propionid/portonide -88 No Yes Yes propionid/portonide -73 No Yes Yes 2.3-pertanectione -75 No Yes	4-methylphenol				
phenytethanone 5 Yes No Benzaldehyde 6 Yes No Benzaldehyde 6 Yes Yes No Benzaldehyde 8 Yes Yes No Citranellal 8 Yes Yes No Geraniol 8 Yes Yes No Cyclohexanone 48 No Yes No Propiony bromide -88 No Yes Yes propiony bromide -88 No Yes Yes 2-pertanedione -55 No Yes Yes 2-propiony choride -88 No Yes Yes 2-propiony choride -39 No Yes Yes 2-propiony choride -30 No Yes </td <td>Carvone</td> <td></td> <td></td> <td></td> <td></td>	Carvone				
Berzaldehyde G Yes Yes No Berzophenone 8 Yes Yes No Citronelal 8 Yes Yes No Ethyl Acetate 8 Yes Yes No Ethyl Acetate 1 No Yes No Methysalicytate 1 3 No Yes No Indue 1 No Yes No Cyctohexanone 44 No Yes No Indue 21 Yes Yes No Perplonyl bromide -88 No Yes Yes propionyl bromide -88 No Yes Yes propionyl bromide -78 No Yes Yes 2-pertanedione -56 No Yes Yes 2-propionyl choride -39 No Yes Yes 2-propionyl choride -30 No	Phenylethanone	5	Yes	Yes	No
Benzophenone B Yes Yes No Citronellal 8 Yes Yes No Ceranol 8 Yes Yes No Ethyl Acatate 13 No Yes No Methylsalicylate 13 No Yes No Cyconexanone 44 No Yes No Indole 21 Yes Yes No Cyconexanone 48 No Yes No Indole 21 Yes Yes No Cyconexanone 48 No Yes Yes propionity dhoride 73 No Yes Yes propionity choride -73 No Yes Yes 2.3-pentanecione -55 No Yes Yes 2.4-petanol -39 No Yes Yes 2.4-petanol -39 No Yes Yes 2.4-petanol -39 No Yes Yes 2.4-petanol -30 No Yes Yes 2.4-petanol -30 No Yes Yes					
Cittonelial B Yes No Ceraniol 8 Yes No Ethyl Acetate 8 Yes No Methylsalicylate 13 No Yes No Dethyl Acetate 13 No Yes No Cycobrexanone 48 No Yes No Cycobrexanone 48 No Yes No Z-methylphenol 24 No Yes No Perspondyl bromide -88 No Yes Yes propionyl bromide -88 No Yes Yes propionyl bromide -73 No Yes Yes 2-petpland -39 No Yes Yes 2-propionicadione -30 No Yes Yes propionicadi -32 No Yes Yes Staptanol -48 Yes Yes Yes Staptanol -16 Yes Yes Yes					
Ethylacitation a Yes No Methylacitydae 13 No Yes No Cycobexanone 48 No Yes No Lindle 21 Yes Yes No 2-methylphenol 24 No Yes No 2-methylphenol 24 No Yes Yes propionyl bromide -88 No Yes Yes propionyl bromide -88 No Yes Yes propionyl bromide -73 No Yes Yes 2-pertanedione -55 No Yes Yes 2-pertanedione -39 No Yes Yes 2-methyl-3-heptanone -26 Yes Yes Yes 2-methyl-3-heptanone -26 Yes Yes Yes 2-methyl-3-heptanone -16 Yes Yes Yes 2-forentylmino)-ethanol -16 Yes Yes Yes 2-forentylmino)-ethanol -16 Yes Yes Yes 2-forentylmino)-ethanol -16 Yes Yes Yes <t< td=""><td></td><td></td><td></td><td></td><td></td></t<>					
Methysalicylate 13 No Yes No Thymol 15 No Yes No Cyclohexanone 48 No Yes No Indole 21 Yes Yes No 2-methylphenol 24 No Yes Yes Yes projonyl bromide 38 No Yes Yes Yes projonyl bromide -73 No Yes Yes Yes projonyl bromide -73 No Yes Yes Yes 2.3-pettanecione -55 No Yes Yes Yes 2.4-petanol -39 No Yes Yes Yes 2.4-petanol -39 No Yes Yes Yes 2.4-petanol -38 No Yes Yes Yes 2.4-petanol -16 Yes Yes Yes Yes 2.5-dimethylhiophene -9 Yes Yes Yes <td< td=""><td></td><td></td><td></td><td></td><td></td></td<>					
Thymon Yes No Cydohexanone 48 No Yes No Indole 21 Yes Yes No Indole 21 Yes Yes No andrivjpruvate -100 No Yes Yes propionyl chornide -88 No Yes Yes propionyl chornide -73 No Yes Yes propionyl chornide -68 No Yes Yes 2-petnancione -55 No Yes Yes 2-petnancione -39 No Yes Yes 2-propionic acid -32 No Yes Yes 2-metnyl-3-heptanone -26 Yes Yes Yes 2-metnyl-3-heptanone -16 Yes Yes Yes 2-metnyl-3-heptanone -11 Yes Yes Yes 2-demetnyl-1-5-heptan-2-ol 0 Yes Yes Yes 2-demetnyl-1-5-heptan-2-ol			Yes		
Cyclothorsanone 48 No Yes No Indole 21 Yes Yes No 2-methylphenol 24 No Yes No projonyl bronide -100 No Yes Yes projonyl bronide -88 No Yes Yes projonyl bronide -73 No Yes Yes projonyl bronide -73 No Yes Yes 2.3-pettanecione -55 No Yes Yes 2.4-petanol -38 No Yes Yes 2.4-petanol -39 No Yes Yes 2.4-petanol -39 No Yes Yes 2.4-petanol -38 No Yes Yes 2.4-petanone -26 Yes Yes Yes 2.5-dimetrylhtiohorheo -9 Yes Yes Yes 2.5-dimetrylhtiohorheo -1 Yes Yes Yes 2.5-dimetry					
2-methylphenol 24 No Yes No methyl pruvale -100 No Yes Yes Yes projonyl bromide -88 No Yes Yes Yes projonyl bromide -73 No Yes Yes Yes projonyl bromide -73 No Yes Yes Yes 2.3-pettanedione -55 No Yes Yes Yes 2.4-petanol -39 No Yes Yes Yes 2.4-petanol -39 No Yes Yes Yes 2.4-petanol -39 No Yes Yes Yes 2.4-petanol -32 No Yes Yes Yes 3-beptanol -16 Yes Yes Yes Yes 2.5-dimetrylhiophene -9 Yes Yes Yes Yes 2.5-dimetrylhiophene -1 Yes Yes Yes Yes 3.4-beptanone					No
methy ipyuvate -100 No Yes Yes projony bronide -88 No Yes Yes projony bronide -73 No Yes Yes projony bronide -68 No Yes Yes projony bronide -68 No Yes Yes 2-heptanol -39 No Yes Yes 2-heptanol -39 No Yes Yes 2-portionic aid -32 No Yes Yes 2-methyl-3-heptanol -39 No Yes Yes 2-methyl-3-heptanone -26 Yes Yes Yes 2-methyl-3-heptanone -16 Yes Yes Yes 4-(methylthio)-1-butanal -15 Yes Yes Yes 1-bepten-2-ol 0 Yes Yes Yes 2-5-dimethylthiophene -9 Yes Yes Yes 1-bepten-3-0l 0 Yes Yes No 3-decanone 1 Yes Yes No 4-methylthiophene 3 Yes Yes No 1-boronbe					
propiony bromide -88 No Yes Yes propiony chorde -73 No Yes Yes Yes 2-apentanedione -68 No Yes Yes Yes 2-apentanedione -65 No Yes Yes Yes 2-heptanol -39 No Yes Yes Yes 2-horp and chore -31 No Yes Yes Yes 2-horp and chore -31 No Yes Yes Yes 2-horp and chore -31 No Yes Yes Yes 3-heptanone -31 No Yes Yes Yes 4-hydroxy-2-butanone -11 Yes Yes Yes Yes 2-denatority hitophene -9 Yes Yes Yes Yes 3-decanone 1 Yes Yes No Yes No 3-nonanone 2 Yes Yes Yes No Yes					
propionity chloride 7-3 No Yes Yes propionidehyde -68 No Yes Yes 2.3-pertanedione -55 No Yes Yes 2.4-pertanol -38 No Yes Yes 2-(propylamino)-ethanol -38 No Yes Yes 2-propylamino)-ethanol -38 No Yes Yes 2-methyl-3-heptanone -32 No Yes Yes 2-methyl-3-heptanone -26 Yes Yes Yes 4-(methylthio)-1-butanal -16 Yes Yes Yes 4-finethylthiophene -3 Yes Yes Yes 1.5-pentanediol 0 Yes Yes Yes 3-decanone 1 Yes Yes No 3-nonanone 2 Yes Yes No 4-heptanone 3 Yes Yes No 1-bromohexane 3 Yes Yes No					
2.3-petranectione -56 No Yes Yes 2-heptanol -39 No Yes Yes 2-(propylamino)-ethanol -38 No Yes Yes propionic acid -32 No Yes Yes 2-methy/3-heptanone -32 No Yes Yes 2-methy/3-heptanone -32 No Yes Yes 3-heptanol -16 Yes Yes Yes 4-methy/hio/1-1-butanal -15 Yes Yes Yes 4-finethy/thiophene -3 Yes Yes Yes 2.5-dimethy/thiophene -3 Yes Yes Yes 1.5-pentanecicit 0 Yes Yes Yes 3-decanone 1 Yes Yes No 3-nonanone 2 Yes Yes No 2-heptanol 2 Yes Yes No 1-bromohexane 3 Yes Yes No 2-heptanol 2 Yes Yes No 1-bromohexane 3 Yes Yes No 1-bromohexane 3 Yes Yes No 2-decanote 5 Yes </td <td>propionyl chloride</td> <td>-73</td> <td>No</td> <td>Yes</td> <td>Yes</td>	propionyl chloride	-73	No	Yes	Yes
2-heptanol -30 No Yes Yes 2-(ropylamio)-ethanol -30 No Yes Yes butyry(abloride -30 No Yes Yes projoinci acid -32 No Yes Yes 2-methyl-3-heptanone -32 No Yes Yes 2-methyl-3-heptanone -26 Yes Yes Yes 3-heptanol -16 Yes Yes Yes 4-methylho)-1-butanal -15 Yes Yes Yes 2-formethylhophene -11 Yes Yes Yes 2-domethylhophene -9 Yes Yes Yes 2-domethylhophene -9 Yes Yes Yes 3-decanone 1 Yes Yes Yes No 3-nonanone 2 Yes Yes No Yes 3-nonanone 2 Yes Yes No Pherylatiane 3 Yes Yes Yes No Pherylatiane 1-bromohexane 3 Yes Yes No Pherylatiane 1-bromohexane 3 Yes Yes No Pherylatiane 1-bromohexane 3 Yes Yes No Pherylatiane 1-bromohexane 5 Yes Yes No 1-bromohexane 5 Yes					
2-(progylamino)-ethanol -30 No Yes Yes butyry choinde -30 No Yes Yes propionic acid -32 No Yes Yes 2-methy-3-heptanone -32 No Yes Yes 3-heptanon -65 Yes Yes Yes 4-methythio)-1-butanal -15 Yes Yes Yes 4-methythio)-1-butanal -15 Yes Yes Yes 5-methyt-3-Inptenz-0 0 Yes Yes Yes 1.5-pentanediol 0 Yes Yes Yes 1.4-heptan-2-ol 0 Yes Yes Yes 3-decanone 1 Yes Yes No 3-nonanone 2 Yes Yes No 4-heptanone 2 Yes Yes No 1-hexanethiol 3 Yes Yes No 1-branchexane 3 Yes Yes No 1-branchexane 3 Yes Yes No	2,3-pentanedione				
butyry choinde -30 No Yes Yes projoinic aid -32 No Yes Yes 2-methyl-3-heptanone -26 Yes Yes Yes 3-heptanol -16 Yes Yes Yes 4-mdroxy-2-butanone -11 Yes Yes Yes 4-mdroxy-2-butanone -11 Yes Yes Yes 2-dimethylhiophene -9 Yes Yes Yes 2-dimethylhiophene -9 Yes Yes Yes 2-decanone 0 Yes Yes Yes 3-decanone 1 Yes Yes No 3-nonanone 2 Yes Yes No 3-nonanone 2 Yes Yes No 1-bromohexane 3 Yes					
2-metpu/s-3-heptanone -26 Yes Yes Yes 3-heptanone -16 Yes Yes Yes 4-(methylthio)-1-butanal -15 Yes Yes Yes 4-(methylthio)-1-butanal -15 Yes Yes Yes 2-dimethylthiophene -11 Yes Yes Yes 2-dimethylthiophene -31 Yes Yes Yes 2-dimethylthiophene -31 Yes Yes Yes 1-bpten-3-ol 0 Yes Yes No 3-decanone 1 Yes Yes No 3-nonanone 2 Yes Yes No 4-heptanone 2 Yes Yes No 1-hexanethiol 3 Yes Yes No	butyryl chloride	-39	No	Yes	Yes
3-heptanol -16 Yes Yes Yes 4-methythio)-1-butanal -16 Yes Yes Yes 4-methythio)-1-butanal -16 Yes Yes Yes 2-brenethythiophene -11 Yes Yes Yes 2-brenethythiophene -0 Yes Yes Yes 1.5-pentanediol 0 Yes Yes Yes 1.5-pentanediol 0 Yes Yes Yes 3-decanne 1 Yes Yes No 3-nonanone 2 Yes Yes No 3-nonanone 2 Yes Yes No 2-heptanone 2 Yes Yes No 2-heptanone 3 Yes Yes No 2-heptanone 3 Yes Yes No 1-bromohexane 3 Yes Yes No 1-hexanethiol 3 Yes Yes No 1-abcranethio 3 Yes Yes No 1-abcranethio 3 Yes Yes No 2.4.5-fimethythiazole 5 Yes					
4-(methythio)-1-butanne 15 [ves Yes Yes 2.5-dimethythiophene -0 Yes Yes Yes 6-methyt-5-hepten-2-ol 0 Yes Yes Yes 1.5-pentanediol 0 Yes Yes Yes 1.5-pentanediol 0 Yes Yes Yes 3-decanone 1 Yes Yes No 3-nonanone 2 Yes Yes No 3-nonanone 2 Yes Yes No 4-heptanone 2 Yes Yes No 1-brombexane 3 Yes </td <td></td> <td></td> <td></td> <td></td> <td></td>					
2.5-dimethythiophene -0 Yes Yes Yes 1.5-pertanediol 0 Yes Yes Yes 3-decanone 1 Yes Yes No 3-conanone 2 Yes Yes No 3-nonanone 2 Yes Yes No 4-heptanone 2 Yes Yes No 2-hexanol 2 Yes Yes No 1-bromohexane 3 Yes Yes No 1-bromhexane 3 Yes Yes No 1-bromhexane 3 Yes Yes No 1-bromkytilane 3 Yes Yes No 2.4.5.firmethythiazole 5 Yes Yes	4-(methylthio)-1-butanal	-15	Yes	Yes	Yes
6-methyl-5-hepten2-ol 0 Ves Yes Yes 1-5-pentanedic 0 Ves Yes Yes 1-bepten3-ol 0 Ves Yes Yes 3-decanone 1 Yes Yes No 3-nonanone 2 Yes Yes No 3-nonanone 2 Yes Yes No 4-heptanone 2 Yes Yes No 2-hexanol 2 Yes Yes No 1-bromohexane 3 Yes Yes No 2.4.5-fimethythibazole 5 Yes					
1-5-perinanctiol 0 Ves Yes Yes 1-bepten-3-ol 0 Ves Yes Yes No 3-decanone 1 Yes Yes No Provision No 3-decanone 1 Yes Yes No Provision No 3-nonanone 2 Yes Yes No Provision Provision 2-hexanol 2 Yes Yes No Provision					
1-hepten-3-ol 0 Ves Yes Ves 3-decanone 1 Yes No pyruvic adid 2 Yes No 3-nonanone 2 Yes No 4-heptanone 2 Yes Yes No 4-heptanone 2 Yes Yes No 2-hexanol 2 Yes Yes No 1-hexanethiol 3 Yes Yes No 1-hexanethiol 3 Yes Yes No 1-idodhexane 3 Yes Yes No 2.4.5 trimethythiazole 5 Yes Yes No 1-idodhexane 6 Yes Yes No cis-3-hexene 5 Yes Yes No i					
pyrukic add 2 Yes Yes No 3-nonanone 2 Yes Yes No 4-beptanone 2 Yes Yes No 2-hexanol 2 Yes Yes No 2-hexanol 2 Yes Yes No 1-boronchexane 3 Yes Yes No 1-hexanethiol 3 Yes Yes No 1-hexanethiol 3 Yes Yes No 1-idodhexane 3 Yes Yes No 1-idodhexane 3 Yes Yes No 2.4.5-trimethythiazole 5 Yes Yes No 1-idodhexane 5 Yes Yes No 2.4.5-trimethythiazole 5 Yes Yes No 2.4.5-trimethythazole 5 Yes Yes No cis-2-hexene 5 Yes Yes No cis-2-hexene 6 Yes Yes No cis-3-hexen-1-ol 10 Yes Yes No cis-3-hexen-1-ol 10 Yes Yes	1-hepten-3-ol	0	Yes	Yes	Yes
2-nonanone 2 Yes Yes No 4-heptanone 2 Yes Yes No 4-heptanone 2 Yes Yes No 1-bromohexane 3 Yes Yes No 1-bromohexane 3 Yes Yes No 1-bromohexane 3 Yes Yes No 1-braznetholo 3 Yes Yes No phenylacetaldehyde 3 Yes Yes No 1-odohexane 3 Yes Yes No 2.4.5-trimethythitazole 5 Yes Yes No ethyl valerate 5 Yes Yes No cis-2-hexene 5 Yes Yes No smethyl-2-petriene 5 Yes Yes No cis-3-hexen-1-ol 10 Yes Yes No 2-acetythtophene 31 No Y		1	N	Nr	N
4-heptanone 2 Yes Yes No 2-hexanol 2 Yes Yes No 1-brombexane 3 Yes Yes No 1-hexanethiol 3 Yes Yes No 1-hexanethiol 3 Yes Yes No 1-hexanethiol 3 Yes Yes No phenylactaidehyde 3 Yes Yes No 1-odohexane 3 Yes Yes No 2.4,5-timethylthiazole 5 Yes Yes No 2.4,5-timethylthiazole 5 Yes Yes No cis-2-hexene 5 Yes Yes No s-methyl-2-pentene 5 Yes Yes No cis-3-hexen-1-ol 10 Yes Yes No fluoroacetone 10 Yes Yes No fluoroacetone 10 Yes Yes No 2-acetylthiophene 31 No Yes No 2-acetylthiophene 31 No Yes No 2-acetylthiophene 10 Yes		2			
2-hexanol 2 Yes Yes No 1-bromohexane 3 Yes Yes No 1-brannehiol 3 Yes Yes No hexylsilane 3 Yes Yes No phenylacetaidehyde 3 Yes Yes No 2.4.5-trimethylbiazole 3 Yes Yes No 2.4.5-trimethylbiazole 5 Yes Yes No 2.4.5-trimethylbiazole 5 Yes Yes No 62-2-hexene 5 Yes Yes No 63-2-hexene 5 Yes Yes No 65-2-hexene 6 Yes Yes No 65-2-hexene 6 Yes Yes No 65-3-hexen-1-01 10 Yes Yes No 1-chiordhexane 18 Yes Yes No 2-acetylhiophene 10 Yes Yes No 2-acetylhiophene 100 Yes Yes No 2-acetylhiophene 100 Yes Yes No 2-schtyl-3.5(b-dimethylyprazine	4-heptanone				
1-hexatehilol 3 Yes Yes No hexylsilane 3 Yes Yes No phenylacetaldehyde 3 Yes Yes No 1-dochexane 3 Yes Yes No 2.4.5-frimethylthiazole 5 Yes Yes No 2.4.5-frimethylthiazole 5 Yes Yes No ethyl valerate 5 Yes Yes No 3-methyl-2-pentene 5 Yes Yes No 3-methyl-2-pentene 6 Yes Yes No 1-chorohexane 8 Yes Yes No 1-chorohexane 10 Yes Yes No 1-chorohexane 10 Yes Yes No fluoroacetone 10 Yes Yes No acetophenone 15 No Yes No 2-acetythitophene 31 No Yes No pridinc 99 Yes Yes No 2-acthythitophene 100 Yes Yes No 2-acthythytoprazine 4 Yes <td>2-hexanol</td> <td>2</td> <td>Yes</td> <td>Yes</td> <td>No</td>	2-hexanol	2	Yes	Yes	No
hexylslane 3 Yes Yes No phenylacetaldehyde 3 Yes Yes No 1-icdohexane 3 Yes Yes No 2.4.5-finnethylthiazole 5 Yes Yes No 2.4.5-finnethylthiazole 5 Yes Yes No cis-2-hexnet 5 Yes Yes No s-methyl-2-pentene 5 Yes Yes No s-methyl-2-pentene 5 Yes Yes No cis-2-hexnet 6 Yes Yes No cis-3-hexen-1-ol 10 Yes Yes No cis-3-hexen-1-ol 10 Yes Yes No fluoroacetone 10 Yes Yes No 2-acelythiophene 31 No Yes No 2-acelythophene 31 No Yes No pridine 99 Yes Yes No 2-acelythiophene 100 Yes Yes No 2-acthythophene 8 Yes Yes No 2-dethythopheratinethylpyrazine					
phenytacetaldehyde 3 Yes Yes No 1-dodhexane 3 Yes Yes No 2.4.5-frimethythiazole 5 Yes Yes No 2.4.5-frimethythiazole 5 Yes Yes No cby Zaherane 5 Yes Yes No dby Zaherane 5 Yes Yes No 3-methyl-2-pentene 5 Yes Yes No methoxyacetone 6 Yes Yes No 1-chiorohexane 8 Yes Yes No 6s-3-hexen-1-01 10 Yes Yes No fluoroacetone 10 Yes Yes No acetophenone 13 No Yes No 2-acetythitophene 31 No Yes No pridinc 99 Yes Yes No 4-zheryt-3;6(b-dimethylpyrazine 8 Yes Yes No 2-sethyl-4;3;0(b-dimethylpyrazine 4 Yes Yes No					
1-iodotexane 3 Yes Yes No 2.4.5-trimethylthiazole 5 Yes Yes No ethyl valerate 5 Yes Yes No cls-2-hexner 5 Yes Yes No S-methyl-2-pertene 5 Yes Yes No S-methyl-2-pertene 5 Yes Yes No S-methyl-2-pertene 6 Yes Yes No I-chlorobexane 8 Yes Yes No cls-3-hexen-1-ol 10 Yes Yes No clavatophenone 15 No Yes No 2-acetythiophene 31 No Yes No pridine 99 Yes Yes No thiazole 100 Yes Yes No 2-acetythiophene 31 No Yes No pridine 99 Yes Yes No 2-acetythiophene 100 Yes Yes No 2-acetythiophene 8 Yes Yes No 2-acetythiophene 9 Yes <			Yes		
ethy Valerate 5 Yes No 65:2-hexene 5 Yes No 3-methyl-2-pentene 5 Yes Yes No 3-methyl-2-pentene 5 Yes Yes No 1-chlorohexane 6 Yes Yes No 1-chlorohexane 8 Yes Yes No 1-chlorohexane 10 Yes Yes No acetophenone 10 Yes Yes No acetophenone 15 No Yes No pyridine 99 Yes Yes No 2-acetylthiophene 31 No Yes No pyridine 99 Yes Yes No 2-acetylthiophene 8 Yes Yes No 2-sethyth3;6/b-dimethylpyrazine 8 Yes Yes No 2-sethyt3;6/b-dimethylpyrazine 26 Yes Yes No	1-iodohexane	3	Yes	Yes	No
cis-2-hexene S Yes No 3-methyl-2-pentene 5 Yes No methoxyacetone 6 Yes Yes No 1-chlorohexene 8 Yes Yes No 1-chlorohexene 10 Yes Yes No flaoroacetone 10 Yes Yes No acetophenone 10 Yes Yes No 2-acetyfithiophene 31 No Yes No pyrdine 99 Yes Yes No 4-zethyf-3.5(b-dimethylpyrazine 8 Yes No 2,5-dimethylpyrazine -4 Yes Yes Yes					
3-methyl-2-pentene 5 Yes No methoxyacetone 6 Yes Yes No 1-chiorohexane 8 Yes Yes No cis-3-hexen-1-ol 10 Yes Yes No fluoroacetone 10 Yes Yes No acetophenone 15 No Yes No 2-acetythiopheno 31 No Yes No pyridine 99 Yes Yes No 2-acetythiophene 31 No Yes No pyrdine 99 Yes Yes No 2-acetythiophene 31 No Yes No 2-acetythiophene 99 Yes Yes No 2-acetythiophene 8 Yes Yes No 2-acetythiophere 8 Yes Yes No 2-acetythiophere 8 Yes Yes No 2-acetythiophere 8 Ye					
methoxyacetone 6 Yes No 1-ohorohexyacetone 8 Yes No cis-3-hexen-1-ol 10 Yes Yes No fluoroacetone 10 Yes Yes No acetophenone 15 No Yes No 2-acetylthiophene 31 No Yes No pridine 99 Yes Yes No thiazole 100 Yes Yes No 2-acthyl-3,5(b-dimethylpyrazine 8 Yes Yes No 2,5-dimethylpyrazine -2 Yes Yes No					
cis-3-baxen-1-ol 10 [Ves Yes No fluoroacetone 10 [Ves Yes No acetophenone 15 No Yes No 2-acetylthiophene 31 No Yes No pridine 99 Yes Yes No thiazole 100 Yes Yes No 2-acetylthiophene 31 No Yes No 2-acetylthiophene 100 Yes Yes No 2-acthyl-3.5(b)-dimethylpyrazine 8 [Yes Yes No 2.5-dimethylpyrazine -8 [Yes Yes No	methoxyacetone	6	Yes	Yes	No
fluoroactone 10 Ves Yes No acetophenone 15 No Yes No 2-acetythiophene 31 No Yes No pyridine 99 Ves Yes No 100 Ves Yes No 2 2-ethyl-3,5(6)-dimethylpyrazine 8 Yes Yes No 2,5-dimethylpyrazine 26 Yes Yes No 2,5-dimethylpyrazine -8 Yes Yes No					
acetophenone 15 No Yes No 2-acetylthiophene 31 No Yes No pyridine 99 Yes Yes No thiazole 100 Yes Yes No 2-ethyl+35 (6)-dimethylpyrazine 8 Yes Yes No 2.5-dimethylpyrazine 26 Yes Yes No 2.6-dimethylpyrazine -8 Yes Yes No					
2-actylthiophene 31 No Yes No pyridine 99 Yes Yes No thiazole 100 Yes Yes No 2-ethyl-3.5(6)-dimethylpyrazine 8 Yes Yes No 2.5-dimethylpyrazine 26 Yes Yes No 2.5-dimethylpyrazine 9 Yes Yes No	acetophenone	15	No	Yes	No
thiazole 100 Yes Yes No 2-ethyl-35(6)-dimethylpyrazine 8 Yes Yes No 2,5-dimethylpyrazine 26 Yes Yes No pyrazine -8 Yes Yes Yes	2-acetylthiophene	31	No		
2-ethyl-3,5(6)-dimethylpyrazine 8 Yes No 2,5-dimethylpyrazine 26 Yes Yes No pyrazine -8 Yes Yes Yes I					
2,5-dimethylpyrazine 26 Yes Yes No pyrazine -8 Yes Yes Yes					
pyrazine -8 Yes Yes Yes	2,5-dimethylpyrazine	26	Yes	Yes	No
	pyrazine	-8	Yes	Yes	Yes
naphthalene -14 Yes Yes Yes	naphthalene	-14	Yes	Yes	Yes

Table 3.7

Table 3.8: Optimized descriptors selected for the Aromatic Activator Screen

Optimized descriptor symbols, brief descriptions, classes, dimensionality, and occurrences are listed for the aromatic activator screen. Descriptors are listed in ascending order of when they were selected into the optimized set. Weights indicate the number of times a descriptor was selected in an optimized descriptor set.

symbol	symbol breif description	class	dimensionality occurrence	occurrence
N.075		atom-centred fragments	2	1
R3v.	R maximal autocorrelation of lag 3 / weighted by atomic van der Waals volumes [GETAWAY descriptors	BETAWAY descriptors	3	7
H.049	H attached to C3(sp3)/C2(sp2)/C3(sp2)/C3(sp)	atom-centred fragments	2	7
nRCHO	number of aldehydes (aliphatic)	functional group counts	1	-
Nn	number of Nitrogen atoms	constitutional descriptors	1	7
ISH	standardized information content on the leverage equality	GETAWAY descriptors	3	7
EEig07d	oments	edge adjacency indices	2	-
piPC04		walk and path counts	2	7
MATS4e	MATS4e Moran autocorrelation - lag 4 / weighted by atomic Sanderson electronegativities 2D autocorrelations	2D autocorrelations	2	7
ESpm14d	ESpm14d Spectral moment 14 from edge adj. matrix weighted by dipole moments	edge adjacency indices	2	-
Mor12m	Mor12m 3D-MoRSE - signal 12 / weighted by atomic masses	3D-MoRSE descriptors	3	1
Toblo 0				

Table 3.8

Table 3.9: Optimized descriptors selected for the Broad Activator

Optimized descriptor symbols, brief descriptions, classes, dimensionality, and occurrences are listed for the broad activator screen. Descriptors are listed in ascending order of when they were selected into the optimized set. Weights indicate the number of times a descriptor was selected in an optimized descriptor set.

		CIASS	anniensionainty occurrence	aniaunono
HNar	Narumi harmonic topological index	topological descriptors	2	1
R3v+	R maximal autocorrelation of lag 3 / weighted by atomic van der Waals volumes	GETAWAY descriptors	З	4
HATS3m	leverage-weighted autocorrelation of lag 3 / weighted by atomic masses	GETAWAY descriptors	3	~
Mor13p	3D-MoRSE - signal 13 / weighted by atomic polarizabilities	3D-MoRSE descriptors	З	-
	standardized information content on the leverage equality	GETAWAY descriptors	С	2
P1s	1st component shape directional WHIM index / weighted by atomic electrotopological states WHIM descriptors	WHIM descriptors	S	-
R4e+	R maximal autocorrelation of lag 4 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors	С	-
nRCHO	number of aldehydes (aliphatic)	functional group counts	-	0
JGI2	mean topological charge index of order2	topological charge indices	2	7
E1u	1st component accessibility directional WHIM index / unweighted	WHIM descriptors	3	2
MATS5m	MATS5m Moran autocorrelation - lag 5 / weighted by atomic masses	2D autocorrelations	2	~
STN	spanning tree number (log)	topological descriptors	2	0
DISPe	d COMMA2 value / weighted by atomic Sanderson electronegativities	geometrical descriptors	3	~
B06.C.O.	B06.C.O. presence/absence of C - O at topological distance 06	2D binary fingerprints	2	~
X4A	average connectivity index chi-4	connectivity indices	2	4
JGI3	mean topological charge index of order3	topological charge indices	2	~
De	D total accessibility index / weighted by atomic Sanderson electronegativities	WHIM descriptors	S	0
	3D-MoRSE - signal 25 / unweighted	3D-MoRSE descriptors	S	~
nRCOX	number of acyl halogenides (aliphatic)	functional group counts	-	~
B03.O.O.	presence/absence	2D binary fingerprints	2	~
nHDon	number of donor atoms for H-bonds (N and O)	functional group counts	-	~
S3e	Moran autocorrelation - lag 3 / weighted by atomic Sanderson electronegativities	2D autocorrelations	2	~
RBF	rotatable bond fraction	constitutional descriptors	-	~
GATS5m	Geary autocorrelation - lag 5 / weighted by atomic masses	2D autocorrelations	2	~
C.008	C.008 CHR2X	atom-centred fragments	2	~
Mor13v	3D-MoRSE - signal 13 / weighted by atomic van der Waals volumes	3D-MoRSE descriptors	Э.	-
R6u.	R maximal autocorrelation of lag 6 / unweighted	GETAWAY descriptors	3	1

Table 3.9

Table 3.10: Optimized descriptors selected for the Inhibitor Screen

Optimized descriptor symbols, brief descriptions, classes, dimensionality, and occurrences are listed for the inhibitor screen. Descriptors are listed in ascending order of when they were selected into the optimized set. Weights indicate the number of times a descriptor was selected in an optimized descriptor set.

ATS1p Bro Gu tots		2D autocorrelations	2	~
				_
	total symmetry index / unweighted	WHIM descriptors	e	9
	th/walk 5 - Randic shape index	Topological indices	2	-
	attached to C0(sp3) with 1X attached to next C	Atom-centred fragments	2	4
H4m Ha	autocorrelation of lag 4 / weighted by mass	GETAWAY descriptors	e	e
		GETAWAY descriptors	8	e
HATS6m leve	by mass	GETAWAY descriptors	e	n
B03[C-O] Pre		2D Atom Pairs	2	-
		Functional group counts	-	2
EEig09r Eig	onance integrals	edge adjacency indices	2	-
	d by atomic masses	3D-MoRSE descriptors	e	e
X5A ave		connectivity indices	2	-
EEig02r Eig	EEig02r Eigenvalue 02 from edge adi, matrix weighted by resonance integrals	edge adjacency indices	2	2
RDF055m Ra		RDF descriptors	3	-
EEig04d Eig	le moments	edge adjacency indices	2	2
ក្ត		2D binary fingerprints	2	-
JGI4 me	an topological charge index of order4	topological charge indices	2	-
RDF085m Ra	eighted by atomic masses	RDF descriptors	93	-
Mor08u 3D		3D-MoRSE descriptors	3	-
MATS5e Mo	ted by atomic Sanderson electronegativities	2D autocorrelations	2	0
B02[C-C] pre		2D binary fingerprints	2	-
		functional group counts	-	-
X4Av ave		connectivity indices	2	~
R7e+ R n	maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors	e	~
EEig08r Eig	Eigenvalue 08 from edge adj. matrix weighted by resonance integrals	edge adjacency indices	2	~
E3s 3rd	3rd component accessibility directional WHIM index / weighted by atomic electrotopological states [WHIM descriptors	HIM descriptors	3	-

Table 3.10

Table 3.11: Top predicted natural library compounds for the aromatic activator,

broad activator, and inhibitor screens

The chemical structure and predicted distance from the known training activators is listed for each predicted odor. All distances represent the minimum optimized descriptor distance to a training set compound, which are listed in gray.

Structure	Distance	Structure	Distance	Structure	Distance
D=C1CCCCC1	0		0	O=(0)2222	
C1=NC=CC=C1	0		0	CC(C(C)=O)=O	
S1C=NC=C1	0	C1=NC=CN1	2.297704		
D=C1CCCCCN1	2.037369	N1N=CC=C1	2.768945	O=C(C(C)=O)C	1.1934
D=C1NCCCC1	2.16724	CC1=CSC=N1		NCCC(O)=O	2.0285
C1=CC=CS1	2.997682	CCCCCC1=NC=CC=C1		O=((O=0)=0	2.5791
D=C1C=CCCC1	3.977348	0110-00-01	3.721854	CCC(N)C(O)=O	2.7529
CC1CCNCC1	4.39789	0001-100(-014-01)0		CC(N(C)C)=O	3.0881
C1=NC=CN1	4.619738	0-0/0-0/000000000	3.778543	CC(C(OC)=O)=C	3.1280
D=C1C=CC=CO1	4.919501	CC1=CN=CC(C)=N1	3.815402	CC(OCC)=O	3.1335
NIN=CC=C1	4.943772	C1=CC=CS1	3.817309	CC(C)/C=N/O	3.169
	5.167015 5.609835		3.82998	O=(O=(O)2)2(C)20	3.1799
C(C)=CC1CC(C)=CCO1	5.751913		3.853768	CC(C)CC(O)=O	3.3184
CC(C)=C[C@H]1C[C@@H](C)CCO1	5.94834		3.889099	C/C(C(O)=O)=C\C	3.4424
	5.94834	CCC1=NC=CN=C1	3.914359	C/C=C(C)/C([O-])=O	3.4529
CC(C)=CC1C=C(C)CCO1	5.971966	CC1=NC=CN=C1OC	4.038081	C=C(C)CCO	3.736
0=C1CC(C)(O)CCO1	6.075926	COC1=NC=CN=C1CC	4.03881	O=C(O)COC	3.778
CC(C)=CC10CCC(C1)C	6.143672	C=CC1=CN=CC(C)=N1	4.048223	CC(C)C(OC)=O	3.80
0C1CCCCC1 01SCCC1	6.220288	CC1=COC=C1	4.074861	CC(C)=CCO	3.874
CIC=CCS1	6.313776	CC1=NC=C(CC)C=C1	4.124326	CC(COC)=O	3.874
)C1(C)C=CCCC1	6.407874	a/a a/a a) a a a a a a a a a a	4.131876	C/C(C=O)=C\C	4.012
0C1(C)CCCC1	6.471678		4.139062	CCC(C)C=O	4.027
)=C1C/C=C\CCCCCCCC01	6.523937	CC1=CC2=C(C=C1)N=CC=C2	4.187466	C=C(O)CCC	4.210
CC(=CCCC(=CCCC1=COC=C1)C)C	6.54101	CCC/C=C/C=C/C/C=C\CCO	4.235145	C=CC(CC)=O	4.220
C1=CC=CC=CC1	6 558737	CC/C=C/C=C/CCCCCCCCCO	4.260037	CC(CC=C)=O	4.255
C1=NC=C(CC)C=C1	6 577361	CC1=CN=C(C(C)CC)C(C)=N1	4.26035	CC(C)CC#N	4.2
1C=CC=C1		CC/C=C\C/C=C\C/C=C\CCO	4.262767	O=C(O)C(N)CO	4.307
N1C=CC=C1		CC1=NC=CN=C1CC(C)C	4.265956	CC(C)CCO	4.368
D=C(NCCC(C)C)C1=CC=CC=C1	6.612483		4.290186	NC(OCC)=O	4.378
CC1SCCN1	6.61741		4.295488	CC(OC)OC	4.394
D=C(OC(C)C)C1=CC=CC=C1		CC(C1=CN=CC(C(C)C)=N1)C	4.295748	C/C=C(C)/CO	4.410
CCCC(C1=CC=CC=C1)=O	6.651088	OCC/C=C\C1=CC=CC=C1	4.312156	C=C(C)C(C)=C	4.446
D=C(N1CCCCC1)C2=CCCCC2	6.675009	000000000000000000000000000000000000000	4.317797	CC(C(C)=C)=O	4.523
CC(C)CC1=NC=CS1	6.701117	CC/C=C\C/C=C\CCCO	4.328344	CCC(C)C#N	4.540
CCCCCCC1CCCC(01)=0	6.717317		4.347131	O=C(O)C(CC)CC	4.545
CCCCCCCC1CCCC(O1)=O	6.743187	022222020/0=2/2	4.35801	CC(CCC)=0	4.576
CC1CCCC(C)N1	6.751586		4.371786	O=(C(C(C)CC)=0	4.608
D=CC1=COC=C1	6.853976		4.375425	O=COCC	4.696
D=C(OCC=C(C)C)C1=CC=CC=C1	6.86057		4.38817	CC(C)(C)C(O)=0	4.786
C1=COC=C1	6.867993	000000000000000000000000000000000000000	4.401625	N[C@@H](C(C)C)C(O)=O	4.809
D=C(C)CC(OCC1=CC=CC=C1)=O	6.899082	CC1C=CCC1	4.413842	CC(C)C[N+]([O-])=O	4.811
C1=CC=CC(O)=C1	6.902425	O=COC/C=C/C1=CC=CC=C1	4.423901	CC(C(O)=O)=C	4.818
D=C(N(CC)CC)CC1=CC=CC=C1	6.905865	CC1=NC=C(CC)N=C1C	4.441315	CC(C(O)CC)=0	4.835
CCC(N1CCCCC1)=O	6.908113	NCCC1=CC=CC=C1	4.45126	CC(C)=CC(O)=O	4.870
C/C(C(OCCC1=CC=CC=C1)=O)=C\C	6.915907	N1=CCCC1	4.455448	CC(OC(C)=C)=O	4.88
CCC(OCCC1=CC=CC=C1)=O	6.94	C/C=C\C=C/CCCCCCCCCO	4.455697	CC(C(C(C)C)=O)=O	4.932
)=C1C/C=C\C/C=C\CCCCCO1	6.96282	C1(CCCC2=CC=CC=C2)=NC=CC=C1	4.48037	0=(0)202	4.94
CCC/C=C\C1CC=CC(O1)=O	6.971452	O=CC1=CC=C(C(C)=C)C=C1	4.484765	CC(0)COC	4.960
CCCCCC1=NC=CC=C1	6.99577	022022222222222222222222222222222222222	4.4849	CC(O)C(CC)=O	4.969
CCCCC/C=C\C1CC=CC(O1)=O	7.00054	CC1-C(SC-N1)CCO	4.495566	O=CN(C)C	4.971
CCCC/C=C\C1CC=CC(O1)=O	7.008492	004-0N-0(0)0(0)00)-N4	4.495643	0=0(0)(0=0)	4.979 5.003
CC(C)=CCC1=C(C)C=CO1	7.01097	00100001	4.507732	O=C(C)/C=C/C	
C/C=C/C(OCC1=CC=CC=C1)=O	7.011722	CC1=C(C)N=CS1	4.507732	CC(C)=CC#N	5.003
CCCCCC1=CC=C1	7.012331	0000/01 10/01 01 01010		CC([C@H](O)C)=0	5.00
CCCC(OCCC1=CC=CC=C1)=O	7.016306	a	4.551649	OC(C)(CC)(C([0-])=0	5.013
CC(CCC1=CC=CC=C1)=O	7.018781		4.551649	0=(0)(0)(0)(0) 0=0	5.020
CC(C)CC(OCCC1=CC=CC=C1)=O	7.0234			C[C@@H](O)CC(O)=O	5.047
CC(SCC1=CC=CO1)C	7.030379		4.559646	CC(C(O)C)=O	5.057
DC1=CC=CC=C1	7.03727	CCCCCC/C=C/CCCCCCO	4.559792	CCC(CO)=C	5.059
C1=CC=C(CCC)C=C1				CC(C)CC=0	5.151
CCC10CC(01)C	7.057154		4.57072	CC(OCC)=S	5.164
CCCCCCCCC(N1CCC(C)CC1)=O	7.066965	CCCCCC/C=C\CO	4.573949	SC(C)C(O)=O	5.213

Table 3.12: Predicted odors validated as activators and inhibitors of the CO₂

receptor

The overall accuracy for CO2 predictions considering all three predicted sets. The accuracy and percentage accuracy are listed for each class.

Activity	Accuracy	Percentage
Activators (>50 spikes/sec)	25/139	18%
Activators (>30 spikes/sec)	42/139	30%
Inhibitors (<-5 spikes/sec)	25/139	18%
	Total	48%

Table 3.12

Table 3.13: Optimized descriptor sets for each Citrus Psyllid ORN

Optimized descriptor symbols and final descriptor-activity correlations are listed for each Citrus Psyllid ORN. Descriptors are listed in ascending order of when they were selected into the optimized set. The number of times a descriptor was selected in an optimized descriptor set represent weights.

RP4_C SP02 Correlation ATS6m 0.807409 0.807409 R5p. ATS5m SP12 Mor29e R7m. R8u. RDF020e Mor23p H.052 0 R8p. 1 Mor16p BEHm7 SP12.1 R6m. EEig08x HATS3p G3u G3u nCb. B07.C.O. R6m1 H7u B04.C.C. EEig11x Z ATS8m RTu. BEHm7.1 R7m1 R8e. C.025		Pl Or RP2_A Correlation 0.8315387		RP2_C Correlation	5 Infective.80 RDF065m JGI6 RDF080v nHDon Mor27e H8v E1u R2v. Mor03m R7m.1 Mor32u H6m H8m Mor16u O.056 Mor27e.1 JGI6.1 EEig12x QYYe.1 R8p.	
Mor16p.1 nRCO						
RP4_C SP02 Correlation ATS6m 0.807409 R5p. ATS5m SP12 Mor29e R7m. R8u. RDF020e Mor23p H.052 0 R8p. 1 Mor16p BEHm7 SP12.1 R6m. EEig08x HATS3p G3u G3u nCb. B07.C.O. R6m1 H7u B04.C.C. EEig11x 2 MATS8m RTu. BEHm7.1 R7m1 R8e. C.025 0.1 H4p CIC3 Mor30u Mor16m R6m2 B07.C.O1 BEHm7.3 EEig11x.1 BEHm7.3 EEig08x.11 R8e1 R7m2 R5p1 SP12.2 BEHm7.4 Mor16p.1 nRCO	ATS5v ATS4e DISPv R7p. H5v nHDon As B05.C.C. nDB E2s Mor26v Infective.80 B05.C.C.1 L.Bw piPC08 G3p RDF080e nR.Cp BELm1 nHDon.1 PJI3 H8u Mor24m DISPv.1 nCconj B05.C.C.2 L2s nHDon.2 H4m G3u nR04 Infective.80.1 nRC0 RDF075e DISPv.2 0.057	RP2_A Correlation	C ESpm10d lation L1m 6558 Mor30p nHDon ESpm10d.1 Mor27p E3m H.051 Mor24p Mor27p.1 HATS8m Mor16u R1u. ESpm06d R4v. Mor13p B04.C.C. L3s EEig08x nHDon.1 Mor27e Mor30m nR.Cs Mor30e Mor10u C.006 R5v.	RP2_C Correlation	R7m QYYe 5 Infective.80 RDF065m JGI6 RDF080v nHDon Mor27e H8v E1u R2v. Mor03m R7m.1 Mor32u H6m H8m Mor16u O.056 Mor27e.1 JGI6.1 EEig12x QYYe.1 R8p.	RP2_B Correlation

	Desc.Symbol		Desc.Symbol		Desc.Symbol	
RP6_A Correlation 0.8951214	nRCHO nCconj	RP6_B Correlation 0.8758008	ATS5v Xu	RP6_C Correlation 0.8019783	SP01 Mor13u	RP7_B Correlation 0.8016844

Table 3.13 Continued

Desc.Symbol	Or	Desc.Symbol
Mor02p	RP7 C	nRCHO
Mor27e	Correlation	EEig10x
R7p.	0.8422402	•
DISPm		EEig03d
Infective.80		RDF020e
JGI5		DISPv
B07.C.C.		Mor30u
HATS4e		PJI3
Mor23p		G3s
Mor32m		GATS2p
CIC2		RDF080e
R7m.		nROH
JGI4		R3p
Mor10m		RDF020e.1
X5A		EEig10x.1
EEig10r		ESpm01d
B07.C.C1		nRCOOR
H3m		H.051
Mor03p		GATS5e
F05.C.O.		H8u
R6m.		H.051.1
JGI5.1		Mor30e
B07.C.C2		nROH.1
Mor27e.1		EEig09x
HATS4e.1		Jhetp
E2e		Mor30u.1
B07.C.C3		RDF020e.2
Mor03m		
B04.C.C.		
EEig10r.1		
CIC2.1		
B07.C.C4		
JGI4.1		

Table 3.13 Continued

Table 3.14: Top predicted natural library compounds for Citrus Psyllid ORNs

The chemical structure and predicted activity are listed for the top predicted activators for each ORN. Compounds in gray are training set odors.

RP2_B		RP2_C		RP4_B	
SMILES	Pred Activity 74.35797		Pred Activity SM	ILES	Pred Activity
C/C1=C\CC(C)(C)/C=C/C(C)=C/CC1 CC(OCCCCC)=0		CCC/C=C/C=O CC(C)=CCCC(C=C)=C		=CC=C(C(C)C)C=C1 C1=CC=CC=C1)=O	163.3939 139.1738
C=C1CC/C=C(C)/CC[C@@]2([H])C(C)(C)C[C@]12[H] C/C(CCC=C(C)C)=C\C=O	71.84607	0=(00)2020 0=000000000000000000000000000000	42.36729 CC(0	C12CCC(C1C2)=C)C	135.1755 128.784
C=C/C(C)=C/CC=C(C)C	58.49042	O=CC1=CC=CC=C1	26.24606 CCC		117.5805
0=22222222 0=222222222 0=22(2)(2)(2)(2)(2)(2)(2)(2)(2)(2)(2)(2)(2		C=CC(O)CCCCC CC1=CCC(C(C)=C)CC1=O	23.14035 CC/0 21.80823 CC(0		116.1112 112.9869
C/C1=C\CC(C)(C)/C=C/C/C(C)=C/CC1	74.35797	C/C=C/CC(OC)=O	51.43602 CCC	(C1=NC=CS1)C	210.9587
0=(0000000)0=0		CCCC=CC=O CC/C=C/CC(OC)=O	45.26686 CCC 44.65782 CC(0	C1=CC=CO1 C)CC1=NC=CS1	201.5245 195.0182
C/C1=C\CC/C(C)=C/C/C(C[C@@H]1C)=C(C)\C	71.24567	CCC(OC)=O	44.38818 CC(0	C1=CC=CC=C1)C	194.1631
CC1=CCCC(=CCC(CC1)C(=C)C)C CC(C)CCC(OCC)=O		CC(=CCCC(=C)C=C)C CCCC/C=C/C=O		=CC=CC=C1CC CC1=CC=CC=C1	193.5604 191.4757
CCCC(OCC(C)C)=0 CC(/C=C/CCCCC)=0		CCCC(OC)=0 C/C=C/C(OC)=0		=CC(CC)=CC=C1 0C1=CC=CC=C1	191.0865 190.5536
CC(OCCCCCC)=0	65.7931	CCC(/C=C/C=O)=O	41.84369 CCC	C1=CC=CC=C1	188.6928
CC1=CC=C(O1)C(C)CC=O O=C/C=C(CCC=C(C)C)\C		CC(/C=C/CCC)=0 CCC/C=C/C(OC)=0	40.55074 CCC 40.52789 CC1		188.517 187.4761
O=(00)000000	63.10904	CC1CCC2=C(C=NC=C12)C	40.00807 CC1	=CSC(C(C)C)=N1	184.7897
CC(/C=C/CCCC)=O CC(CCC=C)C=C(C)C		CCCCC/C=C/C=C CC/C=C/C(OC)=O	39.71849 CC(0	C(OC)C1=CC=CC=C1 C1=CC(C)=CC=C1)C	178.6651 178.4423
CCC(OCCCCC)=0 C=C(C1C/C=C(C)/CC/C=C(C)\CC1)C		CC/C=C/C=C/C=O C=CCC(O)CC=C	39.4017 CC1	=CC=C(CC)C=C1 C2=CC=CC=C2)CO1	177.9384 175.7152
C/C=C/C(OCC(C)C)=O		C=C/C(C)=C/C=C/C(C)C	38.95081 CC1	=CC(CC)=CC=C1C	174.1878
C=C/C(C)=C/CC1C(C)(C)O1 C=C/C(C)=C/CC=C(C)C		CCCCC(OC)=0 O=C(OC)CCC(OC)=0	38.01496 CCC 37.8518 CCC	:1=CC=CN=C1 :1=CC(CC)=CC=C1	174.0245 169.4623
O=(0(0))	56.55607	C=C/C(C)=C/CCC(C)=C	37.74838 CCC	CCC1=CC=CO1	168.622
CCCCC1CCC(O1)=0 COC/C=C(CCC=C(C)C)/C		C/C(C(OC)=O)=C\C C/C=C/C=C/C(OC)=O	37.48334 N#CI 37.47729 CCC	CC1=CC=CC=C1 CC1=CC=CO1	167.7722 166.5448
CC1=C[C@](C(C)(C)CC[C@@H]2C)([H])[C@@](CC1)([H])C2=C	56.43485	CC/C=C/CC(OCC)=O	37.34352 CC1	=CC=C(C(C)C)C=C1	163.3939
CC(CCCCCC=C)=O C=C(O1)C1(C)=CCC=C(C)C		O=C(C)/C=C/C C/C=C/C=C/C=O	37.33052 COC 37.21464 CC(0	CC1=CC=CC=C1 C)CCC#N	163.2257 161.5202
O=C(OC)CC1=CC=CC=C1		COC1=CC=C(C=C)C=C1 CCCC/C=C/C/C=C/C=O	37.11306 SCC	C1=CC=CC=C1	161.2887 160.0841
C=C/C=C(C)/CCC=C(C)C COC/C=C(CCC=C(C)C)/C		CCC(OCC=C)=0	36.4936 CSC	=CC=CC=C1C(C)C :C1=CC=CC=C1	159.0215
C=CC(CCC=C(C)C)C CC(C)CC(CC(C)C)=O		C=CC(CC)=O C=C(C)/C=C/C=C(C)/C=C		:1C2CCOC(O2)(C)O1 =NC=C(CC)C=C1	158.5089 158.0411
OCCCC(OCCC)=0	53.12195	O=C1(C/C=C/C)=CCCC1C	36.06916 CCC	CC1=CC=CC=C1	156.9442
O=[N+](/C=C\C1=CC=CC=C1)[O-] CCCCC(OCC)=O		0=C(0C)CC(0C)=0 CCCCC/C=C\C=C\C=0	36.01778 CSC 36.00254 [C-1#	1=CC=CC=C1 [N+]CC1=CC=CC=C1	156.4088 154.3357
CCCCC/C=C/C=O	52.16527	CCC(OCC/C=C\CC)=O	35.75418 CCC	C10CC(01)C	154.2606
0=(202020)20 0=(200)2(2)2020		CC(C)C(OC)=0 C=C/C=C/C=C\CCCCC		C1=CC=C(CC)C=C1 COC(O1)CC(C)C	153.2292 152.8799
CC(C)=C1CCC(C)C2=C(C(C)CC2)C1	51.6773	CC/C=C/CCC=O CCC(OCCC)=O	35.3759 CCC	C(OC)=S =CC=CC=C1CC	152.8392 152.6492
CC(C1CC=C(C=O)CC1)C O=C(C)C(OCCC(C)C)=O	51.17537	CC/C=C/C=O	35.05646 COC	1=CC=CC=C1	152.1006
O=(02(0)) O=(0=(02(0)) O=(0=(020))		C=C/C=C/CCCC O=COCCC	35.0319 CCC 35.02602 CSC	1=NC=CN=C1	150.7356 148.9938
CC(OC(C)(C1=CC=CC=C1OC)C)=O	51.00987	CCC/C=C/C=C/C=O	35.00791 CC1	=NC=C(CC)N=C1C	144.4554
C=CCC(C)C(OCC)=O O=CCC1=CC=C(C)C=C1C		CC(CC=CC=CC)C O=C(OC)CCCOC		:1=NC(=CN=C1)C OC2(C)C(C)CCC1O2	144.0637 142.4315
COC(C=C)(C)CCC=C(C)C	50.49973	COC1=CC=C(/C=C/C)C=C1	34.60386 CC1	(C)C2CCC(C)=CC12	142.1961
CC1(C)C2CC/C(C)=C\CC/C(C)=C\C12 O=COCCCCCC	50.36754 50.33509	CCCC(O)CCC=C	34.57437 CCC 34.19629 O=C	C1=CC=CC(CC)=C1	141.7605 141.4747
CC(C)=C/C=C/C(C)=C\C CC(C)CCCC(OC)=O		O=CC1=CN=CC=C1 C=C/C(C)=C/C		C=CC2(C(C)C)CC12 D)C1=CC=CC=C1	140.7053 140.5338
C/C(CCC=C(C)C)=N\O	49.90491	C/C=C/C(OCC)=O	33.48005 CC1	=NC=CN=C1CC	139.2927
CC(C)=CC1=CC=CC=C1 CCCCCCCC=O		CCC(/C=C/C)=0 CC(OCCCCC/C=C/CC)=0	33.43157 COC 33.40156 CC(0	C1CC=C(C)CC1 C1=CC=CC=C1)=O	139.2339 139.1738
CC/C=C\CCC=O	48.87246	CCC(OCC)=O	33.32586 CC(0	DC1=CC=CC=C1)=O	137.8998
CC(OC1CCCCC1)=0 CC1CCC=C2C1(C3C(C3(C)C)CC2)C		CC(OC)OC CCCC(OCC/C=C/CC)=O		C1=CC=C(C)C=C1 (C1=C(C)N=C(C)S1)C	137.7904 137.15
O=COCCCCCC	48.08597	CCC/C=C\C(OC)=0 C=C=C(C)CC	33.02956 O=C	(OC)C1=CC=CC=C1C 2CCCC(O2)C(CC)O1	137.0934 136.7338
O=C(OC)C1=CC=CC=C1C	47.67373	O=C(N1C)N(C)C=CC1=O	32.91734 CNC	1=CC=CC=C1	136.328
CCCC(OCCC)=O C=C/C(C)=C/CC=C(C)C		CCCC/C=C/CC=O O=COC1CCCCC1		CC1=CC=CC=C1)=O CC2=CC=CC2)C=CC=C1	135.7478 135.7411
O=COCCCCC	47.10583	C/C=C/C=C/C(OCC)=O	32.70471 C=C	1CCC2(C(C)C)CC12	135.1755
CC(CC1=CC=CC=C1)=O O=[N+](CCC1=CC=CC=C1)[O-]		CCCCC/C=C/C/C=C/CC(OC)=O CCC1=CC=C(C=C)C=C1	32.552 CC(0 32.41418 COC	C)CC#N C1=CC=CC=C1C	134.4416 134.3196
CCCCCC(0C)=0 C=C(C)C(0CCCC(C)C)=0	46.73148	CCCC/C=C/C=C/C=O CC(OC1CCCCCC1)=O	32.03659 CCC 31.94634 CCC	C1CCC(O1)=O	133.6848 132.8239
CCCCCC/C=C/C=O	46.33825	CC(OC(C)C)=O	31.59381 O=C	C1=CC=CC=C1CC	132.788
CC(OCCC/C=C\C)=0 CCCCC1C(CC(=O)O1)C		CC(0/C=C/CCCCCC)=0 CCC/C=C/CCC(0C)=0		=CC=C(C)C(C)=C1 D)(C1=CC=CC=C1)C	131.9495 131.9484
C=C([C@@H]1CC=C(C=O)CC1)C	45.83685	CCCC/C=C/C=C(C)C	31.44217 O=C	(OC)CC1=CC=CC=C1	131.7989
0=000000000000000000000000000000000000		CC(C)=CC(CC(C=C)=C)=O COC1=CC=C(OC)C=C1		C1=CC=C(C)C=C1C C(O)C1=CC=CC=C1	131.7978 131.719
CSSCC1=CC=CO1	45.46385	CC(C/C=C/CC)=O	31.37606 CC(0	0000(131.6372
CCC(C)CCC(OC)=0 O=C(C1CCCCC1)OC		CC(=CCCC(=CC=CC(=O)C)C)C CC1=CCC=CC1	31.37038 CC(0 31.31489 CC1	C1=CN=C(C)C=N1)C =C(C)C=CS1	131.534 130.8618
C=CC(0CCCC)=O CCCCC(/C=C/C=O)=O		CC(C)CCCC(OC)=0 CC(CCC=C(C)C)C=0	31.30609 O=C	OCCC(C)C =CN=C(C)C(CC)=N1	130.8068 129.885
CCCCC/C=C(CC)/C([O-])=O	44.65088	CN1CCCCC1	31.17583 CCC	(C)C#N	129.1444
0=CC1=CC=C(0CC)C=C1 CC(0CCCCCC)(C)=0		CC1=CC=C(C(C)=C)CC1 C=C(C)CCC		CCC1=CC=CC=C1 C1CCCC(01)=0	128.9196 128.6957
CCC(OC1=CC=CC=C1)=O	44.13589	CC(C(OC)=O)=C	31.04751 CCC	CCC1C(C)C1	128.5922
CCCC1=CC=CC=C1 C=C(C1CCC(C)C12CC=C(C)CC2)C		CC/C=C/CC/C=C/C=O CCCC(OCC)=O	30.89184 C#C 30.8423 CC(=	=O)C1=CC=C(C=C1)OC	128.5503 128.3256
CCCCCC1=CC=CO1	43.65871	CCC(C(COC)=O)=C	30.83327 CC1	=CCC2(C1C2)C(C)C	128.1545
CC(C)=CCC1=C(C)C=CO1 CC1=NC=CN=C1CC(C)C	43.43477	C=CC(OCC)=O CC(COC)=O		N(C(C)=O)CCCC1	128.0058 127.756
O=20202020 O=(02)20202020	43.1834	CCC(C)CC(OC)=0 CCCC(OCC/C=C\CC)=0	30.61718 CCC 30.53002 CCC		127.5711 127.5105
CCCCCC(OCC)=O	43.08604	C/C(C(OCC=C)=O)=C\C	30.51805 CCO	COCC	127.4569
C=CCCCCCCC O=C10/C(C2=C1C=CC=C2)=C\CCC		CC(CCC1)OC21CCCO2 CC(/C=C/CC)=O	30.41643 COC 30.40109 CCC	C1=CC=CC=C1OC(C)=O C(C)C(OC)=O	127.3973 127.2072
CCC(C1=CC=CC=C1)=O	42.71533	CC(OC)CC	30.34567 CC(0	C)(C)CC(C)CC	126.9944
CCCC(OC(C(C)=O)C)=O CC1=CCCC(=C)C2CC(C2CC1)(C)C		O=COCCCC CC(/C=C/C(C)C)=O		C1=CC=CC=C1)C=O C1=CC=CC=C1)OCC	126.5322 126.26

Table 3.14

SMLES Pred Activey SMLES Pred Activey				554.4			554.0
DOCUMON No.500 Status Description DOCUMON NO.500 NO.500 NO.500 DOCUMON <th>RP6_B ES Pred Activity</th> <th>Activity</th> <th>Pred</th> <th>RP6_A SMILES</th> <th>Activity</th> <th></th> <th>RP4_C</th>	RP6_B ES Pred Activity	Activity	Pred	RP6_A SMILES	Activity		RP4_C
Control Base Control Base Control Base Control Control Prime Control Base Control Base Control Control Prime Control Base Control Base Control Base Control Control Base Contro Base <	2CCC(C1C2)=C)C 134.0782	55.52031	1100	CC/C=C\CC=O	88.03097	1100	000000
Del del manufactoria Name Concordona Name Concordona Name Del del manufactoria 11 10000000000000000000000000000000000	C=C(C(C)C)C=C1 130.4358 =CC=CC=CC=C1)=O 125.9246	50.76842 55.52031		CCCCCCCC=0 CC/C=C\CC=0	81.96087 70.8636		CC(C1=CCC(C)=CC1)C CCCC(OCC)=O
Bellinkania Biology Biology Biology Biology Biology Biology Biology Biology Biology Biology Biology Biology Biology Biology Biology Biology Biology Biology Biology Biology Biology Biology Biology Biology Biology Biology Biology <td>C(C)C)=O 123.529</td> <td>55.23 115</td> <td></td> <td>CCCC/C=C/CC=O</td> <td>56.16668</td> <td></td> <td>C=C([C@H]1CC=C(C)CC1)C</td>	C(C)C)=O 123.529	55.23 115		CCCC/C=C/CC=O	56.16668		C=C([C@H]1CC=C(C)CC1)C
	SCCC 119.8744	50.84559		0=0000000000000000000000000000000000000	41.21922		D=CC1=CC=CC=C1
	CCCC)=O 106.2103	50.76842		0=2222222	40.3888		CCC/C=C/C=O
	=C\CO 97.64069 =CC=CC=C1)C 154.2561			CCC(CC)C=0 CCCCC(CC)C=0	88.57896 88.03097		CCC(OCCC)=0 CCCCCCO
SECCODO 74183 COCCODO 44.2 1182 COCCODENCION SECCODO 74183 COCCODENCION 44.2 1182 COCCODENCION SECCODO 74184 COCCODENCION 44.2 1182 COCCODENCION SECCODO 74184 COCCODENCION 44.2 1182 COCCODENCION SECCODO 74184 COCCODENCION 44.2 1182 COCCODENCION SECCODO 84.2 100 COCCODENCION 44.2 1182 COCCODENCION SECCODO 84.2 100 COCCODENCION 44.2 100 COCCODENCION SECCODO 84.2 100 COCCODENCION 44.2 100 COCCODENCION SECCODO 84.2 100 COCCODENCION 45.2 20 COUNTRING SECCODO 84.2 100 COUNTRING 45.2 20 COUNTRING COUNTRING SECCODO 84.2 100 COUNTRING 45.2 20 COUNTRING COUNTRING SECCODO 84.2 100 COUNTRING 84.2 20 COUNTRING COUNTRING SECCODO SECCODO SECCODO SECCODO SECODO <td>=CC(C)=CC=C1)C 153.5955</td> <td>44.74221</td> <td></td> <td>CCC(C)CCCC/C=C\CCCCCCC=0</td> <td>82.40683</td> <td></td> <td>NCCCCCN</td>	=CC(C)=CC=C1)C 153.5955	44.74221		CCC(C)CCCC/C=C\CCCCCCC=0	82.40683		NCCCCCN
SEGEDEDPO 7.387 COCCO-COCCO 44.387 COCCO-COCO SEGEDEDPO 7.387 COCCO-COCCO 44.388 COCCO-COCO SEGEDEDPO 7.387 COCCO-COCO 44.388 COCCO-COCO SEGEDEDPO 7.387 COCCO-COCO 44.388 COCCO-COCO SEGEDEDPO 86.388 COCCO-COCO 44.388 COCCO-COCO SEGEDEDPO 86.387 COCCO-COCO- 86.388 COCCO-COCO- SEGEDEDPO 86.387 COCCO-COCO- 86.388 COCCO-COCO- SEGEDEDPORT 86.387 COCCO-COCO- 86.388 COCCO-COCO- SEGEDEDPORT 86.388 COCCO-COCO- 86.388 COCCO-COCO- SEGEDEDPORT 86.388 COCCO-COCO- 86.388 COCCO-COCO- SEGEDEDPORT 86.388 COCCOC							
SCC0000-0 NR80 CCCC000-0 44.812 CCC-0-00-0 SCC0000-0 NR80 CCCC00-0-0 44.812 CCC-0-0-0-0 SCC0000-0 NR80 CCCC00-0-0 44.822 CCC-0-0-0-0-0 SCC0000-0 NR80 CCCC00-0-0 44.822 CCC-0-0-0-0-0-0 SCC0000-0 NR80 CCCC00-0-0 44.828 CCC-0-0-0-0-0-0 SCC0000-0 NR80 CCCC00-0-0-0 44.828 CCC-0-0-0-0-0-0-0-0 SCC0000-0 NR80 CCCC00-0-0-0-0 38.83 CCC-0-0-0-0-0-0-0-0 SCC0000-0 NR80 CCCC00-0-0-0-0 38.83 CCC-0-0-0-0-0-0-0-0-0-0-0 SCC0000-0 NR80 CCCC00-0-0-0-0-0 38.83 CCC-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0	=CC=C01 148.7293	44.03917		CCCCC/C=C\C/C=C\CCCCCCC=O	77.38877		O=(0000)000
SEGECOND-O 13.748 COP-COCCUC-QC-OCCUCCOCCO-Q 41.448 COP-COCUC-QC-OCCUCCO-Q SEGECOND-O 13.748 COP-COCUC-QC-OCCUCCO-Q 41.348 COP-COCUC-QC-OCCUC-Q SEGECOND-O 13.748 COP-COCUC-QC-OCCUC-Q 41.348 COP-COCUC-QC-OCCUC-Q SEGECOND-O 61.778 COP-COCUC-QC-OCCUC-Q 41.348 COP-COCUC-QC-OCCUC-QC-QC-QC-QC-QC-QC-QC-QC-QC-QC-QC-QC-QC	1=NC=CS1)C 143.9979 1=CC=C01 143.4794	43.72791		000000000000000000000000000000000000000			C=CC(CCC)=O
bcbccccipio 81988 bcbcccccipio 41.822 Control-concip bcbcccipio 81988 bcbcccipio 41.822 Control-concip bcbcccipio 81988 bcbcccipio 41.822 Control-concip bcbcccipio 81988 bcbcccipio 41.822 Control-concipio bcbcccipio 81988 bcbcccipio 41.822 Control-concipio bcbcccipio 81988 bcbcccipio 39.848 Control-concipio bcbcccipio 81988 bcbcccipio 39.848 Control-concipio bcbcccipio 81988 bcbcccipio 39.848 Control-concipio bcbcccipio 81988 bcbcccipio 39.931 Control-concipio <t< td=""><td>CC=CN=C1 141.5474</td><td>41.48486</td><td></td><td>CC/C=C\C/C=C\C/C=C\C/C=C\CCCCCC=O</td><td>70.27421</td><td></td><td>0=00000000</td></t<>	CC=CN=C1 141.5474	41.48486		CC/C=C\C/C=C\C/C=C\C/C=C\CCCCCC=O	70.27421		0=00000000
SCCCCCCOPP-0 81988 CCCCCCCCCCC-0 41488 CCC-1-8-C/C/C/H SCCCCCCCCP-0 81984 CCCCCCCCCCC-0 42383 CCCCCCCCCCC-0 SCCCCCCCCCCP-0 81984 CCCCCCCCCCCC-0 328277 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC				CC(C)(C)CC(C)CC=0			
BECCCCC BETME CODCO-0 4.4400 CONSCICUTION BECCCCC BETME CONSCICUTION 4.4000 CONSCICUTION SCOCCCCP-0 BETME CONSCICUTION 3.8401 CONSCICUTION SCOCCCCP-0 BETME CONSCICUTION 3.8401 CONSCICUTION SCOCCCCP-0 J.3.31 CONSCICUTION 3.8401 CONSCICUTION SCOCCCCP-0 J.3.31 CONSCICUTION 3.8401 CONSCICUTION SCOCCCCP-0 J.3.31 CONSCICUTION 3.8401 CONSCICUTION SCOCCCP-0 J.3.8401 CONSCICUTION 3.8401 CONSCICUTION SCOCCCP-0 J.3.8401 CONSCICUTION 3.8401 CONSCICUTION SCOCCCP-0 J.3.8401 CONSCICUTION 3.8401	N=C(C)C(CC)=N1 137.8212	41.34868		CC(C)CC(C)CC=O	67.27872		0=(0=0)20000
DSCC0000000-0 8.388 CONTRACTORNO 8.386 CONTRACTORNO DSCC000000-0 8.387 CONTRACTORNO 8.3827 CONTRACTORNO DSCC000000-0 8.387 CONTRACTORNO 8.3827 CONTRACTORNO DSCC000000-0 8.387 CONTRACTORNO 8.388 CONTRACTORNO DSCC00000-0 8.387 CONTRACTORNO 8.388 CONTRACTORNO DSCC00000	I=CC=CC=C1 136.8536 SC(CC)=N1 135.7359			0=2222222222222222222222222222222222222			0=(000000)
SECCEDDD-D 44.048 C-CCUCDD-D-C 40.0869 SECCEDD-D-C SECCEDDD-D 88.077 C-CC-SCUCDD-D-C 38.077 C-CC-SCUCDD-D-C SECCEDDD-D 88.077 C-CC-SCUCDD-D 38.078 C-CC-SCUCDD-D-C SECCEDDD-D 88.077 C-CC-SCUCDD-D 38.088 C-CC	NC=CN=C1CC 135.369	40.45955		CCCCC#CCCCCCCCCC=0	65.19794		
Chelebellighender 818822 Chelebellighender 818822 Chelebellighender Chelebellighender 81882 Chelebellighender 818824 Chelebellighender Chelebellighender 81784 Construction 81784 Construction Schederlighender 81784 Construction 818842 Construction Schederlighender 81784 Construction 81842 Construction Schederlighender 81784 Construction 81842 Construction Schederlighender 81784 Construction 81784 Construction Schederlighender 81784 Construction 81784 Construction Schederlighender 81784 Construction 81784 Construction Schederlighender 81784 Construction 8	I=CC=CC=C1 134.9309 NC(=CN=C1)C 134. 113	40.06869		C=CCC(C)C=O			CCCCC(OC)=O
SCGCCCCDQ-D 34.473 COLONCOCQ-D 34.473 COLONCOCQ-D SCGCCCDQ-D 37.100 COLONCOCQ-D 37.000 COLONCOCQ-D SCGCCDQ-D 37.000 COLONCOCQ-D 37.000 <	NC(=CN=C1)C 134. 113 CC2(C(C)C)CC12 134.0782	39.8543 39.68227					
Scienceders 8,1784 Coccepto- December 2000 9,7330 Cont-Scienceder- Handler Scienceders 8,1781 Coccepto- December 2000 8,8381 Cont-Scienceders Scienceders 8,1781 Coccepto- December 2000 8,8381 Cont-Scienceders Scienceders 8,1781 Coccepto- December 2000 8,8481 Cont-Scienceders Scienceders 8,1781 Coccepto- December 2000 8,1781 Coccepto- December 2000 8,1781 Coccepto- December 2000 Scienceders 8,1781 Coccepto- December 2000 8,1781 Coccecepto- December 2000 8,1781	C=C(CC)C=C1 133.5617	38.46738		CC/C=C\CCC=O	60.78221		0=(000000)
SEGCCODO-D 88.877 COCCI-COCCI-0 97.000 SER.877 COCCI-COCCI-0 SEGCCODO-D 88.887 COLIC-COCCI-1 SER.887 COCCI-COCCI-0 SEGCCODO-D 97.878 COCCI-COCCI-0 SER.887 COCCI-COCCI-0 SEGCCODO-D 97.878 COCCI-COCCI-0 SER.888 COLIC-COCCI-0 SEGCCODO-D 97.878 COCCI-COCCICCOCOCO-0 SER.878 COCCI-COCCICCOCOCO-0 SEGCCODO-D SER.888 COCCI-COCCICCOCOCO-0 SER.888 COCCI-COCCICCOCO-0 SEGCCODO-D SER.888 COCCI-COCCICCOCO-0 SER.888 COCCI-COCCICCOCO-0 SEGCCODO-D SER.898 COCCI-COCCICCOCO-0 SER.898 COCCI-COCCICCOCO-0 SEGCCODO-D SER.898 COCCI-COCCICCOCO-0 SER.898 COCCIC-COCCICCOCO-0 SEGCCODO-D SER.898 COCCIC-COCCIC-0 SER.898 COCCIC-COCCIC-0 SEGCCODO-D SER.898 COCCIC-COCCIC-0 SER.898 COCCIC-COCCIC-0 SEGCCODO-D SER.898 COCCIC-COCCIC-0 SER.898 COCCIC-COCCIC-0 SEGCCODO-D <td< td=""><td>IC=CN=C1CC 132.9788 SC(C(C)C)=N1 132.7151</td><td>37.37 114</td><td></td><td>CCCCCCCC/C=C\CCCCCCCC=O</td><td>59.32255 58.70435</td><td></td><td>C=C1CCC(C(C)=C)=CC1 CC(C1=CN=C(C)C=N1)C</td></td<>	IC=CN=C1CC 132.9788 SC(C(C)C)=N1 132.7151	37.37 114		CCCCCCCC/C=C\CCCCCCCC=O	59.32255 58.70435		C=C1CCC(C(C)=C)=CC1 CC(C1=CN=C(C)C=N1)C
SECCODED-0 SECON SEGUE SECON SEGUE CCI-N-C-C-C-C-C SUCCODED-0 SUGUE SUGUE<	1=CC=CC=C1 131.8252	37.00024		CCCC/C=C\CCC=O	58.25072		CC(OCCCC)=O
Scied-Coccy-pi-0 84.0072 SCICCCC-0 84.002 Cort-Cocc2(CCIQ)(C)C Scied-Coccy-pi-0 MADD Coccy-Coccy-Coccy-Coccy MADD Coccy-Coc-Coccy-Cocy-Co	C(CC)=CC=C1C 131.1524 NC=CN=C1CC 131.0553						
SIGCCCCOPD-0 97.328 0CCCCC-C-C-C 88.6480 CCCCCCC-C-C-C SIGCCCCOPD-0 88.0480 CCCCCCCCCCC-C-C-C-C 88.0480 CCCCCCCCCCCC-C-C-C-C-C CCCCCCCCCCCCC-C-C-C-C-C-C-C-C-C 88.0480 CCCCCCCCCCCC-C-C-C-C-C-C-C-C 88.0480 CCCCCCCCCCCCC-C-C-C-C-C-C-C-C-C-C-C-C-	CC2(C1C2)C(C)C 130.8624	36.69429		CCCCCCC=0	58.02782		CC(/C=C/C(CC)=O)=O
	C1=CC=CC=C1)C 130.6334	35.66337		0=CCC1=CC=CC=C1			CC(CCC(CC)=0)=0
C1-C0/C0/E0-C1/C0/C0 81.6088 CCCC0/C0-C0-C0 34.002 CCI-C0/C0/C0/C0/C0 D-C0/C0/C0/C0 81.002 CCCC0/C0-C0 34.002 CCI-C0/C0/C0/C0/C0 D-C0/C0/C0/C0 81.002 CCCC0/C0-C0 34.002 CCI-C0/C0/C0/C0/C0 D-C0/C0/C0/C0 81.002 CCCC0/C0-C0 31.004 CCI-C0-C0/C0/C0/C0/C0/C0/C0/C0/C0/C0/C0/C0/C0/C	C(C)C)C 129.5921	34.93723		CCCC/C=C\CCCCCCCCC=O	56.53 117		C=CCCCCC
C1C()=C0C(=0)CC1 5.7786 CC-0 31.773 CC-04N-C-04P-(1C) C4C(C)CCC 5.4786 CCCC-0C0CCCC-0 31.8101 O-(1-AC-C-04P-(1C) C4C(C)CCC 5.4786 CCCC-0C0CCCCC-0 31.8014 O-(1-C-C-02P-(1C) C4C(C)CCC-0 5.4786 CCCC-0C0CCCCCC-0 31.8014 CC(1-C-C-02P-(1C) C4C(C)CCCC-0 5.4418 CCCCC-0CC-0 31.8014 CCCCC+0C-0P-(1C) C4C(C)CCCC-0 5.4418 CCCCC-0CC-0CC-0 31.8014 CCCCC+0C-0P-(1C) C4C(C)CCCC-0 5.8418 CCCCC-0CC-0CC-0CC-0 28.8181 CCCCCC-0CC-0P-(1C) C4C(C)CCCCCCCCCC-0 28.8181 CCCCCC-0CC-0CC-0CC-0 28.8181 CCCCCC-0CC-0CC-0CC-0 C4C(C)CCCCCCCCCCCCC-0 28.8181 CCCCCC-0CCCCCCCCCCC-0 28.8184 CCCCCC-0C-0C-0C-0C-0C-0C-0C-0C-0C-0C-0C-	CC2(C(C)C)CC12 129.4238 22CCOC(02)(C)O1 128.56	34.48002					CC1=CC[C@@H](CC1)C(C)=C
>=CICCDCDC 56.10822 CCCDC=CCCCCCCCC=0 33.2143 CC1+CC-CCC1+DC >=CICCCCCCCCCCCCCC 53.4444 CCCC-CCCCCCCC 31.1441 CC1+CC-CCCCCCCC >=CICCCCCCCCCCCCCCCC 53.4448 CCCC-CCCCCCCCCCC 31.1441 CC1+CC-CCCCCCCCCCC >=CICCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	SC 126.9605	34.2548		CC=0	55.27365		CC(C)C1=CCC(=C)CC1
Discher Conception \$39.400 CDIS-Cher Conception \$1.5990 CDIS-Cher Conception Discher Conception \$3.4410 CDIS-Cher Conception \$1.5990 CDIS-Cher Conception Discher Conception \$3.4410 CDIS-Cher Conception \$1.8310 CONCEPTION Discher Conception \$3.4410 CDIS-Cher Conception \$3.8310 CONCEPTION Discher Conception \$3.8410 CDIS-Cher Conception \$3.8310 CONCEPTION Discher Conception \$3.8410 CDIS-Cher Conception \$3.8310 CONCEPTION Discher Conception \$3.8310 CONCEPTION \$3.8310 CONCEPTION \$3.8310 CONCEPTION Discher Conception \$3.8310 CONCEPTION \$3.8310 CONCEPTION \$3.8310 CONCEPTION Discher Conception \$3.8381 CONCEPTION \$3.8380 CONCEPTION \$3.8300 CONCEPTION Discher Conception \$3.8381 CONCEPTION \$3.8380 CONCEPTION \$3.8300 CONCEPTION Discher Conception \$3.8380 CONCEPTION \$3.8300 CONCEPT	IC=CN=C1OC 126.0013	33,70733		CCCC/C=C\CCCCCCCC=0	55.10922		D=C(OCC)OCC
Dischellicochelle S3.4400 Collechellic-Collechellicoc	=CC=CC=C1)=O 125.9246 1=CC=CN=C1)C 124.8349	33.21461 31.90149		000000000000000000000000000000000000000			D=CNC1=CC=CC=C1 CCCCCC=O
> COUCCUC/COUCCUC-CUC/CUC/CUC/CUC/CUC/CUC/CUC/CUC/CU	C=CC=C1C(C)C 124.8332	31.59909		CC/C=C\C/C=C\C/C=C\CCCCCCCC=O	53.94009		
DAMACDET COCCCCC 31.03740 CCC1+CC[CC]-CC-CC1 DAMACDET COCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CC1=NC=CS1 123.6646 SSCCC 123.6242	31.14121		CC(C1=CC=C(C(C)(C)C)C=C1)C=O CC(C(C)=C(C)(C)(C)CC=C)	53.44199 53.44199		CC1=CCC(CC1)C(C)=C C=C(IC@@H11CC=C(C)CC1)C
D=(D)CHCD=CPG(D)C=C1 \$2.1486 CD(C)CCD=D 28.1734 CD(C)CD(D)=D)CCT D=C)CCCDD 51.8848 CDCCD=CDCDCDCDCDCD 28.3853 CDCI=NCP-CDCT D=C)CCCDD 50.88541 CDCCCDCDCDCDCDCD 28.3853 CDCI=NCP-CDCPCP-CDC D=C)CCCCDCD 50.88541 CDCCCDCDCDCDCDCDCD 28.3953 CDCI=NCPCCPCP-CDCCDCDCDCDCDCDCDCDCDCDCDCDCDCDC	CC(CC)=CC=C1 123.591	31.03749		CC(C)C1=CC=C(C=C1)CC(C)C=O	52.41753		D/N=C/C1=CC=CC=C1
C-CICCCCC[0]CPCC ² 58.8848 CCCCC 28.8148 CCCCCCCCCCCCCCCCC C-COCCCCC 58.8848 CCCCC-CCCCCCCCCCCCCC 28.0869 CIC2C-CCCCCCCCCCCCCCCCC C-CCCCCC 58.8848 CCCCC-CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	C(C)C)=0 123.529 NC=CN=C1 123.5075						CC(CC/C=C/C)=0
DireUb-Cle[C0CC]=0 58.811 CCCC+ClCCCC-0C-ClCCCC-0 28.0884 CCCC+CC+ClCCC-0C-ClCCC-0C-ClCCCC-0 DireClCCDCCD 58.8844 CCCC+ClCCC-ClCCCC-0 28.7534 CCGBN(C-C-CC-ClCCC-0C-ClCCCC-0 DireClCCDCD-0 58.8844 CCCC+ClCCC-ClCCCC-0 28.7534 CCGBN(C-C-ClCCC-0C-ClCCCC-0 DireClCCCCCD-0 58.444 CCCCCC-ClCCCC-0CCCC-0 27.8576 CCCCCCCCCO-0 DireClCCCCCC-0 48.4584 CCCCCCC-ClCCC-0 27.8576 CCCCSCCCCCCCCCCCC-0 DireClCCCCCCO-0 48.4584 CCCCCCCCCCCCCCC-0 27.8576 CCCSSCCC DIRECLCCCCCCCO-0 48.4584 CCCCCCCCCCCCCCC-0 28.6486 CCCC+CCCCCCCCCCCCC-0 DIRECLCCCCCCCO-0 48.4587 CCCCCCCCCCCCCCCCC-0 28.6486 CCCC+CCCCCCCCCCCCC-0 DIRECLCCCCCCCCCCCCCC-0 28.6486 CCCC+CCCCCCCCCCCCC-0 28.6486 CCCC+CCCCCCCCCCCC-0 DIRECLCCCCCCCCCCCC-0 28.6486 CCCC+CCCCCCCCCCCC-0 28.6486 CCC+CCCCCCCCCCCCCC-0 DIRECLCCCCCCCCCCCC-0 28.6486 CCC+CC+CCCCCCCCCC-0 28.6486 CCC+CC+CCCCCCCCCCC-0 DIRECCCCCCCCCCC-0 28.6486	OC(C)=O)CCC1 122.6161	29.61341		CCC=O	51.85418		C=C1CCC(C(C)=C)C=C1
C=CCCCCO 88844 CCC+=CCC+CC+CC+CC+CC+CC+CC+CC+CC+CC+CC+C	IC=C(CC)C=C1 122.4707 IC=CC=CC=C2)CO1 122.2966	29.36574		CCCC/C=C\CCCCCCCCC=O			C/C=C/CCCO
D-CICIC/CIC/CIC/CIC/CIC/CIC/CIC/CIC/CIC/C	CC=C(C=C)C=C1 122.2946	28.85484		CC/C=C/CCCCCCCCC=0			C=CCCCCO
C-CICCCCCCCC 82.0297 CC1-CC-CIC(C)-O(1) CCCCCCC-CICCCCCCCCCCCC 27.8218 CCC1-CC-CIC(C)-O(1)-O CCCCCCCC-CICCCCCCCCCCC 27.8218 CCC1-CC-CIC(C)-O CCCCCCCCCCCCCCCC 27.8218 CCC1-CC-CIC(C)-O CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	I](C1=CC=CC=C1)CO 121.2901 1=CC=CC=C1 120.9415	28.75354		CCCC/C=C/CCC/C=C/CCCCCC=O			D=C(C)CC(OCC)=O
CC-C(C)C-CC-C(C)C 49.2451 CCCCCCCCCC-O 27.5565 CCCC+NC-CNCCC(O)-O CCCC(C-C)C-C)C 49.2432 CCCCCCCCCCC-O 27.5565 CCCCN-NC-CNC-CNCCCC-O CCCC(C-C)C-O)-O 49.0433 CCCCCCCCCCCO-O 27.54716 CCCSCCCCCC-NC-CNCCCC-O CCCCCCCCCCCCCCC-O 27.54716 CCCSCCCCCCCC-NC-CNCCCC-O 28.4482 CCCCCCCCCCCCCC-O CCCCCCCCCCCCCC-O 28.4482 CCCCCCCCCCCCCC-O 28.4482 CCCCCCCCCCCCC-O CCCCCCCCCCCCCCC-O 28.4482 CCCCCCCCCCCCCC-O 28.4482 CCCCCCCCCCCCCCC-O CCCCCCCCCCCCCCCCCC-O 28.4482 CCCCCCCCCCCCCCC-O 28.4482 CCCCCCCCCCCCCC-O CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	1=CC=CC=C1 120.9415 C=C(C(C)=O)O1 120.6793	28.32705					
CCCUC+CO-IC>-O 27.54716 CCCCSCCC CCCUC+CO-IC>-O 27.54716 CCCSSCCC CCCUC+CO-IC>-O 28.6486 CCUC+CO-CO-ISC CCCUC+CO-IC>-O 28.6486 CCUC+CO-CO-ISC CCCUC+CO-IC>-O 28.6486 CCUC+CO-CO-ISC CCUC+CO-IC>-O 28.6486 CCUC+CO-CO-ISC CCUC+CO-IC>-O 28.6486 CCUC+CO-CO-ISC CCUC+CO-IC>-O 28.6486 CCUC+CO-CO-ISC CCUC+CO-IC>-O 28.6486 CCUC+CO-CO-ISC DC-COCOCC 48.0431 CCC-CO-COCCCCO-O 28.6489 CCUC+COCC-ISC DC-COCOCCC 48.0631 CCC-CO-COCCCCO-O 28.9636 CCCI+CO-CO-ISC DC-COCOCCCC-IO 48.0637 CCC-FC-COCCO-O 28.9636 CCCI+CO-CO-ISC DC-COCOCCCC-IO-IO 48.9375 CCI-CO-COCICCC-O 28.9846 CCICI+CO-CO-ISC DCCCICCCCCCIO-IO 28.9846 CCICI-CO-COCICCCCCCO-O 28.9846 CCICI-CO-COCICCCCCCO-O DCCCICCCCCCIO-IO 28.9841 CCICI-CO-COCICCCCCCO-O 28.9841 CCICI-CO-COCICCCCCCO-O DCCIC-IO-COCICICO-IO 2	ICCC(01)=0 120.0403	27.82103		CCCCCC/C=C\CCCCCCCCCC=O	49.62951		CC=C(C)C=CC=C(C)C
CCC/CCCCC)-0 48.0433 CC/CCC-CC/CO/CCCCCCC 28.0446 CC/CCCC/CO/CC+N1C CCCCCCCCD-0 48.4433 CCCCCCCCC-0 28.0446 CC/CCCCC/CO/CC+N1C CCCCCCCCD-0 48.1433 CCCCCCCCCCCCC 28.0446 CC/CCCCCC/CO/CC+N1C DCCCCCCCD-0 48.1433 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	NC=CN=C1C(C)C 119.9674 SCCC 119.8744	27.55956		CCC(C)CCCC(C)CCC=0	49.24534		CC1=CC=C(CC1)C(C)C
CCCC/COCCC>P 48.4738 CC1+CCCC(C1(C)C)CC-O 25.84022 CC12CCCCC(C)CC)C1 CCCCCCCCOP 48.1738 D=C0(C)CCC-O 25.84022 CC12CCCCCCC-C1(C) CCCCCCCCOP 48.1738 D=C0(C)CCC-O 25.1513 CCCCCCCCC-C1(C) CCCCCCCCOP 48.1433 CCCCCCCCC-O 23.9538 CCC1+CCCCCCCCCC D=C0(C)CCCCCCCCCOP 23.9538 CCC1+CCCCCCCCC-O 23.9538 CCC1+CCCCCCCC-O D=C0(C)CCCCCCCCCOP 23.9538 CCC1+CCCCCCCC-O 23.9538 CCC1+CCCCCCCC-O D=C0(C)CCCCCCCCOP 23.9538 CCC1+CCCCCCCC-O 23.9538 CCC1+CCCCCCCC-O DCCCCCCCCCCOPO 23.9538 CCC1+CCCCCCCOPO 23.9538 CCC1+CCCCCCCOPO DCCCCCCCCCCOPO 23.9538 CCC1+CCCCCCCOPO 23.9538 CCC1+CCCCCCCCOPO DCCCCCCCCCCOPO 23.9538 CCC1+CCCCCCCCOPO 23.9538 CCC1+CCCCCCCCOPO DCCCCCCCCCCD 43.9742 CCCCCCCCCCCOPO 23.9538 CCC1+CCCCCCCCOPO DCCCCCCCCCCD 43.9745 CCCCCCCCCCCOPO 23.9717 CC1+NCC-N-N-CCCCCCCCCCCCC DCCCCCCCCCCC	C=CN=C1SC 119.8238	27.33422		CC(CCC=C(C)C)C=O	49.01636		0=(000000000000000000000000000000000000
C-CICCCCCCD-0 48.1739 CC(C)CO ⁻⁰ 25.84202 C-CIC(-CC-C)C(C)C D/C-CICCCCCD 48.1739 CCCCCCCCCCC-0 25.1138 C-CCCCCC-C)C D/C-CICCCCCCCCC-0 25.1138 C-CCCCCCC-C)C 25.1138 C-CCCCCCC-C)C D/C-CICCCCCCCCCCC-0 25.1148 C-CCCCCCCCCCCCCCCC-0 25.1148 C-CCCCCCCCCCCCCCCCC-0 D/C-CICCCCCCCCCCCCCCCCCCCCCCCC-0 25.1148 C-CICCCCCCCCCCCCCCC-0 25.990 CCIC/C-CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	=CN=C(C)C=N1)C 119.3759 CCC(O2)C(CC)O1 119.3573			0=C(0)CCCCCCCC=0 CC1=CCC(C1(C)C)CC=0			
Dice-DCD(D)=D 48.1432 CCCCCCCCC+CCC-D 25.1438 C=CDCC(D) D=COCCCC 48.0883 CCCCCCCCCCCC+D 24.9809 CC1(D)(CCC)=(C)(D)(CC) D=COCCCCC CCL=D)(C=CC)(CC)(C)(C)(C)(C)(C) 24.9809 CC1(D)(CCC)=(C)(C)(D)(C) D=COCCCCC CCL=D)(C=CC)(CC)(C)(C)(C)(C) 23.9807 CC1+CC)(C+C)(D) D=COCCCCC CCL=D)(C=C)(C)(C)(C)(C) 23.9807 CC1+CC)(C+C)(D) D=COCCCCC CCL=D)(C=C)(C)(C)(C)(C) 23.9807 CC1+CC)(C)(C)(C)(C) D=COCCCCC CCL=D)(C=C)(C)(C)(C) 23.9807 CC1+CC)(C)(C)(C)(C) D=COCCCCC CCCC+C)(C)(C)(C)(C) 23.9807 CC1+CC)(C)(C)(C)(C) D=COCCCCC CCCC+C)(C)(C)(C)(C) 23.9807 CC1+CC-C)(C)(C)(C) D=COCCCCC CCCC+C)(C)(C)(C)(C) 23.9817 CC1+CC-C)(C)(C)(C) D=COCCCCC CCCCC+C)(C)(C)(C)(C) 23.9817 CC1+CC-C)(C)(C)(C) D=COCCCCCC CCCCC+C)(C)(C)(C)(C) 23.9817 CC1+CC-C)(C)(C)(C) D=COCCCCCC CCCCC+C)(C)(C)(C)(C) 23.9812 CCC1+CC-C)(C)(C)(C) D=COCCCCCCCCCCCC+D) 13.9717 CCC1+CC-C)(1=CC=CC=C1)C 119.3014	25.62622		CC(C)C=O	48.31301		0=(00000)00=0
D=C0CCCC 48.0831 CCCCCDC=C0CCCCD 25.4488 O=C(1=C)(C)+C)(C)(C)CC1 D=C0CCCCC 48.0587 CCC=C0(CCC)(C)(C)(C)CC1 24.9590 CCC1=C)(C)(C)(C)(C)(C) D=C0CCCCCCD(D=D) 47.8477 CCC=C0CCCCCC-O 23.9846 CC0(C)(C)(C)(C) D=C0CCCCCCC1 47.8477 CCC=C0CCCCCC-O 23.9846 CC0(C)(C)(C)(C) DCCCCCCCCC1 47.8477 CCC=C0CCCCCCC-O 23.9846 CC0(C)(C)(C)(C) DCCCCCCCCCC1 47.8477 CCC=C0CCCCCCCCC-O 23.9846 CC0(C)(C)(C)(C)(C) DCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	I=CC=CC=C1 119.2656 CC(C)C 118.642	25.47008		O=CC(C)CC1=CC=C(C(C)(C)C)C=C1			00000
D=CICOCCCCICOD=0 47.8427 CCC=DCCCCCCCC=0 23.9894 CCCT=CCCCCC+CCCCCCCC=0 DCCCICCCCCCI 47.8447 CCCI=DCCCCCCCCCC=0 23.9894 CCCI=DCCCCCCCCCCC=0 DCCCICCCCCCI 47.8447 CCCI=CCCCCCCCCCCC=0 23.9894 CCI=CCCCCCCCCCCCCC DCCICCCCCCI 47.8447 CCCI=CC-CCICCCCCCCCC 23.9894 CCI=CC-CCICCCCCCCCCCCC DCCICCCCCICIC 47.9817 CCCI=CC-CCICCCCCCCCCCCCC 23.9894 CCI=CC-CCICCCCCCCCCCCCCCCCCCCCCCCCCCCCC	118.2089 118.2089	25.15136		CCCCC/C=C/CCCCC=0	48.08631		D=COCCCC
CCCCCQCQCCCPO 47.8472 CCC-BCCCCCC-O 23.8984 CCCQCCCCCO-D CCCCCCCQCCCCC 47.8472 CCCC-BCCCCCCC-O 22.7878 CC1+CC-CCCCCCCO-D CCCCCCCCCCCC 48.9785 CCCI+CC-CCCCCCCCCCC-O 22.7878 CC1+CC-CCCCCCCCCCCCCCCC-O CCCCCCCCCCCCCCCCCCCCCCCCCCC 22.7878 CC1+CC-CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC)C2CC=C(C)CC21 118.1076 CC(=CC=C1)CO 117.0701	24.59309		CC1=C(C(CCC1)(C)C)CC=O			
DCC1CC0CCC1 47.8478 CCC(PC-CC)-DO 23.5894 CC(DCC(C)C)-D SC(D-CCCCC)-DO 47.8478 CCC(PC-CC)-DO 22.7885 CC10C-C(C)C)(C)-D DCC1CS(C)(D)-CO 48.9785 D-CCC1-CC-C)(C)C-CC 22.7817 CSSC(D-C)(N-C) DCC1CS(C)(D)-CO 48.9785 D-CCC1-CC-C)(C)C-CC 22.85111 CC1ACC-C)(N-C)(N-C) DCC1CS(C)(D)-CO 48.94116 CCC-C-C)(C)CCCCCD 21.9812 CC1COC(C)(N-C)(C) DCC1CS(C)(D)-CO 48.94116 CCC-C-C)(C)CCCCD 21.98121 CC1COC(C)(C)(C)CC1 DCCCCCCCD-D) 45.7853 CCDC-C-C)(C)CCCCCCCCC-D 21.98123 CC1CACC-C)(D)CC1CO DC(C)(C)(C)-CC1-C 45.7853 CC)(C-C)(C)(C)(C)CD-D 19.8745 CC(C)(C)(C)(C)-C DC(N)(N)(C)C-CC1-O 45.8485 CC)(C-C)(C)(C)(C)C1-O 19.8745 CC(C)(C)(C)(C)-D DC(N)(N)(C)C-CC1-O 45.9485 CC)(C)(C)(C)C1-O 19.8745 CC(C)(C)(C)-D DC(N)(N)(C)C-CC1-O 45.9485 CC)(C)(C)(C)C1-O 19.8745 CC(C)(C)(C)-D DC(N)(N)(C)C-CC1-O 19.8745 CC(C)(C)(C)-D 19.8745 CC(C)(C)(1=NC=CN=C1C 116.6756	23.89949		CC/C=C\CCCCCCC=0	47.81427		0=(0=(000)00)000
CCIC=CQ(D)=D 48 9765 0=CCC1=CC=CQ(D)=C-1 22.56 111 CSSCC1=CC=CO1 CCIC=CQ(D)=C 46 9242 CCICQCICQ(D)=CC 21.85717 CSSCC1=CC=CO1 CCIC=CQ(D)=C 46 9441 CCICQCICQCCCCC=C 21.85717 CCICN=CC=CO1 CCICQCICQ(D)=C 46 9441 CCICQCICQCCCCCCCCC 21.85717 CCICN=CC=CO1 CCICQCICQ(D)=C 46 9441 CCICQCICQCCCCCCCCCC 21.87717 CCICN=CC=CICQCCCCCCCCCCCC CCICQCICQ(D)=C 46 94548 CCICQC=CCICQCCCCCCCCCCC 21.87717 CCICN=CC=CICQCCCCCCCCCCCCCCCCCCCC CCICQCICQCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	(C)CC)=O 116.6452	23.35864		CCC(/C=C/C=O)=O	47.64478		DCCC1CCCCC1
SCCC1SQ(s)CoC1 49.2427 C01(C)Q(CC12)C/CC2C-0 22.69 11 C01+MC-Q(C)M-O1 SCCC1SQ(s)CoC1 46.84 16 CCCC2CCCCCCCC-0 21.8915 CCCCCCC1C-CO-1 SCCCC1Q(s)CO 46.84 CCCCCCCCCCCCCC-0 21.8717 CCCCCCCCCCCC-0 SCCCC1Q(s)CO 45.7528 CCCCCCCCCCCCCC-0 21.9733 CCICCCCCCCCCCCC-0 SCCCCC1Q(s)CC 45.7548 CCICCCCCCCCCCC-0 20.4982 O-CCICCCCCCCCCCC-0 SCCCCCCCCCCCCCC-0 19.3237 O-CCICC1C-CCCCCCCCCC-0 19.32415 CCICCCCCCCCCCCC-0 SCCCCCCCCCCCCCCCCCCCCCC-0 19.32415 CCICCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	C1=CC=CO1 116.0629	22.71871		O=CCC1=CC=C(C)C=C1C			
CCCCC(0)-0 ⁻⁰							
Φ=(CC)CCC 45.7828 CCDC2=CO=CD=CCCCCCCCCC=0 21.7833 CC102CC(C)C(C)CCC102 CC(CCCCC)=D=0 45.7448 CC1=CC=C(0)(C)(C)CC-0 20.49628 CC1=CC=C(0)(C)(C)CC1 CC(CCCCC)=D=0 45.7448 CC1=CC=C(0)(C)(C)(C)C-0 20.49628 CC1=CC=C(0)(C)(C)(C)=C1 CC(CCCCC)=D=0 45.9448 CC1=CC=C(0)(C)(C)(C)(C) 19.3237 CC1=CC=C(0)(C)(C)(C) F(N)(C)(N)(C)=C1 45.9448 CC(C)=C1=CC=C(C)(C)(C)(C) 19.3237 CC(C)(C)(C)(C)=C1 F(N)(N)(C)(C)=C1 45.9448 CC(C)(C)(C)(C)(C) 19.31455 CC(C)(C)(C)(C)(C) F(N)(N)(C)(C)=C1 41.9457 CCCCCCCCCCCCCC 19.81455 CC(C)(C)(C)(C)(C) CC(C)(C)(C)(C)(C) 44.9167 CCCCCCCCCCCCCC 19.81455 CC(C)(C)(C)(C)(C) CC(C)(C)(C)(C) 44.9170 CCCCCCCCCCCCCC 19.81455 CC(C)(C)(C)(C)(C) CC(C)(C)(C)(C) 44.9170 CCCCCCCCCCCCCC 19.8145 CC(C)(C)(C)(C) CC(C)(C)(C)(C) 44.9170 CCCCCCCCCCCCCCC 19.8157 CCCCCCCCCCCCCCC CC(C)(C)(C)(C) 43.9183 CCCCCCCCCCCCCCC 19.8145	CC1=CC=CO1 114.4769 NC=CN=C1C(C)=O 114.2716						
CICIC/CIC/CI-CC-IC 45.848 COIC=DOC-CICCCCCCCCC-D 20.1726 CCI=NCOCIC/FCI CICIC/CIC/CIC/CI-CI-CC 45.385 COIC=DOC-CICCCCCCCCC-D 19.3227 COICC/CIC/CIC/CIC/CIC/CIC/CIC/CIC/CIC/CI	C2(C)C(C)CCC102 114.1827	21.27533		CCCC/C=C\C=C\CCCCCCCC=O	45.75258		D=C(CC)CCC
CCCCCCS 45.2983 CC(C1C)(C=C)(C)CC1) ^{-CO} 19.8745 CC(CCC)C2/CCCCCC P(N(T)N)(C)Z=C)(C=C)C=C2)(C) 45.9974 CC(CCC)(C)C=C)(CCCCC 19.8745 CC(CCC)(C)C=C)(CCCCCC CCCCCCC 44.3977 CCCCCC)(C=C)(CCCC) 19.8745 CC(CCC)(C)C)PO CCCCCCCC 44.3977 CCCCCC)(C=C)(C)CCC 19.8783 CC(CCC)(C)C)PO D=C01(C)(C)=D)(C)CCC 19.8782 CC(C)(C)(C)C)PO 19.7742 CC(C)(C)(C)C)PO D=C01(C)(C)=D)(C)CCC 19.8782 CC(C)(C)(C)C)PO 19.8787 CC(C)(C)(C)C)PO D=C01(C)(C)=D)(C)CCC 19.8787 CC(C)(C)(C)C)PO 19.8787 CC(C)(C)(C)C)PO D=C01(C)(C)=D)(C)CCC 19.8787 CC(C)(C)(C)C)PO 19.8787 CC(C)(C)(C)(C)PO D=C01(C)(C)(C)(C)(C)(C)(C)(C)(C)(C))(C) 19.8787 CC(C)(C)(C)(C)PO 19.8787 CC(C)(C)(C)(C)PO D=C01(C)(C)(C)(C)(C)(C)(C)(C)(C)(C)(C))(C) 19.8797 CC(C)(C)(C)(C)PO 19.8797 CC(C)(C)(C)(C)PO D=C01(C)(C)(C)(C)(C)(C)(C)) 19.8797 CC(C)(C)(C)(C)PO 19.8797 CC(C)(C)(C)(C)PO D=C01(C)(C)(C)(C)(C)(C)(C)) 43.8787 <	=CC=C(CC)C=C1 113.986 IC=C(C)N=C1C 112.9504	20.49682		CC1=CC=C(O1)C(C)CC=O			C(C(CCCC)=0)=0
CCCCCCS 452989 C0(C100(C=0)(C)CC1)-0 19.8745 CC(CCSC)-0 (C)(C)(C)(C)-C)(C)(C)(C)(C)(C)(C)(C)(C)(C) (C)(C)(C)(C)-C)(C)(C)(C)(C)(C)(C)(C)(C) (C)(C)(C)(C)-C)(C)(C)(C)(C)(C)(C)(C)(C) (C)(C)(C)(C)(C)(C)(C)(C)(C)(C)(C)(C)(C)()C1=CC=C(C)C=C1 112.6495	19.93297		CCC/C=C/C=C/CCCCCCCCC=O	45.3955		=C(N1C)N(C)C=CC1=O
CCCCCCC 44.3957 CCCCCCCC=0 19.5223 CC(CCC(C)C)=D CCCCCCCC=0 ⁻¹ D-0 44.2915 D=CC10(C)(C)=D(C)CCC1 19.21282 CC(COC(C)C)=D D=C010(C)(C)=D(C)CCC1 19.3182 CC(COC(C)C)=D CC(C)C(C)C)=D D=C010(C)(C)=D(C)CCC1 19.3182 CC(C)(C)(C)C)=D CC(C)(C)(C)C)=D D=C010(C)(C)=D(C)CCC1 19.384 CC(C)(C)(C)C)=D CC(C)(C)(C)C)=D D=C010(C)(C)=D(C)CCCCCCCCCCC 18.3877 D=C(C)(C)(C)C)=D D=C010(C)(C)=D(C)CCCCCCCCCCCCC 18.3877 D=C(C)(C)(C)C)=D D=C010(C)(C)=D(C)CCCCCCCCCCCCCCC 18.3877 D=C(C)(C)(C)C)=D D=C010(C)(C)(C)=C)(C)(C)(C)(C)(C)(C)(C)) 17.3458 C=CCCC1+C)C-CO D=C010(C)(C)(C)(C)(C)(C)(C)(C)(C)(C)(C)) 17.3458 C=CCCC1+C)C-CO D=C010(C)(C)(C)(C)(C)(C)(C)(C)(C)(C)(C)) 18.3487 CCCCC1+C)C-CO D=C010(C)(C)(C)(C)(C)(C)(C)(C)(C)(C)(C)(C)) 18.3448 CCCC(C)(C)(C)(C)(C)(C)(C)(C)(C)) D=C010(C)(C)(C)(C)(C)(C)(C)(C)(C)(C)(C)(C)(C)(SC)=O 112.624	19.87415		CC(C1OC(C=C)(C)CC1)C=0	45.29639		CCCCCS
CCC(C=CC=CC=C)=D 42.917 O=CC1(C)(C)(C)=O)CCC(C 19.1832 CCC(O(C)CC)=D CCC(D)CCCCC) 42.9168 O=CC1(D)(C)C(C)C(C) 19.1832 CCC(O(C)C)C)=D CCC(D)CD(C)C) 44.9764 CCCC=C)CCCCCCCC 19.0844 CCC(C)C)=D CCC(D)C)C)CD(D) 44.9764 CCCC=C)CCCCCCCCCC 19.0844 CCCC(C)=D CCC(D)C)C)D(D) 44.9764 CCCC=C)CCCCCCCCCCC 19.0854 CCCCC+C)C CCC(D)C)D(D) 44.9764 CCCC=C)CCCCCCCCCCCC 19.0854 CCCCC+C)C CCCC(D)C)D(D) 43.9767 O=CCC1+C)CCCCCCCCCCCC 19.0854 CCCCCCCCCCCD CCCC(D)C)D(D) 43.9787 O=CCC1+C)CCCCCCCCCCCCC 16.3844 CCCCCCCCCD> CCCC(C)C)D(D) 43.8388 O=CCCCCCCCCCCCCCD 16.38442 CCCCC(C)C)D CCCCCCCCCCCCCCCCCC 16.38445 CCCCCCCCCCCCCCC 16.38454 CCCCCCCCCCCCCCC CCCCCCCCCCCD 16.38454 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	C(C)C)=0 11 1.6846			CCCCCC/C=C/CCCC=0			CCCCCCC
CCC[C0]@HI[C]C0]=0 44.07494 CCCC ^{CC} CCC ^{CC} CO 19.044 CCCC ^C T ^A CC ^A CC ^A CC ^A CC ^A CC ^A CC ^A	C(CCC)C)=O 110.9251	19.21828		O=CC1C(C(C)=O)CCC1C	44.29157		CC(C1=CC=CC=C1)=O
CCCCで行らに行う	1=NC=CS1 110.2391	19.0844		CCC/C=C\C=C\CCCCCCCCC=O	44.07604		CC([C@@H](C)[C@H](O)CC)=0
CCCCCQ(CD)=0 43,7676 0-C1(Q)C2/C2(CQ)(C)(D)C-0 17,2433 C-CCSSC CC(CC)(C)CD-D 43,4576 0-CCCCC+CC-CC-CC+ 17,3579 CC(CC)(C)CD-D 43,433 0-CCCCC+CCCCCCCCCCC+ 16,3844 CC(C)(C)(C)CD-D 43,383 0-CCCCC+CC-CC+ 16,3844 0-CC+CC+CC+CC+ 16,3844 CCC(C)(C)(C)-D 43,243 CCDC+CC)-CC+ 16,3844 CCC(C)(C)(C)-D 43,243 CCDC+CC+CC+ 16,3844 CCCC+CC)(C)-D 16,3844 CCCC+CC)(C)-D 16,3844 CCCC+CC)(C)-D 16,3844 CCC+CC+CC+ 17,3579 CCC+CC+CC+ 17,3579 CCC+CC+CC+ 17,3579 CCC+CC+CC+C+ 17,3579 CCC+CC+CC+C+ CCC+C+C+C+C+C+C+C+	1=NC=CC=C1)C 109.7006	18.8576		CC1C=C(CCC1C=O)C	44.07124		CC/C(C)=C/C(O)=O
CCC(C[0]0]=D-0 43.67156 0-CCCC1=CC=CC=C1 17.37078 CC(CC(C)CD=D (CCC(C)C[0]=D-0 43.3835 0-CCCC1=CC=CCCC(C)C=D 16.38443 0-CC1=CC=CC(C)C(C)D=D (CCC=C)C(C)C=C0 43.3834 CCDC2=CC=CCCCCCCCCD=0 16.38494 0-CC1=CC=CC(C)C(C)D=D (CCC=C)C=CCCCCCCCCCCCCD=0 16.38495 0-CCCC=CCCCCCCCD=0 (CCC)C=CD=CD=CCCCCCCCCCCCCD=0 16.38496 CCCC(S)CCD=D (CCC)CD=D=CD=CD=CCCCCCCCCCCCD=0 16.38496 CCCC(S)CCD=D (CCC)CCCCCCCD=0 42.3850 CCCCCCCCCCD=0 16.38496 CCCC(S)CCD=D (CCC)CCCCCCD=D 16.38496 CCCC(S)CCD=D (CCC)CCCCCCCCCCD=0 16.38496 CCCC(S)CCD=D (CCC)CCCCCCCCCCCD=0 16.38496 CCCC(S)CCCCCCCD=D (CCC)CCCCCCCCCCCD=0 16.38496 CCCC(S)CCCCCCCD=D (CCC)CCCCCCCCCCCCCCCCD=0 16.38496 CCCC(S)CCCCCCCD=D (CCC)CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	C1=CC=CO1 109.6941 SC 108.6 1	18.75997 17.82453		UUUU/C=C\CCC/C=C/C=C/CCC=O O=C1C(O2)C2(CC(C)(C1)C)C=O	43.82648 43.76267		
CONTINUE2-ONCIN2=01CI=0 43.4838 0=CCCCCCCCCCCCCCCCCCCC<0	(C)CC)=O 107.924	17.35709		O=CCCC1=CC=CC=C1	43.67156		CCC(C(O)=O)=O
EQICCC/E+CC=C01 43.12843 CC/E=CC=CCCCCCCCCC−0 18.8959 CC1=CN=(CC)(C)(C)=N1 CC1CCCC(E)(F)=0 43.9543 CC1=CC=CC=CCCCCCCCCCCC−0 18.85456 CC1=CN=(C)(C)(C)(C)=N1 CC1CCCC(E)(F)=0 43.9178 CC1CC(E)(C)CC=0 18.85456 CCCC(E)(C)CC=0 CC1CCCC(E)(F)=0 42.9178 CC1CC(E)(C)=0 18.85458 CC1CCCCCCCCC-0 18.9188 CC1=C)(C)(C)(C)CC=0 CC1CCCCC(E)(F)=0 42.9187 CC1CCCCCCCCC-0 18.9188 CC1CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC)C(OC)=O 107.4248 =CC=CC(CC)=C1 107.4013	16.94432					=C(N1)NC2=C(NC(N2)=O)C1=O
CCC1CCCCC(0)=0 43.0524 C01C=0CCCCCCC-0 16.85496 CCCC(5)CC0 CC(0)CC-C)=0 42.9705 CCCC(5)CC0C-D CC(0)CCCCC)=0 42.9807 CCCCC(5)CC0C-D CC(0)CCCCC)=0 42.4807 CCCCCCCCCC(5)C=0 16.9328 CCC(5)CC0C-D CCC(5)CCCCCCCCCCCCCCCCC)CO-D 16.95482 CCC(5)CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	:N=C(CC)C(C)=N1 107.3825	16.89059		CC/C=C/C=C\CCCCCCCCCC=O	43.12843		=C(OCC)C1=CC=CO1
CC(N1CCCCC)=)0 42.4807 CCCCCCCCC(C)()C=0 16.738 CCC+C-C-C-C+CC ーのC-C+CCCC 42.3185 0-C(C)=0 16.89382 CCC5(G)SCC C(C)(C)CCCC)=0 42.855 0-C(C)=0 16.8425 CC1CC2+NC=H=C12 C(C)(C)CCCC)=0 16.2432 CC1CC2+NC=H=C12 C(C)=CC(C)CC)=0 16.2434 CC1CC2+NC=H=C12 CC)=CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	SC)CCO 107.1016	16.85496		CC/C=C/C=C\CCCCCCCC=0	43.0524		CCC1CCCC(01)=0
+=CC=CICCCC 42.3187 0=C(C)C=0 16.8982 CCCS(0)SCC :C(C)C(CCCC)=0 42.2856 CC(1=CC=CC=C1)C=0 16.54825 CC1C(CC=CN=C12 :C(C)=CC(CC)=C(C)=CC + CCC=C1CCCCCCCCCC 0 16.29843 CC1(C)C2CCC)=C12	C)C(OCC)=O 107.0201 CC=CC=C1CC 106.9824	16.82522 16.71336		0=0000000000000000000000000000000000000	42.9705 42 48007		CC(UCC=C)=0 CC(N1CCCCCC1)=0
C(C)=CC(OCC)=0 42.0531 C=C/C=C/CCCCCCCCC=0 16.28343 CC1(C)C2CCC(C)=CC12	C)SCCC 106.9291	16.69362		O=C(C)C=O	42.31857		=C/C=C/CCCC
NOT CONCOUNT #2,033 CONCOLOR #2,033 CONCOLOR 10,2000 (U)FUL12 歴代のPCPCPC 44.98418 CCPCPCに日にPCPC日日 15.07413 CCPCPCPC-0	C2=NC=CN=C12 106.774 IC2CCC(C)=CC12 106.7335	16.54825		CC(C1=CC=CC=C1)C=O	42.26556		
	CCCC)=O 106.2103	15.97413		CCCCC/C=C/C(C)CC=O	41.98418		D=C(OC)CCCOC
CC(0)C/C=N/OC 41.96767 CC/C=C/CCCCCCCCC=O 15.75651 CCCC1OC(01)C	IOCC(01)C 105.9842	15.75651		CC/C=C\C=C/CCCCCCCCCC=O	41.96767		C(C)C/C=N/OC
"=CCSCO=C 41.92669 CC/C=CDCCCCCCCCC=O 15.71584 CC1=CC(C(C)=D)=C(D)S1 CCC(C(C)CCC)=O 41.87159 O=CC1(C)CCC(C)=CO 15.27558 CC1=CC(C)(C)=O	C(C(C)=0)=C(C)S1 105.7342 C1CCC(01)=0 105.613						

Table 3.14 Continued

SMILES	RP6_C		RP7 B			RP7_C		
		A	SMILES	Dend	A -+:- :+ -	SMILES	Dead	A
	Pred	Activity 86.13873	0/01=0/00/01/0=0/0/01=0/001	Pred	Activity 126.4586	CC/C=C\CC=O	Pred	Activity 36.52692
CC1=CCC(C(C)=C)CC1=O CCCCCCCO		79.27182 67.29345	C=C1CC/C=C(C)/CC[C@@]2[[H])C(C)(C)C[C@]12[H] CC(C1=CC=CC=C1)=O		119.7731 95.38008	0=000000000000000000000000000000000000		30.50133 16.84203
CC(C1=CCC(C)=CC1)C		65.13451	CCCC(OCC)=0		76.21054	CC/C=C\CC=O		36.52692
OC1=CC=CC=C1C(OC)=O C=C([C@H]1CC=C(C)CC1)C		58.16259 54.28428	CCCCCCO C/C1=C/CC(C)(C)/C=C/C/C(C)=C/CC1		67.77761 126.4586	CCCCCC=O O=CCCSC		33.78351 33.33575
CCCC(OCC)=0		86.13873	CC(C1=CC=CC=C1)=O		95.38008	CC(C)CC=0		31.71206
CCC(OCCC)=0		83.38456	0=(02)(20)(20)(20)(20)(20)(20)(20)(20)(20)		92.59738	CC/C=C/CCC=O		31.37961
CC1=CCC(C(C)=C)CC1=O O=C(OC)CCSC		79.27182 79.13522	CC(CC(C)C)=O)=O CC(CCCC(C)C)=O CCC(C)C)C)=O CCC(C)C(C)C)=O		91.15 114 89.91984	CCC(C)C=0 CCCCCCCC=0		31.0054 30.50133
C=CCCCCC		77.20856 76.38981	CCC(C)C(OC(C)C)=0 CC(CCC=C(C)C)=0		87.99201	0=2020202		29.72137
C=CC(CCCC)=O CCCCC(OC)=O		76.38981 76.16308	CC(C)CC(OC(C)C)=0		87.32837 87.14336	C=CCC(C)C=O O=CCCCC=O		29.40163 28.98876
CC(C)C(CC1)C=CC1=C O=C(C(C)=C1)C=C(C(C)C)C1=O		74.89678 74 12276	CC(0)CCC=C(C)C		83.85426 83.3632	CC/C=C\CCC=0 CC/CC1=CC2=C(C=C1)OCO2)C=0		28.42686 26.77087
0=C(C(C)=C1)C=C(C(C)C)C1=0 0=C1CC(CC)OC(CC)=C1		74.12276 73.47661	CC(0CCCC(C)C)=0 CC(0C(CCC)C)=0		83.3632 82.94325	CC(CC1=CC2=C(C=C1)OCO2)C=O CCCC/C=C/CC=O		26.77087 26.07484
C=CC(O)CCCC		73.1929	O=C(C1=CC=CO1)OC		81.97053	CCCC=0		25.96475
CCC(CCCC)=0 CC/C=C/C(OC)=0		71.946 11 71.24633	CC1=CCC(C2=C1C=CC(=C2)C)C(C)C O=C(C1=CC=CN=C1)C		80.79637 80.65999	CCC(CC)C=0 CC(C)CC(C)CC=0		25.59708 25.02162
CCC(OCC=C)=0		71.24633 71.14553	O=C(C1=CC=CN=C1)C CC(CC(CC(C)C)=O)C		80.58242	CCCCC(CC)C=O		24.15837
O=C1C=C(CC)OC(C)=C1O C=CCSSSC		71.05457 70.38179	O=(323)23(2)20 CC(02(2)2)20(2)20 O=(2=(2)2)20(2)20		80.41422 80.22339	CCCC(C)C=O CC(C)C=O		23.89254 23.88156
C=C1CCC(C(C)=C)=CC1		70.27329	CC1=CCCC(=C)C2CC(C2CC1)(C)C		76.99125	CCCCC=O		23.52 119
NCCCCCC C/C=C/CC(OC)=0		69.99448 69.2848	CC(NCCC(C)C)=0 CC1=CCC(C=CCC(=CCC1)C)(C)C		76.5694 76.23738	CC(SC)CC=0 CC(C1OC(C=C)(C)CC1)C=0		21.55237 21.16626
CC(CC/C=C/C)=O		69.24917	CCCC(OCC)=O		76.21054	O=C1C(O2)C2(CC(C)(C1)C)C=O		18.74665
C=C(C)C(CCC1C)CC1=O O=C1C=C(C)CCC1C(C)C		68.66812 68.14354	N#CC(C1=CC=CC=C1)=O CC(0)CC(OCC)=O		75.54794 75.52013	CCC(C)C[N+]([O-])=0		18.60151 18.52774
C=C(C)C(CCC1C)=CC1=O		67.73656	CC(OCC(CC)=0)=0 CC(OCC=C(C)=0)=0 CC(OCC=C(C)=0)=0		75.43823	CCCCC/C=C\C/C=C\CCC=O SCC1=CC=CO1		18.04152
CC(OCCCC)=0 CCCCCCCO		67.64093 67.29345	CC(0CC=C(C)C)=0 CC(/C=C/C=C(C)C)=0		74.71706 74.55248	O=C(OC)C1=C(C)C=CC=C1O CCCCN=C=O		17.93662 17.56101
C=C1CCC(C(C)=C)C=C1		66.99069	O=C(C1=NC=CC=C1)C		74.49208	O=CCC1=CC=C(C)C=C1C		17.37472
C=C/C=C/C/C=C/C		66.84646	CC(C1=CC=CC=C1)C C/C=C/[C@@H](O)CC(C)C CC1CCC(CC2=C1CCC2C)C(=C)C		74.0 1133	0=CCC1=CC=CC=C1 CC(C1=CC=CC=C1)C=O		17.32718
C/C=C/C(OCC)=O CCOC1=CC=CC=C1		66.64964 65.88814	C/C=C/[C@@H](O)CC(C)C CC1CCC(CC2=C1CCC2C)C(=C)C		73.71874 73.5887	CC(C1=CC=CC=C1)C=O CC1SCCN1		17.29056 17.16448
O=C(N1C)N(C)C2=C(C=CC=C2)C	1=O	65.85213	CC(C)CC(OCC)=O		73.46298	CCC(C)/C=N/OC		17.12756
CC(C)C1=CCC(=C)CC1 CC1=CCC(=CC1)C(C)C		65.65882 65.13451	CCCC(0)CCC 0=C(0)C1=CC=CC=C1		73.3584 73.31343	CC(C)CC[N+]([O-])=O CC(OCC(C)C)=O		16.86213 16.84203
CCC/C=C/C(O)=O		63.74982	CC(C)=C1CCC(C)C2=C(C(C)CC2)C1		72.78 11	SCCCCCCS		16.78584
CCCCCC(O)=0 C=CCCCCCO		63.63551 63.27646	N#CCC1=CC=CC C=C/C(C)=C\C/C=C(C)/CCC=C(C)C		72.23238 71.73195	O=C(01)OCC1C O=C([0-])OS(C)SSC		16.65321 16.58147
CCCC1CCCC(01)=0		62.21691	CCCC(OC(C)C)=0 C=C(C1=CC=CC1)C		71.16331	CC(C)C[N+]([O-])=O		16.55789
CSSSCSC O=C(OCC)CSC		62.04977 61.81868	C=C(C1=CC=C1)C CCCCCC(O)=O		70.22063 70.09967	[O-]C(C[N+](C)(C)C)=O O=COCC=C(C)C		16.53871 16.48318
CC1=NC2=CC=CC=C2N=C1		61.46244	CC(0)CC(0)=0		69.75241	CC(NCC(C)CC)=0		16.48318
CCCC1SC(C)OCC1		61.36557	CC(C)=CC(OCC)=O		69.04661	SCCCCCS		16.24069
O=C1(C/C=C\C)=CCCC1C CC1=C(CCCC)C(CC1)=O		60.99415 60.61307	CC1CCC2=C(CCC(CC12)C(=C)C)C CCC(CCCC)=O		68.915 68.86344	CCCCC/C=C/CCCCC=O CC(C)C(OCC)=O		16.21917 16.10514
CSCCCCO		60.4865	CC(0)C1=CC=CC=C1		68.28692	CCC=O		16.09149
C=C/C=C/CCCC CC1=NC2=CC=CC=C2N=C1C		60.14782 59.98227	000000		67.77761 67.66886	O=C/C(C)=C/CCC1=COC=C1 OC1=C(OC)C=C2CC=COC2=C1		16.08724 16.08161
C/C=C/CCCO		59.95597	CC(CCCCC)=0 CC1=CC2C(C(C)C)CCC(C)C2=CC1		67.50108	CC(NCCC(C)C)=0		16.05204
CC1=CC=C(C(C)=C)CC1 CCCC/C=C/O		59.7741 59.55189	CC1=CC2C(C(C)C)CCC(C)C2=CC1 O=C(C1=NC=CN=C1)C		67.2853 67.07072	O=C(OC)CCSC OC1=CC(C)=CC(OC)=C1C		16.0168 15.84205
O=C(OC)C1=CC=CC=C1SC		59.29277	CC(OC(C)COC)=O		66.89404	C/C(CCC(01)=C1(C)C)=C/C=0		15.74377
CC(C)C/C=N/OC CC(/C=C/CCC)=0		59.19607 59.08062	[C-]#[N+]CC1=CC=CC=C1 SCCC1=CC=CC=C1		66.39249 66.19192			
CC1CCC(C(COC2=O)C)C2C1		58.72099	CC1=C2C=CC=CC2=CC=C1		66.18268			
O=C1C=C(C(C)C)CCC1C OC1=CC=CC=C1C(OC)=O		58.68 119 58.16259	CC(CC/C=C/C)=0 CC(C1=CC2=C(C)C=CC2=C(C)C=C1)C		66.06761 65.222			
CC1=CN=C(CC)C(C)=N1		58.04722	CC(C)(C)CC(C)CCO		65.18269			
CCC(OC1=CC=CC=C1)=O CCC(C)/C=N/OC		57.98341 57.90524	CC1=CC=C(C=O)C=C1 CC(C)CC(O)CC(C)C		64.98162 64.94732			
C=CCSCC=C		57.6607	C=CCC(O)CC=C		64.92842			
O=C1(C/C=C/C)=CCCC1C		57.63992	C=CC1(C)C(C(C)=C)CC(C(C)=C)CC1		64.86062 64.52239			
CC(C1=CN=C(C)C=N1)C CCCC(CCC)=O		56.97493 56.07365	COC(C=C)(CC/C=C(CC)C)(C)(C)(C)(C)(C)(C)(C)(C)(C)(C)(C)		64.52239 64.35953			
CN1C(C2=NC=CC=C2)CCC1		55.89354	O=C1C(CC)CCCC1		64.20792			
0=(CCCCCC)=0 CCC(O)CCCC		55.65697 55.03286	02(20)2222		64.0447 63.7268			
CN1C(CCC1)C2=CC=CN=C2 C12=CC=CC=C1N=CC=N2		54.53139	CC1=CC2C(C(C)C)CCC(C)=C2CC1 CCC(C1=CC=CC=C1)O		63.04465			
C12=CC=CC=C1N=CC=N2 CC1=CC[C@@H](CC1)C(C)=C		54.33279 54.28428	CCC(C1=CC=CC=C1)O O=C(CC)CC		62.80598 62.68223			
CC(C1CC(C(C)=C)C2)(O1)C2=O		54.25887	CC(C(0)CCCC)=0		62.66521			
O=C(N1)N=C2N=CN=C2C1=O O=C1C=CC2=C(O1)C=C(O)C=C2		54.08839 53.91696	CCC(C1=CC=CC=C1)=O CC(C)=CC(C=C(C)C)=O		62.60064 62.25825			
CCC(N1CCCCC1)=0		53.80537	C=CC1=CC=CC=C1		62.19846			
OC1=CC=CC=C1CCC C12=CC=CC=C1N=CC=C2		53.80223 53.64288	O=C(N(C1=O)C)N(C2=C1N(C=N2)C)C CCCCCCS		61.90239 61.85532			
O=C(OCC)C1=CC=CC=C1		53.42226	C=C(C)C(OCC(C)C)=O		61.75396			
O=C(OCC)OCC O=C(C=C1)C=C(CC)C1=O		53.40861 53.16238	CC(C)CC(0)CCC C=C(C1C/C=C(C)/CC/C=C(C)/CC1)C		61.6526 61.64239			
0=C10C2=C(C=CC=C2)C=C1		52.39659	CC1=CC=C(C)/CC/C=C(C)/CC1/C		61.608 11			
O=C(OCC)C1=CC=CC=C1OC		52.29142	CC(0)C(CC)=0		61.58498			
CC(C/C=C/CC)=O CC1COC2C1CCC(=C2)C		52.16263 51.91039	0=C0C(C)C(C)C)C0C(C)C		61.33144 61.20754			
CCC(C1=CC=CC=C1)=O		51.65885	CC1=CCC2(CC1)C(=C)CCCC2(C)C		61.06316			
O=C1C=C(C)CC[C@H]1C(C)=C COC1=CC=CC=C1C(OC)=O		51.52354 51.519 11	C=C1CCCC(C)(C)(C@@)21CCC(C)=CC2 CC(O)C(C)CCCC		61.01872 61.01721			
COC1=CC=CC=C1C(OC)=O OC1=CC=CC=C1C(OCC)=O		51.470 11	COC1=CC=CC=C1C		60.96861			
CCCCCCS OC1CC2CCCCC2CC1		51.09141 50.99655	CCC(C)C(CCC)=0 CC(0C1=CC(C)=CC=C1C(C)C)=0		60.7091 60.625 11			
CCC(OCC=C)=S		49.9 1146	CC1=CC2C(=C(CCCC2(C)C)C)CC1		60.32029			
CCCC(C1=CC=CC=C1)=O CCCCCCCCC		49.87987 49.77356	CCCCCC=0 C=C([C@@H]1C[C@@H]([C@](C=C)(CC1)C)C(C)=C)C		60.2745 60.1139			
		49.71818	CC(0)COCC(0)C		59.55436			
O=C(OC)C1=CC=CC=C1N			C=CC1=CN=CC(C)=N1		59.54975			
O=C(C)CC(OCC)=O		49.69014	C=CC1=CN=CC(C)=N1		50.5050			
O=C(OC)C1=CC=CC=C1N O=C(C)CC(OCC)=O CCC(OCC)=O CSSSSSC O=C1SC2=CC=CC=C2N1		49.69014 49.61974 49.44057 48.96835	CC(0)CCCC CC1=CN=C(C)C(C)CC)=N1 CC1=CN=C(C)C(C(C)CC)=N1 CCC(C(C)C(C)C)=D1=O		59.50504 59.12154			

Table 3.14 Continued

Table 3.15: Optimized descriptor sets for each mammalian OR

Optimized descriptors occurrences, symbol, brief description, class, and dimensionality are listed. A summary of the total number of descriptors selected for the receptor repertoire is provided at the beginning. Descriptors are listed in ascending order of when they were selected into the optimized set. Weights indicate the number of times a descriptor was selected in an optimized descriptor set.

Descriptor Class Type Counts for all Ors GETAWAY descriptors 109 atom-centred fragments 49 ZD autocorrelations 48 Barborner 48 DD-MoRSE descriptors 46 DMMRSE descriptors 43 Tunctional group counts 33 ZD binary fingerprints 26 Burden eigenvalues 23 ZD frequency finders 14 ZD frequency finders 12 atomtypes (Ceruiz2) 111 molecular properties 7 voorstitutional descriptors 6 Randic molecular profiles 5 topological descriptors 6 atomtypes (Ceruiz2) 111 molecular profiles 5 topological (Ceruiz2) 4 information indices 4 generation indices 1 seigenvalue-based indices 1 charge descriptors 0

Dimensionality Counts (Weights Included) Num zero dimensional descriptors: Num one dimensional descriptors: Num two dimensional descriptors: Num three dimensional descriptors:	7 104 176 272
Origin (Weights Included)	
Num Dragon descriptors:	546
Num Cerius2 descriptors:	13
Dimensionality Counts (Weights Excluded)	
Num zero dimensional descriptors:	7
Num one dimensional descriptors:	37
Num two dimensional descriptors:	93
Num two dimensional descriptors: Num three dimensional descriptors:	93 155

Odor Receptor Name	Weight	Symbol	Description	Class	Dimeniona
40R1.1					
		2 Mor17m	3D-MoRSE - signal 17 / weighted by atomic masses	3D-MoRSE descriptors	
		8 H-051 2 R6p+	H attached to alpha-C R maximal autocorrelation of lag 6 / weighted by atomic polarizabilities	atom-centred fragments GETAWAY descriptors	
			3D-MoRSE - signal 23 / weighted by atomic Sanderson electronegativities	3D-MoRSE descriptors	
			3D-MoRSE - signal 30 / weighted by atomic masses R maximal autocorrelation of lag 5 / weighted by atomic van der Waals volumes	3D-MoRSE descriptors GETAWAY descriptors	
		4 R5v+ 1 Mor32e	3D-MoRSE - signal 32 / weighted by atomic Sanderson electronegativities	3D-MoRSE descriptors	
		1 Mor32e 1 JGI7	3D-MoRSE - signal 32 / weighted by atomic Sanderson electronegativities		
			mean topological charge index of order7	topological charge indices	
		2 E1s	1st component accessibility directional WHIM index / weighted by atomic electrotopological states	WHIM descriptors	
		1 nCt 1 nArCO	number of total tertiary C(sp3)	functional group counts	
			number of ketones (aromatic)	functional group counts	
		1 0-058	#NAME?	atom-centred fragments	
		1 B07[C-O]	presence/absence of C - O at topological distance 07	2D binary fingerprints	
		2 GATS2m	Geary autocorrelation - lag 2 / weighted by atomic masses	2D autocorrelations	
		1 RDF110e	Radial Distribution Function - 11.0 / weighted by atomic Sanderson electronegativities	RDF descriptors	
		1 nCconj	number of non-aromatic conjugated C(sp2)	functional group counts	
		1 C-006	CH2RX	atom-centred fragments	
		1 nCrs	number of ring secondary C(sp3)	functional group counts	
		1 GATS7m	Geary autocorrelation - lag 7 / weighted by atomic masses	2D autocorrelations	
		1 C-003	CHR3	atom-centred fragments	
		1 MATS8m	Moran autocorrelation - lag 8 / weighted by atomic masses	2D autocorrelations	
OR106.1			20 M-DCF - stand 25 / weighted by stands as betrakilister	DD Manger dagaster	
		1 Mor25p	3D-MoRSE - signal 25 / weighted by atomic polarizabilities	3D-MoRSE descriptors	
		1 BEHe6	highest eigenvalue n. 6 of Burden matrix / weighted by atomic Sanderson electronegativities	Burden eigenvalues	1
		1 IC1	information content index (neighborhood symmetry of 1-order)	information indices	
		2 C-006	CH2RX	atom-centred fragments	
		2 RTe+	R maximal index / weighted by atomic Sanderson electronegativities	GETAWAY descriptors	
		1 piPC07	molecular multiple path count of order 07	walk and path counts	
		1 RDF045e	Radial Distribution Function - 4.5 / weighted by atomic Sanderson electronegativities	RDF descriptors	
		1 nRCOOH	number of carboxylic acids (aliphatic)	functional group counts	
		1 R7v+	R maximal autocorrelation of lag 7 / weighted by atomic van der Waals volumes	GETAWAY descriptors	
		1 HOMT	HOMA total	geometrical descriptors	
		1 RDF035m	Radial Distribution Function - 3.5 / weighted by atomic masses	RDF descriptors	
		1 H-049	H attached to C3(sp3)/C2(sp2)/C3(sp2)/C3(sp)	atom-centred fragments	
		1 SHP2	average shape profile index of order 2	Randic molecular profiles	
OR107.1					
	1	5 nCq	number of total quaternary C(sp3)	functional group counts	
		1 Mor07v	3D-MoRSE - signal 07 / weighted by atomic van der Waals volumes	3D-MoRSE descriptors	
		1 BELv3	lowest eigenvalue n. 3 of Burden matrix / weighted by atomic van der Waals volumes	Burden eigenvalues	
		1 R4p+	R maximal autocorrelation of lag 4 / weighted by atomic polarizabilities	GETAWAY descriptors	
		1 E1u	1st component accessibility directional WHIM index / unweighted	WHIM descriptors	
		1 JGI4	mean topological charge index of order4	topological charge indices	
		1 DISPv	d COMMA2 value / weighted by atomic van der Waals volumes	geometrical descriptors	
		1 nR06	number of 6-membered rings	constitutional descriptors	
		1 RDF040m	Radial Distribution Function - 4.0 / weighted by atomic masses	RDF descriptors	
		1 R8e+	R maximal autocorrelation of lag 8 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors	
		1 piPC07	molecular multiple path count of order 07	walk and path counts	
		1 L2s	2nd component size directional WHIM index / weighted by atomic electrotopological states	WHIM descriptors	
		1 piPC08	molecular multiple path count of order 08	walk and path counts	
		1 nDB	number of double bonds	constitutional descriptors	
		1 H-051	H attached to alpha-C	atom-centred fragments	
		1 E1m 1 B05[C-0]	1st component accessibility directional WHIM index / weighted by atomic masses presence/absence of C - O at topological distance 05	WHIM descriptors 2D binary fingerprints	
		1 BUS[C-U] 1 BELp3	lowest eigenvalue n. 3 of Burden matrix / weighted by atomic polarizabilities	2D binary fingerprints Burden eigenvalues	
		1 Becho	lowest eigenvalue it. 5 of Burden matrix / weighted by atomic polarizabilities	Burden eigenvaldes	
OR129.1					
		1 Dv	D total accessibility index / weighted by atomic van der Waals volumes	WHIM descriptors	
		2 HATS7e	leverage-weighted autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors	
		1 F01[C-C]	frequency of C - C at topological distance 01	2D frequency fingerprints	
		1 Mor10u	3D-MoRSE - signal 10 / unweighted	3D-MoRSE descriptors	
		1 HATS5m	leverage-weighted autocorrelation of lag 5 / weighted by atomic masses	GETAWAY descriptors	
		2 H1v	H autocorrelation of lag 1 / weighted by atomic van der Waals volumes	GETAWAT descriptors	
		1 Mor11v	3D-MoRSE - signal 11 / weighted by atomic van der Waals volumes	3D-MoRSE descriptors	
		1 Mor11v 1 B05[C-C]	3D-MORSE - signal 11 / weighted by atomic van der Waals volumes presence/absence of C - C at topological distance 05	2D binary fingerprints	
		1 BU5[C-C] 1 RDF085e	presence/absence of C - C at topological distance US Radial Distribution Function - 8.5 / weighted by atomic Sanderson electronegativities	2D binary fingerprints RDF descriptors	
		1 Dm	D total accessibility index / weighted by atomic masses	WHIM descriptors	
		1 H0m	H autocorrelation of lag 0 / weighted by atomic masses	GETAWAY descriptors	
		1 Mor10e	3D-MoRSE - signal 10 / weighted by atomic Sanderson electronegativities	3D-MoRSE descriptors	
		1 D/Dr06	distance/detour ring index of order 6	topological descriptors	
		1 HATS6m	leverage-weighted autocorrelation of lag 6 / weighted by atomic masses	GETAWAY descriptors	
		1 MATS5p	Moran autocorrelation - lag 5 / weighted by atomic polarizabilities	2D autocorrelations	
		1 RDF035m	Radial Distribution Function - 3.5 / weighted by atomic masses	RDF descriptors	
		1 H7e	H autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors	
		1 H0v	H autocorrelation of lag 0 / weighted by atomic van der Waals volumes	GETAWAY descriptors	
		1 R5m	R autocorrelation of lag 5 / weighted by atomic masses	GETAWAY descriptors	
004064					
OR136.1		1 005020m	Padial Distribution Exaction 2.0 / unighted by atomic masses	DDE descriptors	
		1 RDF030m	Radial Distribution Function - 3.0 / weighted by atomic masses	RDF descriptors	
		1 S_dssC	S_dssC	atomtypes (cerius2)	
		1 Mor05m	3D-MoRSE - signal 05 / weighted by atomic masses	3D-MoRSE descriptors	
	1	1 BELe1	lowest eigenvalue n. 1 of Burden matrix / weighted by atomic Sanderson electronegativities	Burden eigenvalues	
			R maximal autocorrelation of lag 5 / unweighted		
		1 R5u+	R maximal autocorrelation of lag 5 / unweighted	GETAWAY descriptors	
		1 R5u+ 1 SHP2	average shape profile index of order 2	GETAWAY descriptors Randic molecular profiles	

Table 3.15

	2 H1v 1 HATS1u	H autocorrelation of lag 1 / weighted by atomic van der Waals volumes leverage-weighted autocorrelation of lag 1 / unweighted	GETAWAY descriptors GETAWAY descriptors
	1 TPSA(NO) 1 piPC06	topological polar surface area using N,O polar contributions molecular multiple path count of order 06	molecular properties walk and path counts
	1 H8m	H autocorrelation of lag 8 / weighted by atomic masses	GETAWAY descriptors
	1 GVWAI-80	Ghose-Viswanadhan-Wendoloski drug-like index at 80%	molecular properties
	1 R1v 1 GATS2m	R autocorrelation of lag 1 / weighted by atomic van der Waals volumes Geary autocorrelation - lag 2 / weighted by atomic masses	GETAWAY descriptors 2D autocorrelations
	1 Mor24e	3D-MoRSE - signal 24 / weighted by atomic Sanderson electronegativities	3D-MoRSE descriptors
	1 EEig09d	Eigenvalue 09 from edge adj. matrix weighted by dipole moments	edge adjacency indices
OR162.1	1 HOMA	Harmonia Ossillator Model of Aromatisity index	geometrical descriptors
	1 HATS5m	Harmonic Oscillator Model of Aromaticity index leverage-weighted autocorrelation of lag 5 / weighted by atomic masses	GETAWAY descriptors
	1 E2e	2nd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities	WHIM descriptors
	1 H2e 1 R6v+	H autocorrelation of lag 2 / weighted by atomic Sanderson electronegativities R maximal autocorrelation of lag 6 / weighted by atomic van der Waals volumes	GETAWAY descriptors GETAWAY descriptors
	1 P2e	2nd component shape directional WHIM index / weighted by atomic Sanderson electronegativities	WHIM descriptors
	1 MATS5p 1 RCI	Moran autocorrelation - lag 5 / weighted by atomic polarizabilities Jug RC index	2D autocorrelations geometrical descriptors
	1 HATS6m	leverage-weighted autocorrelation of lag 6 / weighted by atomic masses	GETAWAY descriptors
	1 RDF035m 1 H1e	Radial Distribution Function - 3.5 / weighted by atomic masses H autocorrelation of lag 1 / weighted by atomic Sanderson electronegativities	RDF descriptors GETAWAY descriptors
	1 nie	H autocorrelation of lag 1 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors
DR170.1	3 C-025	RCRR	atom-centred fragments
	1 F05[C-O]	frequency of C - O at topological distance 05	2D frequency fingerprints
	1 R6v+	R maximal autocorrelation of lag 6 / weighted by atomic van der Waals volumes	GETAWAY descriptors
	2 E2e 1 S_aaCH	2nd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities S_aaCH	WHIM descriptors atomtypes (cerius2)
	2 RTe+	R maximal index / weighted by atomic Sanderson electronegativities	GETAWAY descriptors
	1 R8u+ 1 ATS2p	R maximal autocorrelation of lag 8 / unweighted Broto-Moreau autocorrelation of a topological structure - lag 2 / weighted by atomic polarizabilities	GETAWAY descriptors 2D autocorrelations
	1 MATS5p	Moran autocorrelation - lag 5 / weighted by atomic polarizabilities	2D autocorrelations 2D autocorrelations
	1 RDF045v	Radial Distribution Function - 4.5 / weighted by atomic van der Waals volumes	RDF descriptors
	1 P2p 1 R7p+	2nd component shape directional WHIM index / weighted by atomic polarizabilities R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities	WHIM descriptors GETAWAY descriptors
	1 R5m	R autocorrelation of lag 5 / weighted by atomic masses	GETAWAY descriptors
	1 HOMA	Harmonic Oscillator Model of Aromaticity index	geometrical descriptors
OR184.1	16 1000		stomburge (million)
	1 S_dCH2 1 GATS1m	S_dCH2 Geary autocorrelation - lag 1 / weighted by atomic masses	atomtypes (cerius2) 2D autocorrelations
	1 H-047	H attached to C1(sp3)/C0(sp2)	atom-centred fragments
	1 Qindex 1 DISPv	Quadratic index d COMMA2 value / weighted by atomic van der Waals volumes	topological descriptors geometrical descriptors
	1 L2v	2nd component size directional WHIM index / weighted by atomic van der Waals volumes	WHIM descriptors
	1 nCIC	number of rings	constitutional descriptors
	1 HATS2v 1 Mor07u	leverage-weighted autocorrelation of lag 2 / weighted by atomic van der Waals volumes 3D-MoRSE - signal 07 / unweighted	GETAWAY descriptors 3D-MoRSE descriptors
	1 R7e	R autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors
	1 MPC06 1 EEig09r	molecular path count of order 06 Eigenvalue 09 from edge adj. matrix weighted by resonance integrals	walk and path counts
	1 nCIR	number of circuits	edge adjacency indices constitutional descriptors
	1 RDF045m	Radial Distribution Function - 4.5 / weighted by atomic masses	RDF descriptors
	1 BELp3 1 EEig09d	lowest eigenvalue n. 3 of Burden matrix / weighted by atomic polarizabilities Eigenvalue 09 from edge adj. matrix weighted by dipole moments	Burden eigenvalues edge adjacency indices
	1 L2p	2nd component size directional WHIM index / weighted by atomic polarizabilities	WHIM descriptors
	1 HATS7p	leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities	GETAWAY descriptors
	1 R4p+ 1 Mor10m	R maximal autocorrelation of lag 4 / weighted by atomic polarizabilities 3D-MoRSE - signal 10 / weighted by atomic masses	GETAWAY descriptors 3D-MoRSE descriptors
OR185.1	1 BAC	Balaban centric index	topological descriptors
	1 HATS2m	leverage-weighted autocorrelation of lag 2 / weighted by atomic masses	GETAWAY descriptors
	1 R8u+ 1 X5A	R maximal autocorrelation of lag 8 / unweighted average connectivity index chi-5	GETAWAY descriptors connectivity indices
	1 E1e	1st component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities	
	1 E1e 1 RTe+	1st component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities R maximal index / weighted by atomic Sanderson electronegativities	WHIM descriptors GETAWAY descriptors
	1 E1e 1 RTe+ 1 E2e	R maximal index / weighted by atomic Sanderson electronegativities 2nd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities	WHIM descriptors GETAWAY descriptors WHIM descriptors
	1 E1e 1 RTe+	R maximal index / weighted by atomic Sanderson electronegativities 2nd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities Geary autocorrelation - laq 2 / weighted by atomic masses	WHIM descriptors GETAWAY descriptors
	1 E1e 1 RTe+ 1 E2e 1 GATS2m 1 H1p 1 HATS7p	R maximal index / weighted by atomic Sanderson electronegativities 2nd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic masses H autocorrelation of lag 1 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities	WHIM descriptors GETAWAY descriptors WHIM descriptors 2D autocorrelations GETAWAY descriptors GETAWAY descriptors
	1 E1e 1 RTe+ 1 E2e 1 GATS2m 1 H1p 1 HATS7p 1 RDF035m	R maximal index / weighted by atomic Sanderson electronegativities 2nd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic masses H autocorrelation of lag 1 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic masses	WHIM descriptors GETAWAY descriptors WHIM descriptors 2D autocorrelations GETAWAY descriptors GETAWAY descriptors RDF descriptors
	1 E1e 1 RTe+ 1 E2e 1 GATS2m 1 H1p 1 HATS7p	R maximal index / weighted by atomic Sanderson electronegativities 2nd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic masses H autocorrelation of lag 1 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities	WHIM descriptors GETAWAY descriptors WHIM descriptors 2D autocorrelations GETAWAY descriptors GETAWAY descriptors
OR189.1	1 E1e 1 RTe+ 1 E2e 1 GATS2m 1 H1p 1 HATS7p 1 RDF035m 1 SHP2 1 R2p+	R maximal index / weighted by atomic Sanderson electronegativities 2nd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic masses H autocorrelation of lag 1 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic masses average shape profile index of order 2 R maximal autocorrelation of lag 2 / weighted by atomic polarizabilities	WHIM descriptors GETAWAY descriptors WHIM descriptors 2D autocorrelations GETAWAY descriptors GETAWAY descriptors RDF descriptors Randic molecular profiles GETAWAY descriptors
OR189.1	1 E1e 1 RTe+ 1 E2e 1 GATS2m 1 H1p 1 HATS7p 1 RDF035m 1 SHP2 1 R2p+ 1 nCrs	R maximal index / weighted by atomic Sanderson electronegativities Znd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities H autocorrelation of lag 1 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic masses average shape profile index of order 2 R maximal autocorrelation of lag 2 / weighted by atomic polarizabilities R maximal autocorrelation of lag 2 / weighted by atomic polarizabilities number of ring secondary C(sp3)	WHIM descriptors GETAWAY descriptors WHIM descriptors 2D autocorrelations GETAWAY descriptors GETAWAY descriptors Randic molecular profiles GETAWAY descriptors functional group counts
OR189.1	1 E1e 1 RTe+ 1 E2e 1 GATS2m 1 H1p 1 HATDp 1 RDP055m 1 SD25m 1 R2p+ 1 nCrs 1 V-DIST-mag	R maximal index / weighted by atomic Sanderson electronegativities 2nd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic masses H autocorrelation of lag 1 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic masses average shape profile index of order 2 R maximal autocorrelation of lag 2 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag	WHIM descriptors GETAWAY descriptors WHIM descriptors 2D autocorrelations GETAWAY descriptors GETAWAY descriptors RDF descriptors Randic molecular profiles GETAWAY descriptors
OR189.1	1 E1e 1 RTe+ 1 E2e 1 GATS2m 1 H1p 1 HATS7p 1 ROF035m 1 SHF2 1 R2p+ 1 RCs 1 V-D15T-mag 1 J3D 2 Atype_C_40	R maximal index / weighted by atomic Sanderson electronegativities 2nd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic masses H autocorrelation of lag 1 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 2 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban index Number of Carbon Type 40	WHIM descriptors GETAWAY descriptors 2D autoornelations GETAWAY descriptors GETAWAY descriptors Randic molecular profiles GETAWAY descriptors functional group counts topological (cerius2) geometrical descriptors atomtypes (Cerius2)
OR189.1	1 E1e 1 RTe+ 1 E2e 1 GATS2m 1 H1p 1 HATS7p 1 RDF035m 1 SHP2 1 R2p+ 1 R2p+ 1 Crs 1 V-DIST-mag 1 J3D 2 Atype_C_40 1 EEj11r	R maximal index / weighted by atomic Sanderson electronegativities Znd component accessibility directional WHI index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 2 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by resonance integrals	WHIM descriptors GETAWAY descriptors Dautocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors RDF descriptors GETAWAY descriptors functional group counts topological (certus2) geometrical descriptors atomtypes (Certus2) edge adjacency indices
OR189,1	1 E1e 1 RTe+ 1 E2e 1 GATS2m 1 H1p 1 RJF035m 1 RJF035m 1 RJF02 1 R2p+ 1 R2p+ 1 R2p+ 1 V-DIST-mag 1 J30 2 Atype_C_40 1 EEgi1r 1 R4m 1 Mor07p	R maximal index / weighted by atomic Sanderson electronegativities Znd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic polarizabilities autocorrelation of lag 7 / weighted by atomic masses average shape profile index of order 2 R maximal autocorrelation of lag 2 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by resonance integrals R autocorrelation of lag 4 / weighted by atomic polarizabilities	WHIM descriptors GETAWAY descriptors Dautocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors RDF descriptors GETAWAY descriptors functional group counts topological (cerius2) geometrical descriptors atomtypes (Cerius2) edge adjacency indices GETAWAY descriptors 3D-MORSE descriptors
OR189.1	1 E1e 1 RTe+ 1 E2e 1 GATS2m 1 H1p 1 HATS7p 1 RDF035m 1 SHP2 1 RDF035m 1 RDF035m 1 RDF035m 1 RDF035m 1 J3D 2 Atype C, 40 1 EFig11r 1 R4m 1 Mor07p 1 GVVAI-80	R maximal index / weighted by atomic Sanderson electronegativities 2nd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic masses H autocorrelation of lag 1 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 2 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by resonance integrals R autocorrelation of lag 4 / weighted by atomic polarabilities 3D-MoRSE - signal 07 / weighted by atomic polarabilities 3D-MoRSE - signal 07 / weighted by atomic polarabilities	WHIM descriptors GETAWAY descriptors 2D autocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors RDF descriptors functional group counts topological (ceruis2) geometrical descriptors atomtypes (Ceruis2) edge adjacency indices GETAWAY descriptors 3D-MoRSE descriptors
OR189.1	1 E1e 1 RTe+ 1 E2e 1 GATS2m 1 H1p 1 HATS7p 1 RDF035m 1 SHP2 1 R2p+ 1 R2p+ 1 R2p+ 1 V-DIST-mag 1 J30 2 Atype C_40 1 EEgi1r 1 R4m 1 Mor07p 1 GVWAI-80 1 R07025m	R maximal index / weighted by atomic Sanderson electronegativities Znd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic polarizabilities autocorrelation of lag 2 / weighted by atomic masses average shape profile index of order 2 R maximal autocorrelation of lag 2 / weighted by atomic polarizabilities mumber of ring secondary C(sp3) 1D-Balaban index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by resonance integrals R autocorrelation of lag 4 / weighted by atomic masses 3D-MoRSE - signal 07 / weighted by atomic masses 3D-MoRSE - signal 07 / weighted by atomic masses 3D-MoRSE - signal 07 / weighted by atomic masses	WHIM descriptors GETAWAY descriptors Dautocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors RDF descriptors GETAWAY descriptors functional group counts topological (cerius2) geometrical descriptors atomtypes (Cerius2) edge adjacency indices GETAWAY descriptors 3D-MORSE descriptors
OR189,1	1 E1e 1 RTe+ 1 E2e 1 GATS2m 1 H1p 1 HATS7p 1 RDF035m 1 SHP2 1 R2p+ 1 R2p+ 1 R2p+ 1 CTS 1 V-DIST-mag 1 J30 2 Atype_C_40 1 EEg11r 1 R4m 1 Mor07p 1 GVWAI-80 1 R07025m 1 B07(C-C) 1 R4+	R maximal index / weighted by atomic Sanderson electronegativities Znd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic polarizabilities autocorrelation of lag 2 / weighted by atomic masses average shape profile index of order 2 R maximal autocorrelation of lag 2 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by resonance integrals R autocorrelation of lag 4 / weighted by atomic masses 3D-MoRSE- signal 07 / weighted by atomic polarizabilities Ghose-Viswanadhan-Wendoloski drug-like index at 80% Radial Distribution Function - 2.5 / weighted by atomic masses presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / meighted	WHIM descriptors GETAWAY descriptors Database Quarter and the service GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors RDF descriptors GETAWAY descriptors dometrical descriptors atomtypes (Cerius2) geometrical descriptors atomtypes (Cerius2) edge adjacency indices GETAWAY descriptors 3D-MORSE descriptors 2D binary fingerprints GETAWAY descriptors
OR189.1	1 E1e 1 RTe+ 1 E2e 1 GATS2m 1 H1p 1 HATS7p 1 RDF035m 1 RDF035m 1 RDF035m 1 RDF025m 1 JDD 2 Atype C_40 1 EEge1T 1 RDF025m 1 B07(C-C) 1 R4u+ 1 Mor22e	R maximal index / weighted by atomic Sanderson electronegativities Znd component accessibility directional WHI index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by resonance integrals R autocorrelation of lag 4 / weighted by atomic polarizabilities R autocorrelation of lag 4 / weighted by atomic polarizabilities R autocorrelation of lag 4 / weighted by atomic polarizabilities R autocorrelation of lag 4 / weighted by atomic polarizabilities R autocorrelation of lag 4 / weighted by atomic polarizabilities R autocorrelation of lag 4 / weighted by atomic polarizabilities R maximal autocorrelation of lag 4 / weighted by atomic polarizabilities R maximal autocorrelation of lag 4 / weighted by atomic polarizabilities R autocorrelation of lag 4 / weighted by atomic polarizabilities R autocorrelation of lag 4 / weighted by atomic polarizabilities R autocorrelation of lag 4 / weighted by atomic polarizabilities R autocorrelation of lag 4 / unweighted 3D-MORSE - signal 2D / weighted by atomic Sanderson electronegativities	WHIM descriptors GETAWAY descriptors UMIM descriptors 2D autocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors functional group counts topological (cerus2) geometrical descriptors adop adjaccorrelation GETAWAY descriptors adop adjaccorrelations adop adjaccorrelations Descriptors RDF descriptors RDF descriptors GETAWAY descriptors GETAWAY descriptors 3D-MORSE descriptors SD-MORSE descriptors
OR189.1	1 E1e 1 RTe+ 1 E2e 1 GATS2m 1 H1p 1 HATS7p 1 RDF035m 1 RDF035m 1 RDF035m 1 RDF025m 1 DD 2 Atype C_40 1 EEga1T 1 RDF025m 1 B07(C-C] 1 R4u+ 1 Mor07p 1 CVVAI-80 1 RDF025m 1 B07(C-C] 1 R4u+ 1 Mor22e 1 O-058 1 EEg07d	R maximal index / weighted by atomic Sanderson electronegativities Znd component accessibility directional WHI index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by atomic polarizabilities Gabal Viswanadin Functiones 7 (rug- ike index at 0%, Gabal Sance of C. 4 to topological distance 07 R maximal autocorrelation of lag 4 / unweighted 3D-MoRSE - signal 22 / weighted by atomic Sanderson R autocarelation of lag 4 / unweighted Sanderson electronegativities Fesence/ablesone of C 4 topological distance 07 R maximal autocorrelation of lag 4 / unweighted 3D-MoRSE - signal 22 / weighted by atomic Sanderson electronegativities Fesence/ablesone of C 4 topological distance 07 R maximal autocorrelation of lag 4 / unweighted 3D-MoRSE - signal 22 / weighted by atomic Sanderson electronegativities Fesence/ablesone of C 4 topological distance 07 R maximal autocorrelation of lag 4 / unweighted 3D-MoRSE - signal 22 / weighted by atomic Sanderson electronegativities Fesence/ablesone of C 4 topological distance 07 R maximal autocorrelation of lag 4 / unweighted by atomic Banderson electronegativities Fesence/ablesone of C 4 topological distance 07 R maximal autocorrelation of lag 4 / unweighted by atomic Banderson electronegativities Fesence/ablesone of C 6 topological distance 07 R maximal autocorrelation of lag 4 / unweighted by atomic belatore 07 R maximal autocorrelation of lag 4 / unweighted by atomic belatore 07 R maximal au	WHIM descriptors GETAWAY descriptors UMIM descriptors 2D autocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors RDF descriptors functional group counts topological (cerus2) geometrical descriptors atomtypes (Cerus2) SD-MoRSE descriptors Topological properties RDF descriptors SD-MoRSE descriptors EETAWAY descriptors SD-MoRSE descriptors atom-centred fragments edge adjacency indices
OR189.1	1 E1e 1 RTe+ 1 E2e 1 GATS2m 1 H1p 1 HATDp 1 RATD25m 1 RHP2 1 R2p+ 1 nCrs 1 V-DIST-mag 1 J3D 2 Atype_C_40 1 EEig11r 1 R4m 1 M0701-80 1 R07025m 1 B07(C-C) 1 R4U+ 1 Mor22e 1 O-058	R maximal index / weighted by atomic Sanderson electronegativities Znd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic masses H autocorrelation of lag 1 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic polarizabilities autocorrelation of lag 2 / weighted by atomic masses average shape profile index of order 2 R maximal autocorrelation of lag 2 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban index R autocorrelation of lag 4 / weighted by resonance integrals R autocorrelation of lag 4 / weighted by atomic masses 3D-MoRSE - signal 07 / weighted by atomic masses presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / weighted 3D-MoRSE - signal 22 / weighted by atomic Sanderson electronegativities 3D-MoRSE - signal 22 / weighted by atomic Sanderson electronegativities 3D-MoRSE - signal 22 / weighted by atomic Sanderson electronegativities 3D-MoRSE - signal 22 / weighted by atomic Sanderson electronegativities 3D-MoRSE - signal 22 / weighted by atomic Sanderson electronegativities 8NAME2	WHIM descriptors GETAWAY descriptors UMIM descriptors 2D autocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors functional group counts topological (cerius2) geometrical descriptors atomtypes (Cerius2) edge adjacency indices GETAWAY descriptors molecular properties 2D binary fingerprints GETAWAY descriptors atom-center descriptors atom-center descriptors atom-center descriptors atom-center descriptors
	I ELE I RTe+ I EZe I GATSZm I HIP I HATSYD I ROF035m I SHF2 I RZp+ I NCrs I V-DIST-mag I J30 2 Atype_C_C40 I EEig11r I R4m I Mor07p I GVWAL80 I ROF025m I B07(C-C) I Mor22e I O-058 I EEig07d I EEig11d	R maximal index / weighted by atomic Sanderson electronegativities Znd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 2 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban Index Number of Carbon Type 40 Eigenvalue 11 from edge adj, matrix weighted by resonance integrals Bala Distribution Function - 2.5 / weighted by atomic masses average shape profile index of under 2 R maximal autocorrelation of lag 7 / weighted by resonance integrals R maximal autocorrelation of lag 7 / weighted by resonance integrals R maximal autocorrelation of lag 8 / weighted by atomic masses Bala Distribution Function - 2.5 / weighted by atomic masses presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / weighted by atomic secon electronegativities 3D-MoRSE - signal 22 / weighted by atomic Sanderson electronegativities Eigenvalue 07 from edge adj, matrix weighted by dipole moments Eigenvalue 07 from edge adj, matrix weighted by dipole moments Eigenvalue 11 from edge adj, matrix weighted by dipole moments	WHIM descriptors GETAWAY descriptors GETAWAY descriptors ZD autocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors functional group counts topological (cerius2) geometrical descriptors atomtypes (Cerius2) edge adjacency indices GETAWAY descriptors molecular properties RDF descriptors molecular properties RDF descriptors GDAWAS descriptors descriptors CDD-WASE descriptors edge adjacency indices edge adjacency indices
	1 E1e 1 RTe+ 1 E2e 1 GATS2m 1 H1p 1 HATS7p 1 RDF035m 1 SHP2 1 R2p+ 1 nCrs 1 V-D1ST-mag 1 JD 2 ASype_C_40 1 E6g11r 1 R4m 1 GYP025m 1 ROF025m 1 ROF025m 1 E6g07d 1 E6g11d 1 RF045m	R maximal index / weighted by atomic Sanderson electronegativities Znd component accessibility directional WHI index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by resonance integrals R autocorrelation of lag 4 / weighted by atomic masses 3D-MoRSE - signal 07 / weighted by atomic masses presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / weighted by atomic Rasses presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / weighted by atomic Rasses 2D-MoRSE - signal 22 / weighted by atomic Rasses Presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / uneighted 3D-MoRSE - signal 22 / weighted by atomic Rasses Presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / uneighted 3D-MoRSE - signal 22 / weighted by atomic Rasses Presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / uneighted 3D-MoRSE - signal 22 / weighted by atomic Rasses Presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / uneighted 3D-MoRSE - signal 22 / weighted by atomic Rasses Presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / uneighted 3D-MoRSE - signal 22 / weighted by atomic Rasses Ratial Distribution Function - 4.5 / weighted by atomic Rasses	WHIM descriptors GETAWAY descriptors WHIM descriptors 2D autocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors RDF descriptors functional group counts topological (cerus2) geometrical descriptors atomtypes (Cerus2) edge adjacency indices GETAWAY descriptors atomtypes (Cerus2) edge adjacency indices GETAWAY descriptors 3D-MORSE descriptors atom-centred fragments edge adjacency indices edge adjacency indices
	I ELE I RTe+ I EZe I GATSZm I HIP I RJF035m I RJF02 I RZp+ I RZp+ I RCrs I V-DIST-mag I JD 2 Atype_C_40 I EEgilr I R4m I GOF025m I GOF025m I GOF025m I BOF025m I EEg07d I EEg07d	R maximal index / weighted by atomic Sanderson electronegativities Znd component accessibility directional WHI index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by atomic masses autocorrelation of lag 4 / weighted by atomic masses 3D-MoRSE - signal 27 / weighted by atomic masses 3D-MoRSE - signal 22 / weighted by atomic masses presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / matrix weighted 3D-MoRSE - signal 22 / weighted by atomic masses gresence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / matrix eleghted 3D-MoRSE - signal 22 / weighted by atomic masses gresence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / matrix weighted 3D-MoRSE - signal 22 / weighted by atomic Sanderson electronegativities Eigenvalue 11 from edge adj. matrix weighted by atomic masses Ratial Distribution Function - 4.5 / weighted by atomic masses Ghoose-Viswanadhan-Viendoloski drug-like index at 80% Radial Distribution Function - 4.5 / weighted by atomic masses Ghoose-Viswanadhan-Viendoloski drug-like index at 80% Radial Distribution Function - 4.5 / weighted by atomic masses Ghoose-Viswanadhan-Viendoloski drug-like index at 80%	WHIM descriptors GETAWAY descriptors WHIM descriptors 2D autocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors RDF descriptors functional group counts topological (cerius2) geometrical descriptors atomtypes (Cerius2) edge adjacency indices GETAWAY descriptors 3D-MORSE descriptors 3D-MORSE descriptors 3D-MORSE descriptors atom-centred fragments edge adjacency indices edge adjacency indices RDF descriptors molecular properties RDF descriptors molecular properties RDF descriptors molecular properties RDF descriptors molecular properties Burden eigenvalues
	I ELE I RTe+ I EZe GATSZm I HIP I HATS7p I ROF035m I SHP2 I RZp+ I RZp+ I RZp+ I CTs I V-DIST-mag I J3D 2 Atype C. C40 I EEig11r I R4m I Mor07p I GVWAI-80 I ROF025m I B07IC-CT I R4u+ I Mor022e I O+038 I EEig11d I EEig11d I RDF045m I GVWAI-80 I BELe7 I ROF050m	R maximal index / weighted by atomic Sanderson electronegativities Znd component accessibility directional WHI index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban Index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by resonance integrals R autocorrelation of lag 4 / weighted by atomic masses 3D-MoRSE - signal 07 / weighted by atomic masses 3D-MoRSE - signal 07 / weighted by atomic masses Radial Distribution Function of lag 4 / weighted by atomic masses 3D-MoRSE - signal 07 / weighted by atomic masses 3D-MoRSE - signal 22 / weighted by atomic Sanderson electronegativities R maximal autocorrelation of lag 4 / weighted by atomic masses Radial Distribution Function - 16g 4 / weighted by atomic masses Radial Distribution Function - 4.5 / weighted by atomic sanderson electronegativities Radial Distribution Function - 16g 4 / weighted by atomic Sanderson electronegativities Radial Distribution Function - 5.0 / weighted by atomic masses Radial Distribution Function - 4.5 / weighted by atomic masses Radial Distribution Function - 4.5 / weighted by atomic masses Radial Distribution Function - 5.0 / weighted by atomic Sanderson electronegativities Radial Distribution Function - 5.0 / weighted by atomic Sanderson electronegativities Radial Distribution Function - 5.0 / weighted by atomic Sanderson electronegativities Radial Distribution Function - 5.0 / weighted by atomic Sanderson electronegativities Radial Distribution Function - 5.0 / weighted by atomic Sanderson electronegativities Radial Distribution Function - 5.0 / weighted by atomic Sanderson electronegativities Radial Distri	WHIM descriptors GETAWAY descriptors GETAWAY descriptors ZD autocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors functional group counts topological (cerus2) geometrical descriptors atomtypes (Cerus2) edge adjacency indices GETAWAY descriptors 3D-MoRSE descriptors molecular properties RDF descriptors atom-centred fragments edge adjacency indices edge adjacency indices RDF descriptors molecular properties Burdescriptors RDF descriptors Burdescriptors Burdescriptors RDF descriptors Burdescriptors Burdescriptors Burden eigenvalues RDF descriptors
	1 E1e 1 RTe+ 1 E2e 1 GATS2m 1 H1p 1 HATS7p 1 RDF035m 1 RDF035m 1 V-D1ST-mag 1 JD 2 AAvpe_C_40 1 E6g11r 1 R4m 1 RVm07b 1 RVM1-80 1 R0F025m 1 R0F025m 1 R0F025m 1 R0F025m 1 R0F025m 1 RDF045m 2 GVWAI-80 1 BELe7 1 RDF050m 1 R0F025m	R maximal index / weighted by atomic Sanderson electronegativities Znd component accessibility directional WHI index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by resonance integrals R autocorrelation of lag 4 / weighted by atomic masses 3D-MoRSE - signal 07 / weighted by atomic masses presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / weighted by atomic masses presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / matrix weighted by atomic masses Figenvalue 11 from edge adj. matrix weighted by atomic masses presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / uneighted 3D-MoRSE - signal 22 / weighted by atomic Sanderson electronegativities <i>Balaelistical C</i> - C at topological distance 07 R maximal autocorrelation of lag 4 / uneighted by atomic masses presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / uneighted by atomic masses Figenvalue 11 from edge adj. matrix weighted by atomic masses Radial Distribution Function - 4.5 / weighted by atomic masses Ghose-Viswanadhan-Vendoloski drug-like index at 80% Radial Distribution Function - 4.5 / weighted by atomic masses Ghose-Viswanadhan-Vendonski Murdy-like index at 80% Iowest eigenvalue 0.7 of Murden matrix, weighted by atomic Sanderson electronegativities Radial Distribution Function - 5.0 / weighted by atomic masses Ghose-Viswanadhan-Vendonski drug-like index at 80%	WHIM descriptors GETAWAY descriptors WHIM descriptors 2D autocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors RDF descriptors functional group counts topological (cerius2) geometrical descriptors atomtypes (Cerius2) edge adjacency indices GETAWAY descriptors 3D-MORSE descriptors 3D-MORSE descriptors 3D-MORSE descriptors atom-centred fragments edge adjacency indices edge adjacency indices RDF descriptors molecular properties RDF descriptors molecular properties RDF descriptors molecular properties Burden eigenvalues RDF descriptors molecular properties Burden eigenvalues RDF descriptors 3D-MORSE descriptors
	<pre>LELe LELe LELe LELe LELe LELe LELe LEL</pre>	R maximal index / weighted by atomic Sanderson electronegativities Znd component accessibility directional WHI index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic polarizabilities autocorrelation of lag 1 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by atomic polarizabilities R autocorrelation of lag 4 / weighted by atomic polarizabilities R autocorrelation of lag 4 / weighted by atomic polarizabilities R autocorrelation of lag 4 / weighted by atomic polarizabilities R autocorrelation of lag 4 / weighted by atomic polarizabilities R autocorrelation of lag 4 / weighted by atomic polarizabilities R autocorrelation of lag 4 / uweighted by atomic masses 3D-MoRSE - signal 07 / weighted by atomic masses Badial Distribution Function - 2.5 / weighted by atomic masses 3D-MoRSE - signal 22 / weighted by atomic masses FRAME? Eigenvalue 07 from edge adj. matrix weighted by atomic masses Badial Distribution Function - 4.5 / weighted by atomic masses Badial Distribution Function - 4.5 / weighted by atomic masses Badial Distribution Function - 4.5 / weighted by atomic masses Badial Distribution Function - 4.5 / weighted by atomic masses Badial Distribution Function - 5.0 / weighted by atomic masses Badial Distribution Function - 5.0 / weighted by atomic masses Badial Distribution Function - 5.0 / weighted by atomic Sanderson electronegativities Eigenvalue 11 from edge adj. matrix weighted by atomic masses 3D-MoRSE - signal 14 / weighted by atomic Sanderson electronegativities Eigenvalue 12 from edge adj. matrix weighted by atomic Sanderson electronegativities Badial Distribution Function	WHIM descriptors GETAWAY descriptors GETAWAY descriptors ZD autocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors functional group counts topological (cerus2) geometrical descriptors atomtypes (Cerus2) edge adjacency indices GETAWAY descriptors 3D-MoRSE descriptors molecular properties RDF descriptors atom-centred fragments edge adjacency indices edge adjacency indices RDF descriptors molecular properties Burdescriptors RDF descriptors Burdescriptors Burdescriptors RDF descriptors Burdescriptors Burdescriptors Burden eigenvalues RDF descriptors
	l Eie l RTe+ l E2e GATS2m H1p H4TS7p 1 ROF035m 1 ROF035m 1 ROF035m 1 ROF035m 1 ROF035m 1 J3D 2 Atype_C_C40 1 EFG01r 1 R4m 1 Mor07p 1 GVVAI-80 1 ROF025m 1 B070C-C1 1 R4u+ 1 Mor022e 1 O-058 1 EFG016 1 EFG016 1 ROF045m 2 CVVAI-80 2 EFG016 1 ROF045m 2 ROF045m 2 ROF045m 2 ROF045m 1 ROF045m 2 ROF045m 2 ROF045m 1 ROF045m 2 ROF045m 1 ROF045m 2 ROF045m 1 ROF050m 1	R maximal index / weighted by atomic Sanderson electronegativities Znd component accessibility directional WHI index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by atomic polarizabilities Ghose-Viswanadhan-Wendoloski drug-like index at 80% Radial Distribution Function - 2.5 / weighted by atomic masses 3D-MoRSE - signal 07 / weighted by atomic polarizabilities Ghose-Viswanadhan-Wendoloski drug-like index at 80% Radial Distribution Function - 2.5 / weighted by atomic masses 3D-MoRSE - signal 22 / weighted by atomic sonderson electronegativities <i>RNAME</i> Eigenvalue 07 from edge adj. matrix weighted by dipole moments Eigenvalue 07 from edge adj. matrix weighted by dipole moments Eigenvalue 11 from edge adj. matrix weighted by atomic sanderson electronegativities Radial Distribution Function - 4.5 / weighted by atomic sanderson electronegativities Radial Distribution Function - 4.5 / weighted by atomic masses Ghose-Viswanadhan-Wendoloski drug-like index at 80% Ibowest eigenvalue n. 7 of Burden matrix weighted by atomic sanderson electronegativities Radial Distribution Function - 4.5 / weighted by atomic masses Ghose-Viswanadhan-Wendoloski drug-like index at 80% Ibowest eigenvalue n. 7 of Burden matrix weighted by atomic sanderson electronegativities Eigenvalue 12 from edge adj. matrix weighted by atomic masses Burden at Lorem enters weighted by atomic masse	WHIM descriptors GETAWAY descriptors GETAWAY descriptors ZD autocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors functional group counts topological (ceruia2) geometrical descriptors atomtypes (ceruia2) edge adjacency indices GETAWAY descriptors 3D-MoRSE descriptors atomtypes (descriptors 2D binary fungerprints GETAWAY descriptors 2D binary fungerprints GETAWAY descriptors atom-centred fragments edge adjacency indices edge adjacency indices RDF descriptors atom-centred fragments edge adjacency indices Burden eigenvalues RDF descriptors 3D-MoRSE descriptors atom-centred fragments edge adjacency indices Burden eigenvalues RDF descriptors 3D-MoRSE descriptors Burden eigenvalues Burden eige
	<pre>LELe LELe LELe LELe LELe LELe LELe LEL</pre>	R maximal index / weighted by atomic Sanderson electronegativities Znd component accessibility directional WHI index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by resonance integrals R autocorrelation of lag 4 / weighted by atomic polarizabilities Ghose-Viswanadhan-Wendoloski drug-like index at 80% Radial Distribution Function - 2.5 / weighted by atomic masses 3D-MoRSE - signal 07 / weighted by atomic polarizabilities Ghose-Viswanadhan-Wendoloski drug-like index at 80% Radial Distribution Function - 2.5 / weighted by atomic masses Brawimal autocorrelation of lag 4 / unweighted 3D-MoRSE - signal 22 / weighted by atomic sonderson electronegativities Eigenvalue 07 from edge adj. matrix weighted by dipole moments Eigenvalue 11 from edge adj. matrix weighted by dipole moments Eigenvalue 11 from edge adj. matrix weighted by atomic sonderson electronegativities Radial Distribution Function - 4.5 / weighted by atomic sonderson electronegativities Radial Distribution Function - 4.5 / weighted by atomic sonderson electronegativities Radial Distribution Function - 4.5 / weighted by atomic masses Ghose-Viswanadhan-Wendoloski drug-like index at 80% Ibowest eigenvalue n. 7 of Burden matrix weighted by atomic sonderson electronegativities Eigenvalue 12 from edge adj. matrix weighted by atomic masses Burden at Lorement atomic weighted by atomic masses Burden at Lore	WHIM descriptors GETAWAY descriptors GETAWAY descriptors ZD autocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors functional group counts topological (cerius2) geometrical descriptors atomtypes (Cerius2) edge adjacency indices GETAWAY descriptors molecular properties RDF descriptors molecular properties RDF descriptors molecular properties Burdescriptors molecular properties Burdescriptors molecular properties Burdescriptors molecular properties Burden eigenvalues RDF descriptors edge adjacency indices Burden eigenvalues RDF descriptors edge adjacency indices
	l Eie l RTe+ l E2e GATS2m H1p H4T57p l ROF035m SFMP2 l ROF035m L P075 l C74 V-DIST-mag L3D 2 Atype_C_C40 EE011r I R4m Mor07p GVWAI-80 l ROF025m B070C-C1 l R4u+ Mor022e L0-058 EE001 I ROF025m I ROF045m CVWAI-80 CVWAI-80 I EE011 I ROF045m I ROF045m I ROF045m I ROF045m I ROF045m I ROF045m I ROF045m I ROF050m I Mor14e I EE012 I ROF050m Mor14e I EE021 I ROF050m Mor14e I EE021 I Mor26p I Mor26p I Mor26p	R maximal index / weighted by atomic Sanderson electronegativities Zand component accessibility directional WIM index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by atomic masses 3D-MoRSE - signal 07 / weighted by atomic masses 3D-MoRSE - signal 07 / weighted by atomic masses pravid batencorrelation of lag 4 / weighted by atomic masses pravid batencorrelation of lag 4 / weighted by atomic masses pravid batencorrelation of lag 4 / weighted by atomic masses pravid batencorrel - 2.5 / weighted by atomic masses pravid batencorrel - 3.5 / weighted by atomic masses pravid batencorrel - 4.5 / weighted by atomic masses Eigenvalue 07 from edge adj. matrix weighted by dipole moments Eigenvalue 07 from edge adj. matrix weighted by atomic canses Ghose-Viswanadhan-Wendoloski drug-like index at 80% Radial Distribution Function - 4.5 / weighted by atomic sanderson electronegativities Eigenvalue 11 from edge adj. matrix weighted by atomic sanderson electronegativities Eigenvalue 12 form edge adj. matrix weighted by atomic masses Ghose-Viswanadhan-Wendoloski drug-like index at 80% lowest eigenvalue n. 7 of Burden matrix / weighted by atomic sanderson electronegativities Eigenvalue 12 / modified by atomic masses	WHIM descriptors GETAWAY descriptors GETAWAY descriptors ZD autocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors functional group counts topological (ceruia2) geometrical descriptors atomtypes (ceruia2) edge adjacency indices GETAWAY descriptors 3D-MoRSE descriptors atom-centred fragments edge adjacency indices GETAWAY descriptors atom-centred fragments edge adjacency indices RDF descriptors atom-centred fragments edge adjacency indices RDF descriptors atom-centred fragments edge adjacency indices Burden eigenvalues RDF descriptors 3D-MoRSE descriptors Burden eigenvalues RDF descriptors 3D-MoRSE descriptors 3D-MoRSE descriptors 3D-MoRSE descriptors 3D-MoRSE descriptors 3D-MoRSE descriptors 3D-MoRSE descriptors 3D-MoRSE descriptors 3D-MoRSE descriptors 3D-MoRSE descriptors
	l Eie l RTe+ l E2e GATS2m H1p H4TS7p 1 RDF035m 1 RDF035m 1 RDF035m 1 RDF035m 1 RDF02 1 RDF02 1 RDF02 1 RDF025m 1 B070C-C1 1 R4u+ 1 Mor07p 1 GVVAI-80 1 RDF025m 1 B070C-C1 1 R4u+ 1 Mor07p 1 GVVAI-80 2 GVVAI-80 3	R maximal index / weighted by atomic Sanderson electronegativities Zand component accessibility directional WIII nidex / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by resonance integrals R autocorrelation of lag 4 / weighted by atomic masses 3D-MoRSE - signal 07 / weighted by atomic masses presence/absence of C - C at topological distance 07 # NAMEC Eigenvalue 07 from edge adj. matrix weighted by atomic masses Browence/absence of C - C at topological distance 07 # NAMEC Eigenvalue 07 from edge adj. matrix weighted by domic masses Ghose-Viswanadhan-Wendoloski drug-like index at 80% Radial Distribution Function - 4.5 / weighted by domic masses Ghose-Viswanadhan-Wendoloski drug-like index at 80% Isigenvalue 07 from edge adj. matrix weighted by dipole moments Eigenvalue 07 from edge adj. matrix weighted by dipole moments Eigenvalue 11 from edge adj. matrix weighted by atomic sanderson electronegativities Radial Distribution Function - 4.5 / weighted by atomic sanderson electronegativities Radial Distribution Function - 4.5 / weighted by atomic sanderson electronegativities Eigenvalue 12 from edge adj. matrix weighted by atomic masses Bo-MoRSE - signal 12 / weighted by atomic sanderson electronegativities Eigenvalue 12 from edge adj. matrix weighted by atomic masses Bo-MoRSE - signal 26 / weighted by atomic polarizabilities 10-MoRSE - signal 26 / weighted	WHIM descriptors GETAWAY descriptors GETAWAY descriptors ZD autocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors RDF descriptors functional group counts topological (certus2) edge adjacency indices GETAWAY descriptors Certus2) edge adjacency indices GETAWAY descriptors 3D-MoRSE descriptors molecular properties RDF descriptors atom-centred fragments edge adjacency indices GETAWAY descriptors atom-centred fragments edge adjacency indices GETAWAY descriptors atom-centred fragments edge adjacency indices RDF descriptors molecular properties Buffen eginevalues DFMRSE descriptors molecular properties Buffen eginevalues 3D-MoRSE descriptors molecular properties Buffen eginevalues 3D-MoRSE descriptors atom-centred fragments edge adjacency indices
OR189.1 OR2.1	l Eie l RTe+ l EZe GATS2m l Hip l HATS7p l ROF035m l SHF2 l ROF035m l SHF2 l ROF035m l V-DIST-mag l J3D 2 Atype_C_C40 l EEg11r l RMm l Mor07p GVWAL80 l ROF025m l BOF0C-C1 l Nor22e l ROF025m l EEg11d l EEg11d l ROF045m l ROF045m l ROF045m l ROF045m l ROF045m l ROF045m l ROF045m l ROF045m l Mor14e l EEg12x l Mor24 l BELe7 ROF045m l Mor14e l EEg12x l Mor34 l Mor34m l Mor34m l Mor034 l Mor034	R maximal index / weighted by atomic Sanderson electronegativities Znd component accessibility directional WHI index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic polarizabilities autocorrelation of lag 1 / weighted by atomic masses average shape profile index of order 2 R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities mumber of ring secondary C(sp3) 1D-Balaban index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by resonance integrals R autocorrelation of lag 4 / weighted by atomic masses 3D-MoRSE - signal 70 / weighted by atomic masses 1D-MoRSE - signal 70 / weighted by atomic masses presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / weighted by atomic masses Eigenvalue 21 / from edge adj. matrix weighted by atomic masses presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / weighted by atomic sanderson electronegativities Eigenvalue 17 from edge adj. matrix weighted by dipole moments Eigenvalue 17 from edge adj. matrix weighted by atomic masses Chose-Viswanadhan-Wendoloski drug-like index at 80% Iowest eigenvalue 1.7 for Burden matrix / weighted by atomic Sanderson electronegativities 2D-MoRSE - signal 22 / weighted by atomic masses Ghose-Viswanadhan-Wendoloski drug-like index at 80% Iowest eigenvalue 1.7 for Burden matrix / weighted by atomic Sanderson electronegativities Eigenvalue 1.2 from edge adj. matrix weighted by atomic Sanderson electronegativities Eigenvalue 1.2 from edge adj. matrix weighted by atomic Sanderson electronegativities Eigenvalue 1.2 from edge adj. matrix weighted by atomic Sanderson electronegativities Eigenvalue 1.2 from edge adj. matrix weighted by atomic masses 3D-MoRSE - signal 3D / weighted by atomic masses 3D-MoRSE - sign	WHIM descriptors GETAWAY descriptors GETAWAY descriptors ZD autocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors functional group counts topological (certus2) geometrical descriptors atomtypes (Certus2) edge adjacency indices GETAWAY descriptors anolecular progenties RDF descriptors anolecular progenties RDF descriptors edge adjacency indices GETAWAY descriptors molecular properties Batom-cented fragments edge adjacency indices GETAWAY descriptors molecular properties Batom-cented fragments BATOMARSE descriptors atom-cented fragments Batom-cented fragments Batom-cented fragments BDF descriptors 3D-MoRSE descriptors
	l Eie l RTe+ l E2e GATS2m H1p H4TS7p 1 RDF035m 1 RDF035m 1 RDF035m 1 RDF035m 1 RDF02 1 RDF02 1 RDF02 1 RDF025m 1 B070C-C1 1 R4u+ 1 Mor07p 1 GVVAI-80 1 RDF025m 1 B070C-C1 1 R4u+ 1 Mor07p 1 GVVAI-80 2 GVVAI-80 3	R maximal index / weighted by atomic Sanderson electronegativities Zand component accessibility directional WIII nidex / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by resonance integrals R autocorrelation of lag 4 / weighted by atomic masses 3D-MoRSE - signal 07 / weighted by atomic masses presence/absence of C - C at topological distance 07 # NAMEC Eigenvalue 07 from edge adj. matrix weighted by atomic masses Browence/absence of C - C at topological distance 07 # NAMEC Eigenvalue 07 from edge adj. matrix weighted by domic masses Ghose-Viswanadhan-Wendoloski drug-like index at 80% Radial Distribution Function - 4.5 / weighted by domic masses Ghose-Viswanadhan-Wendoloski drug-like index at 80% Isigenvalue 07 from edge adj. matrix weighted by dipole moments Eigenvalue 07 from edge adj. matrix weighted by dipole moments Eigenvalue 11 from edge adj. matrix weighted by atomic sanderson electronegativities Radial Distribution Function - 4.5 / weighted by atomic sanderson electronegativities Radial Distribution Function - 4.5 / weighted by atomic sanderson electronegativities Eigenvalue 12 from edge adj. matrix weighted by atomic masses Bo-MoRSE - signal 12 / weighted by atomic sanderson electronegativities Eigenvalue 12 from edge adj. matrix weighted by atomic masses Bo-MoRSE - signal 26 / weighted by atomic polarizabilities 10-MoRSE - signal 26 / weighted	WHIM descriptors GETAWAY descriptors GETAWAY descriptors ZD autocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors RDF descriptors functional group counts topological (certus2) edge adjacency indices GETAWAY descriptors Certus2) edge adjacency indices GETAWAY descriptors 3D-MoRSE descriptors molecular properties RDF descriptors atom-centred fragments edge adjacency indices GETAWAY descriptors atom-centred fragments edge adjacency indices GETAWAY descriptors atom-centred fragments edge adjacency indices RDF descriptors molecular properties Buffen eginevalues DFMRSE descriptors molecular properties Buffen eginevalues 3D-MoRSE descriptors molecular properties Buffen eginevalues 3D-MoRSE descriptors atom-centred fragments edge adjacency indices
	l Eie l RTe+ l E2e GATS2m l H1p l HATS7p l RDF035m l SHP2 l RDF035m l SHP2 l RDF035m l SHP2 l RDF02 l RDF02 l RDF02 l RDF02 l RDF025m l B07(C-C) l R4u+ l Mor07p GVWAI-80 l RDF025m l B07(C-C) l R4u+ l RDF045m 2 GVWAI-80 l EEig11d l RDF045m 2 GVWAI-80 l B015 l RDF05 l RD	R maximal index / weighted by atomic Sanderson electronegativities Zand component accessibility directional WHI index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by resonance integrals R autocorrelation of lag 4 / weighted by atomic masses 3D-MoRSE - signal 27 / weighted by atomic masses presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / uneighted by atomic masses presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / uneighted by atomic masses presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / uneighted by atomic masses presence/absence of C - N at topological distance 07 R maximal autocorrelation of lag 4 / uneighted by atomic masses Ghoes-Viswanadhan-Viendoloski drug-like index at 80% Radial Distribution Function - 4.5 / weighted by atomic masses Ghoes-Viswanadhan-Viendoloski drug-like index at 80% Iowest eigenvalue 1.7 of Murden matrix weighted by atomic sanderson electronegativities Radial Distribution Function - 5.0 / weighted by atomic masses 3D-MoRSE - signal 12 / weighted by atomic masses 3D-MoRS	WHIM descriptors GETAWAY descriptors GETAWAY descriptors WHIM descriptors CHAWAY descriptors GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors functional group counts topological (cerus2) geometrical descriptors adge adjacency indices GETAWAY descriptors adge adjacency indices GETAWAY descriptors Topological (cerus2) adge adjacency indices GETAWAY descriptors Topological (cerus2) Diany fungerprints GETAWAY descriptors atom-centred fragments edge adjacency indices Gege adjacency indices RDF descriptors atom-centred fragments edge adjacency indices RDF descriptors Top-MoRSE descriptors Top-MoRSE descriptors Burden eigenvalues RDF descriptors Da-MoRSE descriptors
0R2.1	l Eie l RTe+ l RTe+ l E2e l GATS2m l H1p l HATDp l HATDp l RATD25m l RATD25m l RATD25m l V-DIST-mag l J3D 2 Atype_C_40 l EEig11r l RATD l RATD25m l RATD35m l	R maximal index / weighted by atomic Sanderson electronegativities Zand component accessibility directional WHI index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by resonance integrals R autocorrelation of lag 4 / weighted by atomic masses 3D-MoRSE - signal 07 / weighted by atomic masses presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / weighted by atomic masses presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / uneighted by atomic masses gravence and autocorrelation of lag 4 / uneighted by atomic sanderson electronegativities atuatocorrelation - 4.5 / weighted by atomic masses gravence and the adj. matrix weighted by atomic sanderson electronegativities atuatocorrelation - 4.5 / weighted by atomic masses Ghoese-Viswanadhan-Wendoloski drug-like index at 80% Iowest eigenvalue 11 from edge adj. matrix weighted by atomic sanderson electronegativities Radial Distribution Function - 4.5 / weighted by atomic masses Ghoese-Viswanadhan-Wendoloski drug-like index at 80% Iowest eigenvalue 1.2 from edge adj. matrix weighted by atomic sanderson electronegativities Radial Distribution Function - 5.0 / weighted by atomic masses 3D-MoRSE - signal 14 / weighted by atomic masses Sigenvalue 12 from edge adj. matrix weighted by atomic masses Eigenvalue 12 from edge adj. matrix weighted by atomic masses Eigenvalue 12 from edge adj. matrix weighted b	WHIM descriptors GETAWAY descriptors GETAWAY descriptors ZD autocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors RDF descriptors functional group counts topological (cerius2) geometrical descriptors atomtypes (Cerius2) edge adjacency indices GETAWAY descriptors molecular properties RDF descriptors atomtypes (descriptors atom-centred fragments edge adjacency indices GETAWAY descriptors atom-centred fragments edge adjacency indices RDF descriptors RDF descriptors RDF descriptors RDF descriptors RDF descriptors RDF descriptors BD-MoRSE descriptors BD-MoRSE descriptors SD-MoRSE descriptors SD-MOR
0R2.1	l Eie l RTe+ l E2e GATS2m l H1p l HATS7p l ROF035m l SHP2 l ROF035m l SHP2 l ROF035m l C-DIST-mag l J3D l AType _C_40 l EEig11r l RHm l Mor07p G VWAI-80 l ROF025m l BOF025m l BOF025m l BOF025m l BOF025m l BOF025m l BOF025m l BOF025m l BOF025m l BOF025m l BOF045m l ROF045m l ROF045m l ROF045m l ROF045m l Mor14e l EEig11d l BOF045m l Mor14e l EEig12x l Mor26p l Mor26p l Mor26p l Mor26p l Mor26p l Mor26m l BELe7 l ROF045m l ROF045m l BOF045m l BO	R maximal index / weighted by atomic Sanderson electronegativities Zand component accessibility directional WHI index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by resonance integrals R autocorrelation of lag 4 / weighted by atomic polarizabilities Ghose-Viswanadhan-Wendoloski drug-like index at 00% Bab-MoRSE - signal 07 / weighted by atomic polarizabilities Ghose-Viswanadhan-Wendoloski drug-like index at 00% Presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / unweighted 3D-MoRSE - signal 22 / weighted by atomic masses Bab-MoRSE - signal 22 / weighted by atomic sanderson electronegativities <i>RNAME</i> Eigenvalue 07 from edge adj. matrix weighted by dipole moments Eigenvalue 11 from edge adj. matrix weighted by atomic masses Choose-Viswanadhan-Wendoloski drug-like index at 00% Radial Distribution Function - 4.5 / weighted by atomic masses Choose-Viswanadhan-Wendoloski drug-like index at 00% D-MoRSE - signal 12 / weighted by atomic masses Choose-Viswanadhan-Wendoloski drug-like index at 00% D-MoRSE - signal 14 / weighted by atomic masses Choose-Viswanadhan-Wendoloski drug-like index at 00% D-MoRSE - signal 14 / weighted by atomic masses Choose-Viswanadhan-Wendoloski drug-like index at 00% D-MoRSE - signal 15 / weighted by atomic masses Choose-Viswanadhan-Wendoloski drug-like index at 00% D-MoRSE - signal 16 / weig	WHIM descriptors GETAWAY descriptors GETAWAY descriptors ZD autocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors RDF descriptors RDF descriptors functional group counts topological (cerus2) geometrical descriptors atomtypes (Cerus2) edge adjacency indices GETAWAY descriptors 3D-MoRSE descriptors atomcypes (descriptors atom-centred fragments edge adjacency indices GETAWAY descriptors DD-MoRSE descriptors atom-centred fragments edge adjacency indices RDF descriptors molecular properties Burden eigenvalues RDF descriptors Burden eigenvalues RDF descriptors Burden eigenvalues RDF descriptors 3D-MoRSE descriptors Burden eigenvalues RDF descriptors 3D-MoRSE descriptors 3D-MoRSE descriptors 3D-MoRSE descriptors 2D-MoRSE descriptors 2D binary fingerprints
0R2.1	l Eie l RTe+ l RTe+ l E2e l GATS2m l H1p l HATDp l HATDp l RATD25m l RATD25m l RATD25m l V-DIST-mag l J3D 2 Atype_C_40 l EEig11r l RATD l RATD25m l RATD35m l	R maximal index / weighted by atomic Sanderson electronegativities Zand component accessibility directional WHI index / weighted by atomic Sanderson electronegativities Geary autocorrelation - lag 2 / weighted by atomic polarizabilities leverage-weighted autocorrelation of lag 7 / weighted by atomic polarizabilities Radial Distribution Function - 3.5 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities average shape profile index of order 2 R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities number of ring secondary C(sp3) V-DIST-mag 3D-Balaban index Number of Carbon Type 40 Eigenvalue 11 from edge adj. matrix weighted by resonance integrals R autocorrelation of lag 4 / weighted by atomic masses 3D-MoRSE - signal 07 / weighted by atomic masses presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / weighted by atomic masses presence/absence of C - C at topological distance 07 R maximal autocorrelation of lag 4 / uneighted by atomic masses gravence and autocorrelation of lag 4 / uneighted by atomic sanderson electronegativities atuatocorrelation - 4.5 / weighted by atomic masses gravence and the adj. matrix weighted by atomic sanderson electronegativities atuatocorrelation - 4.5 / weighted by atomic masses Ghoese-Viswanadhan-Wendoloski drug-like index at 80% Iowest eigenvalue 11 from edge adj. matrix weighted by atomic sanderson electronegativities Radial Distribution Function - 4.5 / weighted by atomic masses Ghoese-Viswanadhan-Wendoloski drug-like index at 80% Iowest eigenvalue 1.2 from edge adj. matrix weighted by atomic sanderson electronegativities Radial Distribution Function - 5.0 / weighted by atomic masses 3D-MoRSE - signal 14 / weighted by atomic masses Sigenvalue 12 from edge adj. matrix weighted by atomic masses Eigenvalue 12 from edge adj. matrix weighted by atomic masses Eigenvalue 12 from edge adj. matrix weighted b	 WHIM descriptors GETAWAY descriptors GETAWAY descriptors Dautocorrelations GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors GETAWAY descriptors Roff descriptors Roff descriptors Roff descriptors functional group counts topological (cerus2) geometrical descriptors GETAWAY descriptors GETAWAY descriptors functional group counts topological (cerus2) geometrical descriptors 3D-MoRSE descriptors BOMGRSE descriptors abom-centred fragments edge adjacency indices Gege adjacency indices RDF descriptors BOMRSE descriptores BOMRSE descriptors BOMRSE descri

 $\begin{array}{c}
 1 \\
 2 \\
 3 \\
 1 \\
 2 \\
 3 \\
 1 \\
 2 \\
 3 \\
 1 \\
 2 \\
 3 \\
 1 \\
 2 \\
 3 \\
 1 \\
 2 \\
 3 \\
 1 \\
 2 \\
 3 \\
 1 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\
 2 \\$

Table 3.15 Continued

	3 nRCHO 2 nRCOOH	number of aldehydes (aliphatic) number of carboxylic acids (aliphatic)	functional group counts functional group counts
	1 MATS4m	Moran autocorrelation - lag 4 / weighted by atomic masses	2D autocorrelations
	1 G3s	3st component symmetry directional WHIM index / weighted by atomic electrotopological states	WHIM descriptors
	1 D/Dr05 1 nArCO	distance/detour ring index of order 5 number of ketones (aromatic)	topological descriptors functional group counts
	1 B10[C-C]	presence/absence of C - C at topological distance 10	2D binary fingerprints
	1 MATS6m	Moran autocorrelation - lag 6 / weighted by atomic masses	2D autocorrelations
	1 BEHm7 1 MAXDN	highest eigenvalue n. 7 of Burden matrix / weighted by atomic masses maximal electrotopological negative variation	Burden eigenvalues topological descriptors
	1 L2s	2nd component size directional WHIM index / weighted by atomic electrotopological states	WHIM descriptors
	1 BELe3 1 RDF095u	lowest eigenvalue n. 3 of Burden matrix / weighted by atomic Sanderson electronegativities Radial Distribution Function - 9.5 / unweighted	Burden eigenvalues RDF descriptors
	TKDE0A20	radiar Discribution Function = 9.5 / unweighted	KOF descriptors
10R204.6	1 nCconj	number of non-aromatic conjugated C(sp2)	functional group counts
	1 S_dsCH	S_dsCH	atomtypes (cerius2)
	2 HATS3m	leverage-weighted autocorrelation of lag 3 / weighted by atomic masses	GETAWAY descriptors
	1 DISPv 1 R4u+	d COMMA2 value / weighted by atomic van der Waals volumes R maximal autocorrelation of lag 4 / unweighted	geometrical descriptors GETAWAY descriptors
	2 D/Dr06	distance/detour ring index of order 6	topological descriptors
	1 R6m	R autocorrelation of lag 6 / weighted by atomic masses 3D-MoRSE - signal 10 / weighted by atomic masses	GETAWAY descriptors
	1 Mor10m 1 EEig09r	Eigenvalue 09 from edge adj. matrix weighted by resonance integrals	3D-MoRSE descriptors edge adjacency indices
	1 R7e	R autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors
	1 R3u+ 1 R2v	R maximal autocorrelation of lag 3 / unweighted R autocorrelation of lag 2 / weighted by atomic van der Waals volumes	GETAWAY descriptors GETAWAY descriptors
	1 F05[C-O]	frequency of C - O at topological distance 05	2D frequency fingerprints
	1 HATS7e	leverage-weighted autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors
IOR207.1			
	3 C-025	RCRR	atom-centred fragments
	1 F05[C-O] 1 R6v+	frequency of C - O at topological distance 05 R maximal autocorrelation of lag 6 / weighted by atomic van der Waals volumes	2D frequency fingerprints GETAWAY descriptors
	2 E2e	2nd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities	WHIM descriptors
	1 S_aaCH	S_aaCH B maximal index / weighted by atomic Sanderson electronegativities	atomtypes (cerius2)
	2 RTe+ 1 R8u+	R maximal index / weighted by atomic Sanderson electronegativities R maximal autocorrelation of lag 8 / unweighted	GETAWAY descriptors GETAWAY descriptors
	1 ATS2p	Broto-Moreau autocorrelation of a topological structure - lag 2 / weighted by atomic polarizabilities	2D autocorrelations
	1 MATS5p 1 RDF045v	Moran autocorrelation - lag 5 / weighted by atomic polarizabilities Radial Distribution Function - 4.5 / weighted by atomic van der Waals volumes	2D autocorrelations RDF descriptors
	1 P2p	2nd component shape directional WHIM index / weighted by atomic polarizabilities	WHIM descriptors
	1 R7p+	R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities	GETAWAY descriptors
	1 R5m 1 HOMA	R autocorrelation of lag 5 / weighted by atomic masses Harmonic Oscillator Model of Aromaticity index	GETAWAY descriptors geometrical descriptors
	1 R7v+	R maximal autocorrelation of lag 7 / weighted by atomic van der Waals volumes	GETAWAY descriptors
	1 H1p	H autocorrelation of lag 1 / weighted by atomic polarizabilities	GETAWAY descriptors
MOR273.1			
	1 P2s 2 Jhety	2nd component shape directional WHIM index / weighted by atomic electrotopological states Balaban-type index from van der Waals weighted distance matrix	WHIM descriptors topological descriptors
	1 GATS5m	Geary autocorrelation - lag 5 / weighted by atomic masses	2D autocorrelations
	1 HATS1u	leverage-weighted autocorrelation of lag 1 / unweighted	GETAWAY descriptors
	1 Mor20u 1 JGI6	3D-MoRSE - signal 20 / unweighted mean topological charge index of order6	3D-MoRSE descriptors topological charge indices
	1 R1e	R autocorrelation of lag 1 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors
	1 Mor32u	3D-MoRSE - signal 32 / unweighted	3D-MoRSE descriptors
	1 EEig08r 1 BEHm3	Eigenvalue 08 from edge adj. matrix weighted by resonance integrals highest eigenvalue n. 3 of Burden matrix / weighted by atomic masses	edge adjacency indices Burden eigenvalues
MOR250.1			
108230.1	1 Dv	D total accessibility index / weighted by atomic van der Waals volumes	WHIM descriptors
	6 H-047	H attached to C1(sp3)/C0(sp2)	atom-centred fragments
	1 BEHm5 3 C-006	highest eigenvalue n. 5 of Burden matrix / weighted by atomic masses CH2RX	Burden eigenvalues atom-centred fragments
	2 MATS5p	Moran autocorrelation - lag 5 / weighted by atomic polarizabilities	2D autocorrelations
	1 O-057 2 D/Dr06	phenol / enol / carboxyl OH distance/detour ring index of order 6	atom-centred fragments topological descriptors
	2 Mor24p	3D-MoRSE - signal 24 / weighted by atomic polarizabilities	3D-MoRSE descriptors
	3 P1s	1st component shape directional WHIM index / weighted by atomic electrotopological states	WHIM descriptors
	1 EEig07d 1 R7p+	Eigenvalue 07 from edge adj. matrix weighted by dipole moments R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities	edge adjacency indices GETAWAY descriptors
	3 E1v	1st component accessibility directional WHIM index / weighted by atomic van der Waals volumes	WHIM descriptors
	2 L2s	2nd component size directional WHIM index / weighted by atomic electrotopological states	WHIM descriptors
	2 Mor10e 1 H1v	3D-MoRSE - signal 10 / weighted by atomic Sanderson electronegativities H autocorrelation of lag 1 / weighted by atomic van der Waals volumes	3D-MoRSE descriptors GETAWAY descriptors
	4 R4m	R autocorrelation of lag 4 / weighted by atomic masses	GETAWAY descriptors
	1 RDF035m	Radial Distribution Function - 3.5 / weighted by atomic masses	RDF descriptors
	1 BELm1 2 HATS7m	lowest eigenvalue n. 1 of Burden matrix / weighted by atomic masses leverage-weighted autocorrelation of lag 7 / weighted by atomic masses	Burden eigenvalues GETAWAY descriptors
	1 F04[C-O]	frequency of C - O at topological distance 04	2D frequency fingerprints
	1 B04[0-0] 1 B05[C-C]	presence/absence of O - O at topological distance 04 presence/absence of C - C at topological distance 05	2D binary fingerprints 2D binary fingerprints
	2 C-003	CHR3	atom-centred fragments
	3 H1p	H autocorrelation of lag 1 / weighted by atomic polarizabilities	GETAWAY descriptors
	2 Mor11m 1 EEig07x	3D-MoRSE - signal 11 / weighted by atomic masses Eigenvalue 07 from edge adj. matrix weighted by edge degrees	3D-MoRSE descriptors edge adjacency indices
	3 GVWAI-80	Ghose-Viswanadhan-Wendoloski drug-like index at 80%	molecular properties
	2 JGI7	mean topological charge index of order7	topological charge indices
	3 piPC07 1 nR09	molecular multiple path count of order 07 number of 9-membered rings	walk and path counts constitutional descriptors
	1 RDF060p	Radial Distribution Function - 6.0 / weighted by atomic polarizabilities	RDF descriptors
	1 nRCOOH	number of carboxylic acids (aliphatic)	functional group counts
	1 Mor10m 1 GATS2m	3D-MoRSE - signal 10 / weighted by atomic masses Geary autocorrelation - lag 2 / weighted by atomic masses	3D-MoRSE descriptors 2D autocorrelations
	2 BELe1	lowest eigenvalue n. 1 of Burden matrix / weighted by atomic Sanderson electronegativities	Burden eigenvalues
	1 IC1 1 MATS4m	information content index (neighborhood symmetry of 1-order)	information indices 2D autocorrelations
	1 nArOR	Moran autocorrelation - lag 4 / weighted by atomic masses number of ethers (aromatic)	functional group counts
	1 D/Dr05	distance/detour ring index of order 5	topological descriptors
	1 RDF060u	Radial Distribution Function - 6.0 / unweighted	RDF descriptors
10R256.17	7 BIC	BIC	topological (covius2)
	1 EEig01x	Eigenvalue 01 from edge adi, matrix weighted by edge degrees	topological (cerius2) edge adjacency indices
	6 HATS6m	leverage-weighted autocorrelation of lag 6 / weighted by atomic masses	GETAWAY descriptors
	5 nOHp	number of primary alcohols	functional group counts
	3 S_sssCH 3 nArCO	S_sssCH number of ketones (aromatic)	atomtypes (cerius2) functional group counts
	3 H-049	H attached to C3(sp3)/C2(sp2)/C3(sp2)/C3(sp)	atom-centred fragments
	3 nR=Ct	number of aliphatic tertiary C(sp2)	functional group counts
	3 HTm	H total index / weighted by atomic masses 3D-MoRSE - signal 30 / weighted by atomic van der Waals volumes	GETAWAY descriptors 3D-MoRSE descriptors
	1 Mor30v 2 GATS6m	Geary autocorrelation - lag 6 / weighted by atomic masses	2D autocorrelations
	1 Mor30v 2 GATS6m 1 RDF130m	Geary autocorrelation - lag 6 / weighted by atomic masses Radial Distribution Function - 13.0 / weighted by atomic masses	2D autocorrelations RDF descriptors
	1 Mor30v 2 GATS6m	Geary autocorrelation - lag 6 / weighted by atomic masses	2D autocorrelations

Table 3.15 Continued

	1 C-008	CHR2X	atom-centred fragments
	1 X5A 1 MATS7m	average connectivity index chi-5 Moran autocorrelation - lag 7 / weighted by atomic masses	connectivity indices 2D autocorrelations
	1 Mor24v	3D-MoRSE - signal 24 / weighted by atomic van der Waals volumes	3D-MoRSE descriptors
	1 Mor27e	3D-MoRSE - signal 27 / weighted by atomic Sanderson electronegativities	3D-MoRSE descriptors
	1 EEig09d	Eigenvalue 09 from edge adj. matrix weighted by dipole moments	edge adjacency indices
IOR258.1	3 R1v	R autocorrelation of lag 1 / weighted by atomic van der Waals volumes	GETAWAY descriptors
	1 BELm2	lowest eigenvalue n. 2 of Burden matrix / weighted by atomic masses	Burden eigenvalues
	2 H1p 1 E1u	H autocorrelation of lag 1 / weighted by atomic polarizabilities 1st component accessibility directional WHIM index / unweighted	GETAWAY descriptors WHIM descriptors
	1 HATS2m	leverage-weighted autocorrelation of lag 2 / weighted by atomic masses	GETAWAY descriptors
	1 JGI2 1 R1p	mean topological charge index of order2 R autocorrelation of lag 1 / weighted by atomic polarizabilities	topological charge indices GETAWAY descriptors
	1 B06[C-C]	presence/absence of C - C at topological distance 06	2D binary fingerprints
	1 L2s	2nd component size directional WHIM index / weighted by atomic electrotopological states	WHIM descriptors
	1 DISPm 1 SHP2	d COMMA2 value / weighted by atomic masses average shape profile index of order 2	geometrical descriptors Randic molecular profiles
	1 H1u	H autocorrelation of lag 1 / unweighted	GETAWAY descriptors
	1 P2s	2nd component shape directional WHIM index / weighted by atomic electrotopological states	WHIM descriptors
IOR259.1			
	1 nCb- 1 G3s	number of substituted benzene C(sp2) 3st component symmetry directional WHIM index / weighted by atomic electrotopological states	functional group counts WHIM descriptors
	1 R4m	R autocorrelation of lag 4 / weighted by atomic masses	GETAWAY descriptors
	1 MPC06 1 DISPv	molecular path count of order 06 d COMMA2 value / weighted by atomic van der Waals volumes	walk and path counts geometrical descriptors
	1 R1p	R autocorrelation of lag 1 / weighted by atomic polarizabilities	GETAWAY descriptors
	1 F05[C-O] 1 R2v+	frequency of C - O at topological distance 05 R maximal autocorrelation of lag 2 / weighted by atomic van der Waals volumes	2D frequency fingerprints GETAWAY descriptors
	1 E1u	1st component accessibility directional WHIM index / unweighted	WHIM descriptors
	1 GATS2m	Geary autocorrelation - lag 2 / weighted by atomic masses	2D autocorrelations WHIM descriptors
	1 E2e 1 H1u	2nd component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities H autocorrelation of lag 1 / unweighted	GETAWAY descriptors
IOR260.1	1 RDF110v	Radial Distribution Function - 11.0 / weighted by atomic van der Waals volumes	RDF descriptors
	2 R2m+	R maximal autocorrelation of lag 2 / weighted by atomic masses	GETAWAY descriptors
	1 JGI8 1 Hy	mean topological charge index of order8 hydrophilic factor	topological charge indices molecular properties
	1 0-056	alcohol	atom-centred fragments
	1 H-050 1 MATS8m	H attached to heteroatom Moran autocorrelation - lag 8 / weighted by atomic masses	atom-centred fragments 2D autocorrelations
	1 RDF080e	Radial Distribution Function - 8.0 / weighted by atomic Sanderson electronegativities	RDF descriptors
	1 HATS6m	leverage-weighted autocorrelation of lag 6 / weighted by atomic masses	GETAWAY descriptors
IOR261.1			
	1 RDF110e	Radial Distribution Function - 11.0 / weighted by atomic Sanderson electronegativities	RDF descriptors
	2 C-006 1 RDF075v	CH2RX Radial Distribution Function - 7.5 / weighted by atomic van der Waals volumes	atom-centred fragments RDF descriptors
	1 RDF095u	Radial Distribution Function - 9.5 / unweighted	RDF descriptors
	1 DISPm 1 C-001	d COMMA2 value / weighted by atomic masses CH3R / CH4	geometrical descriptors atom-centred fragments
	1 BEHm8	highest eigenvalue n. 8 of Burden matrix / weighted by atomic masses	Burden eigenvalues
	1 RDF110v	Radial Distribution Function - 11.0 / weighted by atomic van der Waals volumes	RDF descriptors
IOR268.1			
	2 ATS8e 1 C-006	Broto-Moreau autocorrelation of a topological structure - lag 8 / weighted by atomic Sanderson electronega CH2RX	atom-centred fragments
	1 TIE	E-state topological parameter	topological descriptors
	1 RDF050m 3 B09[C-0]	Radial Distribution Function - 5.0 / weighted by atomic masses presence/absence of C - O at topological distance 09	RDF descriptors 2D binary fingerprints
	5 B07[C-C]	presence/absence of C - C at topological distance 07	2D binary fingerprints
	4 H-051	H attached to alpha-C	atom-centred fragments
	3 S_sssCH 1 MATS6m	S_sssCH Moran autocorrelation - lag 6 / weighted by atomic masses	atomtypes (cerius2) 2D autocorrelations
	2 G2p 1 RDF115e	2st component symmetry directional WHIM index / weighted by atomic polarizabilities Radial Distribution Function - 11.5 / weighted by atomic Sanderson electronegativities	WHIM descriptors RDF descriptors
	1 H-049	H attached to C3(sp3)/C2(sp2)/C3(sp2)/C3(sp)	atom-centred fragments
	1 0-057	phenol / enol / carboxyl OH	atom-centred fragments
	1 RDF130u 1 G3u	Radial Distribution Function - 13.0 / unweighted 3st component symmetry directional WHIM index / unweighted	RDF descriptors WHIM descriptors
	1 nRCHO	number of aldehydes (aliphatic)	functional group counts
	1 nArCO 1 nRCOOH	number of ketones (aromatic) number of carboxylic acids (aliphatic)	functional group counts functional group counts
	1 GATS1m	Geary autocorrelation - lag 1 / weighted by atomic masses	2D autocorrelations
	1 nCconj 1 MATS5p	number of non-aromatic conjugated C(sp2) Moran autocorrelation - lag 5 / weighted by atomic polarizabilities	functional group counts 2D autocorrelations
	1 MAISSP	Proton autocorrelation = lag 5 / weighted by atomic polarizabilities	2D autocorrelations
IOR271.1		U standard to be transmission	
	1 H-050 1 PHI	H attached to heteroatom Kier flexibility index	atom-centred fragments topological descriptors
	3 JGI6	mean topological charge index of order6	topological charge indices
	2 RDF075m 2 H-049	Radial Distribution Function - 7.5 / weighted by atomic masses H attached to C3(sp3)/C2(sp2)/C3(sp2)/C3(sp)	RDF descriptors atom-centred fragments
	1 SPH	spherosity	geometrical descriptors
	2 Hy 1 EEig09x	hydrophilic factor Eigenvalue 09 from edge adj. matrix weighted by edge degrees	molecular properties edge adjacency indices
	1 RTu+	R maximal index / unweighted	GETAWAY descriptors
	1 GATS8m 1 nRCOOH	Geary autocorrelation - lag 8 / weighted by atomic masses	2D autocorrelations functional group counts
	1 nRCOOH 1 RDF110p	number of carboxylic acids (aliphatic) Radial Distribution Function - 11.0 / weighted by atomic polarizabilities	RDF descriptors
	1 GATS4m	Geary autocorrelation - lag 4 / weighted by atomic masses	2D autocorrelations
	1 MATS5p 1 R8m+	Moran autocorrelation - lag 5 / weighted by atomic polarizabilities R maximal autocorrelation of lag 8 / weighted by atomic masses	2D autocorrelations GETAWAY descriptors
			and a composition
IOR272.1	1 BLTF96	Verhaar model of Fish base-line toxicity from MLOGP (mmol/I)	molecular properties
	1 DISPe	d COMMA2 value / weighted by atomic Sanderson electronegativities	geometrical descriptors
	1 B08[C-O] 1 HATS6p	presence/absence of C - O at topological distance 08 leverage-weighted autocorrelation of lag 6 / weighted by atomic polarizabilities	2D binary fingerprints GETAWAY descriptors
	1 MATS6m	leverage-weighted autocorrelation of lag 6 / weighted by atomic polarizabilities Moran autocorrelation - lag 6 / weighted by atomic masses	2D autocorrelations
	1 RDF110v	Radial Distribution Function - 11.0 / weighted by atomic van der Waals volumes	RDF descriptors
	1 G3s 1 H-049	3st component symmetry directional WHIM index / weighted by atomic electrotopological states H attached to C3(sp3)/C2(sp2)/C3(sp2)/C3(sp)	WHIM descriptors atom-centred fragments
	1 H-050	H attached to heteroatom	atom-centred fragments
	1 R2m+ 1 GATS8m	R maximal autocorrelation of lag 2 / weighted by atomic masses Geary autocorrelation - lag 8 / weighted by atomic masses	GETAWAY descriptors 2D autocorrelations
	1 HATS5e	leverage-weighted autocorrelation of lag 5 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors
	1 H3m	H autocorrelation of lag 3 / weighted by atomic masses	GETAWAY descriptors
	1 BEHm3	highest eigenvalue n. 3 of Burden matrix / weighted by atomic masses	Burden eigenvalues
IOR273.1			WIND down's
	1 P2s 2 Jhetv	2nd component shape directional WHIM index / weighted by atomic electrotopological states Balaban-type index from van der Waals weighted distance matrix	WHIM descriptors topological descriptors
	1 GATS5m	Geary autocorrelation - lag 5 / weighted by atomic masses	2D autocorrelations
	1 HATS1u	leverage-weighted autocorrelation of lag 1 / unweighted	GETAWAY descriptors

Table 3.15 Continued

NB.3.7.1 Image: Section of					
NO.377.1 I. Burger of the set of		1 Mor20u	3D-MoRSE - signal 20 / unweighted	3D-MoRSE descriptors	
No.277.1 Interface Interface Interface Interface Interface NO.277.1 Interface Interfac			mean topological charge index of order6		
Image: Section of the sectio			3D-MoRSE - signal 32 / unweighted	3D-MoRSE descriptors	
Image: section in the formation is a factor in the formatis factor in the formation is a factor in the format		1 EEig08r	Eigenvalue 08 from edge adj. matrix weighted by resonance integrals	edge adjacency indices	
NGD3.1 Image: Section of the section		1 BEHm3	highest eigenvalue n. 3 of Burden matrix / weighted by atomic masses	Burden eigenvalues	
NURDA1 Image: books of the product o					
NORAL Image: Control in the second of products of the se	MOR277.1	1 HATS3V	leverage-weighted autocorrelation of lag 3 / weighted by atomic van der Waals volumes	GETAWAY descriptors	
NOTE: Image: Section of the section of th			1st component accessibility directional WHIM index / weighted by atomic Sanderson electronegativities		
Home Spectroline			Moran autocorrelation - lag 5 / weighted by atomic masses	2D autocorrelations	
NOR3.1 Image: Imag			2nd component accessibility directional WHIM index / weighted by atomic polarizabilities	WHIM descriptors	
NONSEL Image active probe basis of wind 2 is active active active probe basis of wind 2 is active acti		2 RDF035m 2 R2m+	R maximal autocorrelation of lag 2 / weighted by atomic masses	GETAWAY descriptors	
NONSEL Image active probe basis of wind 2 is active active active probe basis of wind 2 is active acti			R maximal autocorrelation of lag 8 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors	
Heat of the second se			average shape profile index of order 2		
NR33.1 Image: Control in the second sec			Geary autocorrelation - lag 6 / weighted by atomic masses		
NG33-1 Instance of a paint		1 lbetn	Balaban-type index from nolarizability weighted distance matrix	topological descriptors	
HEAL Tool Instant operation in a final matrix / wayled by dation: Statution decompative. Heal to be a statution of the					
NO33.1 information info			Eigenvalue 09 from edge adj. matrix weighted by resonance integrals	edge adjacency indices	
NO33.1 In ac composer a constable during bartering with barter masses In ac composer a constable during bartering with barter masses In accomposer a constable during bartering with barter masses NO33.1 In accomposer a constable during bartering with barter masses In accomposer a constable during bartering with barter masses In accomposer a constable during bartering with barter masses NO33.1 In accomposer a constable during bartering with barter masses In accomposer a constable during bartering with barter masses In accomposer a constable during bartering with barter masses NO33.1 In accomposer a constable during bartering with barter masses In accomposer a constable during bartering with barter masses In accomposer a constable during bartering with bartering		1 BELe3		Burden eigenvalues	
Heat Decision of an entropy of the set of a set o			number or esters (aliphatic) 2nd component accessibility directional WHIM index / unweighted	WHIM descriptors	
NB32.1 		1 JGI5		topological charge indices	
B. S. ACC B. S.			Geary autocorrelation - lag 3 / weighted by atomic masses	2D autocorrelations	
Image: 12.12 Image: 12.12 I			2nd component size directional WHIM index / unweighted	WHIM descriptors	
NOI33.1 Distance of C - 2 at locational distance 00 Distance frequencies Biolic C - 2 NOI33.1 Temper - 0 - 2 Distance frequencies Distance frequencies NOI33.1 Temper - 0 - 2 Distance frequencies Distance frequencies NOI33.1 Temper - 0 - 2 Distance frequencies Distance frequencies NOI33.1 Temper - 0 - 2 Distance frequencies Distance frequencies NOI33.1 Temper - 0 - 2 Distance frequencies Distance frequencies NOI33.1 Temper - 0 - 2 Distance frequencies Distance frequencies NOI33.1 Temper - 0 - 2 Distance frequencies Distance frequencies NOI33.1 Temper - 0 - 2 Distance frequencies Distance frequencies NOI33.1 Temper - 0 - 2 Distance frequencies Distance frequencies NOI33.1 Temper - 0 - 2 Temper - 0 - 2 Temper - 0 - 2 NOI33.1 Temper - 0 - 2 Temper - 0 - 2 Temper - 0 - 2 NOI33.1 Temper - 0 - 2 Temper - 0 - 2 Temper - 0 - 2 NOI33.1 Temper - 0 - 2 Temper - 0 - 2 Temper - 0 - 2 NOI33.1 Temper - 0 - 2 Temper - 0 - 2 Temper - 0 - 2 NOI33.1 Temper - 0 - 2 Temper - 0 - 2 Temper - 0		1 S_dssC 1 G3a	S_dssL 3ct component symmetry directional WHIM index / weighted by atomic Sanderson electronegativities	atomtypes (cerius2)	
Image:		1 B06[C-C]	presence/absence of C - C at topological distance 06	2D binary fingerprints	
Hordson Interface Description Description Hordson Interface Description Description Hordson Interface Description Description Hordson Interface Description Description Hordson Hordson Hordson Description Hordson Hordson Hordson Description Hordson Hordson Hordson Hordson Hordson Hordson		1 L2p	2nd component size directional WHIM index / weighted by atomic polarizabilities	WHIM descriptors	
Hordson Interface Description Description Hordson Interface Description Description Hordson Interface Description Description Hordson Interface Description Description Hordson Hordson Hordson Description Hordson Hordson Hordson Description Hordson Hordson Hordson Hordson Hordson Hordson					
NGR3.1.1 10/05/01 Hother Hother Hother NGR3.1	MOR30.1	1 809[C-0]	presence/absence of C - O at topological distance 09	2D binary fingerprints	
NO23.1 2 0071C 01 bit bit of bit bit bit bit of bit		1 0-056	alcohol	atom-centred fragments	
MRR3.1 Radial Distribution function - 6.5 / weighted by atomic names: Rolf description (CAU) ACR 2015 Reduct Distribution Function - 2.5 / weighted by atomic names: Ref description (CAU) COURT Regeneration of the function - 2.5 / weighted by atomic names: Ref description (CAU) COURT Regeneration of the function - 2.5 / weighted by atomic names: Ref description (CAU) COURT Ref description - 2.5 / weighted by atomic name of the function - 2.5 / weighted by atomic name of the		2 B07[C-O]	presence/absence of C - O at topological distance 07	2D binary fingerprints	
M033.1 Ext of processing in a processing in processing in processing in p			Radial Distribution Function - 8.5 / weighted by atomic van der Waals volumes	RDF descriptors	
MOR33.1 2 C.066 C155X Ltds://initialized/status/sta				atom-centred fragments RDF descriptors	
MOB3.1.1 if Log Log Log Log Log Log Log Log Log		3 C-006	CH2RX	atom-centred fragments	
MOR3.1 Elegination of models all matter weighted by advancements: More special particular in the special matter matter in masses According to the special matter in the special matter in masses According to the special matter in the special matter in masses According to the special matter in the special matter in masses According to the special matter in the special matter in masses According to the special matter in the special matter in masses According to the special matter in the special mat		1 L/Bw	length-to-breadth ratio by WHIM	geometrical descriptors	
MOB3.1.1 21 Composent accessibility directional WHM index / weighted by atomic polarizabilities WHM accession MOB3.1.1 21 Composent accessibility directional WHM index / weighted by atomic masses Direction / Section / S		1 EEig07d	Eigenvalue 07 from edge adj. matrix weighted by dipole moments	edge adjacency indices	
MOR3.1. 2 (MTSTm Gary adsocration - 10 / sequeble by storm masse 30 bits of the sequeble sequeble sequeble by storm masse 30 bits of the sequeble sequeble sequeble by storm masse 30 bits of the sequeble sequeble by store sequeble by sto			Radial Distribution Function - 9.5 / weighted by atomic van der Waals volumes	KDF descriptors	
NG3.1.1 10 Mod21 sequence (1) weighted by atomic masses 10 Mod25 description (1) Mod23 sequence (2) mod (2) mode (2) mode (2) mode (2) mode (2) mode (2) mode (2) mode (2) Mod23 mode (2)					
NOR3.1.1 10.74635 30.74635 10.746355 10.746355 10.746355 10		1 Mor30m	3D-MoRSE - signal 30 / weighted by atomic masses	3D-MoRSE descriptors	
MOB3.1 Cleary autoconstants - lig / velopited by atomic masses Distance methods MOB3.1 Cleary autoconstants - lig / velopited by atomic masses Distance methods MOB3.1 Implicited by atomic masses Distance methods Implicited by atomic masses Distance methods Distance methods Implicited by atomic masses <td></td> <td></td> <td>3D-MoRSE - signal 09 / unweighted</td> <td></td> <td></td>			3D-MoRSE - signal 09 / unweighted		
NOR3.1.1 Close - Waxaaddan Weddexka antimictio- Has index at 80% in the consequence of the ansignation of the ansignatex and ansignater an			Eigenvalue 06 from edge adj. matrix weighted by dipole moments		
NOB3.1. I Res- tor all scattering of a weighted by storic sanderson electronegabilities CETAW// Securitation 2.2 weighted by storic sanderson electronegabilities CETAW// Securitation 2.2 weighted by storic sanderson electronegabilities NOB3.1. I Res- tor all scatter al					
Nor3.1 Radial Distribution Function - 14.0 / weighted by atomic Standerson electronegativities RDF descriptors NOR3.1. I (F0/C-0) frequency of C - 0 at topological distance 07 atomic of topological distance 07 I (F0/C-0) I (F0/C-0) Prequency of C - 0 at topological distance 07 atomic of topological distance 07 I (F0/C-0) I (F0/C-0) Prequency of C - 0 at topological distance 07 atomic of topological distance 07 I (F0/C-0) Prequency of C - 0 at topological distance 07 atomic of topological distance 07 atomic of topological distance 07 I (F0/C-0) Presence/absence of C - 0 at topological distance 09 atomic of topological distance 08 atomic of topological distance 07 I (F0/C-0) Presence/absence of C - 0 at topological distance 08 atomic on topological distance 07 atomic on topological distance 08 I (F0/C-0) Presence/absence of C - 0 at topological distance 08 atomic on topological distance 08 atomic on topological distance 08 I (F0/C-0) Presence/absence of C - 0 at topological distance 08 atomic on topological distance 08 atomic on topological distance 08 I (F0/C-0) Presence/absence of C - 0 at topological distance 08 atomic on topological distance 08 atomic on topological distance 08		1 R6e+	R maximal autocorrelation of lag 6 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors	
NR33.1 Image: sec: sec: sec: sec: sec: sec: sec: se		1 GATS2m	Geary autocorrelation - lag 2 / weighted by atomic masses		
MOR3.1.1 i P07(C-0) i P000000000000000000000000000000000000		1 RDF045e	Radial Distribution Function - 4.5 / weighted by atomic Sanderson electronegativities	RDF descriptors	
MOR3.1.1 i POTC-01 Presence/sector requestry of C - 0 at topological distance 07 requestry of C - 0 at topological distance 04 requestry of C - 0 at topological distance 04 Presence/sector 2D frequestry frequestria 2D frequestry frequestria 2D frequestry of C - 0 at topological distance 04 Presence/sector MOR3.7.1 1 100/CC - 1 requestry of C - 0 at topological distance 04 Presence/sector 2D frequestry frequestria 2D frequestry frequestria atom-cetter of frequestry atom-cetter	MOR33.1				
IDESP		1 F07[C-O]	frequency of C - O at topological distance 07	2D frequency fingerprints	
Image: Projection of the program o		1 nRCOOH	number of carboxylic acids (aliphatic)		
Average 2 Mort/Per 10-MoRSE - signal 17 / weighted by atomic masses 10-MoRSE - descriptors 1 MORA7.1 Charpy mathematical solution 2 Descriptors 2 Descriptors 1 MORA7.1 Descriptors 2 Descriptors 2 Descriptors 1 MORA7.1 Radial Distribution Function - 11.0 / weighted by atomic van der Waals volumes RDF descriptors 1 MORA7.1 Radial Distribution Function - 11.0 / weighted by atomic van der Waals volumes RDF descriptors 1 MORA7.1 H distribution Function - 11.0 / weighted by atomic van der Waals volumes RDF descriptors 1 MORA7.1 H distribution Function - 11.0 / weighted by atomic van der Waals volumes RDF descriptors 1 MORA7.1 H distribution Function - 11.0 / weighted by atomic van der Waals volumes RDF descriptors 1 MORA7.1 H distribution Function - 11.0 / weighted by atomic masses 2 Descriptors 2 MORA7.1 Radial Distribution Function - 1.0 / weighted by atomic masses 2 Descriptors 2 MORA7.1 H distribution Function - 1.0 / weighted by atomic masses 2 Descriptors 2 MORA7.1 H distribution Function - 1.0 / weighted by atomic m					
Image: Provide and the standard of a plan-C attached to a plan-C attached to a plan-C Image: Provide and the standard of the plane of the standard of the standard of the plane of the standard of th			3D-MoRSE - signal 17 / weighted by atomic Sanderson electronegativities	3D-MoRSE descriptors	
MOR37.1 1 C-006 CATS'm 1 MC90 1 MC9		1 H-051	H attached to alpha-C	atom-centred fragments	
MOR37.1 Image: Second		1 C-006	CH2RX	atom-centred fragments	
MOR37.1 1 D09[C-C] 1 preserve/absence of C - 0 at topological distance 09 20 binary fingerprints 20 binary fingerp			Geary autocorrelation - lag / / weighted by atomic masses H attached to beteroatom		
NOR4.1.1 I B091C-O1 10 0036 I B001C-O1 10 0037 I B001C-O1 10 0037 I B001C-O1 10 0037 I B001C-O1 10 0037 10 0037 I B001C-O1 10 0037 10 0037 10 003		1		alom concernagments	
NOR40.1 atcome atcome atcome atcome atcome NOR40.1 2 DPT600 Radial Distribution Function - 11.0 / weighted by atomic van der Waals volumes NDF descriptors Automatical State 3D-M632E atcome atcome atcome NOR41.1 Radial Distribution Function - 11.0 / weighted by atomic Statemon electronegativities 3D-M632E atcome NOR41.1 Garary Mutocorrelation - lag 7 / weighted by atomic masses atcome atcome NOR41.1 graph vertex complexity index information indices information indices NOR41.1 graph vertex complexity index information indices information indices NOR41.1 graph vertex complexity index information indices information indices NOR41.1 graph vertex complexity index information indices information indices NOR41.1 graph vertex complexity index information indices information indices NOR41.1 graph vertex complexity index information indices information indices NOR41.1 graph vertex complexity index information indices information indices Norther graph vertex complexity index information indices information indices Norther graph vertex complexity index informatin information i	MOR37.1				
MOR40.1 2 BDF LOP		1 B09[C-0]	presence/absence of C - O at topological distance 09	2D binary fingerprints	
MOR40.1 2 RDF LLOW Padial Distribution function - 11.0 / weighted by atomic van der Waals volumes RDF descriptors MOR40.1 2 RDF LLOW Padial Distribution function - 11.0 / weighted by atomic Sanderson electronegativities RDF descriptors MOR41.1 1 CADSS* Gearsy autocorrelation - lag 7 / weighted by atomic masses 20 -MoSE descriptors MOR41.1 1 HVcps graph wertex complexity index Information indicas 1 Kappo-3 Kappo-3 Kappo-3 Cantorrelation - lag 7 / weighted by atomic masses 20 -autocorrelation indicas 1 Number 0 cantorrelation - lag 7 / weighted by atomic masses 20 -autocorrelation indicas topological (cerus2) 1 Number 0 cantorrelation - lag 7 / weighted by atomic masses 20 -autocorrelation indicas topological (cerus2) 1 Number 0 cantorrelation - lag 7 / weighted by atomic masses 20 -autocorrelation indicas topological (cerus2) 2 MortDav 20 -MoSE - signal 10 / weighted by atomic masses 20 -autocorrelation indicas topological (cerus2) 2 MortDav 20 -MoSE - signal 20 / weighted by atomic masses 20 -autocorrelation indicas topological (cerus2) 2 MortDav 20 -MoSE - signal 21 / weighted by atomic masses 20 -autocorrelation indicas topological (cerus2) <td></td> <td>1 B08[C-0]</td> <td></td> <td></td> <td></td>		1 B08[C-0]			
PRORALL 2 RDF110V H 4315 thet do alpha-C 1 kor 7/a 2 D-M0RSE - signal 17 / weighted by atomic Sanderson electronegativities RDF descriptors atom centre fragments 2 D-M0RSE - signal 17 / weighted by atomic Sanderson electronegativities RDF descriptors 2 D-M0RSE - signal 17 / weighted by atomic Sanderson electronegativities RDF descriptors 2 D-M0RSE - signal 17 / weighted by atomic masses MOR41.1 I MCpcx 1 GATS7m graph vartex complexity index (apps 3 (apps 3) (apps 4) (apps 3) (apps 4) (apps 4) (1000[0 0]		20 bindi y miger printo	
NOR41.1 1 H 4051 Mort 72 10 Mort 72 (C-006 CH2RX Gats 75m 12 weighted by atomic Sanderson electronegativities Gats 75m 3D-MoSE descriptors atom-centred fragments 2D autocorrelations NOR41.1 1 MCriptor Gats 75m Gats 75m Gats 75m Gats 75m NOR41.1 1 MCriptor Gats 75m Gats 75m Gats 75m Gats 75m NOR41.1 1 MCriptor HCriptor Gats 75m Gats 75m Gats 75m Gats 75m 1 MCriptor HCriptor Gats 75m Gats 75m Gats 75m Gats 75m Gats 75m 2 Mort 75m Gats 75m Gats 75m Gats 75m Gats 75m Gats 75m 3 Mort 75m 10 Mort 75m 10 Mort 75m 10 Mort 75m 10 Mort 75m 3 Mort 75m 10 Mort 75m 10 Mort 75m 10 Mort 75m 10 Mort 75m 3 Mort 75m 10 Mort 75m 10 Mort 75m 10 Mort 75m 10 Mort 75m 3 Mort 75m 10 Mort 75m 10 Mort 75m 10 Mort 75m 10 Mort 75m 3 Mort 75m Gats 75m Gats 75m Gat	MOR40.1				
NOR41.1 3D-MoRSE discriptors 3D-MoRSE discriptors I CO06 CH2XX Co06 Geary autocorrelation - lag 7 / weighted by atomic masses 2D autocorrelations I Hytops graph vertex complexity index information indices I Noppa-3 Kappa-3 topological (carrus) A GATS3m Geary autocorrelation - lag 3 / weighted by atomic masses 2D autocorrelations B RACCOH number of carboxilic calds (alphatic) functional group counts B RACCOH number of carboxilic calds (alphatic) functional group counts 2 MOR3D 3D-MORSE - signal 10 / weighted by atomic masses 3D-MoRSE discriptors 2 MOR3D Redail Distribution Function - Re 5 / weighted by atomic masses 3D-MoRSE discriptors 2 MOR3D Redail Distribution Function - Re 5 / weighted by atomic masses 2D autocorrelations 3 Hofm H autocrrelation - Ling 6 / weighted by atomic masses 2D autocorrelations 3 Hofm H autocrrelation - Ling 6 / weighted by atomic masses 2D autocorrelations 3 Hofm H autocrrelation Function - Re 5 / unweighted by atomic masses 2D autocorrelations 3 Hofm H autocrrelation Function - Re 5 / unweighted by atomic masses 2D autocorrelations 4 BEC Bar 6 - Weighted by atomic masses 2D autocorrelations 1 (GI3 mean to		2 RDF110v	Radial Distribution Function - 11.0 / weighted by atomic van der Waals volumes	RDF descriptors	
MOR41.1 1 C-006 I GATSTM Genry autocorrelation - lag 7 / weighted by atomic masses 2D autocorrelation indices information indices indicates in the indicates indindicates indicates		1 Mor1 7e		3D-MoRSE descriptors	
MORA1.1 Image: More and the second seco				atom-centred fragments	
MORE-11 Information indices information indices I Kappa-3 Kappa-3 Kappa-3 Kappa-3 4 GATS3m Geary autocorrelation - lag 3 / weighted by atomic masses 2D autocorrelations 8 InRCOOH number of carboxylic acids (aliphatic) atom-centred fragments 2 Nor10v 3D-MARSE - signal 10 / weighted by atomic van der Waals volumes 3D-MARSE - disencentred fragments 3 Hinded Edgenalue 06 from edge ad, mattix weighted by atomic polarizabilities RDF descriptors 3 Hinded Edgenalue 06 from edge ad, mattix weighted by atomic masses 2D autocorrelations 3 Hinded Edgenalue 06 from edge ad, mattix weighted by atomic masses 2D autocorrelations 3 Hinded Edgenalue 06 from edge ad, mattix weighted by atomic masses 2D autocorrelations 3 Hinded Edgenalue 06 from edge ad, mattix weighted by atomic polarizabilities Burden eigenvalues 1 GATS2m Geary autocorrelation - lag 5 / weighted by atomic masses 2D autocorrelations 1 GATS2m Real al Distribution Function - 8.5 / unweighted by atomic masses 2D autocorrelations 1 GATS2m Real al Distribution Function - 8.5 / unweighted by atomic masses 2D autocorrelations 1 GATS2m Geary autocorrelation - lag 7 / weighted by atomic polarizabilities WHIM descriptors 1 GATS4m Laprenter addia Distribution Function - 8.5 / unweighted by				2D autocorrelations	
MORE-11 Information indices information indices I Kappa-3 Kappa-3 Kappa-3 Kappa-3 4 GATS3m Geary autocorrelation - lag 3 / weighted by atomic masses 2D autocorrelations 8 InRCOOH number of carboxylic acids (aliphatic) atom-centred fragments 2 Nor10v 3D-MARSE - signal 10 / weighted by atomic van der Waals volumes 3D-MARSE - disencentred fragments 3 Hinded Edgenalue 06 from edge ad, mattix weighted by atomic polarizabilities RDF descriptors 3 Hinded Edgenalue 06 from edge ad, mattix weighted by atomic masses 2D autocorrelations 3 Hinded Edgenalue 06 from edge ad, mattix weighted by atomic masses 2D autocorrelations 3 Hinded Edgenalue 06 from edge ad, mattix weighted by atomic masses 2D autocorrelations 3 Hinded Edgenalue 06 from edge ad, mattix weighted by atomic polarizabilities Burden eigenvalues 1 GATS2m Geary autocorrelation - lag 5 / weighted by atomic masses 2D autocorrelations 1 GATS2m Real al Distribution Function - 8.5 / unweighted by atomic masses 2D autocorrelations 1 GATS2m Real al Distribution Function - 8.5 / unweighted by atomic masses 2D autocorrelations 1 GATS2m Geary autocorrelation - lag 7 / weighted by atomic polarizabilities WHIM descriptors 1 GATS4m Laprenter addia Distribution Function - 8.5 / unweighted by	NOD41 1				
I Kappa-3 Kappa-3 topological (cerius2) 4 GATS3m Geary autocorrelation - lag 3 / weighted by atomic masses 2D autocorrelations B R-COOH number of carboxylic acids (alphatic) 1unctional group counts B R-COOH 3D -MoRSE - signal 10 / weighted by atomic onder Waals volumes 3D -MoRSE descriptors 2 RDF085p Radial Distribution Function - 8.5 / weighted by atomic masses 2D autocorrelation - lag 8 / weighted by atomic masses 2 RDF085p Radial Distribution Function - 8.5 / weighted by atomic masses 2D autocorrelations 3 Biom H autocorrelation - lag 8 / weighted by atomic masses 2D autocorrelations 3 Biom H autocorrelation of lag 6 / weighted by atomic masses 2D autocorrelations 1 BCD Birden matrix / weighted by atomic masses 2D autocorrelations 1 BCD Birden matrix / weighted by atomic masses 2D autocorrelations 1 BCD Birden matrix / weighted by atomic masses 2D autocorrelations 1 BCD Birden matrix / weighted by atomic masses 2D autocorrelations 1 BCD Birden matrix / weighted by atomic colarizabilities Birden matrix / weighted by atomic masses 1 GATS3m Geary autocorrelation all 2 / weighted by atomic masses 2D autocorrelations	MOK41.1	1 HVcox	graph vertex complexity index	information indices	
B number of carboxylic acids (aliphatic) functional group counts 3H-049 H attachet to C3(ap)2(C3(ap)2(C3(ap)2)(C3(ap)2) atom-centred fragments 2R0F05p Radial Distribution Function - 8.5 / weighted by atomic polarizabilities BD7 descriptors 3EEig08r Eigenvalue 08 from edge adj. matrix weighted by resonance integrals edge adjacency indices 4 BIC BC BC topological (centus2) 5 GATS8m Geary autocorrelation - lag 8 / weighted by atomic masses 2D autocorrelations 1 BEHp3 highest eigenvalue 0.8 from edge adj. matrix weighted by atomic masses 2D autocorrelations 1 BEHp3 highest eigenvalue n.3 of Burden matrix / weighted by atomic masses 2D autocorrelations 1 BEHp3 highest eigenvalue n.3 of Burden matrix / weighted by atomic masses 2D autocorrelations 1 GATS2m Radial Distribution Function - 8.5 / unweighted by atomic masses 2D autocorrelations 3 Hof Hautocorrelation - 18.2 / uweighted by atomic masses 2D autocorrelations 3 Hof RDF050v Radial Distribution Function - 5.0 / weighted by atomic masses 2D autocorrelations 3 Hof Hautocorrelation - 18.2 / uweighted by atomic masses 2D autocorrelations 3 Hof RDF050v Radial Distribution Function - 5.0 / weighted by atomic masses 2D autocorrelations 1 RDF050v Radial Distri		1 Kappa-3	Kappa-3	topological (cerius2)	
Bit -049 H attached to C3(q3)/C3(q52)/C3(q52)/C3(q52) atom-centred fragments 2 Mor10v 30-MoRSE - signal 10 / weighted by atomic van der Waals volumes BD MoRSE descriptors 2 RDF085p Radial Distribution Function - 8.5 / weighted by atomic polarizabilities RDF descriptors 4 BIC BIC BIC BIC 5 GKTS8m Geary autocorrelation - lag 8 / weighted by atomic masses GETRWAY descriptors 1 BEG13 Highest eigenvalue 08 for matrix weighted by atomic masses GETRWAY descriptors 1 BEG13 Highest eigenvalue 08 for matrix weighted by atomic polarizabilities BDrd descriptors 1 BEG13 Highest eigenvalue 3.3 Guardiantic masses GETRWAY descriptors 1 BEG13 Highest eigenvalues - 3.3 Guardiantic masses 2D autocorrelations 2 BOP dos 22 3D-MoRSE - signal 22 / weighted by atomic conlegativities 3D -MoRSE descriptors 4 MOR22e 3D-MoRSE - signal 22 / weighted by atomic scalerson electronegativities 3D -MoRSE descriptors 1 BOP dos 22 3D-MoRSE - signal 22 / weighted by atomic conlegativities BD descriptors 2 MOR22e 3D-MoRSE - signal 22 / weighted by atomic conlegativities BD descriptors 1 GKWAI-80 Ghose-Viswamadhan-Wendoloski drug-like index at 80% Inctional gr			Geary autocorrelation - lag 3 / weighted by atomic masses		
Mor10v 3D-MoRSE - signal 10 / weighted by atomic van der Waals volumes 3D-MoRSE descriptors 2 RDF055p Radial Distribution Function - 8.5 / weighted by atomic polarizabilities RDF descriptors 3 EEig08r Eigenvalue 08 from edge adj. matrix weighted by atomic masses 2D autocorrelations 4 BIC BIC GE 5 GATS8m Geary autocorrelation - 1ag 8 / weighted by atomic masses 2D autocorrelations 1 JGT3 mean topological charge index of order3 Burden eigenvalues 1 JGT3 Radial Distribution Function - 8.5 / weighted by atomic masses 2D autocorrelations 1 JGT3 mean topological charge index of order3 Burden eigenvalues 1 JGT3 Radial Distribution Function - 8.5 / weighted by atomic masses 2D autocorrelations 1 JGT3 Radial Distribution Function - 8.5 / weighted by atomic masses 3D-MoRSE eigenvalues 1 GATS2m Geary autocorrelation - 8.5 / weighted by atomic masses 3D-MoRSE eigenvalues 1 GATS2m Geary autocorrelation - 8.5 / weighted by atomic masses 3D-MoRSE eigenvalues 1 GATS2m Geary autocorrelation - 8.5 / weighted by atomic masses 3D-MoRSE eigenvalues 1 GATS2m Geary autocorrelation - 8.5 / weighted by atomic masses 3D-MoRSE eigenvalues 1 GATS2m Geary autocorrelation - 8.5 / weighted by atomic masses 3D-MoRSE eigenvalues 1 G			number or carboxylic acids (aliphatic) H attached to C3(sn3)/C2(sn2)/C3(sn)	runctional group counts atom-centred fragments	
RAFIO Radial Distribution Function - 8.5 / weighted by atomic polarizabilities RDF descriptors 4 EIC BIC		2 Mor10v	3D-MoRSE - signal 10 / weighted by atomic van der Waals volumes	3D-MoRSE descriptors	
4 BIC BIC topological (cerius2) 5 GATSbm Geary autocorrelation of lag 6 / weighted by atomic masses 2D autocorrelations 3 H6m H autocorrelation of lag 6 / weighted by atomic masses GETAWAY descriptors 1 BEHp3 Highest eigenvalues n. 30 Burden matrix / weighted by atomic plarizabilities Burden eigenvalues 1 Cata mean topological charge index of order3 topological charge indices 4 RDF085u Radial Distribution Function - 8.5 / unweighted by atomic masses 2D autocorrelations 3 InCq number of total quaternary C(sp3) functional group counts 1 Etp 11 to component accessibility directional WHIM index / weighted by atomic plarizabilities WHIM descriptors 1 RDF050v Radic shape index RDF descriptors RDF descriptors 1 CWM1-80 Ginose-Viswanadhan-Wendoloski drug-like index at 80% molecular properties 1 CWM1-80 Ginose-Viswanadhan-Wendoloski drug-like index at 80% molecular properties 1 RDF130u Radio Istribution Function - 5.0 / weighted by atomic masses 2D autocorrelations 1 RDF050v Radio Istribution Function - 5.0 / weighted by atomic van der Waals volumes GETAWAY descriptors 1 RDF050v Radio Istribution Function - 5.0 / weighted by atomic wan der Waals volumes GETAWAY descriptors 1 RDF050v Radic Istribution Function - 1.3 / Vieijhted by atomic		2 RDF085p	Radial Distribution Function - 8.5 / weighted by atomic polarizabilities	RDF descriptors	
SGATSSm Geary autocorrelation - lag 8 / weighted by atomic masses 20 autocorrelations' BHM H autocorrelation of lag 6 / weighted by atomic masses GETWAY descriptors 1 BEHp3 highest eigenvalue n.3 of Burden matrix / weighted by atomic masses BUrden eigenvalues 1 GATS2m Radial Distribution Function - 8.5 / unweighted by atomic masses BDF descriptors 4 RDF085u Radial Distribution Function - 8.5 / unweighted by atomic masses 3D-MoRSE eigenvalues 3 InCq number of total quaternary (CR3) BUT descriptors 4 Mor22e 3D-MoRSE eigenvalue 3D-MoRSE eigenvalues BUT descriptors 3 InCq number of total quaternary (CR3) HIM descriptors BUT descriptors 1 RDF050v Radial Distribution Function - 8.0 / weighted by atomic van der Waals volumes BCF descriptors 1 RDF050v Radial Distribution Function - 8.0 / weighted by atomic van der Waals volumes BCF descriptors 1 RDF050v Radial Distribution function - 16.0 / weighted by atomic van der Waals volumes GETWAV descriptors 1 RDF130u Radial Distribution of lag 6 / weighted by atomic van der Waals volumes GETWAV descriptors 1 RDF130u Radial Distribution of lag 6 / weighted by atomic van der Waals volumes GETWAV descriptors 1 RDF130u Radial Distribution function - 13.0 / unweighted by atomic van der Waals volumes BUT descriptors <td></td> <td>3 EEig08r</td> <td>Eigenvalue 08 from edge adj. matrix weighted by resonance integrals</td> <td></td> <td></td>		3 EEig08r	Eigenvalue 08 from edge adj. matrix weighted by resonance integrals		
Mom H autocorrelation of lag 6 / weighted by atomic masses GETAWAY descriptors 1 BEHp3 highest eigenvalues n.3 of Burden matrix / weighted by atomic polarizabilities Burden eigenvalues 1 GLTS mean topological charge index of order3 topological charge indices 4 RDF085u Radial Distribution Function - 8.5 / unweighted RDF descriptors 1 GATS2m Geary autocorrelation - lag 2 / weighted by atomic masses 2D autocorrelations 3 InCq number of total quaternary C(sp3) functional group counts 1 ELp 11 at component accessibility diructional WHM index / weighted by atomic polarizabilities RDF descriptors 1 RDF050v Radic Istribution Function - 5.0 / weighted by atomic van der Waals volumes RDF descriptors 1 RDF050v Radic Istribution Function - 5.0 / weighted by atomic van der Waals volumes RDF descriptors 1 GWM1-80 Ghose-Viswanadhan-Wendoloski drug-like index at 80% molecular properties 1 GWM1-80 Ghose-Viswanadhan-Wendoloski drug-like index at 80% molecular properties 1 HoV H autocorrelation - lag 3 / weighted by atomic masses 2D autocorrelations 1 HoV H autocorrelation - lag 3 / weighted by atomic wan der Waals volumes GETAWAY descriptors 1 RDF130u Radic Istribution Function - 3.3 / weighted by atomic wan der Waals volumes Burden regenvalues 1 HoV H autoc				2D autocorrelations	
MOR5.1 I BEHp3 highest eigenvalue n. 3 of Burden matrix / weighted by atomic polarizabilities Burden eigenvalues 1 JG13 mean topological charge index of order3 RoPF085u Radial Distribution Function - 8.5 / unweighted by atomic masses 2D sutcorrelations 3 InCq number of total quaternary C(g3) Burden eigenvalues Tunctional group counts 1 Exp 12 control Representation - lag 2.7 weighted by atomic solarison electronegativities 3D-MoR5E eigenvalues 3 InCq number of total quaternary C(g3) Incitional group counts WITM descriptors 1 RDP/050v Radial Distribution Function - 6.7 / weighted by atomic van der Waals volumes RDF descriptors 1 RDP/050v Radial Distribution Function - 6.7 / weighted by atomic van der Waals volumes RDF descriptors 1 RDP/050v Radial Distribution Function - 6.7 / weighted by atomic van der Waals volumes RDF descriptors 1 RDP/050v Radial Distribution function - 6.7 / weighted by atomic van der Waals volumes GETWAY descriptors 1 RDP/130u Radial Distribution of lag 6 / weighted by atomic van der Waals volumes GETWAY descriptors 1 H6v H autocorrelation - 13.0 / unweighted atomtypes (Cerius2) atomtypes (Cerius2) 1 RDF130u Radial Distribution Function - 13.0 / unweighted geometrical descriptors Connectivity indices 1 RDF130u Radial Distr		3 H6m	H autocorrelation of lag 6 / weighted by atomic masses	GETAWAY descriptors	
Horbosture Radial Distribution Function - 8.5 / unweighted by atomic masses RDF descriptors 1 GATS2m Geny autocorrelation - lag 2, V weighted by atomic Sanderson electronegativities 3D-MoRSE descriptors 4 Mor22e 3D-MoRSE - signal 22, Weighted by atomic Sanderson electronegativities 3D-MoRSE descriptors 1 RDF050v Radial Distribution Function - 5.0 / weighted by atomic van der Waals volumes RDF descriptors 1 RDF050v Radial Distribution Function - 5.0 / weighted by atomic van der Waals volumes RDF descriptors 1 RDF050v Radial Distribution Function - 5.0 / weighted by atomic van der Waals volumes RDF descriptors 1 RDF050v Radial Distribution Function - 5.0 / weighted by atomic van der Waals volumes RDF descriptors 1 RDF050v Radial Distribution Function - 5.0 / weighted by atomic van der Waals volumes RDF descriptors 1 RDF130u Radial Distribution of Ilag 6 / weighted by atomic van der Waals volumes ZD autocorrelations 1 Atype C_18 Number of Carbon Type 18 atomtypes (Cerius2) 1 RDF130u Radial Distribution Function - 13.0 / unweighted RDF descriptors 1 RDF1400 Indexred RDF descriptors RDF descriptors 1 RDF130u Radial Distribution function - 13.0 / unweighted by atomic van der Waals volumes Burden regenvalues 1 RDF130u Radial Distribution Function - 13.0 / unweighted by atomic van der Waa		1 BEHp3	highest eigenvalue n. 3 of Burden matrix / weighted by atomic polarizabilities	Burden eigenvalues	
I GATS2m Geary autocorrelation - lag 2 / weighted by atomic masses 2D autocorrelations 4 Mor22e 3D-MASE - signal 22 / weighted by atomic masses 3D-MASE - discriptors 3 InCq number of total quaternary C(sp3) functional group counts 1 Elp 11 st componet accessibility directional WHM index / weighted by atomic polarizabilities WHM descriptors 2 PW3 pathwalk 3- Randic shape index RDF descriptors 1 GVWAI-80 Ghose-Viswanadhan-Wendoloski drug-like index at 80% molecular properties 1 G-008 CrR2X atom-correlations of lag 6 / weighted by atomic masses GETRWAY descriptors 1 HoV H autocorrelation - lag 3 / weighted by atomic masses GETRWAY descriptors 1 HAY3m Moran autocorrelation - lag 3 / weighted by atomic masses ZD autocorrelations 1 HAY3m Number of Carbon Type 18 Burden matrix / weighted by atomic wan der Waals volumes Burden regenvalues 1 RDF130u Radial Distribution Function - 13.0 / unweighted Tantonia group counts RDF descriptors 1 BBCf-0 presence/absence of C - 0 at topological distance 05 ZD binary fingerynitis 1 BBC1-0 presence/absence of C - 0 at topological distance 07 ZD requency fingerynitis 1 MCC0H number of adrbylic distance 07 ZD requency fingerynitis 1 MEC1 malecular eccretricity ZD					
Mor22e 3D-MoRSE - signal 22 / weighted by atomic Sanderson electronegativities 3D-MoRSE descriptors functional group counts 1 Etp 12 component accessibility directional WHM index / weighted by atomic polarizabilities WHM descriptors 1 RDF050v Radial Distribution Function - 5.0 / weighted by atomic van der Waals volumes RDF descriptors 2 RVMAI-80 Ghose-Viswanadhan-Wendoloski drug-like index at 80% molecular ecosisities 1 GVWAI-80 Ghose-Viswanadhan-Wendoloski drug-like index at 80% molecular ecosisities 1 GVWAI-80 Ghose-Viswanadhan-Wendoloski drug-like index at 80% molecular ecosisities 1 GVWAI-80 Ghose-Viswanadhan-Wendoloski drug-like index at 80% molecular ecosisities 1 MATS3m Moran autocorrelation - 183 of / weighted by atomic van der Waals volumes 2D autocorrelations atomtypes (Cerius2) 1 BBHV3 highest eigenvalues n.3 of Burden matrix / weighted by atomic van der Waals volumes Burden eigenvalues 1 RRF00 number of Carbon Type 18 Burden matrix / weighted by atomic van der Waals volumes Burden eigenvalues 1 BBHV3 highest eigenvalues n.3 of Burden matrix / weighted by atomic van der Waals volumes Burden eigenvalues 1 RRF010 muber of adehydes (aliphatic) functional group counts 2D binary fingerprints 1 BBCH-0 muber of adehydes (aliphatic) functional group counts 2D binary fingerprints					
MOR5.1 3)nCq number of total quaternary C(sp3) functional group counts 1 El:p 11 st component accessibility directional WHIM index / weighted by atomic polarizabilities WHIM descriptors 1 RDF050v Radial Distribution Function - 5.0 / weighted by atomic van der Waals volumes RDF descriptors 2 PW3 pathwalk 3 - Radic shape index molecular properties 1 G/0.08 GRb2e-Viswanadhan-Wendoloski drug-like index at 80% molecular properties 1 G/0.08 GRb2e-Viswanadhan-Wendoloski drug-like index at 80% molecular properties 1 G/0.08 GRb2e-Viswanadhan-Wendoloski drug-like index at 80% molecular properties 1 HKV H autocorrelation o lag 6 / weighted by atomic masses GETAWAY descriptors 1 MAT33m Moran autocorrelation o lag 6 / weighted by atomic wan der Waals volumes Burden regenvalues 1 Atype_C_18 Number of Carbon Type 18 Burden matrix / weighted by atomic van der Waals volumes Burden regenvalues 1 RDF130u Radial Distribution Function - 13.0 / unweighted functional group counts RDF descriptors 1 RDF130u Radial Distribution Function - 13.0 / unweighted functional group counts RDF descriptors 1 RDF130u Radial Distribution Function - 13.0 / unweighted functional group counts geometric descriptors 1 RDF130u Radial Distribution Function - 13.0 / unweighte		4 Mor22e	3D-MoRSE - signal 22 / weighted by atomic Sanderson electronegativities	3D-MoRSE descriptors	
I RDF050v Radial Distribution Function - 5.0 / weighted by atomic van der Waals volumes RDF descriptors I PW3 path/walk 3 - Radic shape index topological descriptors I GVWAI-80 Ghose-Viswanadhan-Wendoloski drug-like index at 80% molecular properties I C-008 CHR2X atom-centred fragments I H4W H autocorrelation - lag 3 (/ weighted by atomic van der Waals volumes GETAWAY descriptors 1 MATS3m Moran autocorrelation - lag 3 (/ weighted by atomic van der Waals volumes GETAWAY descriptors 1 MATS3m Number of Carbon Type 18 Burden matrix / weighted by atomic van der Waals volumes Burden eigenvalues 1 RDF130u Radial Distribution Function - 13.0 / unweighted topological RDF descriptors 1 RDF130u Radial Distribution Function - 13.0 / unweighted patientic) functional group counts 1 RDF130u Radial Distribution Function - 13.0 / unweighted topological distance 05 2D binary fingerprints 1 RDFC10 number of adeptides (aliphatic) functional group counts 2D fraquenty connectivity indices 1 RDFC10 number of carboxylic acids (aliphatic) functional group counts 2D fraquency fingerprints <		3 nCq	number of total quaternary C(sp3)	functional group counts	
MOR5.1 2 PW3 path/walk 3 - Randic shape index topological descriptors 1 G/WM1-80 Ghose-Viswanadhan-Wendoloski drug-like index at 80% anom-centred fragments 1 C-008 CHR2X atom-centred fragments 1 Hóv H autocorrelation o lag 3 / weighted by atomic wan der Waals volumes GETWAV descriptors 1 Hóv H autocorrelation o lag 3 / weighted by atomic wan der Waals volumes 2D autocorrelations 1 Hóv H autocorrelation o lag 3 / weighted by atomic wan der Waals volumes 2D autocorrelations 1 MATS3m Moran autocorrelation - lag 3 / weighted by atomic wan der Waals volumes Burden eigenvalues 1 RbF130 Radial Distribution Function - 1.0 / unweighted RDF descriptors 1 RbF10 number of aldehydes (aliphatic) functional group counts 1 RbFC0-01 presence/absence of C - 0 at topological distance 05 2D binary fingerprints 1 MKC5.1 inRCOOH number of carboxylic acids (aliphatic) functional group counts 1 RbFC0-01 frequency of C - 0 at topological distance 07 2D frequency fingerprints 2D frequency fingerprints 2D frequency fingerprints 2D frequency fingerprints 1 PO7C0-01 frequency of C - 0 at topological distance 04 2D frequency fingerprints 1 Po4(C-0) frequency of C - 0 at topological distance 04 2D frequency fingerprints					
I GVWAI-80 Gnose-Viswanadhan-Wendolośki drug-like index at 80% molecular properties atom-centred fragments I C-008 C-RR2X atom-centred fragments I H6V H autocorrelation of lag 6 / weighted by atomic wan der Waals volumes GETAWAY descriptors I MATS3m Moran autocorrelation - lag 3 / weighted by atomic masses GETAWAY descriptors I MATS3m Number of Carbon Type 18 atom-centred fragments I BEH*3 highest eigenvalues. 3 of Burden matrix / weighted by atomic van der Waals volumes Burden eigenvalues RDF130u Radial Distribution Function - 13.0 / unweighted RDF RDF descriptors I IRCH0 number of aldehydes (aliphatic) functional group counts RDF descriptors I IRCF presence/absence of C - 0 at topological distance 05 2D binary fingerprints geometrical descriptors I IRCC nolecular eccentricity average connectivity indices connectivity indices I IRCC00 number of adebydical distance 07 2D fraquency fingerprints 2D fraquency fingerprints I IRCC01 frequency of C - 0 at topological distance 04 2D fraquency fingerprints 2D fraquency fingerprints I POCC01 frequency of C			path/walk 3 - Randic shape index		
HGC CHR2X atom-centred fragments 1 HGV H autocorrelation of lag 6 / weighted by atomic wander Waals volumes GETAWAY descriptors 1 MATS3m Moran autocorrelation - lag 3 / weighted by atomic masses 2D autocorrelations 1 Atype C_18 Number of Carbon Type 18 atomtype 18 1 RDF130U Radial Distribution Function - 1.0 / unweighted by atomic wander Waals volumes Burden elgenvalues 1 RDF130U Radial Distribution Function - 1.0 / unweighted functional group counts 1 RDF101 number of aldehydes (aliphatic) functional group counts 1 RDF201 molecular eccentricity geometrical descriptors 1 MRC5.1 InRCOH number of carboxylic acids (aliphatic) functional group counts 1 RDF0100 number of carboxylic acids (aliphatic) functional group counts 1 RDF0100 number of carboxylic acids (aliphatic) functional group counts 1 RDF0100 number of carboxylic acids (aliphatic) functional group counts 1 RDF01000 frequency of C - 0 at topological distance 07 2D frequency fingerprints 2D frequency fingerprints 2D frequency fingerprints 2D frequency fingerprints 1 RDF01000 frequency of C - 0 at topological distance 07 2D frequency fingerprints 1 F04[C-0] frequency of C - 0 at topological distance 04 2D fr		1 GVWAI-80	Ghose-Viswanadhan-Wendoloski drug-like index at 80%	molecular properties	
MAR5.1 IMATS3m Moran autocorrelation - lag 3 / weighted by atomic masses 2D autocorrelations atomtypes (Cerius2) I Atype C_18 Number of Carbon Type 18 atomtypes (Cerius2) I BEHv3 highest eigenvalue n.3 of Burden matrix / weighted by atomic van der Waals volumes Burden eigenvalues I ROF130U Radial Distribution Function - 1.3 0 / unweighted RDF descriptors I ROF101 number of aldehydes (aliphatic) functional group counts I BOF30-01 presence/absence of C - 0 at topological distance 05 2D biary fingerprints I MCC molecular eccentricity geometrical descriptors I MRC5.1 inRCOOH number of carboxylic acids (aliphatic) functional group counts I nRCOOH number of carboxylic acids (aliphatic) functional group counts I nRCOOH number of carboxylic acids (aliphatic) functional group counts I nRCOOH number of carboxylic acids (aliphatic) functional group counts I F04[C-0) frequency of C - 0 at topological distance 07 2D frequency fingerprints I Povid[C-0] frequency of C - 0 at topological distance 04 2D frequency fingerprints I Povid[C-0] frequency of C - 0 at topological distance 04 2D frequency fingerprints I Povid[C-0] frequency fingerprints 3D-MoRSE escriptors I Mori7e 3D-Mo		1 C-008	CHR2X	atom-centred fragments	
I Atype_C_18 Number of Carbon Type 18 atomtypes (Cerius2) I BBH+3 highest eigenvalues.n 3 of Burden matrix / weighted by atomic van der Waals volumes Burden eigenvalues I RDF130u Radial Distribution Function - 13.0 / unweighted Burden eigenvalues I RDF130u Radial Distribution Function - 13.0 / unweighted Burden eigenvalues I RDF130u Radial Distribution Function - 13.0 / unweighted RDF descriptors I RDF130u Radial Distribution Function - 13.0 / unweighted Thome of atomotives I RDF130u presence/absence of C - 0 at topological distance 05 2D binary fingerprints I MECc molecular eccentricity average connectivity indices 1 RDF10-1 interguency of C - 0 at topological distance 07 2D frequency fingerprints 1 F04(C-0) frequency of C - 0 at topological distance 04 2D frequency fingerprints 1 F04(C-0) frequency of C - 0 at topological distance 04 2D frequency fingerprints 1 Ox57 phenol / enol / carboxyl del atomic carboxyl atomic Sanderson electronegativities 1 Mor17e 3D-MoRSE - signal 17 / weighted by atomic Sanderson electronegativities 3D-MoRSE descriptors		1 H6v	H autocorrelation of lag 6 / weighted by atomic van der Waals volumes		
MOR5.1 1 BEHv3 1 highest eigenvalue n. 3 of Burden matrix / weighted by atomic van der Waals volumes BDF descriptors 1 RCF1300 Radia Distribution Function -1 3.0 / unweighted 1 RCF100 1 RC					
I RDF130u Radial Distribution Function - 13.0 / unweighted RDF descriptors I RRCH0 number of aldehydes (aliphatic) functional group counts I B05(C-0) presence/absence of C - 0 at topological distance 05 2D binary fingerprints I MCCc molecular eccentricity average connectivity indices I NCCC number of aldehydes (aliphatic) functional group counts I NCCC number of achory(lic adds (aliphatic) functional group counts I RCOC1 frequency of C - 0 at topological distance 07 2D frequency fingerprints I F04(C-0) frequency of C - 0 at topological distance 04 2D frequency fingerprints I F04(C-0) frequency of C - 0 at topological distance 04 2D frequency fingerprints I 0-057 phenol / enol / carboxyl 04 2D frequency fingerprints I 0-057 abenol / carboxyl 04 atom-centred fragments I Morize 3D-MoRSE - signal 17 / weighted by atomic Sanderson electronegativities 3D-MoRSE descriptors <td></td> <td>1 BEHv3</td> <td>highest eigenvalue n. 3 of Burden matrix / weighted by atomic van der Waals volumes</td> <td>Burden eigenvalues</td> <td></td>		1 BEHv3	highest eigenvalue n. 3 of Burden matrix / weighted by atomic van der Waals volumes	Burden eigenvalues	
NOR5.1 1 [805[C-O] presence/absence of C - O at topological distance 05 2D binary fingerprints geometrical descriptors connectivity indices MOR5.1 1 X2A average connectivity index chi-2 connectivity indices 1 RCOOH number of carboxylic acids (aliphatic) functional group counts 1 [07[C-O] frequency of C - O at topological distance 04 2D frequency fingerprints 1 [07]C-O37 phenol / end / carboxylic carbosylic distance 04 2D frequency fingerprints 1 [07]C-O37 phenol / end / carboxylic distance 04 atomic enterted fragments 1 [07]C-O37 phenol / end / carboxylic absence 04 atomic enterted fragments 1 [07]C-O37 phenol / end / carboxylic absence 04 atomic enterted fragments 1 [07]C-O37 phenol / end / carboxylic absence 04 atomic enterted fragments 1 [07]C-O37 phenol / end / carboxylic absence 04 atomic enterted fragments 1 [07]C-O37 phenol / end /		1 RDF130u	Radial Distribution Function - 13.0 / unweighted	RDF descriptors	
I MEcc 1 X2A molecular eccentricity average connectivity index chi-2 geometrical descriptors connectivity index chi-2 MOR5.1 InRCOOH number of carboxylic acids (aliphatic) 1 F07(C-0) frequency of C - 0 at topological distance 07 1 F04(C-0) frequency of C - 0 at topological distance 04 2D frequency fingerprints 1 F04(C-0) 1 o-057 phenol / enol / carboxyl 1 Mor17e 3D-MoRSE - signal 17 / weighted by atomic Sanderson electronegativities					
MOR5.1 1 X2A average connectivity index chi-2 connectivity indices I nRCOOH number of carboxylic acids (aliphatic) 1 F07[C-0] frequency of C - 0 at topological distance 07 1 F04[C-0] frequency of C - 0 at topological distance 04 1 0-057 phenol / enol / carboxylic Acids and C - 0 at topological distance 04 1 0-057 phenol / enol / carboxylic acids and constrained at atom-centred fragments 1 0-057 phenol / enol / carboxylic acids and constrained at atom-centred fragments 1 0-057 phenol / enol / carboxylic acids and constrained atom-centred fragments 1 0-057 phenol / enol / carboxylic acids and constrained atom-centred fragments 1 0-057 phenol / enol / carboxylic acids and constrained atom-centred fragments 1 0-057 phenol / enol / carboxylic acids and constrained atom-centred fragments 1 0-057 phenol / enol / carboxylic acids and constrained atom-centred fragments 1 0-057 phenol / enol / carboxylic acids atom-centred fragments 1 0-057 phenol / enol / carboxylic acids atom-centred fragments 1 0-057 phenol / enol / carboxylic acids atom-centred fragments 1 0-057 phenol / enol / carboxylic acids atom-centred fragments 1 0-057 phenol / enol / carboxylic acids atom-centred fragments 1 0-057 phenol / enol / carboxylic acids atom-centred fragments 1 0-057 phenol / enol / carboxylic acids atom-centred fragments 1 0-057 phenol / enol / carboxylic acids atom-centred fragments 1 0-057 phenol / enol / carboxylic acids atom-centred fragments 1 0-057 phenol / enol / carboxylic acids atom-centred fragments 1 0-057 phenol / enol / carboxylic acids atom-centred fragments 1 0-057 phenol / enol / carboxylic acids atom-centred fragments 1 0-057 phenol / enol / carboxylic acids atom-centred fragments 1 0-057 phenol / enol / carboxylic acids atom-centred fragments 1 0-057 phenol / enol / carboxylic acids atom-centred fragments 1 0-057 phenol / enol / carboxylic acids atom-centred fragments 1 0-057 phenol / enol / carboxylic acids atom-centred fragments 1 0-057 phenol / enol / carboxylic acids atom-centred fr					
MOR5.1 InRCOOH number of carboxylic acids (aliphatic) functional group counts 1 F07(C-0) frequency of C - 0 at topological distance 07 2D frequency fingerprints 1 F04(C-0) frequency of C - 0 at topological distance 04 2D frequency fingerprints 1 0-057 phenol / enol / carboxyl 0H atom-centred fragments 1 Mor17e 3D-MoRSE - signal 17 / weighted by atomic Sanderson electronegativities 3D-MoRSE descriptors			average connectivity index chi-2	connectivity indices	
1 InRCOOH number of carboxylic acids (aliphatic) functional group counts 1 F07(C-O) frequency of C - 0 a topological distance 07 2D frequency finagerprints 1 F04(C-O) frequency of C - 0 a topological distance 04 2D frequency finagerprints 1 O-057 phenol / enol / carboxyl 0H atom-centred fragments 1 Mor17e 3D-MoRSE - signal 17 / weighted by atomic Sanderson electronegativities 3D-MoRSE descriptors					
1 [F07[C-0] frequency of C - O at topological distance 07 2D frequency fingerprints 1 [F04[C-0] frequency of C - O at topological distance 04 2D frequency fingerprints 1 [O-057 phenol / enol / carboxyl OH atom-centred fragments 1 [Mor17e 3D-MoRSE - signal 17 / weighted by atomic Sanderson electronegativities 3D-MoRSE descriptors	MUR5.1	1 пРСООН	number of carboxylic acids (alinbatic)	functional group counts	
1 [F04[C-O] frequency of C - O at topological distance 04 2D frequency fingerprints 1 0-057 phenol / enol / carboxyi 0H atom-centred fragments 1 Mor17e 3D-MoRSE - signal 17 / weighted by atomic Sanderson electronegativities 3D-MoRSE descriptors		1 F07[C-0]	frequency of C - O at topological distance 07	2D frequency fingerprints	
10-057 phenol / enol / carboxyl OH atom-centred fragments 1 Mor17e 3D-MoRSE - signal 17 / weighted by atomic Sanderson electronegativities 3D-MoRSE descriptors		1 F04[C-0]	frequency of C - O at topological distance 04	2D frequency fingerprints	
ORIA1 ORIAN		1 mor1/e	SuperionSE - Signal 17 / weighted by atomic Sanderson electronegativities	SU-MOKSE descriptors	
	OR1A1				

Table 3.15 Continued

914158. Bit Part State Stat		2 HATS8u	leverage-weighted autocorrelation of lag 8 / unweighted	GETAWAY descriptors	3
1 Espin-Bid Spitchal moment 06 from dege adj. matrix weighted by duois masses edge adj.ecory indices by durine ignerulation 2 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2 0 1 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2D frequency index		1 F1s	1st component accessibility directional WHIM index / weighted by atomic electrotopological states	WHIM descriptors	3
1 Espin-Bid Spitchal moment 06 from dege adj. matrix weighted by duois masses edge adj.ecory indices by durine ignerulation 2 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2 0 1 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2D frequency index					3
1 Espin-Bid Spitchal moment 06 from dege adj. matrix weighted by duois masses edge adj.ecory indices by durine ignerulation 2 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2 0 1 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2D frequency index					-
1 Espin-Bid Spitchal moment 06 from dege adj. matrix weighted by duois masses edge adj.ecory indices by durine ignerulation 2 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2 0 1 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2D frequency index					1
1 Espin-Bid Spitchal moment 06 from dege adj. matrix weighted by duois masses edge adj.ecory indices by durine ignerulation 2 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2 0 1 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2D frequency index					2
1 Espin-Bid Spitchal moment 06 from dege adj. matrix weighted by duois masses edge adj.ecory indices by durine ignerulation 2 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2 0 1 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2D frequency index					2
1 Espin-Bid Spitchal moment 06 from dege adj. matrix weighted by duois masses edge adj.ecory indices by durine ignerulation 2 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2 0 1 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2D frequency index					1
1 Espin-Bid Spitchal moment 06 from dege adj. matrix weighted by duois masses edge adj.ecory indices by durine ignerulation 2 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2 0 1 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2D frequency index		1 Mor21p	3D-MoRSE - signal 21 / weighted by atomic polarizabilities	3D-MoRSE descriptors	3
1 Espin-Bid Spitchal moment 06 from dege adj. matrix weighted by duois masses edge adj.ecory indices by durine ignerulation 2 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2 0 1 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2D frequency index		1 JGI3	mean topological charge index of order3	topological charge indices	2
1 Espin-Bid Spitchal moment 06 from dege adj. matrix weighted by duois masses edge adj.ecory indices by durine ignerulation 2 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2 0 1 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2D frequency index					1
1 Espin-Bid Spitchal moment 06 from dege adj. matrix weighted by duois masses edge adj.ecory indices by durine ignerulation 2 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2 0 1 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2D frequency index					3
1 Espin-Bid Spitchal moment 06 from dege adj. matrix weighted by duois masses edge adj.ecory indices by durine ignerulation 2 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2 0 1 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2D frequency index					1
1 Espin-Bid Spitchal moment 06 from dege adj. matrix weighted by duois masses edge adj.ecory indices by durine ignerulation 2 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2 0 1 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2D frequency index					2
1 Espin-Bid Spitchal moment 06 from dege adj. matrix weighted by duois masses edge adj.ecory indices by durine ignerulation 2 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2 0 1 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2D frequency index			R maximal autocorrelation of lag 6 / weighted by atomic masses		3
1 Espin-Bid Spitchal moment 06 from dege adj. matrix weighted by duois masses edge adj.ecory indices by durine ignerulation 2 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2 0 1 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2D frequency index		1 RDF095u	Radial Distribution Function - 9.5 / unweighted	RDF descriptors	3
1 Espin-Bid Spitchal moment 06 from dege adj. matrix weighted by duois masses edge adj.ecory indices by durine ignerulation 2 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2 0 1 08232 1 St.component accessibility directional WHM index / weighted by atomic electrotopological states 2D frequency index		1 nRCOOH	number of carboxylic acids (aliphatic)	functional group counts	1
OR.222 Ist component accessibility directional WHM index / weighted by atomic electrotopological states WHM descriptors 3 SILE 1 confic-0-1 requency of C - 0 at topological (states 6) 20 requency fragments 12 1 COSIC-0-1 requency of C - 0 at topological (states 6) 20 requency fragments 12 1 COSIC-0-1 requency of C - 0 at topological (states 6) repological (states 6) 1 COSIC-0-1 requency of C - 0 at topological (states 6) repological (states 6) 1 COSIC-0-1 requency fragments 1 1 Hill H attached to ables C CETXWV descriptors 3 2 H-499 H attached to CS(sp)/C(Sp2		1 ESpm06d	Spectral moment 06 from edge adj. matrix weighted by dipole moments	edge adjacency indices	2
OR.222 Ist component accessibility directional WHM index / weighted by atomic electrotopological states WHM descriptors 3 SILE 1 confic-0-1 requency of C - 0 at topological (states 6) 20 requency fragments 12 1 COSIC-0-1 requency of C - 0 at topological (states 6) 20 requency fragments 12 1 COSIC-0-1 requency of C - 0 at topological (states 6) repological (states 6) 1 COSIC-0-1 requency of C - 0 at topological (states 6) repological (states 6) 1 COSIC-0-1 requency fragments 1 1 Hill H attached to ables C CETXWV descriptors 3 2 H-499 H attached to CS(sp)/C(Sp2					2
Bits 1st component accessibility directional WHH index / weighted by atomic electrotopological states WHH descriptors 3 IDEX d COMRA2 value / weighted by atomic value Wasks volumes genometrical descriptors 3 IDEX d COMRA2 value / weighted by atomic value Wasks volumes genometrical descriptors 3 IDEX d COMRA2 value / weighted by atomic value Gene Value value / weighted by atomic value Wasks volumes genometrical descriptors 3 IDEX d COMRA2 value / weighted by atomic masses genometrical descriptors 3 IDEX d COMRA2 value / weighted by atomic washe genometrical descriptors 3 IDEX d COMRA2 value / weighted by atomic value of washs volumes genometrical descriptors 3 IDEX performation of lag / weighted by atomic masses GGTAWAY descriptors 3 IDEX performation of lag / weighted by atomic masses GGTAWAY descriptors 3 IDEX performation of lag / weighted by atomic masses GGTAWAY descriptors 3 IDEX performation of lag / weighted by atomic masses GGTAWAY descriptors 3 IDEX performatinto flag / weighted by atomic masses GGTAWAY desc		1 DECING	lowest eigenvalue in. 5 of barden matrix / weighted by atomic masses	buiden eigenvalues	-
Bits 1st component accessibility directional WHH index / weighted by atomic electrotopological states WHH descriptors 3 IDEX d COMRA2 value / weighted by atomic value Wasks volumes genometrical descriptors 3 IDEX d COMRA2 value / weighted by atomic value Wasks volumes genometrical descriptors 3 IDEX d COMRA2 value / weighted by atomic value Gene Value value / weighted by atomic value Wasks volumes genometrical descriptors 3 IDEX d COMRA2 value / weighted by atomic masses genometrical descriptors 3 IDEX d COMRA2 value / weighted by atomic washe genometrical descriptors 3 IDEX d COMRA2 value / weighted by atomic value of washs volumes genometrical descriptors 3 IDEX performation of lag / weighted by atomic masses GGTAWAY descriptors 3 IDEX performation of lag / weighted by atomic masses GGTAWAY descriptors 3 IDEX performation of lag / weighted by atomic masses GGTAWAY descriptors 3 IDEX performation of lag / weighted by atomic masses GGTAWAY descriptors 3 IDEX performatinto flag / weighted by atomic masses GGTAWAY desc					
0R2W1 1 F06(C-0) frequency of C - 0 at topological distance 06 20 Frequency freqreprints 2 0R3W1 1 CD5FV 4 COMMA2 value / weighted by atomic wind er Wals volumes geometrical descriptors 3 1 CD5FV 4 COMMA2 value / weighted by atomic wind er Wals volumes geometrical descriptors 3 1 CD5FN 4 COMMA2 value / weighted by atomic masses geometrical descriptors 3 1 EBFV6 1 hightest eigenvalues 8 durine marks/ weighted by atomic value 06 atom-centred frequents 1 2 H-049 H atocorrelation of Big J / weighted by atomic masses GGTMAW7 descriptors 3 1 BBFV6 H atocorrelation of Big J / weighted by atomic masses GGTAWA7 descriptors 3 2 F01(C-C) frequency of C - C at topological distance 05 20 Frequency freqreprints 2 2 F01(C-C) frequency of C - C at topological distance 05 20 Frequency freqreprints 2 2 F01(C-C) frequency of C - C at topological distance 05 20 Frequency freqreprints 2 2 F01(C-C) frequency of C - C at topological distance 05 20 Frequency freqreprints 2 2 F05(C-C) presenci/absence of C -	OR2J2				
0R2W1 1 F06(C-0) frequency of C - 0 at topological distance 06 20 Frequency freqreprints 2 0R3W1 1 CD5FV 4 COMMA2 value / weighted by atomic wind er Wals volumes geometrical descriptors 3 1 CD5FV 4 COMMA2 value / weighted by atomic wind er Wals volumes geometrical descriptors 3 1 CD5FN 4 COMMA2 value / weighted by atomic masses geometrical descriptors 3 1 EBFV6 1 hightest eigenvalues 8 durine marks/ weighted by atomic value 06 atom-centred frequents 1 2 H-049 H atocorrelation of Big J / weighted by atomic masses GGTMAW7 descriptors 3 1 BBFV6 H atocorrelation of Big J / weighted by atomic masses GGTAWA7 descriptors 3 2 F01(C-C) frequency of C - C at topological distance 05 20 Frequency freqreprints 2 2 F01(C-C) frequency of C - C at topological distance 05 20 Frequency freqreprints 2 2 F01(C-C) frequency of C - C at topological distance 05 20 Frequency freqreprints 2 2 F01(C-C) frequency of C - C at topological distance 05 20 Frequency freqreprints 2 2 F05(C-C) presenci/absence of C -	1				3
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3	1	1 F06[C-0]	frequency of C - O at topological distance 06	2D frequency fingerprints	2
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3	1				3
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3	1		mean tonological charge index of order5		5
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3	1				
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3	1				1
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3	1				3
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3	1				3
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3	1	1 BEHv8	highest eigenvalue n. 8 of Burden matrix / weighted by atomic van der Waals volumes	Burden eigenvalues	2
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3	1	2 H-049			1
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3	1				5
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3					-
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3					1
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3					5
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3					3
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3		2 F01[C-C]	frequency of C - C at topological distance 01	2D frequency fingerprints	2
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3		2 HATS5p	leverage-weighted autocorrelation of lag 5 / weighted by atomic polarizabilities	GETAWAY descriptors	3
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3					2
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3					5
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3					2
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3					1
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3			leverage-weighted autocorrelation of lag 0 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors	3
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3		1 R7p+	R maximal autocorrelation of lag 7 / weighted by atomic polarizabilities	GETAWAY descriptors	3
OR2W1 2 Disay fingerprints 2 2 B05[C-C] presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic masses RDF descriptors 3 1 RDF110m Radial Distribution Function - 11.0 / weighted by atomic masses RDF descriptors 3 1 RZPM R maximal autocorrelation of lag 7 / weighted by atomic masses CETMWV descriptors 3 1 MATS5p Moran autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 0 RZPC Rautocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 3 R/Pc R autocorrelation of lag 7 / weighted by atomic masses GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 1 Index Balaban Y index Balaban Y index GETAWV descriptors 3 2 RLP4ar R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3		1 VEA2	average eigenvector coefficient sum from adjacency matrix	eigenvalue-based indices	2
PoSIC-C1 presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic polarizabilities BTAWA Reverage-weighted autocorrelation of lag 2 / weighted by atomic masses RDF descriptors 3 1 R2D-1 Ravianal autocorrelation of lag 2 / weighted by atomic masses RDF descriptors 3 1 MATS5p Moran autocorrelation - lag 5 / weighted by atomic masses GETAWAY descriptors 3 1 MATS5p Moran autocorrelation - lag 5 / weighted by atomic masses GETAWAY descriptors 3 1 MATS5m Inverage-weighted autocorrelation of lag 3 / weighted by atomic masses GETAWAY descriptors 3 3 R7e R R autocorrelation of lag 7 / weighted by atomic sanderson electronegativities GETAWAY descriptors 3 1 Mrdex Balaban Y index Index for Daphnia base-line toxicity from MLOGP (mmol/l) molecular properties 1 1 Rofe R autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3 3 2 RLP48 Werhaar model of Daphnia base-line toxicity from MLOGP (mmol/l) molecular properties 1 1 Rofm R autocorre					
PoSIC-C1 presence/absence of C - C at topological distance 05 2D binary fingerprints 2 2 HATS5p leverage-weighted autocorrelation of lag 6 / weighted by atomic polarizabilities BTAWA Reverage-weighted autocorrelation of lag 2 / weighted by atomic masses RDF descriptors 3 1 R2D-1 Ravianal autocorrelation of lag 2 / weighted by atomic masses RDF descriptors 3 1 MATS5p Moran autocorrelation - lag 5 / weighted by atomic masses GETAWAY descriptors 3 1 MATS5p Moran autocorrelation - lag 5 / weighted by atomic masses GETAWAY descriptors 3 1 MATS5m Inverage-weighted autocorrelation of lag 3 / weighted by atomic masses GETAWAY descriptors 3 3 R7e R R autocorrelation of lag 7 / weighted by atomic sanderson electronegativities GETAWAY descriptors 3 1 Mrdex Balaban Y index Index for Daphnia base-line toxicity from MLOGP (mmol/l) molecular properties 1 1 Rofe R autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3 3 2 RLP48 Werhaar model of Daphnia base-line toxicity from MLOGP (mmol/l) molecular properties 1 1 Rofm R autocorre	0R2W1				
1 R2m+ 1 MATS5p R maximal autocorrelation of lag 2 / weighted by atomic masses GETAWAY descriptors 3 0R5P3 - - - Dutocorrelation of lag 3 / weighted by atomic polarizabilities 2D autocorrelations 2D 0R5P3 -	012111			2D hisson financists	
1 R2m+ 1 MATS5p R maximal autocorrelation of lag 2 / weighted by atomic masses GETAWAY descriptors 3 0R5P3 - - - Dutocorrelation of lag 3 / weighted by atomic polarizabilities 2D autocorrelations 2D 0R5P3 -					2
1 R2m+ 1 MATS5p R maximal autocorrelation of lag 2 / weighted by atomic masses GETAWAY descriptors 3 0R5P3 - - - Dutocorrelation of lag 3 / weighted by atomic polarizabilities 2D autocorrelations 2D 0R5P3 -					3
ORSP3 Moran autocorrelation - lag 5 / weighted by atomic polarizabilities ZD autocorrelations Z ORSP3 2 Moran autocorrelation - lag 5 / weighted by atomic polarizabilities ZD autocorrelations Z 0RSP3 2 number of non-aromatic conjugated C(sp2) functional group counts 1 1 HATS3m leverage-weighted autocorrelation of lag 3 / weighted by atomic masses GETAWAY descriptors 3 3 R7a R autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities GETAWAY descriptors 3 1 R7a+ R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3 2 BUTD48 Verhaar model of Daphnis base-line toxicity from MLOGP (mmol/l) molecular properties 1 1 H-047 H attached to C1(sp3)/C0(sp2) atom-centred fragments 1 1 H-047 H attached to C1(sp3)/C0(sp2) atom-centred fragments 2 1 Nor10u 3D AdR52 gatomic masses GETAWAY descriptors 3 3 GATS2m Getary autocorrelation - lag 2 / weighted by atomic masses gatometrical descriptors 3 1 Nor10u 3D AdR52 gatom autocorelation s		1 RDF110m	Radial Distribution Function - 11.0 / weighted by atomic masses	RDF descriptors	3
ORSP3 Moran autocorrelation - lag 5 / weighted by atomic polarizabilities ZD autocorrelations Z ORSP3 2 Moran autocorrelation - lag 5 / weighted by atomic polarizabilities ZD autocorrelations Z 0RSP3 2 number of non-aromatic conjugated C(sp2) functional group counts 1 1 HATS3m leverage-weighted autocorrelation of lag 3 / weighted by atomic masses GETAWAY descriptors 3 3 R7a R autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities GETAWAY descriptors 3 1 R7a+ R maximal autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3 2 BUTD48 Verhaar model of Daphnis base-line toxicity from MLOGP (mmol/l) molecular properties 1 1 H-047 H attached to C1(sp3)/C0(sp2) atom-centred fragments 1 1 H-047 H attached to C1(sp3)/C0(sp2) atom-centred fragments 2 1 Nor10u 3D AdR52 gatomic masses GETAWAY descriptors 3 3 GATS2m Getary autocorrelation - lag 2 / weighted by atomic masses gatometrical descriptors 3 1 Nor10u 3D AdR52 gatom autocorelation s	1	1 R2m+	R maximal autocorrelation of lag 2 / weighted by atomic masses	GETAWAY descriptors	3
ORSP3 2 Incomposition Participate Functional group counts 1 2 number of non-aromatic conjugated C(sp2) functional group counts 1	1				2
2 Incconj number of non-aromatic conjugated C(sp2) functional group counts 1 1 HATS3n leverage-weighted autocorrelation of lag 3 / weighted by atomic masses GETAWAY descriptors 3 3 R7a R autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities GETAWAY descriptors 3 1 Vindex Balaban Y index Information indices 2 1 Kindex R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities GETAWAY descriptors 3 2 BLTD48 Verhaar model of Daphnia base: GETAWAY descriptors 3 1 Ho47 H attached to C1(sp3)/C0(sp2) Batomer enter fragments 1 1 Ho47 H attached to C1(sp3)/C0(sp2) Batomer enter fragments 3 1 Ho47 H attached to C1(sp3)/C0(sp2) Batomer enter fragments 3 3 GATS2m Geary autocorrelation in ag / weighted by atomic masses GETAWAY descriptors 3 3 GATS2m dC0MMAQ value / weighted by atomic masses geometrical descriptors 3 1 BAD10 Montol 10 Junveighted by atomic polarizabilities RDF descriptors 3 1 BAD10-01 presence/absence 07 0- ot attopological distance 04 2D binary fingerprints <	1	1			-
2 Incconj number of non-aromatic conjugated C(sp2) functional group counts 1 1 HATS3n leverage-weighted autocorrelation of lag 3 / weighted by atomic masses GETAWAY descriptors 3 3 R7a R autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities GETAWAY descriptors 3 1 Vindex Balaban Y index Information indices 2 1 Kindex R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities GETAWAY descriptors 3 2 BLTD48 Verhaar model of Daphnia base: GETAWAY descriptors 3 1 Ho47 H attached to C1(sp3)/C0(sp2) Batomer enter fragments 1 1 Ho47 H attached to C1(sp3)/C0(sp2) Batomer enter fragments 3 1 Ho47 H attached to C1(sp3)/C0(sp2) Batomer enter fragments 3 3 GATS2m Geary autocorrelation in ag / weighted by atomic masses GETAWAY descriptors 3 3 GATS2m dC0MMAQ value / weighted by atomic masses geometrical descriptors 3 1 BAD10 Montol 10 Junveighted by atomic polarizabilities RDF descriptors 3 1 BAD10-01 presence/absence 07 0- ot attopological distance 04 2D binary fingerprints <	OBED2				
1 HATS3m leverage-weighted autocorrelation of lag 7 / weighted by atomic masses GETAWAY descriptors 3 3 R7a R autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities GETAWAY descriptors 3 1 Nrdex Balaban Y index Information indices 2 2 R7c+ R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities GETAWAY descriptors 3 2 BTD48 Verhaar model of Daphnia base-line toxicity from MLOGP (mmol/I) molecular properties 1 1 R6m R autocorrelation of lag 6 / weighted by atomic masses GETAWAY descriptors 3 1 H-047 H attached to C1(593)/C0(502) atom-centred fragments 1 1 A4m R autocorrelation of lag 4 / weighted by atomic masses GETAWAY descriptors 3 3 GATS2m Geary autocorrelation - lag 2 / weighted by atomic masses geometrical descriptors 3 3 GATS2m Geary autocorrelation - lag 2 / weighted by atomic masses geometrical descriptors 3 1 DSPm d COMMA2 value / weighted by atomic masses geometrical descriptors 3 2 Mor10u 3D AMRSE - signal 10 / unweighted by atomic masses geometrical descriptors 3 1 DAPGN Radia Distribution Function - 5.0 / weighted by atomic masses Butocorrelation 10 a 2 / weighted by atomic masses Butocorrela	UK3F3				
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3	1				1
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3	1				3
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3	1	3 R7e	R autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors	3
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3				information indicos	- i
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3		1 11Yindex			
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3					23
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3		1 R7e+	R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors	23
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3		1 R7e+ 2 BLTD48	R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities Verhaar model of Daphnia base-line toxicity from MLOGP (mmol/I)	GETAWAY descriptors molecular properties	231
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3		1 R7e+ 2 BLTD48 1 R6m	R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities Verhaar model of Daphnia base-line toxicity from MLOGP (mmol/l) R autocorrelation of lag 6 / weighted by atomic masses	GETAWAY descriptors molecular properties GETAWAY descriptors	2 3 1 3
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3		1 R7e+ 2 BLTD48 1 R6m 1 H-047	R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities Verhaar model of Daphnia base-line toxicity from MLOGP (mmol/I) R autocorrelation of lag 6 / weighted by atomic masses H attached to C1(sp3)/C0(sp2)	GETAWAY descriptors molecular properties GETAWAY descriptors atom-centred fragments	2 3 1 3 1
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3		1 R7e+ 2 BLTD48 1 R6m 1 H-047	R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities Verhaar model of Daphnia base-line toxicity from MLOGP (mmol/I) R autocorrelation of lag 6 / weighted by atomic masses H attached to C1(sp3)/C0(sp2)	GETAWAY descriptors molecular properties GETAWAY descriptors atom-centred fragments	2 3 1 3 1 3
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3		1 R7e+ 2 BLTD48 1 R6m 1 H-047 1 R4m	R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities Verhaar model of Daphnia base-line toxicity from MLOGP (mmol/l) R autocorrelation of lag 6 / weighted by atomic masses H attached to C1(sp3)/C0(sp2) R autocorrelation of lag / weighted by atomic masses	GETAWAY descriptors molecular properties GETAWAY descriptors atom-centred fragments GETAWAY descriptors	2 3 1 3 1 3 2
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3		1 R7e+ 2 BLTD48 1 R6m 1 H-047 1 R4m 3 GATS2m	R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities Verhaar model of Daphnia base-line toxicity from MLOGP (mmol/l) R autocorrelation of lag 6 / weighted by atomic masses H attached to C1(593)(C0(592) R autocorrelation - lag 4 / weighted by atomic masses Geary autocorrelation - lag 2 / weighted by atomic masses	GETAWAY descriptors molecular properties GETAWAY descriptors atom-centred fragments GETAWAY descriptors 2D autocorrelations	2 3 1 3 1 3 2 3
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3		1 R7e+ 2 BLTD48 1 R6m 1 H-047 1 R4m 3 GATS2m 1 DISPm	R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities Verhaar model of Daphina base-line toxicity from MLOGP (mmol/l) R autocorrelation of lag 6 / weighted by atomic masses H attached to C1(sp3)/C0(sp2) R autocorrelation - lag 2 / weighted by atomic masses Geary autocorrelation - lag 2 / weighted by atomic masses d COMMA2 value / weighted by atomic masses	GETAWAY descriptors molecular properties GETAWAY descriptors atom-centred fragments GETAWAY descriptors 2D autocorrelations geometrical descriptors	2 3 1 3 2 2 3
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3		1 R7e+ 2 BLTD48 1 R6m 1 H-047 1 R4m 3 GATS2m 1 DISPm 2 Mor10u	R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities Verhaar model of Daphina base-line toxicity from MLOGP (mmol/I) R autocorrelation of lag 6 / weighted by atomic masses H attached to C1(4p3)/C0(5p2) R autocorrelation of lag 4 / weighted by atomic masses Geary autocorrelation - lag 2 / weighted by atomic masses d COMMA2 value / weighted by atomic masses 3D-MARSE - signal 10 / uweighted	GETAWAY descriptors molecular properties GETAWAY descriptors atom-centred fragments GETAWAY descriptors 2D autocorrelations geometrical descriptors 3D-MoRSE descriptors	2 3 1 3 1 3 2 3 3 3
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3		1 R7e+ 2 BLTD48 1 R6m 1 H-047 1 R4m 3 GATS2m 1 DISPm 2 Mor10u 1 RDF050p	R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities Verhaar model of Daphina base-line toxicity from MLOGP (mmol/I) R autocorrelation of lag 6 / weighted by atomic masses H attached to C1(sp3)/C0(sp2) R autocorrelation - lag 4 / weighted by atomic masses Geary autocorrelation - lag 2 / weighted by atomic masses d COMMA2 value / weighted by atomic masses 30-MkRSE - signal 10 / unweighted Radial Distribution Function - 5.0 / weighted by atomic polarizabilities	GETAWAY descriptors molecular properties GETAWAY descriptors atom-centred fragments GETAWAY descriptors 2D autocorrelations geometrical descriptors 3D-MoRSE descriptors RDF descriptors	2 3 1 3 2 3 3 3 3
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3		1 R7e+ 2 BLTD48 1 R6m 1 H-047 1 R4m 3 GATS2m 1 DIS9m 2 Mor10u 1 RDF050p 1 B04[0-0]	R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities Verhaar model of Daphina base-line toxicity from MLOGP (mm//I) R autocorrelation of lag 6 / weighted by atomic masses H attached to C1(4p3)/C0(5p2) R autocorrelation - lag 2 / weighted by atomic masses Geary autocorrelation - lag 2 / weighted by atomic masses d COMMA2 value / weighted by atomic masses 3D-MARSE - signal 10 / uweighted Radial Distribution Function - 5.0 / weighted by atomic polarizabilities presence/absence of 0 - 0 at topological distance 04	GETAWAY descriptors molecular properties GETAWAY descriptors atom-centred fragments GETAWAY descriptors 2D autocorrelations geometrical descriptors 3D-MoRSE descriptors RDF descriptors 2D binary fingerprints	2 3 1 3 2 3 3 3 3 2 2
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3		1 R7e+ 2 BLTD48 1 R6m 1 H-047 1 R4m 3 GATS2m 1 DIS9m 2 Mor10u 1 RDF050p 1 B04[0-0]	R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities Verhaar model of Daphina base-line toxicity from MLOGP (mm//I) R autocorrelation of lag 6 / weighted by atomic masses H attached to C1(4p3)/C0(5p2) R autocorrelation - lag 2 / weighted by atomic masses Geary autocorrelation - lag 2 / weighted by atomic masses d COMMA2 value / weighted by atomic masses 3D-MARSE - signal 10 / uweighted Radial Distribution Function - 5.0 / weighted by atomic polarizabilities presence/absence of 0 - 0 at topological distance 04	GETAWAY descriptors molecular properties GETAWAY descriptors atom-centred fragments GETAWAY descriptors 2D autocorrelations geometrical descriptors 3D-MoRSE descriptors RDF descriptors 2D binary fingerprints	2 3 1 3 2 3 3 3 3 2 2 2
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3		1 R7e+ 2 BLTD48 1 R6m 1 H-047 1 R4m 3 GATS2m 1 DISPm 2 Mor10u 1 RDF050p 1 B04[0-0] 1 BELm1	R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities Verhaar model of Daphina base-line toxicity from MLOGP (mmol/I) R autocorrelation of lag 6 / weighted by atomic masses H attached to C1(sp3)/C0(sp2) R autocorrelation - lag 2 / weighted by atomic masses Geary autocorrelation - lag 2 / weighted by atomic masses d COMMA2 value / weighted by atomic masses 3D-MoRSE - signal 10 / unweighted Radial Distribution Function - 5.0 / weighted by atomic polarizabilities presence/absence of 0 - 0 at topological distance 04 lowest eigenvalue n. 1 at 68 under maxity. Weighted by atomic masses	GETAWAY descriptors molecular properties GETAWAY descriptors atom-centred fragments GETAWAY descriptors 2D autocorrelations geometrical descriptors 3D-MoRSE descriptors RDF descriptors 2D binary fingerprints Burden eigenvalues	2 3 1 3 2 3 3 3 3 2 2 2 3
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3		1 R7e+ 2 BLTD48 1 R6m 1 H-047 1 R4m 3 GATS2m 1 DI5Pm 2 Mor10u 1 RDF050p 1 B04[0-0] 1 BELm1 1 Mor11v	R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities Verhaar model of Daphina base-line toxicity from MLOGP (mm//I) R autocorrelation of lag 6 / weighted by atomic masses H attached to C1{ap3}/C0(sp2) R autocorrelation - lag 2 / weighted by atomic masses d COMMA2 value / weighted by atomic masses d COMMA2 value / weighted by atomic masses 3D-MARSE - signal 10 / unweighted Radial Distribution Function - 5.0 / weighted by atomic polarizabilities presence/sebsence of 0 - 0 at topological distance 04 lowest eigenvalue n. 1 of Burden matrix / weighted by atomic masses 3D-MARSE - signal 11 / uneighted by atomic van der Waals volumes	GETAWAY descriptors molecular properties GETAWAY descriptors atom-centred fragments GETAWAY descriptors 2D autocorrelations geometrical descriptors RDF descriptors RDF descriptors 2D binary fingerprints Burden eigenvalues 3D-MoRSE descriptors	2 3 1 3 2 3 3 3 2 2 3 2 2 3 3
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3		1 R7e+ 2 BLTD48 1 R6m 1 H-047 1 DLSPm 2 Mor130 1 BD45050 1 B04(0-0) 1 BELm1 1 Mor11v 2 MATS7e	R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities Verhaar model of Daphina base-line toxicity from MLOGP (mmol/1) R autocorrelation of lag 6 / weighted by atomic masses H attached to C1(sp32)/C0(sp2) R autocorrelation - lag 2 / weighted by atomic masses Geary autocorrelation - lag 2 / weighted by atomic masses d COMMA2 value / weighted by atomic masses 3D-MoRSE - signal 10 / unweighted Radial Distribution Function - 5.0 / weighted by atomic polarizabilities presence/absence of 0 - 0 at topological distance 04 lowest eigenvalue n. 1 at gurder matrix / weighted by atomic sanses 3D-MoRSE - signal 11 / weighted by atomic van der Waals volumes leverage-weighted autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities	GETAWAY descriptors molecular properties GETAWAY descriptors atom-contred fragments GETAWAY descriptors 2D autocorrelations geometrical descriptors 3D-MoRSE descriptors 2D binary fingerprints Burden eigenvalues 3D-MoRSE descriptors	2 3 1 3 2 3 3 3 2 2 2 3 3 3 3 3 3 3 3 3
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3		1 R7e+ 2 ELTD48 1 R6m 1 H-047 1 R4m 3 GATS2m 1 DISPm 2 Mor10u 1 RDF050p 1 B04(0-0) 1 BELm1 1 MOr11v 2 HATS7e 1 B05(C-C)	R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities Verhaar model of Daphina base-line toxicity from MLOGP (mm0/I) R autocorrelation of lag 6 / weighted by atomic masses H attached to C1{sp3}/CO(sp2) R autocorrelation - lag 2 / weighted by atomic masses d COMMA2 value / autocorrelation - lag 2 / weighted by atomic polarizabilities presence/sbesnec of 0 - 0 at topological distance 04 lowest eigenvalue n. 1 of Burden matrix / weighted by atomic masses 3D-MARSE - signal 11 / weighted by atomic van der Waals volumes leverage-weighted autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities presence/sbesnec of 0 - 0 at topological distance 04	GETAWAY descriptors molecular properties GETAWAY descriptors atom-centred fragments GETAWAY descriptors 2D autocorrelations geometrical descriptors 3D-MoRSE descriptors 2D binary fingerprints Burden eigenvalues 3D-MoRSE descriptors GETAWAY descriptors 2D binary fingerprints	2 3 1 3 2 3 3 3 3 2 2 3 3 3 2 2 3 3 2 2 3 3 2 2
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3		1 R7e+ 2 BLTD48 1 R6m 3 R4m 3 GATS2m 1 DISPm 2 Mor10u 1 RDF050p 1 B04[0-0] 1 BELm1 1 Mor11v 2 HATS7e 1 B05[C-C] 1 H-049	R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities Verhaar model of Daphina base-line toxicity from MLOGP (mmol/1) R autocorrelation of lag 6 / weighted by atomic masses H attached to C1{scp3}/CO(sp2) R autocorrelation - lag 2 / weighted by atomic masses Geary autocorrelation - lag 2 / weighted by atomic masses d COMMA2 value / weighted by atomic masses 3D-MoRSE - signal 10 / unweighted Radial Distribution Function - 5.0 / weighted by atomic polarizabilities presence/absence of 0 - 0 at topological distance 04 lowest elgenvalue 1.1 / weighted by atomic van der Waals volumes IB-WARSE - signal 11 / weighted by atomic van der Waals volumes leverage-weighted autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities presence/absence of C - C at topological distance 05 H attached to C3(sp3)/C2(Sp2)/C3(sp2)/C3(sp2)	GETAWAY descriptors molecular properties GETAWAY descriptors atom-centred fragments GETAWAY descriptors 2D autocorrelations geometrical descriptors 3D-MoRSE descriptors 2D binary fingerprints Burden eigenvalues 3D-MoRSE descriptors GETAWAY descriptors 2D binary fingerprints atom-centred fragments	2 3 1 3 2 3 3 3 2 2 2 3 3 2 2 3 2 1
1 Mor18p 3D-MoRSE - signal 18 / weighted by atomic polarizabilities 3D-MoRSE descriptors 3		1 77e+ 2 EUT048 1 K6m 1 H-047 1 R4m 3 GATS2m 2 Mor10u 1 RDF050p 1 B04(0-0) 1 BELm1 1 Mor11v 2 HATS7e 1 B05(C-C] 1 H-049 2 B07(C-C)	R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities Verhaar model of Daphina base-line toxicity from MLOGP (mm0/1) R autocorrelation of lag 6 / weighted by atomic masses H attached to C1(sp3)/C0(sp2) R autocorrelation - lag 2 / weighted by atomic masses d COMMA2 value / autopic distance 04 Radial Distribution Function - 5.0 / weighted by atomic polarizabilities presence/sbeence of 0 - 0 at topological distance 04 lowest eigenvalue n. 1 of Burden matrix / weighted by atomic masses 3D-MARSE - signal 11 / weighted by atomic van der Waals volumes leverage-weighted autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities presence/sbeence of 0 - c at topological distance 05 H attached to C3(sp3)/C2(sp2)/C3(sp2)/C3(sp) presence/sbeence of 7	GETAWAY descriptors molecular properties GETAWAY descriptors atom-centred fragments GETAWAY descriptors 2D autocorrelations geometrical descriptors 3D-MoRSE descriptors 2D binary fingerprints Burden eigenvalues 3D-MoRSE descriptors GETAWAY descriptors 2D binary fingerprints atom-centred fragments atom-centred fragments	2 3 1 3 2 3 3 3 2 2 3 3 2 2 1 2
1 HATS2y leverage-weighted autocorrelation of lag 2 / weighted by stomic van der Waals volumes GETAWAY descriptors 3		1 77e+ 2 EUT048 1 K6m 1 H-047 1 R4m 3 GATS2m 2 Mor10u 1 RDF050p 1 B04(0-0) 1 BELm1 1 Mor11v 2 HATS7e 1 B05(C-C] 1 H-049 2 B07(C-C)	R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities Verhaar model of Daphina base-line toxicity from MLOGP (mm0/1) R autocorrelation of lag 6 / weighted by atomic masses H attached to C1(sp3)/C0(sp2) R autocorrelation - lag 2 / weighted by atomic masses d COMMA2 value / autopic distance 04 Radial Distribution Function - 5.0 / weighted by atomic polarizabilities presence/sbeence of 0 - 0 at topological distance 04 lowest eigenvalue n. 1 of Burden matrix / weighted by atomic masses 3D-MARSE - signal 11 / weighted by atomic van der Waals volumes leverage-weighted autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities presence/sbeence of 0 - c at topological distance 05 H attached to C3(sp3)/C2(sp2)/C3(sp2)/C3(sp) presence/sbeence of 7	GETAWAY descriptors molecular properties GETAWAY descriptors atom-centred fragments GETAWAY descriptors 2D autocorrelations geometrical descriptors 3D-MoRSE descriptors 2D binary fingerprints Burden eigenvalues 3D-MoRSE descriptors GETAWAY descriptors 2D binary fingerprints atom-centred fragments atom-centred fragments	
		1 R7e+ 2 BLTD48 1 R6m 3 R4m 3 GATS2m 1 DLSPm 2 Mor10u 1 R5r050p 1 B04[0-0] 1 BLm1 1 Mor11v 2 HATS7e 1 B05[C-C] 1 H-049 2 B07[C-C] 1 RCOOH	R maximal autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities Verhaar model of Daphina base-line toxicity from MLOGP (mmol/1) R autocorrelation of lag 6 / weighted by atomic masses H attached to C1{ep3}/C0(sp2) R autocorrelation - lag 2 / weighted by atomic masses Geary autocorrelation - lag 2 / weighted by atomic masses 3D-MARSE - saighted by atomic masses 3D-MARSE - saight 10 / unweighted Neuronal Distribution Function - 5.0 / weighted by atomic polarizabilities presence/absence of 0 - 0 at topological distance 04 lowest elegenvalue n. 1 at Burdern matrix / weighted by atomic masses 3D-MARSE - signal 11 / weighted by atomic van der Waals volumes leverage-weighted autocorrelation of lag 7 / weighted by atomic Sanderson electronegativities presence/absence of C - C at topological distance 05 h attached to C3(sp3)/C2(sp2)/C3(sp2)/C3(sp2) presence/absence of C - C at topological distance 07 number of carboxylic adds (alphabic)	GETAWAY descriptors molecular properties GETAWAY descriptors atom-centred fragments GETAWAY descriptors 2D autocorrelations geometrical descriptors 3D-MoRSE descriptors 2D binary fingerprints Burden eigenvalues 3D-MoRSE descriptors GETAWAY descriptors 2D binary fingerprints atom-centred fragments 2D binary fingerprints atom-centred fragments 2D binary fingerprints atom-centred fragments 2D binary fingerprints	

Table 3.15 Continued

Table 3.16: Top 100 predicted compounds for each mammalian OR

Chemical name or Pubchem compound ID (CIDs), SMILES strings, and distances, of the top ~100 predicted compounds for each Or. All distances represent the minimum distance based on optimized descriptors to the previously known strongest active compound listed in the gray cells for that particular Or.

Dirthment 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.095600 7.32720 8.426000 8.4260000 8.4260000 8.4260000 8.4260000 8.4260000 8.426000000000000000000000000000000000000
Data Aut3 0.00000000000000000000000000000000000	0.00953033 CLCord-Cord CrCord 00953033 CLCord-Cord CrCord 000954035 CLCord-Cord CrCord 000954035 CLCord-Cord CrCord 000954035 CLCord-Cord CrCord 000954035 CLCord-Cord CrCord 000951386 CLCord-Cord CrCord 000951386 CLCord-Cord CrCord 000951386 CLCO-Cord CrCord 000951386 CLCO-Cord CrCord 000951385 CLCO-Cord CrCord 00095895 CLCO-Cord CrCord 00095985 CLCO-Cord CrCord 00095985 CLCO-Cord CrCord 00095985 CLCO-Cord CrCord 00095985 CLCO-Cord CrCord 00095985 CLCO-Cord CrCord 00095985 CLCO-CO-CO-CO 00095985 CLCO-CO-CO-CO 00095985 CLCO-CO-CO-CO 00095985 CLCO-CO-CO-CO 00095985 CLCO-CO-CO-CO 00095985 CLCO-CO-CO-CO 00095985 CLCO-CO-CO-CO 00095985 CLCO-CO-CO-CO 00095985 CLCO-CO-CO-CO-CO 00095985 CLCO-CO-CO-CO-CO 00095985 CLCO-CO-CO-CO-CO 00095985 CLCO-CO-CO-CO-CO 00095985 CLCO-CO-CO-CO-CO 00095985 CLCO-CO-CO-CO-CO 00095985 CLCO-CO-CO-CO-CO 00095985 CLCO-CO-CO-CO-CO-CO 00095985 CLCO-CO-CO-CO-CO-CO 00095985 CLCO-CO-CO-CO-CO-CO 00095985 CLCO-CO-CO-CO-CO-CO-CO-CO-CO-CO 00095985 CLCO-CO-CO-CO-CO-CO-CO-CO-CO-CO-CO-CO-CO-C
Distance 0.05527457 0.055274576 0.055274576 0.05527457 0.05527457 0.05527457 0.05527457 0.05527457 0.05527457 0.05527457 0.05527457 0.05527457 0.05527457 0.05527457 0.05527457 0.05527457 0.11721877 0.11721877 0.11721877 0.11721877 0.11721877 0.11721877 0.11721877 0.11721877 0.11721877 0.11724877 0.11248777 0.11248777 0.11248777	1.3137171 1.0158771 0.0158771 0.0158771 0.015877 0.015874 0.015874 0.015874 0.015874 0.015874 0.015874 0.01584<
Data SILS State SILS State Construction Construction Construction State State	 2.227979 CECCHCER (= 075K11):2-10 2.22799 CECCHCER (= 075K11):2-10 2.22894 CECCHCER (= 075K11):2-10 2.22894
Datasa SHLS MortJ25-1 0.00125-1 0.00125-0 0.00125-0 0.00125-1 0.00125-0 0.00125-0 0.00125-1 0.00125-0 0.00125-0 0.00125-1 0.00125-0 0.00125-0 0.00125-1 0.00125-0 0.00125-0 0.00125-1 0.00125-0 0.00125-0 0.000125-0 0.00012-0 0.00012-0 0.000125-0 0.00012-0 0.00012-0 0.000125-0 0.000012-0 0.00012-0 0.000012-0 0.000012-0 0.00012-0 0.000012-0 0.000012-0 0.00012-0 0.000012-0 0.000012-0 0.000012-0 0.000012-0 0.000012-0 0.000012-0 0.0000012-0 0.0000012-0 0.0000012-0 0.0000012-0 0.0000012-0 0.0000001-0 0.0000012-0 0.0000012-0 0.000000-0 0.0000012-0 0.0000012-0 0.000000-0 0.0000012-0 0.0000012-0 0.000000-0 0.0000012-0 0.00000010-0 0.000000-0 <	0.033834 GCL=GC_GCC_CCC 0.033834 GCL=GC_GCC_CCC 0.033834 GCL=GC_GCC_CCC 0.033834 GCL=GC_GCC_CCC 0.033834 GCL=GC_GCC_CCCC 0.033834 GCL=GCC_GCC_CCCC 0.033834 GCL=GCC_GCCCCCCC 0.033834 GCL=GCC_GCCCCCCC 0.033834 GCL=GCC_GCCCCCCC 0.033834 GCL=GCC_GCCCCCCC 0.033834 GCL=GCC_GCCCCCCC 0.033834 GCL=GCCCCCCCCCCC 0.033834 GCL=GCCCCCCCCCCC 0.033834 GCL=GCCCCCCCCCCC 0.033834 GCL=GCCCCCCCCCCC 0.033834 GCL=GCCCCCCCCCCCC 0.033834 GCL=GCCCCCCCCCCCC 0.033834 GCL=GCCCCCCCCCCCCC 0.033834 GCCCCCCCCCCCCCCC 0.033834 GCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Auto: Data: auto: auto: auto: creanisticicamiculos: auto: creanisticicamiculos: auto: creanisticicamiculos: auto: creanisticicamiculos: auto: creanisticicamiculos: auto: creanisticicamiculos: auto: auto: auto: auto: <th> 2.397-93 CLICHCCCI (C) C/2012 2.397-94 CLICCCCI (C) C/2012 2.397-94 CLICCCCI (C) C/2012 2.3984-36 CLICCCCI (C) C/2012 2.3984-38 CLICCCI (C) C/2012 2.3984-38 CLICCCCI (C) C/2012 2.3984-38 CLICCCI (C) C/2012 2.3984-38 CLICCCI (C) C/2012 2.3984-38 CLICCCCA (C) C/2012 2.</th>	 2.397-93 CLICHCCCI (C) C/2012 2.397-94 CLICCCCI (C) C/2012 2.397-94 CLICCCCI (C) C/2012 2.3984-36 CLICCCCI (C) C/2012 2.3984-38 CLICCCI (C) C/2012 2.3984-38 CLICCCCI (C) C/2012 2.3984-38 CLICCCI (C) C/2012 2.3984-38 CLICCCI (C) C/2012 2.3984-38 CLICCCCA (C) C/2012 2.
Morto6-1 Morto6-1 1 04-0000-mmin Mil 04-0000-mmin 04-0000-mmin Mil	(0
MIGI 1 MIGI 1 MILS MILS MILS M	сирастельности соверсионального сирастельности со составлисто и составления и составл

i	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.1767846 0.1767846 0.1926777	0.2034395 0.2121746 0.2283565	0.2532418 0.2600318 0.2607831	0.2758744 0.2813197 0.2828428	0.2854501 0.31266	0.3135219 0.3180221	0.3195927 0.3235687	0.3305075 0.3309083	0.3342322 0.3351069	0.3397238 0.3409651	0.3414605 0.3433653	0.3434153 0.3442434	0.344622 0.3462852	0.3564579	0.3619179	0.3655498	0.3752879 0.376413	0.3808107	0.383855	0.3926395	0.3936016	0.3977997	0.400185	0.4105892	0.4112343	0.4130402 0.414148	0.4156558 0.4163652	0.4198651 0.4198651 0.4208217	0.4220633	0.4245487	0.4277974 0.4301193	0.431292	0.4352579 0.4362954	0.4374064 0.4384387	0.4402955	0.4423475 0.4439708	0.4466131 0.4466131	0.4476903	0.4487506 0.4488419	0.4506406 0.451164	0.4513892 0.452722	0.4540705 0.4540705 0.4541750	400 T #0 # 0
Mor204-6	0 CC1 = CC(C0 @H) (CC1 = O)C(=C)C 0 CC1 = CC(C0 H) (CC1 = O)C(=C)C 0 CC1 = CC(C0 H) (CC1 = O)C(=C)C 0 = C10C2 = CC(C=CCE = C)C = C)C(=C)C	0 CC1CCC = CC1=0/CCC 0.09870324 CC1CCC(=CC1=0/CCC)C 0.1234426 C1=CCC=C2C(=C1)C=C0C2=0	0.1310437 C1=CC(=0)MC2=C1C=NC=C2 0.1429018 CC1=CC(=0)C(CC1)CC0 0.1522912 C=CC1=CC=C(C=C1)C(=0)0	0.1569658 COC(=0)C1=CCCC(C1)0 0.1636356 C1=CC2=C(C(=C1)0)C(=0)MC=C2 0.1710732 C1=CC2=C/MC(=0)C=C2)M=C1	0.1711094 C1=CC(=0,NC2=NC=NC=CC) 0.1778983 CN1C2C1C(CC(=C2)C(=0,0CC) 0.1785371 C1=CC2=C7C(=C2)C(=0,0CC) 0.1785371 C1=CC2=C7C(=C2)C=C1)M==C3(C=0,0C=C2)	0.1786504 C=CC1=CN=C(C=C1)C(=0)0 0.1865765 CC(=C)CC1=CCCCC1=0	0.1901121 CC1=CCC(CC1=N0)C(=C)C 0.1926162 C1C(=CC1=0)C2=CC=CC=C2 0.1048855 C0CC-ACC1=0)C2=CC=CC2	0.1949919 C1CC(=0)C2CC1C(=0)C=C2 0.1959073 CCC(=0)C1=CCCC(51)C		0.1966562 C1=CC=C2C(=C1)C=CC(=O)N2 0.1977104 CC1CC=C(C(01)C)C(=O)O	0.200565 CC1(CCC=CLQ=0)0 0.200565 CC1(CCC=CC1)C(=0)0C)C 0.2005665 CC(=C)C1CCC=CC1)C=N0	0.2069094 CC1=CC2(CCCCC22)OC1=0 0.2083482 COC(=0)C1=CCCC(=0)C1		0.2100252 C1=CC2=C(C=CN2)C3=C1C(=0)C=CN3 0.2100582 CCC(=0)C=C1CC CCC1		0.2141855 C1 = CC = C(C=C1)C2 = CC(= 0)MN2 0.2146121 CC(= 0)C1 = CC = CC = C1C=C	0.215491 C1=CN(C(=CN1)C(=0)O)C(=0)O 0.2160998 CCC1CC(=CNC1)C(=0)C	0.2169532 COC1=CC(=NCN1)0C 0.2170895 COC(=0)C1=CCCCC1	0.2172078 COC(=0/C1=CNCCC1 0.2175421 C1=CC2=C(C=CC(=0)N2)N=C1	0.219903 C1=CC=C2C(=C1)C(=O)C=CN2 0.2195299 CC1=CN(C(=O)N(C1=O)C)C	0.2214962 C1=CC2=C3C(=C1)C=CN3C(=O)C=C2 0.223367 C1C=C(C(=O)N1)X2=CC=CC=C2	0.2233632 CC1=CC(=0)CC1C2=CC=CC=C2 0.2238223 CC0C(=0)C1=CMCCC1	0.2242527 CCL=CCC(=C(NL)C/C(=0)0C 0.2246455 CL=CNC(=0/NCL=0)CC=0	0.2258775 cc(=0)c=c1cccccc1 0.2267393 cc(=0)c1=cc(ccc1)0	0.227668 CINCC(C=0X(=C100)(CXC)C 0.227668 CIN=C(C=CN1C(=0)0)ON	0.2277479 CI = CC2 = C(N=C1)N3C(= C2)C= CNC3=0 0.2279199 CI = CNC = 00 C2=NC = CN=C2 = C	0.22795/65 CC1=CC=CC(=C1)C1=C 0.2280567 C1=CC=CCC(=C1)C3=C(N2)C=CNC3=O 0.376594 C1=CC=CC=C1)C3=C(N2)C=CNC3=O	0.2293331 C1=CC2=C(N=CC2=O)N=C1 0.232204 CC1=CC(CC1=O)C(=O)CO 0.33228E8 C-CC1=ANC(-CC1-C) CC(=O)CO	0.232280 C = CCI = MC = C(C = C) / () / (0.3340755 CCL=CC=CC=CC=CC=CC=CC=OC 0.3340754 C1CC2L=CC=CC=CC=CC=CC=OC 0.3341524 C1CC2/CC1 C=C7X'=OOOC=OO	0.2346179 CCICC=CCC01XC=O/O 0.2349258 CCICCC=CC1XC=O/O/CC	0.2357801 C1=CC=C(C=C1)CN 2C(=O)C=CS2 0.2363829 CC0C1=CC(=O)C(C(C1)C)C	0.2367655 CtC(=0)C=CC(01)C2=CC=C02 0.2372365 CC1=CC2=C(C(=C(S2)C)C)C(=0)01	0.2381111 C1=CC2=C(C=C10)C(=0)C=CN2 0.2382502 C#CCN1C=CC(=0)NC1=0	0.2382673 CC1=CC(COC1=0)(C)C 0.2385028 CC1=C(C(=C(C=C1)0)C)C=C	8 8 I	0.23942879 CCN1C(=CN1C(=CN1C1=0)C)C 0.2394289 CCC1=CN1C(=0)N(C1=0)C)C	0.2399.205 CC1 = CC(=C)N(C.2 = N.= NM1.2/S.C.= O 0.2417149 C1 = CC2=CC1 (SC1 (SC1 (SC1 (SC2) C2 C2) 0.2437373 C1 = CM1.C/=.DM2.1 = DV2'.=DV0	0.243914 CIC=CR(NC=C)/NC1=C)/C=C) 0.242014 CIC=CR(NC=CC=CC=CC=C2)/C=O 0.2440488 CC1=C/C7/C1=O/V=2/CO32/C	CCCL	0.24861 CC1=C(NC(N=C1)(0)0)C 0.2468195 C=CC1=CC(=CC=C1)C0)0)C	0.2472258 C1=CN=CC=C1C2=CC(=0)NN2 0.2483911 CC1=C(C=C2C=C(CC2=C1)C(=0)C)C	0.2485717 CC1=CCC(CC1=0)(C(=C)C) 0.2488646 CC(=0)C1=C(CCCC1)CC=C 0.2488027 C1=CC2=CCC=ANC2=0)CC=C	ハイマションズ ひきさ JAD モンジュモンジョーマン トトロ6.85%・D
Mor203-1	5	0.1327919 ECCC=0000000 0.2135794 ECCCC=0000000 0.2135794 ECCCCC=000000 0.2261997 ECCC=0000000	0.2307089 CCCICCC (CC1)C(=0)CC 0.2685227 CC(CCCC0)C 0.270388 CCCICC(C1)C(=0)C	0.2840643 CCC(=0)C=CCCC 0.2858069 CCCCCC(=0)CCC 0.2878607 CC=CC=CCC0	0.2910175 CC(=0)CC1CCCC=C1 0.2952586 C=CC1=CC=C(C=C1)CCC0 0.2973288 CCCCCCCCCCCC)0	0.2995831 C#CC1=CCC(CC1)CC0 0.2998371 CC(CCCC=C)0	0.3024153 CC(=C)CCCC(=0)C 0.3030766 CCCCCLC(=0)C1	0.3045982 CC(C)CCCC(=0)C=C 0.3045982 CC(C)CCCC(=0)C=C 0.3073687 CCCC=C=CCC0	0.3082988 CCCCC(=0)MC 0.3085543 C1CC(=CC=C1)CCCO	0.3109102 C(C=CC=CCC=CCC)0 0.3115366 CC(C)CCNC(=0)C	0.3119773 CC(C)CC=CC60 0.311947 C1CC1=CCCCC0 0.3119305 CC(C)CC=CC(=0)C	0.3127963 CCCC=CC(=O)C 0.3141638 CCCCC1=CC(=O)C1	0.3146093 CC(=0)C=C1CCCCC1 0.314688 CCCCC(=C)CC0	0.3164913 CCCCC(=0)C=C 0.3168748 CC(C)C1=CC=C(CC1)C0	0.3178926 CC(CCC(=0)CC)CC 0.3181635 CC1CCC(CC1)C(=0)C	0.3225541 CC(C)0C1=CCCC=C1 0.3238227 CC1(C01)CCCC=C	0.3280601 CCC(=0)CCC(=C)C 0.329925 CC(=CC)CCC(=0)C	0.3307236 CC(CCC(CC)0)CC 0.3332723 C1CC=C(C=C1)CCC0	0.3341447 CCC(CICCCCC1)0 0.3348343 CC(=C=CCC(=0)C)C	0.3379899 C=CCCCCCCC0 0.3379899 C=CCCCCC#CC0	0.3382412 CC(=0)C=CC1CCCCC1 0.3422228 CCCCCCC(C)0	0.342778 ccccccc(c)0 0.3433717 cc(c1=cc=c(c=c1)c=c)N	0.3455022 CC(=0)CCCICCI=C 0.3455022 C#CCCCCI(CCI)0		0.3515843 CCCCC(CC)N 0.353092 CC(C)OC1=CC=CNC1	0.3530949 CC(C)0C1=CC=CC1 0.3552634 CC(C)0C1=CCC=CC1	0.3593263 CC1=CC=C(C=C1)OCC=C 0.3579266 C =CCCCC1=CC=C(C=C1)O	0.3583624 CICCI=C2CC2CC0 0.3585697 CCCICC(=0)CC1 0.3581307 CCCICCC(=0)CC1	0.3591302 CCCCICCS(=0)CC1 0.3594296 CCCCCICCS(=0)CC1 0.3603129 CCCCCI-CS	0.3640987 CCCC#CCC0 0.3647515 CCCC#CCC0	0.3676689 CCCMC(=0)C=C 0.3676688 CCC(CCC#CC)0	0.3680748 CC(C)C1=CCC(CC1)C0 0.3685367 CN=S(C)C1=CC=CC=C1	0.3697989 C1CCCCC1) 0C =C 0.3697989 C1CCC(CC1) C2=CCC(=0) CC2	0.369876 CLCCC(=C=CCO)CC1 0.3698959 C(CCC=CCC)0	0.3707031 CCCCC1=C(C1=0)C 0.3712612 CCCCCCC(=N)N	0.3719231 CCC ICCC(CC1)CO 0.3727306 CC(C=C)OC1=CNCC=C1	0.3738466 CC(CC/C=C(C)/C)=0 0.375163 CCC(=0)C=C1CCCCC1	0.3764092 CN(C)C(=0)CCC=C=C 0.3764092 CN(C)C(=0)CCC=C=C	0.3776953 CCI(C(01)CCCC=C)C	0.3793322 CO(=CCC(CC)) 0.3796353 C =CCCICCC(CC1)0 0.3803442 C ICC=C(C=C1)MCC0	0.3805739 CCCCCCC(C(C)C)0 0.3815324 CCCCCC#C)0C	0.3823562 CC1=CC=C(C=C1)COCC#C 0.3838065 C1CCC(CC1)CCC0	0.3864021 CC1=CC=C(C=C1)OCC %C 0.3872609 CC(=0)CC1=CCCCC1 0.3872666 CC1=CCCCC1	0.38/3999 001=00100=00120
Mor2-1	0 CC(C6 @H)(C1 = CC = CC = C1)C(= 0)0 0 CC(C6 @H)(C1 = CC = CC = C1)C(= 0)0 0 CC(C6 @H)(C1 = CC = CC = C1)C(= 0)0 0 CC(C2 = 0)0C = CC = CC = C1)C(= 0)0 0 CC(C2 = 0)0C = C2 = CC = C2	0 0000(=0)%(==0)%(==0)%(==0)%(==0)%(==0)%(==0)%(==0)%(==0)%(==0)%(==0)%(==0)%(==0)%(==0)%(==0)%(==0)%(==0)%(==0)%(=0)%(0.06676451 C1CC1(C2=CC=CC=C2)OCCS 0.1183577 C=CCOC(=0)CC1=CC=C(C=C1)0 0.1347063 C0C(=0)Cc1ccc(cc1)0C	0.1680434 CCC(C1=C(C=NC=C1)C0)0C 0.1763185 COC(=0)CC1=CC=CC(=C1)C#N 0.1962587 C1CC54=0Y=0X2=CC=CC=C2C1	0.1976955 CICCI(C2=CC=CC=C2C0) 0.2061102 CC(C)0C(=C)CC=CC=C2C0)0 0.2061102 CC(C)0C(=CU1XM)CC#NCCFN0		0.2097237 CICC2=CC=CC=C2MC(=0)C1 0.2140007 CICC(C2=C(C1)C=CS2)MC(=0)N	0.2209319 CICC(C2=CC=CC=C1NC(=0)0 0.2209319 CICC(C2=CC=CC=C2SC1)0	000	0.2406093 CC(C1=CC=CC=C1N)C(=0)OC 0.241701 C1=CC(=CC(=C1)CN)CC(=0)O	0.2450089 CCOCLECCEC(CEC1)OC 0.2445011 CCOC(=0)CC1=CC=C(C=C1)O 0.2468526 CCN1C(OC2=C1C=C(C=C2)C)	CC(NCN1	0.2532433 CCC(C1=CC=CC=C1)C(=0)OC 0.2564928 COC(=0)CC1=CC=C(C=C1)NN		0.2593795 CCOC(=0)C(C)C1=CC=CN1C 0.2594466 CC#CCOC(=0)CC1=CC=CC=C1	0.2597198 C1=CC=C(C(=C1)CC(=0)0)CN 0.2611222 CN1CC2=C(CC1C(=0)0)SC=C2	0.2773754 CMLC=CC=CLCSCCC(=0)M2C 0.2773754 CMLC=CC=CLC2CCC(=0)M2C	0.2797628 CC1=C2CCCN2C(=0)CCC1 0.2807091 C1=CC=C(C=C1)C(C0)C(=0)0	0.2841142 CC(C1 = CC = CC = C1)C(=0)OC 0.2842825 C1CC2 = C(CC1C(=0)0)SC = C2	0.2861447 CC(C)N1CSC2#CC#CC#CC#C21 0.2869487 CCOC(#0)CC1#CC#CC#CC#C1	0.2904827 CCCIC 2C(CCN2C(=0)0)NC1=0 0.2904898 CCOC1(C2=CCCCN2C(=0)01)C	0.2924971 CCOC(=0)CC1=CC=C(C=C1)N 0.2940839 C1CCC2=C(C(C1)N)N=CC=C2	0.2954905 CNIC(0C2=CC=CC=C21)C 0.2954905 CN(CC1=CC=CC=C1)CC(=S)N	ŏ×.	0.2930856 CN=C1CNCC2=CC=C1)C(=0)0 0.2980856 CN=C1CNCC2=CC=CC=C2S1	0.2987179 CC1=CCC2C(C1)N2C(=0)0C 0.2989803 C=CCC1=CC=CC=C10CCN	0.2939992 CC(C1=CC=CC=C1)C(=0)UC=C 0.3007561 CC1=C(C=CC=C10)C(C)C(=0)0	0.3024095 COCCI=CC=CC=CCCCC 0.3030642 CCICCNCC2=CION=C20C	0.3052182 CC(N(C)CC1=CC=CC=C1)S 0.3065182 CC(N(C)CC1=CC=CC=C1)S 0.3060123 C1CC7=CCC=CS2)C/C1 WC=0	0.3092388 C1=CC(=C2C=C2/(C1)/CC0 0.3092388 C1=CC(=C2C=C2C=C1)/CC0 0.3119717 C7CN1C2=C7=C7=C7=C7=C7/(C1)/CC0	0.31434 CC1=C2C(=CC=C1)MC(=0)CCS2 0.3163057 CC1(OC2=CC=CC=C201)CCN	0.317051 CC1=CC=CC=CIN(C)C(=0)C 0.3172796 CC1=C(C(=CC=C1)C0)OCCC#N	0.3178126 CC1(CC(CC01)0)C2=CN=CS2 0.3199334 C1CC2=C(C=C(C=C2)0)NC(=0)C1		0.325901 CC(C1=CC=CC=C1)C(=0)0C#N 0.3269808 CC(C1=C(C=NC=C1)N)C(=0)0C	0.3273557 CICOC2=CC=CC=CCC(C1N)0 0.3298992 CC(C#N)C1=CC=C(01)CN(C)C	0.3308055 CC1=CC(=C(C=C1)0C)CC(=0)0 0.3320885 CC(C1=CC=CC=C1CN)C(=0)0	0.3344908 CC1=C(C(=CC=C1)C/DCC(=N)N 0.3346634 CC(=C)CC1=CC=CC=C1SC 0.336634 CC(=C)CC1=CC=CC=C1SC	0.3367353 CUCLE-COCE-CUCEC(CEC) 0.3367353 CUECC=C(CEC)(CC(=0)OCCN 0.3367478 CUCLE-CVC1=CC/-CUE-CU-ON	C1=CC=	0.3388549 CC1C(C2=C(CN1)C=CS2)0C 0.3434852 C0C(=0)C(C0)C1=CC=CC=C1	0.3450098 CC(C)C(=C)CIC(N=C01)C(=0)0 0.3470305 CNC(C1=CC=CC=C1)C(=0)0	0.3483415 CCC1(C(=0)N(C(=0)N1C=C)C=C/C 0.3505473 CC1=C(C(=CC=C1)C)OCC(=S)N 0.3510066 CC1=C(C(=CC=C1)C)OCC(=S)N	20001650 PM
Mor189-1		0.0323404 CCL=05(Cgm)14CcL(0)C(=)C 0.0323404 CCL=05(Cgm)1(CCL=0)C(=)C 0.0355811 C[Cgm)12CC[Cgm)1(CL)C(2=0)(C)C 0.0418993 CC1(C2CC1(CC2=0)C)C	0.04258475 CC(=C/CICC=C(C(=0)C1)0 0.04279004 CC1 =CC(=0/C(CC1)C(=C)C 0.04383469 C=C(C)C(CC1C) =CC1=0	0.04396265 CC1CCC(=CC1=0)C(C)C 0.04402903 CC1=CCCC(C1=0)(C)C#C 0.0442424265 CC1=CCCC(C1=0)C(C)C#C	0.046368 CC1=CC(CCC1=0)C(C)C 0.04635459 CC1C2(CCC1(=0)C)C)C 0.04657459 CC1C2(CCC1(=0)C2)C)C 0.04615777 CC1CC=CC(=0)C1)C(C)C	0.0499476669 0=C1C2C(CCCCC22 ACIC)=C 0.049947066 CC1(CCC(CCCCC22 ACIC)=C	0.05012532 CC(C)(C12CCC(=0)C1C2)0 0.0513685 CCC1=C(C(=0)C(CC1)C)C 0.05138185 CCC1=C(C(=0)C(CC1)C)C	0.05282474 CCCCI(CCC(=0)C=C1)C 0.05282474 CCCCI(CCC(=0)C=C1)C 0.05299349 CC(CIC=CCCNI)X(=0)C	0.05360856 CC1=CCC(CC1)C(=C)C=0 0.0536915 CC1(CCC(=0)C=C1C=C)C	0.05373938 CICN(CCCICCN)C=0 0.05481358 0=CIC=C(C)CCCIC(C)C			0.05701812 CC1(CC(=C(C(=0)C1)0)0)C 0.05795114 CC(=C)C1CCC(=CC1)C=0	CC1C2O	41 CC(C)(C 94 C[C@@	0.0595711 CC1(C2C(C1=0)CC=02)C 0.03968833 CC1(CCC(=0)C(=C1)OC)C	0.06004616 CC1(C2CCC1C(=0)C=C2)C 0.06023724 CC1(CC=C(C(=0)C1)C0)C	0.0610729 CC1(CCN(CC1)C(=0)0)N 0.0621596 CC(=CC1CCC=CC1)C=0	0.05224206 CC1CCCC=C1C(=0)C=C 0.06255557 CC1C=C(CCC1(C)C=0)C	0.05260877 CCICCCC2C1=0)(C)C 0.05314167 CCICC(=0)C2(CIC2)C(C)C	CC(C)	0.0636295 C1C(C(C(C1=0)(C0)0)0)N 0.06390911 C1CC2C=CC2C(=0)C1		0.06419423 CN1CC2CCCC(C1)C2=0 0.0645933 CC(C)(C1CCC=CC1=0)O	0.04465735 CC1(C2CC=CC(C2)) 0.04489509 C=CC1CC(C1)C=0)C=C	CC1CC20	0.0669387 6C1=C(C(=0)CCC)X(=C)C 0.06693876 6C1=C(CC(==0)(CC) 0.06712877 6C1=C(CC(=0)(CC)		0.067580182 CC11cC1 =CC1=C/L1/CU/C 0.067581182 CC1 = CC1=CC1 = O/CC1/C 0.06783182 CC1 =CC1CC1 =C(CC1/C1	0.06802411 CC1=C(CC(CT=0)(C)C) 0.0680248 CCTC1C(CT=0)(C)C) 0.0680248 CCTC1CC(CT=0)(C)C)	0.06806372 CC1CCC(LC=0)C(=C)C 0.06819661 CC1=CC(=C)C(=C)C 0.06819661 CC1=CC(=O)C(=C(C)C)CC1	0.0682767 0=C1C(C)=CCC(C(C)C)C1 0.06843499 CC1CNC(CN1C(=0)0)C	0.06849173 CC1(CCN(CC1)C(=0)0)0 0.06864301 CC1(CCN(CC1)C(=0)0)C	0.0686631 CC1(CC(=CC(=O)C1)MC)C 0.06879747 C1CM(CCC1CC0)C=O	0.06883269 CC12CCCC=C10CC2=0 0.06891363 C=C(CC1CCC=CC1)C=0	0.06926642 CC(CICC=C(C=0)CC1)C 0.0693349 CCICC(C(=C1)C)C(=0)C	0.00066745 CCI(CCCM(CI)C(=000)C 0.00082317 CICC2=CC=CC=C(=0)C2MCI	0.07035182 CONTCC(=0)C(C1C)C 0.07031169 CICC(CNC1)CC(C=0)N 0.07035861 CC1CC(CNC1)CCC(C=0)N	0.07114938 CCLCC(=CCNLC/C/=C 0.07114938 CCLCC(=CCNLC/C/=CONC/C/=O/C 0.07113115 CC1=CC//C/C/=-O/O/O/C	0.0712314 DOLE-COCADOCICCE 0.0712314 DICE-CCO-DOCICCE 0.07147205 CCI2CCCC1 YE-ECC	0.07168902 CCICC(=CCCIC(=0)C)C 0.07168178 C1CC=C(C(1)CCC=0)D	0.07210112 CCC(=0)C1(CCOCC1)C 0.07225106 CC(C)(C)C1CC(=0)C=CN1	0.07241177 CC1CC=CCC1(CO)C=0 0.07245435 CC1(CCC(=CO1)OC)C=0 0.07552033 C1CACC1CC/C=0/M	0.01223035 CICKIC-1001
Mor185-1	0 C(=C 0 0=C 0 C1CC	5558	0.4097808 CC(=C)C1=C0C=C1 0.4227823 CCC1=CCC(CC1)0 0.4271719 CCC1CCC(CC1)N	0.4313385 C1CC(=0)C2(C1)CC2 0.4430801 C1CC(=0)C2=C1N=CC=C2 0.4515747 C1CN2CCT=0)CC2=CN1	0.4557655 CIC(CC2CIONC2)N 0.4625187 CIC(CC2CIONC2)N 0.4625187 CIC(CC2CICI)CC2=0	0.472155 C1C2C=CC=CCC(N1)0 0.4769287 C1CCC2(CC1)CC20	0.4788082 C1CCC2=C(C1)C(=O)CN2 0.48704 CCC1=C(CCCC1)O	355	88	0.5103795 CC1=CC(=CCC1)OC 0.5108372 CCC1=CC=CC=CLN 0.5108372 CCC1=CC=CC=CLN	0.513459 CLC(CCLUNCZ)W 0.513459 CC(=C)C1=CNC=C1 0.5130736 CC(C)CLCNCC=C1	0.5160087 CICC2CCC(=0)C3C2(C1)03 0.5162618 CICCC(C2CMCC2C1)N	0.5202251 C1CC2=C(C=C1)NNC(=O)C2 0.5209791 CC(N1CCCCCC1)O	0.5217194 C1CC(=0)C2=C1CC=CC=C2 0.522958 C1C(=0)CMC2=CC=CC=C21	0.5243087 CLOON2CCCOC(=0)C2C1 0.5249237 CLCC2=C(C(=0)WCL)N=CN2	0.531335 COCL=CC(=0)MCCN1 0.5317809 CLCCN2CCMC(=0)CC2C1	0.5349245 C1=CC2=C(NC(=0)C=CN2)N=C1 0.5361614 C1CCC(CC1)C2CCC2=0	0.5376741 CICC2=C(CC1=0)C=CN2 0.5382746 CICC2CC(=0)CCN2C1	0.5403689 CCC1=C(C=MC=C1)C 0.5430105 CC(=0)N1CC2CC1CN2	0.5452694 C1=CC2=C(C=C1S)C=NN2 0.5483312 CC1=C(C=NC=C1)C=C	0.5522314 CLCC2CCC(=0)C=C2C1 0.5534906 C1=CC2=C(C=C1C(=0)0)NC=C02	0.5544272 CN=CICCCC(=0)C1 0.5577659 CI=CC2=CC=CC(=0)N2C=C1	0.5586555 CCIC.2C(COCO2)0C01 0.5609908 CMLCOACCCICO	0.5635416 CIC=CCOC2NIC(=0)C2 0.5649692 CCICCC(=C1)SC	0.565907 C1=CC=CZC(=C1)C(=0)N=C02 0.5676443 C0C1CC(CCC10)C2C02	0.56807 CIC(CNC1C0)S 0.5702246 CICCC2C(CI)CCC(=0)O2	0.5746414 CC(=0/L)=CC=NC=C1 0.5754528 CC(=0/C)C2C1COC2 0.5754528 CC(=0/C)C2C1COC2	0.5797328 COCI=CC2=C(C=C1)C(=O)CC=C2 0.5797328 C1=CC2=C(C(=O)M=CN2)N=C1 0.5797328 C1=CC2=C(C(=O)M=CN2)N=C1	0.580173 CULCC=0./LZ=NNC.NZCL 0.580173 CNLCC2=C(C1)/CNC2 0.586857 C1CCC2/C1)/CCC/02/O	0.589029 CLECCC0020000000000000000000000000000000	0.5975424 C1=CN=CC2=C1C(=0)NN=C2 0.5976542 CC1=CA=CC2=C1C(=0)NN=C2	0.5979454 CIC=CC=C2CICC(=0)C=C2 0.5988352 CICC(=0)C=CC=C1	0.6003185 CC(CLCCCC=C1)N 0.6020785 CCC1=C(C=CN=C1)C	0.6037065 C1=CNC2=NC=NC=C2C1=O 0.6041441 CC1=C(CCCC1)OC	0.6078608 CC(=0)CL2CC(CL)C2 0.608671 CIC(=0)M=NN1C2=CC=CC=C2	0.6094027 COCI=CCC(=N)C=C1 0.6102408 CC1=CC0C2=C1C=CC=N2	0.6115156 COCLECC2 =C(C=C1)C(=O)NCCN2 0.6115773 CN1C=NC2 =C1CCNC2	0.5128066 CC(=O)N1CCCC=C1 0.5128066 CC(=O)N1CCCC=C1 0.5135868 C1CCC2=C/C1VN=C/M1=M2VI	0.0133900 CLCCC2=C(CL)M=C(m=M2/M 0.0155297 CLCCC2=C(CL)CCCC2=0 0.6166073 CLCCC2=C(CL)CCCCC2=0	0.6211655 C1CC2=C(CC=C1)C(=0)CC2 0.62116972 C1=C(CC=C1)C(=0)CC2	C1CC2	0.6226769 CC(=0)N1CC2CC1C02 0.6232394 C1CN(C1=0)C2=CC=C02	0.626257 CICCC2C(CI)CCCC20 0.6275748 COCI=CC=C(C=CI)C(=0)N2CC2 0.6273987 COCCPC1CCC01	100000000000000000000000000000000000000
Mor184-1	0 CCL = CC[C@@H] (CCL = 0XC = CX 0 CCL = CC[C@@H] (CCL = 0XC = CX 0 CCL = CCC[C@H] (CCL = 0XC = CX 0 06619 003 CCL = 0XYC = CX	0.08323528 CCICCCCCCC=0/XC=0 0.078505 CCI=0/CICC=C(CCI=0/XC=0/CI)0 0.0810557 CCI=CCC(CCI=0/XC=C)C=0 0.08323528 CCI(CCCCCI=0/XC=C)	0.09673947 CCLCC(=0)C(C(=0)C1)CC=C 0.1024509 CC1=CC(=0)C(CC1)C(=C)C 0.1030488 CC(=C)CC1(CCCCC1)0	0.1099358 C=CCCLCCC(=0)NC1=0 0.1100806 CC(=C)CLCCC(CC1)C=0 0.1146739 CC1CCCCC(=0)C1)C(=C)C	0.1150157 CC1C(CCC1C(=0.0)) 0.1202605 CC1=CCC(CC10)C=C 0.1202605 CC1=CCC(CC10)C=C)C 0.1237537 CC1=CC1CCCC=CC1X(0)D	0.1254566 CC(=C)CICCC(=CC1)C(=0)N 0.1294035 C=CCCC1C(=0)CCC21=0	0.1318522 CC(CC=C)C1CCCCC1=0 0.1335452 CC1CCCC1(CC=C)CC=0	0.1366252 CC(=C)CC1(CCCCC1)C=0 0.1366252 CC(=C)CC1=CCCCC1)C=0	0.1383896 C=CCICCC(CC1)C(=0)00 0.1389853 CC(=0)C(=C)CICCCCC1	0.1393494 CC(=C)CC1(CCCCC1=0)C 0.1397765 CCCCC(=C)C1(CCCCC1)0	0.142249 COLOCOCOCOCOCOCOCOCOCOCO 0.14513 CC(=C)CICCC(=CC1)C=N0 0.1455027 CC(=C)C(C1=CCCCC1=0)0	0.1477967 C=C(CC1CCCC(=0)C1)C=0 0.1491949 CC1CCCC(=0)C1CC=C	0.1500831 CC(=C)CC1(CCCCC1)C 0.1531366 C=CCC1CC(C1)C(=0)O	0.1534062 CC1C(=0)CC(CC1=0)C(=C)C 0.1549527 CC1(CCCCC1=C)CCC=0	0.1551537 cc(=0/c1(cocc c1)c=c 0.1592257 cc1coc(cc10)c(=c)c	0.1595478 CC1=CCC(CC1)C(=C)CC(=0)C 0.1598404 CC(=C)C1CCCC(=0)C1	0.1613346 CC1=CCC(CC1)C(=C)C=0 0.1615579 CC(=C)CCCCCC1=0	0.1619112 CC(=C)CICCC(CC1)C0 0.1621826 CC1=C(CC(CC1=0)C(=C)C)0	0.1636.204 CCLCCC(CCL)C(=C)C0 0.1664853 CC(=C)C1CCC(CCL)0	0.1687667 CCICCCC(=0)CICC=C 0.1698968 C=CCCCCC1(CCCCCC1)O	0.1706281 CC(=C)C ICCC(=CC1)CCC=0 0.171085 CC(=C)C C(=0)CC1CCCCC1	0.1718966 CC(=C/CCICCCCCC1=0 0.1723568 CC1C(C(0C1=0)C/CCCC=C	0.1726051 cc(=c/cccl(ccccc1)0 0.1731622 ccl(c(=0)cccc1=0/cc=c	0.1745533 CC1=C(C(CC1)C(=C)C)0)0 0.1748691 C=CCC1(CCCCC1)C=0	0.1751408 CC1=CC(C(CC1/C(=C/C)) 0.1754592 C=C1CC(C(=O)O)N	0.175988 CC(=C)CICCC(CC1)(C)0 0.1761884 C=CC1(CCC(=O)CC1)0	0.176395 CC1(CCCC)=CX0X.C1 0.176395 CC1(CCCCC=C)C0C0 0.176595 CC1(CCCCC=C)C0C0	0.1785427 CC(=C)CLCCC(=0)CC1 0.1786124 C=CCCC1(CCCCC1)0 0.181816 CC(-C)C1-CCC-AV-C1VC-VV	0.1812771 CC1=CCC(CC1)(CC=C)0 0.1812771 CC1=CCC(CC1)(CC=C)0 0.18209 C=CCC1(CCCCC1=D00	0.1834068 CCICCC(C(1)0)C(=C)0 0.183408 CCICCC(C(1)0)C(=C)0 0.1838148 CCICCCC(C1=0)CC=C	0.1843654 C1(=0)(=0)C(=CCC(C1)C(=C)C)C 0.1845829 C=CC1(CCC(=CC1)C=0)C=0	0.1848174 CC(=0)CCCC1CCCC1=C 0.1850502 CC(=C)C1CCC(=CC1)C(=0)O	0.18571 C=CCC1CCC(=0)C=C10 0.1867364 CC(=C)C1CCC(C1)(C)C(=0)0	0.1881487 CC(C)C1=CCC(=C)CC1 0.1892903 CC(=C)C1CCC(=C(C1)O)CO	0.1901027 CC1=CCC(CC1)C(C)=C 0.1909013 CC(CCC1C(01)(C)C)C=C	0.1920341 C=CC(=0/C1(CCCCC1/0 0.1925363 CC1=CCC(CC1=N0/C(=C/C	0.1925621 CC(=C/C I(CCCCCI)0 0.192789 CCI(CCCCCI)C(=C)CC(=0	0.1939/3 CC(=C/c(=O)CLCC(=O)CLC 0.1939808 C=CLCC=C(C(=C1)O)C(=O)O 0.1943788 CC(=C)C(CCCC1=O)	0.119417.00 CC(=C)CCLCCCCCCC	0.2012826 CCI(0)CCCC(C(C)=C)C=C1 0.2012818 CCI=0)CCC(C(C)=C)C=C1	0.2033238 C=CICCC(=NNC(=O)N)CC1 0.204286 CC1=CC=C(S1)CC(=C)C(=O)O	0.2047669 C=CCCCICCCC(=0)C1 0.2070898 CC1=C(C(=0)CCC1)CCC=C	0.2073703 CC(=CICCC(01)(C)C=C)C 0.2074198 CC1(CCCC(=0)01)CC=C 0.2074182 C=CCC(CCCC1=0)01	
Mor170-1	0=0100023=010=00=02 0=01000023=010=00=00 0=010002=0(0=0020)=01 0=01002=070=02010=01		COC(=N)C1=CC=CC=C1 C1=CC=C2C(=C1)C(=O)N=CC=N2 C1C2=CC=CC=C2ON=C1C=O				z	CCIECC(=0)C2=CC=CC=C201 CCI=CC(=0)C2=CC=CC=C201 CNIC(=0)C2=CC=CC=CC=C2N=NI	2)C#N	CC(=0)MN=CC1=CC=CC=C1 C1=CC=C2C(=C1)C=CC(=0)M2 CN1C7=CC2=C7=C7=C7=C1M		-		N(2	0	CC1=COC2=CC=CC=CC=C21=0 C1=CC=C2C(=C1)C(=0)OC=N2	C1=CC=C2C(=C1)C(=0)N=C(S2)N CC1CC(=0)C2=CC=CC=C201	CIC(=0)C2=CC=CC=C 20N1 C1=CC(=CC=CIC=0)S	C1=CC=C(C=C1)C=NC=0 C1=CC=C2C(=C1)C=C(C(=0)O2)N	CON IC2 = CC = CC = C2 C1 = 0 C1 = CC = C2 C(=C1)C(= CC(=0)02) N	C=CCOC(=N)C1=CC=CC=C1 C1=CC=C2C(=C1)C(=O)C(=C02)N	C1C0C(=N1)C2=CN=CC=C2 C1=CC=C(C=C1)C=CNC=0	C1=CC=C2C(=C1)C(=0)N=C(N2)NC#N C1=CC=C2C(=C1)C(=0)N=CN2N	C=C1C0C2=CC=CC=C2C1=0 CN(C)C1=CC=C(C=C1)C=0	cc(c(=0)c1=cc=cc=c1)N	CC1=NC2=CC=CC=CZC(=0)01 C1=CC=CZC(=C1)C(=0)C=CN2	CULTCUCZ = CC = CC = CZ =	CCI=CC(=0)C2=CC=CC=C2N1 CCCCOC(=N)C1=CN=CC=C1 CCCCOC(=N)C1=CN=CC=C1	CIOC(=0)C1=CC=CC=C2 C1=CC=CC=CC=C2=C2 C1=C7=C7C1=C1 VC1=C10C=CN02MN	COLLECC=C(C=C1)C=NC#N COC1=CC=C(C=C1)C=NC#N	COC1 = C2C(=CN = N1)C=CC=N2 CN1 C=NC(=O)C2=CC=CC=C21	C1=CC=C2C(=C1)C(=0)N=NS2 C1=CC=C(C=C1)C(=0)N=CS	CNC(=0)C1=CC=C(C=C1)S CNC(=0)C1=CC=CC=C1	CC1=NC(=0)CC(=N1)C2=CN=CC=C2 C1=CC=C2C(=C1)C(=0)C=C02	C1=CC(=CC(=C1)N)C(=0)CN C1=CC=C2C(=C1)C(=0)C=C(N2)N	COC1 = CC = C(C = C 1)C 2 = N NCN = N 2 C1C(= 0)C2 = CC = CC = C2 0S1	CIIC=CC=CC=CZCI=0 CIC=CNZNINC2C3=CC=C(C=C3)0	CIECCE(C=CJ)C=NAC=O CICCIC(=O)NN=CC2=CN=CC=C2 CC1=CC2=CT=CC=C2=CN=C	C=C(C1=CC=CC=C1)0 C=C(C1=CC=CC=C1)0	COCCI=C)/OCC=CC=CC COC1=CC=CC(=C1)C=C=C CCSC(=0)C1=CN=CC=C1	C1=CC=C2C(=C1)C(=0)N=CN2 C1C(=0)C0C2=CC=CC=C21	CICC1NC(=0)C2=CC=CC=C2 CN(C)C1=CC=C(C=C1)C(=0)C#N	CIC2=C(02)C3=CC=CC=C301 C=CCIC0C2=CC=CC=CC1=0 C1=CC=C7C1=C1+CC=C0A4A1=A12+CC	

Table 3.16 Continued

	Distance 0	0.04581804 0.04753237	0.04908247	0.06334015	0.06633087	0.07077628	0.07088963	0.07283703 0.07466881	0.07735112 0.07825345	0.0817986	0.0845592	0.08888077	0.08920102 0.08954888	0.08968592	0.09056786 0.09156643	0.09158454	0.09274995	0.09456447	0.0951854	0.0954759	0.09713763	0.09923997	0.1007118	0.1009531 0.1010144	0.1020273	0.1030238	0.1042897 0.1057732	0.1075921 0.1079465	0.1080846	0.1095993	0.1104009 0.110401	0.1106139	0.1116488	0.1128842	0.112892 0.1143021	0.1151577	0.1158386	0.1167684	0.1186123	0.1214704	0.1216725 0.1234908	0.1238225 0.1249956	0.1269258 0.1297072	0.1299016	0.1319032	V 0.1326711 0.1342538	0.1348869	0.1351912	0.1351973 0.1352406	0.1361757 0.1368982	0.1369147	0.138562	0.1395212	0.1407029	TCOT+T'O	
Mor260-1	Distance SMILES 0 c(= 0) (ccccccccc)0 0 c(cccccccc)5	0.04197753 COC(= 0)(CCCCCCCC)0 0.04197753 COC(= 0)CCNC1=CC=CC=C1 0.09340541 C=CC(=0)CCCCCCCCC(=0)0	0.03240341 C=CC(=C/CCCCCC(=C) 0.0390186 C#CCCCCCC=CC(=O/O	0.1129747 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	0.11715 CCCCCN1 = 0,000	0.1401864 CNC(=0)COC1=CC=C(C=C1)C#N		0.1550444 CCCCCCLCCCCCCL)C(=0)0 0.1553915 CCNCCC1=CC2=C(C=C1)0C02	0.1566442 CC(=0)CCC(=0)NC1=CCCCC1 0.1586167 CCCC1CCC(CC1)CCC(=0)O	0.1601506 COC(=0)C=CCNC1CCCCC1 0.1621343 CCCCC/=0)C=NCCNC/=0)CCCCC1	0.1633878 CNCC1=CC=C(C=C1)N2CCCC2	0.1651134 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	0.1667638 CCCCCCCCCCCCC(=0)CC(=0)0 0.1670003 CCNCC1=CC=C1C(=C1)C(=0)0C	0.1673194 CCCC0C1=CN=C(C=C1)C(=0)0	0.1704537 COC(=0)CMCCC1=CC=CC=C1 0.1718171 CCCCCCCC(=0)NCC	0.1760533 CCCCCCNNLC=NC=NL 0.1825772 CCCCCC1=NC=CCC=C1VC=OVO	0.1861117 CC1=CC=C(C=C1)C=NNC(=O)C	0.1953836 CC1=CC=C(C=C1)NC(=0)COC 0.1961028 C=CC1=CC=C(C=C1)CCCC(=0)0	0.1965068 CCCCC1=CN=C(C=C1)C(=O)NC 0.1998679 CC1=CC=C101VC=NMY7=OVC	0.2033951 CCCCCCCCCC(= 0)0	0.2043851 CCOC(=0)NN=CC1=CC=C(01)C 0.2051726 CCCCCCCOOOC(=0)O	0.2064523 CCOC1=CC=C(C=C1)CCNC 0.2291434 CC1=C1CC=C12NN=CCC=C100C	0.2299909 CCCC(=0)NC1=CN(N=C1)COC	0.2319916 CCCCCCCCCCCCCCCCCCCC 0.2394643 COC1=CC=CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	0.2401632 CC1=CC=C(C=C1)NCC2=CC=NC=C2 0.2412083 CMC1=CC=C/C=C1+C2	0.2420575 CCCCCCCC(=0)NC	0.2441588 CCCCCCCCCCCCCCCC=CC(=0)C1)0 0.2570274 CCCCCC1=CC=C(C(=S)C1)0	0.2599685 CCCCOC1=CN=C(N=C1)C(=O)O 0.2603975 CCOC1=CNC2=C1C=CC(=C2)OC	0.2610168 CCONCLON(CC1)C	0.2620487 CCCCCCCN (C)C (=0)0 0.2637201 C=CCCCCCC(=0)CCCC(=0)0	0.2639623 CC(= 0) CCCCC CCS 0.2643008 CNCC1=NOC(=C1)C2=CN(N=C2)C	0.266331 CC1=CC=C(C=C1)C= CC(=0)NC 0.2674834 CC1=CC=C(C=C1)NCC(=0)NC	0.273599 CCCCCOLICCON1	0.2774421 CCCl = C = C = C = C = C = C = C = C =	0.2779931 CCCCCOCCC(C)S 0.2794787 CCCCCCOC(CC)CS	0.2808203 CCCCCCCCCCC(=0)NC 0.282005 C=CCCCCCC(=0)NC	0.2878304 C1=CC(=CC=CLCCCCXN)C(=0)0 0.2883403 C1C=C1CCCCCCCC	0.2911803 C=CCNC1=CC=C(C=C1)C#N	0.3006473 CN(C/CCNCCI = CC=C01	0.3034644 CCCC1=CC=C(C=CL)NC2=Nc=C(C=N2)cm 0.3034644 CCCC1=CC(=CC=C1)NC(=O)C=C	0.3036508 CCOC(=0)CC1=CC=C(C=C1)NC 0.3040234 C1=CC=C(C=C1)C(=0)CCCC(=0)0	0.3040574 CCCCCCC1=CC=C(C=C1)0 0.3041203 CCC(CCC1=CC=C(C=C1)0)C#N	0.305162 CCC0C1=CC=C(C=C1)C=N0 0.3061267 CCCCCC=O)C1=CC=C(C=C1)O	0.3071959 CC(=0)C=C(C=CC1=CC=CC=C)0	0.3130324 CCCCCCCCCCCCC	0.3138424 C1=CC=C(C=C1)NC2=CC=C(C=C2)C#N 0.3148852 CC(=O)NC1=CC=C(C=C1)OC(=O)C	0.3160575 CC(CCCCOCCC#N)C(=0)0	0.3197115 CC1=CC=C(C=C1)C2=CC(=C(C=C2)C)O	0.3234246 CNC(=0)CCCCCCCC=C 0.3263573 CCCCCCCC(=0)0	0.3264308 CC=CC=NNC(=0)C1=CC=CS1 0.3301505 CCCCCCLCCC(=N0)CC1	0.3326617 CCC(CC)NCCOC(=0)C=C 0.3337109 CCCCCC2(=0)CCCC1=000	0.3351018 CCC1=CC=C(C=C1)NC(=0)C(C)C	0.300/59 COCI = CC = CC = CC = CI NCCC *N	0.342283 CC(=CCL=CC=CC=C(C=CJ)CC(=C)O/ 0.3422433 CCCC1=CC=C(C=CC)CC(=C)O/ 0.342200 CL CCC1=CC=CCC=CCC		
Mor259-1	SMILES 0 C1C2=CC=CC=C20C1=0 0 c1(cccc1)C(=0)c2cccc2	0 0=CL0C2=C(C=CC=C2)C=C1 0.04626341 C1=CC=C2C(=C1)MC(=0)C=N2 0.04664833 C1=CC=C2C(=C1)MC(=N2)C=0	0.00264368 C1 =CC2 =C(N)=C2 =C1) 0.07264368 C1 =CC2 =C(N)=C2 =C1) 0.07238415 C1 =CC2 =C1)	0.08079227 CC(=0)NCL=CC=C(=C1)C(=N)N	0.08123408 CI = CCC = CCC = CI)NC = O)O2	0.08243389 C1=CC=C2C(=C1)NC(=O)NN2	0.08274814 C1=COC(=C1)C2=CC=C(C=C2)0 0.08415395 C=C1C2=CC=CC=C2OC1=0	0.08472221 C1=CC(=CC=CC=C1C(=O)O)NCCC#N 0.08486507 CN=CC1=CC=C(C=C1)C(=O)OC	0.08532597 C1=CC=C2C(=C1)C=C0C2=0 0.08674062 C=CC(=O)NC1=CC=C(C=C1)C(=N)N	0.08754144 C1=CC=C2C(= C1)C=NN2C=0 0.0813503 CN=NNC1=CC=C/C=C1 V/=0)0C	0.08876163 C1=CC=C2C(=C1)C(=C2)N=O	0.0889943 COULECCEC(CECI)NC(E0)CEC 0.08899985 CC(E0)NCLECCEC(CECI)N(C)C	0.0890455 CCC(= 0)C1=CC=C(C=C1)OC 0.09011572 C1=CC=C2C(=C1)C=C(C=N2)O	0.09045361 CCNC1=CC=C(C=C1)N(0)0	0.09100104 CCC(=0)C1=CC=C(C=C1)NO 0.09216601 C1=CC=C2C(=C1)OS2(=0)=0	0.09277338 C1C2=CC=CC=C2S1(=0)=0 0.0831637 CCNC1=CC=CCC=C1 VC=0 VCC	0.09397485 C1=CC=C2C(=C1)C=C2(=0)=0	0.09415977 CL=CC=C2C(=C1)N=C52(=0)=0 0.09510532 COC1=CC=C(C=C1)C(=0)CN			0.09783618 C=NC(=0)C1=CC=C(C=C1)C(=0)N 0.09784775 C1=CC=C2C(=C1)N=CN2N=0	0.09796812 COC1=CC=C(C=C1)NC(=O)N 0.09843545 CC0C(=O)C1=CC=C1)N(C)C	0.09886127 C1=CC2=C(SC(=C2C=C1)0)0	0.09949614 C1=CC(=CC(=C1)N)C2=NC(=0)NN2 0.09987804 CN(C)C1=CC=C(C=C1)NC(=0)N	0.1003145 COC(=0)C1=CC=C(C=C1)NN=C	0.101283 C1C(=0)C=CC2=CC=C2	0.1014415 C1=CC=C2C(=C1)C=CN2C=O 0.1014849 C1=CC=C2C(=C1)N=CN2C=O	0.1015078 C1=CC=C2C(=C1)C=NC(=O)N2 0.1016095 CC1=CC=C1)C2=NOC(=N2)C	0.1016398 CC=CC(=0)NC1=CC=C(=C1)OC	0.1019654 C=CIC=CC(=0)C2=CC=CC=CL2 0.1035476 CC1=NC=C(C2=CC=CC=C12)0	0.1043858 C1=CC(=CC=CLNCC(=0)NC=0)0 0.1044181 CC1=NC(=C01)C2=CC(=CC=C2)N	0.1044385 C1= CC(=CC(=C1)NC(=O)CCS)N 0.1048361 COC1=CC=C1C=C1VC=NNC(=O)N	0.1051196 C1=CC(=CC=C1C=0)C2=NN=C02	0.103548 CI =CC=CC(C=CI)C(=0)NNC2=0 0.105717 COCI =CC=CC(C=CI)C(=0)NNC2=0	0.1058726 CC1=CC=C(C=C1)N2CCNC2=0 0.1058831 C1=CC=C2C(=C1)C=CC(=0)N2	0.1063838 CCC(=0)C1=CC(=CC=C1)OC 0.1065172 CC1=CC=CC(=C1)C2=NC(=0)NN2	0.1070297 C1C2= CC=CC=C2(=0)(=0)01 0.1071082 C=C1C2=CC=CC=C2MC1=0	0.1071924 C1=CC=C2C(=C1)C=C(N2)0	0.1072834 C1 =CC(=CC=CIC=0)C=C(=0)C2=NC=NO2	0.10743594 CI =CC=CC(=CC=CC(=C)C=CC(=C)SC(=C)S 0.1076403 CI =CC(=CC=CC(=C)S)C(=C)S	0.1077243 CC1=CC=C(C=C1)C2CC(=O)C2 0.107799 CC(=O)NN=CC1=CC=C(C=C1)OC	0.1078811 C1=CC=C2C(=C1)C(=NN2)NC=O 0.1080445 C1=CC=C2C(=C1)C(=CN2)C= O	0.1080824 CIC2=CC=CC=C2CNIC=O 0.1081034 C1=CC=C2Cf=C1XCf=CN2NN=O	0.1083373 C1=CC(=CC=CLCCKN)CCC+N	0.10844303 C=CC(=0)MC=CCC(=C1)M 0.1084479 C1C=CC(C=C1)C2=CC=CC=C20	0.1084723 C1=CC(=CC=CLM)N2C=CNC2=0 0.1086097 CC(C1=CC=C(C=C1)C(C)OC)OC	0.1087269 C1=CC(=CC=C1C(=O)0)N=N 0.1087848 C1=CC(=CC=C1C(=O)0)N=N	0.1091177 CIC2=CC=CC=CC=C2C001	0.1091268 CIC=C(NC2=CC=CC=C21)C=0 0.1092127 C=CC(=O)NC1=CC=C(C=C1)0	0.1097492 CC(C)C1=CC=C (C=C1)NC(=O)C 0.1097619 C1=CC2=CN(N=C2C=C1)C=O	0.1103146 C1=CC=C2C(=C1)C=C(C=N2)C=0 0.1103637 C1=CC=C2C=NC=C2=C1)C=0	0.1105087 C1=CC=C2C(=C1)NC(=CN=0)02 0.1107137 C1=CC=C2C(=C1)NC(=C)MC2=0	0.110907 C1=CC=C2C(=C1)C=CC(=N2)C=O	0.1110351 CC1=CC=CC(=CC1)C(C=0)C 0.1110351 CC1=CC(=CC(=CC1)N2C(=O)CC=N2		
Mor258-1	istance SMILES Distance 0 C1C2=CC=CC=C20C1=0 0 0= C10C2=C(C=CC=C2)C=C1	0 ct(=0)Cccccc1 0 ct=ccc=cc(=c1)NC(=0)C=N2 0 cr1 ===================================	0.1277119 CIL CC2 C(N = CN2C = C)C			0.2373345 CC1=NC2=C(C=C1)NC=N2	0.2398072 CMC1=CC=NC=C1 0.2537211 CC1=NC(=NC=C1C#N)C	0.256625 CC1=CCC(=0)CC1 0.266695 C1=COC(=C1)C2=NN=NC=C2	0.2654262 CC1=CC2=NC=NN2C=C1 0.2666345 CC(=0)OCSC	0.2891708 C1COC2=C1C=C(C=C2)C(=O)O	0.2910104 C1=C2N=C(N=CN2N=C)C#N	0.2941937 C1=CC2=C(N=C1)SC(=C2)C=O 0.2947368 C1CC2=C(C=C1)NNC(=O)C2	0.2981597 C1CSN(N1)COC(=0)N 0.2988469 C1CC(SC1)CO	0.3023335 CC1=NN(CS1)C	0.3041483 C1CC2=C(C1)SC(=N2)N 0.3058697 C1C=CC2=CN=NC2=C1	0.3085566 CC1=NC2=C(01)C=CN=N2 0.3135661 C1CN/C1)C2=MC=C03	0.3146737 C1= CC2 = C(N = C1)N = C(N2) C= O	0.319479 CLCRCCI=C(C=NC=CL)N 0.319478 CLCN2C=CC(=O)N2C1	0.3250441 CC1=NC2=C(01)N=NC=C2 0.3351572 C1C=M2C1CC=O	0.3361486 CCLCC=COCL	0.338916 CIC2=CC=CC=CC=CNNIC(=0)0 0.3389186 CI=CSC(=C1)C2=NNN=C2	0.3397872 C1=CC2=C(C=C10)C=C(S2)C(=0)0 0.3415637 CC1=MC3=MC=MC=C2N=C1	0.3432483 C1=CN(N=N1)CC(=O)N	0.3545416 CICNCC(=C1)C=O 0.360758 C1C=CC2=CIC=C2XC(=O)O	0.3633213 CC1=CC2=C(C=C1)C=NC=C2 0.364702 C1C2(=C02)C=NC=C2	0.3713083 CC1=NC2=C(C=C1)NN=C2	0.3728931 C1=CC2=CC(=NN2C=C1)C(=O)O 0.374313 CC1=CC2=C(C=C1C)N=C(N2)N	0.3753883 C1CCOC(=N)C1 0.3809527 CC1CN1C(=0)SC	0.3838605 CICC(OC=CI)C=O	0.3890282 C1=CC=C(C=C1)5C0 0.3897468 CCS(=O)(=O)MC1CC1	0.3888208 C1C= CC(01)OC=0 0.3898445 CN1CCCC(=C1)C=0	0.3946607 CC1= CC2=C(C=C1)OC=C2 0.3944630 CC1-CC5=C1	0.4047688 CCICCC(=0)C01	0.4052417 CMC(=0)NICCIC#N 0.405968 COCI=CC2=NN=C2C=C1	0.4075889 C#CCSCC(=O)N 0.4078831 C1=CC=C2C(=C1)N=CN2N=O	0.4085535 CI(=0)C=CCCC1 0.4213588 CIC2=CC=CC=C2N=C100	0.4240297 CICC2=C(C=CN2C1)C=O 0.42440555 C=C1CCC7=O)C=C1	0.4252747 C1=CN=C2C(=N1)C=C(S2)C(=O)O	0.4264494 CC1=NC2=CN=NC=C2N=C1	0.4276709 CICNC(CNI)C#N	0.4281004 CNC1=NN(C(=O)C=C1)C 0.4287692 CSCCC(=O)O	0.4297029 CC(=O)NN ICC1 0.4309587 C1N=CSN1CC=O	0.4316256 CCC(= 0)C1=NC=NC=C1 0.4323462 C1=CC2+CC4=CC(=C2)SN=C1	0.4329099 C1= CN(N=C1C+N)CO	0.4353019 CSNC(=0)NICC1	0.4356453 CL= CN2C=C(N=CC2=C1)C(=O)O 0.4356482 CL= CC=NC(=C1)N2C=NN=C2	0.4372975 CC1=CC2=C(C=C1)0C02 0.4372975 CC1=CC2=C(C=C1)0C02	0.4392266 CICCINCC(=O)N	0.440694 CICONCIC=0 0.4415777 CC(C#N)OCC=C	0.4417036 COCICCC(=0)01 0.4420935 CICC=C(C=C1)C(=0)N	0.4421728 CC1=NC(=C2C=NN=C2)NN1 0.4453138 CC1=MC3=NC=NC=C2N1	0.4466413 CC(=0)CICSCNI 0.4470504 C1C=C7C1=C7C1=C30M0M13	0.44.70.558 CCL = CCC = CCC = COCC = CCCC = CCCCC = CCCCC = CCCCC = CCCCC = CCCCCC	0.44480569 CCLCC2=CC=C(C=C(C=C)S)C=N1 0.4523235 CNLC2=C(C=C)C(C=C)S)C=N1		
Mor256-17	Distance SMILES D 0 C1C2=CC=CC=C20C1=0 0 0 CCC(=0)C(=0)CC 0	0 C(CCCC)OC(=0)CCCCC 0.3793798 C(=0)(CCCCCCCCC)0 0 3293748 C(=0)(CCCCCCCCC)0	0.384888 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	0.4719471 C(CCCN)/CCC(=0)0	0.4926594 CCCCCCCCCCCCCCV	0.534839 CCCCCCCC(=0)0CCC	0.5353036 CCCCCC(=0)00CCCC 0.5594665 CCCCCCCCCC(=0)N	0.572254 C(CCCC(=0)0)CCCN 0.5755313 C(C)0C(=0)CCCCCCC	0.5820786 C(CCCC)OC(=0)CCCC 0.5914498 C1=CC=C(C=C1)CCCCCCN	0.5925996 CC(=0)NCCCCCCN 0.5891708 CCCCCCNC/=01CCC	351	0.6157112 CCCCCCCCCCCCCCCCCCC	0.620347 C1=CC=C2C(=C1)NC(=0)02 0.6529591 CCCCCCNCC(=0)0	0.659726 C1CCC(CC1)(0)S	0.668126 C1 = CC = C(C = C1) CCC CCN0 0.670643 CC(=0) CCCCCCC(=0) C	0.6741813 C1=CC=C2C(=C1)NC(=O)N2 0.6754651 C1=CC2=CNON2C=C1	0.579814 CCCCCCCC(=0)N	0.6824018 CCC1=NN=C(S1)NC 0.6834855 CCCCCCCCC1=CC=CC=C1	0.6870004 CNCCCCCCCC(=0)0 0.6619384 CCCCCCNC(=0)0C	0.6920565 C#CC1=C(C(=CC=C1)C#C)N	0.6959268 CCCCCCCCC(0)(0)0 0.7001146 COCC0C1=CC=CC=C1	0.706339 CCCCCCCC(=0)COCC 0.7083084 CCCCCCCNC(=0)MC		0.7128538 CMC1=NN=C(S1)NC 0.7133358 CCCCOC(=0)NCCCC	0.7146281 CCCCCCCCCCCCCC	0.7190709 CCCCCCCCCCCC(= 0)NC	0.722355 CCCCCCCCCCCC(=0)C 0.725016 C#CCCCCCCC(=0)O	0.7262696 CCCCCCCCC1=CC=C01 0.7266735 C1CNC2=C1SC=C2	0.727193 CC(C)(CNC1=CC=CC=C1)N	0.7281083 CCCCCCCCCC = 0/N 0.7379573 CCCCCCCOC (= 0/N	0.7390813 C(CCN)CCNCC(=0)0 0.7400931 C1=CC=C(C=C1)0CCNN	0.7418715 CLCNC2=CC(=C(C=C21)0)0 0.7424576 CLCCCC1VNVS	0.7432415 CCCC1=COC(=N1)C2=CC=CC=C2	0.7559961 CC=CC1=CC=C(C=C1)NCC#N	0.7599564 CCC1=CC=C(C=C1)OC(=O)CC 0.764867 C1CCN(CC1)C2=CNC=C2	0.7665449 CCOC(=0)OCCCCCCN 0.7680675 CCCCCCCCCI=0WCO	0.775816 COC(=0)C(=0)CC 0.7768097 CCOC1=MC(=NUNN	0.7769156 CCC(=0)CCCCCCCC(=0)CC	0.78395 CC#CCCC1(OCCO1)C	0.7847848 COLLEC(C(=CL=C1)0C)9C 0.7882237 CCC1=CSC(=N1)CC	0.7885484 CC(=0)0CC1=CC=C(C=C1)N 0.7890455 CCCCCCCCCCC(=0)0CC	00		0.7958007 CCCCCCNN=C(C)C	0.7958813 COCI =CC=C(C=C1)CCC#C	0.797922 CCCCCCCCC(=0)NCCC 0.7983707 C1N2C=CC=CN2C(=0)01	0.7988777 CCCCCCCCCCC(=0)C=C=C 0.7980738 C=CCN/CC =CNL=C	0.7992844 C1=CC(= 0)NC= CC1=0	0.7995076 CCCCCCCCCNICNC=C1 0.8015428 C(CCC(=O)OCCCN)CCN	0.8015852 CCCCCCCCC(=0)00CC 0.8021905 CC(=0)0CCC(C)(C)0	0.8025518 CC(=N)CCCCCC(=N)C 0.803635 CCCCNNVCCC(=NNC	0.8060032 COCOCCI=CC=CC=C1 0.8067357 CCC1=CC=C1C=C1	0.8078429 CCCCCCCCCCCN=C(N)N	0.8080923 CCCCCCCCCCCCC(=0)C	0.903T525 CC(C)(CCCC(=0)M)0	
Mor250-1	Distance SMILES 0 C(=0)(C)s1ccccc1 0 0=C10C2=C(C=CC=C2)C=C1	0 cl(cccc1)OC(=0)C 0.09948513 CCC(=0)OC1=CC=CC=C1 0.1338373 CCC(=0)OC1=CC=C1	0.1371426 C1=CC=C2C(=C1)C=CC(=O)N2 0.1371426 C1=CC=C2C(=C1)C=CC(=O)N2	0.2023979 CCC(=0)C1=CCC=C1	0.2240541 CC(=0)NC1=CC=CC=C1	0.253228 C1=CC=C(C=C1)NOC=0	0.2744787 CIC=CC2=CC=CC(=0)NZC=C1 0.2744787 CIC=C2C=CC=CC20C1=0	0.2756416 C=CLC(=0)0C2=CC=CC=C2N1 0.2810861 C1=CC=C(C=C1)0N=C=0	0.2843047 CC(=0)C=CIC=CCC=C1 0.2902787 C1=CC=C(C=C1)N(C=O)N	0.299426 C1=CC=C(C=C1)NC(C=0)0 0.2071267 CC1=CCC-CCC=C1)VCCO	0.3087009 C1=CC=C(C=C1)ONC=O	0.3129654 CI=CC=C(C=CI/MC(=U)NS 0.3463383 c1(ccccc1)NC=0	0.3527429 C1=CC=C(C=C1)NC(=O)N 0.3589161 CCC(C1=CC=C(C=C1)N)O	0.3614484 CC1=CC=CC=C1C(C)0	0.3668489 C1=CC=C(C=C1)OC#N 0.3705043 CC(C1=CC=C(C=C1)N)O	0.3737975 C=CC1=CN=C(C=C1)C=O 0.3767563 C1=CC=C1CC=C1VCC=OW	0.3781045 CSC(= 0)C1=CC=NC=C1	0.3811/58 CC1=C(C=CC(=C1)C=C/C=C) 0.3818025 CC(C1=CC=CC=CC=C1N)O	52 C1=CC=C(0	0.4036705 CC(NC1=CC=CC=C1)(0)0	0.4068996 C1=CC=C(C=C1)NC(=O)C=O 0.412378 CN(C1=CN=CC=C1)N=O	0.4139083 C=CC(=0)OC1=CN=CC=C1 0.4179807 C1=CC=C(C=C1)C(=0)S	0.4257721 C1=CC=C(C=C1)C(=O)NN	0.4340718 C1=CC=C(C=C1)C(=O)C#N 0.441583 C1=CC=C(C=C1)CC(N)O	0.4427735 C1= CC=C(C=C1)S(=0)N	0.4491596 C=C1C2=CC=CC=CC=C20NC1=0	0.4493704 CION(01)C2=CC=CC=C2 0.4531518 C=C1CC=CC=CL=CIN=C=0	0.453392 COC1= CC=C(CC1)C(=0)N 0.4594144 CCCC(=0)C1=CC=CC=C1	0.4606335 C=CC(=0)C1=CN=CC=C1	0.4610775 C1=CC=C(C=C1/CC(NO/O 0.4628345 C1=CC=C(C=C1/C(=O)SN	0.4660403 CC(=CC=0)C1=CC=CC=C1 0.4667059 CC(=C)C1=CC=C(C=C1)N=C=0	0.468857 C1=CC=C(C=C1)NC(=O)S 0.471485 CC1=CC=C1VC(=O)S	0.4735791 CCC(=0)NC1=CC=CC=C1	0.4854457 CC(=0)NXCI=CC=CC=CI 0.4868151 C1=CC=C(C=C1)OC(=0)NN	0.4880825 CICC1(C2=CC=CC=C2)0 0.491219 C1=CC=C(C=C1)0C=N	0.4976125 C1=CC=C(C=C1)NCN=O 0.4982229 C1=CC=CCC=C1)NCVC=O1N	0.5059386 CS(=0)(=0)CL=CN=CC=C1 0.5067189 C1=CC=C1C=C1VC =0)SO	0.5094009 C#CC(=0)MC1=CC=CC=C1	0.514507 C1=CC=C(C=C1)N=CN0	0.5204479 C=CICCC2=CC=CC=CC=CC1=0	0.5225184 C1=CC=C(C=C1)N(C(=O)N)N 0.524365 CC(0)SC1=CC=CC=C1	0.529635 C1=CC=C(C=C1)ONC(=O)N 0.5340142 C1=CC=C(C=C1)NCOC=O	0.537694 C1=CC=C(C=C1)C2=CC(=0)C2=0 0.5378829 C1=CC=C(C=C1)NC=C=0	0.5390166 c1(cccc1)C(=NO)C	0.5415792 CSC(= 0)C1=CN=CC=C1	0.5419474 C1=CC=C(C=C1)N(C=S)0 0.5442348 C1=CC=C(C=C1)CC=N0	0.5453544 C1=CC=C(C=C1)C(=0)CC=S	0.5456976 C1=CC=C(C=C1)CC(=0)NN	0.5494509 CLCC(CL)(C2=CC=CC=C2)0 0.5496824 C1=CC2=C(C3C(03)C=C2)N=C1	0.5566925 C1=CC=C(C=C1)C(=O)C=O 0.5549933 CNC(=O)C1=C(C=C(C=C1)N)N	0.5563128 C=CIC(=0)CCC2=CC=CC=C12 0.5566175 C1=CC=CCC=C12=NO	0.5581519 C1=CC=C(C=C1)CC#C0	0.5598583 CCI =CC=C(C=C1)OC(=0)C	0.5624856 CC(C1=CC=C(C=C1)C=0)0		
Mor223-1	Distance SMILES 0 C(=C)COC(=0)Cclocccc1 0 c1(ccccc1)COC(=0)C	0 c1(ccccc1)OC(=0)C 0.06933906 C#CCOC(=0)CC1=CC=CC=C1 0.08038855 CCOC(=0)CC1=CC=CC=C1	0.08366296 CCCCC(=0)CC1=CC=CC=C1 0.08366296 CCCCC(=0)CC1=CC=CC=C1	0.108847 CECC(=0)CC1=CC=CC=C1	0.1114792 0.001=CC=CC=C1)CCCCC=0	0.1201505 CCC(=0)0C1=CC=CC=C1	0.124919 CC=C=CC(=0)0CC1=CC=CC=C1 0.1258814 C=CC(=0)0C1=CC=CC=C1	0.1260327 CC(=0)0CCCC1=CC=CC=C1 0.1322961 C=CCC(=0)0CC1=CC=CC=C1	0.1338931 C#CC(=0)OCC1= CC=CC=C1 0.1355292 C1=CC=C(C=C1)CCCC0C= 0	0.1374166 CCCC(=0)0C1=CC=CC=C1 0.1387836 CCCCC(=0)0C1=CC=CC=C1	0.1409284 CCCCC(=0)0C1=CC=CC=C1	0.1409447 COC(=0)CCC1=CC=CC=C1 0.1460253 COC(=0)CCCCC1=CC=C1	0.1465203 CCCCOC(=0)CC1=CC=CC=C1 0.1469559 CC(=0)CC=CC1=CC=CC=C1	0.1485208 COC(=0)CCCC1=CC=CC=C1	0.1501398 C1=CC=C(C=C1)C=CC0C=0 0.1512307 C=C0C(=0)CCC1=CC=CC=C1	0.1514078 C1=CC=C(C=C1)CCCCCOC=O 0.1543114 CC/=OOCCC-C1=C7=C7	0.155389 CC(=C)C(=O)OC1=CC=CC=C1	0.1595091 CC(=0)ACF CC1=CC=CC=C1 0.1596583 COCC(=0)AC1=CC=CC=C1	0.1603431 C=CC(=0)0CCCC1=CC=CC=C1 0.1609765 CCC(=0)0CCCC1=CC=C1	0.1618874 CCCCCC = 0)0C1 = CC = C1	0.1627933 C1=CC=C(C=C1)COC=O 0.1628804 CC(C)OC(=O)CC1=CC=CC=C1	0.1637411 CC(=0)0CCCCC1=CC=CC=C1 0.1681853 COC(=0)CCCCCC1=CC=C1	0.1696474 COC(=0)COCC1=CC=CC=C1	0.1688499 COC(=0)COC1=CC=CC=C1 0.1700087 CCC(=0)OCC=CC1=CC=CC=C1	0.1704098 CCOC(=0)CCC1=CC=CC=C1	0.173784 COC(=0)CC =CC1=CC=CC	0.1760244 CCCC(=0)0CC1=CC=CC=C1 0.1763525 c1(ccccc1)C(C)0C=0	0.1770091 C= CC(=0)0CC=CC1=CC=CC=C1 0.1777917 CCCC(=0)0C0C1=CC=CC=C1	0.1792888 CC(=C)CC(=O)CC1=CC=CC=C1	0.1793112 CC(C)COC(=0)CC1=CC=CC=C1 0.1794657 COC(=0)C=CC1=CC=CC=C1	0.1796827 CC(C)C(=0)OC1=CC=CC=C1 0.1798026 C=COC(=0)COC1=CC=CC=C1	0.139857 C# cc(=0)0cccc1=cc=cc=c1 0.1830238 c1(cccc1)c0cc=0)c=cc	0.1825544 COCC=0)CCC1=CC=CC=C1	0.1826441 CN(C/CC) = 0 XXC1 = CC = C1 0.1836267 CC(=CC(=0)OC1 = CC = C1)C	0.1849264 c1(cccc1)COC(=0)CCCC 0.1852108 CCOC(=0)COCC1=CC=CC=C1	0.186622 CCCOC(=0)CCC1=CC=CC=C1 0.1868345 CCf=0X0CC#CC1=CC=C1	0.1878621 CC(=0)0CNCC1=CC=CC=C1 0.188291 C1=CC=C/C=C100CC0C=0	0.1885667 C1=CC=C(C=C1)CCOC=O	0.1907101 CC(=0)0CCC0C1=CC=CC=C1	0.192518 C=C(COC1=CC=CC=CL)0	0.1930319 COC(=0)C# CC1=CC=CC=C1 0.1938174 CCOC(=0)C0C1=CC=CC=C1	0.1944149 C1=CC=C(C=C1)CCNCC=0 0.1947007 CC(C)CC(=0)0C1=CC=CC=C1	0.1948448 CC(0)OCC1=CC=CC=C1 0.195021 c1(ccccc1)COC(=0)CC=CCC	0.195902 COCC=000CC1=CC=CC=C1	0.1922684 COOC #07 #CC1 #CC #CC #CC	0.2017375 COCCOC(=0)CC1=CC=CC=C1 0.2018451 CCOCC(=0)CC1=CC=CC=C1	0.2028423 CC(=0)CNCC1=CC=CC=C1 0.2028425 CCCCC+OV=CC1=CC=C1	0.2044652 COC(=0)CNCCC1=CC=CC	0.2061299 COCC(=0)CC1=CC=CC=C1 0.2066889 C#CCNNCCC1=CC=CC=C1	0.2080846 C = CCN(CC1 = CC = CC = C1)0 0.2087961 CN(C)N = MCC1 = CC = C1	0.2098703 C1=CC=C(C=C1)CCCN=C=0 0.2099183 C0C/=0.5NCC1=CC=CC=C1	0.2099267 C1=CC=C(C=C1)CCCC00 0.2131813 COC(=-OVCNAC1=-CC=C1	0.212798 C1=CC=C(C=C)CCCC=0 0.212768 C1=CC=C(C=C)CCCC=0	0.2133856 C#CC(=0)COCC1=CC=CC=C1 0.2133856 C#CC(=0)COCC1=CC=CC=C1		Communed
Mor207-1		0 = CIOC2 = C(C=CC=C2)C=C1 C1= CC=C2C(=C1)C=C(NO2)C=0 CC1 = Mr/ = OVC3 = C7 = C7 = C7 M1	CC1NC(=0)C2=CC=CC=C2O1 CN1C=NC2=CC=CC=C2O1	CODE = NCI = CC = CC = CI	CC1 COC2 = CC = CC = C = C = C	CIC2=CC=CC=C2ON= CIC=O			CNNC(=0)C1=CC=CC=C1 CC1=CC(=0)C2=CC=CCC=C201			XCMN	IN		C1=CC=C2C(=C1)C(=0)SN2 C1C(C(=0)C2=CC=CC=C2O1)N	CNLC(=0)C2=CC=CC=C2N=C1N C1=CC=C2C(=C1)C=C(NO2V0	CIC(=CC2=CC=CC=C01)C=0	CL=CC(=CLC(=CLC(=C)CS)S CNC1=CC(=O)C2=CC=CC=C2N1	CCI = NNC2 = CC = C2 C I= O CI = CC = C2 C I V C = O X C = N2	CC1CC(=0)C2=CC=CC=C201	C1= CC=C2C(=C1)C(=O)C =C(O2)N CCCCOC(=N)C1= CN=CC=C1	CC1 = COC2 = CC = CC = C 2C 1= 0 C1C /= O VC2 = CC = CC = C2 ON1	C1=CC=C2C(=C1)C=C(C(=0)02)N	CI=CC(=CC=CIC=0)S CI=CC=C(C=CI)C=NNC=0	C1=CC=C2C(=C1)C(=CC(=0)02)N			C1=CC=C2C(=C1)C(=O)C=NS2 C=C1COC2=CC=CC=C2C1=O	C1C0C(=N1)C2=CN=CC=C2	C = CCOC(=N)C1=CC = CC=C1 C1=CNN(N=C1)C2=CC=C(C=C2)C= 0	C1=CC=C2C(=C1)C(=O)C=CN2 CC1=CC(=O)C2=CC=CC=C2N1	CNLC(C2=CC=CC=C2N=NL)O	CONIC2 = CC = CC = CC = O		17		CN	C1=CC=C2C(=C1)C(=O)C=C(N2)NN	CI=CC=C2C(=C1)C(=O)N=NS2	CIECC=C2C(=C1)C(=0)C=C02 CIEC(=0)C2=CC=CC=C2OS1	CN(C)C1=CC=C(C=C1)C=O COC1=CC=C(C=C1)C=NC#N	CC1=CC2=CC=CC=CC2OC1=O C1=CC=C(C=C1)C=NCC=O	CC1 = NC(=0)CC(=N1)C2=CN=CC=C2 C1 = CC=C1 C(=C1)C2=C02 X0		C=C(C1=CC=CC=C1)C	CICCIC(=0)NN= CC2 =CN=CC=C2 CNIC2 =CC=C2C1=0	CCSC(=0)C1=CN=CC=C1	CIC =CN2N INC2C3 =CC=C(C=C3)0	CIC(=0)C0C2=CC=CC=C21 C1=CC=C2C(=C1)C(=0)N=C(S2)N	C=CC1COC2=CC=CC=C2C1= 0 C1=CC=C2C(=C1)C(=0)N=CN2	CIC2=C(02)C3=CC=CC=C301 C1=CC=CC=C1C/=OW)S	COCI=CN=NC2=CC=CC=C21	CIC(C2=CC=CC=C2OO1)N			Iable 3.10 Continue

	Control C	
Mor30-1	0.00000000000000000000000000000000000	
Mor277-1	 CICREDINGCE-AND CONTRICTORY (CONTRIPUTED CONTRIPUTED CONTRIPUTED	
Mor273-1	 Construction of Construction of C	
Mor 272-1	 C.C.G. ORGANINAL C.C.G. C.C. CARLON, C.C. CARLON, C.C. C.C. CARLON, C.	
Mor271-1	OCCUPATION OCCUPATION OCCUPATION OCCUPATION OPENANCE OPENANCE OPENANCE	
Mor268-1	 0 SECRECCEGN 0 SEC	3 16 Continued
Mor 261-1	Reconstruction Reconstruction	Table 3 16 (

Table 3.16 Continued

	Diama. the second
0r2J2	Anternal Suttact 0100000000000000000000000000000000000
Or 1A1	Othera 91123 00000730 CCCC and CCC and CCCC and CCCC and CCC and CCC and CCC and CCC and CCC and CCC and
Mor5-1	Datasa Bullita 0.13323 0.13324 0.13324 0.13324 0.13334 0.13334 0.13334 0.13334 0.13334 0.13334 0.13334 0.13334 0.13334 0.13334 0.13334 0.124244 0.13334 <
Mor41-1	Data Built 0101-000-000-000-000-000-000-000-000-00
Mor40-1	Anutas and another provided and another provided and another and another provided and another another provided another another another provided another another another provided another anot
Mor37-1	 (1) (1)
Mor33-1	ants ants ants ants ants ants ants ants

;	Distance	0.3110759 0.3586025						0					0.516556					0.545					0)C=C3 0.5684292 0)N32 0.5728021								0.5994571			0.608081		0.6095801				0.6138947 0.6158562				2	0.624421	
Or5P3	SALLES 0 CCI =CC[C@H](CC1=0)C(=C)C 0 CCI =CC[C@H](CC1=0)C(=C)C 0 CCI =CC[C@H](CC1=0)C(=C)C	0=010.2=000001 0=001000001 001=0001001001=00	C1=CC=C2C(=C1)C=CC(=N0)02 C1=CC=C2C(=C1)C=CC(2=S	C1=CC=C2C(=C1)C=C0C2=0 C=C1C2=CC=CC=C20NC1=0	C1=CC=C2C(=C1)C=CC(=0)N2 CC1=C(C(=0)CC1)CC=C	C1=CC(=CC2=C1C=CC(=0)02)S	cc1(c2c1c(=0)c(=c)cc2)c	CCC1 ZCCC(=0)C=C1CC(C2)0	CICC2(CC1)CCC=CC2=0	CTILCTOCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCU	cd =0;0(=0;000#C	cc1=cc2ccccq =0)c2 =cc1	CC1=C2C(=C)C(=0)NC2=CC=C1 C1=C2C(=C(C(=C1)0)OC(=0)C=C1	cc(=0)c1 =ccc2(c1)c(=c)ccc2= cc1 2cc(=0)c=c1cc3c2cc=c3	C=C1CCCCCCC1=0 C1CC2=q(CC=C1)C(=0)CC2 CC1-CC2CCCN32C1=0	C1=CC1=C1/C=C(C(=N)02)C	C1=CC=C2C(=C1)C=CC(=MS2)N C1=CC=C2C(=C1)C=CC(=MS2)N	C1CC(=CC(=0)C1)C2=CC=C52 C1=CC=C2C(=C1)C=CN(C2=0)0	CCI =CSC2=C1C(=0)C(=C)CC2 C1=CC=C2C(=C1)C=C(C(=0)02)A	C1=CC(=0)0C2=CC(=C(C=C21)0 CCC1=C(C2=CC=CC=CC21=N)N	cd =ccd =0 /c=c/c cd =ccd =0 /c=c/c	C=C1C(=C)CC=C1)C=CC(=0)N02 C1=CC(C)C1=CC(001=0)C	C1=CC=C2C(=C1)C3=C(N2)MC(=C	C=CC1=CC=C(C=C1)C(=0)N CC1=CC(=0)CC1CC=C	CICC(=CC(=0)CI)C2CCC=C2 CCC1=CC2CCCCN2C1=0	cc1=cc=ccd(=c1)wc(=0)c=cs2 cc1=c2c=ccd(=0)wc2=cc=c1 c1fcr1=0)c?=cfc=c1c=cr1=c?	C1=CC2=CN=C(C(=0)N=C2C=C1) C1=CC2=CN=C(=C1)C=CN3C2=NNC	C=C1CC2=CC=CC=C20C1=0 CCC(=C)CC1=CCCC1=0	CCI =CC(=0)0C2 =CIC(=C(C=C2) CCI 2CC=CCCICC(=0)C=C2	C=CCC2(CCC=CC2=0)CC=C1 C1CC2(CCC=CC2=0)CC=C1 CC1=C7(-0)MC2=C1C1=C7=C7=C7	0.00208407 CCI =C(CCCI(C)C/=0)OC 0.00208407 CCI =C(CCCI(C)C/=0)OC	C1C2=CC=CC=CZC=C(C1=0)0 CC1=CCC(CC1=0)C2(CO2)C	CCI C=C(C(=0)01)/C2=CC=CS2 CCI =CC(=0)/CCCCI 0C=C	cq c)c1ccc=c1q =0/c cc1=cc(=0)cc1c2=cc=cc=c2 cc1-ccr=cc=cc=cc	CIC2=CC=C2C(=0)C1=CN C1=C72=CC=C2C(=0)C1=CN	CICC2(CC3CC3C=C3)C=CC1=0	C1=CC(=0)C2=C1C3=C(C=C2)N CCC1=C(N2CCCN2C1=0)C	cc(=C)C1=CC=C(C=C1)0 C=C1CCC2(CC1)CC(=0)C=C2	C1=CC=C2C(=C1)C(=CC(=0)02) CC1=CC(=0)CC(CC1)(C)C	cc1 2000(=001=0)0(0)0	cc1 =c(c2=ccc(c(c1)0)(c)c cc1 =c(c2=cc=cc=c2c1=N)N	C1=CC=C(C=C1)C2=CC(=0)MN2 CCC12CCC(=0)C=C1CCCC2=0	CCLUE C(C=U) XI X(C)C C1=CC=C2C(=C1)C=C(C(=0)N2)C CC1=CC2=C/C=C/C=C22(0)	1=002=0	<pre>c1=cc=c2c(=c1)c(= cc1cc(c(=0)c=c1c)</pre>	
i	C)C DISTANCE		000	00	00	0.00049109	699-69000.0	0.00085074	0.00098218	0.00098218	20002100'0	0.00120303	0.00129719	0.00138938	0.00145282 0.00145282	196.24100.0	0.00147361	0.00162884	0.00162884 0.00162884	0.00167839 C 0.00168551	100100100108228	0.00170148							0.00202507	8 CE 802 U0. U 0 .00 208 358 7 04 805 00 0	0.00208407 0.0020895	0.0020895	0.00211915 0.00214114	0.00214114 0.00214114	0.00214114	0.00214114			U	0.0022560	16202200.0				0.00240605 0.00241118	
Or2W1	Growthes Growthiccleani(cc1=0)c(= Growthiccc=c(c)c)cc0	d accecto	ccc(=0)cccccc	q =c)coc(=0)cc1acca1 q/qcc/c=c(c)\c)=c\co	c(=0)ccccc c(=0)ccccc	cccc(ccc=c(c)c)o	CICCCCIC=NC(=0)CO	CCCOC1=CC=C(C=C1)C			cc(c)cccq(c)c1c01 cc(c)cccq(c)c1c01	cc(c)(c)c(=0)0ccc0	cc(c)wc(=0)cc(ccn)n cc(c)wc(=0)cc(ccn)n	ccccc(=c)N	COC(=0)CC1=CC=C(C=C1)C=C CC(C)MCC1=CC=C(C=C1)MC	C=CCCCO C=CCCCCO CT#CCT=0)C1CCCCC1	CC11(CC1C1=C(C=N1)C(C)NC CCCN1C=C(C=N1)C(C)NC	cccc1c(01)cccc=c ccc(c(=0)occ(c)c)MN	ccccctccc(cct)N cccccc#cc(cct)0	CC(C)COC1 =CC=C(C=C1)CO CC1 =CC(=CC(=C1)MC(=0)C(C)C)C	CUTCHECCENCIENCE	cc(c)(ca)cccc=c	cicqoci/ccccN ccc1=Nc(=No1)q(c(cc)N)o	CCCCNIC=C(N=N1)C=C CCCCC1=CC=C(C=C1)OC)MC	CDC(=0)COCC#C C1CCC(CC1)MCC2=CC=CN2	CC(=CCCICCIC=CC=CC=CC CC(=CCCICCIC=O)C	ccc(c)(cccc(=c)c)o	C1 CCCC(C)C)0 C1 CCCC(C)C)0 C1 CCCC(C)C)0	CI CC2 =CC = CC = O/C2NCI	ccc(=0)ccc+cc ccc(=0)ccc+cc	accocciccio accocciccio	cccoccc(=N)oc c1=cc(=cc=c1ccc0)N	C=CCCCC1=NCCC1 CCCCC1=CN=C(C=C1)C	ccccc1c(o1)c(=0)wczcc2	cc(c)cc(=0)c=c(c)c=c	CCCCNIC=C(C(=N1)C)N	cc(=cccc1=Nccc1)c ccccc(=0)c(c)(c)cc	C1 CC1 NCC(=0)/22 =CC=CC=C2 C=CC0C1CC(C1)/C2CC(=0)/C2	CCC1=COC(=N1)MC(=0)C CC1=CC=C(C=C1)C2=MC=C(N2)	ccocctoncot cc(=c)cccc(c)(c=c)N	cc/=cccc=q(c/cc)c	COCCCCAC CC(C)CIC(01)CCCC=C	CC(=CCC1=C(C(=CC=C1)N)N)C CC(=CCC1=C(C(=CC=C1)N)N)C	CCOCC1CC(=C)CC1 CCCCCC1=C(NC=C1)C	c=ccccc#cco ccoct =0)dNcc#c	

CHAPTER IV:

A New Generation of Safe DEET Substitutes that are Strong Olfactory and Gustatory Repellents of Mosquitoes and Flies

INTRODUCTION

Blood-feeding insects transmit deadly diseases such as malaria, Dengue, Filariasis, West Nile Fever, Yellow fever, Sleeping sickness and Leishmaniasis to hundreds of millions of people, causing untold suffering and more than a million deaths every year. Insect repellents can be very effective in reducing vectorial capacity by blocking the contact between blood-seeking insects and humans, however they are seldom used in disease-prone areas of Africa and Asia due to high costs and need for continuous application on skin.

N,*N*-Diethyl-m-toluamide (DEET) has remained the primary insect repellent used for more than 60 years in the developed world. DEET is a solvent, melting several forms of plastics, synthetic fabrics, painted and varnished surfaces(Krajick, 2006). Additionally, DEET has been shown to inhibit mammalian cation channels and human acetylcholinesterase, which is also inhibited by carbamate insecticides commonly used in disease endemic areas (Corbel et al., 2009). These concerns are enhanced by the requirement of direct and continuous application of DEET to every part of exposed skin in concentrations that can be as high as 30-100 percent. Several instances of increased resistance to DEET have also been reported in flies (Reeder et al., 2001), *Anopheles albimanus* (Klun et al., 2004), and *Aedes aegypti* (Stanczyk et al., 2010). Moreover, mosquito strains with resistance to pyrethroid insecticides, the main line of defense against mosquitoes in developing countries, are spreading (Butler, 2011). There is

201

therefore an urgent need to develop safer and improved alternatives to DEET. The other major barrier in developing new repellents is the time and cost of development. It has been suggested that >\$30M and several years may be required for identification (Gupta, 2007) and adequate human-safety analysis of new repellent chemistries.

A major limitation to finding effective substitutes is that the molecular targets in adult mosquitoes through which DEET causes repellence are unknown. Recent studies have put forward a few competing theories about mechanism of action, but demonstration of a causal relationship is lacking. Some reports show that pure DEET causes inhibition (Ditzen et al., 2008) or mild electrophysiological modulations of neural responses to weakly activating odors in *Drosophila* antennal olfactory neurons (Pellegrino et al., 2011), but whether such effects cause repellency in either *Drosophila* or mosquitoes are unknown. On the other hand a DEET-responsive receptor, Or42a, has been identified in the maxillary palps of *Drosophila*, however Or42a is also known to be a broad-spectrum detector for several food-associated odorants that elicit attraction (Syed et al., 2011). Other studies in *Drosophila* have shown that DEET is also detected through bitter taste neurons causing contact-avoidance (Lee et al., 2010; Weiss et al., 2011). Although the three proposed mechanisms confound appropriate target choice for high-throughput screening, *Drosophila* might provide a tractable model for discovery of new DEET substitutes via direct behavioral screening of compounds.

Here, we describe identification of novel repellent odors that are safe, inexpensive, and effective at repelling *D. melanogaster* and *A. aegypti*. We first demonstrate that *D. melanogaster* and *A. aegypti* may utilize their gustatory system and olfactory system to different extents to avoid DEET, with mosquitoes relying more heavily on olfactory pathways. We then use a novel *chemical informatics* approach that

uses supervised training from known repellents to identify important structural features that are responsible for avoidance behavior. Using these features we predict novel repellents from a very large untested odor space comprising a large purchasable odor set and a natural odor library, the latter providing many chemicals that are safe and already approved for human use by both United States and European governmental safety organizations. We select four odors from the 150 natural odor library predictions and demonstrate that all four are able to cause strong avoidance in both D. melanogaster and A. aegypti. Due to the large number of candidates we are able to select new repellents with ideal properties; safe for human consumption, do not dissolve plastics and mild and pleasant aroma. These results suggest that our integrative approach of computational predictions and behavioral analysis can revolutionize the discovery of safe and effective repellent odors that could be very useful in our struggle against the increasing spread of insect disease vector species. Although it has been several years since odor receptors were identified in vertebrates and invertebrates, very few odor receptor targets have been identified for known behavior modifying odorants. This study therefore has broader implications since the approach presented can be used for identification of improved behavior modifying odorants for any organism, even if the target odor receptor is unknown. Moreover upon identification of target receptors, the same methodology can be easily adapted for a receptor-activity based approach.

RESULTS AND DISCUSSION

Contributions of Olfaction and Gustation in DEET Avoidance in Drosophila

In order to select a reliable behavior assay, we first tested for repellency in the well-established T-maze. We found that Drosophila do not avoid the arm containing DEET (10%) in this assay (Figure 4.1A), perhaps due to its low volatility. By introducing a well known repellent CO_2 (0.66%) in the other arm, we asked whether we could observe an effect by forcing flies to enter the DEET arm closer to the DEET source. We find a marginal, but not significant, reduction in avoidance to CO_2 , suggesting that DEET is not an effective olfactory repellent for *Drosophila* in this assay (Figure 4.1A). Drosophila do however show strong avoidance when they are allowed to come in close contact to DEET in a plate-based 2-choice trap assay as described previously(Syed et al., 2011), where they can sense DEET-treated filter paper positioned at the entrance of a trap with both the olfactory and gustatory system (Figure 4.1B). Orco mutant Drosophila that lack functional odor receptors belonging to the Or family show ~30% reduction in avoidance to DEET (Figure 4.1B). The simplest interpretation of these results is that although olfactory receptor pathways participate in the avoidance behavior, the response mediated by the gustatory system is sufficient to generate strong avoidance of Drosophila to DEET.

Aedes aegypti Detect and Avoid DEET Primarily using Olfaction

To test whether the gustatory system of mosquitoes plays a substantial role in DEET repellency as well, we developed a modified hand-in-glove assay (described in Supplementary Methods) (Figures 4.1C, 4.1D, and 4.2). The assay allows us to

quantitatively analyze the repellent effects of DEET on mosquitoes attracted to a human arm, without being able to bite. Female Aedes aegypti mosquitoes show an equally strong avoidance behavior to DEET in both the contact and non-contact versions of the assay (Figure 4.1D). For rare landings, the time spent on the net before escape is marginally lower, but not significantly different, when direct contact with DEET was permitted (Figure 4.1E). In order to test whether the reduction in attraction is caused by a direct detection or a masking/scrambling of skin-odor detection, we measure attraction of female Aedes to humidity and warmth and demonstrate a significant dose-dependent reduction in presence of DEET (Figure 4.1F). These results indicate that the female Aedes primarily use the olfactory system to sense DEET directly and avoid it. This is consistent with previous observations that *Culex quinquefasciatus* (Syed and Leal, 2008) and A. aegypti (Turner et al., 2011) avoid DEET presented as a volatile stimulus directly. In fact a DEET-sensitive neuron type has been identified in *C. guinguefasciatus* (Syed and Leal, 2008) and A. aegypti (Stanczyk et al., 2010), however it is not known whether these neurons are responsible for repellency, or which odor receptors they express. A broadly tuned larval odor receptor AgOr40 has been shown to respond to DEET (Liu et al., 2010; Xia et al., 2008), however its role in avoidance behavior in adults has not been determined.

A Computer can be trained to Predict Repellent Behavior from chemical structure

Since behavior assays in *Drosophila* and mosquitoes appear to differ in requirements for gustatory and olfactory exposure for repellency (Figure 4.1G), we would require use of both systems to reliably identify improved DEET substitutes. However volatile chemical space that can be exploited to find such improved DEET

substitutes is vast (potentially >400,000) thus using behavior assays alone is unfeasible from the perspective of time and cost of chemical purchase. Moreover, since a protein target for DEET action is unknown, high-throughput screening, or sophisticated computational protein-ligand docking based approaches to identify new ligands are also not possible.

To circumvent these problems so as to enable selection of compounds for behavior assays, we developed a novel chemical informatics approach. We hypothesized that the unknown target protein is recognizing specific structural features of DEET and other known structurally related repellents. By identifying structural features that are shared amongst DEET and the known repellent compounds, we can utilize them to rapidly screen an extremely large number of compounds in-silico to identify novel repellents, thus greatly reducing both the cost and time required. We assembled a training set of known repellents that included: the two approved ones DEET (a carboxamide) and picaridin; and also 34 N-acyl piperidiens (Katritzky et al., 2008) that are structurally related to picaridin; eucalyptol, linalool, alpha-thujone, betathujone (Kline et al., 2003; Klocke et al., 1987; Syed and Leal, 2008) and a structurally diverse panels of odors that are not expected to elicit repellency via similar target receptors (Carey et al., 2010; Hallem and Carlson, 2006). The study where the 34 n-acyl piperidiens were identified also showed that a chemical-structure-based approach could be successfully applied to predicting repellency (Katritzky et al., 2008). For our analysis, compounds from different sources were approximated into a single metric of "protection duration" as a rough indicator of repellency. The non-repellent diversifying training set of odors were assigned protection times of zero, while the approved repellents DEET and Picaridin were assigned the highest value since these would have the properties

important for regulatory approval. Compounds were clustered using Euclidean distance and hierarchical clustering based on differences in repellency values, and a set of 5 compounds with the highest activity that clustered together was classified as "training repellents".

We expect that only specific structural features of the repellent odors will interact with target proteins to elicit repellent responses, and not the entire molecule. We assumed that identification of structural features that are shared across repellent odors would enable a search for these features within a large chemical space, potentially identifying novel repellents (Maldonado et al., 2006). We decided to focus on a descriptor-based computational approach that is effective in structure analysis and is efficient in subsequently searching a large chemical space rapidly. We calculated mathematical values for 3,242 molecular descriptors, that describe the 3-D structure of a chemical, for our 201 compound training set and using a Sequential-Forward-Selection method (Haddad et al., 2008) we incrementally identified a unique subset of 18 descriptors that were highly correlated with repellency (correlation of 0.912)(Figures 4.3A, 4.3B, and 4.3C). As expected the repellent odors cluster together in the training set if the optimized descriptor subset is used to calculate Euclidean distance amongst them (Figure 4.3B). These 18 molecular descriptors represent a collection of predominately 2D and 3D descriptor types. Inspection suggests that 6 member rings, carbon-nitrogen distances, tertiary amides, and oxygen placement are prominent in the optimized subset. Interestingly, although repellents are topically applied chemicals, the Ghose-Viswanadhan-Wendoloski drug-like index is selected, which is an aggregate descriptor that usually suggests similarity of chemical features important for drugs (Ghose et al., 1999).

In order to improve the predictive ability of the chemical informatics approach we used the optimized descriptor set to train a Support Vector Machine (SVM), which is a well-known supervised learning approach (Cortes and Vapnik, 1995)(Figure 4.3A). To validate the predictive ability of our approach, we performed 5-fold cross-validation using SVMs on the training set. Each cross-validation run excluded ~20% of the repellents as a test-set, while the remaining repellents were used to train a SVM. We predicted repellency for the withheld test-set odors using the trained SVM. This operation was repeated 5 times, each trial performed excluding a different subset of the training set, and the whole process was repeated 20 times for consistency. A mean Receiver-Operating-Characteristic (ROC) analysis curve representing the prediction accuracy was generated, and the Area-Under-Curve (AUC) value was determined to be 0.994, indicating that the *in-silico* approach was extremely effective in predicting repellents from compounds that are excluded from the training set (Figure 4.3D).

High-Throughput In Silico Screen identifies Safe Natural Odors as repellents

We use the 18 optimized-descriptors and SVM method to screen *in-silico* a large chemical library consisting of >440,000 chemicals from a database called eMolecules of putative volatiles. Upon inspection, we find the top 1,000 predicted compounds (0.23% of hits) represent a structurally diverse group of chemicals that retain some structural features of the known repellents (Figures 4.4A and 4.4B). We computed logP values of the 1,000 compounds to identify ones that are predicted to be lipophilic (logP >4.5) thus allowing for selection of other compounds that are less likely to pass through the skin barrier in topical applications (Walker et al., 2003) (Figure 4.4B). In addition, we

computed the predicted vapor pressures of these chemicals since volatility may predict ability of long-term protection vs. increased spatial domain of action (Figure 4.4B). Taken together the results of the screen present a very large collection of novel predicted repellents with desirable properties, identified via a computationally guided search of odor space.

Although the *in-silico* screen bypasses the challenge of not knowing the protein target, the most significant challenge lies in identifying effective repellent substitutes for DEET that are affordable and safe and that can be rapidly approved for human use. In order to identify compounds that fit these criteria, we applied our *in-silico* screen to an assembled natural odor library consisting of >3,000 chemicals identified as either originating from plants, insects, or vertebrate species or compounds already approved for human use as fragrances, cosmetics or flavors (See Methods). Using the trained SVM and optimized descriptor set on the natural library, we identified the top 150 ranked predicted repellent compounds. Predicted repellents share similarity in some parts of the structure while providing a diverse set of compounds (Figure 4.4C). For example, several anthranilates and pyrazines were identified that represent novel groups of safe and natural compounds, although such compounds were absent from the training set. These 150 compounds were arranged by predicted logP and vapour pressure values to provide a high-priority list of candidates for behavioral testing (Figure 4.4C).

Candidate Natural Odors Strongly Repel Drosophila and mosquitoes

In order to test for repellency we first used *Drosophila melanogaster* in the 2choice trap assay that previously showed DEET repellency (Reeder et al., 2001; Syed et al., 2011). We selected 4 affordable compounds from the list, (Methyl N,N-Dimethyl

anthranilate, Ethyl anthranilate, Butyl anthranilate, 2,3-dimethyl-5-isobutyl pyrizine) the first 3 of which have been thoroughly tested for human use, have excellent safety profiles, a very mild and pleasant aroma like grapes, and have already been approved for human consumption/oral inhalation by the FDA, World Health Organization and European Food Safety Authority (EFSA, 2008; JECF, 2007) (Figure 4.4D). The pyrizine is a natural compound produced by ants as a trail pheromone (Tentschert et al., 2000). All 4 of the predicted compounds showed a very strong repellent effect on *Drosophila* across multiple doses tested using the trap-based 2-choice assay (Reeder et al., 2001; Syed et al., 2011) (Figure 4.4E). The effect was consistent at two different time points, 48 hours and 72 hours after the start of the assay.

One of the major disadvantages of DEET is its property of solubilizing plastics and synthetic materials (Krajick, 2006), which affects its usefulness by the military, and at home. We tested the ability of the 4 repellents to dissolve a 3 x 3mm square of vinyl. The plastic square disappeared completely in DEET within 6 hrs; however in the 4 predicted repellents there was no significant difference in the weight of the vinyl squares after 6 hrs, and even at the 30hr time point (Figure 4.5A).

In order to test whether these promising candidates were in fact repellent to mosquitoes, we performed behavior trials using the modified hand-in-a-cage assay. Notably, we find that all 4 compounds applied at 10% concentration demonstrate substantial repellency. Both the fraction of mosquitoes present on the net window over the arm throughout the duration of the assay, and the cumulative number of mosquitoes present on the net window were substantially lower in the test compounds as compared to solvent controls (Figures 4.5B, 4.5C, 4.6). For the mosquitoes that did land on the

repellent treatment, the escape index, as measured by the frequency of take off, was substantially higher as well (Figure 4.7).

A New Generation of Safe and Effective Repellent Odors

Taken together we have identified a number of affordable and safe compounds with repellent properties, which establishes a significant advance toward the identification of DEET substitutes that are excellent candidates for regulatory approval for human and animal use (Figure 4.5D). This was made possible by a computational screening strategy that identified shared structural features of existing repellents to use for rapid identification of structurally related novel repellent compounds. Apart from the 4 compounds we have behaviorally identified as repellents, we have also used the screen to identify ~1000 novel compounds and ~146 additional natural compounds, many approved for use in human food and cosmetics, that may lead to several additional effective repellents for deadly insects. The repellency strategy can also have great potential if used in combination with other behavior control strategies such as masking of CO₂-mediated attraction behavior or population control by trapping as a part of an integrated pull-mask-push approach (Turner et al., 2011; Turner and Ray, 2009). Since several of these compounds are affordable, repellent for fruit flies and approved for human consumption, they may have implications for control of agricultural pest insects as well that cause billions of dollars in crop loss as well as in protecting animals and pets that have tendencies to lick their skin. Moreover such substitutes may also have implications for control of DEET-resistant insects. We expect such repellents that are safe, affordable and do not solubilize plastics to pave the way for formulations that can

be used in control of insect-human contact in disease endemic areas of the world and to provide an important line of defense against deadly diseases.

Figure 4.1: Contribution of olfaction and gustation in DEET avoidance

(A) Preference index of *Drosophila* in a T-Maze to DEET (10%), CO₂ (0.66%), and opposing gradient of both compounds. N = 8-39 trials, ~40 flies/trial, error bars = s.e.m., ** = p-value < 10⁻⁴. (B) Preference index of *Drosophila* wild-type and *Orco-/-* flies to DEET (10%) in a two choice trap assay measured at 48 hrs and 72 hrs after start. N = 5-10, 10 flies/trial, error bars = s.e.m. ** = p-value < 10^{-3} . (C) Photograph of the hand-inglove assay to measure repellency in mosquitoes. (D) Relative attraction of female Aedes aegypti in hand-in-glove assay measured as a percentage of mosquitoes spending >5-sec on the net covered window of glove, measured at 1 min intervals. (Left) DEET (10%) treated netting placed at the top level allowing contact, or (Right) at the lower level not allowing contact. N=5 trials for each, 10 mosquitoes/trial. (E) Average time spent per mosquito on net for each landing event. (F) Schematic of assay and mean number of female Aedes mosquitoes at net probing a heat and humidity source >5-secs. Mean calculated across 10 time-points, every 30-sec interval. DEET (10%) treated or Acetone (Solvent) treated netting is placed at a distance that mosquitos can not contact. N=3 trials for each, 10 mosquitoes/trial, error bars = s.e.m. p-value ** = < 10⁻ ³, *=<0.05. (G) DEET mediated repellency in *Drosophila* is mediated by both olfaction and gustation in Drosophila while primarily by olfaction in Aedes aegypti.

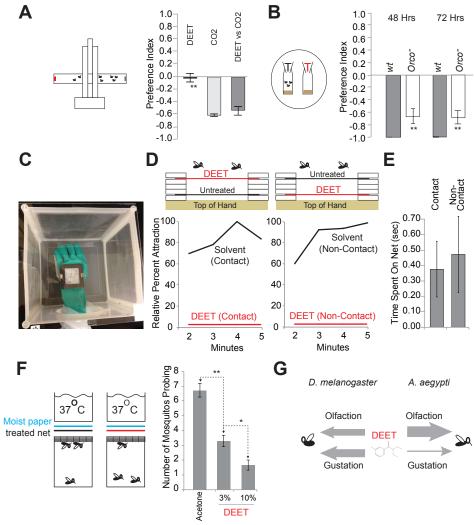


Figure 4.1

Figure 4.2: Mosquito behavioral assay glove setup

The assay glove is assembled in the following order: rubber glove with window cut into the hand, magnet glued around the cut window, control or test odor treatment mesh, three spacer magnets that prevent mosquitoes from biting through to the hand, untreated mesh to prevent mosquitoes from touching the treated mesh, and finally a top magnet. One metal clip is then used on each side of the stack to further reinforce the arrangement of magnets and mesh.

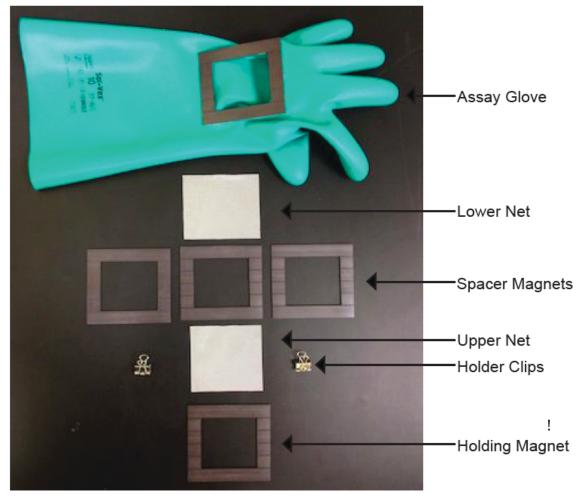


Figure 4.2

Figure 4.3: A chemical informatics method to predict repellency

(A) Overview of the cheminformatics pipeline used to identify novel DEET-like ligands from a larger chemical space. (B) Hierarchical cluster analysis of the 201 odorants of the training set using the optimized descriptor set to calculate distances in chemical space. (C) Repellency-optimized descriptor symbols and brief descriptions arranged according to order in which they were selected for the optimized set. (D) Receiveroperating-characteristic curve (ROC) representing computational validation of repellent predictive ability. The mean true-positive value from 20 independently run 5-fold cross validations is plotted, where ~20% of the dataset was left out of training-set as a test-set for each run. The mean area under the curve (AUC) is provided.

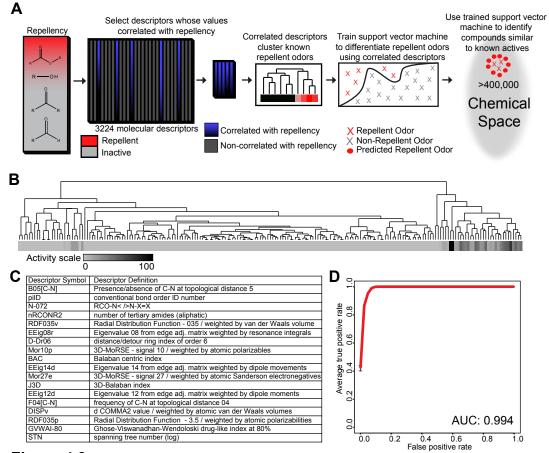


Figure 4.3

Figure 4.4: Identification of repellents using *in-silico* screening of a large chemical space

(A) Examples of two approved repellents DEET and Picaridin, and two unapproved repellents (Katritzky et al., 2008). (B) (Left) Representative predicted repellent odors from the odor library of >400,000. Computationally determined (Middle) LogP values and (Right) vapor pressure values for the top ranked 1000 predicted repellent compounds.
(C) (Left) Representative structures from the top 150 predicted repellent compounds from the natural odor library of >3,000. Computationally determined (Middle) LogP values and (Right) vapour pressure values for the top ranked 150 predicted repellent compounds from the natural odor library of >3,000. Computationally determined (Middle) LogP values and (Right) vapour pressure values for the top ranked 150 predicted repellent compounds. Color arrowheads indicate values for DEET and odors selected for behavior experiments from the natural library indicated in D. (D) Preference index of Drosophila adults to predicted repellents at three different concentrations in a two choice trap assay measured after 24 hrs and after 48 hrs. N = 7-10 trials each treatment at 48 hrs and 3-10 at 24 hrs (trials with <30% participation were excluded), 10 flies/trial, error bars = s.e.m</p>

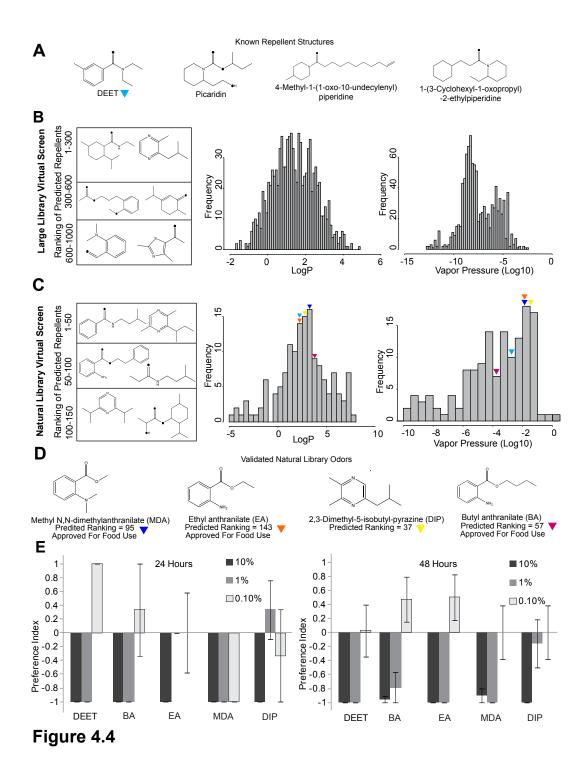


Figure 4.5: A new class of mosquito repellents with desirable safety profiles

(A) Mean weight of vinyl pieces following submersion in indicated compounds for indicated amount of time. N = 3, error bars = s.e.m., *** = p-value < 10⁻⁵. (B) Cumulative percentage of repellency across minutes 2,3,4 and 5 of indicated treatment (10%), in comparison to the appropriate solvent control. N=5 trials/treatment, 40 mosquitoes/trial.
(C) Mean percentage landing as measured by mosquitoes spending at least-5 secs on the protective window of glove, measured at different time-points in the 5-min assay. (D) Summary of desirable properties of new insect repellents reported in this study.

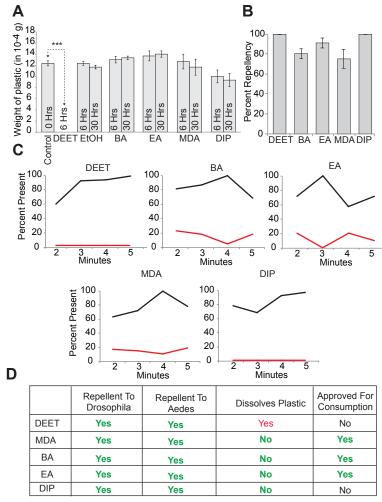


Figure 4.5

Figure 4.6: Mosquito escape index

An index representing the number of mosquitoes that touched and left the behavioral assay glove mesh vs the number that touched the mesh.

Escape Index = (Average Number of mosquitoes that touched and left the mesh during a five second window over the following time points: 1 minute, 2 minutes, 3 minutes, 4 minutes, 5 minutes) / ((Average Number of mosquitoes that touched and left the mesh during a five second window over the following time points: 1 minute, 2 minutes, 3 minutes, 4 minutes, 5 minutes) + (Average Number of mosquitoes that stayed in the mesh during a five second window over the following time points: 1 minute, 2 minutes, 3 minutes, 4 minutes, 5 minutes) + (Average Number of mosquitoes that stayed in the mesh during a five second window over the following time points: 1 minute, 2 minutes, 3 minutes, 4 minutes, 5 minutes)).

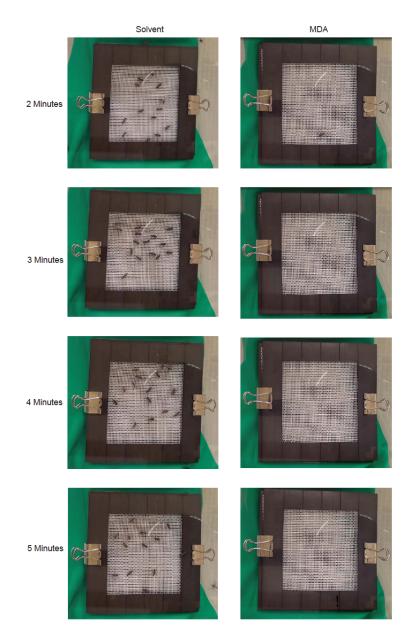
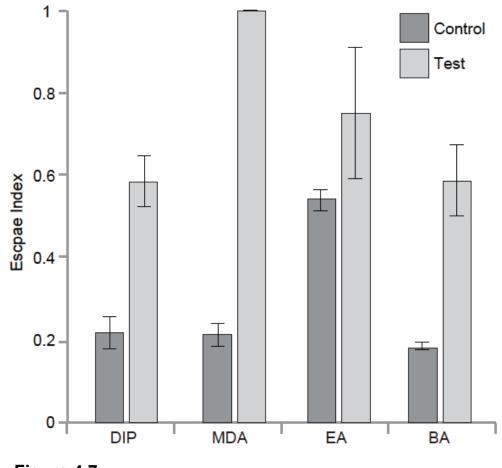


Figure 4.6

Figure 4.7: Natural compounds are effective at repelling *aedes aegypti* in the hand in glove assay

Representative still photographs from specific time-points of video assaying landing of female *Aedes aegypti* on solvent treated and MDA treated netting in the hand-in-glove assay.





CHAPTER V:

Analyzing Termination Dynamics of Prolonged Activating Odors and their Effects on Receptor-Mediated Olfactory Behavior

INTRODUCTION

Successful interpretation of a volatile chemical environment allows an organism to make more informed decisions based upon what could be critically important information. The olfactory system is often utilized by insects and mammals for tasks such as finding food, determining oviposition sites, avoiding predators, and identifying mates (van Naters and Carlson, 2006). These high priority tasks are achieved in part through recognition of odors by large families of Odor receptor (Or) genes that often encode 7-transmembrane proteins that are expressed in the Olfactory Receptor Neurons (ORNs) (Buck and Axel, 1991; Clyne et al., 1999; Dahanukar et al., 2005; de Bruyne and Baker, 2008; Vosshall et al., 1999). Generally, a single functional Or gene, along with an obligate co-receptor Orco, is expressed per odor receptor neuron class, causing neuronal responses to be a direct result of the activity of a single odor receptor protein (Couto et al., 2005; Fishilevich and Vosshall, 2005; Larsson et al., 2004; Vosshall and Hansson, 2011). In this fashion, neurons are able to send environmental information from the periphery to higher brain centers for interpretation and behavioral decisions. Using this system an organism can decode and analyze either single compounds, such as pheromones, or complex blends, such as rotting fruit in the environment.

Activation of ORNs can lead to distinct behavioral responses, attraction and repellency, which can be robustly and reproducibly measured in *Drosophila* larvae (Aceves-Pina and Quinn, 1979; Ayyub et al., 1990; Fishilevich and Vosshall, 2005;

Kreher et al., 2008; Monte et al., 1989). While the degree of behavioral response varies across odors, it is dependent on both the odor stimuli and odor concentration (Kreher et al., 2008). Recently, large numbers of Ors have been decoded using the empty neuron system, providing a wonderful knowledgebase to draw upon for analysis (Hallem and Carlson, 2006; Kreher et al., 2008). By testing a panel of 27 odors against all 21 Ors expressed in *Drosophila* larvae one group was able to analyze the relationship between Or activity and behavioral responses on a systems level for the first time (Kreher et al., 2008). This analysis found that attraction and avoidance can be caused by activation of either multiple Ors or, perhaps more interestingly, by single Ors. It was also shown that odors that activated similar sets of Ors are able to behaviorally mask the presence of each other.

One Or in *Drosophila* in particular, Or42b, has been identified as an odor receptor whose response is explicitly linked to an innate behavioral response (Semmelhack and Wang, 2009). Activation of this Or in the adult, and thus its associated ORN ab1A and glomerulus DM1, by the well-known *Drosophila* attractant apple cider vinegar causes a robust attractive response (Semmelhack and Wang, 2009). It has since been demonstrated that the Or42b associated ORN is a starvation modulated neuron (Root et al., 2011). Starvation increases transcription of short neuropeptide F Receptor (sNPFR1) in ab1A, increasing the neurons response to odor stimuli (Root et al., 2011). This cellular response to starvation was shown to be necessary and more importantly sufficient, for increased food search behavior to apple cider vinegar, suggesting that Or42b and associated ORN ab1A may be hardwired for appetitive choices and critically important for *Drosophila* food searching (Figure 5.1A).

This system provides a powerful tool to investigate whether periphery stimulation by odors alone is sufficient to modify the strengthened food search behavior of starved flies.

Traditionally, odors have been thought to interact with receptors causing one of two unique responses, either activation or inhibition of the neuron in which it is expressed (Dobritsa et al., 2003; Hallem et al., 2004). When considered at a systems level, these two categories of responses allow some odors to activate and others to shut down odor receptor neurons in a combinatorial fashion. Very recently, a third type of response to a receptor-odor interaction has been discovered wherein a receptor is activated for a greatly extended period of time (Montague et al., 2011; Turner et al., 2011). In one analysis a special class of odors called pyrizines were found to cause prolonged activation with a maximum response of ~160 spikes/second that lasted for minutes before returning to baseline in DmOr33b and DmOr59b (Montague et al., 2011). In the other, our lab identified CO₂ detecting ORNs that express members of the gustatory receptor gene family in mosquitoes that demonstrate ultra-prolonged termination kinetics, which can disrupt detection of CO_2 and behavior for several minutes (Turner et al., 2011). Additionally, in a few instances, ORNs have been shown to have a tonic response that lasts up to 10 sec beyond the end of the 0.5 sec stimulus period (Hallem and Carlson, 2006; Hallem et al., 2004). The currently understood effects of ORN activation on behavioral responses have emerged from studying the relationship between a very limited set of receptor-odor interactions (~0.05% of putative and ~5% of known volatiles tested) and associated behavioral responses. As a result, there is potential for new behavioral responses to be observed, especially in regard to the newly identified UP activators, as very little is know about what role differences in temporal aspects of receptor activity will have on behavior.

Here we identify the first UP activators of several Drosophila odor receptors, including for the behaviorally important ab1A ORN, and demonstrate that these odors have profound behavioral effects on Drosophila attraction. We first applied a novel chemical informatics approach to identify structural features that are important for activation of the ab1A neuron. We then utilized these features to perform an in silico screen of a large chemical space, predicting a set of odors which are active on ab1A. We validated the predictive approach computationally and tested a number of compounds using single unit electrophysiology, both showing high success rates. This large number of new ligands enabled us to identify a small set of odors that represent the UP mode of signaling. Odors that cause this UP signaling leave a short-term memory trace, where for minutes after exposure of ab1A to an UP activator the neuronal response to other ab1A ligands is dramatically changed. We demonstrate that even a brief exposure of ab1A to these odorants trigger activity in the neuron in a manner that it looses the ability to subsequently detect other ligands in the environment, which ultimately effects the ability of Drosophila to track towards highly attractive ab1A activating odors. In addition to UP activators, we also discover that an inhibitory odor of ab1A can cause an avoidance behavior that is able to overcome the response to highly attractive odors.

RESULTS

Chemical informatics can be applied to describe activity of the ab1A neuron

Only a small number of odors have been tested on the ab1A associated receptor Or42b, however the testing of these odors represents a significant body of work. In the

largest analysis to date 47 odors were tested on the ab1A neuron in the *Drosophila* antenna using single unit electrophysiology (de Bruyne et al., 2001). In two additional analyses, 27 odors were tested on Or42b using single unit electrophysiology in the "empty neuron" expression system (Dobritsa et al., 2003; Kreher et al., 2008).

Volatile chemical space is vast (potentially >400,000) and can be exploited to find ligands of ab1A, however the cost of purchase and time required to test a large number of compounds to identify UP activators using traditional wet lab techniques could prove to be unfeasible. To circumvent these challenges, we have implemented a novel chemical informatics approach to identify UP activators of ab1A (Figure 5.1B). Our approach allowed us to sidestep these challenges by only purchasing and testing odors that share important structural features with known activating odors of ab1A, thus greatly reducing both the cost and time required for identification. While we did not directly predict UP activators, we greatly increased our efficiency at screening active compounds, some of which we hoped would show UP termination kinetics.

Since we wanted to train our pipeline from the largest and most diverse set of compounds that had been tested for activity on ab1A, we used the deBruyne analysis of 47 odors as our training set. To identify important structural features our chemical informatics pipeline selected molecular descriptors, which are mathematical values that describe the structural features of a chemical, that were highly correlated with the activity of a set of training odors (Figure 5.1B). Molecular descriptors can describe a great deal of features about a molecule, ranging from simple information such as molecular weight to much more complex characteristics such as the relationships between atoms in a 3D space. Using the commercially available Dragon suite we calculated 3,224 molecular descriptors for each of the 47 training odors, producing a broad range of information for

each odor. Calculated descriptors consist of 0, 1, 2, and 3 dimensional information, examples of which are vapor pressure, atom type counts, the number and type of atoms that connect each of the atoms in a molecule, and the 3D distances between atoms in energy minimized molecules, respectively. We then implemented a Sequential Forward Selection (SFS) approach that incrementally grows an optimal subset of molecular descriptors best describing the important structural features of activating odors (Whitney, 1971), which for descriptor optimization we considered to be only the most strongly activating odors (>113 spikes/sec) Figure 5.1B, See Supplemental Methods). The SFS approach began by selecting the single descriptor that is most highly correlated with the activity of the 47 training odors. The approach then iteratively built upon this single descriptor, identifying the second best descriptor when combined with the first. The process continued until a single iteration failed to identify a descriptor that further improved the correlation between activity and the growing descriptor set. The resulting list contained 13 optimized descriptors (Table 5.1).

Interestingly, the SFS approach selected four 1D descriptors, one 2D descriptor and eight 3D descriptors. The optimized descriptor set containing the 1D descriptors focusing on the number of aliphatic esters, number of acceptor atoms for H-bonds, number of hydroxyl groups, and the number of carbon atoms attached to heteroatom, as well as containing a large number of 3D descriptors, suggested that the most important structural features dependent for activity in ab1A are the absence of hydroxyl groups, the presence aliphatic esters, and their placement in the odor molecules 3D space. As expected from descriptor optimization, the ab1A activators cluster tightly together when the training is clustered using Euclidean distances calculated between odors using the optimized descriptor values (Figure 5.1C).

Next we used the optimized set of molecular descriptors to train a Support Vector Machine (SVM) to perform predictions, which is a well known and highly effective machine learning technique (Cortes and Vapnik, 1995) (Figure 5.1B, See Supplemental Methods). We then performed 100 independent 4-fold cross validations to computationally validate the predictive success, which is an established computational approach, followed by a Receiver-Operating-Characteristic (ROC) analysis (See Supplemental Methods). A mean ROC curve representing the prediction accuracy across all 100 iterations was generated and the Area UnderCurve (AUC) value was determined to be 0.999, indicating that our in silico approach to describe the activity of odors on the ab1A neuron using structural features of the odors themselves was almost perfect (Figure 5.1D).

Screening a large untested chemical space in silico

Since the Or-optimized descriptor sets are effective at grouping activating odors based on their structural features and we had successfully trained a SVM to perform predictions based on those descriptors, we next applied them to screen a large chemical space *in silico*. We assembled and calculated molecular descriptors for both an eMolecules library, which contains ~440,000 compounds with similar molecular weight and atom type constraints to known volatiles, and a natural odor library, which contains 3,197 natrually occurring odors (See Methods). We then applied the trained SVM to predict activity for each of the compounds in both libraries using the optimized molecular descriptor set, resulting in a ranked list of candidate agonists for Or42b (ab1A).

Identification of Or42b agonists through an electrophysiological validation of in silico screen

In order to identify agonists of Or42b, some of which we hoped would demonstrate prolonged termination kinetics, as well as to further validate our computational approach, we obtained 15 high ranking odors from our natural odor library predictions. We tested each odor for activity against ab1A and it's associated receptor Or42b using single unit electrophysiology (Figure 5.2A). We observed that all tested odors were agonists of Or42b. 13 Odors were highly active (>100 spikes/sec above spontaneous activity), 1 odor was active (>50 spikes/sec above spontaneous activity). In order to further verify that the response was unequivocally from the Or42b receptor expressed in the ab1A neuron and not from neighboring neurons housed in the same ab1 sensilla, we performed single unit electrophysiology on Or42b -/- flies (Figure 5.2B). We observed a substantial reduction in response, indicating that Or42b is indeed the target receptor for these odors.

Identification of odors for ab1A with unusual ultra-prolonged termination kinetics

It has been proposed that not just frequency of activity, but the temporal properties of a response can potentially be a rich source of information encoded by sensory neurons. For a majority of odors, ORNs show rapid activation and termination kinetics, turning off abruptly shortly after the end of the odor stimulus (de Bruyne et al., 2001; Hallem and Carlson, 2006; Hallem et al., 2004). Now that we had identified several additional activating ligands, we could systematically inspect each odor for large differences in kinetics of response termination. Interestingly, 2 of the *in silico* predicted

odors that we tested using long-term electrophysiology recordings showed an ultraprolonged response that lasted for several minutes beyond the 0.5 sec odor stimulus (Figure 5.3A). In both instances exposure of ab1A to a 0.5-second pulse of an ultraprolonged (UP) activator elicits a strong initial response followed by decrease in the ORN firing rate to approximately half maximal frequency in about 8-10 seconds, after which the ORN has a relatively steady firing rate of ~30-70 spikes/sec above spontaneous activity for several minutes (Figure 5.3A -green line). This unusual pattern of activation is quite different from other equally strong activators that return close to baseline between 2-6 seconds after odor exposure (Figure 5.3A –grey line).

This form of a prolonged response elicited by a short 0.5 second stimulus appears even stronger than the activity pattern evoked by a continuous odor pulse of 30 secs, in which the adaptation of the initial strong response of the neuron occurs rapidly, followed by a low frequency of action potentials throughout the duration of the stimulus (de Bruyne et al., 2001). These observations suggest that the class of UP odors we have identified by cheminformatics have an atypical property to activate ORNs for periods >500 times the duration of the initial 0.5 sec stimulus.

A mechanism for short-term memory of odor exposure

Surprisingly, a brief 0.5-second pre-exposure to an UP activator renders the neuron unresponsive to changes in concentration of other activating odorants that the ORN normally responds to. The UP-activated ORNs are unable to respond to odorants normally for more than 100 seconds, in some cases up to the duration of the entire recording (300 seconds) (Figure 5.3B, green bars). This short-term memory effect is specific to the UP-activators and pre-exposure to regular odorants that activate to

comparable levels does not affect the ability of the ORN to detect subsequent repeated 0.5 second stimuli of an activating odorant (Figure 5.3B, grey bars). This form of change in coding capacity of a peripheral sensory level after ultra-prolonged activation is a novel phenomenon that has not been reported for neurons expressing Odor receptor proteins.

Although termination kinetics has been shown to be a property associated with the receptor (Hallem et al., 2004), it remains to be tested whether this novel type of short-term memory effect could be influenced by odor binding proteins (Wang et al., 2007) found in the sensillum lymph or other factors involved in signal transduction. In order to test directly whether the short-term memory effect depends upon the odor receptor protein, we expressed *Or42b* in the well-established "empty neuron" decoder system (Dobritsa et al., 2003). We find that the UP-activation effect is partially transferred to the Δ halo ab3a neuron upon ectopic expression of *Or42b* (Figure 5.4). Surprisingly, the short-term memory effect is transferred to the acceptor ORN simply by the ectopic misexpression of *Or42b* (Figure 5.4B, blue bars), suggesting that the integration of the two inputs and retention of the memory of prior exposure is maintained at the level of the receptor.

The ability of an animal to respond behaviorally to changes in concentration of a ligand along an odor gradient or navigate along an odor plume in the environment is presumed to depend on two important coding properties of the ORN: sensitivity and rapidity of detecting incremental changes in concentration. Since both these properties are severely compromised upon exposure to UP-odorants, we expect a long-term effect on behavior even after the animal is removed from the vicinity of the UP-odorant. The

Drosophila larvae are ideal for behavioral testing of the short-term memory effects to prior exposure to UP-activators since they have a simpler olfactory system and behavior assays are robust and quantitative (Fishilevich and Vosshall, 2005; Kreher et al., 2005; Kreher et al., 2008; Louis et al., 2008). An antennal receptor Or42b, for which we have identified UP-activators, is expressed in the larval system as well (Fishilevich and Vosshall, 2005; Kreher et al., 2005; Kreher et al., 2008). It has also been demonstrated that Or42b is the exclusive receptor for detection of ethyl acetate at 10⁻⁴ dilution, which causes attractive behavior (Kreher et al., 2008). We performed a two-choice assay where larvae were given 90 seconds to choose between an ethyl acetate (10⁻⁴) side and a solvent side on a plate after they were pre-exposed to either the UP-activator (methyl proprionate), a regular activator of comparable initial strength with normal response termination (methyl isobutyrate), or solvent (paraffin oil) (Figure 5.5A). In solvent preexposed and activator pre-exposed larvae a robust attractive behavior towards ethyl acetate was observed, as expected (Figure 5.5B). However a 10-second pre-exposure to an UP-activator almost completely disrupted attraction. Even a brief 1-second preexposure to an UP-activator was sufficient to cause a significant reduction of attraction towards ethyl acetate (Figure 5.5B). Taken together these results demonstrate that preexposure to a super activator not only disrupts the ability of ab1A to detect odors, but also disrupts behavior elicited by the odorant.

In order to demonstrate that the change in behavior is caused directly by UPactivation of Or42b, we performed a similar pre-exposure experiment on larvae that were genetically manipulated to have only the *Or42b* expressing ORN pair functional. This was achieved by specifically rescuing expression of the obligate co-receptor *Orco* in only

the *Or42b* expressing neurons in an *Orco* mutant background. In both solvent preexposed and activator pre-exposed larvae robust attractive behavior towards ethyl acetate was observed, as expected (Figure 5.5C). However, pre-exposure to the UPactivator completely disrupted attraction towards ethyl acetate (Figure 5.5C). This shows that the olfactory system has the ability to integrate two odor stimuli, separated in time, directly at the level of the peripheral ORN, and compute two dramatically different outputs (change or no-change in firing frequency) to transmit to the CNS depending upon the identity of the first odorant.

Disruption of attraction towards apple cider vinegar in starved larvae

In the natural environment attractive cues are often more complex consisting of blends of odorants and insects. Moreover, the olfactory ability to find food odors may be enhanced by the NPF pathway-mediated starvation response (Root et al., 2011). For example, Or42b neurons were shown to be necessary for the starvation-induced food-search behavior in the adults (Root et al., 2011). In order to test whether exposure of Or42b, which was been demonstrated to be hardwired for behaviorally important appetitive choices, to an UP-activator was sufficient to interfere with the attraction of starved larvae towards complex food odor, we tested them in behavior assays. Surprisingly, a brief pre-exposure of 2-hour starved larvae (Koon et al., 2011) to an Or42b UP-activator was sufficient to dramatically reduce the ability to find an attractive source of apple cider vinegar (Figure 5.5D). This result suggests that The UP-activators may provide a powerful tool for behavior modification to protect against harmful pest species, many of which cause significant loss of agricultural produce and crops globally.

Inhibition of appetitive choice ORN causes strong avoidance response

While we have demonstrated that UP activators disrupt attraction and activators have been previously shown to cause a strong attractive response, the behavioral effect of inhibitors tuned to this receptor alone has not been previously reported. We performed a two-choice assay where larvae were given 90 seconds to choose between the inhibitor Isopentyl formate (10^{-2}) , which was found in this study, and a solvent side (paraffin oil) on a plate. Interestingly, larvae behaviorally avoided the inhibitor, with a preference index of -0.2 (Figure 5.6). These results demonstrate that inhibitors are able to repel insects on their own.

Identification of odors that display Ultra Prolonged activation in additional ORNs

In order to test whether we could identify UP activators of additional Ors, we performed similar chemical informatics analysis for Or22a and Or85b. Here we trained our pipeline using the largest panel available for these receptors, which consists of 109 previously tested odors (Hallem and Carlson, 2006). In chapter 2 we predicted activating odors and validated several additional odors that displayed delayed termination kinetics reminiscent of UP activators (Figure 5.7A). We identified 5 UP activators for Or22a and 1 for 85b (Figures 5.7B, 5.8A), further suggesting that such ultra-prolonged termination kinetics are not properties specific only a select few receptors. The prolonged activation of Or85b by UP activator 2-heptanol elicits a strong initial response similar to the one caused by previously identified Or42b up activators, however the decrease in the ORN firing rate to approximately half maximal frequency requires a greatly extended time of 30 seconds, indicating that activation decay rates can vary significantly (Figure 5.7B).

Visual inspection of the 5 UP-activators of Or22a does not reveal any features that easily distinguish this class from that described for other activators of the same receptor (Figure 5.8B). To investigate whether we could identify an UP-optimized descriptor set that separates UP-activators from a large set of active compounds, we identified a subset of descriptors that cluster the UP-activators close together in a chemical space containing activators of Or22a (Figure 5.7C). We then ranked odors for UP-activation for Or22a, tested one using electrophysiology (Butyl propionate) and found that it had the hallmarks of an UP-activator (Figure 5.7D). These results suggest that the UP-optimized descriptors may be useful to distinguish odorants that cause prolonged activation even from structurally similar odorants.

We found instances where the UP-activator did not show prolonged activation of other ORNs it activates, suggesting that the prolonged response is not caused simply due to a property of the odor (Figure 5.8C). However, we also found that 2-heptanol can cause UP-activation of another ORN that expresses Or85a. These results suggest that although UP-activation is probably caused by specific interaction between odor and receptor, some odors may have properties that can cause prolonged activation in at least two different Or containing neurons.

Once again we find that a brief 0.5-second pre-exposure of these receptors to an UP activator renders the neuron unresponsive to changes in concentration of other activating odorants that the ORN normally responds to (Figure 5.9A). The UP-activated Or22a and Or85b expressing ORNs ab3A and ab3B are unable to respond to odorants normally for more 100 seconds for the case of ab3A and for the duration of the entire recording for ab3B (300 seconds) (Figure 5.9B, green bars). This short-term memory effect again contrasts from pre-exposure to regular odorants where activation to

comparable levels does not affect the ability of the ORN to detect subsequent repeated 0.5 second stimuli of an activating odorant (Figure 5.9B, grey bars).

DISCUSSION

We have designed a computational approach that allows us to identify UP activating odors and investigate their effects on odor receptors, including subsequent odor detection. Our computational pipeline builds an optimal set of molecular descriptors that explain odor activity and predicts Or42b activity to over 400,000 odors by applying them to a trained SVM. All experimentally tested odors either activate or inhibit Or42b, additionally, a number of validated odors exhibited prolonged termination kinetics. Through examination of their effects, we have identified that exposure to these UP odors disrupts the ability of *Drosophila* larvae to track towards highly attractive odors. We have also demonstrated the repellent properties of inhibitory odors of Or42b.

No analyses have been previously performed to computationally identify UP activating odors. Computational approaches have been made at predicting activating ligands, however if compared at the same activity threshold applied in our study (>=50 spikes/second), their success rates were far lower than ours at predicting ligands (25%)(Schmuker et al., 2007). We find that our computational approach was 100% efficient in predicting ligands of Or42b, as all odors tested with electrophysiology were either activators or inhibitors. Additionally, through rational prioritization of odors, the likelihood of identifying odors with unique properties becomes far higher. 13% (2/15) of validated odors displayed UP activation characteristics for Or42b. Without our initial computational prioritization to identify activating odors, this rate would reduce

significantly. For example, if we were screening for UP activators using the same ligand identification success rate of the hand selected training set at 19% (9/47) (de Bruyne et al., 2001), we could roughly expect our accuracy at identifying UP activators to be 13% of the 19%, or 2%. Clearly, a computational approach is advantageous.

The new ligands presented in this study include a small number of novel UPactivators whose discovery expands the olfactory code from activation and inhibition to now include ultra-prolonged activation. Most of these UP-odors, exposure to which is retained as a short-term memory trace by the odor-receptor, are present in natural substances suggesting that they may play a significant role in the natural olfactory behavior of animals. Functional insect odor receptors are thought to act as ion-channels (Sato et al., 2008) as well as GPCRs (Wicher et al., 2008) and have a unique inside-out 7-transmembrane structure (Benton et al., 2006) acting along with a heteromeric partner Orco (Benton et al., 2006; Larsson et al., 2004). Although outside the scope of this study, understanding mechanistically how these odors bind and cause prolonged activation will be of great interest.

We have demonstrated two very important characteristics of these UP activating odors: a brief exposure is sufficient to functionally silence the responses of Or42b, Or85b, and Or22a to normally excitatory odors for greater than 2 minutes and that a brief exposure is sufficient to disrupt robust attractive behavior. Olfactory signals are very important for many biological processes. Identification of subtle changes in odor plume identity and concentration allows for successful navigation by insects to odor sources. For example, casting, which involves identifying the edge of an odor plume and course correcting to towards it's center, is utilized by many species to travel up odor plumes. Our prolonged activators cause the insect to be functionally unable to determine these

concentration changes, leading to a loss of casting ability. By the time the effects of the UP activator wear off the insect could easily have flown far off course. In a case were they do reacquire the plume, they would also reacquire the UP activator, once again causing them to drift off course.

We have also demonstrated a very important characteristic of our inhibitory odor: inhibition of Or42b causes repellent behavior. Additionally, if the inhibitory odor is introduced next to a highly attractive odor for the same Or, it negates attraction. These results suggest that Or42b is not solely hardwired for innate attraction and is instead hardwired for behavior, with activating odors causing attraction and inhibitory odors causing avoidance. Further exploration on the effects of other inhibitory odors on this receptor as well as those for additional receptors should be an important focus.

An emerging area of research is the identification of odors that can modify hostseeking behavior in insect disease vectors, either by virtue of their ability to inhibit ORNs that detect host-seeking cues (Montague et al., 2011; Turner et al., 2011; Turner and Ray, 2009), by activating ORNs that cause avoidance behavior (Syed and Leal, 2008). UP-activators and inhibitors provide a novel paradigm for behavior modification strategies targeting important odor receptors (Figure 5.10). *In silico* screens can thus provide a rational foundation for identification of novel insect repellents and lures that are environmentally safe and can aid in the fight against insect-borne diseases.

Figure 5.1: Activity of a behaviorally important neuron, Ab1A, can be described by an odor receptor neuron-optimized chemical inormatics approach

(A) Activation of Odor Receptor Neuron (ORN) ab1A, and thus glomerulus DM1, leads to a strong attractive response in *Drosophila melanogaster*. (B) Schematic of the cheminfomatics pipeline used to identify novel ligands from a larger chemical space. (C) Receiver-operating-characteristic curve (ROC) representing computational validation of ligand predictive ability of the ORN-optimization approach. The mean true-positive value from 100 independent 4-fold cross validation runs of the Support vector machine (SVM) approach is plotted. (D) Hierarchical cluster analysis of the 46 training set odorants using ORN optimized descriptor sets to calculate distances in chemical space for ab1A. Training set odorant activity is indicated using a color gradient scale. (E) Pharmacophore of odors that are highly active against ab1A.

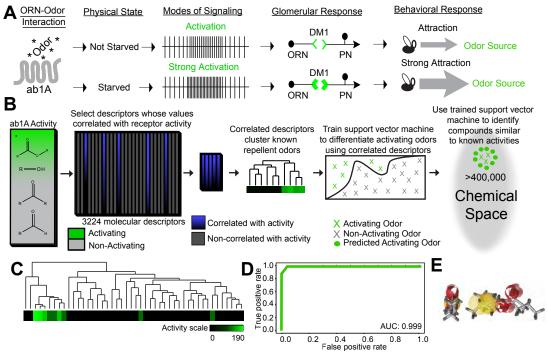


Figure 5.1

Figure 5.2: Electrophysiology validates that ORN-optimized molecular descriptors can successfully identify new ligands for ab1A

Mean increase in response of neuron to 0.5-sec stimulus of indicated predicted odors in **(A)** ab1A (Or42b) ORN; **(B)** and ab1A (Or42b^{-/-}) (10^{-2} dilution). N=3, error bars=s.e.m.

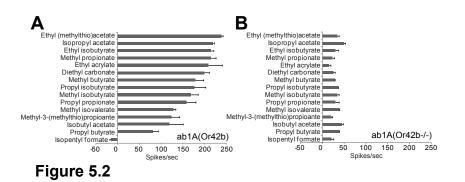


Figure 5.3: Functional identification of Ultra-Prolonged activators and analysis of their long-term effects on ab1A using electrophysiology

(A) Mean long-term response of ab1A to a 0.5- sec stimulus of indicated odor at t=0. Each response curve is depicted in 3 separate graphs with different time windows, 10 sec, 90 sec and 300 sec. N=3, error bars=s.e.m (B) Mean increase in frequency of response of the ab1A to the indicated odor applied at indicated time points after pre-exposure to 0.5-sec odor stimulus indicated (grey=activator, green=UP-activator, blue=UP-activator response in UAS-Or42b expressing ab3A neurons in Δ Halo; Or22a-G4,UAS-Or42b flies). N=5, error bars= s.e.m.

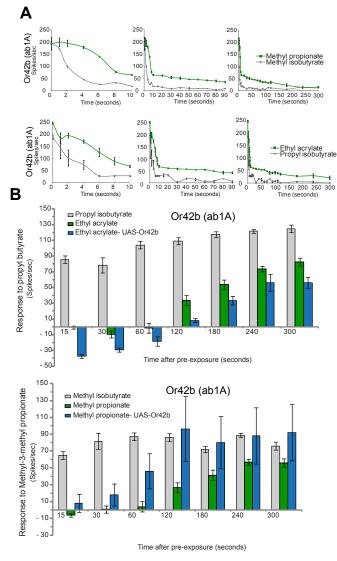


Figure 5.3

Figure 5.4: Ectopic expression confers Or42b UP activation Mean long-term response of Or42b expressing neuron (ab1A) to a 0.5- sec stimulus of indicated odor. Each response curve is depicted in 2 separate graphs with different time windows, 10 sec and 90 sec. UAS-42b recordings were performed in Δ Halo; Or22a-G4,UAS-Or42b flies where ab1A neurons express Or42b. N=3, error bars=s.e.m

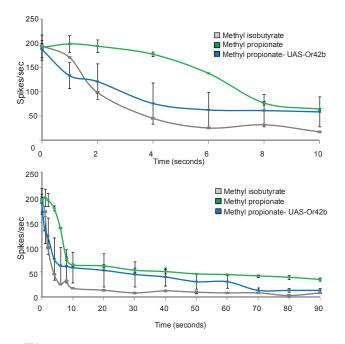


Figure 5.4

Figure 5.5: Behavioral effects of Ultra-Prolonged activators on odor detection in ab1A

(A) Overview of pre-exposure integration into larval two-choice preference assay.

(B) Preference index of *Drosophila* larvae to Ethyl acetate 10^{-4} . Larvae were preexposed to the indicated odors for either 10-sec (left) or 1-sec (right) immediately prior to the preference assays. N=10 (~40 larvae/ trial), error bars=s.e.m. (C) Preference index of *Drosophila* larvae (*w;Or42b-GAL4/UAS-Orco; \Delta Orco/\Delta Orco*) to Ethyl acetate 10^{-4} . Larvae were pre-exposed to the indicated odors for either 10-sec immediately prior to the preference assays. N=10 (~40 larvae/ trial), error bars=s.e.m. (D) Similar experiment as (b) performed on 2-hr starved larvae given a choice between Apple Cider Vinegar (5%) and water. N=20 trials (~40 larvae/trial), error bars=s.e.m. P-values= *<0.05, **<0.001.

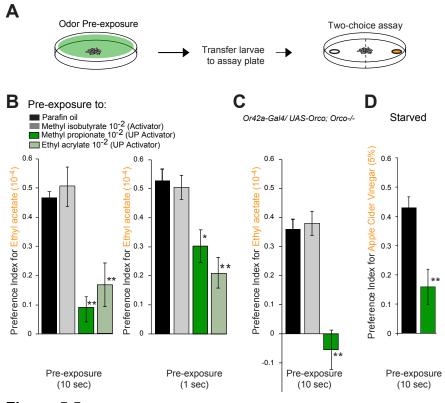




Figure 5.6: Behavioral effects of inhibitory odor on odor detection in ab1A

(A) Overview of larval two-choice preference assay. Red circle denotes inhibitor (iso-amyl formate) placement and empty circle represents solvent (paraffin oil).
(B) Preference index of *Drosophila* larvae to iso-amyl formate 10⁻². Larvae were given a choice between solvent or iso-amyl formate 10⁻² for the preference assay. N=8 (~40 larvae/ trial), error bars=s.e.m.

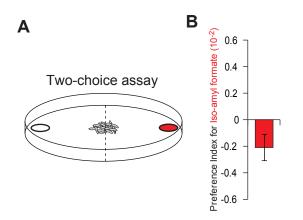


Figure 5.6

Figure 5.7: Functional identification of Ultra-Prolonged activators of additional odor receptors using electrophysiology.

(A) Long-term response of a single Or22a expressing ab3A neuron to a brief 0.5-sec stimulus of ethyl valerate (indicated as a red bar). Action potentials from 0.25-sec windows shown from indicated regions of the response. (B) Mean long-term response of indicated receptor expressing neuron to a 0.5- sec stimulus of indicated odor at t=0. Each response curve is depicted in 3 separate graphs with different time windows, 10 sec, 90 sec and 300 sec. For ease of spike counting ab3B (Or85b) recordings were performed in a Δ Halo (Δ H) mutant background (Dobritsa et al., 2003) where ab3A neuron is unresponsive. N=3, error bars=s.e.m (C) Schematic representing the identification of prolonged activator-specific molecular descriptors that can cluster prolonged activators together in a tree containing all other Or22a activators. (D) Mean long-term response from an ab3A neuron expressing Or22a to a 0.5-sec stimulus of a predicted UP-activator depicted in 2 separate graphs with different time windows, 10 sec and 90 secs. N=3, error bars=s.e.m

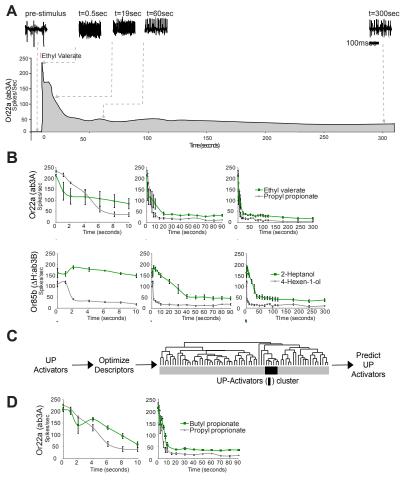


Figure 5.7

Figure 5.8: Identification of ultra-prolonged activating odors for additional Ors

(A) Mean responses from ab3A neurons expressing Or22a across 10 seconds to a 0.5 second odor (10-2) stimulus, red bar. (B) Pharmacophores of Or22a prolonged activators and Or22a activator pharmacophore. (C) Mean responses of indicated receptor expressing neurons to a 0.5 second stimulus of indicated odors (10-2), red bar. For (A) and (C) N=3, error bars=s.e.m.

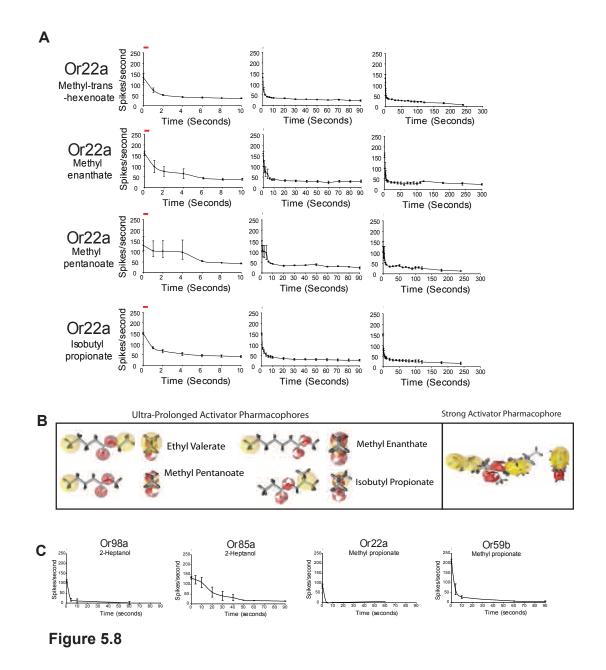


Figure 5.9: Long-term effects of Ultra-Prolonged activators on odor detection

(A) Representative electrophysiology traces of Or85b expressing ab3B neuron starting ~13 sec after a 0.5-sec pre-exposure to an activator (4-hexen-1-ol) or an UP-activator (2- heptanol) with repeated exposures to another activator (5-hexen-1-ol). Boxed area denotes 2-sec regions at 15 sec and 30 sec after pre-exposure where 0.5-sec of 5- hexen-1-ol (black bars) was applied, which are magnified above and below. Ab3B (Or85b) recordings performed in a Δ Halo (Δ H) mutant background (Dobritsa et al., 2003). (B) Mean increase in frequency of response of the indicated neuron to the indicated odor applied at indicated time points after pre-exposure to 0.5-sec odor stimulus indicated (grey=activator, green=UP-activator). N=5, error bars= s.e.m.

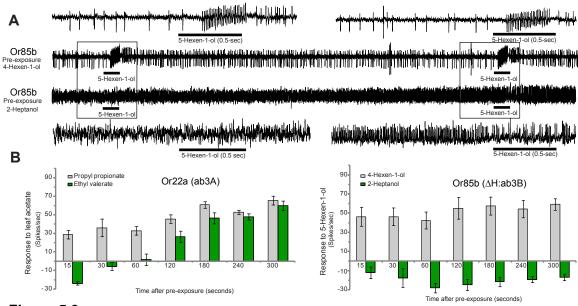


Figure 5.9

Figure 5.10: Modes of signaling and their behavioral responses

Expansion of the known behavioral responses from modes of signaling: inhibition of ab1A leads to repulsion and UP activation of ab1A leads to confusion. Flies are repulsed by inhibitory odors that specifically affect ab1A. Exposure to an UP activator causes flies to be unable to respond to normally attractive odors that activate ab1A.

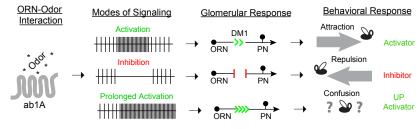


Figure 5.10

Table 5.1: Optimized descriptor sets for ab1A (Or42b) Optimized descriptor symbol, brief description, class, and dimensionality are listed. Descriptors are listed in ascending order of when they were selected into the optimized set.

Optimized Descriptor List			
Symbol	Description	Class	Dimensionality
nRCOOR	number of esters (aliphatic)	Functional group counts	1
Mor10u	signal 10 / unweighted	3D-MoRSE descriptors	3
Mor04m	signal 04 / weighted by mass	3D-MoRSE descriptors	3
R1e+	R maximal autocorrelation of lag 1 / weighted by Sanderson electronegativity	GETAWAY descriptors	3
Mor27m	signal 27 / weighted by mass	3D-MoRSE descriptors	3
nHAcc	number of acceptor atoms for H-bonds (N,O,F)	Functional group counts	1
E1m	1st component accessibility directional WHIM index / weighted by mass	WHIM descriptors	3
GATS5m	Geary autocorrelation of lag 5 weighted by mass	2D autocorrelations	2
nROH	number of hydroxyl groups	Functional group counts	1
R5v	R autocorrelation of lag 5 / weighted by van der Waals volume	GETAWAY descriptors	3
Mor10p	signal 10 / weighted by polarizability	3D-MoRSE descriptors	3
C-006	CH2RX	Atom-centred fragments	1
Mor11e	signal 11 / weighted by Sanderson electronegativity	3D-MoRSE descriptors	3

Table 5.1

CHAPTER VI:

Applying Structure-Based Virtual Screening to Identify Potent Inhibitors of the Tuberculosis Target EthR

INTRODUCTION

While virtual screening is just now becoming an effective tool for modeling and screening odors in mammalian ORs, it is not yet an option for insect Ors, as the structure of receptors for insects have not yet been solved. However, as technologies advance the structures of insect and mammalian odor receptors will undoubtedly be determined in the near future. Once the structures are available, application of structure-based virtual screening approaches to predict ligand binding will be effective tools for predicting receptor-odor interactions. Additionally, application of these approaches will also provide valuable insight into how odors are functionally interacting with the receptors. Structure-based virtual screening can be applied as a standalone method or, as was done with the goldfish Or, it can be applied in combination with ligand-based virtual screening (Triballeau et al., 2008). Comparing the structures of activating or inhibiting compounds using ligand-based approaches, such as molecular descriptors, can quickly and effectively screen millions of compounds. A second screen can then be applied where potential ligands that share important structural features with known actives can be docked into the binding site of a target protein, which is a more time consuming process.

In order to learn the technique of structure-based virtual screening, I performed an external research project under the guidance of Professor Sir. Tom Blundell at the University of Cambridge, UK. Under the guidance of specialists in his laboratory, including Dr. Willaim Pitt, I successfully applied structure-based virtual screening to

identify potent inhibitors of the enzyme EthR, a promising second line drug target currently under investigation for Tuberculosis (TB) treatment.

TB is a major health challenge around the globe. Roughly 1/3 of the world population is infected with *Mycobacterium tuberculosis*, which is responsible to leading to the infectious disease Tuberculosis that is responsible for approximately 2 million deaths each year. The currently approved course of treatment, titled Directly Observed Therapy, Short-Course (DOTS), comprises 2 months of treatment using isoniazide, rifampicin, ethambutol, and pyrazinamide followed by a 4-6 month treatment with only 2 of the aforementioned drugs (Raviglione, 2003). Unfortunately as has been seen repeatedly in bacteria, a multidrug resistant strain has been emerging, with which it is estimated that roughly 50 million people are currently infected (Chan and Iseman, 2002; Mahmoudi and Iseman, 1993). As a response the efficacy of several "second line" drugs have been under investigation and considered increasingly important.

One of these second line drugs ethionamide (ETH) has shown good efficacy, but only at relatively high doses, leading to high rates of side effects (Frenois et al., 2004). ETH functions as a pro-drug, since it needs to be activated by a mycobacterial enzyme prior to being able to perform its antimicrobial effect (Baulard et al., 2000; DeBarber et al., 2000). The activator of ETH has been determined to be EthA protein, which is a monooxygenase that oxidizes ETH, thus activating the compound (Figure 6.1) (Baulard et al., 2000; Vannelli et al., 2002). A repressor gene EthR, which has been shown to transcriptionally regulate expression of EthA through a 55bp operator located in the ethA-R intergenic region, regulates EthA (Aramaki et al., 1995; Engohang-Ndong et al., 2004). Inhibition of EthR leads to increased ETH efficacy, as the prodrug is more readily activated.

Several small molecule inhibitors of EthR have been identified over the last decade. Initial crystal structures of the repressor identified a potential drugable cavity between helices 4 and 9, which contained two dioxane molecules (Dover et al., 2004) (Figure 6.2A). Shortly thereafter another group discovered a naturally bound ligand hexadecyl octanoate which was co-purified and co-crystallized with the repressor (Frenois et al., 2004)(Figure 6.2B). The same group also identified and tested several additional ketone based compounds, identifying benzlacetone as a likely inhibitor of the EthA repressor EthR. Over the years since, a number of groups have identified and co-crystalized additional EthR inhibitors, all of which function within the same long cylindrical cavity (Flipo et al., 2011; Flipo et al., 2012; Willand et al., 2010; Willand et al., 2009) (Figure 6.2C). The efficacy of these compounds ranges from micro to nanomolar.

In an attempt to identify more effective inhibitors of EthR we have applied a combination of both ligand-based and structure-based virtual screening to predict additional putative inhibitors of EthR. As we are able to use our approach to screen a vastly larger chemical space than has previously been inspected, we hoped to identify more potent EthR inhibitors.

RESULTS AND DISCUSSION

Analyzing the ligand binding pocket of EthR

As previously mentioned, a number of inhibitors have formerly been identified and their bound orientations within the EthR cavity had been determined. In addition to these published compounds, several additional molecules have been identified and cocrystallized by Dr. Sachin Surade, a member of the Blundel lab. Analysis of the EthR

structure displays a long narrow cavity that runs between helices 4, 5, 7, 8, and 9 (Figure 6.3). The cavity entrance is open and resides between helices 4, 5, and 7.

By Integrating all solved ligand binding locations and analyzing their orientations in EthR, it appears there are certainly two and possibly up to three distinct binding regions within the EthR cavity (Figures 6.4, 6.5). Very few ligands span the entire length of the cavity. The majority of compounds bind close to the cavity entrance at site 2 and a select few reside deep within the pocket in Site1. A few longer compounds extend into what could be considered site 3, which is an extension of site 2, and leave the binding pocket. From previous analysis it appears that site 2 is the most potent of these cavity positions, however it is important to note that the number of ligands identified for site 1 are limited, making a more thorough analysis required before a final decision can be made. This led us to focus our efforts on identifying and virtually docking ligands into sites 1 and 2 of the protein target, which we will refer to as small site 1 and small site 2. As a select few known ligands reside across both sites, we also performed a separate analysis where we attempted to dock ligands across the entire cavity, which we will call the combined site.

Preparing a Virtual Screening Library

We assembled a virtual library for inhibitory compound screening that contained only commercially available chemicals that were purchasable. Our library contained compounds from the Enamine (advanced library: 204,772 compounds), Maybridge (screening library: 56,000 compounds), and Asinex (merged library: 439,946 compounds) libraries containing 700,930 unique structures. Upon removal of duplicate

molecules shared across libraries (9,661 removed) and molecules containing salts or unappealing atom types, we remained with a sizable chemical library of 588,723 compounds (See Methods).

Compounds identified to bind within small site 1 were duplicates of those bound within small site 2 (Sachin Unpublished). Interestingly, binding site 1 was only occupied when site 2 was filled, raising the possibility that this site may be more challenging to fill. As a result, a single library was docked within both site 1 and site 2 and a separate and larger compound set was created for docking into the combined site.

As it would take a great deal of time to computationally dock >550,000 chemicals into each of our binding sites, we analyzed previously identified ligands to reduce the size of our screening library. We determined structural features that may be important for fitting within the cavity and for binding to EthR. By analyzing known ligands, it appears that the inhibitory cavity of EthR is long and fairly thin, thus all known compounds bound to either site are also relatively thin and unbranched. We also noticed that compounds that bound only into sites 1 or 2 were small, contained at least one aromatic ring, and often contained a ketone within the structure that formed a hydrogen bond within each of the cavities (Asparagine 179 – Site 2, Glutamine 125 -Site 1). Additionally, we identified 2 potential hydrogen bonding sites that are rarely satisfied by any of the known ligands (Asparagine 176 – Site2, Threonine 121 – Site 1). Considering these criteria, we assembled our two separate libraries, one to individually dock into binding sites 1 and 2 and another for the cavity spanning combined site.

We selected compounds for our small ligand library from the full set of >550,000 compounds using the following criteria: <= 3 H-bond acceptors/donors, at least 1 aromatic ring, a molecular weight of less than 250, and had no rings of size greater than

7. As the compounds in this library were relatively small, we were not concerned with removing compounds containing side chain branches that would be to wide for the cavity. These criteria resulted in selection of 38,893 compounds for a small site library that could be docked into binding sites 1 and 2.

We selected our large ligand library by application of both molecular descriptors and machine learning. While the combined site library was also selected from the full set of >550,000 compounds, it needed to contain much larger structures. As there were many compounds with sizes that would span the entire cavity in the full library, a more meticulous criterion was used in its selection. We first attempted to identify a single molecular descriptor from either the commercially available Dragon descriptor suite or pipeline pilot that defined the length and narrowness of a compound. Unfortunately, we were unable to identify such a descriptor. As a result, we compared three different sets of general shape descriptors (Balaban, Chi, and Kappa) for their ability to separate out long thin compounds. At the same time we also compared several machine learning approaches including random forests, support vector machines, and linear discriminate analysis for their ability to separate out the ideal compound shapes using each of the three descriptors. Each of these methods requires both a positive and a negative training set, which in this case would be a set of compounds that inhibit EthR and another set that do not. We assembled a training compound set containing ~20 previously know ligands (positive training set) and, as no negative ligands were known, 100 randomly select ligands from the Asinex library (negative training set) in order to compare each method and descriptor for the ability to separate known binding from non-binding chemicals. Application of the random forest approach trained on balaban descriptor values was the most effective at differentiating the training set with the largest Area

Under the Curve (AUC) of the Reciever Operating Characteristic (ROC) of 0.95. We next applied the random forest technique to discriminate between similar and dissimilar compounds based on their balaban descriptor values, reducing the full original library from 588,723 to 112,692 compounds. As it requires a great deal longer to dock compounds into the long combined binding site, the library was still far too large. We further reduced the size of the large ligand library by randomly selecting 6,000 chemicals meeting the following requirements that were determined based upon the structures of previously identified compounds that bound into the combined cavity: MW > 400, >= 1 aromatic ring, and no ring sizes greater than 6 atoms.

Selecting Docking Structures of EthR

We next selected the crystal structures and binding pockets that would be used to perform the virtually screen of our final compound libraries. In total, 32 previously determined EthR crystal structures were available, consisting of 24 unpublished (Surade Unpublished) and 8 previously published (3G1M, 1T56, 1U9N, 1U9O, 3G1L, 3G1O, 3O8H, and 3O8G) structures. While initial attempts were made to use ensemble docking, which uses multiple crystal structures of the same protein to allow for protein backbone and R group movements, the computational docking time greatly exceeded our time constraints. As a result, we selected a single structure that best defined each binding site for docking.

We identified the single structure that underwent the largest conformational shift in the DNA binding region, which in theory would also cause the largest reduction in repression of EthA, and contained the widest ligand cavity. All protein structures were aligned to their largest alpha helix using Pymol. Each structure was compared for R

group shifts leading to increase or decrease in binding cavity shape. After careful inspection, it appeared that MB1047 and NT06 had the most open configurations in site 2 and site 1, respectively, and were selected for docking (Surade Unpublished). NT06 was also selected for combined site docking as this structure had the largest cavity spanning both binding sites.

Selecting Hydrogen Bond Locations Important for Protein-Ligand Interface

The hydrogen bonding between a ligand and its protein-binding site is critically important for describing the mechanism of attachment. As such, it is essential that we identify which binding locations appear to be important for EthR. Visual analysis of all previously identified ligands, their binding sites, and the protein cavity itself uncovered Asparagine 179 for site 1 and Glutamine 125 for site 2, as being highly important to hydrogen bonding at the protein-ligand interface. Asparagine 176 and Threonine 149 in site 1 and Threonine 121 in site 2 may also play a less substantial role, as evidence for their interactions with known ligands is present, but less pronounced.

Self-Docking and Cross-Docking Validations

We next compared how well the Gold software suite self-docked, which involves docking a ligand back into its own crystal structure, and cross-docked, which involves docking other solved ligands for the same receptor into a crystal structure, for the structures NT06 and MB1047. As we know exactly where each of these compounds should bind, they provide good indicators as to how well the docking software and protein system will work.

For self-Docking, ligands for both NT06 and MB1047 were re-docked into their own solved structures using the GOLD suite (Verdonk et al., 2003). H-Bond weighted constraints for Asparagine 179 in site 1 and Glutamine 125 in site 2 were compared to docking runs where no constraints were implemented. Self-docking runs were often able to successfully reinsert their own ligands back into the correct position and orientation in the receptor (Figures 6.6, 6.7). For our cross-docking analysis, we docked a variety of ligands known to bind to EthR. Cross-docking is a more stringent test of binding as a structure that is used for docking was not solved with a ligand that is attempted to be docked creating a test to see how "accepting" the binding site is compounds with different shapes that are known to bind as well. The analyses yielded promising results, as many of the ligands were positioned very similarly to the natural binding positions of their own solved structures.

We next compared the effectiveness of both the presence and absence of Hbond constraints. Interestingly, docking with and without H-bond constraints provided similar results, indicating that even without constraints this interaction is likely energetically preferred. However, as a large number of known ligands contain H-bond interactions, we feel they will be highly important in discriminating between the tens of thousands of compounds in our virtual screen, many of which may not be able to form this H-bond. As such, we have decided to include constraints for all docking.

Performing structure-based virtual screening on EthR

We performed 3 independent docking experiments. Each experiment attempted to dock a single library into a binding site using the Gold software suite. While the many of the same settings were applied across experiments, several were unique to a binding

site, such as H-bond constraints. Each compound was docked multiple times into a binding site to increase the likelihood of identifying the correct location and orientation in the binding pocket. The structure of the EthR protein was kept rigid for all 3 docking scenarios.

We first docked our small library into the EthR binding site 1 of the solved structure NTO6. Each of the 38,893 compounds from the small site library were independently docked into binding site 1, 10 times. H-bond constraints were applied for both Asparagine 179 and Asparagine 176.

We next docked our small library into the EthR binding site 2 of the solved structure MB1047. Each of the 38,893 compounds from the small site library were independently docked into binding site 2 10 times. An H-bond constraint was applied for Glutamine 125.

Lastly, we docked our combined library into the full EthR cavity of the solved structure NT06, which spans nearly the entire cavity including from deep within the pocket at biding site 1 to binding site 2 and beyond to the opening of the tunnel. Each of the 6,000 structures was independently docked into the cavity 3 times. We had reduced the number of docking iterations to 3 due to computational constraints. As the size of both the ligands and docking cavity was much larger for the combined site, a far longer time was required for each individual docking. All H-bond constraints applied in both sites 1 and 2 were implemented for combined site docking (Asparagine 179, Asparagine 176, Glutamine 125).

Selecting docked ligands for experimental validation

We analyzed Gold docking results using Goldmine, which is an integrated portion of the Gold software suite. The Goldmine package allows for visual inspection and thresholding of docking results based on H-bond constraints and fitness values. Fitness values and H-bond constratins were individually applied to each docking set, resulting in a reduction to 708 compounds for site 2, 619 compounds for site 1, and 69 compounds for the combined site. We then sorted the remaining compounds by H-bond score and visually inspected each docking, selecting the most promising leads. We ultimately decided on 14 compounds for purchase and experimental validation. 6 of the selected compounds originated from binding site 1, 3 from binding site 2, and 5 from the combined site.

Experimental validation of predicted ligands

All experimental validation was performed by Dr Sachin Surade. The 14 compounds were assayed for their inhibition of EhtR binding affinity to the promoter sequence of EthA. Surface Plasmon Resonance (SPR) assays were performed to determine the inhibition caused by each compound at a 50 micro molar concentration. SPR assay activity determined for the compounds ranged from 95% inhibition to 159% activation (Table 6.1). We believe activation values may be a product of interference with the assay itself.

Analysis of predicted ligand binding and experimentally validated activity

We next inspected each of the docking conformations and compared their validated inhibitory values to orientations within their associated binding pocket. It is important to note that predicted binding orientations may not be exactly as they are

when truly bound. Our screening approach only considered the rigid structure of a single enzyme. Since protein structures in cellular conditions are able to shift and flex and many amino acid side chains are able to rotate, the true binding conditions will likely allow for more ligand movement and a better orientation in the binding pocket.

Compound BAS118136, which was docked into site 1, had the highest validated inhibition of 95% (Figure 6.8 (Top)). From analysis of the predicted binding location it appears that two hydrogen bonds may be strengthening the interaction. It appears that the ligand may actually be shifted forward and rotated forming interactions with Glutamine 125 and Glutamine 180, however this is only a hypothesis would need to be determined with a crystal sctructure. The wide shape of the structure placed into binding site 1 should cause a large shift in DNA binding region of EthR, thus reducing the repression of EthA and increasing ETH effectiveness.

Compound T6977356, which is docked into site 2 had the second highest validated inhibiton of 92% (Figure 6.8 (Middle)). From analysis of the predicted binding location it appears that a hydrogen bond with Asparagine 179 is formed. The ligand shape is long and flat, which fits very well into the cavity and spans from the edge of binding site 1 to the cavity opening. This long addition in the cavity should cause a large shift to the backbone of EthR.

Compound T6779777, which is also docked into site 2 had the third highest validated inhibition of 86% (Figure 6.8 (Bottom)). This compound has a very similar orientation in the binding cavity to T6977356. There appears to be a hydrogen bond forming with Asparagine 179, however this molecule contains two additional H-bond accepting oxygen atoms that do not appear to be forming specific interactions. It is possible that the ligand has a slightly different orientation in its naturally bound state.

The SPR analysis determined that 4 additional compounds have inhibitory values that are between 25% and 75% (Figure 6.9). These moderate inhibitors range in shape and size. One was predicted to interact with binding site 1, one is predicted to interact at binding site 2, and two are predicted to interact across the whole combined cavity. All 4 molecules appear to form H-bonds with at least one amino acid. The two compounds from the combined docking set may form multiple H-bond interactions. 3 of the molecules have bi or tri-cyclic rings that are likely effective in expanding the cavity and thus effectively reducing the ability of EthR to bind to the DNA promoter region upstream of EthA.

Finally, 6 of the compounds had validated inhibitory values lower than 25% and were poor inhibitors of EthR (Figure 6.10). Poor inhibitory compounds originated from all three binding sets. Several compounds contained very large side groups including an adamantane group and a bicyclo[2.2.2]octante. Interestingly, several of the compounds validated as activators of EthR. While it is possible these compounds increased the binding affinity of EthR to DNA, it is probably more likely they have some off target effect on the assay itself.

Future directions in validation

Preliminary results presented here show great promise and we will continue validation of these compounds in several ways. Firstly, It will be important to determine IC50 values so that they can be compared to the current best in class inhibitors of EthR. Each of these compounds has been tested for activity at a 50 micro molar concentration. Since two of our compounds caused very high inhibition (>90%), it is possible that these compounds could be as effective as the best in class compounds. Secondly, it will be

important to test for inhibition across multiple assays. The responses of EthR to a compound may change in a different assay. Finally, it will be very important to determine the true binding orientations of the best compounds within the binding pocket. In order to achieve this we will need to co-crystallize compounds into EthR. As EthR has been co-crystallized with a number of other compounds, this should be an achievable goal. It will be very interesting to compare the predicted with the actual ligand orientations in EthR.

The high success rate in identifying highly inhibitory ligands is a testament to the utility that structure-based virtual screening can have on ligand identification. In a period of 6 weeks we assembled a large untested library of >550,000 compounds, applied ligand-based virtual screening to analyze structural features that are important for ligand binding to limit the library sizes for individual binding sites, and performed structurebased virtual screens for 3 independent binding sites on EthR. From our very small experimental validation we find an accuracy of 36% at identifying inhibitors (>50% inhibition), with 14% being very strong inhibitors (>90% inhibition). The ligand specificity of the EthR receptors is almost certainly vastly more selective than for insect odor receptors, as many insect odor receptors are activated or inhibited by an array of structural features and sizes. While the accuracy of this analysis was lower than what we have observed by applying ligand-based virtual screening in insect species (~72% in Drosophila and ~65% in Anopheles), we would expect a far higher success rate in odor receptors by application of a two stage (ligand-based and then structure-based) screen. As the first structures of insect odor receptors and additional mammalian odor receptors become available, application of structure-based virtual screening should be of high priority.

Figure 6.1: Schematics of Ethionamide Activation Pathway

The Ethionamide activation pathway. EthR represses the expression of EthA. EthA is responsible for activating Ethionamide causing the antibacterial effect. By inhibiting our target EthR, a larger amount of Ethionamide is converted into active form, thus increasing the effectiveness of the drug.

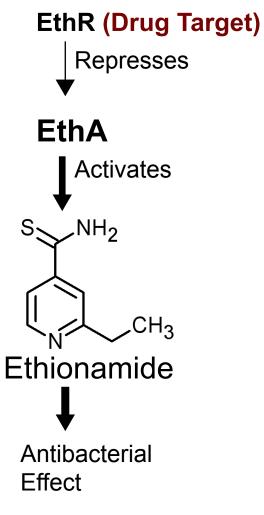




Figure 6.2: Solved EthR structures

(A) The first solved structure of EthR. Fortuitously, the receptor was co-crystallized with two dioxane molecules, allowing for identification of a cavity within the protein. This structure was previously determined, obtained from PDB, and visualized in PyMol (Dover et al., 2004). (B) The first identified structure of EthR bound to a naturally occurring ligand. EthR is bound to hexadecyl octanoate, which spans a very large cavity in EthR. This structure was previously determined, obtained from PDB, and visualized in PyMol (Frenois et al., 2004). (C) An overlay of several bound EthR ligands. Individually co-crystallized structures have been aligned by their largest alpha helix, producing a clear representation of the biding cavity. All structures were previously determined, obtained from PDB, and visualized by PyMol (Dover et al., 2004; Flipo et al., 2011; Frenois et al., 2004; Willand et al., 2010; Willand et al., 2009).

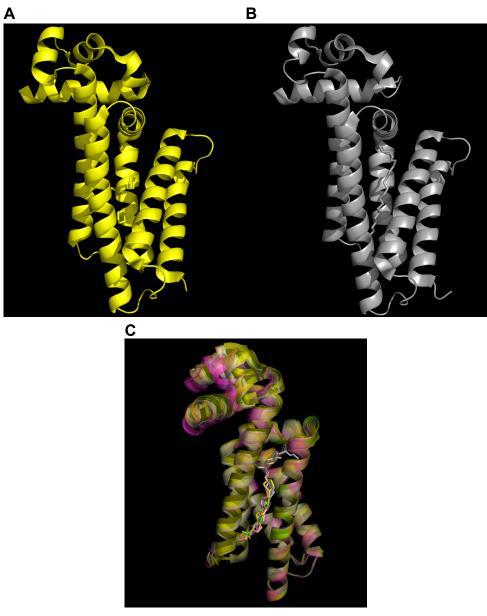


Figure 6.2

Figure 6.3: The shape of the EthR cavity

A structure of EthR (NT06), which was recently solved by members of the Blundell lab, was used along with PyMol to visualize a long and unbranged cylindrical cavity that traverses nearly the entire length of EthR .

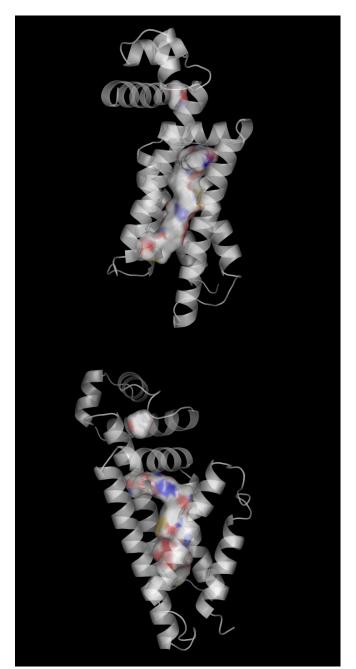


Figure 6.3

Figure 6.4: Previously identified EthR ligands bind within the proposed cavity

Previously determined ligands were oriented into the EthR binding cavity. Three distinct binding regions can be observed. Similar compounds bind into sites 1 and 2. Compounds that extend from the site 2 occupy a hypothetical site 3.

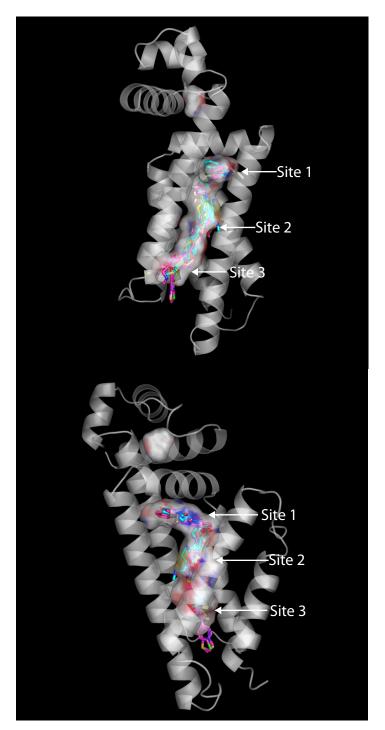


Figure 6.4

Figure 6.5: Visualizing previously identified EthR ligands

Three different views of previously identified EthR ligands residing within the cavity.

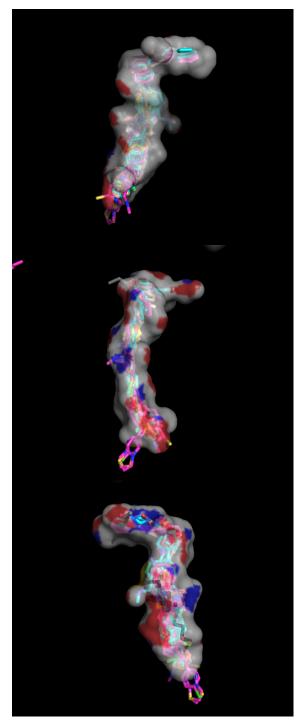


Figure 6.5

Figure 6.6: Single example of successful EthR self-docking

The EthR ligand (brown ligand) has been successfully self-docked back into the correct orientation (yellow ligand) in the EthR binding site 1.

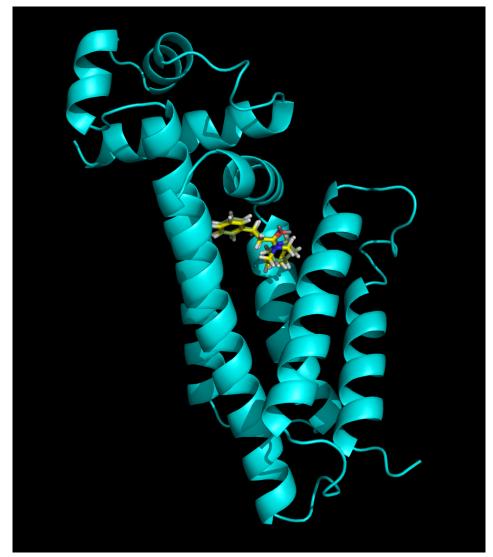




Figure 6.7: The results of many EthR site 1 self-docking runs

The Gold software suite is highly successful at self-docking ligands back into EthR site 1. Each overlayed ligand represents an individual self-docking into binding site 1. The

majority of ligands reside in the correct orientation.



Figure 6.7

Figure 6.8: The predicted orientation of our strongest identified inhibitors in EthR

The resulted docking of our top three strongest validated inhibitors bound into EthR. The percent inhibition represents the inhibition observed by SPR experimental analysis. An individual image is provided for each inhibitor.

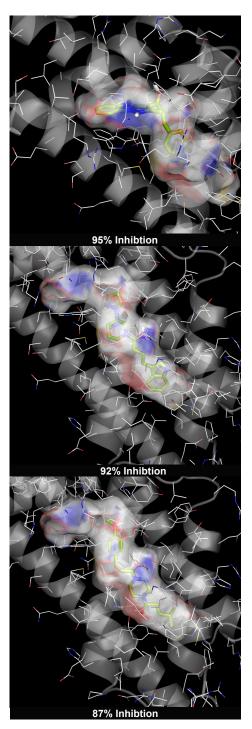


Figure 6.8

Figure 6.9: The predicted orientations of 4 modest inhibitors of EthR

The resulted dockings of our modest validated inhibitors bound into EthR. The percent inhibition represents the inhibition observed by SPR experimental analysis. An individual image is provided for each inhibitor.

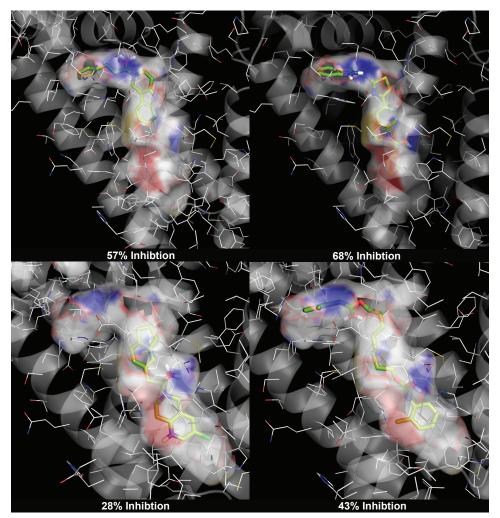


Figure 6.9

Figure 6.10: The predicted orientations of the poor inhibitors of EthR

The resulted dockings of our poor inhibitors bound into EthR. The percent inhibition or activation represents either the inhibition or activation observed by SPR experimental analysis. An individual image is provided for each compound.

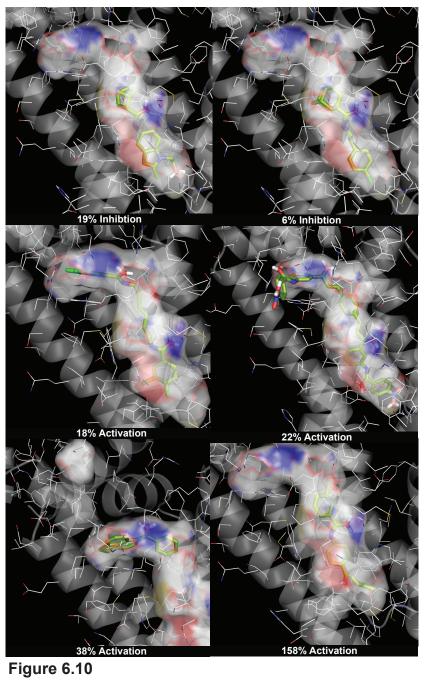


Table 6.1: A breakdown of our structure-based virtual screening accuracy for EthRThe accuracy of our virtual screening approach was validated by SPR. The number ofcompounds that were determined to inhibit EthR are listed by percent inhibition.

Inhibition Criteria	Number of Compounds
> 90% Inhibition	2/14
> 75% Inhibition	3/14
> 50% Inhibition	5/14
> 25% Inhibition	8/14
< 25% Inhibition	6/14

Table 6.1

CHAPTER VII:

Methods

Chemical informatics

Energy minimized 3-D structures were generated using Omega2 software (OpenEye)(Hawkins et al., 2010). Optimized descriptor subsets were iteratively identified from the large Dragon (Talete) and Cerius2 (Accelrys) molecular descriptor sets using a Sequential Forward Selection (SFS) method (Whitney, 1971). The SFS approach functioned by selecting descriptors that increased the correlation between the training set odor distances calculated by activity (spikes/sec) and the growing optimized descriptor set. A 5-fold cross-validation and a receiver-operating-characteristics (ROC) analysis was applied to analyse the performance of the receptor-optimized descriptor sets. Each receptor-optimized descriptor set was then used to rank the combined Natural Odor and Pubchem Libraries (>240,000 compounds) based on each odors distance to a known activator for the corresponding receptor.

Electrophysiology

Extracellular single-sensillum electrophysiology was performed as before (de Bruyne et al., 2001b; Dobritsa et al., 2003; Hallem and Carlson, 2006) with a few modifications. Diagnostic odorants were used to distinguish individual classes of ORNs in sensilla (ab1-ab7) and therefore unequivocally identify the target ORN for testing (de Bruyne et al., 2001b; Hallem et al., 2004). 50ml odor at 10^{-2} dilution in paraffin oil was applied to cotton wool in odor cartridge. Odor stimulus flow = 12ml/second. Due to variability in temporal kinetics of response across various odors, the counting window was shortened

to 250 milliseconds from the start of odor stimulus. A diagnostic panel of odorants were used to distinguish individual classes of sensilla (ab1-ab7) and therefore unequivocally identified the target ORN(de Bruyne et al., 2001a; Hallem et al., 2004).

Natural odor compound library

We assembled a subset of 3197 volatile compounds from annotated origins including plants(Knudsen et al., 2006), insects(El-Sayed, 2009), humans, and a fragrance collection(Sigma-Aldrich, 2007) that may have additional fruit and floral volatiles(Cork and Park, 1996; Curran et al., 2005; Gallagher et al., 2008; Knudsen et al., 2006; Logan et al., 2008; Meijerink et al., 2000; Zeng et al., 1991; Zeng et al., 1996).

Pubchem compound library

We assembled a subset of 241,150 odors from Pubchem, which have similar characteristics to known odor molecules. Compounds met a criteria of MW < 200 and only being composed of the following atoms (C, O, N, H, I, CI, S, F).

eMolecules compound library

We assembled a subset of >440,000 odors from eMolecules(eMolecules), which have similar characteristics to known odor molecules. Compounds met a criteria of MW < 350 and only being composed of the following atoms (C, O, N, H, I, CI, S, F).

Calculation of 3D conformations

The 3-Dimensional structures were predicted for compounds through use of the Omega2 software package(Bostrom et al., 2003; Hawkins et al., 2010). The Omega2 software

package functions in three major stages: assembly of an initial 3D structure from a library of fragments; exhaustive enumeration of all rotatable torsions using values drawn from a knowledge-based list of angles, creating a large number of conformations; and sampling of this set by geometric and energy criteria(Hawkins et al., 2010). The lowest energy 3D conformer for each compound in our Pubchem and Natural compound libraries were stored for use in molecular descriptor calculation.

Calculation of molecular descriptors

Commercially available software packages Cerius2 (200 individual descriptors) and Dragon (3224 individual descriptors) from Accelrys and Talete were used to calculate molecular descriptors from 3D molecular structures. Descriptor values were normalized across compounds to standard scores by subtracting the mean value for each descriptor type and dividing by the standard deviation. Molecular descriptors that did not show variation across compounds were removed. Maximum Common Substructures were determined using an existing algorithm(Cao et al., 2008b). Atom Pairs were computed from the version implemented in ChemmineR(Cao et al., 2008a).

Classification of active compounds

Since we were interested in identifying descriptors which best described active compounds, we needed to first determine which compounds to classify as "active" based on their electrophysiology activity for the receptor being studied. All of the training odors were clustered using hierarchical clustering by activity individually for each Or. The resulting tree can then be pruned such that the branch containing the majority of activating odors (>50 spikes/second) are selected. The activity threshold therefore was

set as the lowest spike/second activity of any odor present in the selected branch.

Calculation of Accumulative Percentage of Actives (APoA)

The accumulative percentage of actives is calculated for each descriptor set individually as previously described (Chen and Reynolds, 2002). Compounds are ranked according to their distance from each known active using the optimized descriptor values as distance, resulting in one set of ranked compound distances from each activating odor. Moving down the list for each of these rankings, ratios are calculated for the number of active compounds observed divided by the total number of compounds inspected, or the APoA. APoA values are averaged across all active compound rankings, creating a single set of mean values representing the APoA for a single Or and descriptor set. Using this approach, ApoA mean values are calculated for each of the 24 Ors separately for each descriptor set used, including optimized sets, all Dragon, all Cerius2, Atom Pair, and Maximum Common Substructure. The Area Under the Curve (AUC) scores were calculated by approximation of the integral under each plotted APoA line.

Determination of optimized descriptor subsets

A compound-by-compound activity distance matrix was calculated using training odor activity data for each of the Ors(Hallem and Carlson, 2006). A separate compound-bycompound descriptor distance matrix was calculated using the 3,424 descriptor values for training odors calculated by Dragon and Cerius2. Active compounds for each Or were identified individually through activity thresholds, as described above. The

correlation between the compound-by-compound activity and compound-by-compound descriptor distance matrices were compared for each actively classified compound, considering their distances to all other compounds. The goal was to identify descriptors that correlate most closely with activity. Using a Sequential Forward Selection (SFS) approach, which involves incrementally adding a single best choice item to growing list in an attempt to produced an optimal final set of items(Whitney, 1971), all descriptors are individually compared for their ability to increase this correlation. The descriptor that correlates best is retained and the process is iteratively used to search for additional descriptors. Each iteration aims to further increases in correlation values. In this manner, the size of the optimized descriptor set increases by one in each iteration, as the best descriptor. This process is halted when all possible descriptor additions in an iteration fails to improve the correlation value from the previous step. This whole process is run independently for each Or resulting in unique descriptor sets that are optimized for each Or.

Clustering Ors by most common descriptors

The first 20 descriptors selected by our optimized descriptor selection algorithm for each Or were used to create an identity matrix. Each row representing an Or and column a specific descriptor. Ors that share common descriptors contain 1s in the same column. This matrix was then converted into an Or-by-Or Euclidean distance matrix and clustered using hierarchical clustering and complete linkage.

Clustering compounds by activity of Or

The responses of each of the Ors that had previously been tested against a panel of compounds were converted into an Or-by-Or Euclidean distance matrix (Hallem and Carlson, 2006). Ors were clustered using hierarchical clustering and complete linkage. Specifically, this was achieved by creating a compound-by-compound distance matrix using the differences in activity between compounds tested on a singe Or. Hierarchical clustering using each Or distance matrix and then identifying the sub cluster which contained the most compounds.

Clustering Ors by predicted ligand space

Percentages of overlapping predictions within the top 500 predicted compounds were calculated pair-wise for all Ors. Euclidean distances were calculated from the similarity between Ors.

Calculation of Or prediction distribution frequencies

Initially, all extreme outliers were removed from the dataset for each Or. On average 5.82 compounds were removed for each Or, resulting in a mean dataset reduction of 0.0024%. Next, all compounds whose distance was greater than 3 standard deviations from the strongest activating compound were removed to reduce outliers. Distribution frequencies were produced for each Or. All compound distances were converted into a percentage of the most distant compound for each Or. Frequencies of compounds in the top 15% were plotted.

Or-ligand interaction map

The Or-ligand interaction map was developed using Cytoscape(Shannon et al., 2003).

Each predicted Or-ligand interaction from the top 500 predicted ligands for all of the Ors listed were used to calculate the map (Figure 5A). All predicted interactions are labelled in purple. In addition all interactions identified in this study and the previous study(Hallem and Carlson, 2006) were included and labeled in gray. All compounds are represented as small black circles and Ors are represented as large colored circles. Or names are provided on the upper right corner of each Or.

Computational validation of ligand-based virtual screening approach (non- SVMs)

We performed 5 independent 5-fold cross-validations. For each independent validation the dataset was divided into 5 equal sized partitions containing roughly 22 compounds each. During each run, one of the partitions is selected for testing, and the remaining 4 sets are used for training. The training process is repeated 5 times with each unique odorant set being used as the test set exactly once. For every training iteration, a unique set of descriptors was calculated from the training compound set. These descriptors were then used to calculate distances of the test set compounds to the closest active compound, exactly as we use to predict ligands in our ligand discovery pipeline. Once test set compounds have been ranked by distance from closest to furthest to a known active in the training set, a receiver operating characteristics (ROC) analysis is used to analyze the performance of our computational ligand prediction approach. Using ROC we were able to determine our predictive ability for the 12 receptors. We decided to perform this validation only on receptors for which sufficient training odors had previously been identified. We consider this to consist of at least one very strongly activating known odor (>150 spikes/sec) and at least five strongly activating odors (>100 spikes/sec), thus allowing for at least one activating odor for each of the 5 test sets in the

cross-validation (DmOr7a, DmOr9a, DmOr10a, DmOr22a, DmOr35a, DmOr43b, DmOr12, DmOr59b, DmOr67a, DmOr67c, DmOr85b, DmOr98a). Test set validations for all 12 Ors were combined and a single ROC curve representing an average across all Ors was plotted (Fig. 2A).

Calculation of LogP and vapor pressure values

SMILES structures of the predicted odors were used with EPI Suite (<u>http://www.epa.gov/oppt/exposure/pubs/episuite.htm</u>) to calculate predicted LogP and Vapor Pressure values.

Repellency behavior testing

Repellency was tested using *Drosophila melanogaster* 2-choice trap assay as described previously (Reeder et al., 2001; Syed et al., 2011).

Preference Index= number of flies in treated trap/(number of flies in treated + control traps).

The Drosophila T-maze assay was conducted as described previously (Turner et al.,

2011; Turner and Ray, 2009).

Preference index = (number of flies in test arm - number of flies in control arm)/(number of flies in test arm + number of flies in control arm).

Repellency was tested in mated and starved *Ae. aegypti* females using a handin-glove assay. Briefly, a gloved hand with an opening exposing skin odorants protected by 2 layers of netting was presented to mosquitoes for 5 min inside a cage and video taped for landing and avoidance responses. Mosquitoes were unable to bite due to the outer protective layer of netting and the inner layer of netting was treated with either test compound (10%) or solvent, such that mosquitoes were able to respond to volatiles but unable to make physical contact. The number of mosquitoes present for more than 5 seconds, and the numbers departing during the same period were counted from the videos at minutes 2,3,4, and 5 mins and repellency percentage and escape index calculated by comparing with similar numbers in solvent treated controls. *Percentage repellency* = 100 x [1 - (mean cumulative number of mosquitoes on the window of treatment for 5 seconds at time points 2,3,4,5 min/ mean cumulative number

of mosquitoes that remained on window of solvent treatment for 5 seconds at time points 2,3,4,5 min)].

Percentage present = average number of mosquitoes on window for 5 seconds at a given time-point across trials. All values were normalized to percentage of the highest value for the comparison, which was assigned a 100 percent present.

Mean Escape Index = (Average Number of mosquitoes in treatment that landed yet left the mesh during a five second window over the following time points: 2 minutes, 3 minutes, 4 minutes, 5 minutes) / (Average Number of mosquitoes that landed yet left the mesh during a five second window over the same time points in (treatment + control)). Each time point has N=5 trials, 40 mosquitoes per trial, Except for EA, where N=4.

The humidity and warmth attraction assay *A. aegypti* were placed in a cylindrical clear acrylic cage covered with insect screen mesh on one end. At 0.5 cm above the cage a moist filter paper and heated source was presented to cause attraction. In between the moist filter paper and the cage either DEET or acetone treated nets were placed far enough above the top of the cage so there could be no contact. For 5 second windows at 30 second intervals throughout the 5 minutes assay the number of

mosquitoes present at the top of the mesh cage were measured and an average was calculated for each condition.

Number of mosquitoes probing = Average number of mosquitoes present at top mesh for 5-sec or more, across the 10 time-point measurements/trial, for 3 trials.

Classification of repellent compounds

Training odors were clustered by their repellency values using Euclidean distance and hierarchical clustering. The resulting cluster containing the majority of strongest repellents was then selected and the repellency threshold for identification of descriptors determined as the lowest protection time within the cluster.

Support Vector Machine (SVM) predictions

The R Package e1071 interface with libsvm, a well established program, was used in the analysis(Chang and Lin, 2001; Karatzoglou et al., 2006). The Tune.SVM function was used to determine optimal gamma (0.01) and cost (100) values. The SVM was trained with the determined optimized descriptors for the training compound set using regression and a radial basis function kernel. The trained SVM then ranked both the eMolecules and natural odor libraries by repellency using their optimized descriptors.

Computational validation of ligand-based virtual screening (SVM)

We performed 20 independent 5-fold cross-validations by dividing the dataset into 5 equal sized partitions containing roughly 40 compounds each. During each run, one of the partitions is selected for testing, and the remaining 4 sets are used for training. The optimized descriptor values for the training set were used in training the SVM to

recognize repellent chemicals. The trained SVM is then used to predict repellent activity for the withheld test set. This process is repeated five times, each trial excluding a different subset of compounds as the training set and assigning the remainder as the test set. The whole process is repeated 20 times to improve consistency. A receiver operating characteristics (ROC) analysis is then used to analyze the performance of our computational repellency prediction approach.

Vinyl solubility assay

One 3 x 3 mm square of 4 gauge vinyl was submerged in 1mL of each test compound in a glass container and stirred at a constant rate on a shaker and checked every 30 minutes until the vinyl square in DEET was completely dissolved (6 Hrs). The vinyl pieces in each of the other compounds was removed, rinsed in ethanol and weighed. The process was repeated at 30 Hrs (24 Hrs after the vinyl square completely disappeared in DEET).

Olfactory avoidance assay trap assay for Drosophila

Trap Assay experiments were preformed as described previously(Reeder et al., 2001)[•] (Syed et al., 2011) with minor modifications. Briefly, traps were made with two 1.5 ml microcentrifuge tubes (USA Scientific) and 200 ul pipette tips (USA Scientific), each cap contained standard cornmeal medium. T-shape piece of filter paper (Whatman #1) was impregnated with 5 ul of acetone (control) or 5 ul of 10%, 1%, 0.10% test odor, diluted in acetone. Traps were placed within a petri dish (100 x 15mm, Fisher) containing 10ml of 1% agarose to provide moisture. Ten flies wCs 4-7days old were used per trial which lasted 48 hours by which time point nearly all flies in the assays had made a choice. For

the 24 hour time point data was considered only if 30% of flies had made a choice, at 48 hours the majority of flies had made choices.

Preference Index= number of flies in treated trap/(number of flies in treated + control traps).

T-maze Assay Methods

Carbon Dioxide and DEET trials were conducted as described previously (Turner and Ray, 2009). Sawyer Jungle Juice 100 Insect Repellent (DEET) was dissolved at 10% in dimethyl sulfoxide (DMSO) and impregnated in a filter paper disc and placed at the bottom of test tube. An equal volume of DMSO impregnated on filter paper disc was used in control arm.

Preference index = (number of flies in test arm - number of flies in control arm)/(number of flies in test arm + number of flies in control arm). For trials with DEET and carbon dioxide, tubes were set up with 10%DEET and DMSO in respective arms. Carbon dioxide was injected into DMSO control tube.

Modified hand-in-glove olfactory repellency assay for mosquitoes

Ae. aegypti mosquitoes (eggs obtained from Benzon Research Inc.) were maintained at ~27 °C and 70% RH on 14h: 10h L: D cycle. Behavioral tests were done with 40 mated, non-blood fed, ~24 hour starved, 4-10 day old females in 30 x 30 x 30 cm cages with a glass top to allow for video recording (Figure 1C, Figure S1). Each test compound solution (500µl) of 10% concentration in acetone solvent was applied evenly to a white rectangular 7 x 6 cm polyester netting (mesh size 26 x 22 holes per square inch) in a glass petri-dish and suspended in the air for 30 minutes to allow solvent evaporation.

The more volatile 2,3-dimethyl-5-isobutyl pyrizine was dissolved in paraffin oil. Acetone or paraffin oil (500µl) served as control. A nitrile glove (Sol-vex) was modified as described in Supplementary Figure 1 such that a 5.8 x 5cm window was present for skin odor exposure. A set of magnetic window frames were designed to secure the treated net ~1.5 mm above skin, and a second untreated netting ~4.5 mm above the treated net in a manner so that mosquitoes were attracted to skin emanations in the open window but unable to contact treated nets with tarsi, or contact and pierce skin. Additionally the test compound had minimal contact with skin. A clean set of glove and magnets were used for every trial. Care was taken that experimenter did not use cosmetics, soap etc on arms. For each trial the arm was first inserted for 5 min and the number landing or escaping test window recorded on video for 5 min period. Solvent controls were always tested prior to treatment. No cage was tested more than once within 1 hour of a testing session and not more than twice on any single day. Videos were analyzed offline on computers and numbers of mosquitoes present for a 5-sec continuous duration were counted every minute. Mosquitoes reliably started accumulating in controls at the 2 min point, and data from this time point was considered for analysis.

Percentage repellency = $100 \times [1 - (\text{mean cumulative number of mosquitoes on the window of treatment for 5 seconds at time points 2,3,4,5 min/ mean cumulative number of mosquitoes that remained on window of solvent treatment for 5 seconds at time points 2,3,4,5 min)].$

Percentage present = average number of mosquitoes on window for 5 seconds at a given time-point across trials. All values were normalized to percentage of the highest value for the comparison, which was assigned a 100 percent present.

Mean Escape Index = (Average Number of mosquitoes in treatment that landed yet left the mesh during a five second window over the following time points: 2 minutes, 3 minutes, 4 minutes, 5 minutes) / (Average Number of mosquitoes that landed yet left the mesh during a five second window over the same time points in (treatment + control)) Each time point has N=5 trials, 40 mosquitoes per trial, Except for EA, where N=4.

Humidity and warmth attraction assay

Experiments with female *Aedes aegypti* for DEET repellency were conducted at 27±1°C and 50-55% under fluorescent lighting from 1400-1700hrs. Each assay lasted 5 minutes. In the humidity-and-heat-attraction assay, 10 females (24hr starved mosquitoes) were held in cylindrical clear acrylic cages (7cm diameter x 5 cm high) covered with insect screen mesh on one end and sealed with clean manila paper on the open end. Mosquitoes were exposed to DEET-treated or acetone(solvent)-treated mesh placed 0.5cm above the screened end of the cage. A 55mm Whatman #1 filter paper disc moistened with 400µL of water was placed over the net to provide humidity. Heat was provided by placing a 148mL dram plastic vial (Thornton Plastics, Utah USA) containing 75mL of water at 37°C over the filter paper. Mosquito behavior around the treated net was recorded on HD video and the number of probing mosquitoes sitting on the top screen mesh for >5-sec were counted every 30-sec interval of the 5-min duration of the assay.

Number of mosquitoes probing = Average number of mosquitoes present at top mesh for 5-sec or more, across the 10 time-point measurements/trial, for 3 trials.

Larval behavior assays

Behavior assays were conducted as in (Kreher et al., 2008) with some modifications. Odorant solution and paraffin oil solvent were presented in small plastic containers fashioned out of inverted eppendorf tube caps. For pre-exposure experiments ~50 larvae per trial were placed on a 1% agarose base in a 90 mm disposable petri dish. 750 ml of odor solution was evenly spread on the lid and it was placed for indicated times (1 sec or 10 sec) on dish. Larvae were gently removed using a paint brush and placed on a separate petridish and assayed for odor preference in the dark for 1 min 30 sec as described above. The mutant *Orco-/-* (previously called *Or83b¹*) (Larsson et al., 2004) was obtained from Bloomington stock center, and the *Or42b-Gal4* flies were a kind gift from Dr. John Carlson.

Assembling of EthR screening library

Three large libraries were assembled consisting of the advanced library from Enamine (204,772 compound), the screening library from Maybridge (56,000 compounds) and the merged library from Asinex (439,946 compounds). All chemical from each library were combined and duplicates or any compound that contained an atom other than C, O, H, N, S, Br, and F were removed. The resulting library contained 588,723 unique structures.

Calculating molecular descriptors for EthR analysis

Molecular descriptors were calculated independently using both the Dragon software (Talete) suite and Pipeline pilot (Accelrys). The 3D conformations for each compound were calculated using the Omega application (OpenEye). Only a single best conformation was saved for each compound resulting in 588,723 unique 3D structures.

These structures were then fed into Dragon, which calculated 3,224 unique molecular descriptor values for each of the compounds. These same structures were also fed into pipeline pilot for descriptor calculation (Balaban, Chi, and Kappa values) and machine learning.

Applying machine learning with Pipeline Pilot

The Pipeline pilot suite was used to compare three different machine learning approaches (Random Forests, Support Vector Machines, and linear discriminate analysis) for their ability to identify what shape characteristics separate compounds that bind into EthR from those that do not. As we only knew compounds that have been effectively docked into the binding site and machine learning techniques require both a positive and negative training set, we had to estimate a set of compounds that would not. We randomly selected 100 compounds from the Asinex library, which as EthR is selective in it's binding, are unlikely to bind into EthR by chance. Each of the three machine learning methods was then individually trained to separate out inhibitors from our hypothetical non-inhibitors based on molecular descriptor values. Each method had a built in built in validation approach, such as cross fold validation or out of bag, that was applied along with a Receiver Operating Characteristic (ROC) analysis to compare between methods.

Performing structure-based virtual screening with Gold

The Gold suite was used for all protein-ligand docking and Goldmine was applied for analysis of docking results. An individual docking run was performed for each of the three binding sites. Other than for the following exceptions, default settings were applied

for the gold algorithm. Protein H-bond constraints were individually applied for each binding site with the following values: Asparagine 179 and Asparagine 176 for binding site 1, Glutamine 125 for binding site 2, and Asparagine 179, Asparagine 176, Glutamine 125 for the combined site. We performed 10 independent docking iterations for both binding site 1 and 2 and 3 independent iterations for the combined binding site. Early termination was allowed if 3 independent iterations failed to improve the rms_tolerance value by better than a value of 1.5. The binding cavity for each of the sites was set to a 10 angstrom radius from the natural ligands bound into site 1 or 2 of structures NT06 and MB1047, respectively. The binding cavity was set to be a 10 angstrom radius from either of the natural bound ligands in both sites 1 and 2 in structure NT06 for the combined site, which created a single site spanning nearly the entire cavity. None of the amino acid side chains were allowed to rotate in any of the docking sets. Both goldscore and chemscore scoring functions were calculated for each binding site.

REFERNCES:

Abuin, L., Bargeton, B., Ulbrich, M.H., Isacoff, E.Y., Kellenberger, S., and Benton, R. (2011). Functional architecture of olfactory ionotropic glutamate receptors. Neuron *69*, 44-60.

Aceves-Pina, E.O., and Quinn, W.G. (1979). Learning in normal and mutant Drosophila larvae. Science *206*, 93-96.

Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., *et al.* (2000). The genome sequence of Drosophila melanogaster. Science *287*, 2185-2195.

Altschul, S.F., Gish, W., Miller, W., Myers, E.W., and Lipman, D.J. (1990). Basic local alignment search tool. J Mol Biol *215*, 403-410.

Aramaki, H., Yagi, N., and Suzuki, M. (1995). Residues important for the function of a multihelical DNA binding domain in the new transcription factor family of Cam and Tet repressors. Protein Eng *8*, 1259-1266.

Araneda, R.C., Kini, A.D., and Firestein, S. (2000). The molecular receptive range of an odorant receptor. Nat Neurosci *3*, 1248-1255.

Ayyub, C., Paranjape, J., Rodrigues, V., and Siddiqi, O. (1990). Genetics of Olfactory Behavior in Drosophila-Melanogaster. J Neurogenet *6*, 243-262.

Baldwin, E., Plotto, A., Manthey, J., McCollum, G., Bai, J.H., Irey, M., Cameron, R., and Luzio, G. (2010). Effect of Liberibacter Infection (Huanglongbing Disease) of Citrus on Orange Fruit Physiology and Fruit/Fruit Juice Quality: Chemical and Physical Analyses. J Agr Food Chem *58*, 1247-1262.

Baulard, A.R., Betts, J.C., Engohang-Ndong, J., Quan, S., McAdam, R.A., Brennan, P.J., Locht, C., and Besra, G.S. (2000). Activation of the pro-drug ethionamide is regulated in mycobaeteria. Journal of Biological Chemistry *275*, 28326-28331.

Belluscio, L., Gold, G.H., Nemes, A., and Axel, R. (1998). Mice deficient in G(olf) are anosmic. Neuron *20*, 69-81.

Benton, R., Sachse, S., Michnick, S.W., and Vosshall, L.B. (2006). Atypical membrane topology and heteromeric function of Drosophila odorant receptors in vivo. PLoS Biol *4*, e20.

Benton, R., Vannice, K.S., Gomez-Diaz, C., and Vosshall, L.B. (2009). Variant Ionotropic Glutamate Receptors as Chemosensory Receptors in Drosophila. Cell *136*, 149-162.

Bohacek, R.S., McMartin, C., and Guida, W.C. (1996). The art and practice of structurebased drug design: A molecular modeling perspective. Med Res Rev *16*, 3-50. Bohbot, J., Pitts, R.J., Kwon, H.W., Rutzler, M., Robertson, H.M., and Zwiebel, L.J. (2007). Molecular characterization of the Aedes aegypti odorant receptor gene family. Insect Mol Biol *16*, 525-537.

Bolton, E.E., Wang, Y., Thiessen, P.A., and S.H., B. (2008). PubChem: Integrated Platform of Small Molecules and Biological Activities In Annual Reports in Computational Chemistry (Washington DC, American Chemical Society).

Bostrom, J., Greenwood, J.R., and Gottfries, J. (2003). Assessing the performance of OMEGA with respect to retrieving bioactive conformations. J Mol Graph Model *21*, 449-462.

Bove, J.M. (2006). Huanglongbing: A destructive, newly-emerging, century-old disease of citrus. J Plant Pathol *88*, 7-37.

Brockhoff, A., Behrens, M., Niv, M.Y., and Meyerhof, W. (2010). Structural requirements of bitter taste receptor activation. P Natl Acad Sci USA *107*, 11110-11115.

Buck, L., and Axel, R. (1991). A Novel Multigene Family May Encode Odorant Receptors - a Molecular-Basis for Odor Recognition. Cell *65*, 175-187.

Butler, D. (2011). Mosquitoes score in chemical war. Nature 475, 19.

Cao, Y., Charisi, A., Cheng, L.C., Jiang, T., and Girke, T. (2008a). ChemmineR: a compound mining framework for R. Bioinformatics *24*, 1733-1734.

Cao, Y., Jiang, T., and Girke, T. (2008b). A maximum common substructure-based algorithm for searching and predicting drug-like compounds. Bioinformatics *24*, i366-374.

Carde, R.T., and Gibson, G. (2010). Long Distance orientation of mosquitoes to host odours and their clues. in Ecology of Vector-Borne Diseases. Vol. 2. Olfaction in Vector-Host Interactions (Wageningen, The Netherlands, Wageningen Academic Publishers).

Carey, A.F., Wang, G.R., Su, C.Y., Zwiebel, L.J., and Carlson, J.R. (2010). Odorant reception in the malaria mosquito Anopheles gambiae. Nature *464*, 66-U77.

Carhart, R.E., Smith, D.H., and Venkataraghavan, R. (1985). Atom Pairs as Molecular-Features in Structure Activity Studies - Definition and Applications. J Chem Inf Comp Sci *25*, 64-73.

Chan, E.D., and Iseman, M.D. (2002). Current medical treatment for tuberculosis. Brit Med J *325*, 1282-1286.

Chang, C., and Lin, C. (2001). Libsvm: A Library for Support Vector Machines.

Chen, X., and Reynolds, C.H. (2002). Performance of similarity measures in 2D fragment-based similarity searching: comparison of structural descriptors and similarity coefficients. J Chem Inf Comput Sci *42*, 1407-1414.

Clyne, P.J., Warr, C.G., and Carlson, J.R. (2000). Candidate taste receptors in Drosophila. Science *287*, 1830-1834.

Clyne, P.J., Warr, C.G., Freeman, M.R., Lessing, D., Kim, J., and Carlson, J.R. (1999). A novel family of divergent seven-transmembrane proteins: candidate odorant receptors in Drosophila. Neuron *22*, 327-338.

Corbel, V., Stankiewicz, M., Pennetier, C., Fournier, D., Stojan, J., Girard, E., Dimitrov, M., Molgo, J., Hougard, J.M., and Lapied, B. (2009). Evidence for inhibition of cholinesterases in insect and mammalian nervous systems by the insect repellent deet. Bmc Biol *7*, -.

Cork, A., and Park, K.C. (1996). Identification of electrophysiologically-active compounds for the malaria mosquito, Anopheles gambiae, in human sweat extracts. Medical and Veterinary Entomology *10*, 269-276.

Cortes, C., and Vapnik, V. (1995). Support-Vector Networks. Mach Learn 20, 273-297.

Couto, A., Alenius, M., and Dickson, B.J. (2005). Molecular, anatomical, and functional organization of the Drosophila olfactory system. Curr Biol *15*, 1535-1547.

Curran, A.M., Rabin, S.I., Prada, P.A., and Furton, K.G. (2005). Comparison of the volatile organic compounds present in human odor using SPME-GC/MS. Journal of Chemical Ecology *31*, 1607-1619.

Dagraca, J.V. (1991). Citrus Greening Disease. Annu Rev Phytopathol 29, 109-136.

Dahanukar, A., Foster, K., van Naters, W.M.V.D.G., and Carlson, J.R. (2001). A Gr receptor is required for response to the sugar trehalose in taste neurons of Drosophila. Nat Neurosci *4*, 1182-1186.

Dahanukar, A., Hallem, E.A., and Carlson, J.R. (2005). Insect chemoreception. Curr Opin Neurobiol *15*, 423-430.

de Bruyne, M., and Baker, T.C. (2008). Odor detection in insects: volatile codes. J Chem Ecol *34*, 882-897.

de Bruyne, M., Clyne, P.J., and Carlson, J.R. (1999). Odor coding in a model olfactory organ: the Drosophila maxillary palp. J Neurosci *19*, 4520-4532.

de Bruyne, M., Foster, K., and Carlson, J. (2001). Odor coding in the Drosophila antenna. Neuron *30*, 537-552.

DeBarber, A.E., Mdluli, K., Bosman, M., Bekker, L.G., and Barry, C.E. (2000). Ethionamide activation and sensitivity in multidrug-resistant Mycobacterium tuberculosis. P Natl Acad Sci USA *97*, 9677-9682.

Ditzen, M., Pellegrino, M., and Vosshall, L.B. (2008). Insect odorant receptors are molecular targets of the insect repellent DEET. Science *319*, 1838-1842.

Dobritsa, A.A., van der Goes van Naters, W., Warr, C.G., Steinbrecht, R.A., and Carlson, J.R. (2003). Integrating the molecular and cellular basis of odor coding in the Drosophila antenna. Neuron *37*, 827-841.

Dobson, C.M. (2004). Chemical space and biology. Nature 432, 824-828.

Dover, L.G., Corsino, P.E., Daniels, I.R., Cocklin, S.L., Tatituri, V., Besra, G.S., and Futterer, K. (2004). Crystal structure of the TetR/CamR family repressor Mycobacterium tuberculosis EthR implicated in ethionamide resistance. Journal of Molecular Biology *340*, 1095-1105.

EFSA (2008). Consideration of Anthranilate derivatives evaluated by JECFA (65th meeting) Opinion of the scientific Panel on Food Additives, Flavourings, Processing Aids and Materials in Contact with Food. The EFSA Journal, 1-24.

El-Sayed, A. (2009). The Pherobase: Database of Insect Pheromones and Semiochemicals.

Engohang-Ndong, J., Baillat, D., Aumercier, M., Bellefontaine, F., Besra, G.S., Locht, C., and Baulard, A.R. (2004). EthR, a repressor of the TetR/CamR family implicated in ethionamide resistance in mycobacteria, octamerizes cooperatively on its operator. Mol Microbiol *51*, 175-188.

Fishilevich, E., and Vosshall, L.B. (2005). Genetic and functional subdivision of the Drosophila antennal lobe. Curr Biol *15*, 1548-1553.

Flipo, M., Desroses, M., Lecat-Guillet, N., Dirie, B., Carette, X., Leroux, F., Piveteau, C., Demirkaya, F., Lens, Z., Rucktooa, P., *et al.* (2011). Ethionamide Boosters: Synthesis, Biological Activity, and Structure-Activity Relationships of a Series of 1,2,4-Oxadiazole EthR Inhibitors. Journal of Medicinal Chemistry *54*, 2994-3010.

Flipo, M., Desroses, M., Lecat-Guillet, N., Villemagne, B., Blondiaux, N., Leroux, F., Piveteau, C., Mathys, V., Flament, M.P., Siepmann, J., *et al.* (2012). Ethionamide Boosters. 2. Combining Bioisosteric Replacement and Structure-Based Drug Design To Solve Pharmacokinetic Issues in a Series of Potent 1,2,4-Oxadiazole EthR Inhibitors. Journal of Medicinal Chemistry *55*, 68-83.

Floriano, W.B., Vaidehi, N., Goddard, W.A., Singer, M.S., and Shepherd, G.M. (2000). Molecular mechanisms underlying differential odor responses of a mouse olfactory receptor. P Natl Acad Sci USA *97*, 10712-10716.

Fox, A.N., Pitts, R.J., Robertson, H.M., Carlson, J.R., and Zwiebel, L.J. (2001). Candidate odorant receptors from the malaria vector mosquito Anopheles gambiae and evidence of down-regulation in response to blood feeding. P Natl Acad Sci USA *98*, 14693-14697. Frenois, F., Engohang-Ndong, J., Locht, C., Baulard, A.R., and Villeret, V. (2004). Structure of EthR in a ligand bound conformation reveals therapeutic perspectives against tuberculosis. Mol Cell *16*, 301-307.

Galizia, C.G., Munch, D., Strauch, M., Nissler, A., and Ma, S.W. (2010). Integrating Heterogeneous Odor Response Data into a Common Response Model: A DoOR to the Complete Olfactome. Chemical Senses *35*, 551-563.

Gallagher, M., Wysocki, J., Leyden, J.J., Spielman, A.I., Sun, X., and Preti, G. (2008). Analyses of volatile organic compounds from human skin. Brit J Dermatol *159*, 780-791.

Ghaninia, M., Ignell, R., and Hansson, B.S. (2007). Functional classification and central nervous projections of olfactory receptor neurons housed in antennal trichoid sensilla of female yellow fever mosquitoes, Aedes aegypti. Eur J Neurosci *26*, 1611-1623.

Ghose, A.K., Viswanadhan, V.N., and Wendoloski, J.J. (1999). A knowledge-based approach in designing combinatorial or medicinal chemistry libraries for drug discovery. 1. A qualitative and quantitative characterization of known drug databases. J Comb Chem *1*, 55-68.

Gillies, M.T. (1980). The Role of Carbon-Dioxide in Host-Finding by Mosquitos (Diptera, Culicidae) - a Review. B Entomol Res *70*, 525-532.

Goldman, A.L., van Naters, W.V., Lessing, D., Warr, C.G., and Carlson, J.R. (2005). Coexpression of two functional odor receptors in one neuron. Neuron *45*, 661-666.

Goto, S., Okuno, Y., Hattori, M., Nishioka, T., and Kanehisa, M. (2002). LIGAND: database of chemical compounds and reactions in biological pathways. Nucleic Acids Research *30*, 402-404.

Grant, A.J., and Oconnell, R.J. (1996). Electrophysiological responses from receptor neurons in mosquito maxillary palp sensilla. Ciba F Symp *200*, 233-253.

Grosse-Wilde, E., Kuebler, L.S., Bucks, S., Vogel, H., Wicher, D., and Hansson, B.S. (2011). Antennal transcriptome of Manduca sexta. P Natl Acad Sci USA *108*, 7449-7454.

Guo, S., and Kim, J. (2007). Molecular evolution of Drosophila odorant receptor genes. Mol Biol Evol *24*, 1198-1207.

Guo, S., and Kim, J. (2010). Dissecting the molecular mechanism of drosophila odorant receptors through activity modeling and comparative analysis. Proteins *78*, 381-399.

Gupta, R.K.a.B., A.K. (2007). Discovery and Design of New Arthropod/Insect Repellents by Computer-Aided Molecular Modeling. In Insect Repellents: principles, methods, and uses, M. Debboun, Frances, S.P., Strickman, D., ed. (Boca Raton, Taylor & Francis Group), pp. 195-228.

Haddad, R., Khan, R., Takahashi, Y.K., Mori, K., Harel, D., and Sobel, N. (2008). A metric for odorant comparison. Nat Methods *5*, 425-429.

Halbert, S.E., and Manjunath, K.L. (2004). Asian citrus psyllids (Sternorrhyncha : Psyllidae) and greening disease of citrus: A literature review and assessment of risk in Florida. Fla Entomol *87*, 330-353.

Hallem, E.A., and Carlson, J.R. (2006). Coding of odors by a receptor repertoire. Cell *125*, 143-160.

Hallem, E.A., Ho, M.G., and Carlson, J.R. (2004). The molecular basis of odor coding in the Drosophila antenna. Cell *117*, 965-979.

Hastie, T., Tibshirani, R., and Friedman, J.H. (2001). The elements of statistical learning : data mining, inference, and prediction : with 200 full-color illustrations (New York, Springer).

Hawkins, P.C.D., Skillman, A.G., Warren, G.L., Ellingson, B.A., and Stahl, M.T. (2010). Conformer Generation with OMEGA: Algorithm and Validation Using High Quality Structures from the Protein Databank and Cambridge Structural Database. Journal of Chemical Information and Modeling *50*, 572-584.

Hendrickson, J.B. (1991). Concepts and Applications of Molecular Similarity - Johnson, Ma, Maggiora, Gm. Science 252, 1189-1189.

Hill, S.R., Hansson, B.S., and Ignell, R. (2009). Characterization of antennal trichoid sensilla from female southern house mosquito, Culex quinquefasciatus Say. Chem Senses *34*, 231-252.

Ishimoto, H., Takahashi, K., Ueda, R., and Tanimura, T. (2005). G-protein gamma subunit 1 is required for sugar reception in Drosophila. Embo J *24*, 3259-3265.

JECF (2007). Safety evaluation of ertain food additives and contaminants. Sixty-fifth meeting of the joint FAO/WHO Expert Committee of Food Additives. WHO Food Additives Series: 56 IPCS, WHO Geneva.

Jefferis, G.S., Potter, C.J., Chan, A.M., Marin, E.C., Rohlfing, T., Maurer, C.R., Jr., and Luo, L. (2007). Comprehensive maps of Drosophila higher olfactory centers: spatially segregated fruit and pheromone representation. Cell *128*, 1187-1203.

Jones, W.D., Cayirlioglu, P., Kadow, I.G., and Vosshall, L.B. (2007). Two chemosensory receptors together mediate carbon dioxide detection in Drosophila. Nature *445*, 86-90.

Kain, P., Chakraborty, T.S., Sundaram, S., Siddiqi, O., Rodrigues, V., and Hasan, G. (2008). Reduced odor responses from antennal neurons of G(q)alpha, phospholipase C beta, and rdgA mutants in Drosophila support a role for a phospholipid intermediate in insect olfactory transduction. Journal of Neuroscience *28*, 4745-4755.

Kaluza, J.F., and Breer, H. (2000). Responsiveness of olfactory neurons to distinct aliphatic aldehydes. J Exp Biol *203*, 927-933.

Karatzoglou, A., Meyer, D., and Hornik, K. (2006). Support Vector Machines in R. J Stat Softw *15*.

Katada, S., Hirokawa, T., Oka, Y., Suwa, M., and Touhara, K. (2005). Structural basis for a broad but selective ligand spectrum of a mouse olfactory receptor: Mapping the odorant-binding site. Journal of Neuroscience *25*, 1806-1815.

Katritzky, A.R., Wang, Z., Slavov, S., Tsikolia, M., Dobchev, D., Akhmedov, N.G., Hall, C.D., Bernier, U.R., Clark, G.G., and Linthicum, K.J. (2008). Synthesis and bioassay of improved mosquito repellents predicted from chemical structure. Proc Natl Acad Sci U S A *105*, 7359-7364.

Keiser, M.J., Setola, V., Irwin, J.J., Laggner, C., Abbas, A.I., Hufeisen, S.J., Jensen, N.H., Kuijer, M.B., Matos, R.C., Tran, T.B., *et al.* (2009). Predicting new molecular targets for known drugs. Nature *462*, 175-U148.

Khafizov, K., Anselmi, C., Menini, A., and Carloni, P. (2007). Ligand specificity of odorant receptors. J Mol Model *13*, 401-409.

Kim, J., and Carlson, J.R. (2002). Gene discovery by e-genetics: Drosophila odor and taste receptors. J Cell Sci *115*, 1107-1112.

Kitchen, D.B., Decornez, H., Furr, J.R., and Bajorath, J. (2004). Docking and scoring in virtual screening for drug discovery: Methods and applications. Nat Rev Drug Discov *3*, 935-949.

Kline, D.L., Bernier, U.R., Posey, K.H., and Barnard, D.R. (2003). Olfactometric evaluation of spatial repellents for Aedes aegypti. Journal of Medical Entomology *40*, 463-467.

Klocke, J.A., Darlington, M.V., and Balandrin, M.F. (1987). Biologically-Active Constituents of North-American Plants .3. 1,8-Cineole (Eucalyptol), a Mosquito Feeding and Ovipositional Repellent from Volatile Oil of Hemizonia-Fitchii (Asteraceae). J Chem Ecol *13*, 2131-2141.

Klun, J.A., Strickman, D., Rowton, E., Williams, J., Kramer, M., Roberts, D., and Debboun, M. (2004). Comparative resistance of Anopheles albimanus and Aedes aegypti to N,N-diethyl-3-methylbenzamide (Deet) and 2-methylpiperidinyl-3-cyclohexen-1-carboxamide (Al3-37220) in laboratory human-volunteer repellent assays. J Med Entomol *41*, 418-422.

Knudsen, J.T., Eriksson, R., Gershenzon, J., and Stahl, B. (2006). Diversity and Distribution of Floral Scent. The Botanical Reveiw 72, 1-120.

Koon, A.C., Ashley, J., Barria, R., DasGupta, S., Brain, R., Waddell, S., Alkema, M.J., and Budnik, V. (2011). Autoregulatory and paracrine control of synaptic and behavioral plasticity by octopaminergic signaling. Nat Neurosci *14*, 190-U275.

Krajick, K. (2006). Medical entomology - Keeping the bugs at bay. Science 313, 36-38.

Kreher, S.A., Kwon, J.Y., and Carlson, J.R. (2005). The molecular basis of odor coding in the Drosophila larva. Neuron *46*, 445-456.

Kreher, S.A., Mathew, D., Kim, J., and Carlson, J.R. (2008). Translation of sensory input into behavioral output via an olfactory system. Neuron *59*, 110-124.

Kurland, M.D., Newcomer, M.B., Peterlin, Z., Ryan, K., Firestein, S., and Batista, V.S. (2010). Discrimination of Saturated Aldehydes by the Rat I7 Olfactory Receptor. Biochemistry *49*, 6302-6304.

Kwon, J.Y., Dahanukar, A., Weiss, L.A., and Carlson, J.R. (2007). The molecular basis of CO2 reception in Drosophila. P Natl Acad Sci USA *104*, 3574-3578.

Lai, P.C., Bahl, G., Gremigni, M., Matarazzo, V., Clot-Faybesse, O., Ronin, C., and Crasto, C.J. (2008). An olfactory receptor pseudogene whose function emerged in humans: a case study in the evolution of structure-function in GPCRs. J Struct Funct Genomics *9*, 29-40.

Larsson, M.C., Domingos, A.I., Jones, W.D., Chiappe, M.E., Amrein, H., and Vosshall, L.B. (2004). Or83b encodes a broadly expressed odorant receptor essential for Drosophila olfaction. Neuron *43*, 703-714.

Lee, Y., Kim, S.H., and Montell, C. (2010). Avoiding DEET through Insect Gustatory Receptors. Neuron *67*, 555-561.

Liu, C., Pitts, R.J., Bohbot, J.D., Jones, P.L., Wang, G., and Zwiebel, L.J. (2010). Distinct olfactory signaling mechanisms in the malaria vector mosquito Anopheles gambiae. PLoS Biol 8.

Logan, J.G., Birkett, M.A., Clark, S.J., Powers, S., Seal, N.J., Wadhams, L.J., Mordue, A.J., and Pickett, J.A. (2008). Identification of human-derived volatile chemicals that interfere with attraction of Aedes aegypti mosquitoes. Journal of Chemical Ecology *34*, 308-322.

Louis, M., Huber, T., Benton, R., Sakmar, T.P., and Vosshall, L.B. (2008). Bilateral olfactory sensory input enhances chemotaxis behavior. Nat Neurosci *11*, 187-199.

Lu, T., Qiu, Y.T., Wang, G., Kwon, J.Y., Rutzler, M., Kwon, H.W., Pitts, R.J., van Loon, J.J.A., Takken, W., Carlson, J.R., *et al.* (2007). Odor coding in the maxillary palp of the malaria vector mosquito Anopheles gambiae. Curr Biol *17*, 1533-1544.

Mahmoudi, A., and Iseman, M.D. (1993). Pitfalls in the Care of Patients with Tuberculosis - Common Errors and Their Association with the Acquisition of Drug-Resistance. Jama-J Am Med Assoc *270*, 65-68.

Maldonado, A.G., Doucet, J.P., Petitjean, M., and Fan, B.T. (2006). Molecular similarity and diversity in chemoinformatics: From theory to applications. Mol Divers *10*, 39-79.

Martin, Y.C., Kofron, J.L., and Traphagen, L.M. (2002). Do structurally similar molecules have similar biological activity? Journal of Medicinal Chemistry *45*, 4350-4358.

Meijerink, J., Braks, M.A.H., Brack, A.A., Adam, W., Dekker, T., Posthumus, M.A., Van Beek, T.A., and Van Loon, J.J.A. (2000). Identification of olfactory stimulants for Anopheles gambiae from human sweat samples. Journal of Chemical Ecology *26*, 1367-1382.

Montague, S.A., Mathew, D., and Carlson, J.R. (2011). Similar Odorants Elicit Different Behavioral and Physiological Responses, Some Supersustained. Journal of Neuroscience *31*, 7891-7899.

Monte, P., Woodard, C., Ayer, R., Lilly, M., Sun, H., and Carlson, J. (1989). Characterization of the Larval Olfactory Response in Drosophila and Its Genetic-Basis. Behav Genet *19*, 267-283.

Nikolova, N., and Jaworska, J. (2004). Approaches to measure chemical similarity - A review. Qsar Comb Sci 22, 1006-1026.

Olsen, S.R., Bhandawat, V., and Wilson, R.I. (2007). Excitatory interactions between olfactory processing channels in the Drosophila antennal lobe. Neuron *54*, 89-103.

Olsen, S.R., and Wilson, R.I. (2008). Lateral presynaptic inhibition mediates gain control in an olfactory circuit. Nature *452*, 956-U953.

Onagbola, E.O., Rouseff, R.L., Smoot, J.M., and Stelinski, L.L. (2011). Guava leaf volatiles and dimethyl disulphide inhibit response of Diaphorina citri Kuwayama to host plant volatiles. J Appl Entomol *135*, 404-414.

Pellegrino, M., Steinbach, N., Stensmyr, M.C., Hansson, B.S., and Vosshall, L.B. (2011). A natural polymorphism alters odour and DEET sensitivity in an insect odorant receptor. Nature.

Pelz, D., Roeske, T., Syed, Z., de Bruyne, M., and Galizia, C.G. (2006). The molecular receptive range of an olfactory receptor in vivo (Drosophila melanogaster Or22a). J Neurobiol *66*, 1544-1563.

Pitts, R.J., Rinker, D.C., Jones, P.L., Rokas, A., and Zwiebel, L.J. (2011). Transcriptome profiling of chemosensory appendages in the malaria vector Anopheles gambiae reveals tissue- and sex-specific signatures of odor coding. Bmc Genomics *12*.

Raviglione, M.C. (2003). The TB epidemic from 1992 to 2002. Tuberculosis 83, 4-14.

Reeder, N.L., Ganz, P.J., Carlson, J.R., and Saunders, C.W. (2001). Isolation of a DEET-insensitive mutant of Drosophila melanogaster (Diptera: Drosophilidae). J Econ Entomol *94*, 1584-1588.

Robertson, H.M., and Kent, L.B. (2009). Evolution of the gene lineage encoding the carbon dioxide receptor in insects. Journal of Insect Science *9*.

Robertson, H.M., Warr, C.G., and Carlson, J.R. (2003). Molecular evolution of the insect chemoreceptor gene superfamily in Drosophila melanogaster. Proc Natl Acad Sci U S A *100 Suppl 2*, 14537-14542.

Rodriguez-Gil, D.J., Treloar, H.B., Zhang, X.H., Miller, A.M., Two, A., Iwema, C., Firestein, S.J., and Greer, C.A. (2010). Chromosomal Location-Dependent Nonstochastic Onset of Odor Receptor Expression. Journal of Neuroscience *30*, 10067-10075.

Root, C.M., Ko, K.I., Jafari, A., and Wang, J.W. (2011). Presynaptic Facilitation by Neuropeptide Signaling Mediates Odor-Driven Food Search. Cell *145*, 133-144.

Root, C.M., Semmelhack, J.L., Wong, A.M., Flores, J., and Wang, J.W. (2007). Propagation of olfactory information in Drosophila. P Natl Acad Sci USA *104*, 11826-11831.

Ruta, V., Datta, S.R., Vasconcelos, M.L., Freeland, J., Looger, L.L., and Axel, R. (2010). A dimorphic pheromone circuit in Drosophila from sensory input to descending output. Nature *468*, 686-U106.

Saito, H., Chi, Q., Zhuang, H., Matsunami, H., and Mainland, J.D. (2009). Odor coding by a Mammalian receptor repertoire. Sci Signal *2*, ra9.

Saito, H., Kubota, M., Roberts, R.W., Chi, Q., and Matsunami, H. (2004). RTP family members induce functional expression of mammalian odorant receptors. Cell *119*, 679-691.

Sanger, F., and Coulson, A.R. (1975). A rapid method for determining sequences in DNA by primed synthesis with DNA polymerase. J Mol Biol *94*, 441-448.

Sato, K., Pellegrino, M., Nakagawa, T., Vosshall, L.B., and Touhara, K. (2008). Insect olfactory receptors are heteromeric ligand-gated ion channels. Nature *452*, 1002-1006.

Sato, K., Tanaka, K., and Touhara, K. (2011). Sugar-regulated cation channel formed by an insect gustatory receptor. P Natl Acad Sci USA *108*, 11680-11685.

Schmuker, M., de Bruyne, M., Hahnel, M., and Schneider, G. (2007). Predicting olfactory receptor neuron responses from odorant structure. Chem Cent J 1, -.

Schneider, G., Schneider, P., and Renner, S. (2006). Scaffold-hopping: How far can you jump? Qsar Comb Sci 25, 1162-1171.

Schwarz, D., Robertson, H.M., Feder, J.L., Varala, K., Hudson, M.E., Ragland, G.J., Hahn, D.A., and Berlocher, S.H. (2009). Sympatric ecological speciation meets pyrosequencing: sampling the transcriptome of the apple maggot Rhagoletis pomonella. Bmc Genomics *10*.

Semmelhack, J.L., and Wang, J.W. (2009). Select Drosophila glomeruli mediate innate olfactory attraction and aversion. Nature *459*, 218-U100.

Shang, Y.H., Claridge-Chang, A., Sjulson, L., Pypaert, M., and Miesenbock, G. (2007). Excitatory local circuits and their implications for olfactory processing in the fly antennal lobe. Cell *128*, 601-612.

Shannon, P., Markiel, A., Ozier, O., Baliga, N.S., Wang, J.T., Ramage, D., Amin, N., Schwikowski, B., and Ideker, T. (2003). Cytoscape: A software environment for integrated models of biomolecular interaction networks. Genome Res *13*, 2498-2504.

Sigma-Aldrich (2007). Flavors and fragarances 2007-2008 catalog. Sigma-Aldrich Fine Chemicals Company, Milquakee, WI.

Singer, M.S. (2000). Analysis of the molecular basis for octanal interactions in the expressed rat I7 olfactory receptor. Chemical Senses *25*, 155-165.

Singer, M.S., and Shepherd, G.M. (1994). Molecular modeling of ligand-receptor interactions in the OR5 olfactory receptor. Neuroreport *5*, 1297-1300.

Smadja, C., Shi, P., Butlin, R.K., and Robertson, H.M. (2009). Large Gene Family Expansions and Adaptive Evolution for Odorant and Gustatory Receptors in the Pea Aphid, Acyrthosiphon pisum. Mol Biol Evol *26*, 2073-2086.

Stanczyk, N.M., Brookfield, J.F., Ignell, R., Logan, J.G., and Field, L.M. (2010). Behavioral insensitivity to DEET in Aedes aegypti is a genetically determined trait residing in changes in sensillum function. P Natl Acad Sci USA *107*, 8575-8580.

Stensmyr, M.C., Giordano, E., Balloi, A., Angioy, A.M., and Hansson, B.S. (2003). Novel natural ligands for Drosophila olfactory receptor neurones. The Journal of experimental biology *206*, 715-724.

Syed, Z., and Leal, W.S. (2008). Mosquitoes smell and avoid the insect repellent DEET. P Natl Acad Sci USA *105*, 13598-13603.

Syed, Z., Pelletier, J., Flounders, E., Chitolina, R.F., and Leal, W.S. (2011). Generic insect repellent detector from the fruit fly Drosophila melanogaster. PLoS ONE *6*, e17705.

Takken, W. (1996). Synthesis and future challenges: The response of mosquitoes to host odours. Ciba F Symp *200*, 302-320.

Tan, P.-N., Steinbach, M., and Kumar, V. (2006). Introduction to data mining, 1st edn (Boston, Pearson Addison Wesley).

Tentschert, J., Bestmann, H.J., Holldobler, B., and Heinze, J. (2000). 2,3-dimethyl-5-(2methylpropyl)pyrazine, a trail pheromone component of Eutetramorium mocquerysi Emery (1899) (Hymenoptera: Formicidae). Naturwissenschaften *87*, 377-380.

Triballeau, N., Van Name, E., Laslier, G., Cai, D., Paillard, G., Sorensen, P.W., Hoffmann, R., Bertrand, H.O., Ngai, J., and Acher, F.C. (2008). High-Potency Olfactory Receptor Agonists Discovered by Virtual High-Throughput Screening: Molecular Probes for Receptor Structure and Olfactory Function. Neuron *60*, 767-774.

Turner, S.L., Li, N., Guda, T., Githure, J., Carde, R.T., and Ray, A. (2011). Ultraprolonged activation of CO2-sensing neurons disorients mosquitoes. Nature *474*, 87-91.

Turner, S.L., and Ray, A. (2009). Modification of CO2 avoidance behaviour in Drosophila by inhibitory odorants. Nature *461*, 277-281.

van der Goes van Naters, W., and Carlson, J.R. (2006). Insects as chemosensors of humans and crops. Nature 444, 302-307.

van Naters, W.V.G., and Carlson, J.R. (2007). Receptors and neurons for fly odors in Drosophila. Curr Biol *17*, 606-612.

Vannelli, T.A., Dykman, A., and de Montellano, P.R.O. (2002). The antituberculosis drug ethionamide is activated by a flavoprotein monooxygenase. Journal of Biological Chemistry *277*, 12824-12829.

Verdonk, M.L., Cole, J.C., Hartshorn, M.J., Murray, C.W., and Taylor, R.D. (2003). Improved protein-ligand docking using GOLD. Proteins-Structure Function and Genetics *52*, 609-623.

Vosshall, L.B., Amrein, H., Morozov, P.S., Rzhetsky, A., and Axel, R. (1999). A spatial map of olfactory receptor expression in the Drosophila antenna. Cell *96*, 725-736.

Vosshall, L.B., and Hansson, B.S. (2011). A unified nomenclature system for the insect olfactory coreceptor. Chemical senses *36*, 497-498.

Walker, J.D., Rodford, R., and Patlewicz, G. (2003). Quantitative structure-activity relationships for predicting percutaneous absorption rates. Environ Toxicol Chem *22*, 1870-1884.

Wang, J.W., Wong, A.M., Flores, J., Vosshall, L.B., and Axel, R. (2003). Two-photon calcium imaging reveals an odor-evoked map of activity in the fly brain. Cell *112*, 271-282.

Wang, P., Lyman, R.F., Shabalina, S.A., Mackay, T.F.C., and Anholt, R.R.H. (2007). Association of polymorphisms in odorant-binding protein genes with variation in olfactory response to benzaldehyde in Drosophila. Genetics *177*, 1655-1665.

Watson, J.D., and Crick, F.H. (1953). Molecular structure of nucleic acids; a structure for deoxyribose nucleic acid. Nature *171*, 737-738.

Weiss, L.A., Dahanukar, A., Kwon, J.Y., Banerjee, D., and Carlson, J.R. (2011). The molecular and cellular basis of bitter taste in Drosophila. Neuron *69*, 258-272.

Whitney, A.W. (1971). Direct Method of Nonparametric Measurement Selection. leee T Comput *C 20*, 1100-&.

Wicher, D., Schafer, R., Bauernfeind, R., Stensmyr, M.C., Heller, R., Heinemann, S.H., and Hansson, B.S. (2008). Drosophila odorant receptors are both ligand-gated and cyclic-nucleotide-activated cation channels. Nature *452*, 1007-1011.

Willand, N., Desroses, M., Toto, P., Dirie, B., Lens, Z., Villeret, V., Rucktooa, P., Locht, C., Baulard, A., and Deprez, B. (2010). Exploring Drug Target Flexibility Using in Situ Click Chemistry: Application to a Mycobacterial Transcriptional Regulator. Acs Chem Biol *5*, 1007-1013.

Willand, N., Dirie, B., Carette, X., Bifani, P., Singhal, A., Desroses, M., Leroux, F., Willery, E., Mathys, V., Deprez-Poulain, R., *et al.* (2009). Synthetic EthR inhibitors boost antituberculous activity of ethionamide. Nat Med *15*, 537-544.

Wilson, R.I., and Laurent, G. (2005). Role of GABAergic inhibition in shaping odorevoked spatiotemporal patterns in the Drosophila antennal lobe. Journal of Neuroscience *25*, 9069-9079.

Wilson, R.I., Turner, G.C., and Laurent, G. (2004). Transformation of olfactory representations in the Drosophila antennal lobe. Science *303*, 366-370.

Wishart, D.S., Knox, C., Guo, A.C., Cheng, D., Shrivastava, S., Tzur, D., Gautam, B., and Hassanali, M. (2008). DrugBank: a knowledgebase for drugs, drug actions and drug targets. Nucleic Acids Research *36*, D901-D906.

World Health Organization. (2011). World malaria report (Geneva, Switzerland, World Health Organization), pp. v.

Xia, Y., Wang, G., Buscariollo, D., Pitts, R.J., Wenger, H., and Zwiebel, L.J. (2008). The molecular and cellular basis of olfactory-driven behavior in Anopheles gambiae larvae. Proc Natl Acad Sci U S A *105*, 6433-6438.

Yao, C.A., and Carlson, J.R. (2010). Role of G-proteins in odor-sensing and CO2sensing neurons in Drosophila. J Neurosci *30*, 4562-4572.

Yao, C.A., Ignell, R., and Carlson, J.R. (2005). Chemosensory coding by neurons in the coeloconic sensilla of the Drosophila antenna. Journal of Neuroscience *25*, 8359-8367.

Zeng, X.N., Leyden, J.J., Lawley, H.J., Sawano, K., Nohara, I., and Preti, G. (1991). Analysis of Characteristic Odors from Human Male Axillae. Journal of Chemical Ecology *17*, 1469-1492. Zeng, X.N., Leyden, J.J., Spielman, A.I., and Preti, G. (1996). Analysis of characteristic human female axillary odors: Qualitative comparison to males. Journal of Chemical Ecology *22*, 237-257.

Zhan, S., Merlin, C., Boore, J.L., and Reppert, S.M. (2011). The Monarch Butterfly Genome Yields Insights into Long-Distance Migration. Cell *147*, 1171-1185.

Zhang, X., and Firestein, S. (2002). The olfactory receptor gene superfamily of the mouse. Nat Neurosci *5*, 124-133.

Zwiebel, L.J., and Takken, W. (2004). Olfactory regulation of mosquito-host interactions. Insect Biochem Molec *34*, 645-652.