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The dipeptidyl peptidase IV inhibitors vildagliptin and K-579 inhibit a phospholipase C: a case of promiscuous scaffolds in proteins

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## RESEARCH ARTICLE

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# The dipeptidyl peptidase IV inhibitors vildagliptin and K-579 inhibit a phospholipase C: a case of promiscuous scaffolds in proteins [v3; ref status: indexed, <http://f1000r.es/51m>]

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## Abstract

The long term side effects of any newly introduced drug is a subject of intense research, and often raging controversies. One such example is the dipeptidyl peptidase-IV (DPP4) inhibitor used for treating type 2 diabetes, which is inconclusively implicated in increased susceptibility to acute pancreatitis. Previously, based on a computational analysis of the spatial and electrostatic properties of active site residues, we have demonstrated that phosphoinositide-specific phospholipase C (PI-PLC) from *Bacillus cereus* is a prolyl peptidase using *in vivo* experiments. In the current work, we first report the inhibition of the native activity of PI-PLC by two DPP4 inhibitors - vildagliptin (LAF-237) and K-579. While vildagliptin inhibited PI-PLC at micromolar concentrations, K-579 was a potent inhibitor even at nanomolar concentrations. Subsequently, we queried a comprehensive, non-redundant set of 5000 human proteins (50% similarity cutoff) with known structures using serine protease (SPASE) motifs derived from trypsin and DPP4. A pancreatic lipase and a gastric lipase are among the proteins that are identified as proteins having promiscuous SPASE scaffolds that could interact with DPP4 inhibitors. The presence of such scaffolds in human lipases is expected since they share the same catalytic mechanism with PI-PLC. However our methodology also detects other proteins, often with a completely different enzymatic mechanism, that have significantly congruent domains with the SPASE motifs. The reported elevated levels of serum lipase, although contested, could be rationalized by

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report



report



report

1 **Rodney Rouse**, U.S. Food and Drug Administration USA

inhibition of lipases reported here. In an effort to further our understanding of the spatial and electrostatic basis of DPP4 inhibitors, we have also done a comprehensive analysis of all 76 known DPP4 structures liganded to inhibitors till date. Also, the methodology presented here can be easily adopted for other drugs, and provide the first line of filtering in the identification of pathways that might be inadvertently affected due to promiscuous scaffolds in proteins.

**2 Mark D Gorrell**, Centenary Institute  
Australia

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**REVISED Amendments from Version 2**

In the current version, we have changed the title, and cited previous research (ref 41 and 54) based on referee suggestions.

We have also included some minor corrections as suggested by a co-author.

**See referee reports**

## Introduction

Oral glucose elicits a greater insulin response than intravenous glucose infusion, a phenomenon known as the incretin effect<sup>1</sup>. This effect is mostly attributed to the intestinally derived hormones glucagon-like peptide-1 (GLP-1) and gastric inhibitory polypeptide (GIP)<sup>2</sup>. These hormones have a very short half-life as they are rapidly inactivated by the ubiquitous enzyme dipeptidyl peptidase-IV (DPP4)<sup>3</sup>. The finding that the incretin effect is impaired in subjects with type 2 diabetes<sup>4</sup> led to two major types of GLP-1 based therapies<sup>5</sup> - intravenously or sub-cutaneously administered GLP-1 mimetics that are resistant to DPP4 (exenatide, liraglutide, etc.)<sup>6</sup>, and the orally administered gliptins that prolong the physiological actions of incretin hormones by inhibiting DPP4 (sitagliptin, vildagliptin, etc.)<sup>7-9</sup>. Due to the multifarious roles played by the DPP4 enzyme<sup>10-12</sup>, the possible side effects of these drugs (acute pancreatitis, pancreatic cancer, etc.<sup>13-15</sup>) are strongly contested by researchers who argue that current statistics are insufficient<sup>16,17</sup> to conclusively attribute these side effects to the otherwise beneficial GLP-1 drugs<sup>18</sup>. Compound promiscuity is another phenomenon that might play a crucial role in determining the side effects of these therapies, although this aspect has rarely been pursued intensively<sup>19</sup>.

Previous work by our group has established the spatial and electrostatic congruence in cognate residue pairs of the active site in proteins with the same functionality (CLASP)<sup>20,21</sup>. CLASP analysis indicated that the phosphoinositide-specific phospholipase C (PI-PLC) from *Bacillus cereus* has spatial and electrostatic congruence with a serine protease motif<sup>22</sup>. This was validated by protease assays, mass spectrometry and by inhibition of the native phospholipase activity of PI-PLC by the well-known serine protease inhibitor AEBSF ( $IC_{50} = 0.018$  mM). The specificity of the protease activity was for a proline in the amino terminal, suggesting that PI-PLC is a prolyl peptidase, similar to the DPP4 enzyme. This finding led us to believe that the gliptins would have similar inhibitory effect on PI-PLC. In the current work, we have confirmed the inhibition of the native phospholipase activity of PI-PLC using two gliptins - vildagliptin<sup>23</sup> (at  $\mu$ -molar concentrations) and K579<sup>24</sup> (at nano-molar concentrations).

Subsequently, we used a motif derived from a DPP4 protein<sup>25</sup>, in addition to the trypsin motif used previously<sup>22</sup>, to query a comprehensive and non-redundant (50% sequence identity) list of ~5000 human proteins with known structures using CLASP, intending to identify other proteins that might be inhibited by the gliptins. From the set of proteins with significant congruent matches with these two motifs, we identified a pancreatic lipase<sup>26</sup> and a gastric lipase<sup>27</sup>,

keeping the context of lipases, acute pancreatitis and GLP-1 based therapies in mind. Our findings rationalize the elevated levels of serum lipase found in patients undergoing DPP4 inhibitor based therapies<sup>28,29</sup>, although these reports are in disagreement with other findings<sup>30,31</sup>. While it is logical and expected to find scaffolds that are congruent to trypsin and DPP4 active sites in lipases based on the current results and our previous findings<sup>22</sup>, we also show the presence of the serine catalytic triad in close proximity to the active site residues of proteins which have a completely different enzymatic mechanism (for example, in glutaminyl cyclase which is a transferase<sup>32</sup>). This corroborates the current belief that convergent evolution occurs more frequently than previously believed<sup>33</sup>. Thus, we propose a rational method to identify proteins that might have unintended and undesirable interactions with newly introduced compounds, and substantiate our claims by demonstrating the inhibition of the native phospholipase activity of PI-PLC from *B. cereus* using gliptins that are used in type 2 diabetes therapy.

## Results

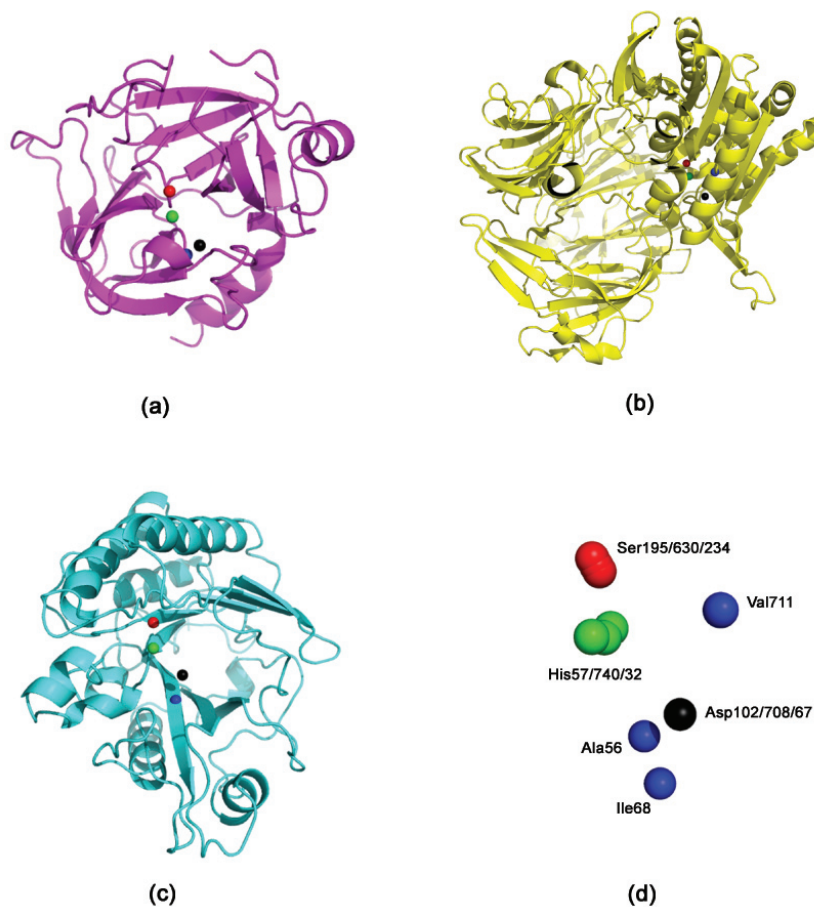
### The active site motifs

The active sites of serine proteases differ in their specificities owing to residues other than the conserved catalytic triad. Thus, in addition to the trypsin motif used previously (Asp102, Ser195 and His57 - PDBid 1A0J)<sup>22</sup> (Motif1), we choose another motif from a DPP4 enzyme (Asp708, Ser630 and His740 - PDBid:1N1M) (Motif2) (Table 1). Apart from the catalytic triad, we chose another non-polar residue in order to increase the specificity of the matches (Ala56 in Motif1 and Val711 in Motif2). This fourth residue is chosen as the closest residue to any one of the catalytic triad residues. Using the ability of CLASP to include stereochemically equivalent residues, this last residue could be matched by another non-polar residue - one of Gly, Ala, Val, Leu, Ile or Met. Further, it has been seen that the second (ac) and fifth (bd) (Table 1) pairwise electrostatic potential differences (EPD) are not discriminatory - thus, this pair is not used to score the EPD difference (although it is included in the distance deviation score).

**Inhibition of phosphoinositide-specific phospholipase C (PI-PLC) using dipeptidyl peptidase-IV (DPP4) inhibitors.** DPP4 (EC 3.4.14.5), a serine protease that is expressed in many tissues (kidney, liver, lung, intestinal membranes, lymphocytes and endothelial cells), cleaves peptides with Pro or Ala residues in the second amino terminal position. Previously, we have experimentally demonstrated the existence of the serine protease domain in PI-PLC from *Bacillus cereus* - both by virtue of its proteolytic activity, and the inhibition of its native activity on phospholipids in the presence of serine protease inhibitors<sup>22</sup>. Furthermore, the specificity of the proteolytic activity indicated that it was a prolyl peptidase - thus, leading us to believe that DPP4 inhibitors should have a similar inhibitory effect on the PI-PLC enzyme. Table 1 shows the presence of a congruent motif in the PI-PLC protein with both Motif1 and Motif2. His32 and Asp67 are known to be a part of the active site scaffold in PI-PLC<sup>22</sup>. These proteins have completely different folds, and thus a superimposition (using both MUSTANG<sup>34</sup> and DECAAF<sup>35</sup>) does not show any detectable similarity in their structures (Supplementary Figure 1). Figure 1 shows the active sites of these proteins, and the superimposition of these proteins

**Table 1. Potential and spatial congruence of the active site residues in proteins queried using two motifs - Motif1 from Trypsin and Motif2 from DPP4.** Rmsd1 and Rmsd2 are the root mean square deviation of the scaffold with respect to Motif1 and Motif2. DPP4 - dipeptidyl peptidase-IV, PI-PLC - phosphoinositide-specific phospholipase C, PLASE - human pancreatic lipase-Related Protein 2, GPASE - human gastric lipase, QC - glutaminyl cyclase. D = Pairwise distance in Å. PD = Pairwise potential difference. APBS writes out the electrostatic potential in dimensionless units of  $kT/e$  where  $k$  is Boltzmann's constant,  $T$  is the temperature in K and  $e$  is the charge of an electron.

PDB	Active site atoms (a,b,c,d)		ab	ac	ad	bc	bd	cd	Rmsd1	Rmsd2
TRYPSIN (1A0J)	D102,S195 H57,A56	D	7.8	5.6	2.9	3.3	9.0	6.9	0	0.5
		PD	-144.1	-39.2	-248.3	104.8	-104.3	-209.1		
DPP4 (1N1M)	D708,S630 H740,V711	D	7.6	5.4	2.6	2.6	6.8	5.4	0.5	0
		PD	-154.4	124.4	-148.8	278.8	5.6	-273.2		
PI-PLC (1PTD)	D67,S234 H32,I68	D	8.2	6.2	4.1	3.8	11.5	9.2	0.6	1.1
		PD	-93.7	39.7	-245.2	133.4	-151.5	-284.8		
PLASE (2OXE)	D195,S171 H282,G235	D	7.7	6.4	4.4	3.0	6.7	5.8	0.5	0.4
		PD	-150.2	26.7	-132.1	176.9	18.2	-158.8		
GPASE (1HLG) Motif1	D324,S153, H353,L326	D	7.5	5.0	2.9	2.7	8.4	6.2	0.2	0.3
		PD	-202.6	-15.0	-272.3	187.6	-69.7	-257.3		
GPASE (1HLG) Motif2	D324,S153 H353,A327	D	7.5	5.0	2.6	2.7	7.1	5.3	0.4	0.1
		PD	-202.6	-15.0	-207.1	187.6	-4.5	-192.1		
QC (3PB4)	D170,S187, H168,G224	D	7.5	4.8	3.4	3.3	10.7	8.0	0.4	0.8
		PD	-92.8	-16.5	-214.0	76.3	-121.2	-197.5		



**Figure 1. The active site residues in Trypsin, DPP4 and PI-PLC.** (a) Trypsin (PDBid:1A0J) (b) DPP4 (PDBid:1N1M); (c) PI-PLC (PDBid:1PTD) (d) Superimposing the active site residues using DE-CAAF<sup>35</sup>. The superimposition can be viewed in Superimposeproteins.p1m in [Dataset 1](#).

based on their catalytic residues<sup>35</sup>. It can be seen that the closest non-polar residue to the catalytic triad in trypsin and PI-PLC (Ala56 in PDBid:1A0J, Ile68 in PDBid:1PTD) is differently placed from Val711 in DPP4 (PDBid:1N1M). This is also indicated by the greater RMSD (root mean square deviation) of the scaffold in PI-PLC to Motif2 as compared to Motif1. The differences in the position of peripheral residues is the source of the diverse specificities exhibited by these proteases. **Figure 2** shows the inhibition of PI-PLC using two gliptins - vildagliptin (LAF-237)<sup>23</sup> and K579<sup>24</sup>. PI-PLC catalyzes hydrolysis of phospholipids to yield diacylglycerol and a phosphoryl alcohol. In the absence of inhibitors enzyme addition to the vesicle suspension causes an increase in turbidity due to vesicle aggregation (**Figure 2 a,c**). Aggregation in turn occurs as a result of formation of the enzyme endproduct diacylglycerol<sup>36,37</sup>. A steady-state is reached under our conditions after 6–8 min. Addition of either LAF-237 (vildagliptin) or K579 leads to an obvious inhibition of the enzyme activity.

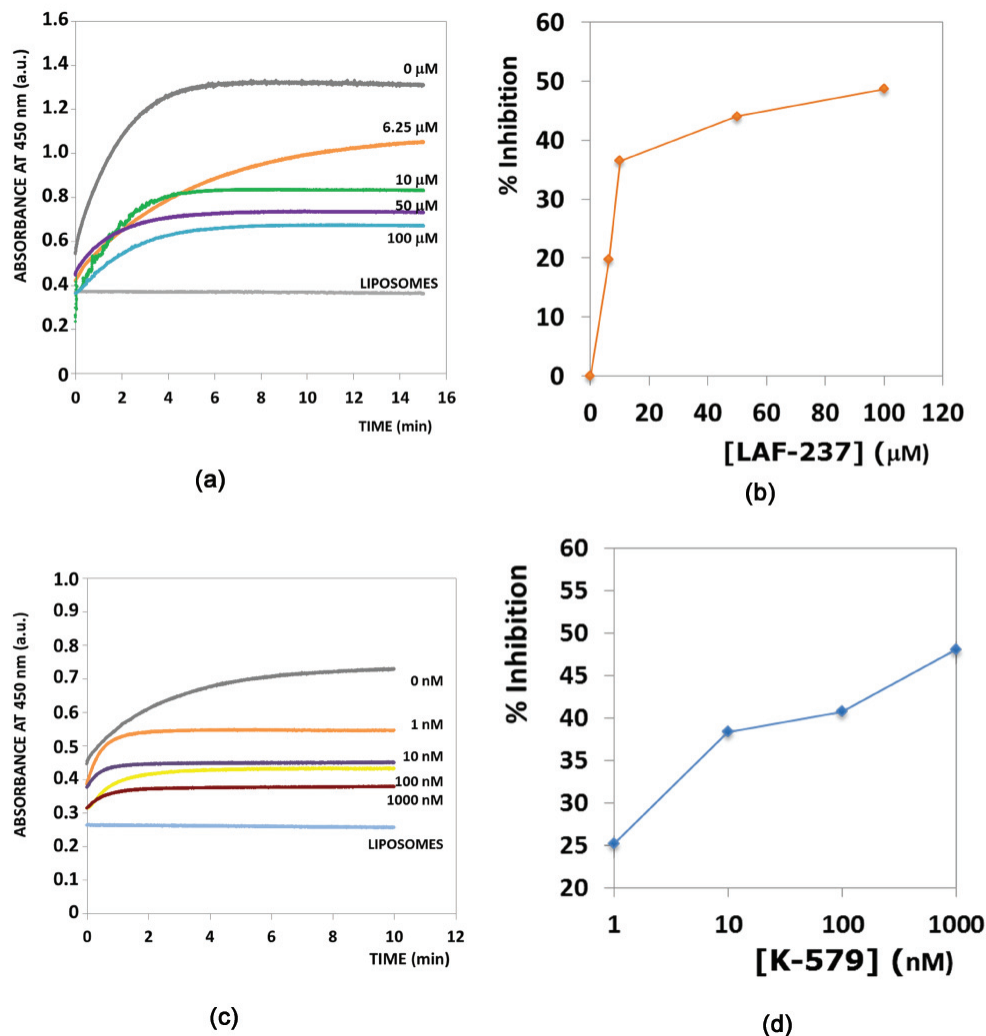
Dose-response curves for the inhibitors are shown in **Figure 2 (b,d)**. K579 is two orders of magnitude more potent than LAF-237 as a PI-PLC inhibitor, with half-maximal inhibitory concentrations  $IC_{50}$  respectively of 1  $\mu$ M and 100  $\mu$ M.

**Phosphoinositide-specific phospholipase C inhibition data using the dipeptidyl peptidase-IV inhibitors K-579 and LAF-237**

12 Data Files

<http://dx.doi.org/10.6084/m9.figshare.880620>

**Querying a non-redundant set of human proteins using Motif1 and Motif2.** Currently, the PDB database has about 25,000 human proteins. Using a identity cutoff of 50%, we chose a set of ~5000 proteins (**Supplementary Table 1**) as the target proteins.



**Figure 2.** PI-PLC inhibition using DPP4 inhibitors. **(a,c)** Time courses of enzyme activity in the presence of varying amounts of inhibitors, respectively LAF-237 and K579. The trace marked LIPOSOMES corresponds to a control in the absence of PI-PLC. **(b,d)** Dose-response effect of inhibitors on PI-PLC activity. Activity was computed as the extent of vesicle aggregation after 10 min enzyme activity.

**Table 2** shows ten proteins which have significant matches with Motif1 and Motif2. Given the context of lipases, acute pancreatitis and GLP-1 based therapies, we picked two proteins - the human pancreatic lipase-related protein 2 (PDBid:2OXE)<sup>26</sup> and a human gastric lipase (PDBid:1HLG)<sup>27</sup> - to demonstrate the distinct possibility that these proteins might be inhibited by DPP4 inhibitors. **Table 1** shows the congruence of the DPP4 motif to these proteins using Motif1 and Motif2. It is interesting to note that the gastric lipase (PDBid:1HLG) has a good match with both motifs - Leu326 in PDBid:1HLG is congruent to Ala56 in PDBid:1A0J, and Ala237 (PDBid:1HLG) is congruent to Val711 (PDBid:1N1M).

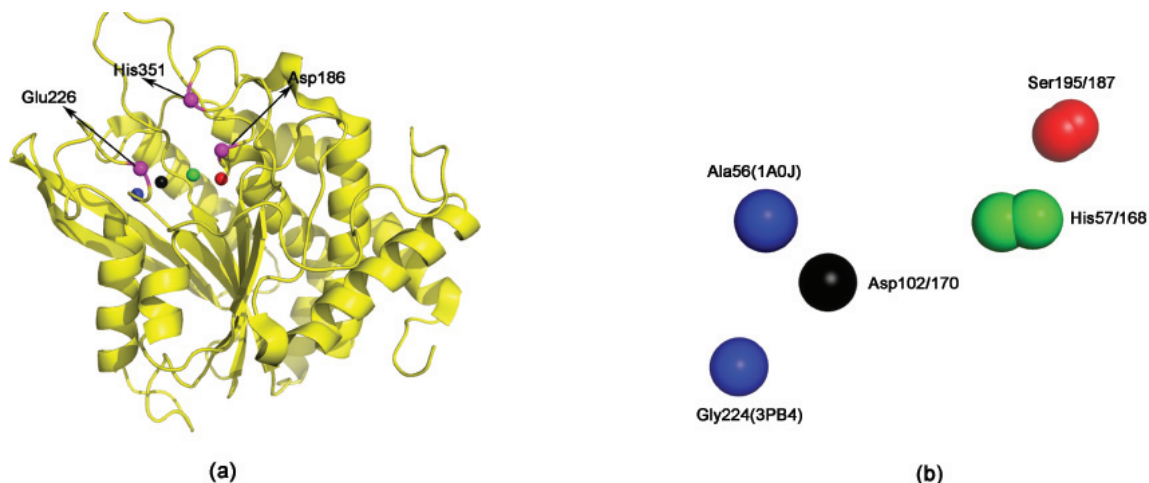
Since both these proteins are lipases (hydrolases), this congruence to Motif1 and Motif2 is expected based on our previous results with PI-PLC<sup>22</sup>. However, our methodology also detects other proteins, often with a completely different enzymatic mechanism from hydrolases. A glutaminyl cyclase (PDBid:3PB4)<sup>32</sup>, a transferase, has a significantly congruent domain with Motif1 (lesser congruence with Motif2, as indicated by the RMSD) (**Table 1**). **Figure 3** shows the proximity of the promiscuous scaffold to the active site of the cyclase, and also the congruence of the scaffold to Motif1.

**Docking vildagliptin to the PIPLC structure.** Since there are no DPP4 structures solved which ligand K-579, a DPP4 protein structure in complex with vildagliptin (PDBid:3W2TA)<sup>38</sup> was used to dock vildagliptin to the PIPLC structure complexed with myo-inositol (PDBid:1PTG)<sup>39</sup> using DOCLASP<sup>40</sup> (**Figure 4**). The Pymol script for visualizing the docking (SupplementaryPymol.p1m) is provided as **Supplementary information**.

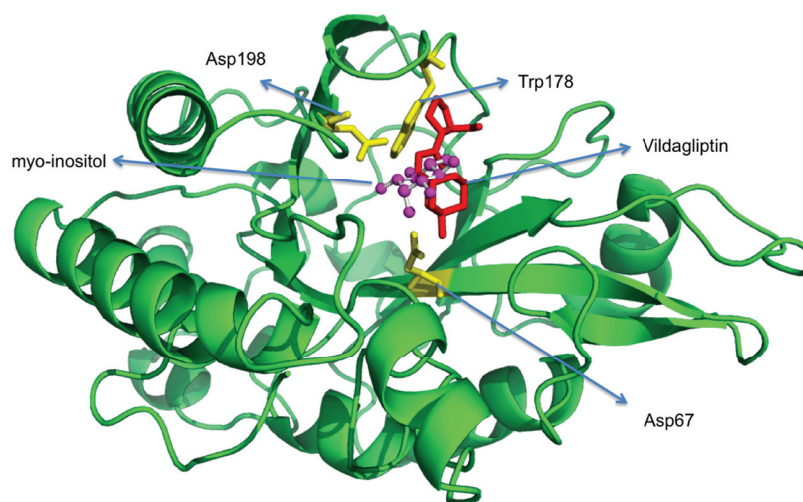
**Statistics of atoms making contact with inhibitors.** There are 76 unique DPP4 inhibitors, defined by three letter codes, for which the

**Table 2. Best matches in the set of ~5000 human proteins.** (a) Motif1 (Asp102, Ser195, His57, Ala56) from Trypsin (b) Motif2 (Asp708, Ser630, His740, Val711) from DPP4.

Motif	PDB	Description	CLASP Score
1	2ANY	Plasma kallikrein, light chain	0.028
1	2OQ5	Transmembrane protease, serine 11E	0.037
1	3U0V	Lysophospholipase-like protein 1	0.041
1	2ODP	Complement C2	0.060
1	1IMJ	CCG1-interacting factor B	0.065
1	3F6U	Vitamin K-dependent protein C heavy chain	0.065
1	1ELV	Complement C1S component	0.068
1	1MD8	C1R complement serine protease	0.068
1	1ORF	Granzyme A	0.070
1	1FJ2	Acyl protein thioesterase 1	0.071
2	1HLG	Gastric lipase	0.042
2	1SPJ	Kallikrein 1	0.114
2	2F83	Coagulation factor XI	0.120
2	1ZJK	Mannan-binding lectin serine protease 2	0.131
2	3QLP	Thrombin light chain	0.145
2	2QXI	Kallikrein-7	0.146
2	2XU7	Histone-binding protein RBBP4	0.174
2	2W2N	Proprotein convertase subtilisin/kexin type 9	0.180
2	2HEH	KIF2C protein	0.195
2	2ANY	Plasma kallikrein, light chain	0.197



**Figure 3. A scaffold congruent to the active site of Trypsin (PDBid:1A0J) in a glutaminyl cyclase (PDBid:3PB4).** (a) The active site residues are marked in magenta. They are seen to be proximal to the identified scaffold. (b) Superimposition of Motif1 and the scaffold in glutaminyl cyclase. The exact pairwise interatomic distance and electrostatic potential differences are specified in **Table 1**.



**Figure 4. Docking vildagliptin to the PI-PLC structure in complex with myo-inositol (PDBid:1PTGA).** Docking done using DOCLASP<sup>40</sup>. The Pymol script for visualizing the docking (SupplementaryPymol.p1m) is provided as [Supplementary information](#).

ligand-DPP4 structure is solved ([Supplementary Table 2](#)). For uniformity, we chose the first four closest atoms from the protein that make contacts to the ligand, excluding hydrophobic interactions. [Table 3](#) shows the number of times each residue in DPP4 makes contact to the ligand. Three residues are ubiquitous in making contacts in all these ligands: Glu205, Glu206 and Tyr662 made contacts in 71, 68 and 63 ligands, respectively. Interestingly, Glu205 and Glu206 have been implicated as critical residues for the enzymatic activity of DPP4 through point mutations<sup>41</sup>. Note, that since only the first four residues were considered, these counts are conservative (and might be more). A recent study has found that inhibitors that bind to residues beyond the extensive subsite (defined as Val207, Ser209, Phe357 and Arg358) increases DPP4 inhibition, as compared to those inhibitors that form a covalent bond with Ser630<sup>38</sup>. [Table 3](#) shows that very few inhibitors make such contacts. We created a library of motifs from these structures that can be used to query any protein using CLASP to determine the possibility that DPP4 inhibitors might bind to it ([Supplementary Table 3](#)), after removing equivalent ones to eliminate redundancy. This table shows the final list of 39 motifs (pruned from the initial 76): this is a comprehensive set of motifs that encapsulates the current knowledge about protein ligand interactions for the DPP4 enzyme. A facet of ligand binding that needs to be accounted for while choosing a motif is the spatial and electrostatic changes that can be induced by ligand binding. Thus, we obtain the residues involved in binding from the holo enzyme, but extract the motif values (pairwise distance and EPD) from the apo enzyme.

## Discussion

The controversy regarding the side effects of the dpp4 inhibitors, particularly with respect to acute pancreatitis and pancreatic cancer, continues unabated. While some researchers feel that it is not acceptable to assume that 'absence of evidence is evidence of absence'<sup>42,43</sup>, others believe that current data are not conclusive and the 'benefits by far outweigh the potential risks'<sup>16</sup>. Adding to the uncertainties are conflicting reports presented by different

groups<sup>28-31</sup>. Notwithstanding the antagonistic views on the subject, it is unanimously accepted that current data are insufficient to establish a causal pathogenic effect of these drugs on such side effects<sup>44</sup>.

**Table 3. Number of times residues from the DPP4 enzyme ligand an inhibitor.** Three residues - Glu205, Glu206 and Tyr662 - make contacts in 71, 68 and 63 ligands, respectively. Note, that since we only choose the first four residues based on proximity of the atoms closest to the ligand, these counts are conservative (and might be actually more).

Residue	Number of ligands
ARG125	11
GLU205	71
GLU206	68
VAL207	1
SER209	3
ARG358	6
TYR547	18
GLN553	1
TYR585	1
TRP629	1
SER630	10
TYR631	12
TYR662	63
ASN710	15



Various database studies have been undertaken in order to ascertain the effects of the GLP-1 therapies. Some studies 'did not find an association between the use of exenatide or sitagliptin and acute pancreatitis' with the caveat that the 'limitations of this observational claims-based analysis cannot exclude the possibility of an increased risk'<sup>45</sup>. On the other hand, other studies have shown that the use of 'sitagliptin or exenatide increased the odds ratio for reported pancreatitis 6-fold as compared with other therapies'<sup>14</sup>. Further, they reported that 'pancreatic cancer was more commonly reported among patients who took sitagliptin or exenatide as compared with other therapies'<sup>14</sup>. Although these studies concern the usage of both GLP-1 mimetics and the orally administered gliptins, and our study exclusively focusses on gliptins, and is not concerned with the GLP-1 mimetics data. The close relationship between chronic pancreatitis and pancreatic cancer is also a subject of intense research<sup>46</sup>. Another administrative database study of US adults with type 2 diabetes reported increased odds of hospitalization for acute pancreatitis for patients undergoing GLP-1 based therapies sitagliptin<sup>13</sup>. Once again, such correlation of GLP-1 based therapies to acute pancreatitis is contested by other studies<sup>47</sup>.

Our findings rationalize the elevated levels of serum lipase found in patients undergoing DPP4 inhibitor based therapies<sup>28,29</sup>, keeping in mind that other studies contradict these reports<sup>30,31</sup>. While several studies have reported that the GLP-1 mimetics do not induce pancreatitis in rats, mouse and/or monkey<sup>48-50</sup>, these studies did not include DPP4 inhibitors, which are the compounds that might be responsible for interactions with pancreatic proteins according to our study. It is to be noted however that these mimetics may have other physiological effects and 'the long-term consequences of sustained GLP-1 receptor activation in the human thyroid remain unknown and merit further investigation'<sup>51</sup>. Once again, the previous study<sup>51</sup> has been challenged by another group who note that 'findings previously reported in rodents may not apply to humans'<sup>52</sup>.

The orally administered gliptins differ in many aspects such as potency, excretion mechanism, target selectivity, half-life, metabolism and possible drug-drug interactions<sup>9,53,54</sup>. This difference is also highlighted in the different concentrations of vildagliptin and K579 that inhibit PI-PLC. A recent study has also noted the differential off-target inhibition of enzymes by vildagliptin and sitagliptin using a high-throughput, multiplexed assay<sup>55</sup>. Interestingly, the PI-PLC scaffold has a better match with the trypsin motif than with the DPP4 motif (Table 1). In order to be able to model these differences in our *in silico* search, it is important to be able to provide flexibility in the scoring mechanism.

To summarize, it has been noted in the case of GLP-1 based therapies that as 'evidence of harm accumulates, but is vigorously discounted' the 'burden of proof now rests with those who wish to convince us of their safety'<sup>43</sup>. Surveillance programs, real-life cohort studies and case-control studies can be supplemented by rational investigations of relevant proteins based on anecdotal reports<sup>56</sup>. The methodology proposed in the current work, which specifically

demonstrates the effects of the DPP4 inhibitors, also presents a rational way of determining the inadvertent interactions of newly designed compounds with proteins, and thus prevent the recurrence of drug induced diseases being detected after considerable damage has already been inflicted on humans subjected to these drugs<sup>57</sup>.

## Materials and methods

### *In silico* analysis

A comprehensive, non-redundant set of ~5000 human proteins (50% identity cutoff) was obtained from the PDB database<sup>58</sup>. The CLASP package (<http://www.sanchak.com/clasp>) used for querying these proteins using motifs from trypsin and DPP4 is written in Perl on Ubuntu<sup>20</sup>. Hardware requirements are modest - all results here are from a simple workstation (8GB ram), and runtimes for analyzing the ~5000 proteins was about 24 hours. Adaptive Poisson-Boltzmann Solver (APBS) and PDB2PQR packages were used to calculate the potential difference between the reactive atoms of the corresponding proteins<sup>59,60</sup>. The APBS parameters and electrostatic potential units were set as described previously in Chakraborty *et al.*<sup>20</sup>. All protein structures were rendered by PyMol (<http://www.pymol.org/>). Protein structures have been superimposed using MUSTANG<sup>34</sup> and DECAAF<sup>35</sup>.

### Protein, substrate and reagents

PI-PLC was purchased from Sigma. Vildagliptin (LAF-237) was obtained from Selleckchem, and K579 was obtained from Santa Cruz.

### PI-PLC assay and inhibition using DPP4 inhibitors

**Vesicle preparation and characterization.** The appropriate lipids were mixed in organic solution, and the solvent was evaporated to dryness under N<sub>2</sub>. Solvent traces were removed by evacuating the lipids for at least 2 hours. The lipids were then swollen in 10 mM Hepes, 150 mM NaCl, pH 7.5 buffer. Large unilamellar vesicles (LUV) were prepared from the swollen lipids by extrusion and sized by using 0.1 μm poresize Nuclepore filters, as described by Ahayauch *et al.*<sup>36</sup>. LUV composition was egg phosphatidylcholine: egg phosphatidylethanolamine: cholesterol at a 2:1:1 mole ratio. The average size of LUV was measured by quasi-elastic light scattering, using a Malvern Zeta-sizer instrument. Lipid concentration, determined by phosphate analysis, was 0.3 mM in all experiments.

**Aggregation Assay.** Enzyme activity was assayed measuring enzyme-induced vesicle aggregation. All assays were carried out at 39°C with continuous stirring, in 10 mM Hepes, 150 mM NaCl buffer (pH 7.5), in the presence of 0.1% BSA for optimum catalytic activity. Enzyme concentration was 0.16 U/mL, and liposomal concentration was 0.3 mM. Lipid aggregation was monitored in a Cary Varian UV-vesicle spectrometer as an increase in turbidity (absorbance at 450 nm) of the sample, as described by Villar *et al.*<sup>37</sup>. The data are average values of two closely similar experiments.

**Analyzing known DPP4 inhibitors with solved structures.** In order to obtain all known structures of DPP4 with inhibitors bound to the

active site, we did a search for the keyword dipeptidyl-peptidase on the PDB database, and choose proteins with DPP4 inhibitors as ligands. There are 76 such unique compounds (defined by three letter codes) that are reported to date (May 2014). We docked the DPP4 inhibitor to the PIPLC active site using DOCLASP<sup>40</sup>.

### Data availability

figshare: Phosphoinositide-specific phospholipase C inhibition data using the dipeptidyl peptidase-IV inhibitors K-579 and LAF-237, <http://dx.doi.org/10.6084/m9.figshare.880620>

### Author contributions

SC, ARR and BA performed the experiments. All authors analyzed the data, and contributed equally to the writing and subsequent refinement of the manuscript.

### Competing interests

No competing interests were disclosed.

### Grant information

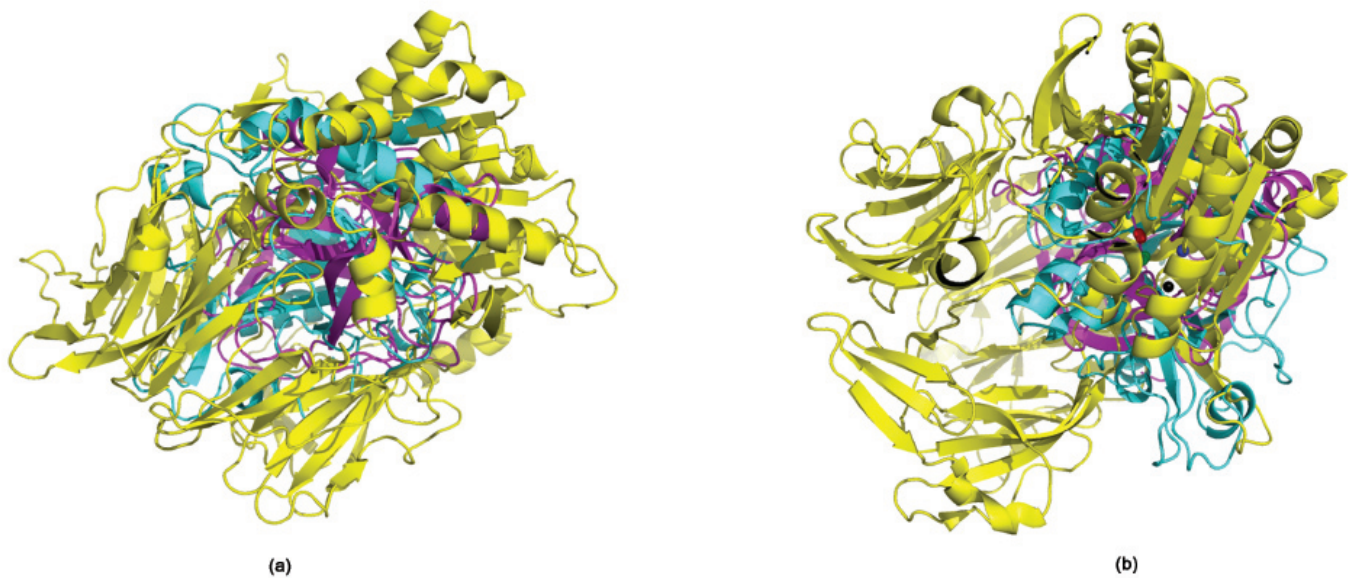
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### Supplementary information

Supplementary Pymol scripts. Click here to access the files. <http://dx.doi.org/10.5256/f1000research.3002.s40929>



**Supplementary Figure 1.** Superimposition of trypsin (PDBid:1A0J - magenta), dipeptidyl peptidase-IV (PDBid:1N1M - yellow) and phosphoinositide-specific phospholipase C (PDBid:1PTD - cyan). It is seen that there is no structural similarity in the two proteins. (a) Using MUSTANG<sup>34</sup>. (b) Using DECAAF<sup>35</sup>.

**Supplementary Table 1. PDB IDs of ~5000 human proteins analyzed in this study.**

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 3HXQ 3HY3 3HYG 3HYM 3HZJ 3I00 3I08 3I28 3I2B 3I2N 3I2V 3I33 3I35 3I3C 3I4A 3I4U 3I4W 3I5R 3I6C  
 3I6U 3I6X 3I84 3I8A 3IAI 3IAR 3IBJ 3ICU 3IDV 3IEI 3IEZ 3IF8 3IFA 3IGK 3IGL 3IH7 3IHJ 3IHR 3IHX  
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 3ISD 3ISQ 3ITU 3IU1 3IU5 3IU6 3IUF 3IUG 3IUY 3IV1 3IVV 3IWL 3IWN 3IWP 3IX0 3IXS 3J0A 3J3D  
 3J3F 3JPN 3JPO 3JPP 3JPQ 3JPR 3JPS 3JPT 3JQH 3JUD 3JUI 3JUY 3JXF 3JXH 3JZY 3K05 3K0J  
 3K0W 3K1R 3K1W 3K1Z 3K26 3K2A 3K2J 3K2O 3K35 3K6G 3K6S 3K7I 3KAN 3KAT 3KB5 3KCI 3KDF  
 3KDV 3KGV 3KGR 3KGV 3KH0 3KHF 3KJD 3KJO 3KJP 3KMD 3KN1 3KN6 3KNB 3KNV 3KOV 3KQ0  
 3KQG 3KQI 3KQS 3KRM 3KS3 3KS9 3KSY 3KT9 3KTM 3KTU 3KTV 3KUP 3KUQ 3KUS 3KUZ 3KVH  
 3KVO 3KVQ 3KVV 3KW6 3KY9 3KZ8 3KZD 3L00 3L11 3L15 3L1X 3L2C 3L2P 3L3C 3L42 3L43 3L46  
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 3LGD 3LH5 3LHR 3LJB 3LJU 3LJW 3LK9 3LL6 3LLH 3LLK 3LLM 3LLP 3LLU 3LM5 3LMN 3LNY  
 3LOF 3LPW 3LQ9 3LQH 3LQM 3LQV 3LRA 3LRE 3LRI 3LRN 3LRQ 3LRR 3LRU 3LS8 3LUC 3LUI  
 3LVR 3LWE 3LWK 3LXX 3LY5 3LYR 3LZB 3M03 3M06 3M1D 3M5B 3M66 3M7P 3M9J 3MA0 3MAX  
 3MAZ 3MB3 3MB4 3MBY 3MCB 3MCE 3MCF 3MDA 3MDF 3MDG 3MDI 3MDM 3MEW 3MFK  
 3MGH 3MGI 3MIJ 3MJG 3MJK 3MK1 3MK4 3MK6 3MMY 3MNG 3MOP 3MOS 3MPX 3MQ4 3MQ7  
 3MQI 3MQL 3MQM 3MQP 3MR2 3MR3 3MR5 3MR6 3MSH 3MT5 3MTC 3MTR 3MTS 3MTT 3MU6  
 3MUJ 3MUM 3MUP 3MUR 3MUT 3MUV 3MVA 3MVB 3MWD 3MX7 3MXH 3MXN 3MXO 3MY1 3N00

3N01 3N2Z 3N3F 3N50 3N5N 3N6S 3N7Q 3N7S 3N8E 3N8I 3N9Y 3NA3 3NAF 3NAR 3NAU 3NBI 3NBN  
 3NCE 3NCL 3NCU 3NDD 3NDQ 3NER 3NEY 3NF1 3NGD 3NGO 3NGQ 3NH6 3NHC 3NHD 3NHE 3NHN  
 3NKB 3NKS 3NMD 3NMR 3NMW 3NMZ 3NNA 3NNC 3NNH 3NO8 3NOI 3NQJ 3NR1 3NR5 3NRX 3NSL  
 3NSZ 3NV1 3NVF 3NWO 3NWH 3NWN 3NWW 3NXA 3NXB 3NXP 3NXU 3NY3 3NY5 3NZL 3O0Z 3O10  
 3O22 3O2G 3O2T 3O36 3O3I 3O46 3O47 3O4R 3O5Q 3O6E 3O70 3O7V 3OAE 3OAD 3OB9 3OBQ 3OCP  
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 3OMZ 3OOI 3OP3 3OP5 3OP8 3OPE 3ORH 3OSE 3OSK 3OSN 3OTC 3OU5 3OUI 3OV1 3OV6 3OVP  
 3OW8 3OX6 3P0C 3P0F 3P0L 3P0U 3P1A 3P1F 3P1J 3P1X 3P23 3P2T 3P3Y 3P49 3P4L 3P57 3P6D  
 3P6Y 3P7G 3P8C 3P8D 3PA6 3PB6 3PBH 3PC7 3PCV 3PD7 3PDF 3PDY 3PE0 3PE6 3PEF 3PFN 3PFS  
 3PFY 3PG6 3PG7 3PGW 3PH9 3PKI 3PLZ 3PM0 3PMI 3PML 3PMN 3PNC 3POW 3POZ 3PP2 3PPD  
 3PQ1 3PRY 3PS5 3PT3 3PTA 3PUA 3PUC 3PUF 3PV7 3PYC 3PZ7 3PZP 3Q01 3Q05 3Q06 3Q0H 3Q0L  
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 3R27 3R2P 3R3I 3R62 3R6B 3R6N 3R7G 3R8J 3R8Q 3R90 3R9A 3R9M 3RAU 3RAY 3RBG 3RBN 3RBS 3RC3 3RCS 3RCS  
 3RCP 3RCQ 3RCW 3RD2 3RDV 3RFE 3RGH 3RGR 3RH4 3RH5 3RH6 3RI4 3RIP 3RIY 3RJD 3RJE  
 3RJF 3RJG 3RJH 3RJI 3RJJ 3RJK 3RJO 3RK6 3RKQ 3RLE 3RLO 3RMU 3RN2 3RN5 3RNJ 3RNU  
 3RPP 3RPX 3RQ4 3RRQ 3RRU 3RSN 3RW6 3RY4 3RZ3 3RZG 3RZH 3RZJ 3RZK 3RZL 3RZM 3RZN  
 3RZV 3S24 3S4Y 3S57 3S58 3S59 3S5A 3S5J 3S5O 3S6W 3S79 3S7R 3S84 3S8I 3S8S 3S8W 3S92 3S93  
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 4A4I 4A5S 4A5X 4A5Z 4A64 4A6D 4A7U 4A82 4A9C 4A9Z 4AA6 4AAA 4ABL 4ABM 4ACQ 4ACR 4AD9  
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 4DQY 4DRI 4DUR 4DVQ 4DWF 4DXT 4DY0 4DYL 4DYO 4DZO 4E1H 4E1I 4E1O 4E34 4E45 4E4H  
 4E54 4E5Y 4E5Z 4E6R 4E74 4E82 4E9E 4E9F 4E9G 4E9M 4EA4 4EA5 4EAR 4EBB 4EBC 4EBD 4EBE  
 4ECQ 4ECR 4ECS 4ECT 4ECU 4ECV 4ECW 4ECX 4ECY 4ECZ 4ED0 4ED1 4ED2 4ED3 4ED5 4ED6  
 4ED7 4ED8 4EEW 4EEY 4EF0 4EFO 4EGL 4EGX 4EHD 4EI1 4EI3 4EIH 4EJN 4EJQ 4EKU 4EKZ 4ELJ  
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 6RLX 7ICE 7ICF 7ICG 7ICH 7ICI 7ICJ 7ICK 7ICL 7ICM 7ICN 7ICO 7ICP 7ICQ 7ICR 7ICS 7ICT 7ICU  
 7ICV 8ICA 8ICB 8ICC 8ICE 8ICF 8ICG 8ICH 8ICI 8ICJ 8ICK 8ICL 8ICM 8ICN 8ICO 8ICP 8ICQ 8ICR  
 8ICS 8ICT 8ICU 8ICV 8ICW 8ICX 8ICY 8ICZ 9ICA 9ICB 9ICC 9ICE 9ICF 9ICG 9ICH 9ICI 9ICJ 9ICK  
 9ICL 9ICM 9ICN 9ICO 9ICP 9ICQ 9ICR 9ICS 9ICT 9ICU 9ICV 9ICW 9ICX 9ICY

**Supplementary Table 2. Residues of DPP4 closest to the bound ligand with possible hydrogen bonds.**

Interactions sorted based on the distance. N: Number of atoms in the ligand, R/A/LA/D: Residue number/Atom of the residue/Atom of ligand/distance between the interacting atoms (in Å). For example, 'E205/OE1/N25/2.7' means that the atom OE1 from Glu205 is at 2.7 Å from the N25 atom of W94 in PDBid:3VJLA. For uniformity, we choose the first four closest atoms. This might result in choosing some atoms which are unlikely to form a hydrogen bond (for example, in PDBid:4J3JA S209/OG is at 4.8 Å from NAQ).

PDB	HET	N	R/A/LA/D	R/A/LA/D	R/A/LA/D	R/A/LA/D
3VJLA	W94	33	E205/OE1/N25/2.7	E206/OE1/N25/2.8	N710/ND2/O33/2.9	Y662/OH/O33/3
2AJ8A	SC3	26	E205/OE2/N13/2.7	E206/OE1/N13/3	Y631/N/O23/3.1	Y547/OH/N7/3.4
2RGUA	356	35	E205/OE2/N27/3	Y662/OH/N27/3.1	Y631/N/O10/3.1	E206/OE2/N27/3.1
4A5SA	N7F	37	E205/OE2/N18/2.7	E206/OE2/N18/2.7	Y662/OH/N18/2.8	Y631/N/O26/3
2QTBA	474	32	E205/OE2/N6/2.7	N710/ND2/O7/2.8	E206/OE1/N6/2.8	R358/NE/N56/2.8
2OGZA	U1N	24	Y631/N/O25/3	E206/OE1/N12/3.1	R125/NH2/O15/3.1	E205/OE2/O15/3.3
2JIDA	GVB	24	E206/OE2/N20/2.8	E205/OE2/N20/2.9	Y662/OH/N20/3	R125/NH1/O25/3.8
2I78B	KIQ	31	Y662/OH/N/3	E205/O/O/4.1	E206/OE1/O/4.2	R669/NH2/O/4.4
3H0CA	PS4	32	E205/OE2/N21/2.7	Y662/OH/N21/2.9	E206/OE2/N21/2.9	Q553/N/O3/3
2AJLI	JNH	24	S630/OG/N3/2.3	E206/OE2/N2/2.5	Y547/OH/N3/2.6	E205/OE2/N2/2.7
2BUBA	FPB	28	E206/OE2/N18/2.5	E205/OE2/N18/2.9	Y662/OH/N18/3	Y547/OH/O16/4.3
4DSAA	D1C	29	E206/OE2/NAY/2.6	E205/O/OBC/3.1	Y662/OH/NAY/3.1	Y585/OH/NAI/3.9
2OPHA	277	23	E205/OE2/N33/2.7	N710/ND2/O32/2.8	Y662/OH/N33/3.1	E206/OE2/N33/3.1
1RWQA	5AP	27	Y662/OH/N21/2.5	E206/OE2/N21/2.8	E205/OE2/N23/2.9	R125/NH2/N1/3.4
2QJRA	PZF	29	E205/OE2/N20/2.6	R358/NE/O18/2.8	E206/OE2/N20/2.9	Y662/OH/N20/3
2FJPA	S14	31	E205/OE2/N30/2.7	N710/ND2/O32/2.8	E206/OE2/N30/2.8	Y547/OH/O33/2.8
2OAEA	AIL	21	E203/OE2/N2/2.8	E204/OE2/N2/2.8	N711/ND2/O8/3.1	Y663/OH/N9/3.1
3G0CA	RUF	27	E205/OE1/N9/3	E206/OE1/N9/3.2	Y631/N/O23/3.4	Y547/OH/N12/3.6
3C43A	315	31	E205/OE2/N6/2.8	Y662/OH/N6/3	N710/ND2/O5/3	E206/OE2/N6/3
3BJMA	BJM	23	S630/OG/N23/2.4	E205/OE2/N7/2.7	E206/OE2/N7/2.7	Y547/OH/O15/2.8
3O95A	01T	26	E206/OE2/N13/2.5	E205/OE1/N13/2.8	Y662/OH/N13/2.8	R125/NH1/O19/3
3G0GA	RUM	24	E205/OE1/N24/2.9	E206/OE1/N24/3.1	Y631/N/O8/3.2	R125/NH2/N17/3.3
2G5PA	ADF	29	S630/OG/N22/2.4	Y662/OH/N8/3.1	Y547/OH/N22/3.1	E206/OE2/N7/3.1
2BUCA	008	26	E206/OE2/N10/2.7	Y662/OH/N10/2.8	E205/OE2/N10/3	Y547/OH/O13/4.5
2QOEA	448	29	E206/OE2/N20/2.7	E205/OE2/N20/2.9	Y662/OH/N20/2.9	Y547/OH/O22/4.6
2OLEA	KR2	30	E206/OE2/NAM/2.7	Y662/OH/NAM/3.6	E205/OE2/NAM/4	Y547/OH/OAP/4.5
3KWFA	B1Q	27	E205/OE2/N21/2.7	N710/ND2/O19/2.7	Y662/OH/N21/3	R125/NH2/O19/3
3SX4A	KXA	58	Y662/OH/N25/2.7	E206/OE2/N25/2.7	E205/OE2/N25/2.8	R125/NH1/O26/3.1
2ONCA	SY1	27	E205/OE1/N1/2.6	Y631/N/O17/3.1	Y547/OH/N18/3.2	E206/OE1/N1/3.4
2I03B	AXD	29	S630/OG/N14/2.4	E206/OE1/N1/2.8	Y662/OH/O16/2.9	Y547/OH/N14/3
3KWJA	23Q	27	E205/OE2/N17/2.6	Y662/OH/N17/2.8	E206/OE2/N17/2.8	S209/OG/O19/3.3
3CCCA	7AC	21	E205/OE1/N20/2.5	Y662/OH/N20/2.7	E206/OE2/N20/3.2	Y631/N/N9/3.3
3SWWA	KXB	25	E205/OE2/N21/2.7	Y662/OH/N21/2.8	E206/OE2/N21/2.9	R125/NH2/N19/3.5
4G1FA	OWG	24	E206/OE2/N9/2.8	Y662/OH/N9/2.9	Y547/OH/N2/3.1	Y631/N/O20/3.1
3C45A	317	30	E205/OE2/N6/2.8	E206/OE2/N6/2.8	Y662/OH/N6/3	Y547/OH/N29/3.7



PDB	HET	N	R/A/LA/D	R/A/LA/D	R/A/LA/D	R/A/LA/D
2G63B	AAF	29	S630/OG/N18/2.4	E205/OE2/N7/2.6	Y662/OH/N8/3.1	Y547/OH/N18/3.1
1X70A	715	28	E206/OE2/N20/2.7	E205/OE2/N20/2.8	Y662/OH/N20/2.8	S209/OG/N27/3.9
2GBIA	XIH	29	E204/OE2/N14/2.3	Y632/N/O/2.8	E203/OE2/N14/3	Y663/OH/N14/3.1
3G0BA	T22	25	E205/OE1/N13/2.5	R125/NH2/N24/3.1	Y631/N/O26/3.2	E206/OE1/N13/3.3
2IITA	872	28	E205/OE2/N20/2.7	Y662/OH/N20/2.8	E206/OE2/N20/2.9	N710/OD1/N20/4.5
4JH0A	1MD	27	Y662/OH/N16/2.7	E206/OE2/N16/2.7	Y547/OH/O1/2.8	E205/OE2/N16/2.9
4LKOA	1WH	25	Y662/OH/N/2.7	E206/OE2/N/2.8	E205/OE2/N/2.9	Y547/OH/O2/3
2RIPA	34Q	25	N710/ND2/O1/2.6	E205/OE2/N3/2.8	Y662/OH/N3/2.8	E206/OE1/N3/2.8
3QBJA	NXZ	25	Y662/OH/N18/2.7	E206/OE2/N18/2.7	N710/ND2/O25/2.8	E205/OE2/N18/2.9
3HACA	361	23	Y662/OH/N23/2.7	E205/OE2/N23/2.8	E206/OE1/N12/4.2	N710/OD1/N23/4.3
3VJMA	W61	32	E205/OE1/N28/2.7	E206/OE1/N28/2.7	Y662/OH/O57/2.9	N710/ND2/O57/2.9
3O9VA	10T	23	Y547/OH/O15/2.5	E206/OE2/N19/2.6	Y662/OH/N19/2.7	E205/OE1/N19/2.8
4DSZA	DC3	26	E206/OE2/NAM/2.8	E205/OE2/NAM/3.1	Y662/OH/NAM/3.1	S209/OG/NAR/4.7
4J3JA	D3C	30	E206/OE2/NAM/2.8	E205/OE2/NAM/3.1	Y662/OH/NAM/3.3	S209/OG/NAQ/4.8
4DTCA	D5C	33	E206/OE2/NAM/2.7	E205/OE2/NAM/3.1	Y662/OH/NAM/3.3	R669/NH2/OAQ/4.2
3OPMA	LUI	28	E205/OE1/N18/2.7	Y662/OH/N18/2.8	E206/OE2/N18/2.9	W629/O/N27/3
2OAGB	DLI	31	E205/OE2/N22/2.5	Y662/OH/N22/2.6	E206/OE2/N22/2.9	R358/NE/O1/3.2
2GBGA	1AD	19	S631/OG/N12/2.4	E203/OE2/N14/2.7	Y548/OH/N12/3	E204/OE2/N14/3.1
2HHAA	3TP	26	E205/OE2/N6/2.7	E206/OE2/N6/2.7	Y662/OH/N6/2.9	N710/ND2/O5/2.9
2QT9A	524	31	E205/OE2/N19/2.6	E206/OE2/N19/2.8	Y662/OH/N19/2.9	N710/ND2/O20/2.9
2OQVA	MA9	32	E206/OE2/N27/2.7	Y662/OH/N27/3	R358/NE/O4/3.1	E205/OE2/N27/3.3
3F8SA	PF2	26	E205/OE2/N3/2.5	Y662/OH/O7/2.8	N710/OD1/O7/3	E206/OE2/N3/3.2
2AJBA	0QG	24	S630/OG/N2/2.4	E205/OE2/N/2.7	HIS740/NE2/O2/2.9	Y662/OH/O/3
2G5TA	ACF	26	S630/OG/N22/2.4	E205/OE2/N7/2.6	Y662/OH/O3/3	N710/ND2/O3/3
3NOXA	6A5	28	E205/OE2/N16/2.4	E206/OE2/N16/2.7	Y662/OH/N16/3	R125/NH2/N4/3.7
3W2TA	LF7	22	S630/OG/N2/2.4	E205/OE1/N12/2.8	Y662/OH/O20/3	E206/OE2/N12/3
3D4LA	605	26	E205/OE2/N15/2.6	R358/NE/O42/2.8	Y662/OH/N15/2.9	V207/O/N41/2.9
2QKYA	13Z	26	S630/OG/O2/2.1	E205/O/O4/2.5	Y547/OH/O2/2.6	E206/OE1/O4/2.8
3Q8WA	AZV	38	R125/NH1/O/2.5	E206/OE2/NAG/2.6	Y662/OH/NAG/2.8	E205/OE2/NAG/2.9
3EIOA	AJH	33	Y585/OH/OBD/2.6	E205/OE2/NBG/2.7	Y662/OH/NBG/2.9	E206/OE2/NBG/2.9
3Q0TA	LGE	26	Y662/OH/N21/2.6	E205/OE2/N21/2.7	E206/OE2/N21/2.9	R125/NH1/O22/3.4
2P8SA	417	58	E205/OE2/N38/2.8	E206/OE2/N38/2.9	Y662/OH/N38/3.2	S209/OG/N34/3.4
2OQIB	GGO	28	E205/OE2/N/2.4	Y662/OH/N/2.7	E206/OE2/N/2.9	R358/NE/O/3.2
4PNZA	2VH	28	E205/OE2/N/2.7	E206/OE2/N/2.8	Y662/OH/N/2.9	Y547/OH/O/3.2
3VJKA	M51	30	E205/OE1/N21/2.9	Y662/OH/O30/2.9	E206/OE1/N21/2.9	N710/ND2/O30/3
3OC0A	B2Q	23	E205/OE2/NS/2.8	S209/OG/OB/2.9	Y662/OH/NS/3.4	E206/OE2/NS/3.5
4N8DA	2KS	24	E206/OE2/N10/2.7	E205/OE2/N10/2.8	Y662/OH/N10/2.8	N710/OD1/N10/4.5
4N8EA	2KV	22	E205/OE2/N15/2.7	E206/OE2/N15/2.7	Y662/OH/N15/2.8	N710/OD1/N15/4.3
2IIVA	565	24	E205/OE2/N20/2.7	Y662/OH/N20/2.8	E206/OE2/N20/2.9	N710/ND2/N20/4.4
3HABA	677	27	E205/OE2/N23/2.7	Y662/OH/N23/2.7	E206/OE1/N12/4.3	N710/OD1/N23/4.4
2I3ZA	LIR	27	E203/OE2/N18/2.5	Y632/N/O9/2.7	Y548/OH/N6/3.4	E204/OE2/N18/3.4

**Supplementary Table 3. Library of non-redundant motifs.** This library of motifs can be used to query any protein using CLASP to determine the possibility that DPP4 inhibitors might bind to it.

PDB	Motif Name	Motif
3VJLA	2OQVA1	GLU205/OE1 GLU206/OE1 TYR662/OH ASN710/ND2
2AJ8A	2OQVA2	GLU205/OE2 GLU206/OE1 TYR547/OH TYR631/N
2RGUA	2OQVA3	GLU205/OE2 GLU206/OE2 TYR631/N TYR662/OH
2QTBA	2OQVA4	GLU205/OE2 GLU206/OE1 ARG358/NE ASN710/ND2
2OGZA	2OQVA5	ARG125/NH2 GLU205/OE2 GLU206/OE1 TYR631/N
2JIDA	2OQVA6	ARG125/NH1 GLU205/OE2 GLU206/OE2 TYR662/OH
2I78B	2OQVA7	GLU205/O GLU206/OE1 TYR662/OH ARG669/NH2
3H0CA	2OQVA8	GLU205/OE2 GLU206/OE2 GLN553/N TYR662/OH
2AJLI	2OQVA9	GLU205/OE2 GLU206/OE2 TYR547/OH SER630/OG
2BUBA	2OQVA10	GLU205/OE2 GLU206/OE2 TYR547/OH TYR662/OH
4DSAA	2OQVA11	GLU205/O GLU206/OE2 TYR585/OH TYR662/OH
2OPHA	2OQVA12	GLU205/OE2 GLU206/OE2 TYR662/OH ASN710/ND2
1RWQA	2OQVA13	ARG125/NH2 GLU205/OE2 GLU206/OE2 TYR662/OH
2QJRA	2OQVA14	GLU205/OE2 GLU206/OE2 ARG358/NE TYR662/OH
2FJPA	2OQVA15	GLU205/OE2 GLU206/OE2 TYR547/OH ASN710/ND2
2OAEA	2OQVA16	GLU205/OE2 GLU206/OE2 TYR662/OH ASN711/ND2
3G0CA	2OQVA17	GLU205/OE1 GLU206/OE1 TYR547/OH TYR631/N
3O95A	2OQVA18	ARG125/NH1 GLU205/OE1 GLU206/OE2 TYR662/OH
3G0GA	2OQVA19	ARG125/NH2 GLU205/OE1 GLU206/OE1 TYR631/N
2G5PA	2OQVA20	GLU206/OE2 TYR547/OH SER630/OG TYR662/OH
3KWFA	2OQVA21	ARG125/NH2 GLU205/OE2 TYR662/OH ASN710/ND2
2I03B	2OQVA22	GLU206/OE1 TYR547/OH SER630/OG TYR662/OH
3KWJA	2OQVA23	GLU205/OE2 GLU206/OE2 SER209/OG TYR662/OH
3CCCA	2OQVA24	GLU205/OE1 GLU206/OE2 TYR631/N TYR662/OH
4G1FA	2OQVA25	GLU206/OE2 TYR547/OH TYR631/N TYR662/OH
2G63B	2OQVA26	GLU205/OE2 TYR547/OH SER630/OG TYR662/OH
2IITA	2OQVA27	GLU205/OE2 GLU206/OE2 TYR662/OH ASN710/OD1
2RIPA	2OQVA28	GLU205/OE2 GLU206/OE1 TYR662/OH ASN710/ND2
3HACA	2OQVA29	GLU205/OE2 GLU206/OE1 TYR662/OH ASN710/OD1
3O9VA	2OQVA30	GLU205/OE1 GLU206/OE2 TYR547/OH TYR662/OH
4DTCA	2OQVA31	GLU205/OE2 GLU206/OE2 TYR662/OH ARG669/NH2
3OPMA	2OQVA32	GLU205/OE1 GLU206/OE2 TRP629/O TYR662/OH
2AJBA	2OQVA33	GLU205/OE2 SER630/OG TYR662/OH HIS740/NE2
2G5TA	2OQVA34	GLU205/OE2 SER630/OG TYR662/OH ASN710/ND2
3W2TA	2OQVA35	GLU205/OE1 GLU206/OE2 SER630/OG TYR662/OH
3D4LA	2OQVA36	GLU205/OE2 VAL207/O ARG358/NE TYR662/OH
2QKYA	2OQVA37	GLU205/O GLU206/OE1 TYR547/OH SER630/OG
3EIOA	2OQVA38	GLU205/OE2 GLU206/OE2 TYR585/OH TYR662/OH
2I3ZA	2OQVA39	GLU205/OE2 GLU206/OE2 TYR547/OH TYR631/N

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Thank you to the authors for developing this paper.

I have some further comments.

1. The primary issue now is the speculation in the title.

The title seeks to extrapolate the obtained data on two compounds to suggest that it is applicable to all DPP-IV inhibitors.

That is, the speculation of this paper is that the presented data is relevant to an entire drug class. The comments and the title should be restricted to one or two of the compounds that were studied in this paper. Moreover, K-579 is not a diabetes drug. In this context, the title needs changing to avoid ambiguity.

I suggest:

“The dipeptidyl peptidase IV inhibitor vildagliptin used in type 2 diabetes inhibits a phospholipase C: a case of promiscuous scaffolds in proteins.”

or

“The dipeptidyl peptidase IV inhibitors vildagliptin and K-579 inhibit a phospholipase C: a case of promiscuous scaffolds in proteins.”

2. This study complements the much broader work using focused, direct technology for measuring and detecting off-target inhibition. That paper is published in Nature Chemical Biology in 2014 ( [Bachovchin \*et al.\* 2014](#)). That study similarly showed that vildagliptin inhibits enzymes other than DPP-IV. That study showed that DPP4 inhibitors differ, such that sitagliptin does not inhibit other enzymes.

The authors need to comment and restrict their conclusions to the compounds that they studied rather than imply that DPP-IV inhibiting compounds that they did not study, such as sitagliptin, have similar characteristics to the compounds that they did study.

3. The data of this study is biochemical yet 16 of the cited references concern the safety of DPP-IV inhibition. The manuscript now carefully does not draw a link to drug safety; the title needs to do the same.
4. As the paper is focused upon DPP-IV structure and function, more papers on this topic could be cited and linked with the data. For example, the author's amendment mentions contacts in DPP-IV at Glu205, Glu206 and Tyr662. The authors could state that Glu205 and Glu206 have been shown to be essential for catalysis by DPP-IV and cite the paper *Abbott et al. (1999)*.

**I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.**

**Competing Interests:** This reviewer recently received a speaker honorarium from Boehringer Ingelheim, which manufactures linagliptin.

Author Response 28 Jan 2015

**Sandeep Chakraborty**, Tata Institute of Fundamental Research, India

We would like to thank you for your positive comments, and your informative suggestions.

We agree with your suggested change in the title. In the latest version, we have also cited the research you have brought to our attention.

**Competing Interests:** No competing interests were disclosed.

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## Version 1

Referee Report 26 March 2014

doi:10.5256/f1000research.3236.r4249



**Mark D Gorrell**

Molecular Hepatology, Centenary Institute, Newtown, NSW, Australia

The successful targeting of DPP4 using small molecule compounds to treat type 2 diabetes has attracted a great deal of attention towards the study of this protease.

The authors applied sophisticated techniques that they have developed in order to discover that two DPP4 inhibitors, including one that is in limited clinical use, can to some extent inhibit the activity of a bacterial lipase (PI-PLC). Many lipases and esterases and hydrolases including DPP4 and related enzymes use the *alpha/beta* hydrolase fold and the authors show how this related protein topology can place the residues in positions that are sufficiently similar to interact with an inhibitor.

The major difficulty with this paper is that it attempts to connect these data with possible clinical outcomes. No evidence for such a link is presented. Therefore, the title and much of the conclusions need to be modified so that they reflect the data without speculation.

Two inhibitors of DPP4, LAF237 and K-579, were studied. K-579 is not in clinical use. LAF237 is licensed in Europe and is known to exhibit some inhibition of the DPP4-related proteases DPP8 and DPP9. The extent of inhibition of DPP8 and DPP9 by LAF237 is believed not to have physiological effects in humans. The IC50 of LAF237 on DPP9 is less than 0.01 mM. The IC50 of LAF237 on bacterial PI-PLC is 0.1mM, which is close to the lower limit of detection of inhibition of an enzyme. No mammalian homolog of PI-PLC was examined.

The literature that the authors cite to suggest that DPP4 inhibition might be detrimental for human health, particularly the pancreas, is data on sitagliptin or exenatide. Exenatide is not a DPP4 inhibitor and sitagliptin is quite different to LAF237, both in protease specificity and in chemical structure. The contact points of LAF237 and sitagliptin in the catalytic site of DPP4 differ considerably. The authors present no data on sitagliptin or any other DPP4 inhibitor (other than LAF237) that in is the clinic.

The images of overlaid catalytic triads of various enzymes presented in Fig 1 and Fig 3 need to be depicted in 3D in order to evaluate how close they are in 3D. Intermolecular distances should be shown on these figures. To convince the reader that LAF237 sits into and makes contacts with enzymes other than DPP4, we need to see the compound docked into the structure of each enzyme of interest.

**I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.**

**Competing Interests:** No competing interests were disclosed.

Author Response 10 Dec 2014

**Sandeep Chakraborty**, Tata Institute of Fundamental Research, India

We would like to thank you for taking the time to review this paper, and also for your insightful comments. We also apologize for the inordinate time taken to respond to your comments. A lot of this time was spent in understanding docking methods, instead of blindly applying this to the problem at hand. A by-product of this learning process was the implementation of a new method (DOCLASP) for docking molecules to proteins<sup>1</sup>. We have docked vildagliptin to the PI-PLC structure complexed with myo-inositol using DOCLASP. Based on your suggestion, we have also done a comprehensive analysis of all 76 known DPP4 structures liganded to inhibitors till date.

Please find out detailed responses to your comments below.

- *The successful targeting of DPP4 using small molecule compounds to treat type 2 diabetes has attracted a great deal of attention towards the study of this protease. The authors applied sophisticated techniques that they have developed in order to discover that two DPP4 inhibitors, including one that is in limited clinical use, can to some extent inhibit the activity of a bacterial lipase (PI-PLC). Many lipases and esterases and hydrolases including DPP4 and related enzymes use the alpha/beta hydrolase fold and the authors show how this related protein topology can place the residues in positions that are sufficiently similar to interact with an inhibitor. The major difficulty with this paper is that it attempts to connect these data with possible clinical outcomes. No evidence for such a link is presented. Therefore, the title and much of the conclusions need to be modified so that they reflect the data without speculation.*

We have tried to keep away from taking sides on the clinical outcomes, since that is not our forte. Also, we believe our title is innocuous in that context - it just speaks of promiscuous scaffolds. We only highlight that if (and only if) our data of PIPLC inhibition holds true for human lipases, then it might provide some arguing points for those worried about the side effects of these drugs.

For example, we say 'The reported elevated levels of serum lipase, although contested, could be rationalized by inhibition of lipases reported here'. If you could kindly point out specifically any speculations that is unwarranted, we will modify those.

- *Two inhibitors of DPP4, LAF237 and K-579, were studied. K-579 is not in clinical use. LAF237 is licensed in Europe and is known to exhibit some inhibition of the DPP4-related proteases DPP8 and DPP9. The extent of inhibition of DPP8 and DPP9 by LAF237 is believed not to have physiological effects in humans.*

Since this study does not emphasize on the clinical relevance of the inhibitions (but on the methodology of finding such interactions), and we are not a group specializing in diabetes, we believe the choice of the inhibitors would not alter our reasoning our conclusions.

- *The IC50 of LAF237 on DPP9 is less than 0.01 mM. The IC50 of LAF237 on bacterial PI-PLC is 0.1mM, which is close to the lower limit of detection of inhibition of an enzyme.*

We agree to this point. However, K-579 was inhibiting even at nanomolar concentrations.

- *No mammalian homolog of PI-PLC was examined.*

We are currently evaluating that possibility.

- *The literature that the authors cite to suggest that DPP4 inhibition might be detrimental for human health, particularly the pancreas, is data on sitagliptin or exenatide. Exenatide is not a DPP4 inhibitor and sitagliptin is quite different to LAF237, both in protease specificity and in chemical structure.*

We were referring to the inhibitor part of the data, but that point needs to be made explicit as you have correctly pointed out. Also, we agree that the possible difference of sitagliptin with LAF237 needs to be stated. We have modified the text to include these criticisms. Once again, we reiterate we intend not to comment on clinical outcomes or debates, but to suggest a rational methodology to act as a guide for tests that look for possible interactions.

- *The contact points of LAF237 and sitagliptin in the catalytic site of DPP4 differ considerably. The authors present no data on sitagliptin or any other DPP4 inhibitor (other than LAF237) that in is the clinic.*

We have included a comprehensive study on the contact points of various inhibitors. Once again, this does not negate any of our conclusions.

- *The images of overlaid catalytic triads of various enzymes presented in Fig 1 and Fig 3 need to be depicted in 3D in order to evaluate how close they are in 3D.*



The 3D images of the superimposition of these enzymes are not pleasing to the eye, since they lack structural homology. However, we have added a PyMol script in case someone wishes to do that (Superimposeproteins.p1m). The script specifies the color coding of the residues.

- *Intermolecular distances should be shown on thee figures.*

Once again, we think that the intermolecular distances clutter the figure. The superimposition gives an approximate idea of the congruence. The exact values are specified in Table 1. We have modified the legend of Fig.3 to specify that.

- *To convince the reader that LAF237 sits into and makes contacts with enzymes other than DPP4, we need to see the compound docked into the structure of each enzyme of interest.*

As mentioned previously, we have docked sitagliptin to PI-PLC using DOCLASP<sup>1</sup>. We have provided the Pymol script as supplementary data to help visualize the docking. There is no solved structure where LAF237 inhibits DPP4.

Once again, we are thankful for the comments. We hope that we have addressed your concerns by the changes that we have made, and that the manuscript will be found suitable in the modified form.

#### References

1. Chakraborty S. *DOCLASP* - Docking ligands to target proteins using spatial and electrostatic congruence extracted from a known holoenzyme and applying simple geometrical transformations [v2; ref status: awaiting peer review, <http://f1000r.es/4pb>] *F1000Research* 2014, **3**:262 (doi: [10.12688/f1000research.5145.2](https://doi.org/10.12688/f1000research.5145.2))

**Competing Interests:** No competing interests were disclosed.

Referee Report 06 March 2014

doi:[10.5256/f1000research.3236.r3818](https://doi.org/10.5256/f1000research.3236.r3818)



#### Rodney Rouse

Division of Applied Regulatory Science, Center for Drug Evaluation and Research, U.S. Food and Drug Administration, Silver Spring, MD, USA

**Disclaimer: I lack the protein chemistry expertise to comment on the assumptions and protein chemistry used in the computational method described in this article.**

The title and abstract are appropriate. The overall experimental design is simple but strong and well suited for this project. The methods were generally well described. The conclusions are not overstated and any implications are justified based on the presented data. The article is very well written.

This is a very interesting study that uses a previously defined computational method, Catalytic Active Site Prediction (CLASP), that compares structural and charge similarities of catalytic sites to identify

functionally similar proteins. This methodology was used to assess the potential for adverse events based on off target effects of the inhibitors of DPP-IV. Using CLASP, the authors had previously indentified a *Bacillus cerus* phosphoinositide specific phospholipase-C (PI-PLC) as similar in active catalytic site to the enzyme, DPP-IV. They used laboratory techniques to verify this finding.

In the present study, the authors demonstrated the ability of two separate DPP-IV inhibitors to significantly reduce the activity of this PI-PLC in the lab. Subsequent to this experimentation, the authors returned CLASP to identify catalytic sites in other proteins that might also be inhibited by DPP-IV inhibitors thereby yielding unforeseen inhibition and biological effects. As applied to the case of DPP-IV inhibitors, which are not extremely specific, the authors identify a number of other proteins that could be promiscuously impacted by DPP-IV inhibitors thereby providing mechanisms for unexpected adverse events. Although the significance of DPP-IV inhibitor related adverse events has yet to be determined, the fact that changes have been reported non-clinically and clinically are undeniable. Eventually, the benefit of these molecules may far outweigh their associated risks, but the authors provide a potential path forward for investigation of unexpected events with this class of drug. If contradictory reports persist, this path may require further illumination.

The approach is theoretically similar to using structural similarities to identify off target receptor binding and consequent biological effects, an expanding approach in safety assessment and in identification of mechanisms for adverse events in the pharmaceutical lifecycle. Similarly, this method could be predictive for off target effects and suggest what those effects might be. However, whether this is a method that can be generally applicable to other molecules is beyond my ability to comment and the scope of this work.

Comments/Suggestions:

1) Were the inhibition experiments done in duplicate, triplicate, etc? Some slight expansion of the protocols would help with attempts to replicate.

**I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.**

**Competing Interests:** No competing interests were disclosed.

Author Response 10 Mar 2014

**Adela Rendón-Ramirez**, Unidad de Biofísica CSIC UPV, Spain

Dear Dr Rouse,

We would like to thank you for taking the time and reviewing our paper. Your positive comments encourage us to further our research in this area.

We concur with your statement - "*Eventually, the benefit of these molecules may far outweigh their associated risks*". And it is our endeavor to improve the accuracy and generality of our method through different compounds. We would specifically like to highlight another case of antagonist binding identified through CLASP, although in this case most alkaline phosphatases were not affected - [Chakraborty et al.\(2012\)](#)

The data for PI-PLC inhibition using DPP4 inhibitors, as shown in Figure 2, are average values of two closely similar experiments. We will revise the manuscript to include this point when we hear

from another referee.

Best regards,

Sandeep Chakraborty and Adela Rendón-Ramirez

**Competing Interests:** No competing interests were disclosed.

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