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Discovery and characterization of chaperone-independent substrates of the CHIP ubiquitin ligase

by
Matthew Callahan

DISSERTATION
Submitted in partial satisfaction of the requirements for degree of
DOCTOR OF PHILOSOPHY

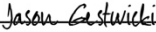
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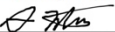
GRADUATE DIVISION
of the
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Dedication & Acknowledgements

Those who have completed a doctorate know that persevering through the inevitable ups and downs requires the support of countless friends and colleagues. It is not hyperbolic to say that my success would not have been possible without the exceptional individuals with whom I have worked over the past five years. Finishing a thesis requires the collective effort of many individuals, and I am forever grateful for the help I received from those acknowledged below.

First, I would like to thank my mentor Jason Gestwicki, and the entire Gestwicki lab, for creating a warm and welcoming environment in which I was able to thrive as a scientist. Jason, thank you for giving me the freedom to pursue my interests and to fail confidently. The low pressure and collaborative environment that you nurture in our group has been instrumental in my scientific and career development. To the lab, thank you for your commiseration, your laughs and smiles, your undying love for Pizza Hacker, your excitement to talk science over a beer on a Friday, your many, many questions at group meeting, and your mentorship and friendship. The sense of community that we shared is something I will forever treasure when looking back on graduate school.

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To my closest friends who have been there through the highs and lows of graduate school: thank you, from the bottom of my heart. It is not easy to be a good friend during a PhD, with endless excuses to stay late in lab and bail on plans. You all didn't bat an eye and were always there for

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To my family: my mother Lori, my sister Lauren, Mike, Sylvia, and Ryan, my Uncle Jeff, my cousins Kelsey & Jake and Taylor & Dani, and my aunt Grace, thank you for always believing in me. Thank you for trusting me to pursue this path, despite the many sacrifices that it requires. And thank you for the many wonderful Thanksgivings, Christmases, and birthdays that buoyed me during the tough times. Finally, to my father David, who left us before I began my PhD: thank you for providing so much love and support throughout my educational journey. I would never have achieved this milestone if not for the sacrifices you made for me. I wish you could have been here to be recognized for your role in making this possible.

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Contributions

The chapters in this dissertation were performed under the guidance of Dr. Jason Gestwicki, with the collaboration and feedback of many Gestwicki lab members. My committee members Dr. Arun Wiita and Dr. Martin Kampmann also provided key scientific guidance that helped make this work successful. Other collaborators that were instrumental in moving this work forward include Molly Hodul and Aimee Kao, as well as Rick Page and his x-ray crystallography team.

Chapter 1 contains the majority of my results, which center around characterization of an interaction between CHIP and a novel regulatory protein, CHIC2. This section is primarily a reprint of a manuscript entitled “Interaction with the membrane-anchored protein CHIC2 constrains the ubiquitin ligase activity of CHIP” written by **Callahan, M.D.**, Hodul, M., Carroll, E.C., Ravalin, M., Nadel, C.M., de Silva, A.R.I., Cupo, A.R., McDermott, L.E., Nix, J.C., Page, R.C., Kao, A.W. and Gestwicki, J.E., which is under review at *Nature Chemical Biology*. At the time of dissertation submission these results are pending publication, though a draft preprint has been published on BioRxiv.

Chapter 2 is a collection of preliminary results that highlight additional chaperone-independent interactors of CHIP beyond CHIC2. Collectively, these results imply that CHIP is engaged in a variety of previously unknown interactions that may be important for regulating its activity.

Matthew Callahan provided the experimentation and manuscript preparation for much of the following dissertation, which is a substantive contribution comparable to other dissertations in Chemistry & Chemical Biology. Jason Gestwicki directed and supervised the research and provided guidance and feedback throughout.

Discovery and characterization of chaperone-independent substrates of the CHIP ubiquitin ligase

Matthew Callahan

Abstract

Protein turnover through endolysosomal degradation and the ubiquitin proteasome system are critical for maintaining protein homeostasis. These pathways protect the cell from accumulation of misfolded proteins, coordinate critical signaling processes, and facilitate recycling pathways that are central to cellular health. An integral member of these systems is the E3 ubiquitin ligase CHIP, which facilitates the turnover of damaged or terminally misfolded proteins. Canonically, substrate recognition by CHIP is dependent on Hsp70 or Hsp90 chaperones, which serve as intermediaries between a misfolded client and CHIP. However, emerging evidence suggests that CHIP also has the capacity to recognize substrates independent of a chaperone binding partner. In this dissertation, we explore the biological relevance of such chaperone-independent substrates by exploring interactions predicted by a biophysical scoring function we previously developed, termed CHIPscore.

In the first chapter, I and others describe one such interaction between CHIP and the relatively uncharacterized, membrane-anchored protein CHIC2. We find that CHIC2 binding strongly attenuates CHIP activity, and that CHIC2 knockout phenocopies CHIP knockout in certain cell types, implying that chaperone-independent interactions can sometimes predominate CHIP's biological functions. Furthermore, loss of the CHIP-CHIC2 interaction induces neurodegeneration and shortens lifespan in *C. elegans*, demonstrating that formation of this chaperone-independent

complex is important in animals. We propose that CHIC2 attenuates CHIP activity at the membrane, offering a novel mechanism by which this ubiquitin ligase can be regulated.

In the second chapter, I explore additional chaperone-independent interactors beyond CHIC2 that are predicted by CHIPscore. In preliminary results, I demonstrate interactions between CHIP and three additional proteins. These proteins are completely uncharacterized and reside at different subcellular localizations, suggesting that CHIP may be regulated at various locations within the cell through mechanisms that are not yet understood. This work opens substantial new avenues upon which future studies should be based.

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Chapter 1: Interaction with the membrane-anchored protein CHIC2 constrains the ubiquitin ligase activity of CHIP

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1.1 Abstract

Maintenance of cellular health requires the proper regulation of E3 ubiquitin ligases. The E3 ligase CHIP is canonically regulated by its interactions with the molecular chaperones Hsp70 and Hsp90, which focus CHIP's ubiquitination activity on misfolded proteins. Here, we report a chaperone-independent interaction of CHIP with the membrane-anchored protein CHIC2, which strongly attenuates CHIP's ligase activity. We show that CHIC2 outcompetes abundant, cytosolic chaperones through its exquisite CHIP selectivity, rather than through enhanced affinity. In proteomic experiments, we find that CHIC2 knockout phenocopies CHIP knockout in certain cell types, implying that chaperone-independent interactions can sometimes predominate CHIP's functions. Furthermore, loss of the CHIP-CHIC2 interaction induces neurodegeneration and shortens lifespan in *C. elegans*, demonstrating that formation of this chaperone-independent complex is important in animals. We propose that CHIC2 attenuates CHIP activity at the membrane, offering a novel mechanism by which this ubiquitin ligase can be regulated.

1.2 Introduction

Ubiquitination regulates a wide range of protein functions, including localization, activity and turnover¹. This post-translational modification (PTM) is achieved through the coordinated action of E1, E2 and E3 ubiquitin ligases, which recognize specific substrates and transfer mono- or poly-ubiquitin chains². There is a long-standing interest in deciphering the regulatory networks responsible for controlling ubiquitination. For example, many ubiquitinated proteins are known to be further processed by the successive action of multiple E3 ligases and/or de-ubiquitinating enzymes (DUBs), which refine the length or connectivity of the ubiquitin chains³. The relative activity and substrate selectivity of the E3 ligases themselves are also regulated, through processes

such as PTMs⁴ and changes in oligomeric state⁵. Finally, modulation of E3 ligase activity through specific protein-protein interactions is also possible, as illustrated by proteins such as Emi1, which regulates the cell cycle by acting as a pseudosubstrate inhibitor of the anaphase promoting complex/cyclosome (APC/C)⁶. Together, these observations illustrate the wide variety of mechanisms by which protein ubiquitination can be regulated.

The carboxy-terminus of Hsp70 interacting protein (CHIP) is an E3 ubiquitin ligase that is canonically associated with polyubiquitination and turnover of damaged or terminally misfolded proteins⁷. CHIP is highly expressed in the brain, and its activity is particularly important for the degradation of proteins important in neurodegenerative diseases⁸. CHIP is composed of a coiled-coil domain that mediates dimerization, a U-box domain that recruits E2 conjugating enzymes, and a tetratricopeptide repeat (TPR) domain. The TPR domain of CHIP is known to bind a conserved EEVD motif that is located at the extreme C-termini of the cytosolic chaperones heat shock protein 70 (Hsp70) and heat shock protein 90 (Hsp90)⁹. Crystal structures of EEVD-containing peptides bound to CHIP's TPR domain have shown that key molecular contacts include coordination of the aspartate and terminal carboxylic acids by cationic residues in CHIP's TPR domain, termed the "two-carboxylate clamp"¹⁰. This protein-protein interaction (PPI) is believed to recruit CHIP to misfolded proteins, with the chaperones acting as adapters to localize CHIP's activity. However, recent work has identified other proteins that contain EEVD-like motifs^{11,12}, suggesting that chaperones are not the only partners of CHIP (**Figure 1.1a**). Moreover, CHIP also recognizes some substrates, such as interferon regulatory factor 1 (IRF1) and microtubule-associated protein tau (MAPT), independent of a chaperone or EEVD-like motif^{13,14}. Together, these observations suggest that CHIP has a wider set of potential partners than previously

anticipated. However, Hsp70s and Hsp90s are highly abundant proteins, so the relative contributions of chaperone-dependent and chaperone-independent mechanisms are not yet clear.

To better understand what other proteins might bind to CHIP, we recently screened large-scale peptide libraries that resemble the EEVD motif¹. This screen revealed CHIP's preference for each amino acid within the five C-terminal positions of a substrate, resulting in an algorithm, termed CHIPScore, that predicts the affinity of short peptide motifs for CHIP's TPR domain. To test this algorithm, we used it to design an optimized ligand, termed CHIPOpt (Ac-LWWPD), that binds 50-fold tighter than the Hsp70 and Hsp90 sequences. Here, we reasoned that CHIPScore might also be used to search for potential non-canonical CHIP partners in the human genome. Specifically, we hypothesized that other proteins might contain previously unrecognized, EEVD-like motifs that would bind CHIP and potentially serve as chaperone-independent regulators of its E3 ligase functions. Indeed, by combining CHIPScore with functional genomics data in the Cancer Dependency Map (DepMap), we report here that the relatively uncharacterized, membrane-anchored protein CHIC2 is a strong and biologically important binding partner of CHIP. We show that CHIC2 contains an EEVD-like motif that binds to CHIP *in vitro* and in cells, and that this interaction is chaperone-independent. We find that CHIC2 binding dramatically reduces CHIP ubiquitin ligase activity *in vitro*, suggesting that it locally restricts CHIP function at the cell surface and vesicles where CHIC2 is typically localized. Using a chemoproteomic assay, we show that CHIC2 effectively out-competes the abundant chaperones Hsp70 and Hsp90, seemingly because of its exquisite selectivity for CHIP over other TPR domain containing proteins. Moreover, using quantitative proteomics we show that loss of CHIC2 phenocopies CHIP knockout in some cells, but not others, suggesting that the CHIC2-CHIP axis may predominate over the canonical,

chaperone-mediated mechanism in certain contexts. Finally, we show that the interaction between CHIC2 and CHIP is evolutionarily conserved, and that disrupting CHIC2's EEVD-like motif induces premature aging and neurodegeneration in *C. elegans*. We propose that CHIC2 is an important, chaperone-independent regulator of CHIP function, and that its activity sometimes predominates over CHIP's canonical, chaperone-mediated mechanisms.

1.3 Results

Direct C-terminal binding mediates CHIP's interaction with the membrane-anchored protein CHIC2.

We previously developed a biophysics-based scoring function, termed CHIPScore, that predicts the affinity of CHIP's TPR domain for putative EEVD-like sequences at the extreme C-terminus of open reading frames (ORFs)¹¹. To prioritize biologically important hits for further study, we searched the DepMap database¹⁵ for genes that shared a genetic co-dependency with CHIP and then ranked the C-terminal sequences of those proteins using CHIPScore. We hypothesized that this approach would focus on the most biologically important, direct interactors of CHIP. This search process revealed a striking relationship with the relatively uncharacterized protein, CHIC2, which was a significant outlier in both its genetic interaction and predicted binding affinity for CHIP (**Figure 1.1b**).

To test whether CHIC2's C-terminus might indeed bind to CHIP's TPR domain *in vitro*, we tested peptides corresponding to either the last five (Ac-IFRPD) or ten (Ac-LPKTPIFRPD) amino acids of CHIC2 and monitored their binding to CHIP's TPR domain using a fluorescence polarization (FP) assay. Consistent with a canonical carboxylate clamp binding mode, both of the peptides

displaced a fluorescent tracer from CHIP's TPR domain, while mutation of their C-terminal aspartic acids abolished binding (**Figure 1.1c**). Next, to determine if the CHIC2-CHIP interaction also occurs in cells, we performed co-immunoprecipitation experiments. We expressed a myc-tagged CHIC2 protein in HEK293T cells and found that it bound endogenous CHIP. Importantly, mutation of the critical, C-terminal aspartic acid in CHIC2 (CHIC2^{D165A}) was also sufficient to completely abolish binding (**Figure 1.1d**), re-enforcing the importance of CHIC2's C-terminus in recruiting CHIP. We also noticed that the immunoprecipitated complexes were depleted of Hsp70 and Hsp90, implying that CHIC2 displaces chaperone from both binding sites in an immunoprecipitated CHIP dimer. To understand how CHIC2's C-terminus might compete with the canonical EEVD motifs of Hsp70 and Hsp90, we solved the crystal structure of the CHIC2 peptide (EFLPKTPIFRPD) bound to CHIP's TPR domain (residues 21-154). This 1.63 Å co-structure confirmed interactions between the terminal aspartic acid and the two-carboxylate clamp residues in CHIP: K30 and K95 (**Figure 1.1f, inset**). The overall binding pose of the CHIC2 peptide is highly similar to known CHIP ligands, such as the Hsp70 EEVD motif¹⁶ or CHIPOpt. For example, the phenylalanine and isoleucine in the CHIC2 peptide contact the "hydrophobic shelf" that is formed by F99, mimicking interactions made by the tryptophan and leucine in CHIPOpt. A feature unique to CHIC2 is an internal hydrogen bond between the arginine sidechain and peptide backbone that likely helps to enforce the bound conformation (**Figure 1.7**). Together, these findings confirm that CHIC2 has a validated EEVD-like motif that binds to CHIP's TPR domain *in vitro* and in cells.

CHIC2 is named for its cysteine-rich hydrophobic (CHIC) domain, which is constitutively palmitoylated and known to localize CHIC2 to the plasma membrane and vesicles¹⁷. To validate

this finding, we generated HEK293 Flp-In cells expressing mEGFP-CHIC2 under a doxycycline-inducible promoter. This platform allowed us to titrate CHIC2 expression to a minimal level (**Figure 1.8b**), limiting the potential for mislocalization due to overexpression. We then performed live-cell confocal imaging experiments, which revealed that CHIC2 is indeed localized to plasma membrane and vesicular compartments (**Figure 1.1e**). This localization disappeared upon treatment with the broad-spectrum palmitoylation inhibitor, 2-bromopalmitate (25 μ M) (**Figure 1.1e**), confirming the importance of this PTM in anchoring CHIC2 to the membrane. Deletion of CHIC2's C-terminus (CHIC2- Δ IFRPD) did not substantially alter its subcellular localization but it did increase total levels of the protein (**Figure 1.8a**), suggesting that the interaction with CHIP is not required for localization but that it may be partially responsible for regulating CHIC2's stability. Indeed, treatment with either bortezomib or bafilomycin increased CHIC2 levels (**Figure 1.1e**). However, we observed a more significant accumulation of total CHIC2 upon bafilomycin treatment (**Figure 1.8c**), suggesting that the protein is predominantly cleared through lysosomal degradation.

Given that the co-IP results showed that CHIC2 binds CHIP in cells, we hypothesized that the C-terminus of CHIC2 might be positioned away from the membrane, enabling it to recruit CHIP. An AlphaFold2 predicted structure of CHIC2 supports this idea, with the membrane-anchoring cysteines of the CHIC motif being positioned at the end of a helix-turn-helix, leaving the C-terminus exposed (**Figure 1.1f**). To test whether CHIP can be directly recruited to the membrane by CHIC2, we attempted to observe their colocalization in the GFP-CHIC2 Flp-In cells. However, we did not observe substantial CHIP re-localization upon CHIC2 overexpression (**Figure 1.8d**). In contrast, CHIP over-expression did reduce CHIC2 levels and partially disrupted its vesicular

localization, effects that required an intact CHIC2 C-terminus (**Figure 1.8d**). Interestingly, this effect only occurred in cells expressing CHIP at the highest levels (**Figure 1.8d**). Because both CHIC2 and cytosolic chaperones must compete for the same site on CHIP's TPR domain, we speculate that chaperone-free CHIP levels may need to reach a certain threshold before CHIC2 can be substantially bound.

The CHIC2 C-terminus outcompetes chaperone binding to CHIP using selectivity rather than affinity.

What governs the competition between CHIC2 and chaperones for limited pools of CHIP? To better understand this process, we first compared the relative affinity of various C-terminal peptides using saturation FP assays. Designed peptides, such as CHIPOpt (LWWPD) and IWWPD¹⁸ bind CHIP's TPR domain with affinities that exceed the canonical Hsp70 sequence (IEEVD) (**Figure 1.2a**). We anticipated that CHIC2, because it is expressed at substantially lower abundance than chaperones, might exploit a similar set of interactions to achieve tight binding, thus outcompeting the moderate affinity of the chaperones. Surprisingly, we found that the measured affinity of the labeled CHIC2 peptide (IFRPD, K_d 148 ± 6 nM) was not substantially tighter than that of Hsp70 (**Figure 1.2a**). Because the sequences of high affinity peptides such as CHIPOpt should be evolutionarily accessible, we wondered why CHIC2 retained a modest affinity sequence and how it might compete with abundant chaperones.

CHIP belongs to a family of ~30 carboxylate-clamp containing TPR proteins (CC-TPR proteins) that are predicted to bind EEVD motifs¹⁹. Hsp70 and Hsp90 are known to bind many of these TPR proteins, and competition between them is thought to help regulate protein homeostasis²⁰. Thus,

we considered that an alternative way for CHIC2 to compete with Hsp70s and Hsp90s would be to enhance its selectivity for CHIP's TPR domain over the other CC-TPR proteins. In other words, increased binding specificity might allow CHIC2 to effectively “seek out” free CHIP within the cell, while the chaperones are partitioned amongst the large number of other CC-TPR proteins (**Figure 1.2d**). As an initial test of this idea, we used FP to explore binding of C-termini from Hsp70, Hsp90, and CHIC2 to the relatively highly expressed CC-TPR protein HOP. While Hsp70 and Hsp90 had affinities for HOP that were in the expected, low micromolar range (Hsp70 K_d 4.4 μ M, Hsp90 K_d 1.6 μ M), the CHIC2 peptide was incapable of binding (**Figure 1.2b**). This result provided a first clue that CHIC2 might prefer CHIP over related CC-TPR proteins.

To test this hypothesis more broadly, we developed a chemical proteomics assay. Specifically, we coupled the IEEVD and MEEVD peptides from Hsp70 and Hsp90 to a biotin handle and diazirine photo-crosslinker (**Figure 1.2c**). We envisioned that, together, these probes might pull down the carboxylate clamp containing TPR proteins, including CHIP and HOP (**Figure 1.2d**). Using that system, we could then treat with the CHIC2-derived, C-terminal peptide and measure which interactions are inhibited using quantitative mass spectrometry (**Figure 1.2e**). After treatment of 293T cell lysates with a combination of the Hsp70- and Hsp90-derived probes and UV light, we confirmed that this chemoproteomics platform allows detection of up to 16 CC-TPR proteins in a given experiment (**Figure 1.2d, blue circles**). In key controls, we found that both probes showed UV-dependent enrichment and were effectively competed by unmodified versions of their parent peptides (**Figure 1.9**). Then, we treated the lysates with competitors and determined the extent to which each TPR protein was displaced. First, we confirmed that neither the Hsp70 nor Hsp90 peptides (50 μ M) were highly selective; addition of these peptides displaced most of the CC-TPR

proteins equally. In contrast, the designed ligand (CHIPOpt, 1 μ M) was selective for CHIP as expected (**Figure 1.2f**). Strikingly, we found that the CHIC2 peptide (50 μ M) was exquisitely selective for CHIP amongst CC-TPR proteins (**Figure 1.2f**), despite its modest affinity.

To explore whether this selectivity is inherent in the C-terminus of CHIC2, we generated chimeras of full length CHIC2 in which the native C-terminus (IFRPD) is replaced with the Hsp70 sequence (IEEVD) or the tighter binding designed peptides (LWWPD and IWWPD). We expressed the chimeras in 293T cells and measured binding to CHIP by co-IP. In those experiments, we found that deleting the terminal aspartic acid (IFRPA) blocked the interaction (**Figure 1.2g**), as expected, and that the native and engineered sequences all bound similar levels of CHIP. However, fusion of IEEVD to CHIC2 did not reduce binding of the chimera to CHIP, nor did it confer binding to HOP, suggesting that interactions outside of CHIC2's C-terminal motif must also contribute to selectivity. Thus, a combination of the IFRPD peptide's intrinsic selectivity and PPIs outside the C-terminal region are responsible for mediating CHIC2's selective interaction with CHIP in cells.

CHIC2 binding promotes a dramatic reduction in CHIP ubiquitin ligase activity.

Binding of CHIP to Hsp70's EEVD motif leads to rapid polyubiquitination of Hsp70 *in vitro*²¹, so we expected a similar mechanism for the CHIC2 complex. To our surprise, *in vitro* ubiquitination experiments demonstrated that full length, human CHIC2 (see Methods) was exclusively and weakly mono-ubiquitinated (**Figure 1.3a-b, red stars**). This low level of ubiquitination might be expected if CHIC2 was somehow restricting CHIP's enzyme activity, a possibility that can be conveniently measured by examining the auto-ubiquitination of CHIP. Indeed, when we increased the levels of CHIC2, the amount of CHIP auto-ubiquitination was drastically reduced (**Figure**

1.3a-b). To further test whether CHIC2 may inhibit CHIP's ligase activity, and to rule out alternative effects on E1-mediated ubiquitin activation or E2 ubiquitin charging, we performed CHIP activity assays using a pre-charged E2 conjugate. Equimolar amounts of CHIC2 significantly reduced both E2 discharge and CHIP autoubiquitination in this context (**Figure 1.3c**), whereas super-stoichiometric amounts completely prevented discharge of the E2 conjugate. Therefore, CHIP's ability to catalyze ubiquitin transfer seems to be dramatically reduced in the presence of CHIC2. To probe whether CHIC2 might also inhibit CHIP in the presence of a benchmark, physiological substrate, we added CHIC2 to reactions of CHIP with the microtubule associated-protein tau (MAPT/tau). Again, we found that CHIC2 largely blocked ubiquitin transfer to tau (**Figure 1.3d**). Importantly, adding a peptide derived from CHIC2's EEVD-like motif was not able to fully replicate this effect (**Figure 1.3d**), suggesting that CHIC2's full inhibitory activity required the intact protein. Taken together, these data support a model in which CHIC2 acts as a pseudosubstrate inhibitor of CHIP, using its EEVD-like motif to hinder recruitment of Hsp70 and, once fully bound, exploiting additional protein-protein interactions to reduce CHIP's baseline catalytic activity.

Substrate recognition by CHIC2 and CHIP is highly coordinated in some cell types, but not others.

We next wondered what effect CHIC2's inhibitory activity might have on the proteome. CHIP and CHIC2 have been shown to regulate the levels of two members of the cytokine receptor family: interferon gamma receptor (IFNGR)^{18,22,23} and a subunit of multiple related cytokine receptors, CSF2RB²⁴. These studies suggest that a CHIC2-CHIP complex may primarily regulate recycling and/or turnover of cytokine receptors. However, CHIP is also reported to regulate the levels of a

variety of non-cytokine receptors, such as CFTR²⁵, INSR²⁶ and GHR²⁷, so we wanted to more broadly explore the substrate scope of the CHIC2-CHIP complex. Accordingly, we generated CRISPR knockouts of either CHIC2 or CHIP in the glioblastoma line U251-MG (for characterization, see **Figure 1.10**) and then performed multiplexed quantitative proteomics to identify proteins that change abundance after deletion. We found that relatively few proteins were strongly regulated by knockout of either CHIC2 or CHIP (**Figure 1.4a**). Strikingly, however, a majority of the affected proteins were shared between the CHIC2 and CHIP knockouts (**Figure 1.4e**) and the fold-changes of these hits were also highly correlated (**Figure 1.4b**). This correlation was also true at the pathway level (**Figure 1.4c**), with two of the most impacted pathways being linked to cell surface receptor biology (**Figure 1.4d**). Other affected pathways included various intracellular responses, such as fatty acid metabolism, which might be due to direct or indirect effects of the knockouts. Importantly, these studies only explored changes in protein abundance, while the CHIC2-CHIP complex might also have effects on protein trafficking or other pathways. Nevertheless, the striking correlation between the proteins impacted by CHIC2 and CHIP knockout suggests that, in these cells (see below), a large majority of CHIP's ability to regulate protein turnover seems to be mediated by the chaperone-independent, CHIC2 complex.

CHIP is highly expressed in the brain, and we found it compelling that U251-MG, a brain-derived cell line, exhibits chaperone-independent regulation through CHIC2. However, CHIP has been shown to work with chaperones in other contexts as well²⁸. Therefore, to test whether cells from a different lineage might likewise display chaperone-independent regulation, we repeated the multiplexed quantitative proteomics experiments in a leukemia cell line, K562. In that cell type, we found a smaller amount of overlap between the proteins impacted by CHIC2 or CHIP knockout

(**Figure 1.11**), resulting in a substantially weaker correlation between the fold-changes of CHIC2 and CHIP hits at the protein and pathway level. This effect was not due to a lack of interaction between CHIC2 and CHIP in K562 cells, as CHIC2 levels were reliably increased upon CHIP knockout in the same manner as in U251 cells (**Figure 1.4f**). These results suggest that CHIP function depends less on the regulatory activity of CHIC2 in K562 cells, when compared to U251 cells. Another interesting observation from these comparative proteomics studies is that the responsive proteins and pathways were substantially different in the U251 and K562 cell lines (**Figure 1.11c-e**), consistent with CHIP's role in regulating a broad, rather than narrow, set of substrates.

To further explore this cell type difference, we compared our proteomics datasets to those from previously reported CHIP knockout in melanoma cell lines²³. While known CHIP substrates, such as IFNGR and JAK1, were some of the most significantly regulated substrates in these cell lines, they were substantially less significant hits in either U251 or K562 cells (**Figure 1.12a**) and the effect on IFNGR abundance was variable in experiments using K562 cells (**Figure 1.12b**). However, we noted that CHIC2 knockout partially stabilized IFNGR in both the U251 and K562 cell lines and increased its cell surface levels (**Figure 1.12c-e**), suggesting that some proportion of CHIP-mediated IFNGR regulation might typically depend on CHIC2. Together, these results highlight the complex nature of CHIP substrate regulation, and suggest that CHIC2 plays a key, and sometimes dominant, role in CHIP regulation depending on the cell type.

Loss of the CHIC2 / CHIP interaction leads to decreased longevity & neurodegeneration in *C. elegans*.

Our findings thus far suggest that chaperone-dependent and chaperone-independent mechanisms of CHIP function are both important, and that CHIC2 can be a dominant regulator of CHIP in some contexts. This model inspired us to consider the evolutionary origins of CHIC2. CHIC2 is a highly conserved protein across metazoans, and the C-terminal EEVD-like motif that is responsible for interacting with CHIP is also conserved (**Figure 1.5a**). As an initial test as to whether the orthologs of CHIC2 and CHIP from another organism interact, we expressed CHIC (also known as TAG-266, the *C. elegans* ortholog of CHIC2) and CHN-1 (the *C. elegans* ortholog of CHIP) in 293T cells and confirmed that they bind in a manner that requires the same C-terminal aspartate (**Figure 1.5b**).

C. elegans is an ideal model for further studying the biological roles of this complex because both CHIP and its orthologue CHN-1 have been shown to regulate longevity^{26,28}. Thus, we hypothesized that disruption of the CHIC-CHN-1 interaction might phenocopy this effect, but only if much of CHN-1's activity is mediated through CHIC. As an initial test of this idea, we knocked out CHIC and found that surprisingly, it had a substantially more detrimental effect on worm longevity than CHN-1 knockout (**Figure 1.5c**). Given our observation that CHIC2 inhibits CHIP ligase activity (see Fig. 3), we reasoned that toxic gain-of-function upon removal of CHIC inhibitory activity might contribute to this strong phenotype. However, the CHN-1/CHIC double knockout did not restore viability to the level of the CHN-1 knockout, suggesting that CHIC may have additional functions beyond simply attenuating CHN-1 activity. In order to exclude potential CHN-1-independent impacts of CHIC knockout, we next used CRISPR editing to replace the endogenous

CHIC gene with a mutant lacking the terminal aspartate residue (CHIC D-A). This edit phenocopied CHIC knockout (**Figure 1.5c**), rigorously confirming that the interaction with CHN-1 is essential for proper CHIC function. Taken together, these results show that the chaperone-independent interaction between CHIC and CHN-1 is essential for longevity in an animal.

As in mammals, CHIC and CHN-1 are highly expressed in the *C. elegans* nervous system^{29,30}. Thus, we were curious whether disruption of the CHIC/CHN-1 interaction might be sufficient to impact neuronal health. Using an imaging assay³¹, we found that CHN-1 and CHIC knockout worms exhibited abnormal neuronal branching and increased puncta in PVD neurons (**Figure 1.5e**, arrows, & **Figure 1.5f**), consistent with impaired neuronal health and neurodegeneration. The knockout strains also showed significantly less peripheral neuronal development (**Figure 1.5g**). Again, even mutation of a single amino acid in the C-terminus of CHIC (CHIC D-A) was sufficient to trigger these phenotypes. Together, these results validate the importance of CHIC2's interaction with CHIP in an organismal context. The stringent conservation of this interaction and its dramatic impact on longevity and neuronal health support a fundamental biological role for chaperone-independent regulation of CHIP in metazoans.

1.4 Discussion

CHIP has been implicated in a wide variety of biological processes³². For example, mutations in CHIP are linked to severe neurodegenerative disease in humans^{33,34} and the CHIP^{-/-} mouse develops inclusions of tau³⁵. It has previously been assumed that these functions are largely a product of CHIP working in concert with the molecular chaperones, Hsp70 and Hsp90³⁶. In that canonical mode, the chaperones bind to misfolded proteins and recruit CHIP with their EEVD motifs, favoring polyubiquitination and turnover. Here, we have described an alternative interaction with the membrane-anchored protein, CHIC2, that competes with chaperone binding and restricts CHIP function. Surprisingly, we found that this chaperone-independent role can sometimes predominate, as the proteomic changes induced by CHIC2 and CHIP knockout can largely phenocopy one another in U251 cells (see Figure 1.4). Furthermore, mutating a single aspartate that blocks binding to the CHIC2 ortholog, CHIC, induces premature aging and neurodegeneration in *C. elegans* (see Figure 1.5). These results demonstrate a significant and previously underappreciated role for CHIC2 in shaping CHIP's overall biological functions.

Hsp70s and Hsp90s are highly abundant proteins, reaching ~1% of soluble protein content in some cells³⁷. At first glance, it seems challenging for CHIC2 to compete amongst this large pool of EEVD motifs, especially because its affinity is not substantially different than those of the chaperones (see Figure 1.2). Indeed, in K562 cells, the effects of CHIP and CHIC2 knockout were somewhat decoupled (see Figure 1.11), suggesting that, broadly, CHIP does prefer to work with other partners such as chaperones in that cell line. How then do we harmonize these contrasting examples of chaperone-dependent and chaperone-independent CHIP function? Our chemoproteomics results (see Figure 1.2) provide a key insight here, because CHIC2 seems to use

selectivity, rather than outright affinity, as one way to tip the balance in its favor. As a framework, we envision a model in which the relative expression of CHIP and its partners dictates whether chaperone-dependent or chaperone-independent mechanisms will dominate (**Figure 1.6**). Briefly, while chaperones must interact with a large pool of other CC-TPR proteins, CHIC2 has an EEVD-like motif that is selective for CHIP. Thus, formation of the CHIC2/CHIP complex is only sensitive to the amount of free CHIP, whereas formation of a chaperone-bound CHIP complex is dependent on both the relative concentrations of the chaperones and their many other binding partners. This distinct selectivity may also allow cells to regulate the behavior of CHIP independently from related CC-TPR proteins.

Within this model, it is interesting to speculate that the ability of CHIC2 to interact with CHIP might be further tuned under specific conditions. For example, the levels of Hsp70 and Hsp90 are highly elevated by heat shock, and CHIP is known to regulate their return to basal expression following resolution of stress⁷. Thus, CHIP may be transiently displaced from CHIC2 under such conditions. Conversely, phosphorylation of Hsp70's EEVD motif is known to block its interaction with CHIP, but not other CC-TPR proteins³⁸, which might transiently free CHIP to bind CHIC2. Given the link between CHIC2 and cell surface receptor regulation, this may be a way for cells to change how they respond to external stimuli (*e.g.* cytokines^{22,24}) when internal stress pathways are activated. In other words, the relative expression levels of CHIC2, CHIP, and chaperones might dictate the “set point” at which the transition from chaperone-dependent to chaperone-independent CHIP function occurs across cell types. This model could partially explain the cell-type specificity that we observed in our proteomics experiments. While we are far from fully modelling this complex network of PPIs, we propose that the balance of relative affinities, PTMs and protein

concentrations seems likely to dictate the partners of CHIP, shaping its substrates, localization, and function in dynamic ways.

Because of its subcellular localization, it seems likely that CHIC2 would predominantly shape CHIP's behavior at the membrane (**Figure 1.6**). While it is not yet clear what exact mechanisms are at play, there are several compelling possibilities that deserve future consideration. Given our *in vitro* ubiquitination results (see Fig 1.3), monoubiquitination of CHIC2 seem likely to occur in this environment. Indeed, a band consistent with the molecular weight of monoubiquitinated CHIC2 disappears upon CHIP knockout in U251 cells, despite total CHIC2 levels increasing (see Fig 1.4f). Monoubiquitination has been strongly linked to vesicular transport³⁹, which may serve to modulate endocytic trafficking of receptors such as CSF2RB²⁴. Thus, monoubiquitination of CHIC2, and potentially nearby substrates, could be involved in regulation of receptor trafficking. Mono-ubiquitination of CHIP itself has also been recently shown to change its oligomeric state and processivity⁴⁰, so modulation of CHIP's autoubiquitination activity by CHIC2 might also be a contributing factor. Finally, it is also possible that CHIC2 may simply serve to inhibit CHIP's chaperone-dependent activity in specific, membrane-proximal regions, thus protecting some substrates from degradation. We propose that key clues to these possible mechanisms might emerge by studying the dysfunction of CHIC2 in disease. Deletion or fusion of CHIC2 is observed in certain leukemias and systemic mastocytosis^{41,42}, and copy number variations at the CHIC2 locus are common across multiple cohorts in The Cancer Genome Atlas. Therefore, studying these disease systems may uncover key substrates and mechanisms of the CHIC2/CHIP complex.

1.5 Figures

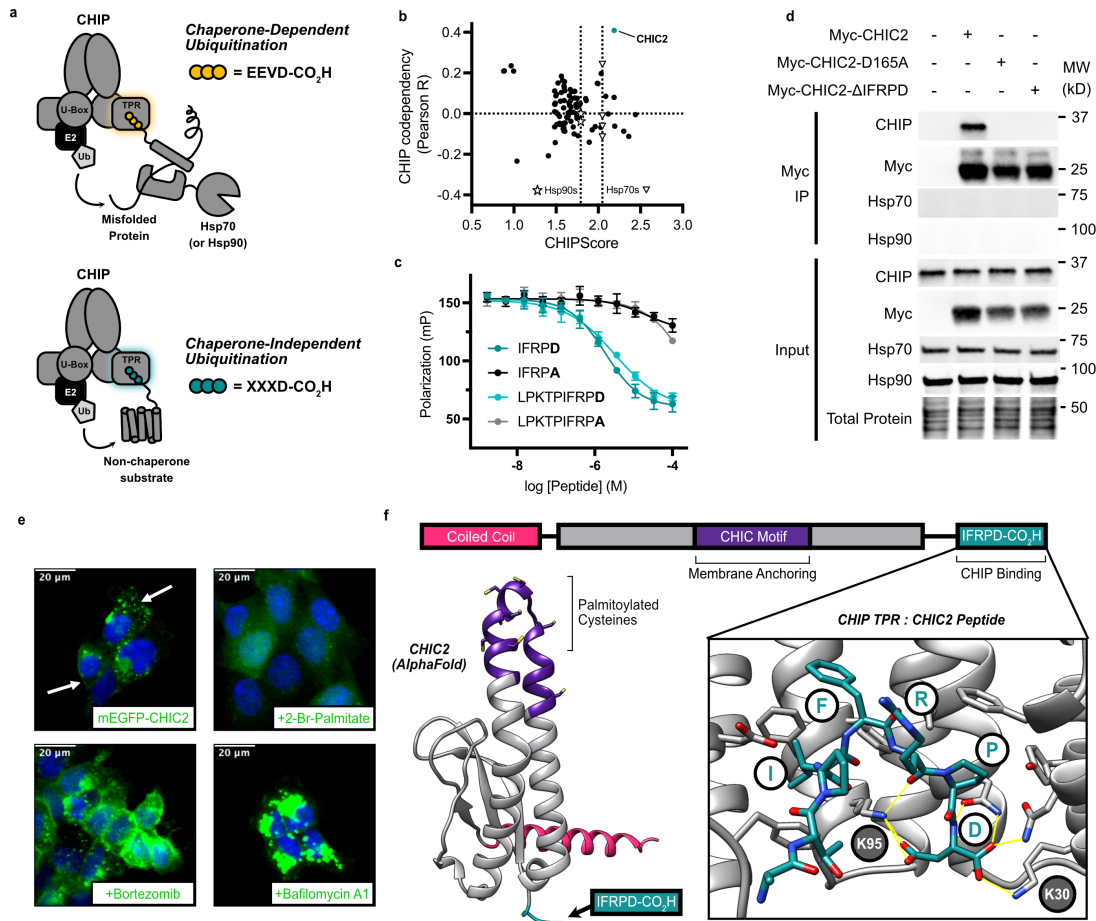


Figure 1.1 Direct C-terminal binding mediates CHIP's interaction with the membrane-anchored protein CHIC2

a) Schematic comparing the canonical, chaperone-dependent mechanism of CHIP to the chaperone-independent mechanism. Both processes are rooted in recognition of C-terminal aspartic acids within EEVD-like motifs. **b)** A combined ranking of putative CHIP substrates using CHIPscore and genetic codependency from the Cancer DepMap reveals a functional interaction between CHIC2 and CHIP. For reference, CHIP's canonical partners, Hsp70 (open triangles) and Hsp90 (open stars), are highlighted. **c)** Competitive displacement of a fluorescence polarization tracer from CHIP's TPR domain by 5 or 10 amino acid peptides derived from CHIC2's C-terminus. Mutation of the C-terminal aspartate abolishes binding. Error bars represent S.D. of 4 replicate datapoints from 1 of 3 representative experiments. **d)** Co-immunoprecipitation of CHIC2 and CHIP from HEK293T cells. Data is representative of 3 independent biological experiments. **e)** Live-cell fluorescence microscopy of dox-inducible Flp-In T-REX HEK-293 cells expressing mEGFP-CHIP2. CHIC2 localization to the plasma membrane and vesicles is shown (arrows). Inhibitors: 2-bromo-palmitate (palmitoylation inhibitor); bortezomib (proteasome inhibitor); bafilomycin A1 (lysosome inhibitor). **f)** CHIC2 domain architecture and AlphaFold2 predicted structure, highlighting the membrane-binding CHIC domain and the EEVD-like, C-terminal motif. Co-crystal structure of the CHIC2 peptide bound to CHIP's TPR domain (inset; 1.63 Å resolution) reveals the expected interactions between the terminal aspartate and the two-carboxylate clamp residues K30 and K95 (also see Figure 1.7).

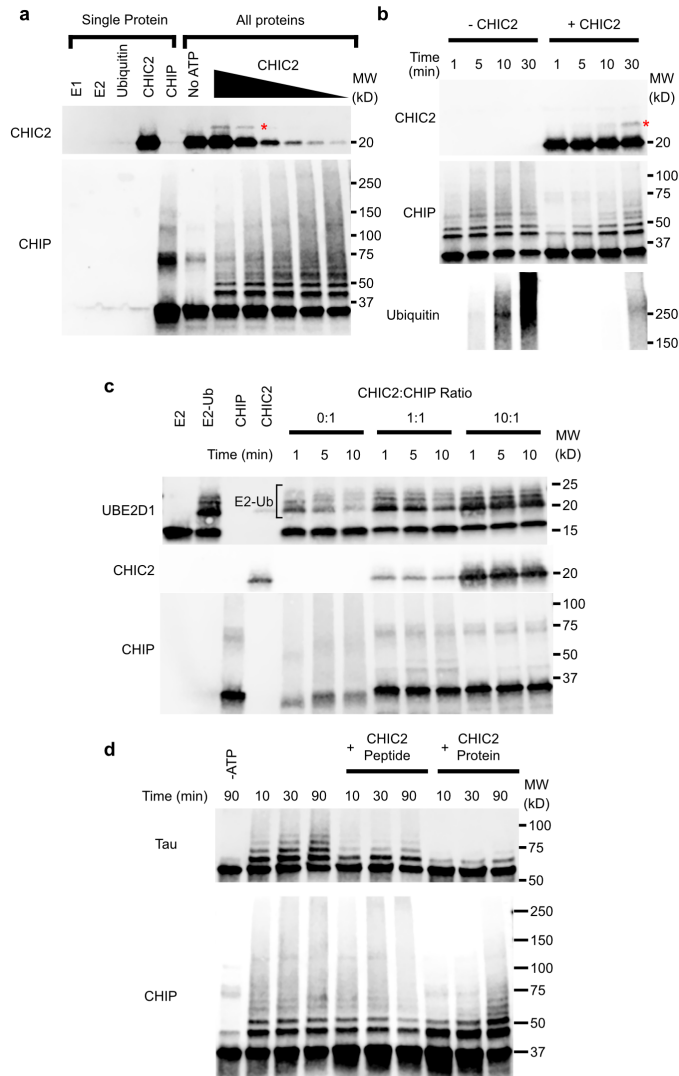


Figure 1.3 CHIC2 is monoubiquitinated and inhibits CHIP E3 ligase activity *in vitro*.

a) *In vitro* ubiquitination reactions of CHIC2 (maximum 5 μ M; serial 2-fold dilutions) and CHIP (0.5 μ M; see Methods). Reactions were quenched after 10 minutes at RT. **b)** Time course of the CHIC2 (5 μ M) ubiquitination reactions, performed as in panel a. **c)** Ubiquitination reactions using CHIP (0.5 μ M) and pre-loaded UBE2D1-ubiquitin conjugate (0.5 μ M; performed in the absence of ATP, ubiquitin or E1 enzyme; see Methods). Saturating concentrations of CHIC2 (10:1) inhibit CHIP's ability to discharge E2 thioester conjugates. **d)** Ubiquitination of the known CHIP substrate tau is inhibited by CHIC2 protein (5 μ M), but not CHIC2 peptide (50 μ M). All results in this figure are representative of experiments performed in independent duplicates.

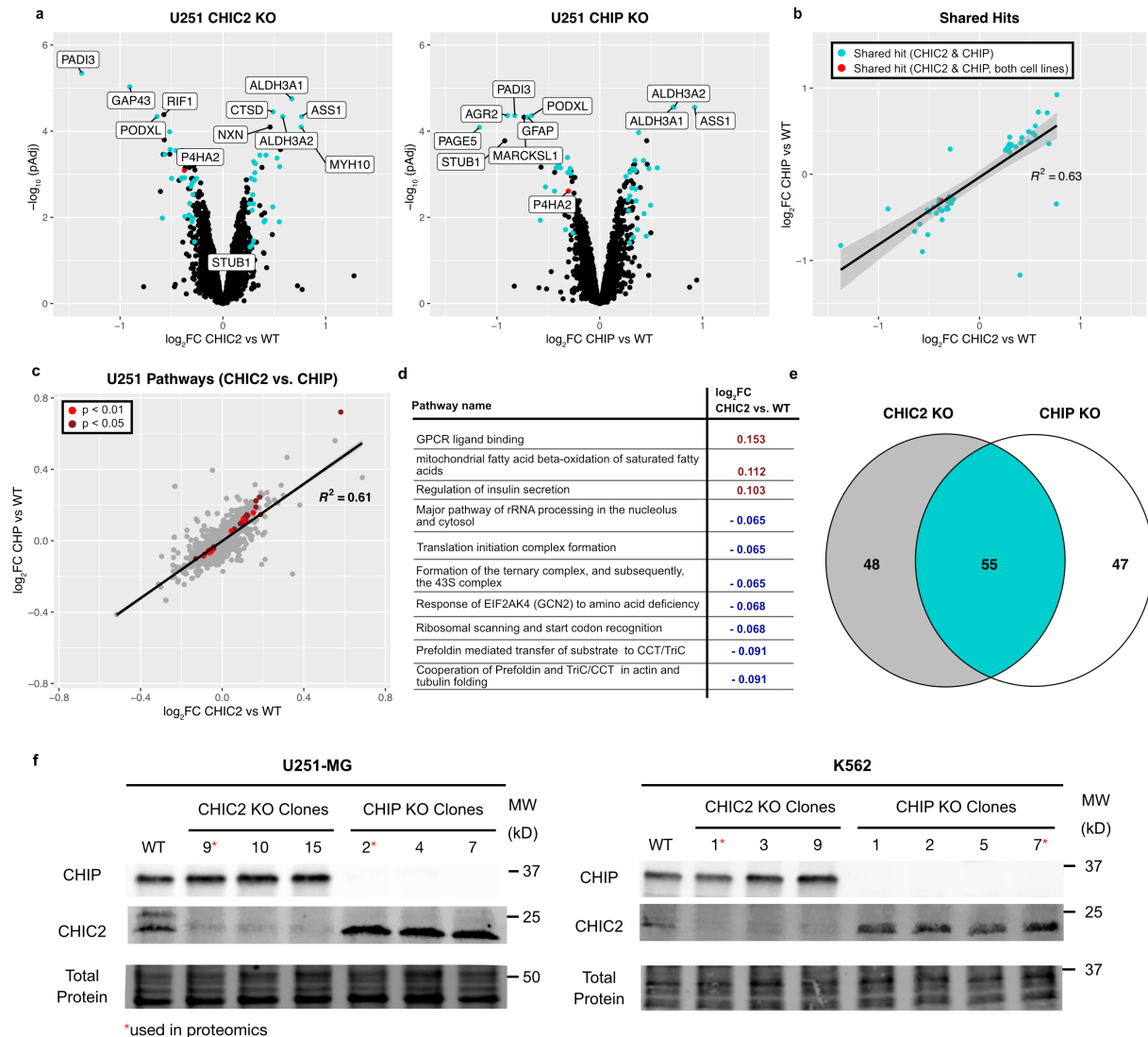


Figure 1.4 Substrate recognition by CHIC2 and CHIP is highly coordinated, but cell-type dependent

a) Results of TMT quantitative proteomics experiments, performed on parent U251-MG and CHIC2 and CHIP knockout U251-MG cells. Proteins with a $\log_2FC > 0.25$ and a Benjamini-Hochberg adjusted p -value < 0.05 were considered hits. Blue dots indicate proteins whose abundance is significantly affected in both knockout conditions. **b)** Shared hits between CHIC2 and CHIP knockout have highly correlated fold-changes. Red dot indicates the one hit that is shared with the cell line K562 (see **Figure 1.11**). **c)** Analysis of pathways from the Reactome database that are affected by CHIC2 or CHIP knockout, using the correlation-adjusted mean rank gene set test (Camera)⁴³. **d)** Top ten pathways ($p < 0.01$) identified as being shared between the CHIC2 and CHIP knockouts. **e)** Venn diagram of proteins that are differentially affected by CHIC2 and CHIP knockout ($\log_2FC > 0.25$, $p_{Adj} < 0.05$). **f)** Western blots showing that CHIC2 levels are elevated by CHIP knockout in both U251 and K562 cells. At least three separate clones are shown for each knockout, with the red star indicating the clone used for proteomic experiments. See **Figure 1.10** for characterization of the clones. Results are representative of experiments performed in independent triplicates.

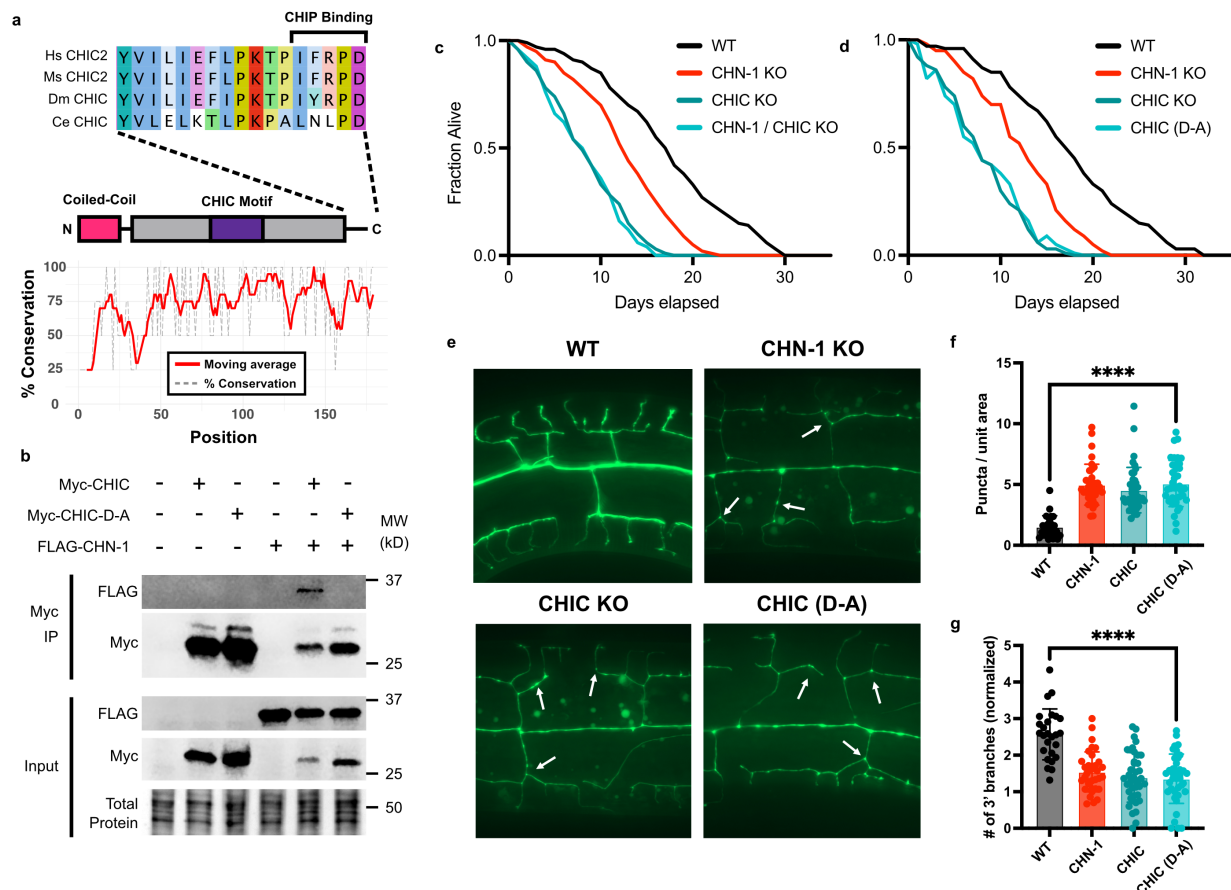


Figure 1.5 Loss of the CHIC2/CHIP interactions leads to decreased longevity and neurodegeneration in *C. elegans*

a) Sequence alignment of CHIC2 and CHIP orthologs from human, mouse, fruit fly, and worm illustrate a high degree of conservation, including in the C-terminal EEVD-like motif that binds CHIP (upper inset). **b)** Results of co-immunoprecipitation experiments from HEK393T cells expressing *C. elegans* myc-CHIC (ortholog of CHIC2) and FLAG-CHN-1 (ortholog of CHIP). Data is representative of 2 independent biological experiments. **c)** Results of longevity assays in *C. elegans*. Data represent the average of 3 independent experiments using 75 animals each. **d)** Results of longevity assays with a CRISPR-edited strain in which CHIC's C-terminal Asp is replaced with Ala (CHIC D-A), showing that loss of the CHIC/CHN-1 interaction decreases longevity. **e)** Knockout and mutant strains display increased rates of PVD neuron degeneration in the strain *wlds51*, which selectively expresses GFP in this cell type. Formation of bead-like puncta on the PVD dendrite (arrows) is indicative of neurodegeneration. **f)** Quantification of neurodegenerative puncta as in panel e). Puncta were counted by a blinded observer, and then normalized to the total area of each image. At least 25 animals per strain were quantified, and data are representative of 3 independent biological experiments. **** $p < 0.0001$ by Welch's *t*-test. **g)** Loss of branched PVD neuron density in mutant strains. Dendrite branches were quantified by a blinded observer who counted junctions moving outward from the central axon. The number of 3' branches was normalized to the number of parental (1', 2') branches. At least 25 animals per strain were quantified, and data are representative of 3 independent biological experiments. **** $p < 0.0001$ by Welch's *t*-test.

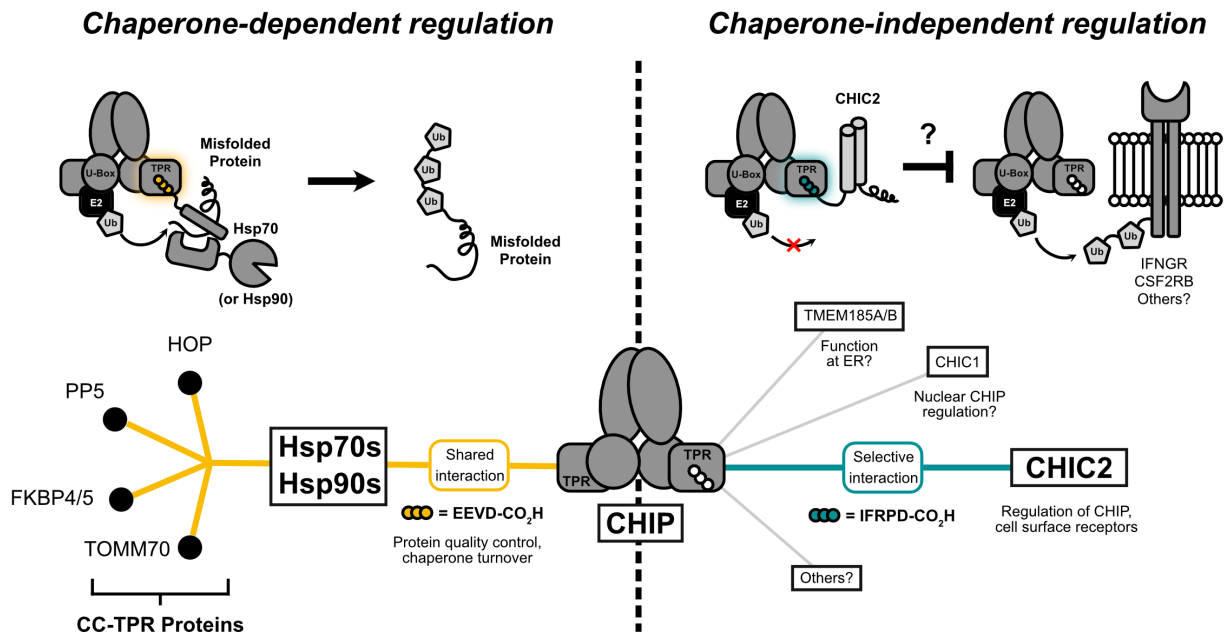


Figure 1.6 A model for context-specific regulation of CHIP.

Competition between chaperone-dependent (left) and chaperone-independent (right) interactions dictate CHIP behavior in different contexts. Binding of "free" CHIP (center) to various partners is governed by the relative expression levels of Hsp70s & Hsp90s, CC-TPR proteins, and chaperone-independent interactors such as CHIC2. Since CHIC2 interacts selectively with CHIP, its interaction is influenced by free CHIP levels but not that of numerous other CC-TPR proteins. Relative levels of free chaperone and CHIP may therefore determine the "set point" at which formation of the CHIC2/CHIP complex occurs in different cell types. Other factors such as PTMs, chaperone upregulation under stress, or subcellular localization may further tune this behavior. This complex web of interactions likely drives the cell-type specificity of CHIP behavior and its response to various stressors.

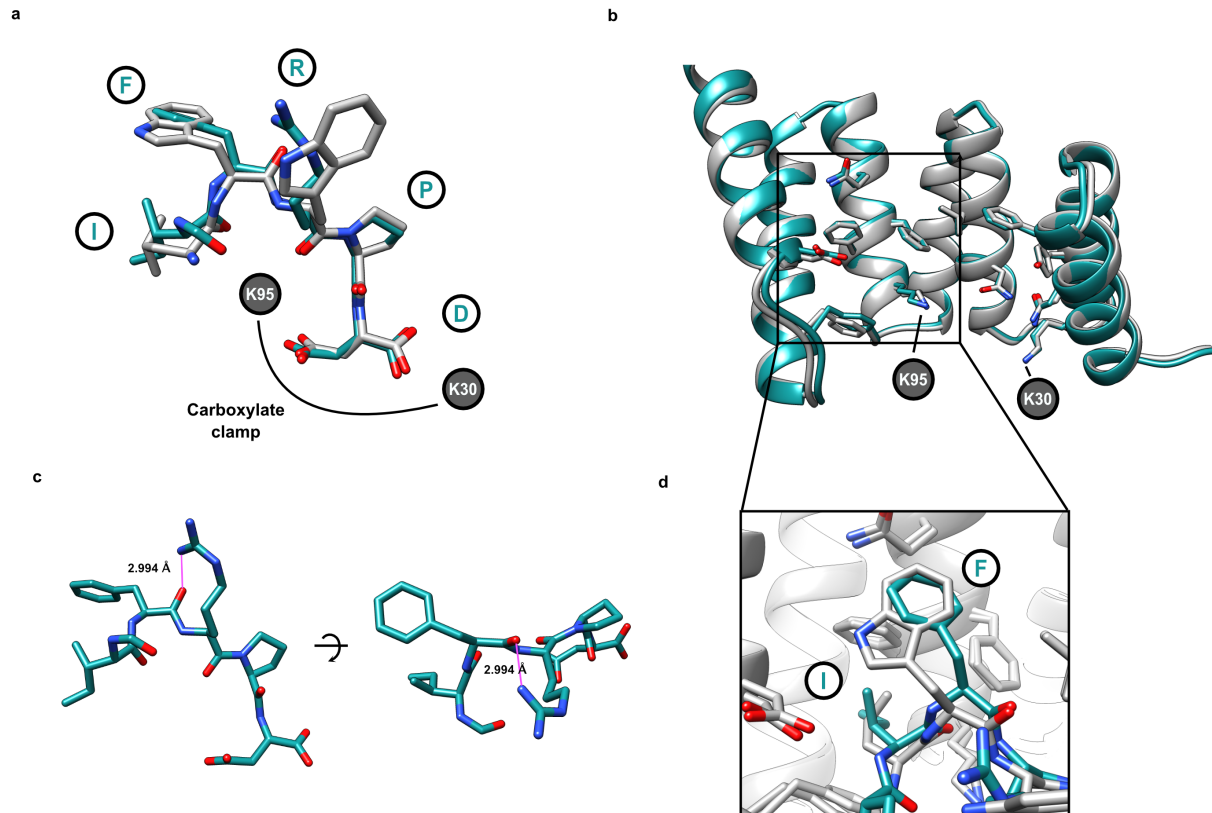


Figure 1.7 CHIC2's EEVD-like motif bound to CHIP's TPR domain adopts a similar conformation as the benchmark CHIPOpt.

a) Overlay of the CHIP-bound conformation of the last five amino acids of CHIC2 peptide (IFRPD, cyan) and CHIPOpt (LWWPD, gray) demonstrates a similar binding pose. **b)** Comparison of CHIP's TPR domains bound to either peptide (see panel a) also suggests a similar structure. **c)** An internal hydrogen bond between the P3 arginine side chain and the peptide backbone in the CHIC2 peptide may help pre-organize or stabilize the CHIP-binding mode. **d)** Similar contacts define the "hydrophobic shelf" in CHIP's TPR domain and its interactions with the P5 isoleucine and P4 phenylalanine in CHIC2, compared to the P4 valine and P5 tryptophan in CHIPOpt. We speculate that the slight differences in backbone conformation may be enforced by the internal hydrogen bond highlighted in panel c).

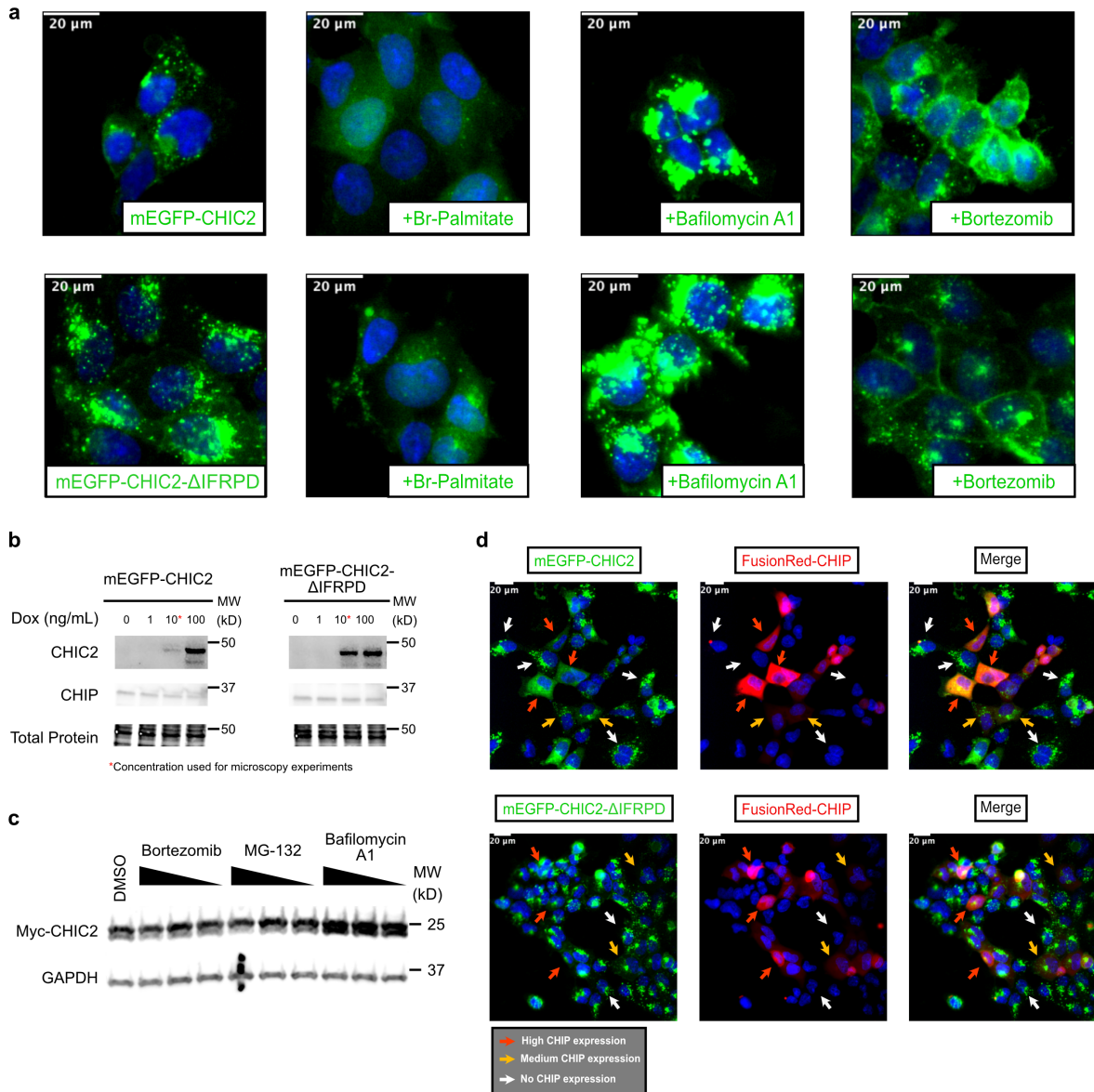


Figure 1.8 Subcellular localization of CHIC2 in response to inhibitor treatment and CHIP overexpression.

a) Live-cell imaging of dox-inducible HEK293 Flp-In cells expressing either GFP-CHIC2-WT or GFP-CHIC2- Δ IFRPD. The C-terminal mutant exhibits higher basal expression levels of CHIC2, suggesting that CHIP is involved in CHIC2 clearance. Bafilomycin treatment induces a substantial accumulation of both WT CHIC2 and CHIC2- Δ IFRPD relative to bortezomib, suggesting that the lysosome is predominantly responsible for clearance, regardless of CHIP's involvement. **b)** Western blots showing GFP-CHIC2 levels in response to doxycycline titration. The minimal amount of doxycycline that induced observable expression (10 ng/mL) was used in microscopy experiments. **c)** Western blots showing the results of transfection of HEK293T cells with Myc-CHIC2, followed by a 4 hour treatment with proteasome (bortezomib or MG-132) and lysosome (bafilomycin) inhibitors, suggesting that CHIC2 is predominantly degraded in the lysosome. Compounds were serially diluted 1:10 from 10 μ M (bortezomib, MG132) or 1 μ M (bafilomycin A1). (Figure caption continued on the next page.)

(Figure caption continued from the previous page.) **d)** Live cell microscopy, showing that high levels of FusionRed-CHIP overexpression (red arrows) result in a substantial relocalization of CHIC2-WT, but not Δ IFRPD. Intermediate expression of FusionRed-CHIP (yellow arrows) are not sufficient, suggesting that CHIP expression must reach a critical level to relocalize CHIC2. To limit the impact of degradation, cells were treated with bafilomycin (100 nM) for 4 hours prior to imaging.

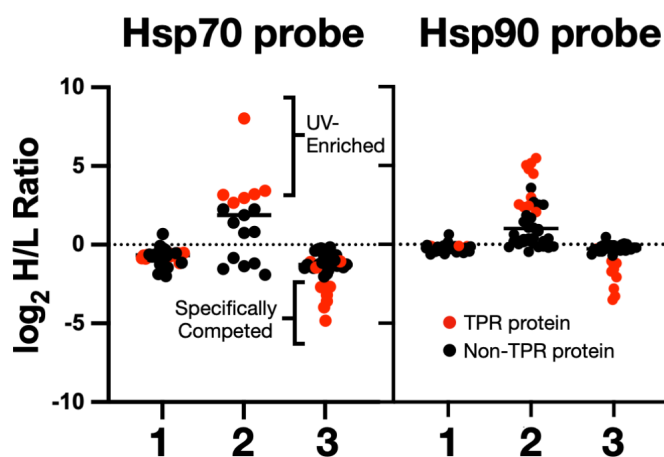


Figure 1.9 TPR protein enrichment by Hsp70 and Hsp90 photoprobes.

1) Equal concentrations of Hsp70 or Hsp90 probes (10 μ M; see **Fig 2c**) were added to both light and heavy channels, demonstrating balanced incorporation of isotopic labels. **2)** Results from experiments in which either Hsp70 or Hsp90 probe (10 μ M) was added to each channel, but the light channel was not exposed to UV light, demonstrating specific crosslinking and enrichment. **3)** Hsp70 or Hsp90 peptide competitor (100 μ M) was added to the heavy channel prior to crosslinking. For all experiments, H/L ratios were directly exported from MaxQuant.

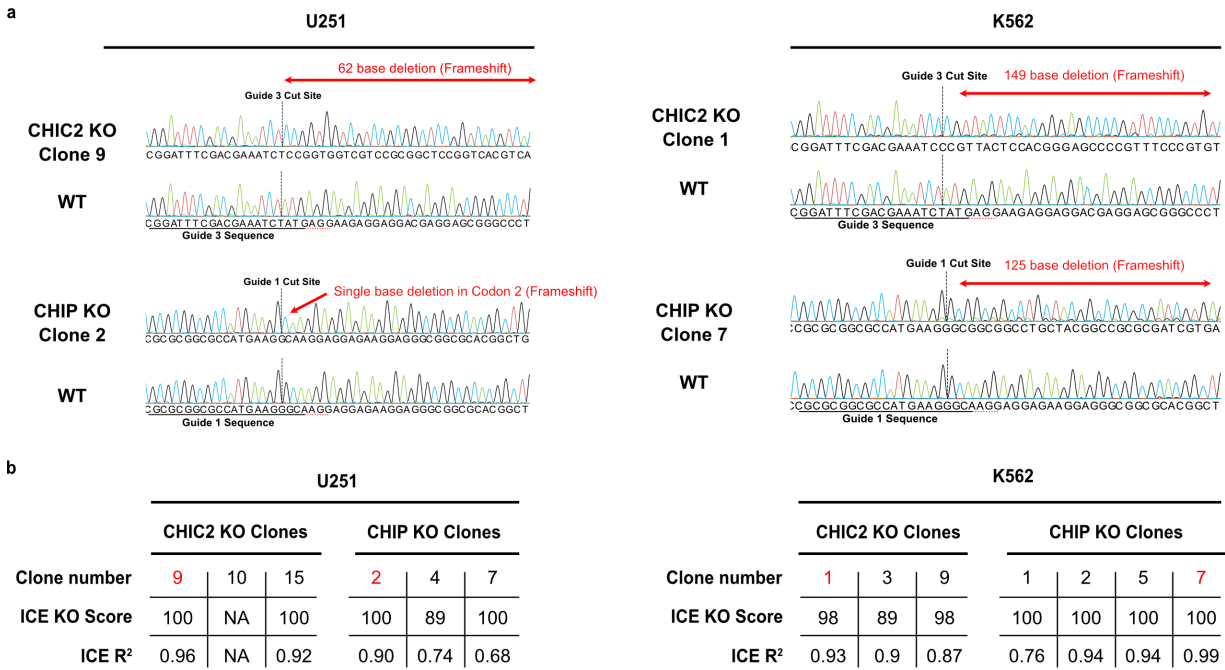


Figure 1.10 Characterization of CHIC2 and CHIP knockout clones.

a) Sanger traces of selected knockout clones highlighting indels around the CRISPR cut sites. Guide sequences are underlined in the WT sequence. **b)** Summary of Sanger sequencing analysis for all clones using the Synthego ICE analysis software. NA indicates that ICE failed to generate a score from the sequencing files.

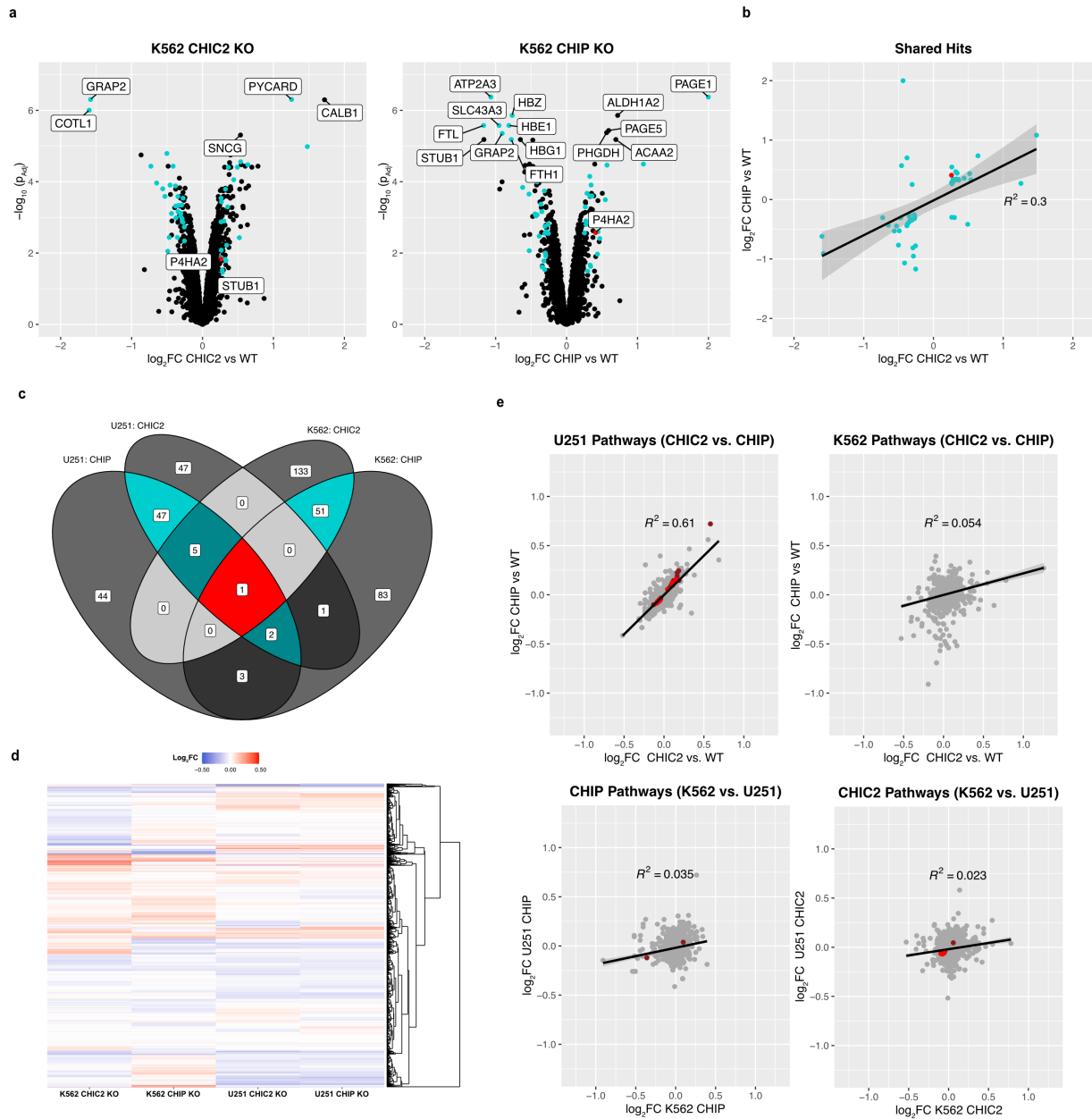


Figure 1.11 Proteomic changes in response to CHIC2 and CHIP knockout in K562 cells, highlighting cell type differences.

a) Results of TMT quantitative proteomics of CHIC2 and CHIP knockout in K562 cells. Proteins with a $\log_2FC > 0.25$ and a Benjamini-Hochberg adjusted p -value < 0.05 were considered hits. Blue dots indicate proteins for which the change in abundance is shared between the two knockouts. **b)** Plot of the fold-change in protein abundance, comparing the CHIC2 and CHIP knockout and showing the poor correlation between the shared hits. Some hits are elevated in abundance in one knockout and reduced in the other. Red dot indicates the one hit that is shared with the U251 cell line (see **Figure 4**). **c)** Venn diagram of hits shared between knockout conditions in the U251 and K562 cell lines, showing that the majority of overlapping hits are shared within a cell line rather than across a cell line or gene. (Figure caption continued on the next page.)

(Figure caption continued from the previous page.) **d)** Heatmap of proteomic fold-changes (KO vs. WT). Hierarchical clustering reveals a strong relationship within, but not across, cell lines. **e)** Pathway analysis from the Reactome database, using the correlation-adjusted mean rank gene set test (Camera)⁴³. Pathways that are differentially regulated in response to CHIC2 or CHIP knockout are not shared between cell lines.

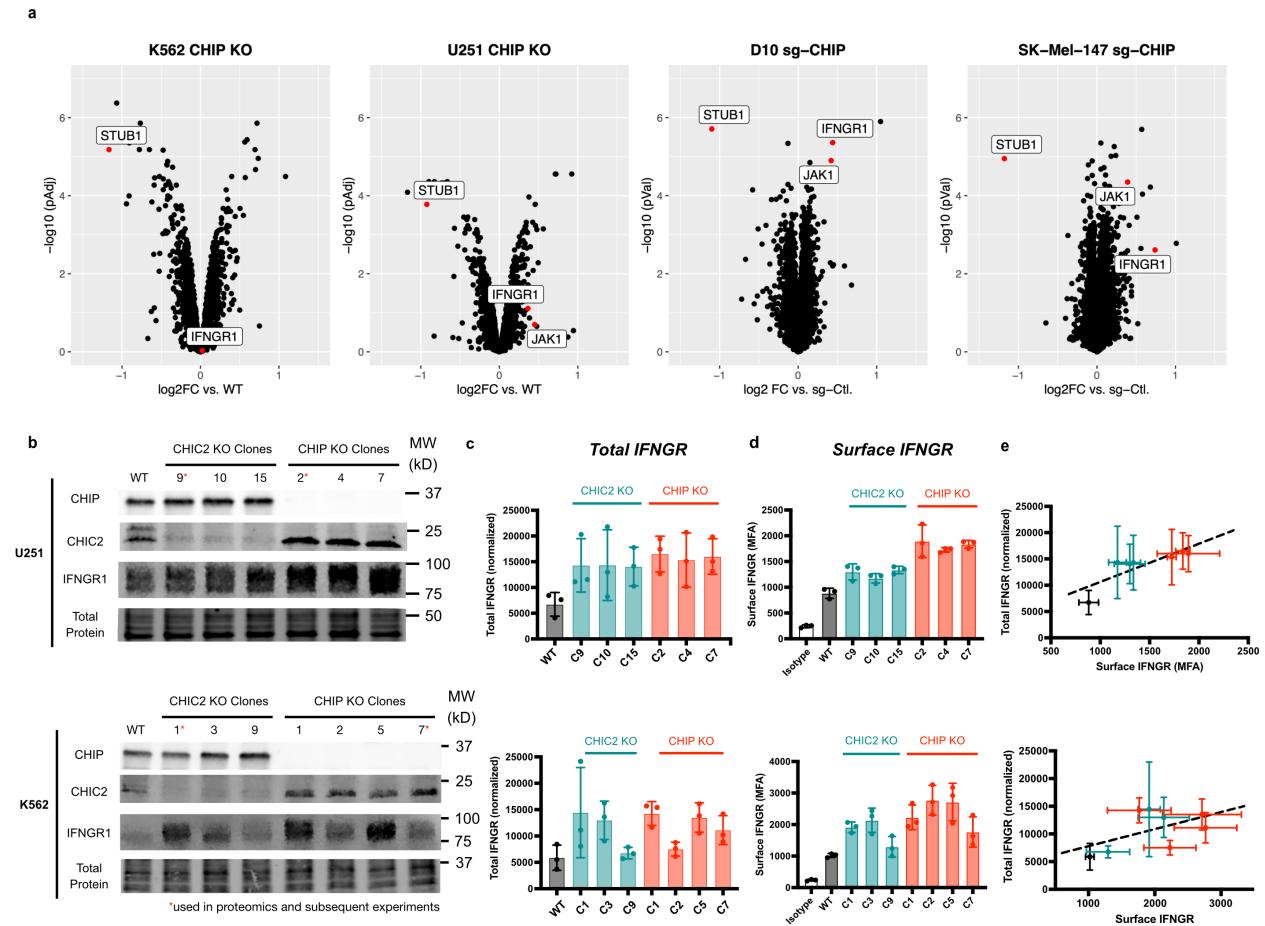


Figure 1.12 Cell-type dependent regulation of IFNGR by CHIP and CHIC2.

a) Comparison of quantitative proteomics datasets from different CHIP knockout cell lines, highlighting the cell-type-dependent regulation of IFNGR. The results from the D10 and SK-Mel-147 cell lines is re-plotted from Apriamashvili et al²³. Note that IFNGR1 and JAK1 were only identified by a single peptide in the K562 and U251 cell lines. **b)** Western blots of U251 and K562 knockout clones, showing that IFNGR upregulation in response to CHIC2 or CHIP knockout is consistent across clones in U251 cells, but more variable in K562 cells. In contrast, CHIC2 levels are consistently elevated upon CHIP knockout. **c)** Quantification of three independent western blotting experiments as in **b)**. Error bars represent the S.D. of all the experiments. **d)** Flow cytometry analysis of surface IFNGR upon CHIC2 and CHIP knockout, showing increases in IFNGR surface levels. Error bars represent the S.D. of three independent biological experiments. **e)** Correlation of total and surface levels of IFNGR in response to knockout of CHIC2 (blue dots) and CHIP (red dots) across various clones, highlighting the strong correlation across clones in U251, but not K562. Error bars represent the S.D. of all the experiments.

1.6 Tables

Table 1.1 Data collection and refinement statistics for CHIP-TPR : CHIC2 crystal structure

| Data Collection | |
|--|-----------------------------|
| X-ray source | Beamline ALS 4.2.2 |
| Wavelength (Å) | 1.000020 |
| Resolution range (Å) ^b | 46.53 – 1.63 (1.688 – 1.63) |
| Space group | <i>P</i> 1 2 ₁ 1 |
| <i>a</i> , <i>b</i> , <i>c</i> (Å) | 46.53, 82.36, 78.39 |
| <i>a</i> , <i>b</i> , <i>g</i> (°) | 90, 90.03, 90 |
| Reflections ^b | 498,239 (50,246) |
| Unique reflections ^b | 71,293 (7,022) |
| Multiplicity ^b | 7.0 (7.2) |
| Completeness (%) ^b | 96.4 (94.6) |
| Mean <i>I</i> /sigma (<i>I</i>) ^b | 8.52 (0.88) |
| Wilson B-factor (Å ²) | 20.6 |
| CC _{1/2} ^b | 0.998 (0.652) |

| Refinement | |
|--|--------------------|
| PDB ID | 8SUV |
| Number of reflections ^b | 71,065 (6,976) |
| Reflections used for R_{free} ^b | 1,540 (136) |
| R_{work} / R_{free} | 0.274 / 0.290 |
| Number of atoms (protein/ligands/water) | 4,395 / 20 / 404 |
| Average B factors (protein/ligands/water) | 32.5 / 37.7 / 31.2 |
| Model Quality | |
| Bond length rmsd (Å) | 0.012 |
| Bond angle rmsd (°) | 1.550 |
| Ramachandran favored (%) | 98.1 |
| Ramachandran allowed (%) | 100 |
| Ramachandran outliers (%) | 0 |
| Poor rotamers (%) ^b | 0.22 |
| Clashscore ^b | 4.79 |

| Model Quality | |
|--|--|
| Clash percentile ^b | 94 th percentile (N=1,784; all resolutions) |
| MolProbity score ^b | 1.25 |
| MolProbity score percentile ^b | 99 th percentile (N=27,675; all resolutions) |

^a Data for the highest resolution shell is represented by the values in parentheses within the table.

^b Values calculated using MolProbity v4.5.2⁴⁴.

1.7 Supplemental Files

Supplemental Dataset 1.1: TMT quantitative proteomics of CHIC2 and CHIP knockout cells

Processed proteomics data, including differential expression of proteins relative to wild-type U251 and K562 cells.

Supplemental Dataset 1.2: Chemoproteomic selectivity of peptides amongst TPR cochaperone proteins

Processed chemoproteomics data of peptide selectivity amongst TPR cochaperone proteins.

1.8 Materials and Methods

DepMap analysis

The top 100 co-dependencies of CHIP (by CRISPR) were downloaded from the Cancer Dependency Map (22Q1 release), and the CHIPScore calculated for each. The top 100 CHIP-scoring proteins in the proteome were also selected (independent of DepMap association), and their genetic codependency with CHIP was also extracted. Proteins without a C-terminal aspartic acid were excluded from the analysis, as were genes not screened by CRISPR in the DepMap.

Fluorescence polarization

Saturation binding: CHIP was serially diluted to 2X its final concentration in assay buffer (25 mM HEPES pH 7.4, 50 mM KCl, 0.01% Triton X-100, 1mM TCEP). Protein dilutions were then mixed 1:1 with a 2X tracer (FAM-Ahx-Peptide) solution in assay buffer + 2% DMSO to yield a final concentration of 1 nM tracer + 1% DMSO. From the resulting dilutions, an aliquot (18 μ L) was pipetted into black, low-volume 384-well plates (Corning 4511) and incubated at RT for 15 minutes. Fluorescence polarization was measured on a BioTek H4 plate reader. Raw polarization data (mP) was normalized to buffer controls, then plotted relative to $\log_{10}[\text{Protein}]$. Data was fit to the $\log[\text{agonist}]$ vs. response model with variable slope in GraphPad PRISM 9.0, and K_d values were extrapolated from half-maximal effective concentration (EC_{50}). HOP saturation binding was performed in the same manner, except that the final tracer concentration was 10 nM and the data was collected on a SpectraMax M5 plate reader (Molecular Devices).

Competition binding: Peptide competitors were prepared as an 11-point serial dilution at 2X concentration in assay buffer + 2% DMSO. These were then mixed 1:1 with a 2X solution of CHIPOpt tracer (FITC-Ahx-LWWPD) and CHIP protein (43 nM and 20 nM, respectively) to yield

a final concentration of 10 nM tracer, 21.5 nM CHIP, and 1% DMSO. An aliquot of the resulting dilutions (18 μ L) were then plated and incubated as above, and the resulting polarization data collected on a BioTek H4 plate reader. Raw polarization data (mP) was plotted relative to \log_{10} [peptide competitor], and data was fit to the \log [inhibitor] vs. response model with variable slope in GraphPad PRISM 9.0.

Peptides & tracers

All peptides were purchased from GenScript as >95% pure N-terminally acetylated peptides unless otherwise indicated. Tracers were prepared identically, with the addition of an N-terminal hexanoic acid linker and FAM fluorophore in place of the acetyl group. Peptide sequences are as follows: IEEVD (Hsp70), MEEVD (Hsp90), IFRPD (CHIC2), LWWPD (CHIPOpt). Synthesis of peptide photo-crosslinkers was performed as previously described¹¹, with the following modifications: Following synthesis of the base peptide (M/IEEVD) on Wang resin, an orthogonally protected lysine residue (Fmoc-Lys(Mtt)) was coupled to its N-terminus. MTT deprotection was afforded by incubation with 3% TFA in DCM for 30 minutes at RT. The resin was then washed 3x with DCM, methanol, and DMF. Biotin conjugation was carried out using 1.7 eq. of Biotin-NHS and 20 eq. NMM in 500 μ L of DMF while shaking for 1h at RT. Conjugation was then repeated. Following Fmoc deprotection in 4-methylpiperidine, NHS diazirine (Thermo cat. 26167) was attached to the N-terminus using the same conditions. Peptides were cleaved off the resin with 500 μ L of cleavage solution (95% trifluoroacetic acid 2.5% water 2.5% triisopropylsilane) while shaking for 1 h, then precipitated in 20 mL cold 1:1 diethyl ether: hexanes. Crude peptides were solubilized in a 1:1:1 mixture DMSO: water: acetonitrile and purified by high-performance liquid chromatography (HPLC) on an Agilent Pursuit 5 C18 column

(5 mm bead size, 150 × 21.2mm) using an Agilent PrepStar 218 series preparative HPLC. The mobile phase consisted of A, water 0.1% trifluoroacetic acid and B, acetonitrile 0.1% trifluoroacetic acid. Solvent was removed under reduced atmosphere and purity >95% was confirmed by liquid chromatography-mass spectrometry (LCMS). DMSO stocks were prepared at a concentration of 10 mM based on the gross peptide mass.

Protein purification

CHIP, CHIP K30A, HOP, and Tau were purified as previously described^{11,45,46}. CHIC2 (human, His-tagged) was expressed from a pMCSG7 vector with an N-terminal tobacco etch virus- (TEV)-cleavable 6His Tag. Palmitoylated cysteines (C88, C90, and C92-96) were mutated to serine as previously described¹⁷ (C6S mutant) to enable expression in Rosetta BL21 (DE3) cells. *E. coli* were grown in terrific broth (TB) at 37 °C, induced with 1mM IPTG in log phase, and grown for 3 hrs at 37 °C. Cells were collected and stored as frozen pellets at -80 °C. Pellets were resuspended in binding buffer (50 mM HEPES pH 7.4, 150 mM NaCl, 5 mM TCEP) supplemented with protease inhibitors (Roche cOmplete), sonicated, clarified, and supernatant was bound to Ni-NTA His-Bind Resin (Novagen) for 1hr at 4 °C. Resin was washed with ~10 column volumes of binding buffer, then protein was eluted from the resin with His elution buffer (50 mM HEPES pH 7.4, 150 mM NaCl, 5 mM TCEP, 500 mM imidazole). N-terminal His tag was removed by overnight dialysis with TEV protease at 4 °C. Digested material was applied to His-Bind resin to remove cleaved His tag, undigested material and TEV protease. Protein was further purified by size exclusion chromatography (SEC) (Superdex 75) in 50 mM HEPES pH 7.4, 150 mM NaCl, 5mM TCEP and 10% glycerol.

Protein production for X-ray crystallography

Human CHIP₂₁₋₁₅₄-TPR domain was expressed and purified as previously described⁴⁷. HsCHIC₂₁₅₄₋₁₆₅-c-term peptide at >95% purity was purchased from Lifetein. Lyophilized HsCHIC₂₁₅₄₋₁₆₅ -c-term peptide was dissolved in 25 mM HEPES pH 7.5 and 50 mM NaCl. Briefly, HsCHIP₂₁₋₁₅₄-TPR was amplified by PCR from the full-length human CHIP construct and cloned into the pHis||2 expression vector to encode for HsCHIP₂₁₋₁₅₄-TPR with an amino-terminal His₆ tag and an intervening TEV protease cleavage site. The HsCHIP₂₁₋₁₅₄-TPR plasmid was transformed into Rosetta2(DE3) *Escherichia coli* competent cells. Expression cultures in Terrific Broth (Fisher BioReagents) were grown at 37 °C until OD₆₀₀ reached 1.0, cooled on ice for 15 minutes, and induced by addition of 400 μM isopropyl β-D-1-thiogalactopyranoside (IPTG). Growth was continued for 20 hours at 18 °C after addition of IPTG prior to harvesting by centrifugation for 10 min at 8,000 × g. Frozen cells suspensions were thawed and lysed overnight with slow rotation at 4 °C. Lysate was clarified by centrifugation at 17,000 × g for 45 minutes, followed by filtration of lysate supernatant through a 0.45μM filter (Fisher Scientific). His₆-HsCHIP₂₁₋₁₅₄-TPR was purified by Ni²⁺-affinity chromatography using a 5mL HisTrap HP column (GE Healthcare) loaded in 25 mM HEPES pH 7.5 and 50 mM NaCl. Nonspecifically bound proteins were washed away with 50 mM imidazole and His₆-HsCHIP₂₁₋₁₅₄-TPR eluted in 500 mM imidazole. TEV protease was added at a protease:target protein ratio of 1:20 (w/w), and the mixture was incubated overnight in the presence of 5 mM β-mercaptoethanol. The protein mixture was loaded across a 5mL HisTrap HP column and the flowthrough was collected for further purification by size exclusion chromatography on a HiLoad 16/60 Superdex 75 column. Fractions were analyzed by SDS-PAGE and fractions containing pure HsCHIP₂₁₋₁₅₄-TPR were concentrated, frozen drop-wise in liquid nitrogen, and stored at -80 °C.

CRISPR KO cell line generation

Knockouts were generated using the Synthego Gene Knockout Kit v2 according to the manufacturer's protocol. Briefly, 500K cells were electroporated with Cas9-RNP complexes using a Lonza nucleofector kit (Program T-016 for K562, T-020 for U251) and grown in 6-well dishes. 72h after nucleofection, pooled knockouts were collected and assayed by western blot. Genomic DNA was extracted using the Qiagen DNEasy kit and PCR of the target loci analyzed using the Synthego ICE tool to confirm high knockout efficiency. Following knockout confirmation, clonal lines were isolated according to Giuliano et al.⁴⁸, then screened by western blot. Selected clones were again genotyped by PCR and ICE analysis (see Figure 1.10), and confirmed mycoplasma negative (ATCC assay) prior to banking.

Western blotting

Adherent cells were collected by scraping in ice-cold PBS, while centrifugation for 5 min @ 300xg was used for suspension cells. The resulting pellet was washed 1x with PBS, then snap frozen for storage or lysed directly in RIPA buffer (50 mM Tris pH 8.0, 150 mM NaCl, 1% Nonidet P40, 0.5% sodium deoxycholate, 0.1% SDS) supplemented with Roche cOmplete protease inhibitor cocktail. Lysates were incubated for 30 min on ice, then centrifuged at 21,000xg for 10 minutes at 4 °C. The soluble fraction was quantified by BCA assay and normalized to a concentration of 2 mg/mL, then mixed with 3X reducing Laemmli buffer and denatured for 5 minutes at 95 °C. Protein (20 µg) was loaded onto a 4-20% mini-TGX Stain-Free gel, and separated at 200V for 35 mins. For endogenous CHIC2 blots, which required more input for reliable protein detection, 50 to 100 µg material was loaded and the gel was stacked at 60V for 30 mins, followed by separation

at 160V for 45 mins. Stain free gels were then activated for 45s using a Chemidoc imager (Bio-Rad), and transferred to 0.2 μ m nitrocellulose membranes using the Bio-Rad Trans-Blot Turbo system. Blots were blocked in Intercept TBS blocking buffer (LI-COR) for 30 mins at RT, then incubated with primary antibody in blocking buffer overnight at 4 °C. The following day, blots were washed three times for 5 min each with TBS + 0.05% tween-20 (TBS-T), then incubated with 1:10,000 secondary antibodies (LI-COR) for 1h at RT. Blots were then washed for 3x5 min in TBS-T and imaged on a LI-COR Fc imaging system.

Immunoprecipitation

293T cells were seeded at a density of 500K cells / well in a 6-well plate (Corning 3335), grown overnight, then transfected using Lipofectamine-3000 according to the manufacturer's protocol. The following day, cells were harvested in ice-cold PBS, then lysed in ice-cold NP-40 lysis buffer (25 mM Tris-HCl pH 7.4, 150 mM NaCl, 1mM EDTA, 1% NP-40, 5% glycerol, Roche cOmplete protease inhibitor cocktail) by trituration followed by incubation on ice for 10 minutes. Lysates were centrifuged for 10 mins at 21,000xg, and the soluble fraction was harvested and quantified by BCA assay. An input sample was retained, and 100 μ g of lysate was then diluted to a final volume of 500 μ L in IP lysis buffer. Diluted lysate was added to 20 μ L of anti-myc magnetic resin (Pierce cat. 88843) or anti-FLAG magnetic resin (Millipore M8823) in a 1.5 mL low-binding tube (Eppendorf), then incubated at RT for 3 hours with end-over-end rotation. Following incubation, beads were washed with 3x500 μ L of IP lysis buffer. Proteins were then eluted by heating to 95 °C in 50 μ L of 1X Laemmli buffer for 5 mins, and processed for Western blotting as above.

***In vitro* ubiquitination**

Assays were conducted by preparing a solution of 50 nM E1, 500 nM E2, 125 μ M ubiquitin, 500 nM CHIP, 1.25 mM ATP / Mg, and 500 nM substrate in ubiquitination buffer (50 mM Tris, 50 mM KCl, pH 8.0). Reactions were prepared by generating 4 separate 4X stocks of E1/E2/ubiquitin, Ligase/Substrate, CHIC2 / peptide, and ATP+Mg²⁺ in ubiquitination buffer. Protein stocks were combined in equal ratios and equilibrated at RT for 10 minutes, followed by addition of the ATP+Mg²⁺ stock and mixing by pipette to ensure homogeneity. Aliquots of each reaction were removed at the indicated timepoints and quenched in 3X Laemmli buffer. E1 (E-304), UBE2D1 (E2-616), UBE2D1-Ub (E2-800), and Ubiquitin (U-100H) were all purchased from R&D Biosystems.

Competitive chemoproteomics assays

SILAC lysate prep: HEK293T cells were cultured in SILAC DMEM (Thermo) supplemented with 10% dialyzed FBS (Gibco), 483 μ M light or heavy Arginine (Sigma A8094 or Cambridge Isotope CNLM-539), and 1 mM light or heavy lysine (Sigma L9037 or Cambridge Isotope CNLM-291). Cell pellets were harvested and washed 2x with ice-cold PBS, then lysed on ice for 10 minutes in M-PER (Thermo) supplemented with Roche cOmplete protease inhibitor. Lysates were centrifuged at 21,000xg for 10 mins at 4 °C and the soluble fraction quantified by BCA assay, then normalized to a concentration of 2 mg/mL. Lysates were then aliquoted, snap frozen, and stored at -80 °C for future use.

Sample prep & crosslinking: For each sample, 0.5 mg each of light and heavy proteome was pipetted into separate wells of a 96-well PCR plate in 5 x 50 μ L aliquots. 2X solutions of

crosslinking probe (10 μ M each Hsp70 + Hsp90) +/- peptide competitor (100 μ M) were prepared in M-PER at a concentration of 2% DMSO. Each peptide solution (5 x 50 μ L) was then mixed 1:1 with the aliquoted lysate in the PCR plate (light lysate - competitor, heavy lysate + competitor) to yield a final solution of 1 mg/mL proteome, 5 μ M Hsp70/90 probes, +/- 50 μ M competitor, 1% DMSO. The resulting samples were incubated for 15 minutes at RT in the dark, then crosslinked under 365nm UV light in the PCR plate for 10 minutes using a 48W nail curing lamp (Sun X9 plus). No-UV controls were prepared as a single 250 μ L aliquot in an amber 1.5mL tube (Eppendorf). Following crosslinking, light and heavy aliquots for each sample were pooled in a single 15 mL falcon tube to yield 1 mg of total proteome per sample.

Protein enrichment & digestion: Pre-chilled methanol (-30 $^{\circ}$ C; 13 mL) was added to each sample, followed by incubation at -30 $^{\circ}$ C overnight to allow complete precipitation to occur. The next day, proteomes were pelleted for 10 mins at 3000xg at 4 $^{\circ}$ C. The resulting pellet was washed with 2x1 mL of chilled 1:1 methanol:chloroform, then the pellet was resuspended in 3 mL cold 4:1 methanol:chloroform and centrifuged. The pellet was briefly air-dried, resuspended in 500 μ L of freshly prepared 6M Urea, 0.2% SDS in PBS, then tip sonicated for 2x30 s at 40% power to ensure complete re-solubilization. Resuspended proteins were diluted with 1 mL of 0.2% SDS in PBS (2M Urea final), then added to 200 μ L of Pierce magnetic streptavidin resin (cat. # 8817) in a 2 mL low-binding tube (Eppendorf). Proteins were captured by continuous rotation at room temperature for 1.5 hours. Using a magnetic rack, beads were then washed with 2x1.75 mL of 0.2% SDS, changing to a new low-binding tube after each wash. Beads were then washed with 2x1.75 mL PBS, then 1.75 mL LC-MS water, and transferred to a new tube during the final wash. Beads were resuspended in 100 μ L of 8M Urea in 100 mM TEAB, mixed well, then reduced by

addition of 4 μ L of 0.5 M TCEP and incubation for 30 min at RT. Cysteines were alkylated with 8 μ L of 0.5 M iodoacetamide at RT in the dark for 30 min, and residual iodoacetamide was quenched by addition of 4 μ L 1 M DTT. Urea was diluted to 1 M by addition of 700 μ L of 100 mM TEAB, then 2 μ g of MS-grade trypsin/lys-C mix was added for on-bead digestion overnight at RT with end-over-end mixing. The following day, supernatants were removed and acidified with 200 μ L of 10% TFA, then desalted on Thermo SOLA SPE cartridges (cat # 03-150-391). Desalted peptides were dried on a Speedvac, resuspended in 2% acetonitrile with 0.1% formic acid with sonication, and analyzed by LC-MS/MS.

LC-MS/MS analysis: 1 μ g of peptides were injected onto a Thermo Scientific EASY-Spray C18 column (150 mm length, 75 μ m diameter, 3 μ m particle size) attached to a Dionex UltiMate 3000 NanoRSLC UHPLC. Separation was achieved using a 30-minute linear gradient from 3-40% acetonitrile / 0.1% formic acid at a flow rate of 300 nl/min, followed by a ramp to 80% acetonitrile for column wash prior to re-equilibration. Spectra were acquired on a Thermo Scientific Q-Exactive+ mass spectrometer running a top-12 method. MS1 spectra were acquired from 350-1500 m/z at a resolution of 70,000, with an AGC target of 3e6 and a maximum injection time of 180 ms. MS2 spectra were acquired at a resolution of 35,000 with an isolation width of 1.7 m/z, AGC target of 2e5, maximum injection time of 180 ms, and normalized collision energy of 27. Dynamic exclusion was set to 20s. Data was searched against a non-redundant human proteome database (Uniprot, downloaded 10/2019) using MaxQuant version 1.6.7. N-terminal acetylation and M oxidation were specified as variable modifications, and cysteine carbamidomethylation as a fixed modification. Heavy arginine and lysine modifications were specified as Arg10 and Lys8, respectively. For quantification, min ratio count was set to 2, unique and razor peptides were

allowed, and the “re-quantify” option was turned on. All other parameters were set as default. For quantitative analysis of TPR protein binding (as in Fig 2f), data were imported into Skyline for further refinement. A spectral library was generated from the MaxQuant search results, and peptides imported using a FASTA file containing all human CC-TPR proteins. Integration boundaries were manually inspected to ensure consistency across samples, and peptides exhibiting interferences or low quality spectra were excluded. The resulting light/heavy ratios were then exported and plotted in GraphPad PRISM 9.0.

TMT quantitative proteomics

Sample preparation: U251 cells were plated in 6-well plates at a density of 750K cells per well and grown until confluent, then harvested by scraping in ice-cold PBS. K562 cells were plated in 12-well plates at a density of 500K / mL, grown for 24h, then harvested by centrifugation. Cells were washed with 3x1 mL of PBS, then snap frozen prior to further processing using a PreOmics iST-NHS kit. Briefly, pellets were thawed and resuspended in 50 μ L of LYSE-NHS solution, then incubated at 95C for 10 minutes with intermittent vortexing every 2 minutes. DNA was sheared by bath sonication until lysates appeared clear, then protein concentration was determined by BCA assay and normalized to 1 mg/mL. Each sample (20 μ L) was then transferred to a 0.6 mL low-binding tube (Eppendorf) for digestion and labeling. DIGEST solution (20 μ L) was added to each sample, and samples were incubated at 37 °C and 500rpm on a thermomixer for 3 hours. Acetonitrile (15 μ L, LCMS-grade) was then added to each sample to achieve a concentration of ~30% v/v, followed by 100 μ g of TMT label (5 μ L of 20 μ g/ μ L stock). The labeling reaction was carried out at room temperature for 1h at 500 rpm on the thermomixer, then quenched with 6 μ L of 10% hydroxylamine (1% final) and incubation for 15 minutes at 500 rpm. STOP solution (40

μL) was then added, and samples were shaken for an additional 1 minute. Samples were pipetted up and down to ensure homogeneity, then pooled into a single tube. The pooled sample was then split between 2 PreOmics iST cartridges for desalting, and the eluates combined and dried on a Speedvac. Desalted peptides were then resuspended in 600 μL of 0.1% TFA with sonication, and half of the sample (~90 μg) was fractionated using the Pierce high pH reversed phase fractionation kit (cat # 84868). 8 fractions were collected at 12.5, 15, 17.5, 20, 22.5, 25, 50, and 80% acetonitrile and dried to completion via Speedvac. Peptide fractions were resuspended in 10 μL of 2% ACN / 0.1% FA, sonicated, and analyzed by LC-MS/MS.

LC-MS/MS analysis: 1 μg of peptides were injected onto a Thermo Scientific EASY-Spray C18 column (150 mm length, 75 μm diameter, 3 μm particle size) attached to a Dionex UltiMate 3000 NanoRSLC UHPLC. Separation was achieved using a 120-minute method composed of a linear gradient from 4-24% acetonitrile over 80 minutes at a flow rate of 200 nl/min, followed by a further ramp to 56% acetonitrile over 25 minutes at 300 nl/min, then a final ramp to 80% acetonitrile for column wash prior to re-equilibration. Spectra were acquired on a Thermo Scientific Q-Exactive+ mass spectrometer running a top-15 method. MS1 spectra were acquired from 375-1400 m/z at a resolution of 70,000, with an AGC target of 3e6 and a maximum injection time of 50 ms. MS2 spectra were acquired at a resolution of 35,000 with an isolation width of 0.7 m/z, AGC target of 1e5, maximum injection time of 100 ms, and normalized collision energy of 32. Dynamic exclusion was set to 30s. Samples were searched against a non-redundant human Uniprot database (downloaded 02/2023) using MaxQuant version 1.6.7. N-acetylation and M oxidation were included as variable modifications, and +113.084 Da was included as a fixed cysteine modification, per PreOmics protocol. MS2 TMT intensities were corrected for isotopic impurities

according to the manufacturer's CoA. All other settings were default. Reverse and contaminant matches were removed using Perseus, then protein intensities were median normalized and analyzed for differential expression using NormalyzerDE⁴⁹. Data was then exported for further analysis in R. Only proteins with 2 or more unique peptides were included unless otherwise indicated.

Flow cytometry

0.5 - 2 million cells were harvested by light dissociation using TrypLE (Gibco cat. 12-605-010) for 5 minutes at 37C followed by quenching with a 5x volume of complete media. Cell pellets were washed with 2mL of ice-cold FACS buffer (PBS (-Ca, Mg), 1% dialyzed FBS, 5 mM EDTA, 0.02% sodium azide), then resuspended in 100 μ L of FACS buffer on ice. 2 μ L of conjugated antibody (anti CD119-PE, Miltenyi Biotec cat # 130125874) or isotype control (IgG1-PE, Miltenyi Biotec cat # 130113450) was spiked into each sample, briefly vortexed, and incubated in the dark for 10 minutes. The antibody solution was diluted with 1.9 mL FACS buffer, then cells were centrifuged for 5 minutes at 300xg. The resulting pellet was resuspended in 500 μ L of FACS buffer, strained, and analyzed directly on a BD LSRFortessa X-14 flow cytometer. FlowJo software was used to select a viable, single-cell population based on forward and side scatter profiles, and IFNGR-positive cells were gated based on the isotype control.

Cell culture

All cell lines were maintained at 37C and 5% CO₂. HEK293T, HEK293 Flp-In T-REX, and U251 cells were maintained in DMEM (Gibco cat. # 11995065). K562 cells were maintained in IMDM (Gibco cat. # 12440053). All media was supplemented with 10% HI FBS (Gibco cat # 10438026).

Live-cell imaging

HEK-293 Flp-In T-REX cells expressing mEGFP-CHIC2 constructs were generated according to the manufacturer's instructions (<https://www.thermofisher.com/order/catalog/product/R78007>). Cells were seeded in 6-well plates, then transfected using LTX-3000 as above. The following day, cells were trypsinized and seeded at a density of 25,000 cells / well in 96-well imaging plates (Greiner cat. 655090), then allowed to grow overnight in media containing 10 ng/mL doxycycline. Prior to imaging the next day, cells were treated for 4 hours with the appropriate compound in complete media (100 nM Bafilomycin A1, 50 nM bortezomib), with the exception of Bromopalmitate which was added at a concentration of 25 μ M immediately upon dox induction the prior day. Following compound treatment, nuclei were stained with 5 μ g/mL Hoechst 33342 in HBSS for 5 minutes. Cells were washed with HBSS, then returned to complete media for imaging. Images were collected on an IN Cell 2000 confocal microscope and analyzed in Fiji.

Crystallization, X-ray crystallographic diffraction data collection, and structural refinement.

Crystals of the CHIP₂₁₋₁₅₄-TPR:CHIC2₁₅₄₋₁₆₅-c-term complex were obtained by sitting drop vapor diffusion in 96-well IntelliPlates (Art Robbins) set up with a Phoenix crystallization robot (Art Robbins). Protein and peptide were combined at 7 mg/mL concentration with a 3:1 peptide:protein ratio) was mixed with crystallization conditions from MCSG1-4 (Microlytic) and BCS sparse matrix crystallization screens at volumes of 400 nL CHIP/CHIC2 and 400 nL condition. Crystals of were harvested and frozen in liquid nitrogen within one month of setting up sitting drop vapor diffusion trials. Crystals were frozen in liquid nitrogen 60-90 days after setting up sitting drop

vapor diffusion trials. The CHIP₂₁₋₁₅₄-TPR:CHIC₂₁₅₄₋₁₆₅-c-term complex was crystallized in 0.05 M Magnesium sulfate heptahydrate 0.1 M HEPES pH 7.5, and 28 % v/v PEG Smear Medium. Harvested crystals were swished through LV CryoOil (MiTeGen) for cryoprotection immediately prior to freezing in liquid nitrogen. X-ray diffraction data were collected on beamline 4.2.2 at 1.000020 Å wavelength at the Advanced Light Source at Lawrence Berkeley National Laboratory. X-ray diffraction data were processed in XDS⁵⁰, followed by molecular replacement with PHASER⁵¹ using our prior CHIP-TPR structure (PDB ID 4KBQ, chain A) as the molecular replacement search model. Model building and refinement were performed iteratively using PHENIX⁵² and Coot⁵³. Coordinates and experimental data for the CHIP₂₁₋₁₅₄-TPR:CHIC₂₁₅₄₋₁₆₅-c-term complex were deposited in the PDB with accession code 8SUV. Geometrical and stereochemical validation was conducted using MolProbity⁴⁴. All figures were prepared using UCSF Chimera⁵⁴.

***C. elegans* Assays**

Strains – The following strains were used for experiments described in this manuscript:

N2 (Bristol) wild-type, *chn-1 (by155)* I, *tag-266 (ok2462)* III, *tag-266 (syb5138)* III, *wlds51 (PF49H12.4::GFP)*. All strains were maintained at 20 °C as described previously⁵⁵.

Longevity – Briefly, a timed egg lay was performed to gather an age-synchronized population of animals. Animals were plated on 60-mm NGM agar plates containing a thin lawn of OP50 *Escherichia coli* spotted the day before the experiment. Each day, or every other day, the number of living and dead worms were recorded until there were no living animals remaining. Longevity

assays were performed using 75 animals over 3 independent experiments by an experimenter blinded to the genotypes of the animals being tested.

Quantification of PVD Degeneration – Fluorescence imaging of *wlds51* ($P_{F49H12.4}::GFP$) was performed as follows. *wlds51* expresses GFP in the neuronal pair PVDR and PVDL, which have extensive dendritic branching. Quantification of PVD neurodegeneration was performed as described³¹. Briefly, Larval-stage 4 (L4) animals were immobilized in a droplet of M9 containing 2.5 mM Levamisole (Tetramisole, Sigma) and placed on a 2% agarose pad. PVD neurons were imaged using 20× magnification on a Zeiss Axio Imager M2. Animals were scored for PVD neuron branching and bead-like puncta in dendrites. Degeneration assays were performed using 30 animals over 3 independent experiments by an experimenter blinded to the genotypes of the animals being tested.

Antibodies

Rb CHIP (Abcam EPR4447, 1:2000), Ms CHIC2 (sc-515175, 1:500), Rb Myc (sc-789, 1:500), Ms Hsp70 (SCBT sc-137239, 1:500), Ms Hsp90 (SCBT sc-13119, 1:500), Rb STIP1/HOP (Abcam EPR6605, 1:2000), Ms Tau5 (Invitrogen AHB0042, 1:1000), Ms Ubiquitin (CST 3936, 1:2000), Rb UBE2D1 (Invitrogen PA576645, 1:2000), Rb FLAG (CST 14793, 1:2000), Rb GAPDH (CST 2118S, 1:2000), Ms Tubulin (CST 2144S, 1:2000), Ms IFNGR (sc-28363, 1:500), anti CD119-PE (Miltenyi Biotec 130125874), IgG1-PE (Miltenyi Biotec 130113450).

Data availability

Raw proteomic data have been deposited to the ProteomeXchange consortium via the PRIDE partner repository with the identifiers PXD043803 (TMT proteomics of CHIC2 and CHIP knockout) and PXD043804 (competitive chemoproteomics of TPR cochaperone proteins). Processed proteomic data are provided in the supplementary information.

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1.10 Author Contributions

M.D.C. conceived the study, designed, and performed experiments. M.H. designed and performed *C. elegans* experiments. E.C.C. and C.M.N. aided in protein expression / purification and helped design experiments. M.R. designed and helped develop the chemical proteomics assay. A.R.I.S., A.R.C., L.E.M., J.C.N., and R.C.P. performed X-ray crystallography and structure refinement. M.C. and J.G. wrote the manuscript, and all authors approved the final version.

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Chapter 2: Beyond CHIC2: Discovery of additional chaperone-independent CHIP substrates

2.1 Abstract

In this second chapter, I explore additional chaperone-independent interactors beyond CHIC2 that are predicted by CHIPscore. In preliminary results, I demonstrate interactions between CHIP and three additional proteins: CHIC1, TMEM185A, and TMEM185B. These proteins are completely uncharacterized and reside at different subcellular localizations, suggesting that CHIP may be regulated at various locations within the cell through mechanisms that are not yet understood. This work opens substantial new avenues upon which future studies should be based.

2.2 Introduction

In the previous chapter, I demonstrated the biological importance of a chaperone-independent interaction between CHIP and the membrane-anchored protein CHIC2. This discovery was motivated in large part by an association between CHIC2 and CHIP in the Cancer Dependency Map database, which suggested that their interaction was biologically important and motivated us to explore it in depth. However, other putative substrates predicted by CHIPscore do not exhibit such an association in the DepMap or other functional genomics databases. Therefore, it is unclear which substrates predicted by CHIPscore might be biologically relevant in cells.

This problem is compounded by the fact that CHIPscore is imperfect. CHIPscore is based on binding data from a combinatorial peptide library screen¹, which measured the affinity of each sidechain along CHIP's TPR. To predict the binding affinity of an untested peptide sequence, the contribution of each individual amino acid based on this screening data is summed to yield its

CHIPscore (**Figure 2.1a**). This scoring function can then be applied to the entire proteome to predict potential CHIP substrates. While this approach successfully enriches for peptides with significantly improved affinity relative to the Hsps, it neglects the potential for both positive and negative cooperativity between amino acids when they are linked together in the same peptide. Thus, CHIPscore may predict false positive binding events.

Here, I empirically test CHIPscore's predictions in order to screen out such false positives, then use additional published datasets to reveal novel, biologically relevant interactors of CHIP. Through this process I uncover interactions between CHIP and three additional proteins: CHIC1, TMEM185A, and TMEM185B, proteins that are completely uncharacterized and reside at various subcellular localizations. Together with our findings regarding CHIC2, these results imply that there are substantial features of CHIP's functions that are not currently understood.

2.3 Results

An empirical assessment of CHIPscore highlights limitations and opportunities

In order to screen out false-positive C-termini predicted by CHIPscore, I used a competition fluorescence polarization assay to empirically determine the affinity of each peptide within the human proteome that is predicted to bind with higher affinity than Hsp90 (**Figure 2.1a**). Given the limitations of CHIPscore discussed above, it was not surprising that the correlation between CHIPscore and affinity in this assay was only modest (**Figure 2.1b**). Nevertheless, many of the known chaperone-independent interactors that have been characterized by us or others were

present in this dataset (**Figure 2.1b, blue circles**), demonstrating the utility of CHIPscore in prioritizing putative substrates for future studies.

These experiments also allowed us to exclude several putative interactors that did not bind at all (**Figure 2.1c**). Several factors likely contributed to this discrepancy between CHIPscore's predictions and reality. For the CD72 peptide (Ac-FRFPD), steric clashes between the P5 phenylalanine and the "hydrophobic shelf" formed by F99 in CHIP's TPR domain likely prohibited binding. For CTSL2 and ACHG (Ac-LLPPD and Ac-LPSPD), prolines at positions other than P2 likely disrupted the ability for the peptides to bind in their canonical "kinked" conformation within CHIP's TPR¹. Finally, the P3 glycine in TXLNB (Ac-LEGVD) likely impaired binding by increasing the entropic cost paid. However, the complete lack of binding we observed is surprising for this peptide, and thus there may be additional factors at play, too.

Together, these results highlight that a CHIPscore greater than Hsp90 is useful as a binary classifier for putative interactors, but that the overall scoring function needs further refinement in order to serve as a rank-ordering system. Incorporation of score penalties that take into account steric clashes or conformational constraints would likely improve CHIPscore's accuracy, and should be considered in future work.

Comparison of CHIC2 and its paralog CHIC1 reveals a distinct subcellular localization

During our initial work on CHIC2, we noted that there is also a paralog within the human proteome, CHIC1, that possesses a substantially similar domain architecture (**Figure 2.2a**). The two proteins are nearly identical in primary sequence, except for a long, disordered N-terminal

extension in CHIC1. Both proteins also possess the same membrane-targeting CHIC motif and share identical C-terminal sequences (IFRPD). Indeed, CHIC1 is able to recruit CHIP in the same fashion as CHIC2, an interaction that shares the same dependency on its C-terminal aspartate (**Figure 2.2c**). Given these similarities, we were therefore surprised that CHIC1 did not also share a similar relationship with CHIP in the DepMap database.

A first clue came when we performed immunofluorescence in HEK293 cells, which revealed that a myc-tagged CHIC1 construct is predominantly nuclear localized (**Figure 2.2b**). This is in stark contrast to CHIC2, which appeared primarily in the vesicles and was excluded from the nucleus (**Figure 2.2b**). This result suggests that the N-terminal extension in CHIC1 possesses a nuclear localization sequence; however, searching this sequence through various online tools did not reveal a canonical motif of any kind. Therefore, CHIC1 may transit into the nucleus through a non-canonical transport mechanism.

In order to further explore potential differences in the subcellular environments occupied by CHIC2 and CHIC1, we performed APEX proximity labeling with each protein (**Figure 2.3**). Both fusion constructs expressed well and were able to efficiently label proteins in their proximity (**Figure 2.3b**), enabling us to carry out a TMT 6-plex proteomics experiment (**Figure 2.3a**). We also included cytosolic (FLAG-APEX-NES) and ER-membrane targeted (ERM-APEX) constructs in order to calculate relative enrichment ratios. Unfortunately, however, fusion with the APEX enzyme appeared to interfere with the localization of both constructs relative to their untagged versions (**Figure 2.3d**), inducing what appeared to be substantial ER-localization. In addition, the nuclear localization of APEX-CHIC1 was perturbed, further supporting the importance of

CHIC1's N-terminus in mediating this localization. These limitations necessitate caution when interpreting the proteomics data, as artefactual mislocalization may have altered the results.

Nevertheless, examining the proteomics data reveals some interesting trends. Relative to the cytosolic construct, APEX-CHIC2 enriched for a variety of vesicular and membrane-associated components, including endosomes, phagocytic vesicles, and components of the lysosome (**Figure 2.3c**). While the enclosed nature of vesicles limits our ability to assign direct CHIC2 interactors with this approach, these results are consistent with our hypothesis that CHIC2 is trafficked to the plasma membrane and then internalized through the endocytic pathway. Surprisingly, the primary interactors that we observed for APEX-CHIC1 were components of the ribosome and nucleus (**Figure 2.3c**). Since ribosomes anchor to the cytosolic face of the ER membrane, we first thought that this might be caused by the putative ER-mislocalization that we observed in our microscopy experiments. However, the ERM-APEX construct, which is localized to this same location, did not show an enrichment for the same ribosomal components, suggesting that this enrichment was not artefactual.

Upon examination of microscopy data from the Human Protein Atlas², we noticed that endogenous CHIC1 is substantially localized to nuclear speckles and other nuclear bodies. Since ribosomes are assembled within the nucleolus, localization of CHIC1 to this location or a proximal nuclear compartment could explain the enrichment for ribosomes and nuclear proteins in our dataset. This is intriguing since CHIP and other proteostasis factors are known to translocate to the nucleolus upon stress³. Therefore, CHIC1's role might be to restrict CHIP function at a distinct subcellular location to CHIC2, perhaps when CHIP changes its localization in response to proteotoxic stress.

However, given the preliminary nature of this data and the limitations discussed above, substantial validation would be required to confirm this hypothesis.

Identification of TMEM185A and TMEM185B as chaperone-independent CHIP substrates

In search of additional biological evidence for chaperone-independent interactors beyond the DepMap, I turned to a recently published dataset that characterized the proteomic changes induced upon CHIP knockout in two different melanoma cell lines⁴. Analysis of these datasets revealed significant increases in the levels of two proteins with high CHIPscores, TMEM185A and TMEM185B (**Figure 2.4a**). Strikingly, TMEM185B was the most significantly upregulated protein in response to CHIP knockout in D10 cells, suggesting a strong interaction between it and CHIP. Indeed, plotting the fold-change of TMEM185A/B compared to their CHIPscores produces results similar to that observed with CHIC2, suggesting that these chaperone-independent CHIP complexes might be biologically important (**Figure 2.4b**).

TMEM185A and TMEM185B are 7-transmembrane proteins of unknown function that are expressed in the endoplasmic reticulum² (**Figure 2.5b**), and their domain architecture suggests a topology that is capable of CHIP recruitment through similar EEVD-like motifs at their C-termini (**Figure 2.5a**). Indeed, co-IP studies in 293T cells showed that these proteins form a chaperone-independent complex with CHIP (**Figure 2.5c**), and previous affinity-purification MS studies of CHIP have also identified these two proteins as interactors⁵. CHIC2 was excluded from this complex (**Figure 2.5c**), suggesting that TMEM185A/B assemble a distinct complex with CHIP at the ER. While the functions of these protein complexes are not yet known, their existence implies

that chaperone-independent interactions may regulate CHIP function at yet another, distinct subcellular localization.

2.4 Discussion

In this chapter, I extended our findings beyond CHIC2 to include 3 additional chaperone-independent CHIP substrates: CHIC1, TMEM185A, and TMEM185B. Despite its sequence similarity to CHIC2, CHIC1 appears likely to regulate CHIP function in the nucleus as opposed to the membrane. While preliminary, our proximity labeling data also suggests a potential link between CHIC1 and ribosomal biology in the nucleus that merits further investigation. Finally, CHIP's interaction with the entirely uncharacterized proteins TMEM185A/B presents yet another mystery that needs solving. Together, these results imply a substantial role for chaperone-independent interactors in shaping CHIP behavior at distinct subcellular localizations. Formation of such complexes may be further modulated by response to stress stimuli, as previous work has revealed hundreds of additional EEVD-like motifs that are generated by proteolysis¹. We anticipate that additional, important CHIP partners remain to be discovered and characterized.

These discoveries also have significant implications for our understanding of the cell biology of the broader TPR cochaperone family. TPR cochaperones have historically been assumed to only interact with EEVD motifs; however, our work suggests that selective TPR binding by non-EEVD ligands may be more widespread than currently appreciated. The binding groove of CC-TPRs is only loosely conserved, raising the possibility that additional selective, c-terminal interactions may have evolved between particular family members and as-yet undiscovered binding partners. We are intrigued by the potential for such interactions to modulate chaperone complexes within subcellular microenvironments, providing opportunities to tailor the behavior of the proteostasis

network to the needs of sub-proteomes within the cell. Future studies should seek to determine the generality of this mechanism.

2.5 Figures

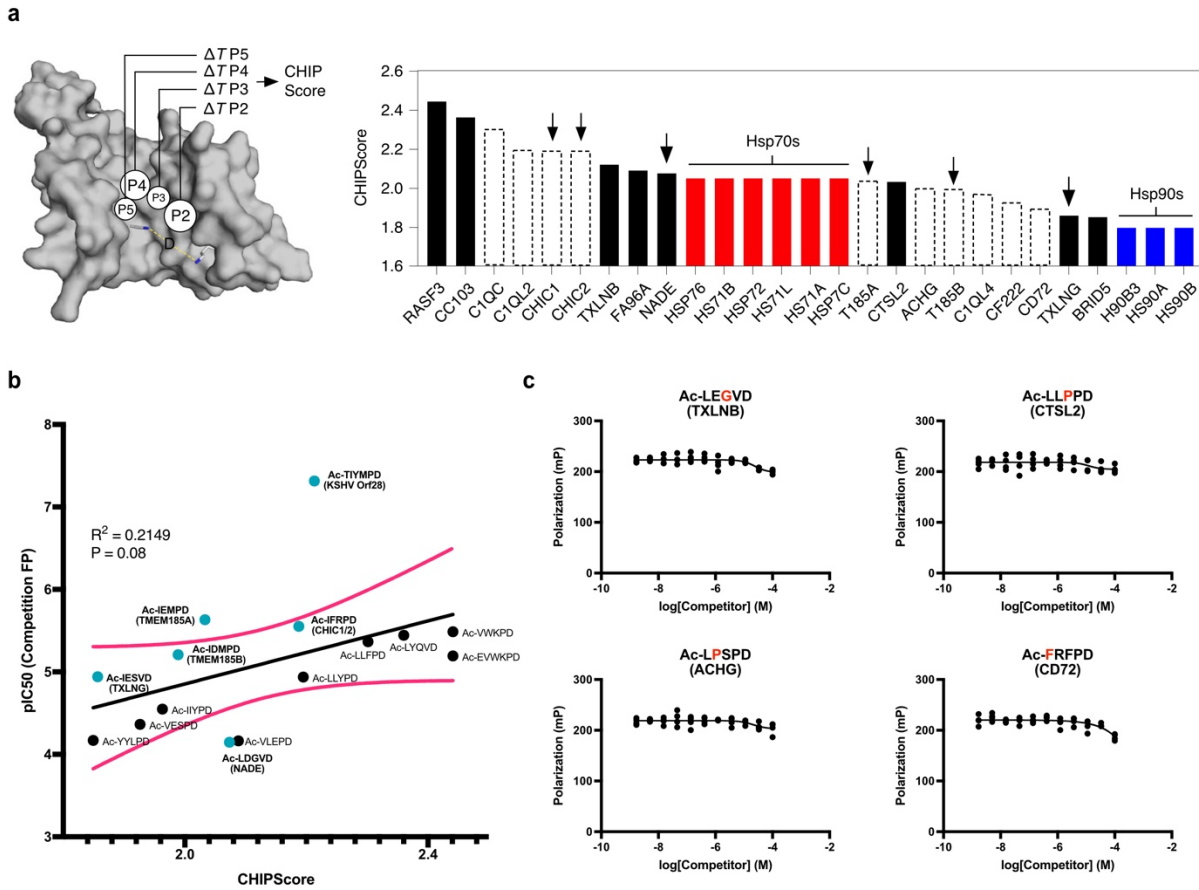


Figure 2.1 Empirical validation of CHIPscore using competition FP

a) Overview of the CHIPScore calculation and its predicted binding partners within the human C-terminome (adapted from Ravalin et al.¹). The set of peptides with a higher CHIPscore than Hsp90 is relatively small, though it contains many of the known chaperone-independent binders characterized by us or others (arrows). **b)** The correlation between CHIPscore and the empirically determined CHIP binding affinity of 5-mer peptides corresponding to the sequences in panel a) is relatively low. Nevertheless, this set has a relatively high percentage of true interactors (blue dots), indicating CHIPscore's utility as a binary classifier rather than rank-ordering function. Peptides that did not bind (and thus had no pIC50) were excluded from the plot and correlation calculation. **c)** Four peptides that were predicted by CHIPscore to bind, but did not validate. The amino acids that were likely responsible for introducing negative cooperativity or steric clashes, thus perturbing binding, are highlighted in red.

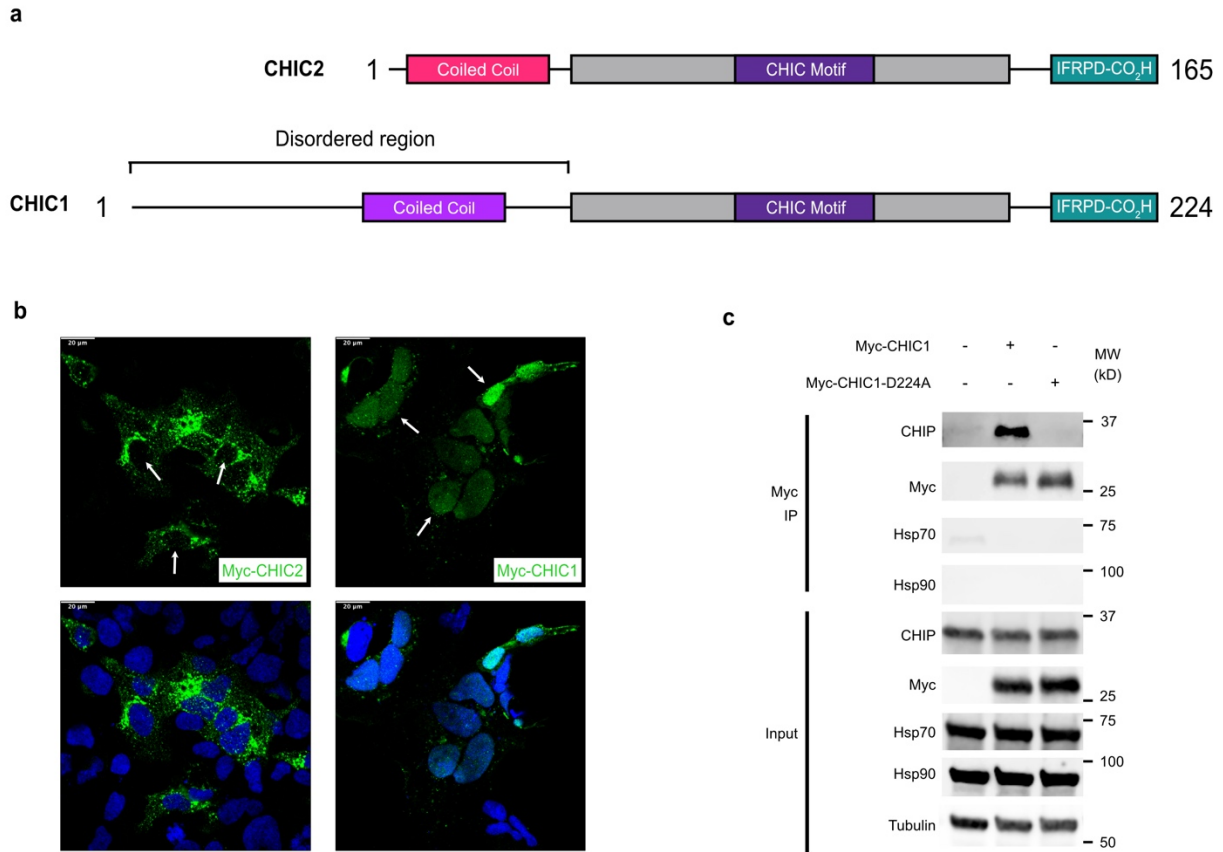


Figure 2.2 Comparison of the domain architecture and subcellular localization of CHIC2 and CHIC1

a) Domain architecture of CHIC2 and CHIC1. The proteins differ primarily in their N-terminal regions, where CHIC1 has a long, disordered region as compared to CHIC2's short coiled-coil. This region is likely responsible for the nuclear localization that we observe, though it does not contain a NLS as predicted by various online tools. The EEVD-like motif shared by both proteins is colored in blue. **b)** Immunofluorescence microscopy results demonstrating nuclear localization of myc-CHIC1 (arrows) in HEK293 cells, compared to the primarily vesicular localization of myc-CHIC2. Myc-CHIC2 seems excluded from the nucleus (arrows). Scale bars (upper left) are 20 μm . **c)** Co-immunoprecipitation of myc-CHIC1 and CHIP in HEK293T cells demonstrates a dependence on the equivalent C-terminal aspartate as in CHIC2. Results are representative of independent experiments performed in duplicate.

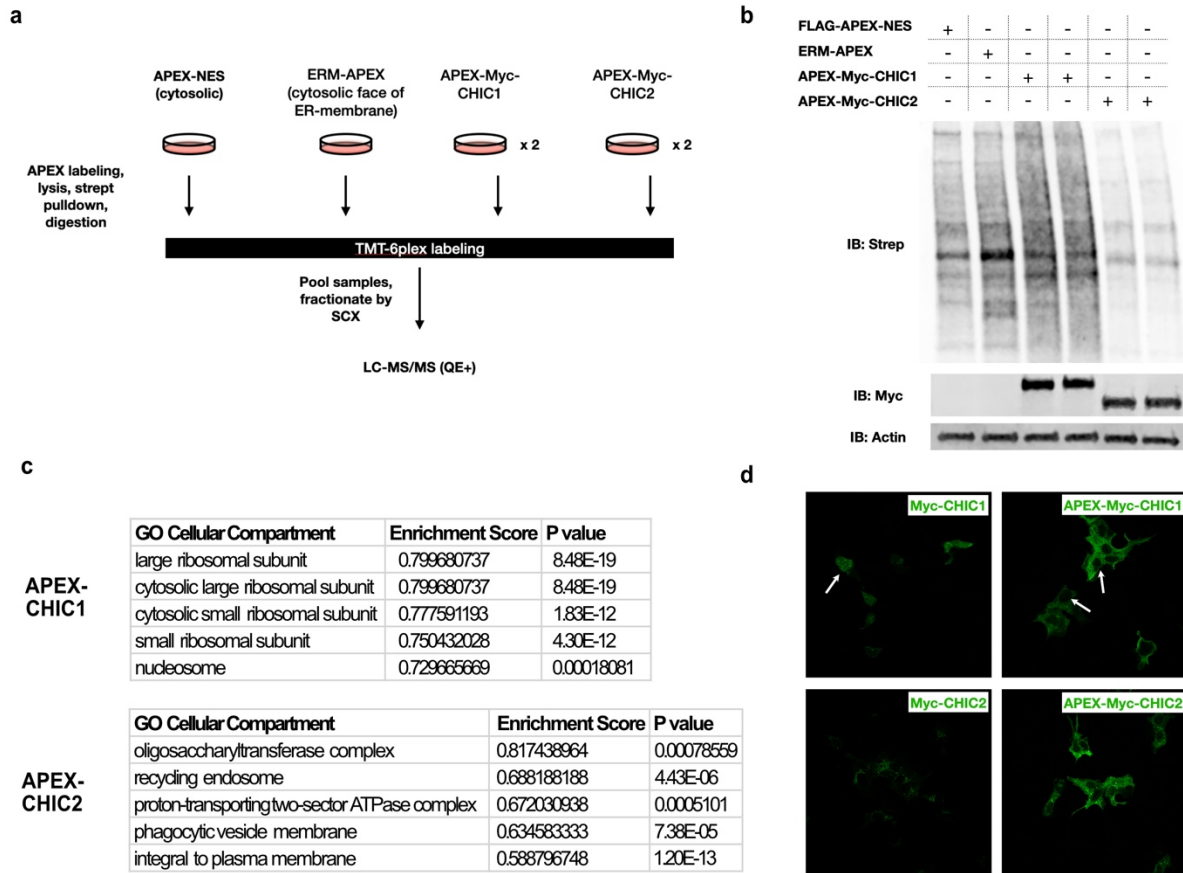


Figure 2.3 An APEX proximity labeling approach for comparing the interactome of CHIC1 and CHIC2

a) Design of the TMT 6-plex proteomics experiment. **b)** Western blots demonstrating effective APEX-mediated biotinylation (streptavidin blot) by all 4 constructs in the experiment. **c)** GO enrichment analysis of proteins enriched by CHIC1 and CHIC2 APEX constructs relative to the cytosolic control (FLAG-APEX-NES). The top 5 GO Cellular Compartments are listed for each construct. **d)** Immunofluorescence in HEK293 cells demonstrating the impact of N-terminal APEX fusion on the localization of CHIC1 and CHIC2. Both proteins, but especially CHIC1, are significantly relocalized relative to their myc-tagged counterparts. Therefore, the APEX proteomics results must be interpreted with caution.

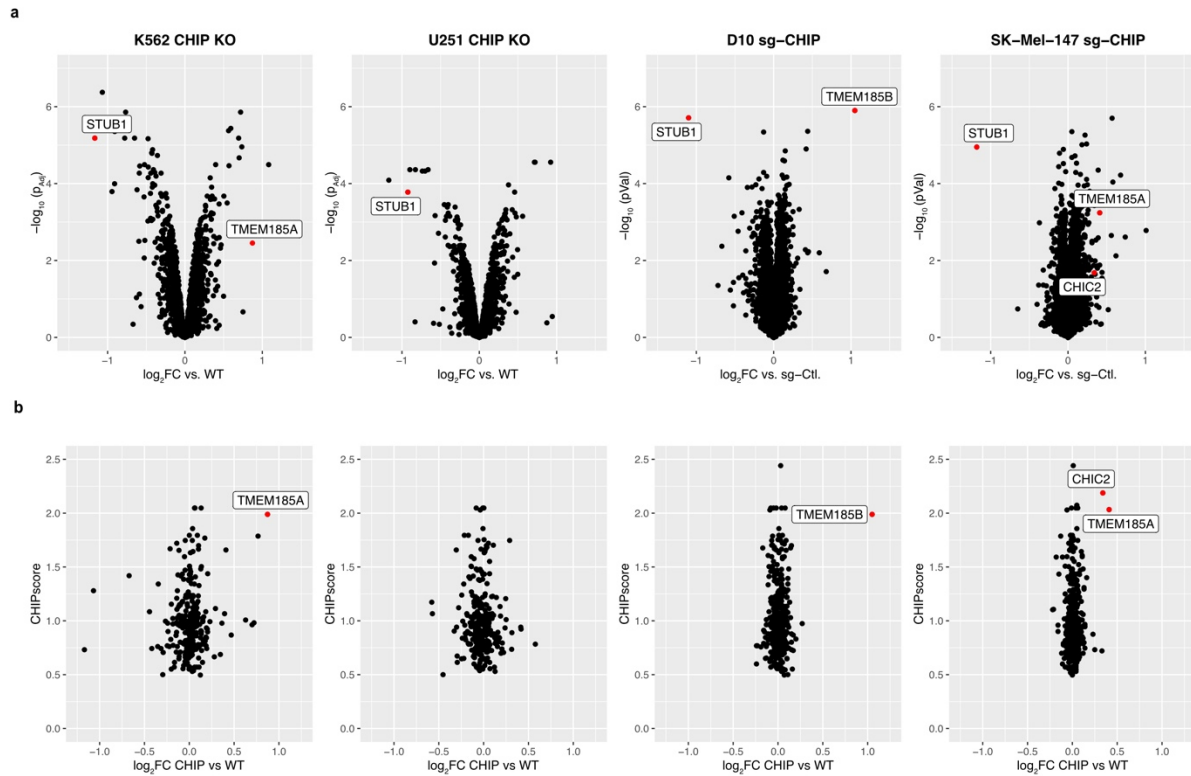


Figure 2.4 Proteomics of CHIP knockout across various cell types reveals significant regulation of the uncharacterized proteins TMEM185A and TMEM185B

a) Quantitative proteomics demonstrates that the levels of TMEM185A/B are consistently elevated in response to CHIP knockout across cell lines. In D10 cells, TMEM185B is the most strongly regulated protein. Note that TMEM185A was only identified by a single peptide in K562 cells, and was not identified in U251. **b)** Similar to what is observed for CHIC2, plotting the fold-change of TMEM185A/B compared to their CHIPScores suggests that these chaperone-independent CHIP complexes might be biologically important.

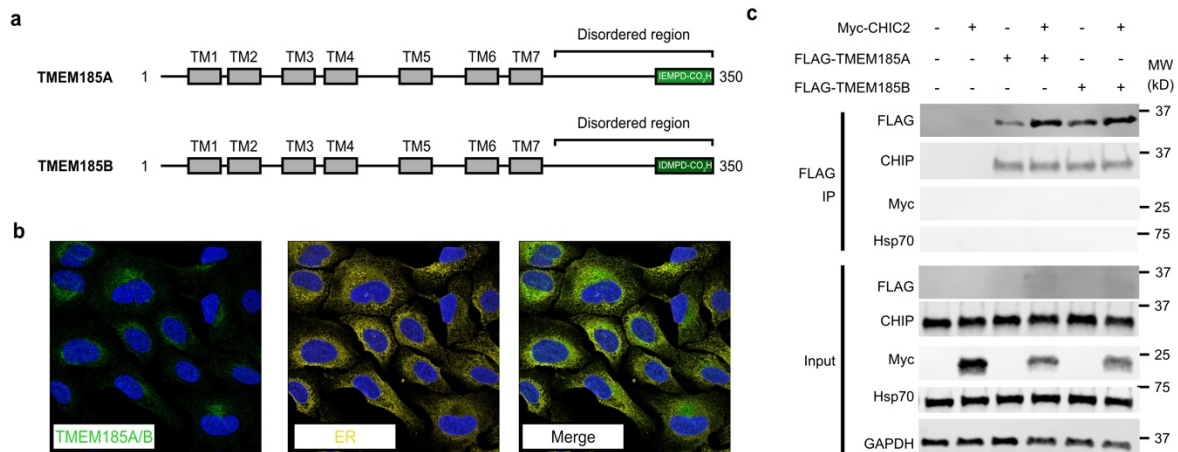


Figure 2.5 Domain architecture and subcellular localization of TMEM185A and TMEM185B

a) Domain architecture of TMEM185A/B, which are 7-transmembrane proteins of unknown function. The EEVD-like motif of each protein is highlighted in green. **b)** Immunofluorescence microscopy from the Human Protein Atlas² reveals a putative ER localization for TMEM185A/B in U2-OS cells. Antibody HPA071744 (which cannot discriminate between the two proteins) was used for staining, and nuclei were stained with DAPI. **c)** Co-immunoprecipitation of TMEM185A and TMEM185B from HEK293T cells shows an interaction with CHIP, but that CHIC2 is excluded. Moreover, over-expression of CHIC2 does not seem to interfere with the TMEM185A/B interaction with CHIP. Together, these results suggest that the TMEM185A/B and CHIC2 complexes with CHIP are distinct.

2.6 Supplemental files

Supplemental Dataset 2.1: APEX proteomics of CHIC2 and CHIC1.

Processed proteomics data from APEX proximity labeling experiment (MaxQuant output).

Supplemental Dataset 2.2: GO enrichment analysis of proteins

Enrichment analysis of protein compartments and families relative to a cytosolic construct (FLAG-APEX).

2.7 Materials and Methods

For western blotting, immunoprecipitation, fluorescence polarization, and quantitative proteomics of CHIP knockout lines, see Chapter 1 Methods.

Immunofluorescence

HEK-293 cells were seeded on poly-lysine coated coverslips in 12-well dishes and grown overnight. The following day, cells were transfected using LTX-3000 according to the manufacturer's protocol, then grown overnight. The next day, cells were stained according to Stadler et al⁶. Briefly, media was aspirated and cells were fixed using 4% PFA in media (DMEM + 10% FBS) on ice for 15 minutes. Fixed wells were washed 2x with PBS at RT, then incubated overnight at 4C in 500 μ L of primary antibody (1 μ g/mL Ms anti myc, Invitrogen cat. #13-500) diluted in blocking / permeabilization buffer (PBS + 4% FBS, 0.1% saponin). The next day, primary antibody was aspirated and cells washed in PBS for 4x10 mins at RT. Secondary antibody (Invitrogen anti-MS AF-488, cat # A-11001) was diluted to 1 μ g/mL in blocking / permeabilization buffer, and 500 μ L added to each well for 1.5 hours at RT. Nuclei were stained with 1 μ g/mL Hoescht 33342 in PBS for 5 minutes, then cells were washed with PBS for 4x10 mins at RT. Coverslips were mounted onto slides using ProLong Gold Antifade Mountant (Thermo cat #P10144) and allowed to cure overnight at RT while protected from light. Images were collected on a Leica SP8 confocal microscope, and processed in Fiji.

APEX Proteomics

APEX labeling & protein enrichment

Briefly, HEK293 cells were plated at a density of 6.0×10^6 cells / 10 mL media in 10 cm dishes, then grown overnight. The following day, cells were transfected with the appropriate APEX

constructs using LTX-3000 according to the manufacturer's protocol, then grown overnight. The following day, media was aspirated and replaced with 10 mL of pre-warmed complete DMEM containing 500 μ M of biotin-phenol, then cells were incubated at 37C for 1 hour. Labeling was initiated by addition of 10 μ L of 1M H₂O₂, followed by immediate swirling of the plate. After 60s of incubation, labeling media was aspirated and the reaction quenched by washing with 3x5mL of ice-cold quenching buffer (DPBS supplemented with 10 mM sodium ascorbate, 5 mM Trolox, 10 mM sodium azide). Cells were harvested in 5mL of quenching buffer + 5mM EDTA, spun down at 300xg for 5 minutes, then snap-frozen. Sample preparation for mass spectrometry was then performed as in Kalocsay et al.⁷.

LC-MS/MS analysis

1 μ g of peptides were injected onto a Thermo Scientific EASY-Spray C18 column (150 mm length, 75 μ m diameter, 3 μ m particle size) attached to a Dionex UltiMate 3000 NanoRSLC UHPLC. Separation was achieved using a 120-minute method composed of a linear gradient from 4-24% acetonitrile over 80 minutes at a flow rate of 200 nl/min, followed by a further ramp to 56% acetonitrile over 25 minutes at 300 nl/min, then a final ramp to 80% acetonitrile for column wash prior to re-equilibration. Spectra were acquired on a Thermo Scientific Q-Exactive+ mass spectrometer running a top-15 method. MS1 spectra were acquired from 375-1400 m/z at a resolution of 70,000, with an AGC target of 3e6 and a maximum injection time of 50 ms. MS2 spectra were acquired at a resolution of 35,000 with an isolation width of 0.7 m/z, AGC target of 1e5, maximum injection time of 100 ms, and normalized collision energy of 32. Dynamic exclusion was set to 30s. Samples were searched against a non-redundant human Uniprot database using MaxQuant version 1.6.7. N-acetylation and M oxidation were included as variable

modifications, and cysteine carbamidomethylation was included as a fixed modification. MS2 TMT intensities were corrected for isotopic impurities according to the manufacturer's CoA. All other settings were default. Reverse and contaminant matches were removed, and additional analyses were performed in Perseus.

2.8 Acknowledgements

We would like to thank Arun Wiita and Emilio Ramos for their assistance in conducting and interpreting our proteomics experiments.

2.9 References

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