1. Li, M., Hsieh, K.-Y., Liu, H., Zhang, S., Gao, Y., Gong, Q., Zhang, K.*, **Chang, C.-I***, and Li, S.* (2026) "Bifurcated assembly pathway and dual function of MtaLonC revealed by cryo-EM analysis." *Fundamental Research* 6, 879-884. (First published online April 19, 2024)
2. Wang, H.-J., Kuan, Y.-E., Ho, M.-R.*, and **Chang, C.-I*** (2025) "Structural basis for the allosteric activation of Lon by the heat shock protein LarA." *Nature Communications*, 16, 2212.
3. Wang, S., Huang, C.-H., Lin, T.-S., Yeh, Y.-Q., Fan, Y.-S., Wang, S.-W., Tseng, H.-C., Huang, S.-J., Chang, Y.-Y., Jeng, U-S., **Chang, C.-I**, and Tzeng, S.-R.* (2024) "Structural basis for recruitment of peptidoglycan endopeptidase MepS by lipoprotein NlpI." *Nature Communications*, 15, 5461.
4. Li, S.*, Hsieh, K.-Y., Kuo, C.-I, Lin, T.-C., Lee, S.-H., Chen, Y.-R., Wang, C.-H., Ho. M.-R., Ting, S.-Y., Zhang, K.*, and **Chang, C.-I*** (2023) "A *5+1* assemble-to-activate mechanism of the Lon proteolytic machine." *Nature Communications* 14, 7340.
5. Wang, H.-J., Hernández-Rocamora, V.M., Kuo, C.-I, Hsieh, K.-Y., Lee, S.-H., Ho, M.-R., Tu, Z., Vollmer, W.*, and **Chang, C.-I*** (2023) "Structural basis for the hydrolytic activity of the transpeptidase-like protein DpaA to detach Braun's lipoprotein from peptidoglycan." *mBio*, 14, e0137923.
6. Lee, M.-S., Hsieh, K.-Y., Kuo, C.-I, Lee, S.-H., Garde, S., Reddy, M., and **Chang, C.-I*** (2022) "Structural basis for the peptidoglycan editing activity of YfiH." *mBio*, 13, e03646-21.
7. Li, S., Hsieh, K.-Y., Kuo, C.-I, Su, S.-C., Huang, K.-F., Zhang, K.*, and **Chang, C.-I*** (2021) "Processive cleavage of substrate at individual proteolytic active sites of the Lon protease complex." *Science Advances,* 7, eabj9537.
8. Li, S., Hsieh, K.-Y., Kuo, C.-I, Lee, S.-H., Pintilie ,G.D., Zhang, K.*, and **Chang, C.-I*** (2021) "Complete three-dimensional structures of the Lon protease translocating a protein substrate." *Science Advances,* 7, eabj7835.
9. Li, S., Hsieh, K.-Y., Su, S.-C., Pintilie, G.D., Zhang, K.*, and **Chang, C.-I*** (2021) "Molecular basis for ATPase-powered substrate translocation by the Lon AAA+ protease." *Journal of Biological Chemistry*, 297, 101239.
10. Tzeng, S.-R.*, Tseng, Y.-C., Lin, C.-C., Hsu, C.-Y., Huang, S.-J., Kuo, Y.-T., and **Chang, C.-I*** (2021) "Molecular insights into substrate recognition and discrimination by the N-terminal domain of Lon AAA+ protease." *eLife,* 10, e64056.
11. Chueh, C.-K., Som, N., Ke, L.-C., Ho, M.-R., Reddy, M., and **Chang, C.-I*** (2019) Structural basis for the differential regulatory roles of the PDZ domain in C-terminal processing proteases. *mBio 10, e01129-19*.
12. Su, M.-Y., Som, N., Wu, C.-Y., Su, S.-C., Kuo, Y.-T., Ke, L.-C., Ho, M.-R., Tzeng, S.-R., Teng, C.-H., Mengin-Lecreulx, D., Reddy, M., and **Chang, C.-I*** (2017) Structural basis of adaptor-mediated protein degradation by the tail-specific PDZ-protease Prc. *Nature Communications*, 8, 1516.
13. Lin, C.-C., Su, S.-C., Su, M.-Y., Liang, P.-H., Fang, C.-C., Wu, S.-H., and **Chang, C.-I*** (2016) Structural insights into the allosteric operation of the Lon AAA+ protease. *Structure*, 24, 667-675.
14. Su, S.-C., Lin, C.-C., Tai, H.-C., Ho, M.-R., Chang, M., Babu, S., Liao, J.-H., Wu, S.-H, Chang, Y.-C., Lim, C., and **Chang, C.-I*** (2016) Structural basis for the magnesium-dependent activation and hexamerization of the Lon AAA+ protease. *Structure*, 24, 676-686.

15. Meyer, P.A., Socias, S., Key, J., Ransey, E., Tjon, E.C., Buschiazzo, A., Lei, M., Botka, C., Withrow, J., Neau, D.B., Rajashankar, K., Anderson, K.S., Baxter, R., Blacklow, S., Boggon, T., Bonvin, A., Borek, D, Brett, T., Caflisch, A., **Chang, C.-I**, Chazin, W., Corbett, K.D., Cosgrove, M., Crosson, S., Dhe-Paganon, S., Di Cera, E., Drennan, C., Eck, M., Eichman, B., Fan, Q., Ferre-D'Amare, A., Fraser, J.S., Fromme, J.C., Garcia, K.C., Gaudet, R., Gong, P., Harrison, S, Heldwein, E., Jia, Z., Keenan, R., Kruse, A, Kvansakul, M., McLellan, J., Modis, Y., Nam, Y., Otwinowski, Z., Pai, E.F., Pereira, P.J.B., Petosa, C., Raman, C.S., Rapoport, T., Roll-Mecak, A., Rosen, M., Rudenko, G., Schlessinger, J., Schwartz, T., Shamoo, Y., Sondermann, H., Tao, Y., Tolia, N., Tsodikov, O.V., Westover, K.D., Wu, H., Foster, I., Maia, F, Gonen, T., Kirchhausen, T., Diederichs, K., Crosas, M., and Sliz, P.* (2016) Data publication with the structural biology data grid supports live analysis. *Nature Communications*, 7, 10882.
16. Qi, J., Singh, S., Cai, Q., Li, L., Liu, H., McDonald, T., Lin, A., Bhatia, R., Huang, W.-J., **Chang, C.-I**, and Kuo, Y.-H.* (2015) Inhibition of HDAC8 reactivates p53 and abrogates leukemia stem cell activity in CBFβ-SMMHC associated acute myeloid leukemia. *Cell Stem Cell,* 17(5), 597-610.
17. Su, M.-Y., Peng, W.-H., Ho, M.-R., Su, S.-C., Chang, Y.-C., Chen, G.-C.*, **Chang, C.-I*** (2015). Structure of yeast Ape1 and its role in autophagic vesicle formation. *Autophagy*, 11(9),1580-1593.
18. Chao, S.-W., Su, M.-Y., Chiou, L.-C., Chen, L.-C., **Chang, C.-I***, Huang, W.-J.* (2015) Total Synthesis of Hispidulin and the Structural Basis for Its Inhibition of Proto-oncogene Kinase Pim-1. *Journal of Natural Products*, 78(8),1969-1976.
19. Lee, S.-C., Lin, C.-C., Wang, C.-H., Wu, P.-L., Huang, H-.W., **Chang, C.-I**, and Wu, W.-G.* (2014) Endocytotic routes of cobra cardiotoxins depend on the spatial distribution of positively charged and hydrophobic domains to target distinct types of sulfated glycoconjugates on Cell Surface. *J. Biol. Chem.,* 289, 20170-81.
20. Li, J.-K., Liao, J.-H., Li, H., Kuo, C.-I, Huang, K.-F., Yang, L.-W., Wu, S.-H., and **Chang, C.-I*** (2013) The N-terminal substrate-recognition domain of a LonC protease exhibits structural and functional similarity to cytosolic chaperones. *Acta Cryst., D69*, 1789-1797.
21. Su, M.-Y., Kuo, C.-I, Chang, C.-F., and **Chang, C.-I*** (2013) Three-dimensional structure of human NLRP10/PYNOD pyrin domain reveals a homotypic interaction site distinct from its mouse homologue. *PLOS ONE,* 8(7), e67843.
22. Liao, J.-H., Ihara, K., Kuo, C.-I, Huang, K.-F**,** Wakatsuki, S., Wu, S.-H., and **Chang, C.-I*** (2013) Structures of an ATP-independent Lon-like protease and its complexes with covalent inhibitors. *Acta Cryst., D*69, 1395-1402.
23. Liao, J.-H., Kuo, C.-I, Huang, Y.-Y., Lin, Y.-C., Lin, Y.-C., Yang, C.-Y., Wu, W.-L., Chang, W.-H., Liaw, Y.-C., Lin, L.-H., **Chang, C.-I***, and Wu, S.-H.* (2012) A Lon-like protease with no ATP-powered unfolding activity**.** *PLOS ONE,* 7(7), e40226.
24. Huang, W.-J.*, Chao S.-W., Yang, C.-Y., Lin, Y.-C., Yang, P., and **Chang, C.-I*** (2012) Synthesis and biological evaluation of ortho aryl *N*-hydroxycinnamides as potent histone deacetylase 8 isoform-selective inhibitors. *ChemMedChem,* 7(10), 1815-24.
25. Su, M.-Y., **Chang, C.-I***, and Chang, C.-F.* (2012) ^{1}H, ^{13}C and ^{15}N resonance assignments of the pyrin domain from human PYNOD. *Biomol. NMR Assign.,* DOI 10.1007/s12104-012-9396-8.

26. Huang, W.-J., Chen, C.-C., Chao S.-W., Yu C.-C., Yang, C.-Y., Guh, J.-W., Lin, Y.-C., Kuo, C.-I, Yang, P., and **Chang, C.-I*** (2011) Synthesis and evaluation of aliphatic-chain hydroxamates capped with osthole derivatives as histone deacetylase inhibitors. *Eur. J. Med. Chem.,* 46(9), 4042-4049.
27. Huang, W.-J., Chen, C.-C., Chao S.-W., Lin, Y.-C., Lee, S.-S., Hsu, F.-L., Lu, Y.-L., Hung M.-F., and **Chang, C.-I*** (2010) Synthesis of *N*-hydroxycinnamides capped with a naturally occurring moiety as inhibitors of histone deacetylases. *ChemMedChem,* 5(4), 598-607.
28. Baxter, R.H.G., **Chang, C.-I**, Chelliah Y., Blandin S., Levashina E., and Deisenhofer, J.* (2007) Structural basis for conserved complement factor-like function in the antimalarial protein TEP1. *PNAS*, 104(28), 11615-20.
29. **Chang, C.-I*** and Deisenhofer, J.* (2007) The peptidoglycan recognition proteins LCa and LCx. *Cellular and Molecular Life Sciences,* 64(11), 1395-402.
30. **Chang, C.-I**, Chelliah, Y., Borek, D., Mengin-Lecreulx, D., and Deisenhofer, J.* (2006) Structure of tracheal cytotoxin in complex with a heterodimeric pattern-recognition receptor. *Science*, 311(5768), 1761-4.
31. **Chang, C.-I**, Ihara, K., Chelliah, Y., Mengin-Lecreulx, D., Wakatsuki, S., and Deisenhofer, J.* (2005) Structure of the ectodomain of *Drosophila* innate immune receptor PGRP-LCa suggests a novel mechanism for pattern recognition. *PNAS*, 102(29), 10279-84.
32. **Chang, C.-I**, Pili-Floury, S., Hervé, M., Parquet, C., Chelliah, Y., Lemaitre, B., Mengin-Lecreulx, D., and Deisenhofer, J.* (2004) A *Drosophila* pattern recognition receptor contains a peptidoglycan docking groove and unusual L,D-carboxypeptidase activity. *PLoS Biology*, 2(9), 1293-13027.
33. Goldsmith, E. J.*, Cobb, M. H., and **Chang, C.-I** (2004) Structure of MAPKs. *Methods Mol Biol.,* 250, 127-44.
34. Goldsmith, E. J.* and **Chang, C.-I** (2002) Another twist in helix C and a missing pocket. *Structure,* 10, 888-889.
35. **Chang, C.-I**, Xu, B.-e, Akella R., Cobb, M. H., and Goldsmith, E. J.* (2002) Crystal structures of MAP kinase p38 complexed to the docking sites on its nuclear substrate MEF2A and activator MKK3b. *Mol. Cell,* 9, 1241-1249.

(*: corresponding author)