

## List of Selected PDB Structures

Target 1 - ACHE - 6O4W (Gerlits et al., 2019)

Target 2 - ADORA2A - 4EIY (Liu et al., 2012)

Target 2 - ADORA2A - 4UHR (Lebon et al., 2015)

Target 3 - ADRA1A - 7YM8 (Toyoda et al., 2023)

Target 3 - ADRA1A - 7YMJ (Toyoda et al., 2023)

Target 4 - ADRA2A - 6KUX (Qu et al., n.d.)

Target 4 - ADRA2A - 7EJ8 (Xu et al., 2022)

Target 5 - AR - 2AM9 (Pereira de Jésus-Tran et al., 2006)

Target 5 - AR - 2AX9 (Bohl et al., 2005)

Target 6 - ADRB1 - 7BU7 (X. Xu et al., 2021)

Target 6 - ADRB1 - 7BVQ (X. Xu et al., 2021)

Target 7 - ADRB2 - 4LDE (Ring et al., 2013)

Target 7 - ADRB2 - 6PS2 (Ishchenko et al., 2019)

Target 8 - BRD4 - 6FO5 (Hoffer et al., 2018)

Target 9 - CNR1 - 5U09 (Shao et al., 2016)

Target 9 - CNR1 - 5XRA (Hua et al., 2017)

Target 10 - CNR2 - 5ZTY (Li et al., 2019)

Target 10 - CNR2 - 8GUR (Li et al., 2023)

Target 11 - CTSD - 4OD9 (Grädler et al., 2014)

Target 12 - CCKAR - 7F8Y (X. Zhang et al., 2021)

Target 12 - CCKAR - 7MBX (Mobbs et al., 2021)

Target 13 - CCKAR - 7F8W (X. Zhang et al., 2021)

Target 14 - PTGS1 - 6Y3C (Miciaccia et al., 2021)

Target 15 - PTGS2 - 5IKR (Orlando & Malkowski, 2016)

Target 16 - CYP1A2 - 2HI4 (Sansen et al., 2007)

Target 17 - CYP2B6 - 3IBD (Gay et al., 2010)

Target 18 - CYP2C19 - 4GQS (Reynald et al., 2012)

Target 19 - CYP2C8 - 2NNJ (Schoch et al., 2008)

Target 20 - CYP2C9 - 5A5I (Skerratt et al., 2016a)

Target 21 - CYP2D6 - 3TBG (Wang et al., 2015)

Target 22 - CYP2E1 - 3E6I (Porubsky et al., 2008)

Target 23 - CYP3A4 - 3NXU (Sevrioukova & Poulos, 2010)

Target 24 - CYP3A5 - 5VEU (Hsu et al., 2018)

Target 25 - OPRD1 - 4N6H (Fenalti et al., 2014)

Target 25 - OPRD1 - 6PT3 (Claff et al., 2019)

Target 26 - DRD1 - 7JVP (Zhuang et al., 2021)

Target 27 - DRD1 - 7JVR (Zhuang et al., 2021)

Target 27 - DRD2 - 6CM4 (Wang et al., 2018)

Target 28 - DRD3 - 3PBL (Chien et al., 2010)

Target 28 - DRD3 - 7CMV (P. Xu et al., 2021)

Target 29 - SLC6A3 - 8Y2F (Li et al., 2024)

Target 29 - SLC6A3 - 9EO4 (Nielsen et al., 2024)

Target 30 - MAP2K7 - 6YG5 (Schröder et al., 2020)

Target 30 - MAP2K7 - 6YZ4 (Schröder et al., 2020)

Target 31 - EDNRA - 8HCQ (Ji et al., 2023)

Target 31 - EDNRA - 8XVK (Hou et al., 2024)

Target 32 - EGFR - 4WKQ (Yosaatmadja et al., n.d.)

Target 32 - EGFR - 8A27 (Obst-Sander et al., 2022)

Target 33 - ESR1 - 3ERD (Shiau et al., 1998)

Target 33 - ESR1 - 6IAR (Scott et al., 2019)

Target 34 - FGFR1 - 5EW8 (Patani et al., 2016)

Target 35 - PTK2 - 4EBV (Iwatani et al., 2013)

Target 35 - PTK2 - 6YOJ (Berger et al., 2021)

Target 36 - GPBAR1 - 9GYO (Castel et al., n.d.)

Target 37 - SLC6A1 - 7Y7Y (Zhu et al., 2023)

Target 37 - SLC6A1 - 7Y7Z (Zhu et al., 2023)

Target 38 - GABRA1/GABRB2/GABRG2 - 6X3X (Kim et al., 2020)

Target 39 - NR3C1 - 1M2Z (Bledsoe et al., 2002)

Target 39 - NR3C1 - 4LSJ (Carson et al., 2014)

Target 40 - GRIN1/GRIN2A - 5H8N (Hackos et al., 2016)

Target 40 - GRIN1/GRIN2A - 5H8Q (Hackos et al., 2016)

Target 40 - GRIN1/GRIN2A - 7EU7 (Y. Zhang et al., 2021)

Target 41 - GSK3B - 1Q5K (Bhat et al., 2003)

Target 42 - KCNH2 - 8ZYQ (Miyashita et al., 2024)

Target 43 - HRH1 - 3RZE (Shimamura et al., 2011)

Target 43 - HRH1 - 8YN2 (Zhang et al., 2024)

Target 44 - HRH2 - 7UL3 (Robertson et al., 2022)

Target 44 - HRH2 - 8YN3 (Zhang et al., 2024)

Target 45 - INSR - 5E1S (Sanderson et al., 2015)

Target 46 - OPRK1 - 4DJH (Wu et al., 2012)

Target 46 - OPRK1 - 8DZR (Han et al., 2023)

Target 47 - MRGPRX2 - 7S8O (Cao et al., 2021)

Target 48 - MAOA - 2Z5X (Son et al., 2008)

Target 49 - MAOB - 2V5Z (Binda et al., 2007)

Target 50 - OPRM1 - 8EFO (Zhuang et al., 2022)

Target 51 - MALT1 - 7AK0 (Pissot Soldermann et al., 2020)

Target 52 - CHRM1 - 6WJC (Maeda et al., 2020)

Target 52 - CHRM1 - 6ZFZ (Brown et al., 2021)

Target 53 - CHRM2 - 5ZKC (Suno et al., 2018)

Target 53 - CHRM2 - 7T8X (Xu et al., 2023)

Target 54 - CHRM3 - 8EA0 (Zhang et al., 2022)

Target 55 - NTRK1 - 5JFW (Skerratt et al., 2016b)

Target 56 - TACR3 - 8JBF (Sun et al., 2023)

Target 57 - CHRNA4/CHRNA2 - 8ST2 (Mazzaferro et al., 2024)

Target 58 - SLC6A2 - 8WGR (Tan et al., 2024)

Target 58 - SLC6A2 - 8ZP2 (Song & Wu, 2024)

Target 59 - RORA - 1N83 (Kallen et al., 2002)

Target 60 - ABCB1 - 8Y6H (Hamaguchi-Suzuki et al., 2024)

Target 61 - PDE3A - 7L28 (Garvie et al., 2021)

Target 62 - PDE4D - 1Y2K (Card et al., 2005)

Target 63 - PIK3CG - 3L54 (Knight et al., 2010)

Target 64 - PGR - 1SQN (Madauss et al., 2004)

Target 64 - PGR - 4OAR (Petit-Topin et al., 2014)

Target 65 - PDK1 - 2Q8G (Kato et al., 2007)

Target 66 - RARA - 5K13 (Hughes et al., 2016)

Target 66 - RARA - 9GFE (Perdriau et al., 2025)

Target 67 - ROCK1 - 3V8S (Li et al., 2012)

Target 68 - ROCK2 - 7JNT (Hu et al., 2020)

Target 69 - ATM - 7NI4 (Stakyte et al., 2021)

Target 70 - STK35 - Q8TDR2 (SWISS-MODEL, 2025a)

Target 71 - AURKA - 5OS5 (McIntyre et al., 2017)

Target 71 - AURKA - 5OSF (McIntyre et al., 2017)

Target 71 - AURKA - 8SSO (Kim et al., 2023)

Target 72 - AURKB - 4AF3 (Elkins et al., 2012)

Target 73 - HTR1A - 8PJK (Ullrich et al., 2023)

Target 74 - HTR1B - 4IAR (Wang et al., 2013)

Target 74 - HTR1B - 5V54 (Yin et al., 2018)

Target 75 - HTR2A - 7WC6 (Cao et al., 2022)

Target 75 - HTR2A - 7WC8 (Cao et al., 2022)

Target 76 - HTR2B - 4IB4 (Wacker et al., 2013)

Target 76 - HTR2B - 6DS0 (McCorvy et al., 2018)

Target 77 - HTR3A - 8BLB (López-Sánchez et al., 2024)

Target 78 - HTR6 - 8JLZ (Pei et al., 2023)

Target 79 - SLC6A4 - 5I73 (Coleman et al., 2016)

Target 79 - SLC6A4 - 6DZZ (Coleman et al., 2019)

Target 79 - SLC6A4 - 7TXT (Singh et al., 2023)

Target 80 - SCN5A - 7DTC (Li et al., 2021)

Target 81 - KIT - 4UOI (Garner et al., 2014)

Target 82 - LCK - 1QPJ (Zhu et al., 1999)

Target 82 - LCK - 2PLO (Jacobs et al., 2008)

Target 83 - SRC - 1Y57 (Cowan-Jacob et al., 2005)

Target 83 - SRC - 7NG7 (Temps et al., 2021)

Target 84 - FLT1 - 3HNG (Tresaugues et al., n.d.)

Target 85 - KDR - 3VO3 (Miyamoto et al., 2013)

Target 86 - AVPR1A - P37288 (SWISS-MODEL, 2025b)

Target 87 - CACNA1C - 8FHS (Gao et al., 2023)

Target 87 - CACNA1C - 8WE8 (Gao et al., 2023)

Target 87 - CACNA1C - 8WEA (Gao et al., 2023)

Target 88 - KCNQ1 - 7XNN (Ma et al., 2022)

Target 88 - KCNQ1 - 7XNN additional 1 (Yang et al., 2013)

Target 88 - KCNQ1 - 7XNN additional 2 (Seeböhm et al., 2003)

## References

- Berger, B. T., Amaral, M., Kokh, D. B., Nunes-Alves, A., Musil, D., Heinrich, T., Schröder, M., Neil, R., Wang, J., Navratilova, I., Bomke, J., Elkins, J. M., Müller, S., Frech, M., Wade, R. C., & Knapp, S. (2021). Structure-kinetic relationship reveals the mechanism of selectivity of FAK inhibitors over PYK2. *Cell Chem Biol*, 28(5), 686-698.e687. <https://doi.org/10.1016/j.chembiol.2021.01.003>
- Bhat, R., Xue, Y., Berg, S., Hellberg, S., Ormö, M., Nilsson, Y., Radesäter, A. C., Jerning, E., Markgren, P. O., Borgegård, T., Nylöf, M., Giménez-Cassina, A., Hernández, F., Lucas, J. J., Díaz-Nido, J., & Avila, J. (2003). Structural insights and biological effects of glycogen synthase kinase 3-specific inhibitor AR-A014418. *J Biol Chem*, 278(46), 45937-45945. <https://doi.org/10.1074/jbc.M306268200>
- Binda, C., Wang, J., Pisani, L., Caccia, C., Carotti, A., Salvati, P., Edmondson, D. E., & Mattevi, A. (2007). Structures of human monoamine oxidase B complexes with selective noncovalent inhibitors: safinamide and coumarin analogs. *J Med Chem*, 50(23), 5848-5852. <https://doi.org/10.1021/jm070677y>
- Bledsoe, R. K., Montana, V. G., Stanley, T. B., Delves, C. J., Apolito, C. J., McKee, D. D., Consler, T. G., Parks, D. J., Stewart, E. L., Willson, T. M., Lambert, M. H., Moore, J. T., Pearce, K. H., & Xu, H. E. (2002). Crystal structure of the glucocorticoid receptor ligand binding domain reveals a novel mode of receptor dimerization and coactivator recognition. *Cell*, 110(1), 93-105. [https://doi.org/10.1016/s0092-8674\(02\)00817-6](https://doi.org/10.1016/s0092-8674(02)00817-6)
- Bohl, C. E., Miller, D. D., Chen, J., Bell, C. E., & Dalton, J. T. (2005). Structural basis for accommodation of nonsteroidal ligands in the androgen receptor. *J Biol Chem*, 280(45), 37747-37754. <https://doi.org/10.1074/jbc.M507464200>
- Brown, A. J. H., Bradley, S. J., Marshall, F. H., Brown, G. A., Bennett, K. A., Brown, J., Cansfield, J. E., Cross, D. M., de Graaf, C., Hudson, B. D., Dwomoh, L., Dias, J. M., Errey, J. C., Hurrell, E., Liptrot, J., Mattedi, G., Molloy, C., Nathan, P. J., Okrasa, K., . . . Tobin, A. B. (2021). From structure to clinic: Design of a muscarinic M1 receptor agonist with potential to treatment of Alzheimer's disease. *Cell*, 184(24), 5886-5901.e5822. <https://doi.org/10.1016/j.cell.2021.11.001>

- Cao, C., Kang, H. J., Singh, I., Chen, H., Zhang, C., Ye, W., Hayes, B. W., Liu, J., Gumpfer, R. H., Bender, B. J., Slocum, S. T., Krumm, B. E., Lansu, K., McCorvy, J. D., Kroeze, W. K., English, J. G., DiBerto, J. F., Olsen, R. H. J., Huang, X. P., . . . Roth, B. L. (2021). Structure, function and pharmacology of human itch GPCRs. *Nature*, 600(7887), 170-175. <https://doi.org/10.1038/s41586-021-04126-6>
- Cao, D., Yu, J., Wang, H., Luo, Z., Liu, X., He, L., Qi, J., Fan, L., Tang, L., Chen, Z., Li, J., Cheng, J., & Wang, S. (2022). Structure-based discovery of nonhallucinogenic psychedelic analogs. *Science*, 375(6579), 403-411. <https://doi.org/10.1126/science.abc8615>
- Card, G. L., Blasdel, L., England, B. P., Zhang, C., Suzuki, Y., Gillette, S., Fong, D., Ibrahim, P. N., Artis, D. R., Bollag, G., Milburn, M. V., Kim, S. H., Schlessinger, J., & Zhang, K. Y. (2005). A family of phosphodiesterase inhibitors discovered by cocrystallography and scaffold-based drug design. *Nat Biotechnol*, 23(2), 201-207. <https://doi.org/10.1038/nbt1059>
- Carson, M. W., Luz, J. G., Suen, C., Montrose, C., Zink, R., Ruan, X., Cheng, C., Cole, H., Adrian, M. D., Kohlman, D. T., Mabry, T., Snyder, N., Condon, B., Maletic, M., Clawson, D., Pustilnik, A., & Coghlan, M. J. (2014). Glucocorticoid receptor modulators informed by crystallography lead to a new rationale for receptor selectivity, function, and implications for structure-based design. *J Med Chem*, 57(3), 849-860. <https://doi.org/10.1021/jm401616g>
- Castel, J., Botzanowski, T., Brooks, I., Frechard, A., Bey, G., Schroeter, M., Del nero, E., Debaene, F., Ciesielski, F., Zeyer, D., Cianferani, S., & Morales, R. (n.d.). *Deciphering molecular determinants of GPCR-G protein receptor interactions by complementary integrative structural biology methods [Manuscript in preparation]*. <https://doi.org/10.2210/pdb9GYO/pdb>
- Chien, E. Y., Liu, W., Zhao, Q., Katritch, V., Han, G. W., Hanson, M. A., Shi, L., Newman, A. H., Javitch, J. A., Cherezov, V., & Stevens, R. C. (2010). Structure of the human dopamine D3 receptor in complex with a D2/D3 selective antagonist. *Science*, 330(6007), 1091-1095. <https://doi.org/10.1126/science.1197410>
- Claff, T., Yu, J., Blais, V., Patel, N., Martin, C., Wu, L., Han, G. W., Holleran, B. J., Van der Poorten, O., White, K. L., Hanson, M. A., Sarret, P., Gendron, L., Cherezov, V., Katritch, V., Ballet, S., Liu, Z. J., Müller, C. E., & Stevens, R. C. (2019). Elucidating the active  $\delta$ -opioid receptor crystal structure with peptide and small-molecule agonists. *Sci Adv*, 5(11), eaax9115. <https://doi.org/10.1126/sciadv.aax9115>
- Coleman, J. A., Green, E. M., & Gouaux, E. (2016). X-ray structures and mechanism of the human serotonin transporter. *Nature*, 532(7599), 334-339. <https://doi.org/10.1038/nature17629>

- Coleman, J. A., Yang, D., Zhao, Z., Wen, P. C., Yoshioka, C., Tajkhorshid, E., & Gouaux, E. (2019). Serotonin transporter-ibogaine complexes illuminate mechanisms of inhibition and transport. *Nature*, 569(7754), 141-145. <https://doi.org/10.1038/s41586-019-1135-1>
- Cowan-Jacob, S. W., Fendrich, G., Manley, P. W., Jahnke, W., Fabbro, D., Liebetanz, J., & Meyer, T. (2005). The crystal structure of a c-Src complex in an active conformation suggests possible steps in c-Src activation. *Structure*, 13(6), 861-871. <https://doi.org/10.1016/j.str.2005.03.012>
- Elkins, J. M., Santaguida, S., Musacchio, A., & Knapp, S. (2012). Crystal structure of human aurora B in complex with INCENP and VX-680. *J Med Chem*, 55(17), 7841-7848. <https://doi.org/10.1021/jm3008954>
- Fenalti, G., Giguere, P. M., Katritch, V., Huang, X. P., Thompson, A. A., Cherezov, V., Roth, B. L., & Stevens, R. C. (2014). Molecular control of  $\delta$ -opioid receptor signalling. *Nature*, 506(7487), 191-196. <https://doi.org/10.1038/nature12944>
- Gao, S., Yao, X., Chen, J., Huang, G., Fan, X., Xue, L., Li, Z., Wu, T., Zheng, Y., Huang, J., Jin, X., Wang, Y., Wang, Z., Yu, Y., Liu, L., Pan, X., Song, C., & Yan, N. (2023). Structural basis for human Ca(v)1.2 inhibition by multiple drugs and the neurotoxin calciseptine. *Cell*, 186(24), 5363-5374.e5316. <https://doi.org/10.1016/j.cell.2023.10.007>
- Garner, A. P., Gozgit, J. M., Anjum, R., Vodala, S., Schrock, A., Zhou, T., Serrano, C., Eilers, G., Zhu, M., Ketzer, J., Wardwell, S., Ning, Y., Song, Y., Kohlmann, A., Wang, F., Clackson, T., Heinrich, M. C., Fletcher, J. A., Bauer, S., & Rivera, V. M. (2014). Ponatinib inhibits polyclonal drug-resistant KIT oncoproteins and shows therapeutic potential in heavily pretreated gastrointestinal stromal tumor (GIST) patients. *Clin Cancer Res*, 20(22), 5745-5755. <https://doi.org/10.1158/1078-0432.Ccr-14-1397>
- Garvie, C. W., Wu, X., Papanastasiou, M., Lee, S., Fuller, J., Schnitzler, G. R., Horner, S. W., Baker, A., Zhang, T., Mullahoo, J. P., Westlake, L., Hoyt, S. H., Toetzel, M., Ranaghan, M. J., de Waal, L., McGaunn, J., Kaplan, B., Piccioni, F., Yang, X., . . . Greulich, H. (2021). Structure of PDE3A-SLFN12 complex reveals requirements for activation of SLFN12 RNase. *Nat Commun*, 12(1), 4375. <https://doi.org/10.1038/s41467-021-24495-w>
- Gay, S. C., Shah, M. B., Talakad, J. C., Maekawa, K., Roberts, A. G., Wilderman, P. R., Sun, L., Yang, J. Y., Huelga, S. C., Hong, W. X., Zhang, Q., Stout, C. D., & Halpert, J. R. (2010). Crystal structure of a cytochrome P450 2B6 genetic variant in complex with the inhibitor 4-(4-chlorophenyl)imidazole at 2.0-Å resolution. *Mol Pharmacol*, 77(4), 529-538. <https://doi.org/10.1124/mol.109.062570>
- Gerlits, O., Ho, K. Y., Cheng, X., Blumenthal, D., Taylor, P., Kovalevsky, A., & Radić, Z. (2019). A new crystal form of human acetylcholinesterase for exploratory room-temperature crystallography studies. *Chem Biol Interact*, 309, 108698. <https://doi.org/10.1016/j.cbi.2019.06.011>

- Grädler, U., Czodrowski, P., Tsaklakidis, C., Klein, M., Werkmann, D., Lindemann, S., Maskos, K., & Leuthner, B. (2014). Structure-based optimization of non-peptidic Cathepsin D inhibitors. *Bioorg Med Chem Lett*, 24(17), 4141-4150. <https://doi.org/10.1016/j.bmcl.2014.07.054>
- Hackos, D. H., Lupardus, P. J., Grand, T., Chen, Y., Wang, T. M., Reynen, P., Gustafson, A., Wallweber, H. J., Volgraf, M., Sellers, B. D., Schwarz, J. B., Paoletti, P., Sheng, M., Zhou, Q., & Hanson, J. E. (2016). Positive Allosteric Modulators of GluN2A-Containing NMDARs with Distinct Modes of Action and Impacts on Circuit Function. *Neuron*, 89(5), 983-999. <https://doi.org/10.1016/j.neuron.2016.01.016>
- Hamaguchi-Suzuki, N., Adachi, N., Moriya, T., Yasuda, S., Kawasaki, M., Suzuki, K., Ogasawara, S., Anzai, N., Senda, T., & Murata, T. (2024). Cryo-EM structure of P-glycoprotein bound to triple elacridar inhibitor molecules. *Biochem Biophys Res Commun*, 709, 149855. <https://doi.org/10.1016/j.bbrc.2024.149855>
- Han, J., Zhang, J., Nazarova, A. L., Bernhard, S. M., Krumm, B. E., Zhao, L., Lam, J. H., Rangari, V. A., Majumdar, S., Nichols, D. E., Katritch, V., Yuan, P., Fay, J. F., & Che, T. (2023). Ligand and G-protein selectivity in the  $\kappa$ -opioid receptor. *Nature*, 617(7960), 417-425. <https://doi.org/10.1038/s41586-023-06030-7>
- Hoffer, L., Voitovich, Y. V., Raux, B., Carrasco, K., Muller, C., Fedorov, A. Y., Derviaux, C., Amouric, A., Betzi, S., Horvath, D., Varnek, A., Collette, Y., Combes, S., Roche, P., & Morelli, X. (2018). Integrated Strategy for Lead Optimization Based on Fragment Growing: The Diversity-Oriented-Target-Focused-Synthesis Approach. *J Med Chem*, 61(13), 5719-5732. <https://doi.org/10.1021/acs.jmedchem.8b00653>
- Hou, J., Liu, S., Zhang, X., Tu, G., Wu, L., Zhang, Y., Yang, H., Li, X., Liu, J., Jiang, L., Tan, Q., Bai, F., Liu, Z., Miao, C., Hua, T., & Luo, Z. (2024). Structural basis of antagonist selectivity in endothelin receptors. *Cell Discov*, 10(1), 79. <https://doi.org/10.1038/s41421-024-00705-9>
- Hsu, M. H., Savas, U., & Johnson, E. F. (2018). The X-Ray Crystal Structure of the Human Mono-Oxygenase Cytochrome P450 3A5-Ritonavir Complex Reveals Active Site Differences between P450s 3A4 and 3A5. *Mol Pharmacol*, 93(1), 14-24. <https://doi.org/10.1124/mol.117.109744>
- Hu, Z., Wang, C., Sitkoff, D., Cheadle, N. L., Xu, S., Muckelbauer, J. K., Adam, L. P., Wexler, R. R., & Quan, M. L. (2020). Identification of 5H-chromeno[3,4-c]pyridine and 6H-isochromeno[3,4-c]pyridine derivatives as potent and selective dual ROCK inhibitors. *Bioorg Med Chem Lett*, 30(21), 127474. <https://doi.org/10.1016/j.bmcl.2020.127474>
- Hua, T., Vemuri, K., Nikas, S. P., Laprairie, R. B., Wu, Y., Qu, L., Pu, M., Korde, A., Jiang, S., Ho, J. H., Han, G. W., Ding, K., Li, X., Liu, H., Hanson, M. A., Zhao, S., Bohn, L. M., Makriyannis, A., Stevens, R. C., & Liu, Z. J. (2017). Crystal structures of agonist-bound human cannabinoid receptor CB(1). *Nature*, 547(7664), 468-471. <https://doi.org/10.1038/nature23272>



- Hughes, N. E., Bleisch, T. J., Jones, S. A., Richardson, T. I., Doti, R. A., Wang, Y., Stout, S. L., Durst, G. L., Chambers, M. G., Oskins, J. L., Lin, C., Adams, L. A., Page, T. J., Barr, R. J., Zink, R. W., Osborne, H., Montrose-Rafizadeh, C., & Norman, B. H. (2016). Identification of potent and selective retinoic acid receptor gamma (RAR $\gamma$ ) antagonists for the treatment of osteoarthritis pain using structure based drug design. *Bioorg Med Chem Lett*, 26(14), 3274-3277. <https://doi.org/10.1016/j.bmcl.2016.05.056>
- Ishchenko, A., Stauch, B., Han, G. W., Batyuk, A., Shiriaeva, A., Li, C., Zatsepin, N., Weierstall, U., Liu, W., Nango, E., Nakane, T., Tanaka, R., Tono, K., Joti, Y., Iwata, S., Moraes, I., Gati, C., & Cherezov, V. (2019). Toward G protein-coupled receptor structure-based drug design using X-ray lasers. *IUCr*, 6(Pt 6), 1106-1119. <https://doi.org/10.1107/s2052252519013137>
- Iwatani, M., Iwata, H., Okabe, A., Skene, R. J., Tomita, N., Hayashi, Y., Aramaki, Y., Hosfield, D. J., Hori, A., Baba, A., & Miki, H. (2013). Discovery and characterization of novel allosteric FAK inhibitors. *Eur J Med Chem*, 61, 49-60. <https://doi.org/10.1016/j.ejmech.2012.06.035>
- Jacobs, M. D., Caron, P. R., & Hare, B. J. (2008). Classifying protein kinase structures guides use of ligand-selectivity profiles to predict inactive conformations: structure of Ick/imatinib complex. *Proteins*, 70(4), 1451-1460. <https://doi.org/10.1002/prot.21633>
- Ji, Y., Duan, J., Yuan, Q., He, X., Yang, G., Zhu, S., Wu, K., Hu, W., Gao, T., Cheng, X., Jiang, H., Eric Xu, H., & Jiang, Y. (2023). Structural basis of peptide recognition and activation of endothelin receptors. *Nat Commun*, 14(1), 1268. <https://doi.org/10.1038/s41467-023-36998-9>
- Kallen, J. A., Schlaeppli, J. M., Bitsch, F., Geisse, S., Geiser, M., Delhon, I., & Fournier, B. (2002). X-ray structure of the hROR $\alpha$  LBD at 1.63 Å: structural and functional data that cholesterol or a cholesterol derivative is the natural ligand of ROR $\alpha$ . *Structure*, 10(12), 1697-1707. [https://doi.org/10.1016/s0969-2126\(02\)00912-7](https://doi.org/10.1016/s0969-2126(02)00912-7)
- Kato, M., Li, J., Chuang, J. L., & Chuang, D. T. (2007). Distinct structural mechanisms for inhibition of pyruvate dehydrogenase kinase isoforms by AZD7545, dichloroacetate, and radicicol. *Structure*, 15(8), 992-1004. <https://doi.org/10.1016/j.str.2007.07.001>
- Kim, C., Ludewig, H., Hadzipasic, A., Kutter, S., Nguyen, V., & Kern, D. (2023). A biophysical framework for double-drugging kinases. *Proc Natl Acad Sci U S A*, 120(34), e2304611120. <https://doi.org/10.1073/pnas.2304611120>
- Kim, J. J., Gharpure, A., Teng, J., Zhuang, Y., Howard, R. J., Zhu, S., Noviello, C. M., Walsh, R. M., Jr., Lindahl, E., & Hibbs, R. E. (2020). Shared structural mechanisms of general anaesthetics and benzodiazepines. *Nature*, 585(7824), 303-308. <https://doi.org/10.1038/s41586-020-2654-5>

- Knight, S. D., Adams, N. D., Burgess, J. L., Chaudhari, A. M., Darcy, M. G., Donatelli, C. A., Luengo, J. I., Newlander, K. A., Parrish, C. A., Ridgers, L. H., Sarpong, M. A., Schmidt, S. J., Van Aller, G. S., Carson, J. D., Diamond, M. A., Elkins, P. A., Gardiner, C. M., Garver, E., Gilbert, S. A., . . . Dhanak, D. (2010). Discovery of GSK2126458, a Highly Potent Inhibitor of PI3K and the Mammalian Target of Rapamycin. *ACS Med Chem Lett*, 1(1), 39-43. <https://doi.org/10.1021/ml900028r>
- Lebon, G., Edwards, P. C., Leslie, A. G., & Tate, C. G. (2015). Molecular Determinants of CGS21680 Binding to the Human Adenosine A2A Receptor. *Mol Pharmacol*, 87(6), 907-915. <https://doi.org/10.1124/mol.114.097360>
- Li, R., Martin, M. P., Liu, Y., Wang, B., Patel, R. A., Zhu, J. Y., Sun, N., Pireddu, R., Lawrence, N. J., Li, J., Haura, E. B., Sung, S. S., Guida, W. C., Schonbrunn, E., & Sebt, S. M. (2012). Fragment-based and structure-guided discovery and optimization of Rho kinase inhibitors. *J Med Chem*, 55(5), 2474-2478. <https://doi.org/10.1021/jm201289r>
- Li, X., Chang, H., Bouma, J., de Paus, L. V., Mukhopadhyay, P., Paloczi, J., Mustafa, M., van der Horst, C., Kumar, S. S., Wu, L., Yu, Y., van den Berg, R., Janssen, A. P. A., Lichtman, A., Liu, Z. J., Pacher, P., van der Stelt, M., Heitman, L. H., & Hua, T. (2023). Structural basis of selective cannabinoid CB(2) receptor activation. *Nat Commun*, 14(1), 1447. <https://doi.org/10.1038/s41467-023-37112-9>
- Li, X., Hua, T., Vemuri, K., Ho, J. H., Wu, Y., Wu, L., Popov, P., Benchama, O., Zvonok, N., Locke, K., Qu, L., Han, G. W., Iyer, M. R., Cinar, R., Coffey, N. J., Wang, J., Wu, M., Katritch, V., Zhao, S., . . . Liu, Z. J. (2019). Crystal Structure of the Human Cannabinoid Receptor CB2. *Cell*, 176(3), 459-467.e413. <https://doi.org/10.1016/j.cell.2018.12.011>
- Li, Y., Wang, X., Meng, Y., Hu, T., Zhao, J., Li, R., Bai, Q., Yuan, P., Han, J., Hao, K., Wei, Y., Qiu, Y., Li, N., & Zhao, Y. (2024). Dopamine reuptake and inhibitory mechanisms in human dopamine transporter. *Nature*, 632(8025), 686-694. <https://doi.org/10.1038/s41586-024-07796-0>
- Li, Z., Jin, X., Wu, T., Zhao, X., Wang, W., Lei, J., Pan, X., & Yan, N. (2021). Structure of human Na(v)1.5 reveals the fast inactivation-related segments as a mutational hotspot for the long QT syndrome. *Proc Natl Acad Sci U S A*, 118(11). <https://doi.org/10.1073/pnas.2100069118>
- Liu, W., Chun, E., Thompson, A. A., Chubukov, P., Xu, F., Katritch, V., Han, G. W., Roth, C. B., Heitman, L. H., AP, I. J., Cherezov, V., & Stevens, R. C. (2012). Structural basis for allosteric regulation of GPCRs by sodium ions. *Science*, 337(6091), 232-236. <https://doi.org/10.1126/science.1219218>
- López-Sánchez, U., Munro, L. J., Ladefoged, L. K., Pedersen, A. J., Brun, C. C., Lyngby, S. M., Baud, D., Juillan-Binard, C., Pedersen, M. G., Lummis, S. C. R., Bang-Andersen, B., Schiøtt, B., Chipot, C., Schoehn, G., Neyton, J., Dehez, F., Nury, H., & Kristensen, A. S. (2024). Structural determinants for activity of the antidepressant vortioxetine at human and rodent 5-HT(3) receptors. *Nat Struct Mol Biol*, 31(8), 1232-1242. <https://doi.org/10.1038/s41594-024-01282-x>

- Ma, D., Zhong, L., Yan, Z., Yao, J., Zhang, Y., Ye, F., Huang, Y., Lai, D., Yang, W., Hou, P., & Guo, J. (2022). Structural mechanisms for the activation of human cardiac KCNQ1 channel by electro-mechanical coupling enhancers. *Proc Natl Acad Sci U S A*, 119(45), e2207067119. <https://doi.org/10.1073/pnas.2207067119>
- Madauss, K. P., Deng, S. J., Austin, R. J., Lambert, M. H., McLay, I., Pritchard, J., Short, S. A., Stewart, E. L., Uings, I. J., & Williams, S. P. (2004). Progesterone receptor ligand binding pocket flexibility: crystal structures of the norethindrone and mometasone furoate complexes. *J Med Chem*, 47(13), 3381-3387. <https://doi.org/10.1021/jm030640n>
- Maeda, S., Xu, J., FM, N. K., Clark, M. J., Zhao, J., Tsutsumi, N., Aoki, J., Sunahara, R. K., Inoue, A., Garcia, K. C., & Kobilka, B. K. (2020). Structure and selectivity engineering of the M(1) muscarinic receptor toxin complex. *Science*, 369(6500), 161-167. <https://doi.org/10.1126/science.aax2517>
- Mazzaferro, S., Kang, G., Natarajan, K., Hibbs, R. E., & Sine, S. M. (2024). Structural bases for stoichiometry-selective calcium potentiation of a neuronal nicotinic receptor. *Br J Pharmacol*, 181(13), 1973-1992. <https://doi.org/10.1111/bph.16321>
- McCorvy, J. D., Wacker, D., Wang, S., Agegnehu, B., Liu, J., Lansu, K., Tribo, A. R., Olsen, R. H. J., Che, T., Jin, J., & Roth, B. L. (2018). Structural determinants of 5-HT(2B) receptor activation and biased agonism. *Nat Struct Mol Biol*, 25(9), 787-796. <https://doi.org/10.1038/s41594-018-0116-7>
- McIntyre, P. J., Collins, P. M., Vrzal, L., Birchall, K., Arnold, L. H., Mpamhanga, C., Coombs, P. J., Burgess, S. G., Richards, M. W., Winter, A., Veverka, V., Delft, F. V., Merritt, A., & Bayliss, R. (2017). Characterization of Three Druggable Hot-Spots in the Aurora-A/TPX2 Interaction Using Biochemical, Biophysical, and Fragment-Based Approaches. *ACS Chem Biol*, 12(11), 2906-2914. <https://doi.org/10.1021/acscchembio.7b00537>
- Miciaccia, M., Belviso, B. D., Iaselli, M., Cingolani, G., Ferorelli, S., Cappellari, M., Loguercio Polosa, P., Perrone, M. G., Caliendo, R., & Scilimati, A. (2021). Three-dimensional structure of human cyclooxygenase (hCOX)-1. *Sci Rep*, 11(1), 4312. <https://doi.org/10.1038/s41598-021-83438-z>
- Miyamoto, N., Sakai, N., Hirayama, T., Miwa, K., Oguro, Y., Oki, H., Okada, K., Takagi, T., Iwata, H., Awazu, Y., Yamasaki, S., Takeuchi, T., Miki, H., Hori, A., & Imamura, S. (2013). Discovery of N-[5-({2-[(cyclopropylcarbonyl)amino]imidazo[1,2-b]pyridazin-6-yl}oxy)-2-methylphenyl]-1,3-dimethyl-1H-pyrazole-5-carboxamide (TAK-593), a highly potent VEGFR2 kinase inhibitor. *Bioorg Med Chem*, 21(8), 2333-2345. <https://doi.org/10.1016/j.bmc.2013.01.074>
- Miyashita, Y., Moriya, T., Kato, T., Kawasaki, M., Yasuda, S., Adachi, N., Suzuki, K., Ogasawara, S., Saito, T., Senda, T., & Murata, T. (2024). Improved higher resolution cryo-EM structures reveal the binding modes of hERG channel inhibitors. *Structure*, 32(11), 1926-1935.e1923. <https://doi.org/10.1016/j.str.2024.08.021>

- Mobbs, J. I., Belousoff, M. J., Harikumar, K. G., Piper, S. J., Xu, X., Furness, S. G. B., Venugopal, H., Christopoulos, A., Danev, R., Wootten, D., Thal, D. M., Miller, L. J., & Sexton, P. M. (2021). Structures of the human cholecystokinin 1 (CCK1) receptor bound to Gs and Gq mimetic proteins provide insight into mechanisms of G protein selectivity. *PLoS Biol*, 19(6), e3001295. <https://doi.org/10.1371/journal.pbio.3001295>
- Nielsen, J. C., Salomon, K., Kalenderoglou, I. E., Bargmeyer, S., Pape, T., Shahsavar, A., & Loland, C. J. (2024). Structure of the human dopamine transporter in complex with cocaine. *Nature*, 632(8025), 678-685. <https://doi.org/10.1038/s41586-024-07804-3>
- Obst-Sander, U., Ricci, A., Kuhn, B., Friess, T., Koldewey, P., Kuglstatter, A., Hewings, D., Goergler, A., Steiner, S., Rueher, D., Imhoff, M. P., Raschetti, N., Marty, H. P., Dietzig, A., Rynn, C., Ehler, A., Burger, D., Kornacker, M., Schaffland, J. P., . . . Jaeschke, G. (2022). Discovery of Novel Allosteric EGFR L858R Inhibitors for the Treatment of Non-Small-Cell Lung Cancer as a Single Agent or in Combination with Osimertinib. *J Med Chem*, 65(19), 13052-13073. <https://doi.org/10.1021/acs.jmedchem.2c00893>
- Orlando, B. J., & Malkowski, M. G. (2016). Substrate-selective Inhibition of Cyclooxygenase-2 by Fenamic Acid Derivatives Is Dependent on Peroxide Tone. *J Biol Chem*, 291(29), 15069-15081. <https://doi.org/10.1074/jbc.M116.725713>
- Patani, H., Bunney, T. D., Thiagarajan, N., Norman, R. A., Ogg, D., Breed, J., Ashford, P., Potterton, A., Edwards, M., Williams, S. V., Thomson, G. S., Pang, C. S., Knowles, M. A., Breeze, A. L., Orengo, C., Phillips, C., & Katan, M. (2016). Landscape of activating cancer mutations in FGFR kinases and their differential responses to inhibitors in clinical use. *Oncotarget*, 7(17), 24252-24268. <https://doi.org/10.18632/oncotarget.8132>
- Pei, Y., Wen, X., Guo, S. C., Yang, Z. S., Zhang, R., Xiao, P., & Sun, J. P. (2023). Structural insight into the selective agonist ST1936 binding of serotonin receptor 5-HT6. *Biochem Biophys Res Commun*, 671, 327-334. <https://doi.org/10.1016/j.bbrc.2023.05.126>
- Perdriau, C., Luton, A., Zimmer, K., Neuville, M., Saragaglia, C., Peluso-Iltis, C., Osz, J., Kauffmann, B., Collie, G. W., Rochel, N., Guichard, G., & Pasco, M. (2025). Guanidinium-Stapled Helical Peptides for Targeting Protein-Protein Interactions. *Angew Chem Int Ed Engl*, 64(5), e202416348. <https://doi.org/10.1002/anie.202416348>
- Pereira de Jesus-Tran, K., Côté, P. L., Cantin, L., Blanchet, J., Labrie, F., & Breton, R. (2006). Comparison of crystal structures of human androgen receptor ligand-binding domain complexed with various agonists reveals molecular determinants responsible for binding affinity. *Protein Sci*, 15(5), 987-999. <https://doi.org/10.1110/ps.051905906>

- Petit-Topin, I., Fay, M., Resche-Rigon, M., Ulmann, A., Gainer, E., Rafestin-Oblin, M. E., & Fagart, J. (2014). Molecular determinants of the recognition of ulipristal acetate by oxo-steroid receptors. *J Steroid Biochem Mol Biol*, 144 Pt B, 427-435.  
<https://doi.org/10.1016/j.jsbmb.2014.08.008>
- Pissot Soldermann, C., Simic, O., Renatus, M., Erbel, P., Melkko, S., Wartmann, M., Bigaud, M., Weiss, A., McSheehy, P., Endres, R., Santos, P., Blank, J., Schuffenhauer, A., Bold, G., Buschmann, N., Zoller, T., Altmann, E., Manley, P. W., Dix, I., . . . Régnier, C. H. (2020). Discovery of Potent, Highly Selective, and In Vivo Efficacious, Allosteric MALT1 Inhibitors by Iterative Scaffold Morphing. *J Med Chem*, 63(23), 14576-14593.  
<https://doi.org/10.1021/acs.jmedchem.0c01245>
- Porubsky, P. R., Meneely, K. M., & Scott, E. E. (2008). Structures of human cytochrome P-450 2E1. Insights into the binding of inhibitors and both small molecular weight and fatty acid substrates. *J Biol Chem*, 283(48), 33698-33707.  
<https://doi.org/10.1074/jbc.M805999200>
- Qu, L., Zhou, Q. T., Wu, D., & Zhao, S. W. (n.d.). *Crystal structures of the alpha2A adrenergic receptor in complex with an antagonist RSC [Manuscript in preparation]*.  
<https://doi.org/10.2210/pdb6KUX/pdb>
- Reynald, R. L., Sansen, S., Stout, C. D., & Johnson, E. F. (2012). Structural characterization of human cytochrome P450 2C19: active site differences between P450s 2C8, 2C9, and 2C19. *J Biol Chem*, 287(53), 44581-44591. <https://doi.org/10.1074/jbc.M112.424895>
- Ring, A. M., Manglik, A., Kruse, A. C., Enos, M. D., Weis, W. I., Garcia, K. C., & Kobilka, B. K. (2013). Adrenaline-activated structure of  $\beta$ 2-adrenoceptor stabilized by an engineered nanobody. *Nature*, 502(7472), 575-579.  
<https://doi.org/10.1038/nature12572>
- Robertson, M. J., Papasergi-Scott, M. M., He, F., Seven, A. B., Meyerowitz, J. G., Panova, O., Peroto, M. C., Che, T., & Skiniotis, G. (2022). Structure determination of inactive-state GPCRs with a universal nanobody. *Nat Struct Mol Biol*, 29(12), 1188-1195.  
<https://doi.org/10.1038/s41594-022-00859-8>
- Sanderson, M. P., Apgar, J., Garin-Chesa, P., Hofmann, M. H., Kessler, D., Quant, J., Savchenko, A., Schaaf, O., Treu, M., Tye, H., Zahn, S. K., Zoephel, A., Haaksma, E., Adolf, G. R., & Kraut, N. (2015). BI 885578, a Novel IGF1R/INSR Tyrosine Kinase Inhibitor with Pharmacokinetic Properties That Dissociate Antitumor Efficacy and Perturbation of Glucose Homeostasis. *Mol Cancer Ther*, 14(12), 2762-2772.  
<https://doi.org/10.1158/1535-7163.Mct-15-0539>
- Sansen, S., Yano, J. K., Reynald, R. L., Schoch, G. A., Griffin, K. J., Stout, C. D., & Johnson, E. F. (2007). Adaptations for the oxidation of polycyclic aromatic hydrocarbons exhibited by the structure of human P450 1A2. *J Biol Chem*, 282(19), 14348-14355.  
<https://doi.org/10.1074/jbc.M611692200>

- Schoch, G. A., Yano, J. K., Sansen, S., Dansette, P. M., Stout, C. D., & Johnson, E. F. (2008). Determinants of cytochrome P450 2C8 substrate binding: structures of complexes with montelukast, troglitazone, felodipine, and 9-cis-retinoic acid. *J Biol Chem*, 283(25), 17227-17237. <https://doi.org/10.1074/jbc.M802180200>
- Schröder, M., Tan, L., Wang, J., Liang, Y., Gray, N. S., Knapp, S., & Chaikuad, A. (2020). Catalytic Domain Plasticity of MKK7 Reveals Structural Mechanisms of Allosteric Activation and Diverse Targeting Opportunities. *Cell Chem Biol*, 27(10), 1285-1295.e1284. <https://doi.org/10.1016/j.chembiol.2020.07.014>
- Scott, J. S., Bailey, A., Buttar, D., Carbajo, R. J., Curwen, J., Davey, P. R. J., Davies, R. D. M., Degorce, S. L., Donald, C., Gangl, E., Greenwood, R., Groombridge, S. D., Johnson, T., Lamont, S., Lawson, M., Lister, A., Morrow, C. J., Moss, T. A., Pink, J. H., & Polanski, R. (2019). Tricyclic Indazoles-A Novel Class of Selective Estrogen Receptor Degradation Antagonists. *J Med Chem*, 62(3), 1593-1608. <https://doi.org/10.1021/acs.jmedchem.8b01837>
- Seeböhm, G., Chen, J., Strutz, N., Culberson, C., Lerche, C., & Sanguinetti, M. C. (2003). Molecular determinants of KCNQ1 channel block by a benzodiazepine. *Mol Pharmacol*, 64(1), 70-77. <https://doi.org/10.1124/mol.64.1.70>
- Sevrioukova, I. F., & Poulos, T. L. (2010). Structure and mechanism of the complex between cytochrome P4503A4 and ritonavir. *Proc Natl Acad Sci U S A*, 107(43), 18422-18427. <https://doi.org/10.1073/pnas.1010693107>
- Shao, Z., Yin, J., Chapman, K., Grzemska, M., Clark, L., Wang, J., & Rosenbaum, D. M. (2016). High-resolution crystal structure of the human CB1 cannabinoid receptor. *Nature*, 540(7634), 602-606. <https://doi.org/10.1038/nature20613>
- Shiau, A. K., Barstad, D., Loria, P. M., Cheng, L., Kushner, P. J., Agard, D. A., & Greene, G. L. (1998). The structural basis of estrogen receptor/coactivator recognition and the antagonism of this interaction by tamoxifen. *Cell*, 95(7), 927-937. [https://doi.org/10.1016/S0092-8674\(00\)81717-1](https://doi.org/10.1016/S0092-8674(00)81717-1)
- Shimamura, T., Shiroishi, M., Weyand, S., Tsujimoto, H., Winter, G., Katritch, V., Abagyan, R., Cherezov, V., Liu, W., Han, G. W., Kobayashi, T., Stevens, R. C., & Iwata, S. (2011). Structure of the human histamine H1 receptor complex with doxepin. *Nature*, 475(7354), 65-70. <https://doi.org/10.1038/nature10236>
- Singh, I., Seth, A., Billesbølle, C. B., Braz, J., Rodriguiz, R. M., Roy, K., Bekele, B., Craik, V., Huang, X. P., Boytsov, D., Pogorelov, V. M., Lak, P., O'Donnell, H., Sandtner, W., Irwin, J. J., Roth, B. L., Basbaum, A. I., Wetsel, W. C., Manglik, A., . . . Rudnick, G. (2023). Structure-based discovery of conformationally selective inhibitors of the serotonin transporter. *Cell*, 186(10), 2160-2175.e2117. <https://doi.org/10.1016/j.cell.2023.04.010>



- Skerratt, S. E., Andrews, M., Bagal, S. K., Bilsland, J., Brown, D., Bungay, P. J., Cole, S., Gibson, K. R., Jones, R., Morao, I., Nedderman, A., Omoto, K., Robinson, C., Ryckmans, T., Skinner, K., Stuppel, P., & Waldron, G. (2016b). The Discovery of a Potent, Selective, and Peripherally Restricted Pan-Trk Inhibitor (PF-06273340) for the Treatment of Pain. *J Med Chem*, 59(22), 10084-10099. <https://doi.org/10.1021/acs.jmedchem.6b00850>
- Skerratt, S. E., de Groot, M. J., & Phillips, C. (2016a). Discovery of a novel binding pocket for CYP 2C9 inhibitors: crystallography, pharmacophore modelling and inhibitor SAR [10.1039/C6MD00011H]. *MedChemComm*, 7(5), 813-819. <https://doi.org/10.1039/C6MD00011H>
- Son, S. Y., Ma, J., Kondou, Y., Yoshimura, M., Yamashita, E., & Tsukihara, T. (2008). Structure of human monoamine oxidase A at 2.2-Å resolution: the control of opening the entry for substrates/inhibitors. *Proc Natl Acad Sci U S A*, 105(15), 5739-5744. <https://doi.org/10.1073/pnas.0710626105>
- Song, A., & Wu, X. (2024). Mechanistic insights of substrate transport and inhibitor binding revealed by high-resolution structures of human norepinephrine transporter. *Cell Res*, 34(11), 810-813. <https://doi.org/10.1038/s41422-024-01024-0>
- Stakyte, K., Rotheneder, M., Lammens, K., Bartho, J. D., Grädler, U., Fuchß, T., Pehl, U., Alt, A., van de Logt, E., & Hopfner, K. P. (2021). Molecular basis of human ATM kinase inhibition. *Nat Struct Mol Biol*, 28(10), 789-798. <https://doi.org/10.1038/s41594-021-00654-x>
- Sun, W., Yang, F., Zhang, H., Yuan, Q., Ling, S., Wang, Y., Lv, P., Li, Z., Luo, Y., Liu, D., Yin, W., Shi, P., Xu, H. E., & Tian, C. (2023). Structural insights into neurokinin 3 receptor activation by endogenous and analogue peptide agonists. *Cell Discov*, 9(1), 66. <https://doi.org/10.1038/s41421-023-00564-w>
- Suno, R., Lee, S., Maeda, S., Yasuda, S., Yamashita, K., Hirata, K., Horita, S., Tawaramoto, M. S., Tsujimoto, H., Murata, T., Kinoshita, M., Yamamoto, M., Kobilka, B. K., Vaidehi, N., Iwata, S., & Kobayashi, T. (2018). Structural insights into the subtype-selective antagonist binding to the M(2) muscarinic receptor. *Nat Chem Biol*, 14(12), 1150-1158. <https://doi.org/10.1038/s41589-018-0152-y>
- SWISS-MODEL. (2025a). Homology model of human Serine/threonine-protein kinase 35 Q8TDR2 <https://swissmodel.expasy.org/repository/uniprot/Q8TDR2>
- SWISS-MODEL. (2025b). Homology model of human Vasopressin V1a receptor P37288 <https://swissmodel.expasy.org/repository/uniprot/P37288>
- Tan, J., Xiao, Y., Kong, F., Zhang, X., Xu, H., Zhu, A., Liu, Y., Lei, J., Tian, B., Yuan, Y., & Yan, C. (2024). Molecular basis of human noradrenaline transporter reuptake and inhibition. *Nature*, 632(8026), 921-929. <https://doi.org/10.1038/s41586-024-07719-z>

- Temps, C., Lietha, D., Webb, E. R., Li, X. F., Dawson, J. C., Muir, M., Macleod, K. G., Valero, T., Munro, A. F., Contreras-Montoya, R., Luque-Ortega, J. R., Fraser, C., Beetham, H., Schoenherr, C., Lopalco, M., Arends, M. J., Frame, M. C., Qian, B. Z., Brunton, V. G., . . . Unciti-Broceta, A. (2021). A Conformation Selective Mode of Inhibiting SRC Improves Drug Efficacy and Tolerability. *Cancer Res*, 81(21), 5438-5450. <https://doi.org/10.1158/0008-5472.Can-21-0613>
- Toyoda, Y., Zhu, A., Kong, F., Shan, S., Zhao, J., Wang, N., Sun, X., Zhang, L., Yan, C., Kobilka, B. K., & Liu, X. (2023). Structural basis of  $\alpha(1A)$ -adrenergic receptor activation and recognition by an extracellular nanobody. *Nat Commun*, 14(1), 3655. <https://doi.org/10.1038/s41467-023-39310-x>
- Tresaugues, L., Roos, A., Arrowsmith, C. H., Berglund, H., Bountra, C., Collins, R., Edwards, A. M., Flodin, S., Flores, A., Graslund, S., Hammarstrom, M., Johansson, A., Johansson, I., Karlberg, T., Kotenyova, T., Moche, M., Nyman, T., Persson, C., Kragh-Nielsen, T., . . . Nordlund, P. (n.d.). *Crystal structure of VEGFR1 in complex with N-(4-Chlorophenyl)-2-((pyridin-4-ylmethyl)amino)benzamide [Manuscript in preparation]*. <https://doi.org/10.2210/pdb3HNG/pdb>
- Ullrich, A., Schneider, J., Braz, J. M., Neu, E., Staffen, N., Stanek, M., Bláhová, J., Hove, T., Albert, T., Allikalt, A., Löber, S., Bhardwaj, K., Rodriguez-Rosado, S., Fink, E., Rasmussen, T., Hübner, H., Inoue, A., Shoichet, B. K., Basbaum, A. J., . . . Gmeiner, P. (2023). Discovery of a functionally selective serotonin 5-HT<sub>1A</sub> receptor agonist for the treatment of pain. *bioRxiv*, 2023.2009.2011.557127. <https://doi.org/10.1101/2023.09.11.557127>
- Wacker, D., Wang, C., Katritch, V., Han, G. W., Huang, X. P., Vardy, E., McCorvy, J. D., Jiang, Y., Chu, M., Siu, F. Y., Liu, W., Xu, H. E., Cherezov, V., Roth, B. L., & Stevens, R. C. (2013). Structural features for functional selectivity at serotonin receptors. *Science*, 340(6132), 615-619. <https://doi.org/10.1126/science.1232808>
- Wang, A., Stout, C. D., Zhang, Q., & Johnson, E. F. (2015). Contributions of ionic interactions and protein dynamics to cytochrome P450 2D6 (CYP2D6) substrate and inhibitor binding. *J Biol Chem*, 290(8), 5092-5104. <https://doi.org/10.1074/jbc.M114.627661>
- Wang, C., Jiang, Y., Ma, J., Wu, H., Wacker, D., Katritch, V., Han, G. W., Liu, W., Huang, X. P., Vardy, E., McCorvy, J. D., Gao, X., Zhou, X. E., Melcher, K., Zhang, C., Bai, F., Yang, H., Yang, L., Jiang, H., . . . Xu, H. E. (2013). Structural basis for molecular recognition at serotonin receptors. *Science*, 340(6132), 610-614. <https://doi.org/10.1126/science.1232807>
- Wang, S., Che, T., Levit, A., Shoichet, B. K., Wacker, D., & Roth, B. L. (2018). Structure of the D2 dopamine receptor bound to the atypical antipsychotic drug risperidone. *Nature*, 555(7695), 269-273. <https://doi.org/10.1038/nature25758>



- Wu, H., Wacker, D., Mileni, M., Katritch, V., Han, G. W., Vardy, E., Liu, W., Thompson, A. A., Huang, X. P., Carroll, F. I., Mascarella, S. W., Westkaemper, R. B., Mosier, P. D., Roth, B. L., Cherezov, V., & Stevens, R. C. (2012). Structure of the human  $\kappa$ -opioid receptor in complex with JDTic. *Nature*, 485(7398), 327-332. <https://doi.org/10.1038/nature10939>
- Xu, J., Cao, S., Hübner, H., Weikert, D., Chen, G., Lu, Q., Yuan, D., Gmeiner, P., Liu, Z., & Du, Y. (2022). Structural insights into ligand recognition, activation, and signaling of the  $\alpha$ (2A) adrenergic receptor. *Sci Adv*, 8(9), eabj5347. <https://doi.org/10.1126/sciadv.abj5347>
- Xu, J., Wang, Q., Hübner, H., Hu, Y., Niu, X., Wang, H., Maeda, S., Inoue, A., Tao, Y., Gmeiner, P., Du, Y., Jin, C., & Kobilka, B. K. (2023). Structural and dynamic insights into supra-physiological activation and allosteric modulation of a muscarinic acetylcholine receptor. *Nat Commun*, 14(1), 376. <https://doi.org/10.1038/s41467-022-35726-z>
- Xu, P., Huang, S., Mao, C., Krumm, B. E., Zhou, X. E., Tan, Y., Huang, X. P., Liu, Y., Shen, D. D., Jiang, Y., Yu, X., Jiang, H., Melcher, K., Roth, B. L., Cheng, X., Zhang, Y., & Xu, H. E. (2021). Structures of the human dopamine D3 receptor-G(i) complexes. *Mol Cell*, 81(6), 1147-1159.e1144. <https://doi.org/10.1016/j.molcel.2021.01.003>
- Xu, X., Kaundl, J., Clark, M. J., Hübner, H., Hirata, K., Sunahara, R. K., Gmeiner, P., Kobilka, B. K., & Liu, X. (2021). Binding pathway determines norepinephrine selectivity for the human  $\beta$ (1)AR over  $\beta$ (2)AR. *Cell Res*, 31(5), 569-579. <https://doi.org/10.1038/s41422-020-00424-2>
- Yang, T., Smith, J. A., Leake, B. F., Sanders, C. R., Meiler, J., & Roden, D. M. (2013). An allosteric mechanism for drug block of the human cardiac potassium channel KCNQ1. *Mol Pharmacol*, 83(2), 481-489. <https://doi.org/10.1124/mol.112.081513>
- Yin, W., Zhou, X. E., Yang, D., de Waal, P. W., Wang, M., Dai, A., Cai, X., Huang, C. Y., Liu, P., Wang, X., Yin, Y., Liu, B., Zhou, Y., Wang, J., Liu, H., Caffrey, M., Melcher, K., Xu, Y., Wang, M. W., . . . Jiang, Y. (2018). Crystal structure of the human 5-HT(1B) serotonin receptor bound to an inverse agonist. *Cell Discov*, 4, 12. <https://doi.org/10.1038/s41421-018-0009-2>
- Yosaatmadja, Y., Squire, C. J., McKeage, M., & Flanagan, J. U. (n.d.). 1.85 angstrom structure of EGFR kinase domain with gefitinib [Manuscript in preparation]. <https://doi.org/10.2210/pdb4wkq/pdb>
- Zhang, S., Gumpfer, R. H., Huang, X. P., Liu, Y., Krumm, B. E., Cao, C., Fay, J. F., & Roth, B. L. (2022). Molecular basis for selective activation of DREADD-based chemogenetics. *Nature*, 612(7939), 354-362. <https://doi.org/10.1038/s41586-022-05489-0>

- Zhang, X., He, C., Wang, M., Zhou, Q., Yang, D., Zhu, Y., Feng, W., Zhang, H., Dai, A., Chu, X., Wang, J., Yang, Z., Jiang, Y., Sensfuss, U., Tan, Q., Han, S., Reedtz-Runge, S., Xu, H. E., Zhao, S., . . . Zhao, Q. (2021). Structures of the human cholecystokinin receptors bound to agonists and antagonists. *Nat Chem Biol*, 17(12), 1230-1237. <https://doi.org/10.1038/s41589-021-00866-8>
- Zhang, X., Liu, G., Zhong, Y. N., Zhang, R., Yang, C. C., Niu, C., Pu, X., Sun, J., Zhang, T., Yang, L., Zhang, C., Li, X., Shen, X., Xiao, P., Sun, J. P., & Gong, W. (2024). Structural basis of ligand recognition and activation of the histamine receptor family. *Nat Commun*, 15(1), 8296. <https://doi.org/10.1038/s41467-024-52585-y>
- Zhang, Y., Ye, F., Zhang, T., Lv, S., Zhou, L., Du, D., Lin, H., Guo, F., Luo, C., & Zhu, S. (2021). Structural basis of ketamine action on human NMDA receptors. *Nature*, 596(7871), 301-305. <https://doi.org/10.1038/s41586-021-03769-9>
- Zhu, A., Huang, J., Kong, F., Tan, J., Lei, J., Yuan, Y., & Yan, C. (2023). Molecular basis for substrate recognition and transport of human GABA transporter GAT1. *Nat Struct Mol Biol*, 30(7), 1012-1022. <https://doi.org/10.1038/s41594-023-00983-z>
- Zhu, X., Kim, J. L., Newcomb, J. R., Rose, P. E., Stover, D. R., Toledo, L. M., Zhao, H., & Morgenstern, K. A. (1999). Structural analysis of the lymphocyte-specific kinase Lck in complex with non-selective and Src family selective kinase inhibitors. *Structure*, 7(6), 651-661. [https://doi.org/10.1016/s0969-2126\(99\)80086-0](https://doi.org/10.1016/s0969-2126(99)80086-0)
- Zhuang, Y., Wang, Y., He, B., He, X., Zhou, X. E., Guo, S., Rao, Q., Yang, J., Liu, J., Zhou, Q., Wang, X., Liu, M., Liu, W., Jiang, X., Yang, D., Jiang, H., Shen, J., Melcher, K., Chen, H., . . . Xu, H. E. (2022). Molecular recognition of morphine and fentanyl by the human  $\mu$ -opioid receptor. *Cell*, 185(23), 4361-4375.e4319. <https://doi.org/10.1016/j.cell.2022.09.041>
- Zhuang, Y., Xu, P., Mao, C., Wang, L., Krumm, B., Zhou, X. E., Huang, S., Liu, H., Cheng, X., Huang, X. P., Shen, D. D., Xu, T., Liu, Y. F., Wang, Y., Guo, J., Jiang, Y., Jiang, H., Melcher, K., Roth, B. L., . . . Xu, H. E. (2021). Structural insights into the human D1 and D2 dopamine receptor signaling complexes. *Cell*, 184(4), 931-942.e918. <https://doi.org/10.1016/j.cell.2021.01.027>