Stanford



Ron Dror

Cheriton Family Professor and Professor, by courtesy, of Structural Biology and of Molecular & Cellular Physiology

Computer Science

Curriculum Vitae available Online

CONTACT INFORMATION

- **Faculty Administrator**

  Suzanne Lessard - Faculty Administrator

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Bio

BIO

Ron Dror is the Cheriton Family Professor of Computer Science in the Stanford Artificial Intelligence Lab. Dr. Dror leads a research group that uses molecular simulation and machine learning to elucidate biomolecular structure, dynamics, and function, and to guide the development of more effective medicines. He collaborates extensively with experimentalists in both academia and industry.

Before moving to Stanford, Dr. Dror served as second-in-command of D. E. Shaw Research, a hundred-person company, having joined as its first hire. He designed computer hardware, software, and algorithms that accelerate molecular dynamics simulations by orders of magnitude, and applied these simulations to the study of protein function, protein folding, and protein-drug interactions.

Dr. Dror earned a PhD in Electrical Engineering and Computer Science at MIT, where he developed machine learning methods for computer vision and genomics. He earned an MPhil in Biological Sciences as a Churchill Scholar at the University of Cambridge, as well as undergraduate degrees in Mathematics and in Electrical and Computer Engineering at Rice University, summa cum laude. He has been awarded a Fulbright Scholarship and fellowships from the National Science Foundation, the Department of Defense, and the Whitaker Foundation, as well as two Gordon Bell Prizes and several Best Paper awards. His work has been highlighted by Science as a top-10 breakthrough of the year.

ACADEMIC APPOINTMENTS

- Professor, Computer Science
- Professor (By courtesy), Molecular and Cellular Physiology
- Professor (By courtesy), Structural Biology
- Member, Bio-X
- Faculty Affiliate, Institute for Human-Centered Artificial Intelligence (HAI)
- Joint Faculty, Institute for Computational and Mathematical Engineering (ICME)
- Faculty Fellow, Sarafan ChEM-H
- Member, Wu Tsai Neurosciences Institute

HONORS AND AWARDS

- Cheriton Family Professorship, Stanford University (2023)
- Best Paper Award, Conference on Neural Information Processing Systems (NeurIPS), Datasets and Benchmarks Track (2021)
- Ravi Faculty Scholar, Stanford University (2018)
- Gordon Bell Prize (Performance), ACM (2014)
- Best Paper Award, International Parallel and Distributed Processing Symposium (2013)
- Best Paper Award, ACM/IEEE Conference on Supercomputing (SC11) (2011)
- Top 10 Breakthroughs of the Year, Science Magazine (2010)
- Best Paper Award, ACM/IEEE Conference on Supercomputing (SC09) (2009)
- Gordon Bell Prize (Special Achievement), ACM (2009)
- Profiled in feature on “EECS Alums: Major Players and Thinkers", MIT Department of Electrical Engineering and Computer Science (2009)
- Best Paper Award, ACM/IEEE Conference on Supercomputing (SC06) (2006)

LINKS

- Dror Lab: http://drorlab.stanford.edu/

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

My lab’s research focuses on computational biology, with an emphasis on 3D molecular structure. We combine two approaches: (1) Bottom-up: given the basic physics governing atomic interactions, use simulations to predict molecular behavior; (2) Top-down: given experimental data, use machine learning to predict molecular structures and properties. We collaborate closely with experimentalists and apply our methods to the discovery of safer, more effective drugs.

Teaching

COURSES

2026-27

- Computational Biology: Structure and Organization of Biomolecules and Cells: BIOE 279, BIOPHYS 279, BMDS 245, CME 279, CS 279 (Aut)
- Seminar in Artificial Intelligence in Healthcare: CS 522 (Aut)

2025-26

- Seminar in Artificial Intelligence in Healthcare: CS 522 (Aut)

2024-25

- Computational Biology: Structure and Organization of Biomolecules and Cells: BIOE 279, BIOMEDIN 279, BIOPHYS 279, CME 279, CS 279 (Aut)
- Seminar in Artificial Intelligence in Healthcare: CS 522 (Aut)

2023-24

- Computational Biology: Structure and Organization of Biomolecules and Cells: BIOE 279, BIOMEDIN 279, BIOPHYS 279, CME 279, CS 279 (Aut)
- Seminar in Artificial Intelligence in Healthcare: CS 522 (Aut)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Ziwei Chen, Chiho Im, Jinho Kim, Richard Shuai, Arpita Singhal

Orals Evaluator

Ziwei Chen

Doctoral Dissertation Advisor (AC)

EJ Fine, Hyelim Kang, Rohan Koodli, Anasthasia Shilov, Briana Sobecks

Master's Program Advisor

Ayush Agarwal, Suchir Agarwal, Keira Cornwell, Kenny Dao, Jessica Ding, Richard Fang, Mete Gumusayak, Uzma Hamid, James Han, Alexander Jeon, Samarth Kadaba, Zachary Lawrence, Brian Lim, Christina Peng, Jiaming Shen, Shreya Singh, Mihajlo Stojkovic, Vineet Vinod

Doctoral Dissertation Co-Advisor (AC)

Jessica Karaguesian, Aviv Korman, Jay Shenoy

Doctoral (Program)

Ayush Pandit, Daniel Richman

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Data Science (PhD Program)
- Biophysics (PhD Program)
- Molecular and Cellular Physiology (PhD Program)
- Neurosciences (PhD Program)
- Structural Biology (PhD Program)

Publications

PUBLICATIONS

- **Geometric Deep Learning for Structure-Based Ligand Design.** *ACS central science*
  Powers, A. S., Yu, H. H., Suriana, P., Koodli, R. V., Lu, T., Paggi, J. M., Dror, R. O.
  2023; 9 (12): 2257-2267

- **Geometric deep learning of RNA structure.** *Science (New York, N.Y.)*
  Townshend, R. J., Eismann, S., Watkins, A. M., Rangan, R., Karelina, M., Das, R., Dror, R. O.
  2021; 373 (6558): 1047-1051

- **How GPCR Phosphorylation Patterns Orchestrate Arrestin-Mediated Signaling.** *Cell*
  Latorraca, N. R., Masureel, M., Hollingsworth, S. A., Heydenreich, F. M., Suomivuori, C., Brinton, C., Townshend, R. J., Bouvier, M., Kobilka, B. K., Dror, R. O.
  2020

- **Molecular mechanism of biased signaling in a prototypical G protein-coupled receptor.** *Science (New York, N.Y.)*
  Suomivuori, C., Latorraca, N. R., Wingler, L. M., Eismann, S., King, M. C., Kleinhenz, A. L., Skiba, M. A., Staus, D. P., Kruse, A. C., Lefkowitz, R. J., Dror, R. O.
  2020; 367 (6480): 881–87

- **Molecular mechanism of GPCR-mediated arrestin activation** *NATURE*
  Latorraca, N. R., Wang, J. K., Bauer, B., Townshend, R. J. L., Hollingsworth, S. A., Olivieri, J. E., Xu, H., Sommer, M. E., Dror, R. O.
  2018; 557 (7705): 452-+

- **Structural basis of opioid receptor activation by PCP and ketamine.** *Nature structural & molecular biology*
  Jiang, Q., Han, J., Fine, E. J., Ramos-Gonzalez, N., Rangari, V. A., Ruiz, M. V., Critz, M. L., Suomivuori, C. M., Wang, J., Albert, T. L., Whiddon, K., Li, K., Robertson, et al
  2026

- **Structural dynamics of kappa opioid receptor interactions with β-arrestin 1.** *Nature communications*
  Han, J., Fine, E. J., Jiang, Q., Zhuang, Y., Suomivuori, C. M., Chen, Z. W., Denn, E., Whiddon, K., Li, K., Evers, A. S., Fuller, J., Carter, J., Fay, et al
  2026
- **Structural insights into coffee bitter taste perception by TAS2R43 receptor.** *Nature structural & molecular biology*
  Kim, Y., Gumpper, R. H., Zhuang, Y., Dror, R. O., Roth, B. L.
  2026; 33 (4): 701-710
- **Molecular mechanism of exchange coupling in CLC chloride/proton antiporters.** *Nature communications*
  Aydin, D., Chien, C. T., Kreiter, J., Nava, A. R., Portasikova, J. M., Fojtik, L., Sobecks, B. L., Mosquera, C., Man, P., Dror, R. O., Chiu, W., Maduke, M.
  2026
- **Protein Structural Model Selection Informed by Comparison of Predicted Ligand Binding Poses.** *Journal of chemical information and modeling*
  Karelina, M., Dror, R. O.
  2025
- **Structure and mechanism of the mitochondrial calcium transporter NCLX.** *Nature*
  Fan, M., Tsai, C. W., Zhang, J., Zhang, J., Krishnan, A. R., Liu, T. Y., Huang, Y. L., Aydin, D., Du, S., Sobecks, B. L., Rodriguez, M. X., Reiter, A. H., Bertozzi, et al
  2025
- **The polypharmacology of psychedelics reveals multiple targets for potential therapeutics.** *Neuron*
  Jain, M. K., Gumpper, R. H., Slocum, S. T., Schmitz, G. P., Madsen, J. S., Tummino, T. A., Suomivuori, C. M., Huang, X. P., Shub, L., DiBerto, J. F., Kim, K., DeLeon, C., Krumm, et al
  2025
- **Structural insights into lipid chain-length selectivity and allosteric regulation of FFA2.** *Nature communications*
  Kugawa, M., Kawakami, K., Kise, R., Suomivuori, C. M., Tsujimura, M., Kobayashi, K., Kojima, A., Inoue, W. J., Fukuda, M., Matsui, T. E., Fukunaga, A., Koyanagi, J., Kim, et al
  2025; 16 (1): 2809
- **A cryptic pocket in CB1 drives peripheral and functional selectivity** *NATURE*
  Rangari, V., O'Brien, E. S., Powers, A. S., Slivicki, R. A., Bertels, Z., Appourchaux, K., Aydin, D., Ramos-Gonzalez, N., Mwirigi, J., Lin, L., Mangutov, E., Sobecks, B. L., Awad-Agbaria, et al
  2025
- **Structure of mitochondrial pyruvate carrier and its inhibition mechanism** *NATURE*
  He, Z., Zhang, J., Xu, Y., Fine, E. J., Suomivuori, C., Dror, R. O., Feng, L.
  2025
- **Systematic analysis of biomolecular conformational ensembles with PENSA.** *The Journal of chemical physics*
  Vogele, M., Thomson, N. J., Truong, S. T., McAvity, J., Zachariae, U., Dror, R. O.
  2025; 162 (1)
- **RNA-Puzzles Round V: blind predictions of 23 RNA structures.** *Nature methods*
  Bu, F., Adam, Y., Adamiak, R. W., Antczak, M., de Aquino, B. R., Badepally, N. G., Batey, R. T., Baulin, E. F., Boinski, P., Boniecki, M. J., Bujnicki, J. M., Carpenter, K. A., Chacon, et al
  2024
- **A non-canonical mechanism of GPCR activation.** *Nature communications*
  Powers, A. S., Khan, A., Paggi, J. M., Latorraca, N. R., Souza, S., Di Salvo, J., Lu, J., Soisson, S. M., Johnston, J. M., Weinglass, A. B., Dror, R. O.
  2024; 15 (1): 9938
- **Signaling Modulation Mediated by Ligand Water Interactions with the Sodium Site at μOR.** *ACS central science*
  Ople, R. S., Ramos-Gonzalez, N., Li, Q., Sobecks, B. L., Aydin, D., Powers, A. S., Faouzi, A., Polacco, B. J., Bernhard, S. M., Appourchaux, K., Sribhashyam, S., Eans, S. O., Tsai, et al
  2024; 10 (8): 1490-1503
- **Signaling Modulation Mediated by Ligand Water Interactions with the Sodium Site at μOR** *ACS CENTRAL SCIENCE*

Ople, R. S., Ramos-Gonzalez, N., Li, Q., Sobecks, B. L., Aydin, D., Powers, A. S., Faouzi, A., Polacco, B. J., Bernhard, S. M., Appourchaux, K., Sribhashyam, S., Eans, S. O., Tsai, et al
2024

- **The Art and Science of Molecular Docking.** *Annual review of biochemistry*
  Paggi, J. M., Pandit, A., Dror, R. O.
  2024

- **CryoEM structures of the human CLC-2 voltage-gated chloride channel reveal a ball-and-chain gating mechanism.** *eLife*
  Xu, M., Neelands, T., Powers, A. S., Liu, Y., Miller, S. D., Pintilie, G. D., Bois, J. D., Dror, R. O., Chiu, W., Maduke, M.
  2024; 12

- **GPR161 structure uncovers the redundant role of sterol-regulated ciliary cAMP signaling in the Hedgehog pathway.** *Nature structural & molecular biology*
  Hoppe, N., Harrison, S., Hwang, S. H., Chen, Z., Karelina, M., Deshpande, I., Suomivuori, C. M., Palicharla, V. R., Berry, S. P., Tschaikner, P., Regele, D., Covey, D. F., Stefan, et al
  2024

- **How accurately can one predict drug binding modes using AlphaFold models?** *eLife*
  Karelina, M., Noh, J. J., Dror, R. O.
  2023; 12

- **Xanomeline displays concomitant orthosteric and allosteric binding modes at the M4 mAChR.** *Nature communications*
  Burger, W. A., Pham, V., Vuckovic, Z., Powers, A. S., Mobbs, J. I., Laloudakis, Y., Glukhova, A., Wootten, D., Tobin, A. B., Sexton, P. M., Paul, S. M., Felder, C. C., Danev, et al
  2023; 14 (1): 5440

- **Structural basis for ion selectivity in potassium-selective channelrhodopsins.** *Cell*
  Tajima, S., Kim, Y. S., Fukuda, M., Jo, Y., Wang, P. Y., Paggi, J. M., Inoue, M., Byrne, E. F., Kishi, K. E., Nakamura, S., Ramakrishnan, C., Takaramoto, S., Nagata, et al
  2023

- **Bias profile and efficacy-driven selectivity of xanomeline at the muscarinic acetylcholine receptor family**
  Valant, C., Powers, A., Pham, V., Burger, W., van der Westhuizen, E., Barnes, N., Paul, S., Christopoulos, A., Thal, D., Felder, C., Dror, R.
  WILEY.2023: 666-667

- **A positively tuned voltage indicator for extended electrical recordings in the brain.** *Nature methods*
  Evans, S. W., Shi, D., Chavarha, M., Plitt, M. H., Taxidis, J., Madruga, B., Fan, J. L., Hwang, F., van Keulen, S. C., Suomivuori, C., Pang, M. M., Su, S., Lee, et al
  2023; 20 (7): 1104-1113

- **Structural basis for activation of CB1 by an endocannabinoid analog.** *Nature communications*
  Krishna Kumar, K., Robertson, M. J., Thadhani, E., Wang, H., Suomivuori, C. M., Powers, A. S., Ji, L., Nikas, S. P., Dror, R. O., Inoue, A., Makriyannis, A., Skiniotis, G., Kobilka, et al
  2023; 14 (1): 2672

- **Protein model quality assessment using rotation-equivariant transformations on point clouds.** *Proteins*
  Eismann, S., Suriana, P., Jing, B., Townshend, R. J., Dror, R. O.
  2023

- **Constrained catecholamines gain β2AR selectivity through allosteric effects on pocket dynamics.** *Nature communications*
  Xu, X., Shonberg, J., Kaindl, J., Clark, M. J., Stößel, A., Maul, L., Mayer, D., Hübner, H., Hirata, K., Venkatakrishnan, A. J., Dror, R. O., Kobilka, B. K., Sunahara, et al
  2023; 14 (1): 2138

- **Molecular mechanism of biased signaling at the kappa opioid receptor.** *Nature communications*
  El Daibani, A., Paggi, J. M., Kim, K., Laloudakis, Y. D., Popov, P., Bernhard, S. M., Krumm, B. E., Olsen, R. H., Diberto, J., Carroll, F. I., Katritch, V., Wünsch, B., Dror, et al
  2023; 14 (1): 1338

- **Structural basis of efficacy-driven ligand selectivity at GPCRs.** *Nature chemical biology*

Powers, A. S., Pham, V., Burger, W. A., Thompson, G., Laloudakis, Y., Sexton, P. M., Paul, S. M., Christopoulos, A., Thal, D. M., Felder, C. C., Valant, C., Dror, R. O.
2023

- **Insights into distinct signaling profiles of the OR activated by diverse agonists.** *Nature chemical biology*
  Qu, Q., Huang, W., Aydin, D., Paggi, J. M., Seven, A. B., Wang, H., Chakraborty, S., Che, T., DiBerto, J. F., Robertson, M. J., Inoue, A., Suomivuori, C., Roth, et al
  2022

- **Signaling snapshots of a serotonin receptor activated by the prototypical psychedelic LSD.** *Neuron*
  Cao, C., Barros-Alvarez, X., Zhang, S., Kim, K., Damgen, M. A., Panova, O., Suomivuori, C., Fay, J. F., Zhong, X., Krumm, B. E., Gumpper, R. H., Seven, A. B., Robertson, et al
  2022

- **Autoantibody mimicry of hormone action at the thyrotropin receptor.** *Nature*
  Faust, B., Billesbølle, C. B., Suomivuori, C. M., Singh, I., Zhang, K., Hoppe, N., Pinto, A. F., Diedrich, J. K., Muftuoglu, Y., Szkudlinski, M. W., Saghatelian, A., Dror, R. O., Cheng, et al
  2022

- **Cryo-EM, Protein Engineering, and Simulation Enable the Development of Peptide Therapeutics against Acute Myeloid Leukemia.** *ACS central science*
  Zhang, K., Horikoshi, N., Li, S., Powers, A. S., Hameedi, M. A., Pintilie, G. D., Chae, H., Khan, Y. A., Suomivuori, C., Dror, R. O., Sakamoto, K. M., Chiu, W., Wakatsuki, et al
  2022; 8 (2): 214-222

- **Structural basis for channel conduction in the pump-like channelrhodopsin ChRmine.** *Cell*
  Kishi, K. E., Kim, Y. S., Fukuda, M., Inoue, M., Kusakizako, T., Wang, P. Y., Ramakrishnan, C., Byrne, E. F., Thadhani, E., Paggi, J. M., Matsui, T. E., Yamashita, K., Nagata, et al
  1800

- **Atypical structural snapshots of human cytomegalovirus GPCR interactions with host G proteins.** *Science advances*
  Tsutsumi, N., Maeda, S., Qu, Q., Vogele, M., Jude, K. M., Suomivuori, C., Panova, O., Waghray, D., Kato, H. E., Velasco, A., Dror, R. O., Skiniotis, G., Kobilka, et al
  1800; 8 (3): eabl5442

- **Leveraging nonstructural data to predict structures and affinities of protein-ligand complexes.** *Proceedings of the National Academy of Sciences of the United States of America*
  Paggi, J. M., Belk, J. A., Hollingsworth, S. A., Villanueva, N., Powers, A. S., Clark, M. J., Chemparathy, A. G., Tynan, J. E., Lau, T. K., Sunahara, R. K., Dror, R. O.
  1800; 118 (51)

- **Structure and mechanism of the SGLT family of glucose transporters.** *Nature*
  Han, L., Qu, Q., Aydin, D., Panova, O., Robertson, M. J., Xu, Y., Dror, R. O., Skiniotis, G., Feng, L.
  2021

- **Selective G protein signaling driven by substance P-neurokinin receptor dynamics.** *Nature chemical biology*
  Harris, J. A., Faust, B., Gondin, A. B., Damgen, M. A., Suomivuori, C., Veldhuis, N. A., Cheng, Y., Dror, R. O., Thal, D. M., Manglik, A.
  2021

- **Structure and mechanism of blood-brain-barrier lipid transporter MFSD2A.** *Nature*
  Wood, C. A., Zhang, J., Aydin, D., Xu, Y., Andreone, B. J., Langen, U. H., Dror, R. O., Gu, C., Feng, L.
  2021

- **Gold nanoparticles and tilt pairs to assess protein flexibility by cryo-electron microscopy.** *Ultramicroscopy*
  Jagota, M., Townshend, R. J., Kang, L., Bushnell, D. A., Dror, R. O., Kornberg, R. D., Azubel, M.
  2021; 227: 113302

- **Simple biochemical features underlie transcriptional activation domain diversity and dynamic, fuzzy binding to Mediator.** *eLife*
  Sanborn, A. L., Yeh, B. T., Feigerle, J. T., Hao, C. V., Townshend, R. J., Lieberman-Aiden, E., Dror, R. O., Kornberg, R. D.
  2021; 10

- **Delineating the Ligand-Receptor Interactions That Lead to Biased Signaling at the μ-Opioid Receptor.** *Journal of chemical information and modeling*
  Kelly, B., Hollingsworth, S. A., Blakemore, D. C., Owen, R. M., Storer, R. I., Swain, N. A., Aydin, D., Torella, R., Warmus, J. S., Dror, R. O.
  2021
- **Hierarchical,rotation-equivariant neural networks to select structural models of protein complexes.** *Proteins*
  Eismann, S., Townshend, R. J., Thomas, N., Jagota, M., Jing, B., Dror, R. O.
  2020
- **Structural and functional characterization of G protein-coupled receptors with deep mutational scanning.** *eLife*
  Jones, E. M., Lubock, N. B., Venkatakrishnan, A. J., Wang, J., Tseng, A. M., Paggi, J. M., Latorraca, N. R., Cancilla, D., Satyadi, M., Davis, J. E., Babu, M. M., Dror, R. O., Kosuri, et al
  2020; 9
- **Angiotensin and biased analogs induce structurally distinct active conformations within a GPCR.** *Science (New York, N.Y.)*
  Wingler, L. M., Skiba, M. A., McMahon, C., Staus, D. P., Kleinhenz, A. L., Suomivuori, C., Latorraca, N. R., Dror, R. O., Lefkowitz, R. J., Kruse, A. C.
  2020; 367 (6480): 888–92
- **Determining How GPCR Phosphorylation Patterns Affect Arrestin-Mediated Signaling**
  Latorraca, N. R., Dror, R. O.
  CELL PRESS.2020: 319A
- **Structure of a GRK5-Calmodulin Complex Reveals Molecular Mechanism of GRK Activation and Substrate Targeting.** *Molecular cell*
  Komolov, K. E., Sulon, S. M., Bhardwaj, A. n., van Keulen, S. C., Duc, N. M., Laurinavichyute, D. K., Lou, H. J., Turk, B. E., Chung, K. Y., Dror, R. O., Benovic, J. L.
  2020
- **Structure of hepcidin-bound ferroportin reveals iron homeostatic mechanisms.** *Nature*
  Billesbølle, C. B., Azumaya, C. M., Kretsch, R. C., Powers, A. S., Gonen, S. n., Schneider, S. n., Arvedson, T. n., Dror, R. O., Cheng, Y. n., Manglik, A. n.
  2020
- **Structure and mechanism of the cation-chloride cotransporter NKCC1.** *Nature*
  Chew, T. A., Orlando, B. J., Zhang, J., Latorraca, N. R., Wang, A., Hollingsworth, S. A., Chen, D., Dror, R. O., Liao, M., Feng, L.
  2019
- **Smoothened stimulation by membrane sterols drives Hedgehog pathway activity.** *Nature*
  Deshpande, I., Liang, J., Hedeen, D., Roberts, K. J., Zhang, Y., Ha, B., Latorraca, N. R., Faust, B., Dror, R. O., Beachy, P. A., Myers, B. R., Manglik, A.
  2019
- **Conformational transitions of a neurotensin receptor1-Gi1complex.** *Nature*
  Kato, H. E., Zhang, Y., Hu, H., Suomivuori, C., Kadji, F. M., Aoki, J., Krishna Kumar, K., Fonseca, R., Hilger, D., Huang, W., Latorraca, N. R., Inoue, A., Dror, et al
  2019
- **How Effectively Can Adaptive Sampling Methods Capture Spontaneous Ligand Binding?** *JOURNAL OF CHEMICAL THEORY AND COMPUTATION*
  Betz, R. M., Dror, R. O.
  2019; 15 (3): 2053–63
- **Diverse GPCRs exhibit conserved water networks for stabilization and activation** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Venkatakrishnan, A. J., Ma, A. K., Fonseca, R., Latorraca, N. R., Kelly, B., Betz, R. M., Asawa, C., Kobilka, B. K., Dror, R. O.
  2019; 116 (8): 3288–93
- **Structure of a Signaling Cannabinoid Receptor 1-G Protein Complex** *CELL*
  Kumar, K., Shalev-Benami, M., Robertson, M. J., Hu, H., Banister, S. D., Hollingsworth, S. A., Latorraca, N. R., Kato, H. E., Hilger, D., Maeda, S., Weis, W. I., Farrens, D. L., Dror, et al
  2019; 176 (3): 448-+

- **Angiotensin Analogs with Divergent Bias Stabilize Distinct Receptor Conformations.** *Cell*
  Wingler, L. M., Elgeti, M., Hilger, D., Latorraca, N. R., Lerch, M. T., Staus, D. P., Dror, R. O., Kobilka, B. K., Hubbell, W. L., Lefkowitz, R. J.
  2019
- **Cryptic pocket formation underlies allosteric modulator selectivity at muscarinic GPCRs.** *Nature communications*
  Hollingsworth, S. A., Kelly, B. n., Valant, C. n., Michaelis, J. A., Mastromihalis, O. n., Thompson, G. n., Venkatakrishnan, A. J., Hertig, S. n., Scammells, P. J., Sexton, P. M., Felder, C. C., Christopoulos, A. n., Dror, et al
  2019; 10 (1): 3289
- **End-to-End Learning on 3D Protein Structure for Interface Prediction. Advances in Neural Information Processing Systems** *Conference on Neural Information Processing Systems (NeurIPS)*
  Townshend, R., Bedi, R., Suriana, P., Dror, R. O.
  2019: 15642–15651
- **End-to-End Learning on 3D Protein Structure for Interface Prediction**
  Townshend, R. J. L., Bedi, R., Suriana, P. A., Dror, R. O.
  edited by Wallach, H., Larochelle, H., Beygelzimer, A., d'Alche-Buc, F., Fox, E., Garnett, R.
  NEURAL INFORMATION PROCESSING SYSTEMS (NIPS).2019
- **Structure of a Signaling Cannabinoid Receptor 1-G Protein Complex.** *Cell*
  Krishna Kumar, K., Shalev-Benami, M., Robertson, M. J., Hu, H., Banister, S. D., Hollingsworth, S. A., Latorraca, N. R., Kato, H. E., Hilger, D., Maeda, S., Weis, W. I., Farrens, D. L., Dror, et al
  2018
- **Publisher Correction: Structural insights into binding specificity, efficacy and bias of a beta2AR partial agonist.** *Nature chemical biology*
  Masureel, M., Zou, Y., Picard, L., van der Westhuizen, E., Mahoney, J. P., Rodrigues, J. P., Mildorf, T. J., Dror, R. O., Shaw, D. E., Bouvier, M., Pardon, E., Steyaert, J., Sunahara, et al
  2018
- **Structural insights into binding specificity, efficacy and bias of a beta2AR partial agonist.** *Nature chemical biology*
  Masureel, M., Zou, Y., Picard, L., van der Westhuizen, E., Mahoney, J. P., Rodrigues, J. P., Mildorf, T. J., Dror, R. O., Shaw, D. E., Bouvier, M., Pardon, E., Steyaert, J., Sunahara, et al
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