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 & Cellular Physiology
- Professor (By courtesy), Structural Biology
- Member, Bio-X
- Faculty Affiliate, Institute for Human-Centered Artificial Intelligence (HAI)
- Member, 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

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)

2022-23

- Computational Biology: Structure and Organization of Biomolecules and Cells: BIOE 279, BIOMEDIN 279, BIOPHYS 279, CME 279, CS 279 (Aut)
- Computational Biology: Structure of Biomolecules: OSPMADRD 70 (Win)

2021-22

- 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)

2020-21

- 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

Postdoctoral Faculty Sponsor

Yuxuan Zhuang

Doctoral Dissertation Advisor (AC)

Masha Karelina, Rohan Koodli, Briana Sobecks

Master's Program Advisor

Shreya D'Souza, Akankshita Dash, Poojit Hegde, Brent Ju, Aakriti Lakshmanan, Zachary Lawrence, Ivan Liongson, Michael Maffezzoli, Lucia Morris, Finsam Samson

Doctoral Dissertation Co-Advisor (AC)

Jessica Karaguesian, Aviv Korman

Doctoral (Program)

Ayush Pandit, Daniel Richman

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Informatics (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. L., Hollingsworth, S. A., Olivieri, J. E., Xu, H., Sommer, M. E., Dror, R. O.
  2018; 557 (7705): 452-+

- **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 #2AR 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. L., Bedi, R., Suriana, P. A., Dror, R. O., 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
  2018; 14 (11): 1059–66

- **Entry from the Lipid Bilayer: A Possible Pathway for Inhibition of a Peptide G Protein-Coupled Receptor by a Lipophilic Small Molecule** *BIOCHEMISTRY*
  Bokoch, M. P., Jo, H., Valcourt, J. R., Srinivasan, Y., Pan, A. C., Capponi, S., Grabe, M., Dror, R. O., Shaw, D. E., DeGrado, W. F., Coughlin, S. R.
  2018; 57 (39): 5748–58

- **Structural basis for sigma(1) receptor ligand recognition** *NATURE STRUCTURAL & MOLECULAR BIOLOGY*
  Schmidt, H. R., Betz, R. M., Dror, R. O., Kruse, A. C.
  2018; 25 (10): 981-+

- **Molecular Dynamics Simulation for All.** *Neuron*
  Hollingsworth, S. A., Dror, R. O.
  2018; 99 (6): 1129–43

- **Structural mechanisms of selectivity and gating in anion channelrhodopsins.** *Nature*
  Kato, H. E., Kim, Y. S., Paggi, J. M., Evans, K. E., Allen, W. E., Richardson, C., Inoue, K., Ito, S., Ramakrishnan, C., Fenno, L. E., Yamashita, K., Hilger, D., Lee, et al
  2018

- **Crystal structure of the natural anion-conducting channelrhodopsin GtACR1.** *Nature*
  Kim, Y. S., Kato, H. E., Yamashita, K., Ito, S., Inoue, K., Ramakrishnan, C., Fenno, L. E., Evans, K. E., Paggi, J. M., Dror, R. O., Kandori, H., Kobilka, B. K., Deisseroth, et al
  2018

- **Structure of the μ-opioid receptor-Gi protein complex.** *Nature*
  Koehl, A., Hu, H., Maeda, S., Zhang, Y., Qu, Q., Paggi, J. M., Latorraca, N. R., Hilger, D., Dawson, R., Matile, H., Schertler, G. F., Granier, S., Weis, et al
  2018

- **Catalytic activation of beta-arrestin by GPCRs** *NATURE*
  Eichel, K., Jullie, D., Barsi-Rhyne, B., Latorraca, N. R., Masureel, M., Sibarita, J., Dror, R. O., von Zastrow, M.
  2018; 557 (7705): 381-+

- **One receptor, many partners: How do GPCRs stimulate diverse signaling proteins?**
  Dror, R.
  AMER CHEMICAL SOC.2018

- **Molecular simulation and machine learning for the design of finely tuned drugs**
  Dror, R.
  AMER CHEMICAL SOC.2018

- **G(i)- and G(s)-coupled GPCRs show different modes of G-protein binding** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Van Eps, N., Altenbach, C., Caro, L. N., Latorraca, N. R., Hollingsworth, S. A., Dror, R. O., Ernst, O. P., Hubbell, W. L.
  2018; 115 (10): 2383–88

- **Mechanism of Substrate Translocation in an Alternating Access Transporter**
  Latorraca, N. R., Fastman, N. M., Feng, L., Dror, R. O.
  CELL PRESS.2018: 207A

- **Structure-inspired design of beta-arrestin-biased ligands for aminergic GPCRs** *NATURE CHEMICAL BIOLOGY*
  McCorvy, J. D., Butler, K. V., Kelly, B., Rechsteiner, K., Karpiak, J., Betz, R. M., Kormos, B. L., Shoichet, B. K., Dror, R. O., Jin, J., Roth, B. L.
  2018; 14 (2): 126-+

- **Structure-inspired design of #-arrestin-biased ligands for aminergic GPCRs** *Nature Chemical Biology*
  McCorvy, J. D., Butler, K. V., Kelly, B., Rechsteiner, K., Karpiak, J., Betz, R. M., Kormos, B. L., Shoichet, B. K., Dror, R. O., Jin, J., Roth, B. L.
  2018: 126-134

- **D-4 dopamine receptor high-resolution structures enable the discovery of selective agonists** *SCIENCE*
  Wang, S., Wacker, D., Levit, A., Che, T., Betz, R. M., McCorvy, J. D., Venkatakrishnan, A. J., Huang, X., Dror, R. O., Shoichet, B. K., Roth, B. L.
  2017; 358 (6361): 381-+

- **Mechanism of substrate translocation in an alternating access transporter**
  Dror, R.
  AMER CHEMICAL SOC.2017

- **Revealing the structural basis for GPCR signaling through atomic-level simulation**
  Dror, R.
  AMER CHEMICAL SOC.2017

- **Structural and Functional Analysis of a beta(2)-Adrenergic Receptor Complex with GRK5** *CELL*
  Komolov, K. E., Du, Y., Nguyen Minh Duc, N. M., Betz, R. M., Rodrigues, J. P., Leib, R. D., Patra, D., Skiniotis, G., Adams, C. M., Dror, R. O., Chung, K. Y., Kobilka, B. K., Benovic, et al
  2017; 169 (3): 407-?

- **Mechanism of Substrate Translocation in an Alternating Access Transporter** *CELL*
  Latorraca, N. R., Fastman, N. M., Venkatakrishnan, A. J., Frommer, W. B., Dror, R. O., Feng, L.
  2017; 169 (1): 96-?

- **Crystal Structure of an LSD-Bound Human Serotonin Receptor.** *Cell*
  Wacker, D., Wang, S., McCorvy, J. D., Betz, R. M., Venkatakrishnan, A. J., Levit, A., Lansu, K., Schools, Z. L., Che, T., Nichols, D. E., Shoichet, B. K., Dror, R. O., Roth, et al
  2017; 168 (3): 377-389 e12

- **GPCR Dynamics: Structures in Motion** *CHEMICAL REVIEWS*
  Latorraca, N. R., Venkatakrishnan, A. J., Dror, R. O.
  2017; 117 (1): 139-155

- **Identification of phosphorylation codes for arrestin recruitment by G protein-coupled receptors** *Cell*
  Zhou, X. E., He, Y., de Waal, P. W., Gao, X., Kang, Y., Van Eps, N., Yin, Y., Pal, K., Goswami, D., White, T. A., Barty, A., Latorraca, N. R., Chapman, et al
  2017: 457-469

- **Identification of Phosphorylation Codes for Arrestin Recruitment by G Protein-Coupled Receptors.** *Cell*
  Zhou, X. E., He, Y. n., de Waal, P. W., Gao, X. n., Kang, Y. n., Van Eps, N. n., Yin, Y. n., Pal, K. n., Goswami, D. n., White, T. A., Barty, A. n., Latorraca, N. R., Chapman, et al
  2017; 170 (3): 457–69.e13

- **Mechanism of intracellular allosteric #2AR antagonist revealed by X-ray crystal structure.** *Nature*
  Liu, X. n., Ahn, S. n., Kahsai, A. W., Meng, K. C., Latorraca, N. R., Pani, B. n., Venkatakrishnan, A. J., Masoudi, A. n., Weis, W. I., Dror, R. O., Chen, X. n., Lefkowitz, R. J., Kobilka, et al
  2017; 548 (7668): 480–84

- **Mechanism of intracellular allosteric #2AR antagonist revealed by X-ray crystal structure** *Nature*
  Liu, X., Ahn, S., Kahsai, A. W., Meng, K. C., Latorraca, N. R., Pani, B., Venkatakrishnan, A., Masoudi, A., Weis, W. I., Dror, R. O., Chen, X., Lefkowitz, R. J., Kobilka, et al
  2017: 480-484

- **D4 dopamine receptor high-resolution structures enable the discovery of selective agonists** *Science*
  Wang, S., Wacker, D., Levit, A., Che, T., Betz, R. M., McCorvy, J. D., Venkatakrishnan, A., Huang, X. P., Dror, R. O., Shoichet, B. K., Roth, B. L.
  2017: 381-386

- **Structural and functional analysis of a #2-adrenergic receptor complex with GRK5** *Cell*
  Komolov, K. E., Du, Y., Duc, N. M., Betz, R. M., Rodrigues, J. M., Leib, R. D., Patra, D., Skiniotis, G., Adams, C. M., Dror, R. O., Chung, K. Y., Kobilka, B. K., Benovic, et al
  2017: 407-421

- **Crystal Structure of a Full-Length Human Tetraspanin Reveals a Cholesterol-Binding Pocket** *CELL*
  Zimmerman, B., Kelly, B., McMillan, B. J., Seegar, T. C., Dror, R. O., Kruse, A. C., Blacklow, S. C.

2016; 167 (4): 1041-?

- **Revealing Atomic-Level Mechanisms of Protein Allostery with Molecular Dynamics Simulations** *PLOS COMPUTATIONAL BIOLOGY*
  Hertig, S., Latorraca, N. R., Dror, R. O.
  2016; 12 (6)

- **Molecular Basis of Ligand Dissociation from the Adenosine A(2A) Receptor** *MOLECULAR PHARMACOLOGY*
  Guo, D., Pan, A. C., Dror, R. O., Mocking, T., Liu, R., Heitman, L. H., Shaw, D. E., IJzerman, A. P.
  2016; 89 (5): 485-491

- **Structural insights into mu-opioid receptor activation** *NATURE*
  Huang, W., Manglik, A., Venkatakrishnan, A. J., Laeremans, T., Feinberg, E. N., Sanborn, A. L., Kato, H. E., Livingston, K. E., Thorsen, T. S., Kling, R. C., Granier, S., Gmeiner, P., Husbands, et al
  2015; 524 (7565): 315-?

- **Structural basis for nucleotide exchange in heterotrimeric G proteins** *SCIENCE*
  Dror, R. O., Mildorf, T. J., Hilger, D., Manglik, A., Borhani, D. W., Arlow, D. H., Philippsen, A., Villanueva, N., Yang, Z., Lerch, M. T., Hubbell, W. L., Kobilka, B. K., Sunahara, et al
  2015; 348 (6241): 1361-1365

- **Identifying localized changes in large systems: Change-point detection for biomolecular simulations** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Fan, Z., Dror, R. O., Mildorf, T. J., Piana, S., Shaw, D. E.
  2015; 112 (24): 7454-7459

- **Structural basis for chemokine recognition and activation of a viral G protein-coupled receptor** *SCIENCE*
  Burg, J. S., Ingram, J. R., Venkatakrishnan, A. J., Jude, K. M., Dukkipati, A., Feinberg, E. N., Angelini, A., Waghray, D., Dror, R. O., Ploegh, H. L., Garcia, K. C.
  2015; 347 (6226): 1113-1117

- **Insights into the Role of Asp79(2.50) in beta(2) Adrenergic Receptor Activation from Molecular Dynamics Simulations** *BIOCHEMISTRY*
  Ranganathan, A., Dror, R. O., Carlsson, J.
  2014; 53 (46): 7283-7296

- **Anton 2: Raising the bar for performance and programmability in a special-purpose molecular dynamics supercomputer** *SC14: INTERNATIONAL CONFERENCE FOR HIGH PERFORMANCE COMPUTING, NETWORKING, STORAGE AND ANALYSIS*
  Shaw, D. E., Grossman, J. P., Bank, J. A., Batson, B., Butts, J. A., Chao, J. C., Deneroff, M. M., Dror, R. O., Even, A., Fenton, C. H., Forte, A., Gagliardo, J., Gill, et al
  2014: 41-53

- **The role of ligands on the equilibria between functional States of a g protein-coupled receptor.** *Journal of the American Chemical Society*
  Kim, T. H., Chung, K. Y., Manglik, A., Hansen, A. L., Dror, R. O., Mildorf, T. J., Shaw, D. E., Kobilka, B. K., Prosser, R. S.
  2013; 135 (25): 9465-9474

- **Hardware Support for Fine-Grained Event-Driven Computation in Anton 2** *ACM SIGPLAN NOTICES*
  Grossman, J. P., Kuskin, J. S., Bank, J. A., Theobald, M., Dror, R. O., Ierardi, D. J., Larson, R. H., Ben Schafer, U., Towles, B., Young, C., Shaw, D. E.
  2013; 48 (4): 549-560

- **The Dynamic Process of beta(2)-Adrenergic Receptor Activation** *CELL*
  Nygaard, R., Zou, Y., Dror, R. O., Mildorf, T. J., Arlow, D. H., Manglik, A., Pan, A. C., Liu, C. W., Fung, J. J., Bokoch, M. P., Thian, F. S., Kobilka, T. S., Shaw, et al
  2013; 152 (3): 532-542

- **The dynamic process of #2-adrenergic receptor activation** *Cell*
  Nygaard, R., Zou, Y., Dror, R. O., Mildorf, T. J., Arlow, D. H., Manglik, A., Pan, A. C., Liu, C. W., Fung, J. J., Bokoch, M. P., Thian, F. S., Kobilka, T. S., Shaw, et al
  2013: 532-542

- **Extending the generality of molecular dynamics simulations on a special-purpose machine** *IEEE 27TH INTERNATIONAL PARALLEL AND DISTRIBUTED PROCESSING SYMPOSIUM (IPDPS 2013)*
  Scarpazza, D. P., Ierardi, D. J., Lerer, A. K., Mackenzie, K. M., Pan, A. C., Bank, J. A., Chow, E., Dror, R. O., Grossman, J. P., Killebrew, D., Moraes, M. A., Predescu, C., Salmon, et al

2013: 933-945

- **Structural basis for modulation of a GPCR by allosteric drugs** *Nature*
  Dror, R. O., Green, H. F., Valant, C., Borhani, D. W., Valcourt, J. R., Pan, A. C., Arlow, D. H., Canals, M., Lane, J. R., Rahmani, R., Baell, J. B., Sexton, P. M., Christopoulos, et al
  2013: 295-299

- **High-resolution crystal structure of human protease-activated receptor 1** *NATURE*
  Zhang, C., Srinivasan, Y., Arlow, D. H., Fung, J. J., Palmer, D., Zheng, Y., Green, H. F., Pandey, A., Dror, R. O., Shaw, D. E., Weis, W. I., Coughlin, S. R., Kobilka, et al
  2012; 492 (7429): 387-?

- **Refinement of protein structure homology models via long, all-atom molecular dynamics simulations** *PROTEINS-STRUCTURE FUNCTION AND BIOINFORMATICS*
  Raval, A., Piana, S., Eastwood, M. P., Dror, R. O., Shaw, D. E.
  2012; 80 (8): 2071-2079

- **Evaluating the Effects of Cutoffs and Treatment of Long-range Electrostatics in Protein Folding Simulations** *PLOS ONE*
  Piana, S., Lindorff-Larsen, K., Dirks, R. M., Salmon, J. K., Dror, R. O., Shaw, D. E.
  2012; 7 (6)

- **Oncogenic Mutations Counteract Intrinsic Disorder in the EGFR Kinase and Promote Receptor Dimerization** *CELL*
  Shan, Y., Eastwood, M. P., Zhang, X., Kim, E. T., Arkhipov, A., Dror, R. O., Jumper, J., Kuriyan, J., Shaw, D. E.
  2012; 149 (4): 860-870

- **Structure and dynamics of the M3 muscarinic acetylcholine receptor** *NATURE*
  Kruse, A. C., Hu, J., Pan, A. C., Arlow, D. H., Rosenbaum, D. M., Rosemond, E., Green, H. F., Liu, T., Chae, P. S., Dror, R. O., Shaw, D. E., Weis, W. I., Wess, et al
  2012; 482 (7386): 552-556

- **Systematic Validation of Protein Force Fields against Experimental Data** *PLOS ONE*
  Lindorff-Larsen, K., Maragakis, P., Piana, S., Eastwood, M. P., Dror, R. O., Shaw, D. E.
  2012; 7 (2)

- **Biomolecular Simulation: A Computational Microscope for Molecular Biology** *ANNUAL REVIEW OF BIOPHYSICS, VOL 41*
  Dror, R. O., Dirks, R. M., Grossman, J. P., Xu, H., Shaw, D. E.
  2012; 41: 429-452

- **Computationally efficient molecular dynamics integrators with improved sampling accuracy** *MOLECULAR PHYSICS*
  Predescu, C., Lippert, R. A., Eastwood, M. P., Ierardi, D., Xu, H., Jensen, M. O., Bowers, K. J., Gullingsrud, J., Rendleman, C. A., Dror, R. O., Shaw, D. E.
  2012; 110 (9-10): 967-983

- **Mechanism of voltage gating in K+ channels** *Science*
  Jensen, M. O., Jogini, V., Borhani, D. W., Lefler, A. E., Dror, R. O., Shaw, D. E.
  2012: 229-233

- **How Fast-Folding Proteins Fold** *SCIENCE*
  Lindorff-Larsen, K., Piana, S., Dror, R. O., Shaw, D. E.
  2011; 334 (6055): 517-520

- **Pathway and mechanism of drug binding to G-protein-coupled receptors** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Dror, R. O., Pan, A. C., Arlow, D. H., Borhani, D. W., Maragakis, P., Shan, Y., Xu, H., Shaw, D. E.
  2011; 108 (32): 13118-13123

- **How Does a Drug Molecule Find Its Target Binding Site?** *JOURNAL OF THE AMERICAN CHEMICAL SOCIETY*
  Shan, Y., Kim, E. T., Eastwood, M. P., Dror, R. O., Seeliger, M. A., Shaw, D. E.
  2011; 133 (24): 9181-9183

- **OVERCOMING COMMUNICATION LATENCY BARRIERS IN MASSIVELY PARALLEL SCIENTIFIC COMPUTATION** *IEEE MICRO*

Dror, R. O., Grossman, J. P., Mackenzie, K. M., Towles, B., Chow, E., Salmon, J. K., Young, C., Bank, J. A., Batson, B., Deneroff, M. M., Kuskin, J. S., Larson, R. H., Moraes, et al

2011; 31 (3): 8-19

- **Structure and function of an irreversible agonist-beta(2) adrenoceptor complex** *NATURE*

  Rosenbaum, D. M., Zhang, C., Lyons, J. A., Holl, R., Aragao, D., Arlow, D. H., Rasmussen, S. G., Choi, H., DeVree, B. T., Sunahara, R. K., Chae, P. S., Gellman, S. H., Dror, et al

  2011; 469 (7329): 236-240

- **Activation mechanism of the #2-adrenergic receptor** *Proceedings of the National Academy of Sciences of the United States of America*

  Dror, R. O., Arlow, D. H., Maragakis, P., Mildorf, T. J., Pan, A. C., Xu, H., Borhani, D. W., Shaw, D. E.

  2011: 18684-18689

- **Radix-8 Digit-by-Rounding: Achieving High-Performance Reciprocals, Square Roots, and Reciprocal Square Roots** *2011 20TH IEEE SYMPOSIUM ON COMPUTER ARITHMETIC (ARITH-20)*

  Butts, J. A., Tang, P. T., Dror, R. O., Shaw, D. E.

  2011: 149-158

- **Structure and function of an irreversible agonist–#2 adrenoceptor complex** *Nature*

  Rosenbaum, D. M., Zhang, C., Lyons, J. A., Holl, R., Aragao, D., Arlow, D. H., Rasmussen, S. F., Choi, H. J., DeVree, B. T., Sunahara, R. K., Chae, P. S., Gellman, S. H., Dror, et al

  2011: 236-240

- **Atomic-Level Characterization of the Structural Dynamics of Proteins** *SCIENCE*

  Shaw, D. E., Maragakis, P., Lindorff-Larsen, K., Piana, S., Dror, R. O., Eastwood, M. P., Bank, J. A., Jumper, J. M., Salmon, J. K., Shan, Y., Wriggers, W.

  2010; 330 (6002): 341-346

- **Equipartition and the Calculation of Temperature in Biomolecular Simulations** *JOURNAL OF CHEMICAL THEORY AND COMPUTATION*

  Eastwood, M. P., Stafford, K. A., Lippert, R. A., Jensen, M. O., Maragakis, P., Predescu, C., Dror, R. O., Shaw, D. E.

  2010; 6 (7): 2045-2058

- **Exploring atomic resolution physiology on a femtosecond to millisecond timescale using molecular dynamics simulations** *JOURNAL OF GENERAL PHYSIOLOGY*

  Dror, R. O., Jensen, M. O., Borhani, D. W., Shaw, D. E.

  2010; 135 (6): 555-562

- **Improved side-chain torsion potentials for the Amber ff99SB protein force field** *PROTEINS-STRUCTURE FUNCTION AND BIOINFORMATICS*

  Lindorff-Larsen, K., Piana, S., Palmo, K., Maragakis, P., Klepeis, J. L., Dror, R. O., Shaw, D. E.

  2010; 78 (8): 1950-1958

- **Principles of conduction and hydrophobic gating in K+ channels** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*

  Jensen, M. O., Borhani, D. W., Lindorff-Larsen, K., Maragakis, P., Jogini, V., Eastwood, M. P., Dror, R. O., Shaw, D. E.

  2010; 107 (13): 5833-5838

- **Improved Twiddle Access for Fast Fourier Transforms** *IEEE TRANSACTIONS ON SIGNAL PROCESSING*

  Bowers, K. J., Lippert, R. A., Dror, R. O., Shaw, D. E.

  2010; 58 (3): 1122-1130

- **Minimizing thermodynamic length to select intermediate states for free-energy calculations and replica-exchange simulations (vol 80, 046705, 2009)** *PHYSICAL REVIEW E*

  Shenfeld, D. K., Xu, H., Eastwood, M. P., Dror, R. O., Shaw, D. E.

  2009; 80 (4)

- **Automated Event Detection and Activity Monitoring in Long Molecular Dynamics Simulations** *JOURNAL OF CHEMICAL THEORY AND COMPUTATION*

  Wriggers, W., Stafford, K. A., Shan, Y., Piana, S., Maragakis, P., Lindorff-Larsen, K., Miller, P. J., Gullingsrud, J., Rendleman, C. A., Eastwood, M. P., Dror, R. O., Shaw, D. E.

  2009; 5 (10): 2595-2605

- **Long-timescale molecular dynamics simulations of protein structure and function** *CURRENT OPINION IN STRUCTURAL BIOLOGY*

  Klepeis, J. L., Lindorff-Larsen, K., Dror, R. O., Shaw, D. E.

2009; 19 (2): 120-127

- **A conserved protonation-dependent switch controls drug binding in the Abl kinase** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Shan, Y., Seeliger, M. A., Eastwood, M. P., Frank, F., Xu, H., Jensen, M. O., Dror, R. O., Kuriyan, J., Shaw, D. E.
  2009; 106 (1): 139-144

- **Elucidating membrane protein function through long-timescale molecular dynamics simulation** *2009 ANNUAL INTERNATIONAL CONFERENCE OF THE IEEE ENGINEERING IN MEDICINE AND BIOLOGY SOCIETY, VOLS 1-20*
  Dror, R. O., Jensen, M. O., Shaw, D. E.
  2009: 2340-2342

- **. Identification of two distinct inactive conformations of the #2-adrenergic receptor reconciles structural and biochemical observations** *Proceedings of the National Academy of Sciences of the United States of America*
  Dror, R. O., Arlow, D. H., Borhani, D. W., Jensen, M. O., Piana, S., Shaw, D. E.
  2009: 4689-4694

- **Dynamic control of slow water transport by aquaporin 0: Implications for hydration and junction stability in the eye lens** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Jensen, M. O., Dror, R. O., Xu, H., Borhani, D. W., Arkin, I. T., Eastwood, M. P., Shaw, D. E.
  2008; 105 (38): 14430-14435

- **Anton, a special-purpose machine for molecular dynamics simulation** *COMMUNICATIONS OF THE ACM*
  Shaw, D. E., Deneroff, M. M., Dror, R. O., Kuskin, J. S., Larson, R. H., Salmon, J. K., Young, C., Batson, B., Bowers, K. J., Chao, J. C., Eastwood, M. P., Gagliardo, J., Grossman, et al
  2008; 51 (7): 91-97

- **Microsecond molecular dynamics simulation shows effect of slow loop dynamics on backbone amide order parameters of proteins** *JOURNAL OF PHYSICAL CHEMISTRY B*
  Maragakis, P., Lindorff-Larsen, K., Eastwood, M. P., Dror, R. O., Klepeis, J. L., Arkin, I. T., Jensen, M. O., Xu, H., Trbovic, N., Friesner, R. A., Palmer, A. G., Shaw, D. E.
  2008; 112 (19): 6155-6158

- **Hierarchical Simulation-Based Verification of Anton, a Special-Purpose Parallel Machine** *2008 IEEE INTERNATIONAL CONFERENCE ON COMPUTER DESIGN*
  Grossman, J. P., Salmon, J. K., Ho, C. R., Ierardi, D. J., Towles, B., Batson, B., Spengler, J., Wang, S. C., Mueller, R., Theobald, M., Young, C., Gagliardo, J., Deneroff, et al
  2008: 340-347

- **Incorporating Flexibility in Anton, a Specialized Machine for Molecular Dynamics Simulation** *2008 IEEE 14TH INTERNATIONAL SYMPOSIUM ON HIGH PEFORMANCE COMPUTER ARCHITECTURE*
  Kuskin, J. S., Young, C., Grossman, J. P., Batson, B., Deneroff, M. M., Dror, R. O., Shaw, D. E.
  2008: 315-326

- **High-Throughput Pairwise Point Interactions in Anton, a Specialized Machine for Molecular Dynamics Simulation** *2008 IEEE 14TH INTERNATIONAL SYMPOSIUM ON HIGH PEFORMANCE COMPUTER ARCHITECTURE*
  Larson, R. H., Salmon, J. K., Dror, R. O., Deneroff, M. M., Young, C., Grossman, J. P., Shan, Y., Klepeis, J. L., Shaw, D. E.
  2008: 303-314

- **Mechanism of Na+/H+ antiporting** *SCIENCE*
  Arkin, I. T., Xu, H., Jensen, M. O., Arbely, E., Bennett, E. R., Bowers, K. J., Chow, E., Dror, R. O., Eastwood, M. P., Flitman-Tene, R., Gregersen, B. A., Klepeis, J. L., Kolossvary, et al
  2007; 317 (5839): 799-803

- **A common, avoidable source of error in molecular dynamics integrators** *JOURNAL OF CHEMICAL PHYSICS*
  Lippert, R. A., Bowers, K. J., Dror, R. O., Eastwood, M. P., Gregersen, B. A., Klepeis, J. L., Kolossvary, I., Shaw, D. E.
  2007; 126 (4)

- **Zonal methods for the parallel execution of range-limited N-body simulations** *JOURNAL OF COMPUTATIONAL PHYSICS*
  Bowers, K. J., Dror, R. O., Shaw, D. E.
  2007; 221 (1): 303-329

- **The midpoint method for parallelization of particle simulations** *JOURNAL OF CHEMICAL PHYSICS*
  Bowers, K. J., Dror, R. O., Shaw, D. E.
  2006; 124 (18)
- **Gaussian split Ewald: A fast Ewald mesh method for molecular simulation** *JOURNAL OF CHEMICAL PHYSICS*
  Shan, Y. B., Klepeis, J. L., Eastwood, M. P., Dror, R. O., Shaw, D. E.
  2005; 122 (5)
- **Statistical characterization of real-world illumination** *JOURNAL OF VISION*
  Dror, R., WILLSKY, A. S., Adelson, E. H.
  2004; 4 (9): 821-837
- **Bayesian estimation of transcript levels using a general model of array measurement noise** *JOURNAL OF COMPUTATIONAL BIOLOGY*
  Dror, R. O., Murnick, J. G., Rinaldi, N. J., Marinescu, V. D., Rifkin, R. M., Young, R. A.
  2003; 10 (3-4): 433-452
- **Real-world illumination and the perception of surface reflectance properties** *JOURNAL OF VISION*
  Fleming, R. W., Dror, R. O., Adelson, E. H.
  2003; 3 (5): 347-368
- **Accuracy of velocity estimation by Reichardt corr¬elators** *Journal of the Optical Society of America A*
  Dror, R. O., O'Carroll, D. C., Laughlin, S. B.
  2001: 241-252
- **A mathematical criterion based on phase response curves for stability in a ring of coupled oscillators** *BIOLOGICAL CYBERNETICS*
  Dror, R., Canavier, C. C., Butera, R. J., Clark, J. W., Byrne, J. H.
  1999; 80 (1): 11-23
- **Phase response characteristics of model neurons determine which patterns are expressed in a ring circuit model of gait generation** *BIOLOGICAL CYBERNETICS*
  Canavier, C. C., Butera, R. J., Dror, R. O., Baxter, D. A., Clark, J. W., Byrne, J. H.
  1997; 77 (6): 367-380
- **A search for best constants in the Hardy-Littlewood maximal theorem** *Journal of Fourier Analysis and Applications*
  Dror, R. O., Ganguli, S., Strichartz, R. S.
  1996: 473-486