Ron O. Dror

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PROFESSIONAL EXPERIENCE

Cheriton Family Professor, Stanford University 2014–present

Faculty member in the Departments of Computer Science and, by courtesy, Molecular and Cellular Physiology and Structural Biology. Affiliated with the Stanford Artificial Intelligence Lab, the Institute for Computational and Mathematical Engineering, Bio-X, ChEM-H, and the Biophysics and Biomedical Informatics Programs. Lead a research group that applies machine learning and physics-based simulation to structural biology in order to explain the workings of living systems and develop better medicines. Developed two new computational biology courses whose enrollment grew eight-fold over three years.

Senior Research Scientist and Special Advisor to the Chairman, D. E. Shaw Research 2002–2014

Second in command of a 110-person research group focused on accelerating simulations of biomolecules, whose work was highlighted by *Science* as one of the top ten scientific breakthroughs of 2010. Helped build the group after starting as the first hire, and managed interdisciplinary projects together with founder and chief scientist David E. Shaw. Oversaw the group's operations; managed substantial parts of the design process for Anton, a special-purpose molecular dynamics supercomputer, and Desmond, a fast molecular dynamics software package for standard computer clusters; and played a leadership role in various projects involving application of molecular dynamics simulations to proteins and ligands of biological and pharmaceutical interest.

Lead Artificial Intelligence Engineer, Arch Healthcare 2001–2002

Developed image-processing software to detect signs of cancer in mammograms.

EDUCATION

Massachusetts Institute of Technology 2002
Ph.D. in Electrical Engineering and Computer Science
Advisors: Alan Willsky and Edward Adelson
Research area: Machine learning and statistical inference for computer vision and genomics

University of Cambridge 1998
M.Phil. in Biological Sciences (Churchill Scholar)
Advisor: Simon Laughlin
Research area: Computational and experimental neuroscience (visual motion detection)

Rice University 1997
B.S. in Electrical Engineering and B.A. in Mathematics
Summa cum laude (1st in class)

AWARDS

Cheriton Family Professorship, Stanford University	2023
Best Paper Award, Conference on Neural Information Processing Systems (NeurIPS), Datasets & Benchmarks	2021
Intel Outstanding Researcher Award	2021
Ravi Faculty Scholar, Stanford University	2018
Gordon Bell Prize (Performance)	2014
Best Paper Award, International Parallel and Distributed Processing Symposium	2013
Best Paper Award, ACM/IEEE Conference on Supercomputing (SC11)	2011
Science Magazine Breakthrough of the Year runner-up (one of nine projects)	2010
Gordon Bell Prize (Special Achievement)	2009
Best Paper Award, ACM/IEEE Conference on Supercomputing (SC09)	2009
Profiled by MIT EECS Dept. in feature on "EECS Alums: Major Players and Thinkers"	2009
Best Paper Award, ACM/IEEE Conference on Supercomputing (SC06)	2006
Whitaker Foundation Fellowship in Biomedical Engineering	1999–2002
National Defense Science and Engineering Graduate Fellowship	1998–2001
Churchill Scholarship	1997–1998
National Science Foundation Graduate Fellowship	declined, 1998
Fulbright Scholarship	declined, 1997
MSTP Fellowship, Harvard-MIT M.D./Ph.D. Program	declined, 1997
Elected to Phi Beta Kappa, Sigma Xi, Tau Beta Pi, and Eta Kappa Nu	1996–2001
Graham Baker Studentship, highest scholastic standing in Rice University class	1996
William Marsh Rice Scholarship (full tuition)	1993–1997
Bronze Medalist, International Mathematical Olympiad (Istanbul, Turkey)	1993
National Merit Scholarship and National Science Scholarship	1992

PUBLICATION SUMMARY

I have published over 140 papers, including over 30 in *Nature*, *Science*, and *Cell*, generally considered the most selective scientific journals. My papers have been cited over 40,000 times, and my h-index is 85.

In the publication list below:
* indicates senior/corresponding authorship
† indicates papers based entirely on work done since arriving at Stanford

JOURNAL PAPERS

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

2. N. Hoppe, S. Harrison, S.H. Hwang, Z. Chen, M. Karelina, I. Deshpande, C.M. Suomivuori, V.R. Palicharla, S.P. Berry, P. Tschaikner, D. Regele, D.F. Covey, E. Stefan, D.S. Marks, J.F. Reiter, **R.O. Dror**, A.S. Evers, S. Mukhopadhyay, A. Manglik. GPR161 structure uncovers the redundant role of sterol-regulated ciliary cAMP signaling in the Hedgehog pathway. *Nature Structural & Molecular Biology* (2024).†

3. A.S. Powers, H.H. Yu, P. Suriana, R.V. Koodli, T. Lu, J.M. Paggi, **R.O. Dror***. Geometric Deep Learning for Structure-Based Ligand Design. *ACS Central Science* (2023).†

4. M. Karelina, J.J. Noh, **R.O. Dror***. How accurately can one predict drug binding modes using AlphaFold models? *eLife* (2023).†

5. W.A. Burger, V. Pham, Z. Vuckovic, A.S. Powers, J.I. Mobbs, Y. Laloudakis, A. Glukhova, D. Wootten, A.B. Tobin, P.M. Sexton, S.M. Paul, C.C. Felder, R. Radostin, **R.O. Dror***, A. Christopoulos, C. Valant, and D.M. Thal. Xanomeline displays concomitant orthosteric and allosteric binding modes at the M4 mAChR. *Nature Communications*, 14(1): 5440 (2023).†

6. S. Tajima, Y.S. Kim, M. Fukuda, Y.J. Jo, P.Y. Wang, J.M. Paggi, M. Inoue, E.F.X. Byrne, K.E. Kishi, S. Nakamura, C. Ramakrishnan, S. Takaramoto, T. Nagata, M. Konno, M. Sugiura, K. Katayama, T.E. Matsui, K. Yamashita, S. Kim, H. Ikeda, J. Kim, H. Kandori**, R.O. Dror**, K. Inoue, K. Deisseroth, and H.E. Kato. Structural basis for ion selectivity in potassium-selective channelrhodopsins. *Cell* 186(20):4325-4344.e26 (2023).†

7. X. Xu, J. Shonberg, J. Kaindl, M.J. Clark, A. Stößel, L. Maul, D. Mayer, H. Hübner, K. Hirata, A.J. Venkatakrishnan, **R.O. Dror**, B.K. Kobilka, R.K. Sunahara, X. Liu and P. Gmeiner. Constrained catecholamines gain β2AR selectivity through allosteric effects on pocket dynamics. *Nature Communications* (2023).†

8. K.K. Kumar, M.J. Robertson, E. Thadhani, H. Wang, C.M. Suomivuori, A.S. Powers, L. Ji, S.P. Nikas, **R.O. Dror**, A. Inoue, A. Makriyannis, G. Skiniotis and B. Kobilka. Structural basis for activation of CB1 by an endocannabinoid analog. *Nature Communications* (2023).†

9. A.S. Powers, V. Pham, W.A. C. Burger, G. Thompson, Y. Laloudakis, P.M. Sexton, S.M. Paul, A. Christopoulos, D.M. Thal, C.C. Felder, C. Valant and **R.O. Dror***. Structural basis of efficacy-driven ligand selectivity at GPCRs. *Nature Chemical Biology* (2023).†

10. A.E. Daibani, J.M. Paggi, K. Kim, Y.D. Laloudakis, P. Popov, S.M. Bernhard, B.E. Krumm, R.H.J. Olsen, J. Diberto, F.I. Carroll, V. Katritch, B. Wünsch, **R.O. Dror*** and T. Che. Molecular mechanism of biased signaling at the kappa opioid receptor. *Nature Communications* (2023).†

11. A.S. Powers, V. Pham, W.A. C. Burger, G. Thompson, Y. Laloudakis, P.M. Sexton, S.M. Paul, A. Christopoulos, D.M. Thal, C.C. Felder, C. Valant, and **R.O. Dror***. Structural basis of efficacy-driven ligand selectivity at GPCRs. *Nature Chemical Biology* **19**:805–814 (2023).†

12. S. Eismann, P. Suriana, B. Jing, R.J.L. Townshend, and **R.O. Dror***. Protein model quality assessment using rotation-equivariant transformations on point clouds. *Proteins* **91**:1089–1096 (2023).†

13. Q. Qu, W. Huang, D. Aydin, J.M. Paggi, A.B. Seven, H. Wang, S. Chakraborty, T. Che, J.F. DiBerto, M.J. Robertson, A. Inoue, C.-M, Suomivuori, B.L. Roth, S. Majumdar, **R.O. Dror***, B.K. Kobilka, and G. Skiniotis. Insights into distinct signaling profiles of the μOR activated by diverse agonists. *Nature Chemical Biology* (2022).†

14. B. Faust, C.B. Billesbølle, C.-M. Suomivuori, I. Singh, K. Zhang, N. Hoppe, A.F.M. Pinto, J.K. Diedrich, Y. Muftuoglu, M.W. Szkudlinski, A. Saghatelian, **R.O. Dror**, Y. Cheng, A. Manglik. Autoantibody mimicry of hormone action at the thyrotropin receptor. *Nature* **609**:846–853 (2022).†

15. C. Cao, X. Barros-Álvarez, S. Zhang, K. Kim, M.A. Dämgen, O. Panova, C.-M. Suomivuori, J.F. Fay, X. Zhong, B.E. Krumm, R.H. Gumpper, A.B. Seven, M.J. Robertson, N.J. Krogan, R. Hüttenhain, D.E. Nichols, **R.O. Dror***, G. Skiniotis, B.L. Roth. Signaling snapshots of a serotonin receptor activated by the prototypical psychedelic LSD. *Neuron* **110**:P3154-3167.E7, (2022).†

16. K. Zhang, N. Horikoshi, S. Li, A.S. Powers, M.A. Hameedi, G.D. Pintilie, H.-D. Chae, Y.A. Khan, C.-M. Suomivuori, R.O. Dror, K.M. Sakamoto, W. Chiu, S. Wakatsuki. Cryo-EM, protein engineering, and simulation enable the development of peptide therapeutics against acute myeloid leukemia. *ACS Central Science* **8**:214–222 (2022).†

17. K.E. Kishi, Y.S. Kim, M. Fukuda, M. Inoue, T. Kusakizako, P.Y. Wang, C. Ramakrishnan, E.F. Byrne, E. Thadhani, J.M. Paggi, T.E. Matsui, K. Yamashita, T., M. Shibata, N, Nomura, S. Iwata, O. Nureki, **R.O. Dror**, K. Inoue, K. Deisseroth, and H.E. Kato. Structural basis for channel conduction in the pump-like channelrhodopsin ChRmine. *Cell* **185**: 672-689 (2022).†

18. N. Tsutsumi, S. Maeda, Q. Qu, M. Vögele, K.M. Jude, C.-M. Suomivuori, O. Panova, D. Waghray, H.E. Kato, A. Velasco, **R.O. Dror**, G. Skiniotis, B.K. Kobilka, and K.C. Garcia. Atypical structural snapshots of human cytomegalovirus GPCR interactions with host G proteins. *Science Advances* **8**:eabl5442 (2022).†

19. J.A. Harris, B. Faust, A.B. Gondin, M.A. Dämgen, C.-M. Suomivuori, N.A. Veldhuis, Y. Cheng, **R.O. Dror***, D.M. Thal, and A. Manglik. Selective G protein signaling driven by substance P–neurokinin receptor dynamics. *Nature Chemical Biology* **18**:109-115 (2022).†

20. L. Han, Q. Qu, D. Aydin, O. Panova, M.J. Robertson, Y. Xu, **R.O. Dror**, G. Skiniotis, and L. Feng. Structure and mechanism of the SGLT family of glucose transporters. *Nature* **601:**274–279 (2022).†

21. R.J.L. Townshend, S. Eismann, A.M. Watkins, R. Rangan, M. Karelina, R. Das, and **R.O. Dror***. Geometric deep learning of RNA structure. *Science* **373**:1047–1051 (2021). **Cover story.**†

22. J.M. Paggi, J.A. Belk, S.A. Hollingsworth, N. Villanueva, A.S. Powers, M.J. Clark, A.G. Chemparathy, J.E. Tynan, T.K. Lau, R.K. Sunahara, and **R.O. Dror***. Leveraging non-structural data to predict structures and affinities of protein–ligand complexes. *Proceedings of the National Academy of Sciences of the United States of America*. **118**:e2112621118 (2021).†

23. C.A.P. Wood, J. Zhang, D. Aydin, Y. Xu, B.J. Andreone, U.H. Langen, **R.O. Dror**, C. Gu, L. Feng. Structure and mechanism of blood–brain-barrier lipid transporter MFSD2A. *Nature* **596:**444–448 (2021).†3

24. B. Kelly, S.A. Hollingsworth, D.C. Blakemore, R.M. Owen, R.I. Storer, N.A. Swain, D. Aydin, R. Torella, J.S. Warmus, and **R.O. Dror***. Delineating the ligand–receptor interactions that lead to biased signaling at the μ-opioid receptor. *Journal of Chemical Informatics and Modeling* **61**:3696–3707 (2021).†

25. A.L. Sanborn, B.T. Yeh, J.T. Feigerle, C.V. Hao, R.J.L. Townshend, E.L. Aiden, **R.O. Dror**, and R.D Kornberg. Simple biochemical features underlie transcriptional activation domain diversity and dynamic, fuzzy binding to Mediator. *eLife* **10**:e68068 (2021).†

26. M. Jagota, R.J.L. Townshend, L. Kang, D.A. Bushnell, **R.O. Dror**, R.D. Kornberg, and M. Azubel. Gold nanoparticles and tilt pairs to assess protein flexibility by cryo-electron microscopy. *Ultramicroscopy* **227**:1133026 (2021).†

27. K.E. Komolov, S.M. Sulon, A. Bhardwaj, S.C. van Keulen, N.M. Duc, D.K. Laurinavichyute, H.J. Lou, B.E.T. Ka, Y. Chung, **R.O. Dror**, and J.L. Benovic. Structure of a GRK5-calmodulin complex reveals molecular mechanism of GRK activation and substrate targeting. *Molecular Cell* **81**:323-339 (2021).†

28. C.-M. Suomivuori, N.R. Latorraca, L.M. Wingler, S. Eismann, M.C. King, A.L.W. Kleinhenz, M.A. Skiba, D.P. Staus, A.C. Kruse, R.J. Lefkowitz, and **R.O. Dror***. Molecular mechanism of biased signaling in a prototypical G protein–coupled receptor. *Science* **367**:881–887 (2020).†

29. N.R. Latorraca, M. Masureel, S.A. Hollingsworth, F.M. Heydenreich, C.-M. Suomivuori, C. Brinton, R.J.L. Townshend, M. Bouvier, B.K. Kobilka, and **R.O. Dror***. How GPCR phosphorylation patterns orchestrate arrestin-mediated signaling. *Cell* **183**:1813–1825 (2020).†

30. L.M. Wingler, M.A. Skiba, C. McMahon, D.P. Staus, A.W. Kleinhenz, C.-M. Suomivuori, N.R. Latorraca, **R.O. Dror.**, R.J. Lefkowitz, and A.C. Kruse. Angiotensin and biased analogs induce structurally distinct active conformations within a GPCR. *Science* **367**:888–892 (2020).†

31. S. Eismann, R.J.L. Townshend, N. Thomas, M. Jagota, B. Jing, and **R.O. Dror***. Hierarchical, rotation-equivariant neural networks to select structural models of protein complexes. *Proteins* **89**:493–501 (2020).†

32. C.B. Billesbølle, C.M. Azumaya, R.C. Kretsch, A.S. Powers, S. Gonen, S. Schneider, T. Arvedson, **R.O. Dror**, Y. Cheng, and A. Manglik. Structure of hepcidin-bound ferroportin reveals iron homeostatic mechanisms. *Nature* **586**:80–811 (2020).†

33. E.M. Jones, N.B. Lubock, A.J. Venkatakrishnan, J. Wang, A.M. Tseng, J.M. Paggi, N.R. Latorraca, D. Cancilla, M. Satyadi, J.E. Davis, M.M. Babu, **R.O. Dror***, and S. Kosuri. Structural and Functional Characterization of G Protein-Coupled Receptors with Deep Mutational Scanning. *eLife* **9**:e54895 (2020).†

34. T.A. Chew, B.J. Orlando, J. Zhang, N.R. Latorraca, A. Wang, S.A. Hollingsworth, D.H. Chen, **R.O. Dror**, M. Liao and L. Feng. Structure and mechanism of the cation–chloride cotransporter NKCC1. *Nature* **572**:488–492 (2019).†

35. S.A. Hollingsworth, B. Kelly, C. Valant, J.A. Michaelis, O. Mastromihalis, G. Thompson, A.J. Venkatakrishnan, S. Hertig, P.J. Scammells, P.M. Sexton, C.C. Felder, A. Christopoulos and **R.O. Dror***. Cryptic pocket formation underlies allosteric modulator selectivity at muscarinic GPCRs. *Nature Communications* **10**:3289 (2019).†

36. H.E. Kato, Y. Zhang, H. Hu, C.M. Suomivuori, F.M.N. Kadji, J. Aoki, K.K. Kumar, R. Fonseca, D. Hilger, W. Huang, N. R. Latorraca, A. Inoue, **R.O. Dror**, B.K. Kobilka and G. Skiniotis. Conformational transitions of a neurotensin receptor 1–Gi1 complex. *Nature* **572**:80–85 (2019).†

37. I. Deshpande, J. Liang, D. Hedeen, K.J. Roberts, Y. Zhang, B. Ha, N.R. Latorraca, B. Faust, **R.O. Dror**, P.A. Beachy, B.R. Myers and A. Manglik. Smoothened stimulation by membrane sterols drives Hedgehog pathway activity. *Nature* **571**:284–288 (2019).†

38. A.J. Venkatakrishnan, A. Ma, R. Fonseca, N.R. Latorraca, B. Kelly, R.M. Betz, C. Asawa, B.K. Kobilka, and **R.O. Dror***. Diverse GPCRs exhibit conserved water networks for stabilization and activation. *Proceedings of the National Academy of Sciences of the United States of America* **116**:3288–3292 (2019).†

39. L.M. Wingler, E. Matthias, D. Hilger, N.R. Latorraca, M.T. Lerch, D.P. Staus, **R.O. Dror***, B.K. Kobilka, W.L. Hubbell, and R.J. Lefkowitz. Angiotensin analogs with divergent bias stabilize distinct receptor conformations. *Cell* **176**:468–478 (2019).†

40. R. Betz and **R.O. Dror***. How effectively can adaptive sampling methods capture spontaneous ligand binding? *Journal of Chemical Theory and Computation* **15**:2053–2063 (2019).†

41. K.K. Kumar, M. Shalev-Benami, M.J. Robertson, H. Hu, S.D. Banister, S.A. Hollingsworth, N.R. Latorraca, H.E. Kato, D. Hilger, S. Maeda, W.I. Weis, D.L. Farrens, **R.O. Dror**, S.V. Malhotra, B.K. Kobilka, and G. Skiniotis. Structure of a signaling cannabinoid receptor 1-G protein complex. *Cell* **176**:448–458 (2019).†

42. S.A. Hollingsworth and **R.O. Dror***. Molecular dynamics simulation for all. *Neuron* **99**:1129–1143 (2018).†

43. H.E. Kato, Y.S. Kim, J.M. Paggi, K.E. Evans, W.E. Allen, C. Richardson, K. Inoue, S. Ito, C. Ramakrishnan, Lief E. Fenno, K. Yamashita, D. Hilger, S.Y. Lee, A. Berndt, K. Shen, H. Kandori, **R.O. Dror**, B.K. Kobilka, and K. Deisseroth. Structural mechanisms of selectivity and gating in anion channelrhodopsins. *Nature* **561**:349–354 (2018).†

44. Y.S. Kim, H.E. Kato, K. Yamashita, S. Ito, K. Inoue, C. Ramakrishnan, L.E. Fenno, K.E. Evans, J.M. Paggi, **R.O. Dror**, H. Kandori, B.K. Kobilka, and K. Deisseroth. Crystal structure of a natural anion-conducting channelrhodopsin GtACR1. *Nature* **561**:343–348 (2018).†

45. H.R. Schmidt, R.M. Betz, **R.O. Dror**, and A.C. Kruse. Structural basis for sigma-1 receptor ligand recognition. *Nature Structural & Molecular Biology* **25**:981-987 (2018).†

46. N.R. Latorraca, J.K. Wang, B. Bauer, R.J.L. Townshend, S.A. Hollingsworth, J.E. Olivieri, H.E. Xu, M.E. Sommer, and **R.O. Dror***. Molecular mechanism of GPCR-mediated arrestin activation. *Nature* **557**:452–456 (2018).†

47. K. Eichel, D. Jullié, B. Barsi-Rhyne, N.R. Latorraca, M. Masureel, J. Sibarita, **R.O. Dror**, and M. von Zastrow. Catalytic activation of β-arrestin by GPCRs. *Nature* **557**:381–386 (2018).†

48. A. Koehl, H. Hu, S. Maeda, Y. Zhang, Q. Qu, J.M. Paggi, N.R. Latorraca, D. Hilger, R. Dawson, H. Matile, G.F.X. Schertler, S. Granier, W.I. Weis, **R.O. Dror**, A. Manglik, G. Skiniotis, B.K. Kobilka. Structure of the μ opioid receptor-Gi protein complex. *Nature* **558**:547–552 (2018).†

49. N. van Eps, C. Altenbach, L.N. Caro, N.R. Latorraca, S.A. Hollingsworth, **R.O. Dror**, O.P. Ernst and W.L. Hubbell. Gi- and Gs-coupled GPCRs show different modes of G-protein binding. *Proceedings of the National Academy of Sciences of the United States of America* **115**:2383-2388 (2018).†

50. J.D. McCorvy, K.V. Butler, B. Kelly, K. Rechsteiner, J. Karpiak, R.M. Betz, B.L. Kormos, B.K. Shoichet, **R.O. Dror***, J. Jin, B.L. Roth. Structure-inspired design of β-arrestin-biased ligands for aminergic GPCRs. *Nature Chemical Biology* **14**:126–134 (2018).†

51. M. Masureel, Y. Zou, L. Picard, E. Westhuizen, J.P. Mahoney, J.P.G.L. Rodrigues, T.J. Mildorf, **R.O. Dror**, D.E. Shaw, M. Bouvier, E. Pardon, J. Steyaert, R.K. Sunahara, W.I. Weis, C. Zhang, and B.K. Kobilka. Structural insights into binding specificity, efficacy and bias of a β2AR partial agonist. *Nature Chemical Biology* **14**:1059–1066 (2018).

52. M.P. Bokoch, H. Jo, J.R. Valcourt, Y. Srinivasan, A.C. Pan, S. Capponi, M. Grabe, **R.O. Dror**, D.E. Shaw, W.F. DeGrado, and S.R. Coughlin. Entry from the lipid bilayer: a possible pathway for inhibition of a peptide G protein-coupled receptor by a lipophilic small molecule. *Biochemistry* **57**:5748–5758 (2018).

53. S. Wang, D. Wacker, A. Levit, T. Che, R.M. Betz, J.D. McCorvy, A.J. Venkatakrishnan, X.-P. Huang, **R.O. Dror**, B.K. Shoichet, and B.L. Roth. D4 dopamine receptor high-resolution structures enable the discovery of selective agonists. *Science* **358**: 381–386 (2017).†

54. X. Liu, S. Ahn, A.W. Kahsai, K.C. Meng, N.R. Latorraca, B. Pani, A.J. Venkatakrishnan, A. Masoudi, W.I. Weis, **R.O. Dror**, X. Chen, R.J. Lefkowitz, and B.K. Kobilka. Mechanism of intracellular allosteric β_2AR antagonist revealed by X-ray crystal structure. *Nature* **548**: 480–484 (2017).†

55. X.E. Zhou, Y. He, P.W. de Waal, X. Gao, Y. Kang, N. Van Eps, Y. Yin, K. Pal, D. Goswami, T.A. White, A. Barty, N.R. Latorraca, H.N. Chapman, W.L. Hubbell, **R.O. Dror**, R.C. Stevens, V. Cherezov, V.V. Gurevich, P.R. Griffin, O.P. Ernst, K. Melcher, and H.E. Xu. Identification of phosphorylation codes for arrestin recruitment by G protein-coupled receptors. *Cell* **170**: 457–469 (2017).†

56. N.R. Latorraca, N.M. Fastman, A.J. Venkatakrishnan, W.B. Frommer, **R.O. Dror***, and L. Feng. Mechanism of substrate translocation in an alternating access transporter. *Cell* **169**: 96-107 (2017).†

57. D. Wacker, S. Wang, J.D. McCorvy, R.M. Betz, A.J. Venkatakrishnan, A. Levit, K. Lansu, Z. Schools, T. Che, D.E. Nichols, B.K. Shoichet, **R.O. Dror***, and B.L. Roth. Crystal structure of an LSD-bound human serotonin receptor. *Cell* **168**: 377-389 (2017). **Cover story.**†

58. K.E. Komolov, Y. Du, N.M. Duc, R.M. Betz, J.P.G.L.M. Rodrigues, R.D. Leib, D. Patra, G. Skiniotis, C.M. Adams, **R.O. Dror**, K.Y. Chung, B.K. Kobilka, and J.L. Benovic. Structural and functional analysis of a β2-adrenergic receptor complex with GRK5. *Cell* **169**: 407-421 (2017).†

59. N.R. Latorraca, A.J. Venkatakrishnan, and **R.O. Dror*.** GPCR dynamics: structures in motion. *Chemical Reviews* **117:** 139–155 (2017).†

60. Crystal structure of a full-length human tetraspanin reveals a cholesterol-binding pocket. B. Zimmerman, B. Kelly, T. Seegar, B.J. McMillan, **R.O. Dror**, A.C. Kruse, and S. Blacklow. *Cell* **167**: 1041–1051 (2016).†

61. S. Hertig, N.R. Latorraca, and **R.O. Dror***. Revealing atomic-level mechanisms of protein allostery with molecular dynamics simulations. *PLOS Computational Biology*. **12**: e1004746 (2016).†

62. D. Guo, A.C. Pan, **R.O. Dror**, T. Mocking, R. Liu, L. Heitman, D.E. Shaw, and A.P. IJzerman. Molecular basis of ligand dissociation from the adenosine A_{2A} receptor. *Molecular Pharmacology* **89**: 485–491 (2016).

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TEACHING

Summary

I created two completely new computational biology courses, CS 279 and CS 371, after arriving at Stanford in 2014. The former has grown from 17 to 180 students, and the latter has grown from 5 to 45 students. I also coordinated two for-credit seminar series in computational biomedicine, which have attracted thousands of students. Comments on recent student evaluations include:

> "Best class I've taken at Stanford so far. Ron is an incredible lecturer that makes the most complex topics seem simple."
>
> "One of the best teachers I've had at Stanford in all four years as an undergrad … one of the best courses I've taken at Stanford."

Computer Science (CS) 279: Computational Biology: Structure and Organization of Biomolecules and Cells

Cross-listed in Computational and Mathematical Engineering, Bioengineering, Biophysics, and Biomedical Informatics
Stanford, 2014, 2015, 2016, 2017, 2019, 2020, 2021, 2022, 2023
http://cs279.stanford.edu
Computational techniques for investigating and designing the three-dimensional structure and dynamics of biomolecules and cells. These computational methods play an increasingly important role in drug discovery, medicine, bioengineering, and molecular biology. Course topics include protein structure prediction, protein design, drug screening, molecular simulation, cellular-level simulation, image analysis for microscopy, and methods for solving structures from crystallography and electron microscopy data.

Computer Science (CS) 371: Computational Biology in Four Dimensions

Cross-listed in Computational and Mathematical Engineering, Biophysics, and Biomedical Informatics
Stanford, 2014, 2016, 2017, 2018
http://cs371.stanford.edu
Cutting-edge research on computational techniques for investigating and designing the three-dimensional structure and dynamics of biomolecules, cells, and everything in between. These techniques, which draw on approaches ranging from physics-based simulation to machine learning, play an increasingly important role in drug discovery, medicine, bioengineering, and molecular biology. Course is devoted primarily to reading, presentation, discussion, and critique of papers describing important recent research developments.

Computer Science (CS) 229: Machine Learning

Stanford, 2018
http://cs229.stanford.edu
Topics: statistical pattern recognition, linear and non-linear regression, non-parametric methods, exponential family, GLMs, support vector machines, kernel methods, model/feature selection, learning theory, VC dimension, clustering, density estimation, EM, dimensionality reduction, ICA, PCA, reinforcement learning and adaptive control, Markov decision processes, approximate dynamic programming, and policy search. Prerequisites: linear algebra, and basic probability and statistics.

Computer Science (CS) 522: Seminar on Artificial Intelligence in Healthcare

Stanford, 2017, 2018, 2019, 2020, 2021, 2023
Artificial intelligence is poised to make radical changes in healthcare, transforming areas such as diagnosis, genomics, surgical robotics, and drug discovery. In the coming years, artificial intelligence has the potential to lower healthcare costs, identify more effective treatments, and facilitate prevention and early detection of diseases. This class features prominent researchers, physicians,

entrepreneurs, and venture capitalists, all sharing their thoughts on the future of healthcare. Each year, I run this course in collaboration with a different set of student organizers.

Computer Science (CS) 109: Introduction to Probability for Computer Scientists

Stanford, 2015

Topics include: counting and combinatorics, random variables, conditional probability, independence, distributions, expectation, point estimation, and limit theorems. Applications of probability in computer science including machine learning and the use of probability in the analysis of algorithms.

Computational and Mathematical Engineering (CME) 500: Seminar on Computation and Mathematics in Biology

Stanford, 2014

This course serves as the main seminar series of the Institute for Computational and Mathematical Engineering. My version featured experts on a variety of topics in computational and mathematical biology.