

Eric Gouaux

List of Publications by Year in descending order

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Version: 2024-02-01

147
papers

29,796
citations

7672

79
h-index

11282

141
g-index

170
all docs

170
docs citations

170
times ranked

19868
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Visualizing the binding mode of the antidepressant vilazodone on the serotonin transporter by cryo-EM. <i>Biophysical Journal</i> , 2022, 121, 26a. | 0.2 | 0 |
| 2 | The intracellular domain of homomeric glycine receptors modulates agonist efficacy. <i>Journal of Biological Chemistry</i> , 2021, 296, 100387. | 1.6 | 17 |
| 3 | Mechanism of gating and partial agonist action in the glycine receptor. <i>Cell</i> , 2021, 184, 957-968.e21. | 13.5 | 77 |
| 4 | Hippocampal AMPA receptor assemblies and mechanism of allosteric inhibition. <i>Nature</i> , 2021, 594, 448-453. | 13.7 | 52 |
| 5 | Extracellular loops of the serotonin transporter act as a selectivity filter for drug binding. <i>Journal of Biological Chemistry</i> , 2021, 297, 100863. | 1.6 | 8 |
| 6 | Image collection strategies for single particle cryoEM. <i>Microscopy and Microanalysis</i> , 2021, 27, 1904-1906. | 0.2 | 0 |
| 7 | The antidepressant drug vilazodone is an allosteric inhibitor of the serotonin transporter. <i>Nature Communications</i> , 2021, 12, 5063. | 5.8 | 45 |
| 8 | Molecular mechanism of prestin electromotive signal amplification. <i>Cell</i> , 2021, 184, 4669-4679.e13. | 13.5 | 61 |
| 9 | Architecture and assembly mechanism of native glycine receptors. <i>Nature</i> , 2021, 599, 513-517. | 13.7 | 39 |
| 10 | Putting the Pieces Together: the Hair Cell Transduction Complex. <i>JARO - Journal of the Association for Research in Otolaryngology</i> , 2021, 22, 601-608. | 0.9 | 11 |
| 11 | Illumination of serotonin transporter mechanism and role of the allosteric site. <i>Science Advances</i> , 2021, 7, eabl3857. | 4.7 | 58 |
| 12 | Molecular structures and conformations of protocadherin-15 and its complexes on stereocilia elucidated by cryo-electron tomography. <i>ELife</i> , 2021, 10, . | 2.8 | 6 |
| 13 | Light-coupled cryo-plunger for time-resolved cryo-EM. <i>Journal of Structural Biology</i> , 2020, 212, 107624. | 1.3 | 23 |
| 14 | Chemical and structural investigation of the paroxetine-human serotonin transporter complex. <i>ELife</i> , 2020, 9, . | 2.8 | 53 |
| 15 | The His-Gly motif of acid-sensing ion channels resides in a reentrant α -loop TM implicated in gating and ion selectivity. <i>ELife</i> , 2020, 9, . | 2.8 | 64 |
| 16 | Autoimmune receptor encephalitis in mice induced by active immunization with conformationally stabilized holoreceptors. <i>Science Translational Medicine</i> , 2019, 11, . | 5.8 | 60 |
| 17 | NMDA Receptors TM Structural Asymmetry. <i>Microscopy and Microanalysis</i> , 2019, 25, 1218-1219. | 0.2 | 3 |
| 18 | Strategy for Compositional Analysis of the Hair Cell Mechanotransduction Complex Using TIRF Microscopy. <i>Microscopy and Microanalysis</i> , 2019, 25, 1266-1267. | 0.2 | 1 |

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|----|--|------|-----------|
| 19 | HOTSPUR: A Real-time Interactive Preprocessing System for Cryo-EM Data. <i>Microscopy and Microanalysis</i> , 2019, 25, 1212-1213. | 0.2 | 4 |
| 20 | Serotonin transporter-ibogaine complexes illuminate mechanisms of inhibition and transport. <i>Nature</i> , 2019, 569, 141-145. | 13.7 | 187 |
| 21 | Structure and mechanism of AMPA receptor auxiliary protein complexes. <i>Current Opinion in Structural Biology</i> , 2019, 54, 104-111. | 2.6 | 38 |
| 22 | Architecture and subunit arrangement of native AMPA receptors elucidated by cryo-EM. <i>Science</i> , 2019, 364, 355-362. | 6.0 | 134 |
| 23 | Insights into the mechanism and pharmacology of neurotransmitter sodium symporters. <i>Current Opinion in Structural Biology</i> , 2019, 54, 161-170. | 2.6 | 42 |
| 24 | Ibogaine Binds Human Serotonin Transporter in Multiple Functional States. <i>Biophysical Journal</i> , 2019, 116, 557a. | 0.2 | 0 |
| 25 | Structural, functional, and behavioral insights of dopamine dysfunction revealed by a deletion in <i>SLC6A3</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3853-3862. | 3.3 | 35 |
| 26 | Gating mechanisms of acid-sensing ion channels. <i>Nature</i> , 2018, 555, 397-401. | 13.7 | 177 |
| 27 | Mechanism of NMDA receptor channel block by MK-801 and memantine. <i>Nature</i> , 2018, 556, 515-519. | 13.7 | 177 |
| 28 | Mechanism of NMDA Receptor Channel Block by MK-801 and Memantine. <i>Biophysical Journal</i> , 2018, 114, 24a-25a. | 0.2 | 1 |
| 29 | Structural basis for recognition of diverse antidepressants by the human serotonin transporter. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 170-175. | 3.6 | 114 |
| 30 | Mechanisms for Zinc and Proton Inhibition of the GluN1/GluN2A NMDA Receptor. <i>Cell</i> , 2018, 175, 1520-1532.e15. | 13.5 | 85 |
| 31 | Cryo-EM structure of the benzodiazepine-sensitive $\alpha 2\beta 2\gamma 2$ tri-heteromeric GABA _A receptor in complex with GABA. <i>ELife</i> , 2018, 7, . | 2.8 | 126 |
| 32 | Divalent cation and chloride ion sites of chicken acid sensing ion channel 1a elucidated by x-ray crystallography. <i>PLoS ONE</i> , 2018, 13, e0202134. | 1.1 | 33 |
| 33 | Thermostabilization and purification of the human dopamine transporter (hDAT) in an inhibitor and allosteric ligand bound conformation. <i>PLoS ONE</i> , 2018, 13, e0200085. | 1.1 | 18 |
| 34 | Expression and purification of a functional heteromeric GABA _A receptor for structural studies. <i>PLoS ONE</i> , 2018, 13, e0201210. | 1.1 | 6 |
| 35 | Activation and Desensitization Mechanism of AMPA Receptor-TARP Complex by Cryo-EM. <i>Biophysical Journal</i> , 2018, 114, 125a. | 0.2 | 0 |
| 36 | Structure of mouse protocadherin 15 of the stereocilia tip link in complex with LHFPL5. <i>ELife</i> , 2018, 7, . | 2.8 | 73 |

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|----|--|------|-----------|
| 37 | Cryo-EM structures of the triheteromeric NMDA receptor and its allosteric modulation. <i>Science</i> , 2017, 355, . | 6.0 | 134 |
| 38 | Activation and Desensitization Mechanism of AMPA Receptor-TARP Complex by Cryo-EM. <i>Cell</i> , 2017, 170, 1234-1246.e14. | 13.5 | 111 |
| 39 | Structure and symmetry inform gating principles of ionotropic glutamate receptors. <i>Neuropharmacology</i> , 2017, 112, 11-15. | 2.0 | 65 |
| 40 | Architecture of fully occupied GluA2 AMPA receptorâ€TARP complex elucidated by cryo-EM. <i>Nature</i> , 2016, 536, 108-111. | 13.7 | 100 |
| 41 | X-ray structures and mechanism of the human serotonin transporter. <i>Nature</i> , 2016, 532, 334-339. | 13.7 | 527 |
| 42 | Mechanism of NMDA Receptor Inhibition and Activation. <i>Cell</i> , 2016, 165, 704-714. | 13.5 | 175 |
| 43 | X-ray structures define human P2X3 receptor gating cycle and antagonist action. <i>Nature</i> , 2016, 538, 66-71. | 13.7 | 191 |
| 44 | Thermostabilization, Expression, Purification, and Crystallization of the Human Serotonin Transporter Bound to S-citalopram. <i>Journal of Visualized Experiments</i> , 2016, , . | 0.2 | 14 |
| 45 | X-ray structures of <i>Drosophila</i> dopamine transporter in complex with nisoxetine and reboxetine. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 506-508. | 3.6 | 147 |
| 46 | Neurotransmitter and psychostimulant recognition by the dopamine transporter. <i>Nature</i> , 2015, 521, 322-327. | 13.7 | 357 |
| 47 | Glycine receptor mechanism elucidated by electron cryo-microscopy. <i>Nature</i> , 2015, 526, 224-229. | 13.7 | 370 |
| 48 | Thermostabilization of the Human Serotonin Transporter in an Antidepressant-Bound Conformation. <i>PLoS ONE</i> , 2015, 10, e0145688. | 1.1 | 21 |
| 49 | How LeuT shapes our understanding of the mechanisms of sodiumâ€coupled neurotransmitter transporters. <i>Journal of Physiology</i> , 2014, 592, 863-869. | 1.3 | 96 |
| 50 | X-Ray Structure of Acid-Sensing Ion Channel 1â€Snake Toxin Complex Reveals Open State of a Na ⁺ -Selective Channel. <i>Cell</i> , 2014, 156, 717-729. | 13.5 | 264 |
| 51 | Screening and large-scale expression of membrane proteins in mammalian cells for structural studies. <i>Nature Protocols</i> , 2014, 9, 2574-2585. | 5.5 | 532 |
| 52 | X-ray structures of GluCl in apo states reveal a gating mechanism of Cys-loop receptors. <i>Nature</i> , 2014, 512, 333-337. | 13.7 | 236 |
| 53 | Structure and Dynamics of AMPA Receptor GluA2 in Resting, Pre-Open, and Desensitized States. <i>Cell</i> , 2014, 158, 778-792. | 13.5 | 186 |
| 54 | X-ray structures of AMPA receptorâ€cone snail toxin complexes illuminate activation mechanism. <i>Science</i> , 2014, 345, 1021-1026. | 6.0 | 110 |

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|----|--|------|-----------|
| 55 | NMDA receptor structures reveal subunit arrangement and pore architecture. <i>Nature</i> , 2014, 511, 191-197. | 13.7 | 441 |
| 56 | Imaged by Cryo-EM, Activated and Desensitized GluA2 Glutamate Receptors Show Extreme Flexibility. <i>Biophysical Journal</i> , 2014, 106, 30a. | 0.2 | 0 |
| 57 | Structural basis for action by diverse antidepressants on biogenic amine transporters. <i>Nature</i> , 2013, 503, 141-145. | 13.7 | 125 |
| 58 | X-ray structure of dopamine transporter elucidates antidepressant mechanism. <i>Nature</i> , 2013, 503, 85-90. | 13.7 | 549 |
| 59 | Unanticipated parallels in architecture and mechanism between ATP-gated P2X receptors and acid sensing ion channels. <i>Current Opinion in Structural Biology</i> , 2013, 23, 277-284. | 2.6 | 34 |
| 60 | Novel Dicarboxylate Selectivity in an Insect Glutamate Transporter Homolog. <i>PLoS ONE</i> , 2013, 8, e70947. | 1.1 | 7 |
| 61 | Insights into transport mechanism from LeuT engineered to transport tryptophan. <i>EMBO Journal</i> , 2012, 31, 228-235. | 3.5 | 45 |
| 62 | Structures of LeuT in bicelles define conformation and substrate binding in a membrane-like context. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 212-219. | 3.6 | 103 |
| 63 | 1PT103 Mechanism of ATP binding and channel activation in P2X receptors (The 50th Annual Meeting of Tj ETQq1 1 0.784314 rgBT / 0.0) | 1.0 | 0 |
| 64 | A Fluorescence-Detection Size-Exclusion Chromatography-Based Thermostability Assay for Membrane Protein Precrystallization Screening. <i>Structure</i> , 2012, 20, 1293-1299. | 1.6 | 222 |
| 65 | Substrate binds in the S1 site of the F253A mutant of LeuT, a neurotransmitter sodium symporter homologue. <i>EMBO Reports</i> , 2012, 13, 861-866. | 2.0 | 39 |
| 66 | X-ray structures of LeuT in substrate-free outward-open and apo inward-open states. <i>Nature</i> , 2012, 481, 469-474. | 13.7 | 488 |
| 67 | Molecular mechanism of ATP binding and ion channel activation in P2X receptors. <i>Nature</i> , 2012, 485, 207-212. | 13.7 | 460 |
| 68 | Structural plasticity and dynamic selectivity of acid-sensing ion channel-spider toxin complexes. <i>Nature</i> , 2012, 489, 400-405. | 13.7 | 245 |
| 69 | Architecture, Symmetry and Mechanism of Ionotropic Glutamate Receptors. <i>Biophysical Journal</i> , 2011, 100, 363a. | 0.2 | 0 |
| 70 | Principles of activation and permeation in an anion-selective Cys-loop receptor. <i>Nature</i> , 2011, 474, 54-60. | 13.7 | 899 |
| 71 | Amino Terminal Domains of the NMDA Receptor Are Organized as Local Heterodimers. <i>PLoS ONE</i> , 2011, 6, e19180. | 1.1 | 30 |
| 72 | The New York Consortium on Membrane Protein Structure (NYCOMPS): a high-throughput platform for structural genomics of integral membrane proteins. <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 191-199. | 1.2 | 57 |

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| 73 | Neurotransmitter/sodium symporter orthologue LeuT has a single high-affinity substrate site. <i>Nature</i> , 2010, 468, 1129-1132. | 13.7 | 117 |
| 74 | Dynamic Superresolution Imaging of Endogenous Proteins on Living Cells at Ultra-High Density. <i>Biophysical Journal</i> , 2010, 99, 1303-1310. | 0.2 | 364 |
| 75 | Molecular bases of cyclodextrin adapter interactions with engineered protein nanopores. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 8165-8170. | 3.3 | 108 |
| 76 | Pore Architecture and ion Sites of Acid Sensing ion Channels and P2X Receptors. <i>Biophysical Journal</i> , 2010, 98, 610a. | 0.2 | 1 |
| 77 | The molecular logic of sodium-coupled neurotransmitter transporters. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2009, 364, 149-154. | 1.8 | 50 |
| 78 | Crystal structure and association behaviour of the GluR2 amino-terminal domain. <i>EMBO Journal</i> , 2009, 28, 1812-1823. | 3.5 | 146 |
| 79 | Unlocking the molecular secrets of sodium-coupled transporters. <i>Nature</i> , 2009, 459, 347-355. | 13.7 | 308 |
| 80 | Crystal structure of the ATP-gated P2X4 ion channel in the closed state. <i>Nature</i> , 2009, 460, 592-598. | 13.7 | 680 |
| 81 | X-ray structure, symmetry and mechanism of an AMPA-subtype glutamate receptor. <i>Nature</i> , 2009, 462, 745-756. | 13.7 | 966 |
| 82 | Pore architecture and ion sites in acid-sensing ion channels and P2X receptors. <i>Nature</i> , 2009, 460, 599-604. | 13.7 | 422 |
| 83 | Structure and Mechanism of a Na ⁺ -Independent Amino Acid Transporter. <i>Science</i> , 2009, 325, 1010-1014. | 6.0 | 299 |
| 84 | A Competitive Inhibitor Traps LeuT in an Open-to-Out Conformation. <i>Science</i> , 2008, 322, 1655-1661. | 6.0 | 418 |
| 85 | Coupling substrate and ion binding to extracellular gate of a sodium-dependent aspartate transporter. <i>Nature</i> , 2007, 445, 387-393. | 13.7 | 473 |
| 86 | Antidepressant binding site in a bacterial homologue of neurotransmitter transporters. <i>Nature</i> , 2007, 448, 952-956. | 13.7 | 391 |
| 87 | Structure of acid-sensing ion channel 1 at 1.9 Å resolution and low pH. <i>Nature</i> , 2007, 449, 316-323. | 13.7 | 979 |
| 88 | Measurement of Conformational Changes accompanying Desensitization in an Ionotropic Glutamate Receptor. <i>Cell</i> , 2006, 127, 85-97. | 13.5 | 206 |
| 89 | Fluorescence-Detection Size-Exclusion Chromatography for Precrystallization Screening of Integral Membrane Proteins. <i>Structure</i> , 2006, 14, 673-681. | 1.6 | 628 |
| 90 | Crystal structure of a bacterial homologue of Na ⁺ /Cl ⁻ -dependent neurotransmitter transporters. <i>Nature</i> , 2005, 437, 215-223. | 13.7 | 1,564 |

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| 91 | Subunit arrangement and function in NMDA receptors. <i>Nature</i> , 2005, 438, 185-192. | 13.7 | 694 |
| 92 | AMPA Receptor Binding Cleft Mutations That Alter Affinity, Efficacy, and Recovery from Desensitization. <i>Journal of Neuroscience</i> , 2005, 25, 3752-3762. | 1.7 | 112 |
| 93 | Principles of Selective Ion Transport in Channels and Pumps. <i>Science</i> , 2005, 310, 1461-1465. | 6.0 | 853 |
| 94 | Crystal Structure of the <i>Vibrio cholerae</i> Cytolysin (VCC) Pro-toxin and its Assembly into a Heptameric Transmembrane Pore. <i>Journal of Molecular Biology</i> , 2005, 350, 997-1016. | 2.0 | 122 |
| 95 | Mechanism of Partial Agonist Action at the NR1 Subunit of NMDA Receptors. <i>Neuron</i> , 2005, 47, 71-84. | 3.8 | 174 |
| 96 | Mechanism of Positive Allosteric Modulators Acting on AMPA Receptors. <i>Journal of Neuroscience</i> , 2005, 25, 9027-9036. | 1.7 | 220 |
| 97 | Structure of a glutamate transporter homologue from <i>Pyrococcus horikoshii</i> . <i>Nature</i> , 2004, 431, 811-818. | 13.7 | 758 |
| 98 | Structure and function of AMPA receptors. <i>Journal of Physiology</i> , 2004, 554, 249-253. | 1.3 | 124 |
| 99 | High resolution crystallographic studies of α -hemolysin-phospholipid complexes define heptamer-lipid head group interactions: Implication for understanding protein-lipid interactions. <i>Protein Science</i> , 2004, 13, 1503-1511. | 3.1 | 74 |
| 100 | A novel member of the split $\beta\alpha\beta$ fold: Solution structure of the hypothetical protein YML108W from <i>Saccharomyces cerevisiae</i> . <i>Protein Science</i> , 2003, 12, 1136-1140. | 3.1 | 27 |
| 101 | Mechanisms of activation, inhibition and specificity: crystal structures of the NMDA receptor NR1 ligand-binding core. <i>EMBO Journal</i> , 2003, 22, 2873-2885. | 3.5 | 430 |
| 102 | Structural basis for modulation and agonist specificity of HCN pacemaker channels. <i>Nature</i> , 2003, 425, 200-205. | 13.7 | 540 |
| 103 | Structural basis for partial agonist action at ionotropic glutamate receptors. <i>Nature Neuroscience</i> , 2003, 6, 803-810. | 7.1 | 364 |
| 104 | Arresting and releasing Staphylococcal α -hemolysin at intermediate stages of pore formation by engineered disulfide bonds. <i>Protein Science</i> , 2003, 12, 997-1006. | 3.1 | 62 |
| 105 | <i>Vibrio cholerae</i> cytolysin is composed of an α -hemolysin-like core. <i>Protein Science</i> , 2003, 12, 379-383. | 3.1 | 42 |
| 106 | Trimeric Subunit Stoichiometry of the Glutamate Transporters from <i>Bacillus caldotenax</i> and <i>Bacillus stearothermophilus</i> . <i>Biochemistry</i> , 2003, 42, 12981-12988. | 1.2 | 93 |
| 107 | Competitive Antagonism of AMPA Receptors by Ligands of Different Classes: Crystal Structure of ATPO Bound to the GluR2 Ligand-Binding Core, in Comparison with DNQX. <i>Journal of Medicinal Chemistry</i> , 2003, 46, 214-221. | 2.9 | 101 |
| 108 | Three-Dimensional Structure of the Ligand-Binding Core of GluR2 in Complex with the Agonist (S)-ATPA: Implications for Receptor Subunit Selectivity. <i>Journal of Medicinal Chemistry</i> , 2003, 46, 872-875. | 2.9 | 59 |

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| 109 | Probing the Function, Conformational Plasticity, and Dimer-Dimer Contacts of the GluR2 Ligand-Binding Core: A Studies of 5-Substituted Willardiines and GluR2 S1S2 in the Crystal. <i>Biochemistry</i> , 2003, 42, 5201-5213. | 1.2 | 82 |
| 110 | β -Barrel membrane protein folding and structure viewed through the lens of β -hemolysin. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2003, 1609, 19-27. | 1.4 | 95 |
| 111 | Tuning activation of the AMPA-sensitive GluR2 ion channel by genetic adjustment of agonist-induced conformational changes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5736-5741. | 3.3 | 139 |
| 112 | A Vibrational Spectroscopic Investigation of Interactions of Agonists with GluR0 a Prokaryotic Glutamate Receptor. <i>Biochemistry</i> , 2002, 41, 1602-1608. | 1.2 | 21 |
| 113 | Mechanism of Activation and Selectivity in a Ligand-Gated Ion Channel: A Structural and Functional Studies of GluR2 and Quisqualate. <i>Biochemistry</i> , 2002, 41, 15635-15643. | 1.2 | 109 |
| 114 | GluR2 ligand-binding core complexes: importance of the isoxazolol moiety and 5-substituent for the binding mode of AMPA-type agonists. <i>FEBS Letters</i> , 2002, 531, 173-178. | 1.3 | 39 |
| 115 | Structural Basis for AMPA Receptor Activation and Ligand Selectivity: Crystal Structures of Five Agonist Complexes with the GluR2 Ligand-binding Core. <i>Journal of Molecular Biology</i> , 2002, 322, 93-109. | 2.0 | 155 |
| 116 | Structure-based functional design of chemical ligands for AMPA-subtype glutamate receptors. <i>Journal of Molecular Neuroscience</i> , 2002, 19, 113-116. | 1.1 | 6 |
| 117 | Mechanism of glutamate receptor desensitization. <i>Nature</i> , 2002, 417, 245-253. | 13.7 | 650 |
| 118 | Mechanisms for ligand binding to GluR0 ion channels: crystal structures of the glutamate and serine complexes and a closed apo state. <i>Journal of Molecular Biology</i> , 2001, 311, 815-836. | 2.0 | 141 |
| 119 | High Level Production, Characterization and Construct Optimization of the Ionotropic Glutamate Receptor Ligand Binding Core. <i>Tetrahedron</i> , 2000, 56, 9409-9419. | 1.0 | 4 |
| 120 | Mechanisms for Activation and Antagonism of an AMPA-Sensitive Glutamate Receptor. <i>Neuron</i> , 2000, 28, 165-181. | 3.8 | 874 |
| 121 | Functional characterization of a potassium-selective prokaryotic glutamate receptor. <i>Nature</i> , 1999, 402, 817-821. | 13.7 | 304 |
| 122 | Crystal structure of staphylococcal LukF delineates conformational changes accompanying formation of a transmembrane channel. <i>Nature Structural Biology</i> , 1999, 6, 134-140. | 9.7 | 220 |
| 123 | A new protein folding screen: Application to the ligand binding domains of a glutamate and kainate receptor and to lysozyme and carbonic anhydrase. <i>Protein Science</i> , 1999, 8, 1475-1483. | 3.1 | 111 |
| 124 | Probing the Folding and Unfolding of Wild-Type and Mutant Forms of Bacteriorhodopsin in Micellar Solutions: A Evaluation of Reversible Unfolding Conditions. <i>Biochemistry</i> , 1999, 38, 15380-15387. | 1.2 | 63 |
| 125 | Structure of a glutamate-receptor ligand-binding core in complex with kainate. <i>Nature</i> , 1998, 395, 913-917. | 13.7 | 646 |
| 126 | Roll out the barrel. <i>Nature Structural Biology</i> , 1998, 5, 931-932. | 9.7 | 11 |

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| 127 | It's not just a phase: crystallization and X-ray structure determination of bacteriorhodopsin in lipidic cubic phases. <i>Structure</i> , 1998, 6, 5-10. | 1.6 | 19 |
| 128 | Single potassium ion seeks open channel for transmembrane travels: tales from the KcsA structure. <i>Structure</i> , 1998, 6, 1221-1226. | 1.6 | 3 |
| 129 | Probing the ligand binding domain of the GluR2 receptor by proteolysis and deletion mutagenesis defines domain boundaries and yields a crystallizable construct. <i>Protein Science</i> , 1998, 7, 2623-2630. | 3.1 | 86 |
| 130 | Crystallization of the $\hat{\pm}$ -hemolysin heptamer solubilized in decyldimethyl- and decyldiethylphosphine oxide. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 276-278. | 2.5 | 4 |
| 131 | $\hat{\pm}$ -Hemolysin from <i>Staphylococcus aureus</i> : An Archetype of $\hat{1}^2$ -Barrel, Channel-Forming Toxins. <i>Journal of Structural Biology</i> , 1998, 121, 110-122. | 1.3 | 233 |
| 132 | [4] Membrane protein crystallization: Application of sparse matrices to the $\hat{\pm}$ -hemolysin heptamer. <i>Methods in Enzymology</i> , 1997, 276, 60-74. | 0.4 | 24 |
| 133 | Channel-forming toxins: tales of transformation. <i>Current Opinion in Structural Biology</i> , 1997, 7, 566-573. | 2.6 | 158 |
| 134 | Designed protein pores as components for biosensors. <i>Chemistry and Biology</i> , 1997, 4, 497-505. | 6.2 | 280 |
| 135 | Overexpression of a glutamate receptor (GluR2) ligand binding domain in <i>Escherichia coli</i> : Application of a novel protein folding screen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 13431-13436. | 3.3 | 148 |
| 136 | The long and short of colicin action: the molecular basis for the biological activity of channel-forming colicins. <i>Structure</i> , 1997, 5, 313-317. | 1.6 | 34 |
| 137 | $\hat{\pm}$ -Hemolysin, $\hat{3}$ -hemolysin, and leukocidin from <i>Staphylococcus aureus</i> : Distant in sequence but similar in structure. <i>Protein Science</i> , 1997, 6, 2631-2635. | 3.1 | 116 |
| 138 | Structure of Staphylococcal alpha -Hemolysin, a Heptameric Transmembrane Pore. <i>Science</i> , 1996, 274, 1859-1865. | 6.0 | 2,237 |
| 139 | Overexpression of bacteriorhodopsin in <i>Escherichia coli</i> as a water-soluble fusion to maltose binding protein: Efficient regeneration of the fusion protein and selective cleavage with trypsin. <i>Protein Science</i> , 1996, 5, 456-467. | 3.1 | 32 |
| 140 | Total Gene Synthesis: Novel Single-Step and Convergent Strategies Applied to the Construction of a 779 Base Pair Bacteriorhodopsin Gene. <i>Journal of the American Chemical Society</i> , 1994, 116, 8799-8800. | 6.6 | 39 |
| 141 | Subunit stoichiometry of staphylococcal alpha-hemolysin in crystals and on membranes: a heptameric transmembrane pore. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 12828-12831. | 3.3 | 245 |
| 142 | Crystal structure of CTP-ligated T state aspartate transcarbamoylase at 2.5 Å resolution: Implications for ATCase mutants and the mechanism of negative cooperativity. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 15, 147-176. | 1.5 | 64 |
| 143 | Crystal structure of the Glu-239→Gln mutant of aspartate carbamoyltransferase at 3.1-Å resolution: an intermediate quaternary structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1989, 86, 8212-8216. | 3.3 | 16 |
| 144 | Structural transitions in crystals of native aspartate carbamoyltransferase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1989, 86, 845-848. | 3.3 | 19 |

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| 145 | Three-dimensional structure of carbamoyl phosphate and succinate bound to aspartate carbamoyltransferase.. Proceedings of the National Academy of Sciences of the United States of America, 1988, 85, 4205-4208. | 3.3 | 79 |
| 146 | The catalytic mechanism of Escherichia coli aspartate carbamoyltransferase: A molecular modelling study. Biochemical and Biophysical Research Communications, 1987, 142, 893-897. | 1.0 | 68 |
| 147 | Activation and Desensitization Mechanism of AMPA Receptor - TARP Complex by cryo-EM. SSRN Electronic Journal, 0, , . | 0.4 | 0 |