

Eric Gouaux

List of Publications by Year in descending order

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147
papers

29,796
citations

7672

79
h-index

11282

141
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170
all docs

170
docs citations

170
times ranked

19868
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of Staphylococcal alpha -Hemolysin, a Heptameric Transmembrane Pore. <i>Science</i> , 1996, 274, 1859-1865.	6.0	2,237
2	Crystal structure of a bacterial homologue of Na ⁺ /Cl ⁻ -dependent neurotransmitter transporters. <i>Nature</i> , 2005, 437, 215-223.	13.7	1,564
3	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
4	X-ray structure, symmetry and mechanism of an AMPA-subtype glutamate receptor. <i>Nature</i> , 2009, 462, 745-756.	13.7	966
5	Principles of activation and permeation in an anion-selective Cys-loop receptor. <i>Nature</i> , 2011, 474, 54-60.	13.7	899
6	Mechanisms for Activation and Antagonism of an AMPA-Sensitive Glutamate Receptor. <i>Neuron</i> , 2000, 28, 165-181.	3.8	874
7	Principles of Selective Ion Transport in Channels and Pumps. <i>Science</i> , 2005, 310, 1461-1465.	6.0	853
8	Structure of a glutamate transporter homologue from <i>Pyrococcus horikoshii</i> . <i>Nature</i> , 2004, 431, 811-818.	13.7	758
9	Subunit arrangement and function in NMDA receptors. <i>Nature</i> , 2005, 438, 185-192.	13.7	694
10	Crystal structure of the ATP-gated P2X4 ion channel in the closed state. <i>Nature</i> , 2009, 460, 592-598.	13.7	680
11	Mechanism of glutamate receptor desensitization. <i>Nature</i> , 2002, 417, 245-253.	13.7	650
12	Structure of a glutamate-receptor ligand-binding core in complex with kainate. <i>Nature</i> , 1998, 395, 913-917.	13.7	646
13	Fluorescence-Detection Size-Exclusion Chromatography for Precrystallization Screening of Integral Membrane Proteins. <i>Structure</i> , 2006, 14, 673-681.	1.6	628
14	X-ray structure of dopamine transporter elucidates antidepressant mechanism. <i>Nature</i> , 2013, 503, 85-90.	13.7	549
15	Structural basis for modulation and agonist specificity of HCN pacemaker channels. <i>Nature</i> , 2003, 425, 200-205.	13.7	540
16	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
17	X-ray structures and mechanism of the human serotonin transporter. <i>Nature</i> , 2016, 532, 334-339.	13.7	527
18	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

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19	Coupling substrate and ion binding to extracellular gate of a sodium-dependent aspartate transporter. <i>Nature</i> , 2007, 445, 387-393.	13.7	473
20	Molecular mechanism of ATP binding and ion channel activation in P2X receptors. <i>Nature</i> , 2012, 485, 207-212.	13.7	460
21	NMDA receptor structures reveal subunit arrangement and pore architecture. <i>Nature</i> , 2014, 511, 191-197.	13.7	441
22	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
23	Pore architecture and ion sites in acid-sensing ion channels and P2X receptors. <i>Nature</i> , 2009, 460, 599-604.	13.7	422
24	A Competitive Inhibitor Traps LeuT in an Open-to-Out Conformation. <i>Science</i> , 2008, 322, 1655-1661.	6.0	418
25	Antidepressant binding site in a bacterial homologue of neurotransmitter transporters. <i>Nature</i> , 2007, 448, 952-956.	13.7	391
26	Glycine receptor mechanism elucidated by electron cryo-microscopy. <i>Nature</i> , 2015, 526, 224-229.	13.7	370
27	Structural basis for partial agonist action at ionotropic glutamate receptors. <i>Nature Neuroscience</i> , 2003, 6, 803-810.	7.1	364
28	Dynamic Superresolution Imaging of Endogenous Proteins on Living Cells at Ultra-High Density. <i>Biophysical Journal</i> , 2010, 99, 1303-1310.	0.2	364
29	Neurotransmitter and psychostimulant recognition by the dopamine transporter. <i>Nature</i> , 2015, 521, 322-327.	13.7	357
30	Unlocking the molecular secrets of sodium-coupled transporters. <i>Nature</i> , 2009, 459, 347-355.	13.7	308
31	Functional characterization of a potassium-selective prokaryotic glutamate receptor. <i>Nature</i> , 1999, 402, 817-821.	13.7	304
32	Structure and Mechanism of a Na ⁺ -Independent Amino Acid Transporter. <i>Science</i> , 2009, 325, 1010-1014.	6.0	299
33	Designed protein pores as components for biosensors. <i>Chemistry and Biology</i> , 1997, 4, 497-505.	6.2	280
34	X-Ray Structure of Acid-Sensing Ion Channel "Snake Toxin Complex Reveals Open State of a Na ⁺ -Selective Channel. <i>Cell</i> , 2014, 156, 717-729.	13.5	264
35	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
36	Structural plasticity and dynamic selectivity of acid-sensing ion channel "spider toxin complexes. <i>Nature</i> , 2012, 489, 400-405.	13.7	245

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37	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
38	Î±-Hemolysin from <i>Staphylococcus aureus</i> : An Archetype of Î²-Barrel, Channel-Forming Toxins. <i>Journal of Structural Biology</i> , 1998, 121, 110-122.	1.3	233
39	A Fluorescence-Detection Size-Exclusion Chromatography-Based Thermostability Assay for Membrane Protein Precrystallization Screening. <i>Structure</i> , 2012, 20, 1293-1299.	1.6	222
40	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
41	Mechanism of Positive Allosteric Modulators Acting on AMPA Receptors. <i>Journal of Neuroscience</i> , 2005, 25, 9027-9036.	1.7	220
42	Measurement of Conformational Changes accompanying Desensitization in an Ionotropic Glutamate Receptor. <i>Cell</i> , 2006, 127, 85-97.	13.5	206
43	X-ray structures define human P2X3 receptor gating cycle and antagonist action. <i>Nature</i> , 2016, 538, 66-71.	13.7	191
44	Serotonin transporter-ibogaine complexes illuminate mechanisms of inhibition and transport. <i>Nature</i> , 2019, 569, 141-145.	13.7	187
45	Structure and Dynamics of AMPA Receptor GluA2 in Resting, Pre-Open, and Desensitized States. <i>Cell</i> , 2014, 158, 778-792.	13.5	186
46	Gating mechanisms of acid-sensing ion channels. <i>Nature</i> , 2018, 555, 397-401.	13.7	177
47	Mechanism of NMDA receptor channel block by MK-801 and memantine. <i>Nature</i> , 2018, 556, 515-519.	13.7	177
48	Mechanism of NMDA Receptor Inhibition and Activation. <i>Cell</i> , 2016, 165, 704-714.	13.5	175
49	Mechanism of Partial Agonist Action at the NR1 Subunit of NMDA Receptors. <i>Neuron</i> , 2005, 47, 71-84.	3.8	174
50	Channel-forming toxins: tales of transformation. <i>Current Opinion in Structural Biology</i> , 1997, 7, 566-573.	2.6	158
51	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
52	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
53	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
54	Crystal structure and association behaviour of the GluR2 amino-terminal domain. <i>EMBO Journal</i> , 2009, 28, 1812-1823.	3.5	146

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55	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
56	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
57	Cryo-EM structures of the triheteromeric NMDA receptor and its allosteric modulation. <i>Science</i> , 2017, 355, .	6.0	134
58	Architecture and subunit arrangement of native AMPA receptors elucidated by cryo-EM. <i>Science</i> , 2019, 364, 355-362.	6.0	134
59	Cryo-EM structure of the benzodiazepine-sensitive $\alpha 1\beta 2\gamma 2S$ tri-heteromeric GABAA receptor in complex with GABA. <i>ELife</i> , 2018, 7, .	2.8	126
60	Structural basis for action by diverse antidepressants on biogenic amine transporters. <i>Nature</i> , 2013, 503, 141-145.	13.7	125
61	Structure and function of AMPA receptors. <i>Journal of Physiology</i> , 2004, 554, 249-253.	1.3	124
62	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
63	Neurotransmitter/sodium symporter orthologue LeuT has a single high-affinity substrate site. <i>Nature</i> , 2010, 468, 1129-1132.	13.7	117
64	α -Hemolysin, β -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
65	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
66	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
67	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
68	Activation and Desensitization Mechanism of AMPA Receptor-TARP Complex by Cryo-EM. <i>Cell</i> , 2017, 170, 1234-1246.e14.	13.5	111
69	X-ray structures of AMPA receptor-cone snail toxin complexes illuminate activation mechanism. <i>Science</i> , 2014, 345, 1021-1026.	6.0	110
70	Mechanism of Activation and Selectivity in a Ligand-Gated Ion Channel: Structural and Functional Studies of GluR2 and Quisqualate. <i>Biochemistry</i> , 2002, 41, 15635-15643.	1.2	109
71	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
72	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

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73	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
74	Architecture of fully occupied GluA2 AMPA receptor-TARP complex elucidated by cryo-EM. <i>Nature</i> , 2016, 536, 108-111.	13.7	100
75	How LeuT shapes our understanding of the mechanisms of sodium-coupled neurotransmitter transporters. <i>Journal of Physiology</i> , 2014, 592, 863-869.	1.3	96
76	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
77	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
78	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
79	Mechanisms for Zinc and Proton Inhibition of the GluN1/GluN2A NMDA Receptor. <i>Cell</i> , 2018, 175, 1520-1532.e15.	13.5	85
80	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
81	Three-dimensional structure of carbamoyl phosphate and succinate bound to aspartate carbamoyltransferase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1988, 85, 4205-4208.	3.3	79
82	Mechanism of gating and partial agonist action in the glycine receptor. <i>Cell</i> , 2021, 184, 957-968.e21.	13.5	77
83	High resolution crystallographic studies of β -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
84	Structure of mouse protocadherin 15 of the stereocilia tip link in complex with LHFPL5. <i>ELife</i> , 2018, 7, .	2.8	73
85	The catalytic mechanism of <i>Escherichia coli</i> aspartate carbamoyltransferase: A molecular modelling study. <i>Biochemical and Biophysical Research Communications</i> , 1987, 142, 893-897.	1.0	68
86	Structure and symmetry inform gating principles of ionotropic glutamate receptors. <i>Neuropharmacology</i> , 2017, 112, 11-15.	2.0	65
87	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
88	The His-Gly motif of acid-sensing ion channels resides in a reentrant β -loop implicated in gating and ion selectivity. <i>ELife</i> , 2020, 9, .	2.8	64
89	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
90	Arresting and releasing Staphylococcal β -hemolysin at intermediate stages of pore formation by engineered disulfide bonds. <i>Protein Science</i> , 2003, 12, 997-1006.	3.1	62

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91	Molecular mechanism of prestin electromotive signal amplification. <i>Cell</i> , 2021, 184, 4669-4679.e13.	13.5	61
92	Autoimmune receptor encephalitis in mice induced by active immunization with conformationally stabilized holoreceptors. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	60
93	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
94	Illumination of serotonin transporter mechanism and role of the allosteric site. <i>Science Advances</i> , 2021, 7, eabl3857.	4.7	58
95	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
96	Chemical and structural investigation of the paroxetine-human serotonin transporter complex. <i>ELife</i> , 2020, 9, .	2.8	53
97	Hippocampal AMPA receptor assemblies and mechanism of allosteric inhibition. <i>Nature</i> , 2021, 594, 448-453.	13.7	52
98	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
99	Insights into transport mechanism from LeuT engineered to transport tryptophan. <i>EMBO Journal</i> , 2012, 31, 228-235.	3.5	45
100	The antidepressant drug vilazodone is an allosteric inhibitor of the serotonin transporter. <i>Nature Communications</i> , 2021, 12, 5063.	5.8	45
101	<i>Vibrio cholerae</i> cytolysin is composed of an alpha-hemolysin-like core. <i>Protein Science</i> , 2003, 12, 379-383.	3.1	42
102	Insights into the mechanism and pharmacology of neurotransmitter sodium symporters. <i>Current Opinion in Structural Biology</i> , 2019, 54, 161-170.	2.6	42
103	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
104	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
105	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
106	Architecture and assembly mechanism of native glycine receptors. <i>Nature</i> , 2021, 599, 513-517.	13.7	39
107	Structure and mechanism of AMPA receptor auxiliary protein complexes. <i>Current Opinion in Structural Biology</i> , 2019, 54, 104-111.	2.6	38
108	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

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109	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
110	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
111	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
112	Overexpression of bacterioopsin 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
113	Amino Terminal Domains of the NMDA Receptor Are Organized as Local Heterodimers. <i>PLoS ONE</i> , 2011, 6, e19180.	1.1	30
114	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
115	[4] Membrane protein crystallization: Application of sparse matrices to the β -hemolysin heptamer. <i>Methods in Enzymology</i> , 1997, 276, 60-74.	0.4	24
116	Light-coupled cryo-plunger for time-resolved cryo-EM. <i>Journal of Structural Biology</i> , 2020, 212, 107624.	1.3	23
117	A Vibrational Spectroscopic Investigation of Interactions of Agonists with GluR0 a Prokaryotic Glutamate Receptor. <i>Biochemistry</i> , 2002, 41, 1602-1608.	1.2	21
118	Thermostabilization of the Human Serotonin Transporter in an Antidepressant-Bound Conformation. <i>PLoS ONE</i> , 2015, 10, e0145688.	1.1	21
119	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
120	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
121	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
122	The intracellular domain of homomeric glycine receptors modulates agonist efficacy. <i>Journal of Biological Chemistry</i> , 2021, 296, 100387.	1.6	17
123	Crystal structure of the Glu-239---Gln mutant of aspartate carbamoyltransferase at 3.1-A 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
124	Thermostabilization, Expression, Purification, and Crystallization of the Human Serotonin Transporter Bound to α -citalopram. <i>Journal of Visualized Experiments</i> , 2016, , .	0.2	14
125	Roll out the barrel. <i>Nature Structural Biology</i> , 1998, 5, 931-932.	9.7	11
126	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

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127	Extracellular loops of the serotonin transporter act as a selectivity filter for drug binding. Journal of Biological Chemistry, 2021, 297, 100863.	1.6	8
128	Novel Dicarboxylate Selectivity in an Insect Glutamate Transporter Homolog. PLoS ONE, 2013, 8, e70947.	1.1	7
129	Structure-based functional design of chemical ligands for AMPA-subtype glutamate receptors. Journal of Molecular Neuroscience, 2002, 19, 113-116.	1.1	6
130	Expression and purification of a functional heteromeric GABAA receptor for structural studies. PLoS ONE, 2018, 13, e0201210.	1.1	6
131	Molecular structures and conformations of protocadherin-15 and its complexes on stereocilia elucidated by cryo-electron tomography. ELife, 2021, 10, .	2.8	6
132	Crystallization of the $\hat{1}\pm$ -hemolysin heptamer solubilized in decyldimethyl- and decyldiethylphosphine oxide. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 276-278.	2.5	4
133	High Level Production, Characterization and Construct Optimization of the Ionotropic Glutamate Receptor Ligand Binding Core. Tetrahedron, 2000, 56, 9409-9419.	1.0	4
134	HOTSPUR: A Real-time Interactive Preprocessing System for Cryo-EM Data. Microscopy and Microanalysis, 2019, 25, 1212-1213.	0.2	4
135	Single potassium ion seeks open channel for transmembrane travels: tales from the KcsA structure. Structure, 1998, 6, 1221-1226.	1.6	3
136	NMDA Receptors TM Structural Asymmetry. Microscopy and Microanalysis, 2019, 25, 1218-1219.	0.2	3
137	Pore Architecture and ion Sites of Acid Sensing ion Channels and P2X Receptors. Biophysical Journal, 2010, 98, 610a.	0.2	1
138	Mechanism of NMDA Receptor Channel Block by MK-801 and Memantine. Biophysical Journal, 2018, 114, 24a-25a.	0.2	1
139	Strategy for Compositional Analysis of the Hair Cell Mechanotransduction Complex Using TIRF Microscopy. Microscopy and Microanalysis, 2019, 25, 1266-1267.	0.2	1
140	Architecture, Symmetry and Mechanism of Ionotropic Glutamate Receptors. Biophysical Journal, 2011, 100, 363a.	0.2	0
141	1PT103 Mechanism of ATP binding and channel activation in P2X receptors(The 50th Annual Meeting of Tj ETQq1 1 0.784314 rgBT / 0v	0.0	0
142	Imaged by Cryo-EM, Activated and Desensitized GluA2 Glutamate Receptors Show Extreme Flexibility. Biophysical Journal, 2014, 106, 30a.	0.2	0
143	Activation and Desensitization Mechanism of AMPA Receptor-TARP Complex by Cryo-EM. Biophysical Journal, 2018, 114, 125a.	0.2	0
144	lhogaine Binds Human Serotonin Transporter in Multiple Functional States. Biophysical Journal, 2019, 116, 557a.	0.2	0

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145	Image collection strategies for single particle cryoEM. <i>Microscopy and Microanalysis</i> , 2021, 27, 1904-1906.	0.2	0
146	Activation and Desensitization Mechanism of AMPA Receptor - TARP Complex by cryo-EM. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
147	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