

Eric Gouaux

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

143 papers	24,755 citations	75 h-index	157 g-index
170 ext. papers	27,840 ext. citations	20.2 avg, IF	7.36 L-index

#	Paper	IF	Citations
143	Illumination of serotonin transporter mechanism and role of the allosteric site. <i>Science Advances</i> , 2021 , 7, eabl3857	14.3	4
142	Putting the Pieces Together: the Hair Cell Transduction Complex. <i>JARO - Journal of the Association for Research in Otolaryngology</i> , 2021 , 22, 601-608	3.3	2
141	Hippocampal AMPA receptor assemblies and mechanism of allosteric inhibition. <i>Nature</i> , 2021 , 594, 448-453	55.4	12
140	Extracellular loops of the serotonin transporter act as a selectivity filter for drug binding. <i>Journal of Biological Chemistry</i> , 2021 , 297, 100863	5.4	2
139	The intracellular domain of homomeric glycine receptors modulates agonist efficacy. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100387	5.4	9
138	Mechanism of gating and partial agonist action in the glycine receptor. <i>Cell</i> , 2021 , 184, 957-968.e21	56.2	28
137	Image collection strategies for single particle cryoEM. <i>Microscopy and Microanalysis</i> , 2021 , 27, 1904-1906	6.5	
136	The antidepressant drug vilazodone is an allosteric inhibitor of the serotonin transporter. <i>Nature Communications</i> , 2021 , 12, 5063	17.4	10
135	Molecular mechanism of prestin electromotive signal amplification. <i>Cell</i> , 2021 , 184, 4669-4679.e13	56.2	10
134	Architecture and assembly mechanism of native glycine receptors. <i>Nature</i> , 2021 , 599, 513-517	50.4	7
133	Molecular structures and conformations of protocadherin-15 and its complexes on stereocilia elucidated by cryo-electron tomography.. <i>ELife</i> , 2021 , 10,	8.9	1
132	Chemical and structural investigation of the paroxetine-human serotonin transporter complex. <i>ELife</i> , 2020 , 9,	8.9	19
131	The His-Gly motif of acid-sensing ion channels resides in a reentrant 'loop' implicated in gating and ion selectivity. <i>ELife</i> , 2020 , 9,	8.9	26
130	Light-coupled cryo-plunger for time-resolved cryo-EM. <i>Journal of Structural Biology</i> , 2020 , 212, 107624	3.4	3
129	HOTSPUR: A Real-time Interactive Preprocessing System for Cryo-EM Data. <i>Microscopy and Microanalysis</i> , 2019 , 25, 1212-1213	0.5	4
128	Serotonin transporter-ibogaine complexes illuminate mechanisms of inhibition and transport. <i>Nature</i> , 2019 , 569, 141-145	50.4	89
127	Structure and mechanism of AMPA receptor - auxiliary protein complexes. <i>Current Opinion in Structural Biology</i> , 2019 , 54, 104-111	8.1	22

126	Architecture and subunit arrangement of native AMPA receptors elucidated by cryo-EM. <i>Science</i> , 2019 , 364, 355-362	33.3	73
125	Insights into the mechanism and pharmacology of neurotransmitter sodium symporters. <i>Current Opinion in Structural Biology</i> , 2019 , 54, 161-170	8.1	24
124	Structural, functional, and behavioral insights of dopamine dysfunction revealed by a deletion in. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 3853-3862	11.5	21
123	Autoimmune receptor encephalitis in mice induced by active immunization with conformationally stabilized holoreceptors. <i>Science Translational Medicine</i> , 2019 , 11,	17.5	27
122	NMDA Receptors' Structural Asymmetry. <i>Microscopy and Microanalysis</i> , 2019 , 25, 1218-1219	0.5	0
121	Strategy for Compositional Analysis of the Hair Cell Mechanotransduction Complex Using TIRF Microscopy. <i>Microscopy and Microanalysis</i> , 2019 , 25, 1266-1267	0.5	
120	Gating mechanisms of acid-sensing ion channels. <i>Nature</i> , 2018 , 555, 397-401	50.4	97
119	Mechanism of NMDA receptor channel block by MK-801 and memantine. <i>Nature</i> , 2018 , 556, 515-519	50.4	107
118	Structural basis for recognition of diverse antidepressants by the human serotonin transporter. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 170-175	17.6	70
117	Expression and purification of a functional heteromeric GABAA receptor for structural studies. <i>PLoS ONE</i> , 2018 , 13, e0201210	3.7	4
116	Structure of mouse protocadherin 15 of the stereocilia tip link in complex with LHFPL5. <i>ELife</i> , 2018 , 7,	8.9	36
115	Author response: Structure of mouse protocadherin 15 of the stereocilia tip link in complex with LHFPL5 2018 ,		2
114	Mechanisms for Zinc and Proton Inhibition of the GluN1/GluN2A NMDA Receptor. <i>Cell</i> , 2018 , 175, 1520-1532.e15	56.2	155
113	Cryo-EM structure of the benzodiazepine-sensitive $\alpha 1 \beta \gamma$ tri-heteromeric GABA receptor in complex with GABA. <i>ELife</i> , 2018 , 7,	8.9	81
112	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	3.7	16
111	Thermostabilization and purification of the human dopamine transporter (hDAT) in an inhibitor and allosteric ligand bound conformation. <i>PLoS ONE</i> , 2018 , 13, e0200085	3.7	14
110	Cryo-EM structures of the triheteromeric NMDA receptor and its allosteric modulation. <i>Science</i> , 2017 , 355,	33.3	96
109	Activation and Desensitization Mechanism of AMPA Receptor-TARP Complex by Cryo-EM. <i>Cell</i> , 2017 , 170, 1234-1246.e14	56.2	71

108	Structure and symmetry inform gating principles of ionotropic glutamate receptors. <i>Neuropharmacology</i> , 2017 , 112, 11-15	5.5	41
107	X-ray structures define human P2X(3) receptor gating cycle and antagonist action. <i>Nature</i> , 2016 , 538, 66-71	50.4	134
106	Thermostabilization, Expression, Purification, and Crystallization of the Human Serotonin Transporter Bound to S-citalopram. <i>Journal of Visualized Experiments</i> , 2016 ,	1.6	11
105	Architecture of fully occupied GluA2 AMPA receptor-TARP complex elucidated by cryo-EM. <i>Nature</i> , 2016 , 536, 108-11	50.4	79
104	X-ray structures and mechanism of the human serotonin transporter. <i>Nature</i> , 2016 , 532, 334-9	50.4	364
103	Mechanism of NMDA Receptor Inhibition and Activation. <i>Cell</i> , 2016 , 165, 704-14	56.2	129
102	X-ray structures of Drosophila dopamine transporter in complex with nisoxetine and reboxetine. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 506-508	17.6	119
101	Neurotransmitter and psychostimulant recognition by the dopamine transporter. <i>Nature</i> , 2015 , 521, 322-7	50.4	259
100	Glycine receptor mechanism elucidated by electron cryo-microscopy. <i>Nature</i> , 2015 , 526, 224-9	50.4	287
99	Thermostabilization of the Human Serotonin Transporter in an Antidepressant-Bound Conformation. <i>PLoS ONE</i> , 2015 , 10, e0145688	3.7	13
98	X-ray structure of acid-sensing ion channel 1-snake toxin complex reveals open state of a Na(+)-selective channel. <i>Cell</i> , 2014 , 156, 717-29	56.2	192
97	Screening and large-scale expression of membrane proteins in mammalian cells for structural studies. <i>Nature Protocols</i> , 2014 , 9, 2574-85	18.8	331
96	X-ray structures of GluCl in apo states reveal a gating mechanism of Cys-loop receptors. <i>Nature</i> , 2014 , 512, 333-7	50.4	201
95	Structure and dynamics of AMPA receptor GluA2 in resting, pre-open, and desensitized states. <i>Cell</i> , 2014 , 158, 778-792	56.2	150
94	X-ray structures of AMPA receptor-cone snail toxin complexes illuminate activation mechanism. <i>Science</i> , 2014 , 345, 1021-6	33.3	93
93	NMDA receptor structures reveal subunit arrangement and pore architecture. <i>Nature</i> , 2014 , 511, 191-7	50.4	346
92	How LeuT shapes our understanding of the mechanisms of sodium-coupled neurotransmitter transporters. <i>Journal of Physiology</i> , 2014 , 592, 863-9	3.9	73
91	Structural basis for action by diverse antidepressants on biogenic amine transporters. <i>Nature</i> , 2013 , 503, 141-5	50.4	112

90	X-ray structure of dopamine transporter elucidates antidepressant mechanism. <i>Nature</i> , 2013 , 503, 85-90	50.4	448
89	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, 277-84	8.1	31
88	Novel dicarboxylate selectivity in an insect glutamate transporter homolog. <i>PLoS ONE</i> , 2013 , 8, e70947	3.7	5
87	A fluorescence-detection size-exclusion chromatography-based thermostability assay for membrane protein precrystallization screening. <i>Structure</i> , 2012 , 20, 1293-9	5.2	172
86	Substrate binds in the S1 site of the F253A mutant of LeuT, a neurotransmitter sodium symporter homologue. <i>EMBO Reports</i> , 2012 , 13, 861-6	6.5	36
85	X-ray structures of LeuT in substrate-free outward-open and apo inward-open states. <i>Nature</i> , 2012 , 481, 469-74	50.4	394
84	Molecular mechanism of ATP binding and ion channel activation in P2X receptors. <i>Nature</i> , 2012 , 485, 207-12	50.4	377
83	Structural plasticity and dynamic selectivity of acid-sensing ion channel-spider toxin complexes. <i>Nature</i> , 2012 , 489, 400-5	50.4	206
82	Insights into transport mechanism from LeuT engineered to transport tryptophan. <i>EMBO Journal</i> , 2012 , 31, 228-35	13	41
81	Structures of LeuT in bicelles define conformation and substrate binding in a membrane-like context. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 212-9	17.6	91
80	1PT103 Mechanism of ATP binding and channel activation in P2X receptors(The 50th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2012 , 52, S85	0	
79	Principles of activation and permeation in an anion-selective Cys-loop receptor. <i>Nature</i> , 2011 , 474, 54-60	50.4	787
78	Amino terminal domains of the NMDA receptor are organized as local heterodimers. <i>PLoS ONE</i> , 2011 , 6, e19180	3.7	29
77	Neurotransmitter/sodium symporter orthologue LeuT has a single high-affinity substrate site. <i>Nature</i> , 2010 , 468, 1129-32	50.4	109
76	Dynamic superresolution imaging of endogenous proteins on living cells at ultra-high density. <i>Biophysical Journal</i> , 2010 , 99, 1303-10	2.9	301
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, 8165-70	11.5	87
74	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, 191-9		48
73	Review. The molecular logic of sodium-coupled neurotransmitter transporters. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2009 , 364, 149-54	5.8	45

72	Crystal structure and association behaviour of the GluR2 amino-terminal domain. <i>EMBO Journal</i> , 2009 , 28, 1812-23	13	134
71	Unlocking the molecular secrets of sodium-coupled transporters. <i>Nature</i> , 2009 , 459, 347-55	50.4	274
70	Crystal structure of the ATP-gated P2X(4) ion channel in the closed state. <i>Nature</i> , 2009 , 460, 592-8	50.4	583
69	X-ray structure, symmetry and mechanism of an AMPA-subtype glutamate receptor. <i>Nature</i> , 2009 , 462, 745-56	50.4	804
68	Pore architecture and ion sites in acid-sensing ion channels and P2X receptors. <i>Nature</i> , 2009 , 460, 599-604	50.4	366
67	Structure and mechanism of a Na ⁺ -independent amino acid transporter. <i>Science</i> , 2009 , 325, 1010-4	33.3	260
66	A competitive inhibitor traps LeuT in an open-to-out conformation. <i>Science</i> , 2008 , 322, 1655-61	33.3	350
65	Coupling substrate and ion binding to extracellular gate of a sodium-dependent aspartate transporter. <i>Nature</i> , 2007 , 445, 387-93	50.4	402
64	Antidepressant binding site in a bacterial homologue of neurotransmitter transporters. <i>Nature</i> , 2007 , 448, 952-6	50.4	355
63	Structure of acid-sensing ion channel 1 at 1.9 Å resolution and low pH. <i>Nature</i> , 2007 , 449, 316-23	50.4	837
62	Fluorescence-detection size-exclusion chromatography for precrystallization screening of integral membrane proteins. <i>Structure</i> , 2006 , 14, 673-81	5.2	513
61	Measurement of conformational changes accompanying desensitization in an ionotropic glutamate receptor. <i>Cell</i> , 2006 , 127, 85-97	56.2	184
60	AMPA receptor binding cleft mutations that alter affinity, efficacy, and recovery from desensitization. <i>Journal of Neuroscience</i> , 2005 , 25, 3752-62	6.6	103
59	Principles of selective ion transport in channels and pumps. <i>Science</i> , 2005 , 310, 1461-5	33.3	672
58	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	6.5	106
57	Mechanism of partial agonist action at the NR1 subunit of NMDA receptors. <i>Neuron</i> , 2005 , 47, 71-84	13.9	164
56	Mechanism of positive allosteric modulators acting on AMPA receptors. <i>Journal of Neuroscience</i> , 2005 , 25, 9027-36	6.6	200
55	Crystal structure of a bacterial homologue of Na ⁺ /Cl ⁻ -dependent neurotransmitter transporters. <i>Nature</i> , 2005 , 437, 215-23	50.4	1374

54	Subunit arrangement and function in NMDA receptors. <i>Nature</i> , 2005 , 438, 185-92	50.4	601
53	Structure of a glutamate transporter homologue from <i>Pyrococcus horikoshii</i> . <i>Nature</i> , 2004 , 431, 811-8	50.4	684
52	Structure and function of AMPA receptors. <i>Journal of Physiology</i> , 2004 , 554, 249-53	3.9	105
51	High resolution crystallographic studies of alpha-hemolysin-phospholipid complexes define heptamer-lipid head group interactions: implication for understanding protein-lipid interactions. <i>Protein Science</i> , 2004 , 13, 1503-11	6.3	61
50	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, 5736-41	11.5	132
49	Arresting and releasing Staphylococcal alpha-hemolysin at intermediate stages of pore formation by engineered disulfide bonds. <i>Protein Science</i> , 2003 , 12, 997-1006	6.3	26
48	Mechanisms of activation, inhibition and specificity: crystal structures of the NMDA receptor NR1 ligand-binding core. <i>EMBO Journal</i> , 2003 , 22, 2873-85	13	382
47	Structural basis for modulation and agonist specificity of HCN pacemaker channels. <i>Nature</i> , 2003 , 425, 200-5	50.4	482
46	Structural basis for partial agonist action at ionotropic glutamate receptors. <i>Nature Neuroscience</i> , 2003 , 6, 803-10	25.5	336
45	Arresting and releasing Staphylococcal Hemolysin at intermediate stages of pore formation by engineered disulfide bonds. <i>Protein Science</i> , 2003 , 12, 997-1006	6.3	58
44	<i>Vibrio cholerae</i> cytolysin is composed of an alpha-hemolysin-like core. <i>Protein Science</i> , 2003 , 12, 379-83	6.3	35
43	Trimeric subunit stoichiometry of the glutamate transporters from <i>Bacillus caldotenax</i> and <i>Bacillus stearothermophilus</i> . <i>Biochemistry</i> , 2003 , 42, 12981-8	3.2	87
42	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, 214-21	8.3	97
41	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, 872-5	8.3	57
40	Probing the function, conformational plasticity, and dimer-dimer contacts of the GluR2 ligand-binding core: studies of 5-substituted willardiines and GluR2 S1S2 in the crystal. <i>Biochemistry</i> , 2003 , 42, 5201-13	3.2	76
39	Beta-barrel membrane protein folding and structure viewed through the lens of alpha-hemolysin. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2003 , 1609, 19-27	3.8	91
38	Structure-based functional design of chemical ligands for AMPA-subtype glutamate receptors. <i>Journal of Molecular Neuroscience</i> , 2002 , 19, 113-6	3.3	6
37	Mechanism of glutamate receptor desensitization. <i>Nature</i> , 2002 , 417, 245-53	50.4	588

36	A vibrational spectroscopic investigation of interactions of agonists with GluR0, a prokaryotic glutamate receptor. <i>Biochemistry</i> , 2002 , 41, 1602-8	3.2	21
35	Mechanism of activation and selectivity in a ligand-gated ion channel: structural and functional studies of GluR2 and quisqualate. <i>Biochemistry</i> , 2002 , 41, 15635-43	3.2	100
34	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, 173-8	3.8	38
33	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	6.5	150
32	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, 815-36	6.5	133
31	High Level Production, Characterization and Construct Optimization of the Ionotropic Glutamate Receptor Ligand Binding Core. <i>Tetrahedron</i> , 2000 , 56, 9409-9419	2.4	4
30	Mechanisms for activation and antagonism of an AMPA-sensitive glutamate receptor: crystal structures of the GluR2 ligand binding core. <i>Neuron</i> , 2000 , 28, 165-81	13.9	798
29	Functional characterization of a potassium-selective prokaryotic glutamate receptor. <i>Nature</i> , 1999 , 402, 817-21	50.4	265
28	Crystal structure of staphylococcal LukF delineates conformational changes accompanying formation of a transmembrane channel. <i>Nature Structural Biology</i> , 1999 , 6, 134-40		197
27	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, 1475-83	6.3	105
26	Probing the folding and unfolding of wild-type and mutant forms of bacteriorhodopsin in micellar solutions: evaluation of reversible unfolding conditions. <i>Biochemistry</i> , 1999 , 38, 15380-7	3.2	61
25	Structure of a glutamate-receptor ligand-binding core in complex with kainate. <i>Nature</i> , 1998 , 395, 913-7	50.4	608
24	Roll out the barrel. <i>Nature Structural Biology</i> , 1998 , 5, 931-2		8
23	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	5.2	19
22	Single potassium ion seeks open channel for transmembrane travels: tales from the KcsA structure. <i>Structure</i> , 1998 , 6, 1221-6	5.2	3
21	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, 2623-30	6.3	84
20	Crystallization of the alpha-hemolysin heptamer solubilized in decyldimethyl- and decyldiethylphosphine oxide. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998 , 54, 276-8		4
19	alpha-Hemolysin from <i>Staphylococcus aureus</i> : an archetype of beta-barrel, channel-forming toxins. <i>Journal of Structural Biology</i> , 1998 , 121, 110-22	3.4	207

18	[4] Membrane protein crystallization: Application of sparse matrices to the Hemolysin heptamer. <i>Methods in Enzymology</i> , 1997 , 276, 60-74	1.7	18
17	Channel-forming toxins: tales of transformation. <i>Current Opinion in Structural Biology</i> , 1997 , 7, 566-73	8.1	143
16	Designed protein pores as components for biosensors. <i>Chemistry and Biology</i> , 1997 , 4, 497-505		251
15	Overexpression of a glutamate receptor (GluR2) ligand binding domain in Escherichia coli: application of a novel protein folding screen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997 , 94, 13431-6	11.5	145
14	The long and short of colicin action: the molecular basis for the biological activity of channel-forming colicins. <i>Structure</i> , 1997 , 5, 313-7	5.2	32
13	alpha-Hemolysin, gamma-hemolysin, and leukocidin from Staphylococcus aureus: distant in sequence but similar in structure. <i>Protein Science</i> , 1997 , 6, 2631-5	6.3	90
12	Structure of staphylococcal alpha-hemolysin, a heptameric transmembrane pore. <i>Science</i> , 1996 , 274, 1859-66	33.3	1967
11	Overexpression of bacterio-opsin in Escherichia coli 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, 456-67	6.3	29
10	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	16.4	36
9	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, 12828-31	11.5	222
8	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, 147-76	4.2	59
7	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, 8212-6	11.5	16
6	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, 845-8	11.5	17
5	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, 4205-8	11.5	66
4	The catalytic mechanism of Escherichia coli aspartate carbamoyltransferase: a molecular modelling study. <i>Biochemical and Biophysical Research Communications</i> , 1987 , 142, 893-7	3.4	60
3	Chemical and structural investigation of the paroxetine-human serotonin transporter complex		1
2	Conserved His-Gly motif of acid-sensing ion channels resides in a reentrant [bop] implicated in gating and ion selectivity		1
1	Mechanism of gating and partial agonist action in the glycine receptor		2

