

Harel Weinstein

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374
ext. papers

18,720
ext. citations

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#	Paper	IF	Citations
301	[19] Integrated methods for the construction of three-dimensional models and computational probing of structure-function relations in G protein-coupled receptors. <i>Methods in Neurosciences</i> , 1995 , 25, 366-428		1974
300	Functional selectivity and classical concepts of quantitative pharmacology. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2007 , 320, 1-13	4.7	870
299	Tas1r3, encoding a new candidate taste receptor, is allelic to the sweet responsiveness locus Sac. <i>Nature Genetics</i> , 2001 , 28, 58-63	36.3	439
298	Molecular mechanisms of ligand interaction with the gonadotropin-releasing hormone receptor. <i>Endocrine Reviews</i> , 1997 , 18, 180-205	27.2	417
297	Agonists induce conformational changes in transmembrane domains III and VI of the beta2 adrenoceptor. <i>EMBO Journal</i> , 1997 , 16, 6737-47	13	332
296	The mechanism of a neurotransmitter:sodium symporter--inward release of Na ⁺ and substrate is triggered by substrate in a second binding site. <i>Molecular Cell</i> , 2008 , 30, 667-77	17.6	308
295	Allosteric communication between protomers of dopamine class A GPCR dimers modulates activation. <i>Nature Chemical Biology</i> , 2009 , 5, 688-95	11.7	294
294	Hinges, swivels and switches: the role of prolines in signalling via transmembrane alpha-helices. <i>Trends in Pharmacological Sciences</i> , 2000 , 21, 445-51	13.2	269
293	The binding sites for cocaine and dopamine in the dopamine transporter overlap. <i>Nature Neuroscience</i> , 2008 , 11, 780-9	25.5	260
292	Crosstalk in G protein-coupled receptors: changes at the transmembrane homodimer interface determine activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 17495-500	11.5	252
291	Substrate-modulated gating dynamics in a Na ⁺ -coupled neurotransmitter transporter homologue. <i>Nature</i> , 2011 , 474, 109-13	50.4	244
290	Structural instability of a constitutively active G protein-coupled receptor. Agonist-independent activation due to conformational flexibility. <i>Journal of Biological Chemistry</i> , 1997 , 272, 2587-90	5.4	238
289	A comprehensive structure-based alignment of prokaryotic and eukaryotic neurotransmitter/Na ⁺ symporters (NSS) aids in the use of the LeuT structure to probe NSS structure and function. <i>Molecular Pharmacology</i> , 2006 , 70, 1630-42	4.3	232
288	Single-molecule dynamics of gating in a neurotransmitter transporter homologue. <i>Nature</i> , 2010 , 465, 188-93	50.4	213
287	Functional microdomains in G-protein-coupled receptors. The conserved arginine-cage motif in the gonadotropin-releasing hormone receptor. <i>Journal of Biological Chemistry</i> , 1998 , 273, 10445-53	5.4	196
286	Related contribution of specific helix 2 and 7 residues to conformational activation of the serotonin 5-HT _{2A} receptor. <i>Journal of Biological Chemistry</i> , 1995 , 270, 16683-8	5.4	183
285	A misconception concerning the electronic density distribution of an atom. <i>Theoretica Chimica Acta</i> , 1975 , 38, 159-163		173

284	Single-molecule analysis of ligand efficacy in β AR-G-protein activation. <i>Nature</i> , 2017 , 547, 68-73	50.4	164
283	Binding of an octylglucoside detergent molecule in the second substrate (S2) site of LeuT establishes an inhibitor-bound conformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 5563-8	11.5	160
282	PDZBase: a protein-protein interaction database for PDZ-domains. <i>Bioinformatics</i> , 2005 , 21, 827-8	7.2	160
281	A cluster of aromatic residues in the sixth membrane-spanning segment of the dopamine D2 receptor is accessible in the binding-site crevice. <i>Biochemistry</i> , 1998 , 37, 998-1006	3.2	160
280	Ion/substrate-dependent conformational dynamics of a bacterial homolog of neurotransmitter:sodium symporters. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 822-9	17.6	157
279	. <i>Nature Genetics</i> , 2001 , 28, 58-63	36.3	144
278	Three-dimensional representations of G protein-coupled receptor structures and mechanisms. <i>Methods in Enzymology</i> , 2002 , 343, 329-71	1.7	143
277	Structure and dynamics of calmodulin in solution. <i>Biophysical Journal</i> , 1998 , 74, 1622-39	2.9	132
276	Some relations between electronic distribution and electronegativity. <i>Journal of Chemical Physics</i> , 1979 , 71, 4218-4220	3.9	131
275	A detailed interpretation of OH radical footprints in a TBP-DNA complex reveals the role of dynamics in the mechanism of sequence-specific binding. <i>Journal of Molecular Biology</i> , 2000 , 304, 55-68	6.5	123
274	Psychotomimetics as anticholinergic agents. I. 1-Cyclohexylpiperidine derivatives: anticholinesterase activity and antagonistic activity to acetylcholine. <i>Biochemical Pharmacology</i> , 1974 , 23, 1263-81	6	123
273	Transport domain unlocking sets the uptake rate of an aspartate transporter. <i>Nature</i> , 2015 , 518, 68-73	50.4	120
272	Mapping the binding site pocket of the serotonin 5-Hydroxytryptamine _{2A} receptor. Ser3.36(159) provides a second interaction site for the protonated amine of serotonin but not of lysergic acid diethylamide or bufotenin. <i>Journal of Biological Chemistry</i> , 1996 , 271, 14672-5	5.4	118
271	Residues in the seventh membrane-spanning segment of the dopamine D2 receptor accessible in the binding-site crevice. <i>Biochemistry</i> , 1996 , 35, 11278-85	3.2	116
270	Ca(2+)-binding and structural dynamics in the functions of calmodulin. <i>Annual Review of Physiology</i> , 1994 , 56, 213-36	23.1	113
269	An intracellular interaction network regulates conformational transitions in the dopamine transporter. <i>Journal of Biological Chemistry</i> , 2008 , 283, 17691-701	5.4	108
268	Characterization of novel cathepsin K mutations in the pro and mature polypeptide regions causing pycnodysostosis. <i>Journal of Clinical Investigation</i> , 1999 , 103, 731-8	15.9	107
267	Conformational dynamics of ligand-dependent alternating access in LeuT. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 472-9	17.6	102

266	Structural and dynamic effects of cholesterol at preferred sites of interaction with rhodopsin identified from microsecond length molecular dynamics simulations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 76, 403-17	4.2	100
265	Signal transduction by a 5-HT ₂ receptor: a mechanistic hypothesis from molecular dynamics simulations of the three-dimensional model of the receptor complexed to ligands. <i>Journal of Medicinal Chemistry</i> , 1993 , 36, 934-8	8.3	100
264	Conserved helix 7 tyrosine acts as a multistate conformational switch in the 5HT _{2C} receptor. Identification of a novel "locked-on" phenotype and double revertant mutations. <i>Journal of Biological Chemistry</i> , 2002 , 277, 36577-84	5.4	99
263	The substrate-driven transition to an inward-facing conformation in the functional mechanism of the dopamine transporter. <i>PLoS ONE</i> , 2011 , 6, e16350	3.7	99
262	The role of a conserved proline residue in mediating conformational changes associated with voltage gating of Cx32 gap junctions. <i>Biophysical Journal</i> , 1999 , 76, 2887-98	2.9	98
261	Conformational Memories and the Exploration of Biologically Relevant Peptide Conformations: An Illustration for the Gonadotropin-Releasing Hormone. <i>Journal of the American Chemical Society</i> , 1996 , 118, 5580-5589	16.4	98
260	Augmenting drug-carrier compatibility improves tumour nanotherapy efficacy. <i>Nature Communications</i> , 2016 , 7, 11221	17.4	96
259	Thermodynamic basis for promiscuity and selectivity in protein-protein interactions: PDZ domains, a case study. <i>Journal of the American Chemical Society</i> , 2006 , 128, 12766-77	16.4	96
258	Two 5-HT receptors linked to adenylate cyclase in guinea pig hippocampus are discriminated by 5-carboxamidotryptamine and spiperone. <i>European Journal of Pharmacology</i> , 1985 , 109, 427-9	5.3	89
257	The study of G-protein coupled receptor oligomerization with computational modeling and bioinformatics. <i>FEBS Journal</i> , 2005 , 272, 2926-38	5.7	87
256	On the use of the transmembrane domain of bacteriorhodopsin as a template for modeling the three-dimensional structure of guanine nucleotide-binding regulatory protein-coupled receptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1992 , 89, 4009-12	11.5	87
255	Membrane driven spatial organization of GPCRs. <i>Scientific Reports</i> , 2013 , 3, 2909	4.9	86
254	Identification of a small-molecule inhibitor of the PICK1 PDZ domain that inhibits hippocampal LTP and LTD. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 413-8	11.5	86
253	Functional role of a conserved motif in TM6 of the rat mu opioid receptor: constitutively active and inactive receptors result from substitutions of Thr6.34(279) with Lys and Asp. <i>Biochemistry</i> , 2001 , 40, 13501-9	3.2	85
252	Ligand-dependent conformations and dynamics of the serotonin 5-HT _{2A} receptor determine its activation and membrane-driven oligomerization properties. <i>PLoS Computational Biology</i> , 2012 , 8, e1002473	5.473	84
251	Localized Molecular Orbitals. <i>Advances in Atomic and Molecular Physics</i> , 1971 , 7, 97-140		84
250	PIP ₂ regulates psychostimulant behaviors through its interaction with a membrane protein. <i>Nature Chemical Biology</i> , 2014 , 10, 582-589	11.7	83
249	Experimental conditions can obscure the second high-affinity site in LeuT. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 207-11	17.6	82

248	Crooked tail (Cd) model of human folate-responsive neural tube defects is mutated in Wnt coreceptor lipoprotein receptor-related protein 6. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 12843-8	11.5	81
247	Prokink: a protocol for numerical evaluation of helix distortions by proline. <i>Protein Engineering, Design and Selection</i> , 2000 , 13, 603-6	1.9	81
246	A locus of the gonadotropin-releasing hormone receptor that differentiates agonist and antagonist binding sites. <i>Journal of Biological Chemistry</i> , 1995 , 270, 18853-7	5.4	80
245	Missense dopamine transporter mutations associate with adult parkinsonism and ADHD. <i>Journal of Clinical Investigation</i> , 2014 , 124, 3107-20	15.9	80
244	Elucidating the Mechanism of Membrane Destabilization by the Preferred Modes of Insertion of the Sars-Cov2 Fusion Peptide. <i>Biophysical Journal</i> , 2021 , 120, 110a	2.9	78
243	Ion-controlled conformational dynamics in the outward-open transition from an occluded state of LeuT. <i>Biophysical Journal</i> , 2012 , 103, 878-88	2.9	77
242	State-dependent conformations of the translocation pathway in the tyrosine transporter Tyt1, a novel neurotransmitter:sodium symporter from <i>Fusobacterium nucleatum</i> . <i>Journal of Biological Chemistry</i> , 2006 , 281, 26444-54	5.4	77
241	Quantitative modeling of membrane deformations by multihelical membrane proteins: application to G-protein coupled receptors. <i>Biophysical Journal</i> , 2011 , 101, 2092-101	2.9	76
240	Structural models for dimerization of G-protein coupled receptors: the opioid receptor homodimers. <i>Biopolymers</i> , 2002 , 66, 317-25	2.2	76
239	Spontaneous inward opening of the dopamine transporter is triggered by PIP2-regulated dynamics of the N-terminus. <i>ACS Chemical Neuroscience</i> , 2015 , 6, 1825-37	5.7	75
238	Prediction of heterodimerization interfaces of G-protein coupled receptors with a new subtractive correlated mutation method. <i>Protein Engineering, Design and Selection</i> , 2002 , 15, 881-5	1.9	75
237	Steric hindrance mutagenesis in the conserved extracellular vestibule impedes allosteric binding of antidepressants to the serotonin transporter. <i>Journal of Biological Chemistry</i> , 2012 , 287, 39316-26	5.4	74
236	Antagonism of histamine-activated adenylate cyclase in brain by D-lysergic acid diethylamide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1977 , 74, 5697-701	11.5	74
235	NbIT--a new information theory-based analysis of allosteric mechanisms reveals residues that underlie function in the leucine transporter LeuT. <i>PLoS Computational Biology</i> , 2014 , 10, e1003603	5	68
234	A knowledge-based scale for the analysis and prediction of buried and exposed faces of transmembrane domain proteins. <i>Bioinformatics</i> , 2004 , 20, 1822-35	7.2	66
233	Chloride binding site of neurotransmitter sodium symporters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 8489-94	11.5	65
232	Constitutive activation of the mu opioid receptor by mutation of D3.49(164), but not D3.32(147): D3.49(164) is critical for stabilization of the inactive form of the receptor and for its expression. <i>Biochemistry</i> , 2001 , 40, 12039-50	3.2	65
231	A proposed structure for transmembrane segment 7 of G protein-coupled receptors incorporating an asn-Pro/Asp-Pro motif. <i>Biophysical Journal</i> , 1998 , 75, 601-11	2.9	65

230	The functional microdomain in transmembrane helices 2 and 7 regulates expression, activation, and coupling pathways of the gonadotropin-releasing hormone receptor. <i>Journal of Biological Chemistry</i> , 1999 , 274, 28880-6	5.4	65
229	The fourth transmembrane segment of the dopamine D2 receptor: accessibility in the binding-site crevice and position in the transmembrane bundle. <i>Biochemistry</i> , 2000 , 39, 12190-9	3.2	64
228	Multiple interactions of the Asp(2.61(98)) side chain of the gonadotropin-releasing hormone receptor contribute differentially to ligand interaction. <i>Biochemistry</i> , 2000 , 39, 8133-41	3.2	64
227	A flexible docking procedure for the exploration of peptide binding selectivity to known structures and homology models of PDZ domains. <i>Journal of the American Chemical Society</i> , 2005 , 127, 14072-9	16.4	63
226	Modeling activated states of GPCRs: the rhodopsin template. <i>Journal of Computer-Aided Molecular Design</i> , 2006 , 20, 437-48	4.2	62
225	Molecular basis of partial agonism: orientation of indoleamine ligands in the binding pocket of the human serotonin 5-HT _{2A} receptor determines relative efficacy. <i>Molecular Pharmacology</i> , 2003 , 63, 36-43	4.3	62
224	Mechanisms of nucleophilic addition to activated double bonds: 1,2- and 1,4-Michael addition of ammonia. <i>Journal of the American Chemical Society</i> , 1993 , 115, 8263-8269	16.4	62
223	Molecular determinants for the complex binding specificity of the PDZ domain in PICK1. <i>Journal of Biological Chemistry</i> , 2005 , 280, 20539-48	5.4	61
222	Allosteric Mechanisms of Molecular Machines at the Membrane: Transport by Sodium-Coupled Symporters. <i>Chemical Reviews</i> , 2016 , 116, 6552-87	68.1	59
221	Dynamic models of G-protein coupled receptor dimers: indications of asymmetry in the rhodopsin dimer from molecular dynamics simulations in a POPC bilayer. <i>Journal of Computer-Aided Molecular Design</i> , 2006 , 20, 405-16	4.2	59
220	Molecular dynamics simulations of peptides and proteins with a continuum electrostatic model based on screened Coulomb potentials. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 51, 109-25	4.2	59
219	A juxtamembrane mutation in the N terminus of the dopamine transporter induces preference for an inward-facing conformation. <i>Molecular Pharmacology</i> , 2009 , 75, 514-24	4.3	56
218	Structural analysis of carboxypeptidase A and its complexes with inhibitors as a basis for modeling enzyme recognition and specificity. <i>Biopolymers</i> , 1985 , 24, 1721-58	2.2	56
217	A functional selectivity mechanism at the serotonin-2A GPCR involves ligand-dependent conformations of intracellular loop 2. <i>Journal of the American Chemical Society</i> , 2014 , 136, 16044-54	16.4	55
216	Modeling membrane deformations and lipid demixing upon protein-membrane interaction: the BAR dimer adsorption. <i>Biophysical Journal</i> , 2009 , 97, 1626-35	2.9	55
215	Comparative modeling and molecular dynamics studies of the delta, kappa and mu opioid receptors. <i>Protein Engineering, Design and Selection</i> , 1997 , 10, 1019-38	1.9	55
214	Toward realistic modeling of dynamic processes in cell signaling: quantification of macromolecular crowding effects. <i>Journal of Chemical Physics</i> , 2007 , 127, 155105	3.9	55
213	Neurofilament (NF) assembly; divergent characteristics of human and rodent NF-L subunits. <i>Journal of Biological Chemistry</i> , 1998 , 273, 5101-8	5.4	53

212	Molecular dynamics simulation of the hydrated d(CGCGAATTCGCG) ₂ dodecamer. <i>Journal of the American Chemical Society</i> , 1993 , 115, 1526-1537	16.4	53
211	A theoretical investigation of histamine tautomerism. <i>Journal of Medicinal Chemistry</i> , 1984 , 27, 1531-4	8.3	52
210	The behavioral effects of phencyclidines may be due to their blockade of potassium channels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1981 , 78, 7792-6	11.5	52
209	Gating mechanism of the extracellular entry to the lipid pathway in a TMEM16 scramblase. <i>Nature Communications</i> , 2018 , 9, 3251	17.4	51
208	The binding sites for benztropines and dopamine in the dopamine transporter overlap. <i>Neuropharmacology</i> , 2011 , 60, 182-90	5.5	49
207	Protein diffusion on charged membranes: a dynamic mean-field model describes time evolution and lipid reorganization. <i>Biophysical Journal</i> , 2008 , 94, 2580-97	2.9	49
206	Ligand-induced domain motion in the activation mechanism of a G-protein-coupled receptor. <i>Protein Engineering, Design and Selection</i> , 1994 , 7, 1441-8	1.9	49
205	Substrate-dependent proton antiport in neurotransmitter:sodium symporters. <i>Nature Chemical Biology</i> , 2010 , 6, 109-16	11.7	48
204	Key issues in the computational simulation of GPCR function: representation of loop domains. <i>Journal of Computer-Aided Molecular Design</i> , 2002 , 16, 841-53	4.2	48
203	Effects of tobacco smoke on gene expression and cellular pathways in a cellular model of oral leukoplakia. <i>Cancer Prevention Research</i> , 2008 , 1, 100-11	3.2	47
202	Molecular electrostatic potentials-II. <i>Tetrahedron</i> , 1975 , 31, 915-923	2.4	47
201	A Markov State-based Quantitative Kinetic Model of Sodium Release from the Dopamine Transporter. <i>Scientific Reports</i> , 2017 , 7, 40076	4.9	46
200	Not just an oil slick: how the energetics of protein-membrane interactions impacts the function and organization of transmembrane proteins. <i>Biophysical Journal</i> , 2014 , 106, 2305-16	2.9	46
199	A surface on the G protein beta-subunit involved in interactions with adenylyl cyclases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997 , 94, 2711-4	11.5	46
198	Electrostatic Potentials as Descriptors of Molecular Reactivity: The Basis for Some Successful Predictions of Biological Activity 1981 , 309-334		45
197	Why GPCRs behave differently in cubic and lamellar lipidic mesophases. <i>Journal of the American Chemical Society</i> , 2012 , 134, 15858-68	16.4	44
196	Gbeta subunit interacts with a peptide encoding region 956-982 of adenylyl cyclase 2. Cross-linking of the peptide to free Gbetagamma but not the heterotrimer. <i>Journal of Biological Chemistry</i> , 1996 , 271, 26445-8	5.4	43
195	Polarity conserved positions in transmembrane domains of G-protein coupled receptors and bacteriorhodopsin. <i>FEBS Letters</i> , 1994 , 337, 207-12	3.8	43

194	Structural motifs as functional microdomains in G-protein-coupled receptors: Energetic considerations in the mechanism of activation of the serotonin 5-HT _{2A} receptor by disruption of the ionic lock of the arginine cage*. <i>International Journal of Quantum Chemistry</i> , 2002 , 88, 65-75	2.1	42
193	Molecular dynamics simulations predict a tilted orientation for the helical region of dynorphin A(1-17) in dimyristoylphosphatidylcholine bilayers. <i>Biophysical Journal</i> , 2000 , 79, 2331-44	2.9	42
192	Mechanism of the Association between Na ⁺ Binding and Conformations at the Intracellular Gate in Neurotransmitter:Sodium Symporters. <i>Journal of Biological Chemistry</i> , 2015 , 290, 13992-4003	5.4	41
191	Conformational rearrangements to the intracellular open states of the LeuT and ApcT transporters are modulated by common mechanisms. <i>Biophysical Journal</i> , 2010 , 99, L103-5	2.9	41
190	Membrane localization is critical for activation of the PICK1 BAR domain. <i>Traffic</i> , 2008 , 9, 1327-43	5.7	41
189	Quantum chemical studies on molecular determinants for drug action. <i>Annals of the New York Academy of Sciences</i> , 1981 , 367, 434-51	6.5	41
188	Structural intermediates in a model of the substrate translocation path of the bacterial glutamate transporter homologue GltPh. <i>Journal of Physical Chemistry B</i> , 2012 , 116, 5372-83	3.4	40
187	Molecular dynamics simulations of transducin: interdomain and front to back communication in activation and nucleotide exchange. <i>Journal of Molecular Biology</i> , 2004 , 338, 469-81	6.5	40
186	Computational modeling of the N-terminus of the human dopamine transporter and its interaction with PIP ₂ -containing membranes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015 , 83, 952-69	4.2	39
185	Structural probing of a microdomain in the dopamine transporter by engineering of artificial Zn ²⁺ binding sites. <i>Biochemistry</i> , 2000 , 39, 15836-46	3.2	39
184	Theoretical treatment of multiple site reactivity in large molecules. <i>Chemical Physics Letters</i> , 1975 , 30, 441-447	2.5	39
183	Computational approaches to detect allosteric pathways in transmembrane molecular machines. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016 , 1858, 1652-62	3.8	38
182	The cost of living in the membrane: a case study of hydrophobic mismatch for the multi-segment protein LeuT. <i>Chemistry and Physics of Lipids</i> , 2013 , 169, 27-38	3.7	38
181	The local environment at the cytoplasmic end of TM6 of the mu opioid receptor differs from those of rhodopsin and monoamine receptors: introduction of an ionic lock between the cytoplasmic ends of helices 3 and 6 by a L6.30(275)E mutation inactivates the mu opioid receptor and reduces the constitutive activity of its T6.34(279)K mutant. <i>Biochemistry</i> , 2002 , 41, 11972-80	3.2	37
180	Functional role of the spatial proximity of Asp114(2.50) in TMH 2 and Asn332(7.49) in TMH 7 of the mu opioid receptor. <i>FEBS Letters</i> , 1999 , 447, 318-24	3.8	37
179	Does TATA matter? A structural exploration of the selectivity determinants in its complexes with TATA box-binding protein. <i>Biophysical Journal</i> , 1997 , 73, 640-52	2.9	36
178	A pincer-like configuration of TM2 in the human dopamine transporter is responsible for indirect effects on cocaine binding. <i>Neuropharmacology</i> , 2005 , 49, 780-90	5.5	36
177	Certain 1,4-disubstituted aromatic piperidines and piperazines with extreme selectivity for the dopamine D ₄ receptor interact with a common receptor microdomain. <i>Molecular Pharmacology</i> , 2004 , 66, 1491-9	4.3	36

176	Probing conformational changes in neurotransmitter transporters: a structural context. <i>European Journal of Pharmacology</i> , 2003 , 479, 3-12	5.3	36
175	Structural dynamics of calmodulin and troponin C. <i>Protein Engineering, Design and Selection</i> , 1991 , 4, 625-37	1.9	36
174	Mechanisms of Lipid Scrambling by the G Protein-Coupled Receptor Opsin. <i>Structure</i> , 2018 , 26, 356-367.	5.3	35
173	Ab initio computational modeling of loops in G-protein-coupled receptors: lessons from the crystal structure of rhodopsin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 64, 673-90	4.2	35
172	A New Computational Method for Membrane Compressibility: Bilayer Mechanical Thickness Revisited. <i>Biophysical Journal</i> , 2019 , 116, 487-502	2.9	34
171	PDZ binding to the BAR domain of PICK1 is elucidated by coarse-grained molecular dynamics. <i>Journal of Molecular Biology</i> , 2011 , 405, 298-314	6.5	34
170	"Specific binding" of 3H-phencyclidine: artifacts of the rapid filtration method. <i>Life Sciences</i> , 1980 , 26, 2011-22	6.8	34
169	GPCRmd uncovers the dynamics of the 3D-GPCRome. <i>Nature Methods</i> , 2020 , 17, 777-787	21.6	34
168	Trefoil factor family-1 mutations enhance gastric cancer cell invasion through distinct signaling pathways. <i>Gastroenterology</i> , 2006 , 130, 1696-706	13.3	33
167	On the ion selectivity in Ca-binding proteins: the cyclo(-L-Pro-Gly-)3 peptide as a model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1989 , 86, 7880-4	11.5	33
166	Reactivities of acrylic and methacrylic acids in a nucleophilic addition model of their biological activity. <i>Journal of the American Chemical Society</i> , 1988 , 110, 1701-1707	16.4	33
165	Topology of Type II REases revisited; structural classes and the common conserved core. <i>Nucleic Acids Research</i> , 2007 , 35, 2227-37	20.1	32
164	Gramicidin Increases Lipid Flip-Flop in Symmetric and Asymmetric Lipid Vesicles. <i>Biophysical Journal</i> , 2019 , 116, 860-873	2.9	31
163	A mechanistic role of Helix 8 in GPCRs: Computational modeling of the dopamine D2 receptor interaction with the GIPC1-PDZ-domain. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015 , 1848, 976-83	3.8	31
162	The second sodium site in the dopamine transporter controls cation permeation and is regulated by chloride. <i>Journal of Biological Chemistry</i> , 2014 , 289, 25764-73	5.4	30
161	Cholesterol modulates the membrane effects and spatial organization of membrane-penetrating ligands for G-protein coupled receptors. <i>Journal of Physical Chemistry B</i> , 2010 , 114, 12046-57	3.4	30
160	Comparison of the amino acid residues in the sixth transmembrane domains accessible in the binding-site crevices of mu, delta, and kappa opioid receptors. <i>Biochemistry</i> , 2001 , 40, 8018-29	3.2	30
159	Molecular Dynamics Simulation of Membranes and a Transmembrane Helix. <i>Journal of Computational Physics</i> , 1999 , 151, 358-387	4.1	30

158	The membrane protein LeuT in micellar systems: aggregation dynamics and detergent binding to the S2 site. <i>Journal of the American Chemical Society</i> , 2013 , 135, 14266-75	16.4	29
157	Ligand selectivity of D2 dopamine receptors is modulated by changes in local dynamics produced by sodium binding. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2009 , 328, 40-54	4.7	29
156	Substrate-induced unlocking of the inner gate determines the catalytic efficiency of a neurotransmitter:sodium symporter. <i>Journal of Biological Chemistry</i> , 2015 , 290, 26725-38	5.4	28
155	A partially-open inward-facing intermediate conformation of LeuT is associated with Na release and substrate transport. <i>Nature Communications</i> , 2018 , 9, 230	17.4	28
154	Structure-activity relationships of a small-molecule inhibitor of the PDZ domain of PICK1. <i>Organic and Biomolecular Chemistry</i> , 2010 , 8, 4281-8	3.9	28
153	Hallucinogen actions on 5-HT receptors reveal distinct mechanisms of activation and signaling by G protein-coupled receptors. <i>AAPS Journal</i> , 2006 , 7, E871-84	3.7	27
152	Differences in conformational properties of the second intracellular loop (IL2) in 5HT(2C) receptors modified by RNA editing can account for G protein coupling efficiency. <i>Protein Engineering, Design and Selection</i> , 2001 , 14, 409-14	1.9	27
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