

Vadim Cherezov

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.

159 papers	26,910 citations	72 h-index	164 g-index
178 ext. papers	29,987 ext. citations	15.1 avg, IF	6.76 L-index

#	Paper	IF	Citations
159	Molecular mechanisms of metabotropic GABA receptor function. <i>Science Advances</i> , 2021 , 7,	14.3	10
158	Structural insights on ligand recognition at the human leukotriene B4 receptor 1. <i>Nature Communications</i> , 2021 , 12, 2971	17.4	4
157	Structural insights into ligand recognition and activation of angiotensin receptors. <i>Trends in Pharmacological Sciences</i> , 2021 , 42, 577-587	13.2	6
156	The ligand-bound state of a G protein-coupled receptor stabilizes the interaction of functional cholesterol molecules. <i>Journal of Lipid Research</i> , 2021 , 62, 100059	6.3	7
155	MicroED structure of the human adenosine receptor determined from a single nanocrystal in LCP. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	9
154	Molecular basis for lipid recognition by the prostaglandin D receptor CRTH2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	1
153	Single Peptide Backbone Surrogate Mutations to Regulate Angiotensin GPCR Subtype Selectivity. <i>Chemistry - A European Journal</i> , 2020 , 26, 10690-10694	4.8	3
152	Structural basis of the activation of a metabotropic GABA receptor. <i>Nature</i> , 2020 , 584, 298-303	50.4	49
151	Virtual discovery of melatonin receptor ligands to modulate circadian rhythms. <i>Nature</i> , 2020 , 579, 609-614	34.4	88
150	XFEL and NMR Structures of Francisella Lipoprotein Reveal Conformational Space of Drug Target against Tularemia. <i>Structure</i> , 2020 , 28, 540-547.e3	5.2	5
149	On the Origin of the Anomalous Behavior of Lipid Membrane Properties in the Vicinity of the Chain-Melting Phase Transition. <i>Scientific Reports</i> , 2020 , 10, 5749	4.9	7
148	Harnessing the power of an X-ray laser for serial crystallography of membrane proteins crystallized in lipidic cubic phase. <i>IUCrJ</i> , 2020 , 7, 976-984	4.7	8
147	Structural insights into melatonin receptors. <i>FEBS Journal</i> , 2020 , 287, 1496-1510	5.7	18
146	Small-wedge synchrotron and serial XFEL datasets for Cysteinyl leukotriene GPCRs. <i>Scientific Data</i> , 2020 , 7, 388	8.2	0
145	Structure-Based Virtual Screening of Ultra-Large Library Yields Potent Antagonists for a Lipid GPCR. <i>Biomolecules</i> , 2020 , 10,	5.9	3
144	Beyond structure: emerging approaches to study GPCR dynamics. <i>Current Opinion in Structural Biology</i> , 2020 , 63, 18-25	8.1	21
143	An outlook on using serial femtosecond crystallography in drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2019 , 14, 933-945	6.2	16

142	Structural basis of ligand recognition at the human MT melatonin receptor. <i>Nature</i> , 2019 , 569, 284-288	50.4	98
141	XFEL structures of the human MT melatonin receptor reveal the basis of subtype selectivity. <i>Nature</i> , 2019 , 569, 289-292	50.4	77
140	The lipid phase preference of the adenosine A receptor depends on its ligand binding state. <i>Chemical Communications</i> , 2019 , 55, 5724-5727	5.8	6
139	Chemical tools for membrane protein structural biology. <i>Current Opinion in Structural Biology</i> , 2019 , 58, 278-285	8.1	6
138	Structure-based mechanism of cysteinyl leukotriene receptor inhibition by antiasthmatic drugs. <i>Science Advances</i> , 2019 , 5, eaax2518	14.3	41
137	High-viscosity injector-based pink-beam serial crystallography of microcrystals at a synchrotron radiation source. <i>IUCrJ</i> , 2019 , 6, 412-425	4.7	30
136	Toward G protein-coupled receptor structure-based drug design using X-ray lasers. <i>IUCrJ</i> , 2019 , 6, 1106-1119	11.9	28
135	Elucidating the active μ opioid receptor crystal structure with peptide and small-molecule agonists. <i>Science Advances</i> , 2019 , 5, eaax9115	14.3	38
134	Structural basis of ligand selectivity and disease mutations in cysteinyl leukotriene receptors. <i>Nature Communications</i> , 2019 , 10, 5573	17.4	31
133	Crystal structure of misoprostol bound to the labor inducer prostaglandin E receptor. <i>Nature Chemical Biology</i> , 2019 , 15, 11-17	11.7	23
132	Structure of the Nanobody-Stabilized Active State of the Kappa Opioid Receptor. <i>Cell</i> , 2018 , 172, 55-67.e15	36.2	205
131	High-throughput in situ X-ray screening of and data collection from protein crystals at room temperature and under cryogenic conditions. <i>Nature Protocols</i> , 2018 , 13, 260-292	18.8	31
130	Structural biology of G protein-coupled receptors: new opportunities from XFELs and cryoEM. <i>Current Opinion in Structural Biology</i> , 2018 , 51, 44-52	8.1	18
129	Serial Femtosecond Crystallography of G Protein-Coupled Receptors. <i>Annual Review of Biophysics</i> , 2018 , 47, 377-397	21.1	31
128	Advances in Structure Determination of G Protein-Coupled Receptors by SFX 2018 , 301-329		1
127	Computational design of thermostabilizing point mutations for G protein-coupled receptors. <i>ELife</i> , 2018 , 7,	8.9	40
126	Fast iodide-SAD phasing for high-throughput membrane protein structure determination. <i>Science Advances</i> , 2017 , 3, e1602952	14.3	27
125	Chemically Stable Lipids for Membrane Protein Crystallization. <i>Crystal Growth and Design</i> , 2017 , 17, 3502-3511	35.1	19

124	Structure of the full-length glucagon class B G-protein-coupled receptor. <i>Nature</i> , 2017 , 546, 259-264	50.4	141
123	Crystal structure of a multi-domain human smoothened receptor in complex with a super stabilizing ligand. <i>Nature Communications</i> , 2017 , 8, 15383	17.4	62
122	Structure of CC Chemokine Receptor 5 with a Potent Chemokine Antagonist Reveals Mechanisms of Chemokine Recognition and Molecular Mimicry by HIV. <i>Immunity</i> , 2017 , 46, 1005-1017.e5	32.3	106
121	Crystallization of Membrane Proteins: An Overview. <i>Methods in Molecular Biology</i> , 2017 , 1607, 117-141	1.4	13
120	Structural basis for selectivity and diversity in angiotensin II receptors. <i>Nature</i> , 2017 , 544, 327-332	50.4	128
119	A Bright Future for Serial Femtosecond Crystallography with XFELs. <i>Trends in Biochemical Sciences</i> , 2017 , 42, 749-762	10.3	102
118	Structural insights into the extracellular recognition of the human serotonin 2B receptor by an antibody. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 8223-8228	11.5	43
117	Identification of Phosphorylation Codes for Arrestin Recruitment by G Protein-Coupled Receptors. <i>Cell</i> , 2017 , 170, 457-469.e13	56.2	225
116	Critical Role of Water Molecules in Proton Translocation by the Membrane-Bound Transhydrogenase. <i>Structure</i> , 2017 , 25, 1111-1119.e3	5.2	8
115	Serial millisecond crystallography of membrane and soluble protein microcrystals using synchrotron radiation. <i>IUCrJ</i> , 2017 , 4, 439-454	4.7	103
114	Serial Femtosecond Crystallography of Membrane Proteins. <i>Advances in Experimental Medicine and Biology</i> , 2016 , 922, 151-160	3.6	6
113	Native phasing of x-ray free-electron laser data for a G protein-coupled receptor. <i>Science Advances</i> , 2016 , 2, e1600292	14.3	85
112	X-ray laser diffraction for structure determination of the rhodopsin-arrestin complex. <i>Scientific Data</i> , 2016 , 3, 160021	8.2	40
111	Preparation and Delivery of Protein Microcrystals in Lipidic Cubic Phase for Serial Femtosecond Crystallography. <i>Journal of Visualized Experiments</i> , 2016 ,	1.6	16
110	Serial femtosecond crystallography datasets from G protein-coupled receptors. <i>Scientific Data</i> , 2016 , 3, 160057	8.2	8
109	The Fragment Molecular Orbital Method Reveals New Insight into the Chemical Nature of GPCR-Ligand Interactions. <i>Journal of Chemical Information and Modeling</i> , 2016 , 56, 159-72	6.1	73
108	Fast iodide-SAD phasing for membrane protein structure determination. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016 , 72, s199-s199	1.7	2
107	Structure of CC chemokine receptor 2 with orthosteric and allosteric antagonists. <i>Nature</i> , 2016 , 540, 458-461	50.4	168

106	Structural biology. Crystal structure of the chemokine receptor CXCR4 in complex with a viral chemokine. <i>Science</i> , 2015 , 347, 1117-22	33.3	262
105	Crystal structure of rhodopsin bound to arrestin by femtosecond X-ray laser. <i>Nature</i> , 2015 , 523, 561-7	50.4	572
104	Structure of the Angiotensin receptor revealed by serial femtosecond crystallography. <i>Cell</i> , 2015 , 161, 833-44	56.2	262
103	GPCR structure, function, drug discovery and crystallography: report from Academia-Industry International Conference (UK Royal Society) Chicheley Hall, 1-2 September 2014. <i>Naunyn-Schmiedeberg's Archives of Pharmacology</i> , 2015 , 388, 883-903	3.4	30
102	Fluorescence Recovery After Photobleaching in Lipidic Cubic Phase (LCP-FRAP): A Precrystallization Assay for Membrane Proteins. <i>Methods in Enzymology</i> , 2015 , 557, 417-37	1.7	10
101	Two disparate ligand-binding sites in the human P2Y1 receptor. <i>Nature</i> , 2015 , 520, 317-21	50.4	239
100	The Importance of Ligand-Receptor Conformational Pairs in Stabilization: Spotlight on the N/OFQ G Protein-Coupled Receptor. <i>Structure</i> , 2015 , 23, 2291-2299	5.2	53
99	Structural Basis for Ligand Recognition and Functional Selectivity at Angiotensin Receptor. <i>Journal of Biological Chemistry</i> , 2015 , 290, 29127-39	5.4	111
98	Nucleation and Growth of Membrane Protein Crystals In Mesophase: A Fluorescence Microscopy Study. <i>Crystal Growth and Design</i> , 2015 , 15, 5656-5660	3.5	8
97	A novel inert crystal delivery medium for serial femtosecond crystallography. <i>IUCrJ</i> , 2015 , 2, 421-30	4.7	108
96	Serial femtosecond crystallography of soluble proteins in lipidic cubic phase. <i>IUCrJ</i> , 2015 , 2, 545-51	4.7	50
95	Serial femtosecond X-ray diffraction of enveloped virus microcrystals. <i>Structural Dynamics</i> , 2015 , 2, 041730	3.0	10
94	Ternary structure reveals mechanism of a membrane diacylglycerol kinase. <i>Nature Communications</i> , 2015 , 6, 10140	17.4	27
93	Lipidic cubic phase serial millisecond crystallography using synchrotron radiation. <i>IUCrJ</i> , 2015 , 2, 168-76	4.7	161
92	Generic GPCR residue numbers - aligning topology maps while minding the gaps. <i>Trends in Pharmacological Sciences</i> , 2015 , 36, 22-31	13.2	259
91	Structural basis for bifunctional peptide recognition at human μ -opioid receptor. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 265-8	17.6	133
90	Structure of a class C GPCR metabotropic glutamate receptor 1 bound to an allosteric modulator. <i>Science</i> , 2014 , 344, 58-64	33.3	406
89	Lipidic cubic phase injector facilitates membrane protein serial femtosecond crystallography. <i>Nature Communications</i> , 2014 , 5, 3309	17.4	416

88	Structure of the human P2Y ₁₂ receptor in complex with an antithrombotic drug. <i>Nature</i> , 2014 , 509, 115-8	50.4	272
87	Allosteric sodium in class A GPCR signaling. <i>Trends in Biochemical Sciences</i> , 2014 , 39, 233-44	10.3	314
86	Molecular control of μ -opioid receptor signalling. <i>Nature</i> , 2014 , 506, 191-6	50.4	355
85	Functional assay for T4 lysozyme-engineered G protein-coupled receptors with an ion channel reporter. <i>Structure</i> , 2014 , 22, 149-55	5.2	6
84	Two classes of cholesterol binding sites for the μ AR revealed by thermostability and NMR. <i>Biophysical Journal</i> , 2014 , 107, 2305-12	2.9	35
83	Structural basis for Smoothened receptor modulation and chemoresistance to anticancer drugs. <i>Nature Communications</i> , 2014 , 5, 4355	17.4	175
82	Preparation of microcrystals in lipidic cubic phase for serial femtosecond crystallography. <i>Nature Protocols</i> , 2014 , 9, 2123-34	18.8	93
81	Agonist-bound structure of the human P2Y ₁₂ receptor. <i>Nature</i> , 2014 , 509, 119-22	50.4	222
80	Femtosecond crystallography of membrane proteins in the lipidic cubic phase. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2014 , 369, 20130314	5.8	40
79	Constitutive phospholipid scramblase activity of a G protein-coupled receptor. <i>Nature Communications</i> , 2014 , 5, 5115	17.4	78
78	Lipidic Cubic Phase Technologies for Structural Studies of Membrane Proteins 2014 , 289-314		5
77	Structure of the human glucagon class B G-protein-coupled receptor. <i>Nature</i> , 2013 , 499, 444-9	50.4	312
76	The role of a sodium ion binding site in the allosteric modulation of the A(2A) adenosine G protein-coupled receptor. <i>Structure</i> , 2013 , 21, 2175-85	5.2	98
75	Structure-based ligand discovery targeting orthosteric and allosteric pockets of dopamine receptors. <i>Molecular Pharmacology</i> , 2013 , 84, 794-807	4.3	69
74	Serial femtosecond crystallography of G protein-coupled receptors. <i>Science</i> , 2013 , 342, 1521-4	33.3	367
73	Structure of the CCR5 chemokine receptor-HIV entry inhibitor maraviroc complex. <i>Science</i> , 2013 , 341, 1387-90	33.3	505
72	The GPCR Network: a large-scale collaboration to determine human GPCR structure and function. <i>Nature Reviews Drug Discovery</i> , 2013 , 12, 25-34	64.1	207
71	Structure-function of the G protein-coupled receptor superfamily. <i>Annual Review of Pharmacology and Toxicology</i> , 2013 , 53, 531-56	17.9	758

70	Integrated nonlinear optical imaging microscope for on-axis crystal detection and centering at a synchrotron beamline. <i>Journal of Synchrotron Radiation</i> , 2013 , 20, 531-40	2.4	31
69	Structural features for functional selectivity at serotonin receptors. <i>Science</i> , 2013 , 340, 615-9	33.3	492
68	Structural basis for molecular recognition at serotonin receptors. <i>Science</i> , 2013 , 340, 610-4	33.3	370
67	Structure of the human smoothened receptor bound to an antitumour agent. <i>Nature</i> , 2013 , 497, 338-43	50.4	375
66	Hydrogen bonding of cholesterol in the lipidic cubic phase. <i>Langmuir</i> , 2013 , 29, 8031-8	4	24
65	Towards protein-crystal centering using second-harmonic generation (SHG) microscopy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013 , 69, 843-51		25
64	Crystal structure of a voltage-gated K ⁺ channel pore module in a closed state in lipid membranes.. <i>Journal of Biological Chemistry</i> , 2013 , 288, 3476	5.4	78
63	Fusion partner toolchest for the stabilization and crystallization of G protein-coupled receptors. <i>Structure</i> , 2012 , 20, 967-76	5.2	272
62	Crystal structures of the outer membrane domain of intimin and invasin from enterohemorrhagic E. coli and enteropathogenic Y. pseudotuberculosis. <i>Structure</i> , 2012 , 20, 1233-43	5.2	69
61	Crystal structure of a voltage-gated K ⁺ channel pore module in a closed state in lipid membranes. <i>Journal of Biological Chemistry</i> , 2012 , 287, 43063-70	5.4	19
60	Structural basis for allosteric regulation of GPCRs by sodium ions. <i>Science</i> , 2012 , 337, 232-6	33.3	714
59	Diversity and modularity of G protein-coupled receptor structures. <i>Trends in Pharmacological Sciences</i> , 2012 , 33, 17-27	13.2	348
58	1.4 X-Ray Crystallography: Crystallization 2012 , 34-63		
57	Structure of the nociceptin/orphanin FQ receptor in complex with a peptide mimetic. <i>Nature</i> , 2012 , 485, 395-9	50.4	383
56	Structure of the human μ opioid receptor in complex with JDTic. <i>Nature</i> , 2012 , 485, 327-32	50.4	695
55	Characterization of lipid matrices for membrane protein crystallization by high-throughput small angle X-ray scattering. <i>Methods</i> , 2011 , 55, 342-9	4.6	28
54	GPCR stabilization using the bicelle-like architecture of mixed sterol-detergent micelles. <i>Methods</i> , 2011 , 55, 310-7	4.6	66
53	Structure of an agonist-bound human A2A adenosine receptor. <i>Science</i> , 2011 , 332, 322-7	33.3	706

52	High resolution structure of the ba3 cytochrome c oxidase from <i>Thermus thermophilus</i> in a lipidic environment. <i>PLoS ONE</i> , 2011 , 6, e22348	3.7	94
51	Crystallization of membrane proteins in lipidic mesophases. <i>Journal of Visualized Experiments</i> , 2011 ,	1.6	17
50	Structure of the human histamine H1 receptor complex with doxepin. <i>Nature</i> , 2011 , 475, 65-70	50.4	630
49	Lipidic cubic phase technologies for membrane protein structural studies. <i>Current Opinion in Structural Biology</i> , 2011 , 21, 559-66	8.1	165
48	Development of an Automated High Throughput LCP-FRAP Assay to Guide Membrane Protein Crystallization in Lipid Mesophases. <i>Crystal Growth and Design</i> , 2011 , 11, 1193-1201	3.5	45
47	LCP-Tm: an assay to measure and understand stability of membrane proteins in a membrane environment. <i>Biophysical Journal</i> , 2010 , 98, 1539-48	2.9	55
46	Structure of the human dopamine D3 receptor in complex with a D2/D3 selective antagonist. <i>Science</i> , 2010 , 330, 1091-5	33.3	938
45	Structures of the CXCR4 chemokine GPCR with small-molecule and cyclic peptide antagonists. <i>Science</i> , 2010 , 330, 1066-71	33.3	1432
44	Recent progress in the structure determination of GPCRs, a membrane protein family with high potential as pharmaceutical targets. <i>Methods in Molecular Biology</i> , 2010 , 654, 141-68	1.4	49
43	Conserved binding mode of human beta2 adrenergic receptor inverse agonists and antagonist revealed by X-ray crystallography. <i>Journal of the American Chemical Society</i> , 2010 , 132, 11443-5	16.4	297
42	Nonlinear optical imaging of integral membrane protein crystals in lipidic mesophases. <i>Analytical Chemistry</i> , 2010 , 82, 491-7	7.8	66
41	Rastering strategy for screening and centring of microcrystal samples of human membrane proteins with a sub-10 microm size X-ray synchrotron beam. <i>Journal of the Royal Society Interface</i> , 2009 , 6 Suppl 5, S587-97	4.1	138
40	Analysis of full and partial agonists binding to beta2-adrenergic receptor suggests a role of transmembrane helix V in agonist-specific conformational changes. <i>Journal of Molecular Recognition</i> , 2009 , 22, 307-18	2.6	100
39	Crystallizing membrane proteins using lipidic mesophases. <i>Nature Protocols</i> , 2009 , 4, 706-31	18.8	516
38	Crystal Structures of the β -Adrenergic Receptor. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2009 , 217-230	0.1	
37	A specific cholesterol binding site is established by the 2.8 Å structure of the human beta2-adrenergic receptor. <i>Structure</i> , 2008 , 16, 897-905	5.2	794
36	Insights into the mode of action of a putative zinc transporter CzcB in <i>Thermus thermophilus</i> . <i>Structure</i> , 2008 , 16, 1378-88	5.2	75
35	LCP-FRAP Assay for Pre-Screening Membrane Proteins for in Meso Crystallization. <i>Crystal Growth and Design</i> , 2008 , 8, 4307-4315	3.5	55

34	In meso crystal structure and docking simulations suggest an alternative proteoglycan binding site in the OpcA outer membrane adhesin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 24-34	4.2	37
33	The 2.6 angstrom crystal structure of a human A2A adenosine receptor bound to an antagonist. <i>Science</i> , 2008 , 322, 1211-7	33.3	1549
32	. <i>IEEE Transactions on Automation Science and Engineering</i> , 2007 , 4, 129-140	4.9	13
31	Crystallization and preliminary X-ray diffraction analysis of a soluble domain of the putative zinc transporter CztB from <i>Thermus thermophilus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007 , 63, 673-7		3
30	High-resolution crystal structure of an engineered human beta2-adrenergic G protein-coupled receptor. <i>Science</i> , 2007 , 318, 1258-65	33.3	2776
29	Membrane protein crystallization in lipidic mesophases. A mechanism study using X-ray microdiffraction. <i>Faraday Discussions</i> , 2007 , 136, 195-212; discussion 213-29	3.6	48
28	GPCR engineering yields high-resolution structural insights into beta2-adrenergic receptor function. <i>Science</i> , 2007 , 318, 1266-73	33.3	1173
27	The Membrane Protein Data Bank. <i>Cellular and Molecular Life Sciences</i> , 2006 , 63, 36-51	10.3	151
26	Controlling the passage of light through metal microchannels by nanocoatings of phospholipids. <i>Journal of Physical Chemistry B</i> , 2006 , 110, 21719-27	3.4	14
25	Room to move: crystallizing membrane proteins in swollen lipidic mesophases. <i>Journal of Molecular Biology</i> , 2006 , 357, 1605-18	6.5	220
24	Transmembrane peptides stabilize inverted cubic phases in a biphasic length-dependent manner: implications for protein-induced membrane fusion. <i>Biophysical Journal</i> , 2006 , 90, 200-11	2.9	39
23	Molecular organization of cholesterol in unsaturated phosphatidylethanolamines: X-ray diffraction and solid state 2H NMR reveal differences with phosphatidylcholines. <i>Journal of the American Chemical Society</i> , 2006 , 128, 5375-83	16.4	77
22	In meso structure of the cobalamin transporter, BtuB, at 1.95 Å resolution. <i>Journal of Molecular Biology</i> , 2006 , 364, 716-34	6.5	88
21	Picolitre-scale crystallization of membrane proteins. <i>Journal of Applied Crystallography</i> , 2006 , 39, 604-605	5.8	15
20	Strength of thermal undulations of phospholipid membranes. <i>Physical Review E</i> , 2005 , 72, 061913	2.4	22
19	Interaction of Polyunsaturated Fatty Acids with Cholesterol: A Role in Lipid Raft Phase Separation. <i>Macromolecular Symposia</i> , 2005 , 219, 73-84	0.8	4
18	A simple and inexpensive nanoliter-volume dispenser for highly viscous materials used in membrane protein crystallization. <i>Journal of Applied Crystallography</i> , 2005 , 38, 398-400	3.8	24
17	Membrane protein crystallization in lipidic mesophases with tailored bilayers. <i>Structure</i> , 2004 , 12, 2113-24	3.2	83

16	Order from disorder, corralling cholesterol with chaotic lipids. The role of polyunsaturated lipids in membrane raft formation. <i>Chemistry and Physics of Lipids</i> , 2004 , 132, 79-88	3.7	54
15	A robotic system for crystallizing membrane and soluble proteins in lipidic mesophases. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 1795-807		114
14	Rational design of lipid for membrane protein crystallization. <i>Journal of Structural Biology</i> , 2004 , 148, 169-75	3.4	66
13	Order from disorder, corralling cholesterol with chaotic lipidsThe role of polyunsaturated lipids in membrane raft formation. <i>Chemistry and Physics of Lipids</i> , 2004 , 132, 79-88	3.7	134
12	The kinetics of non-lamellar phase formation in DOPE-Me: relevance to biomembrane fusion. <i>Journal of Membrane Biology</i> , 2003 , 195, 165-82	2.3	49
11	Nano-volume plates with excellent optical properties for fast, inexpensive crystallization screening of membrane proteins. <i>Journal of Applied Crystallography</i> , 2003 , 36, 1372-1377	3.8	44
10	Interaction of cholesterol with a docosahexaenoic acid-containing phosphatidylethanolamine: trigger for microdomain/raft formation?. <i>Biochemistry</i> , 2003 , 42, 12028-37	3.2	81
9	Too hot to handle? Synchrotron X-ray damage of lipid membranes and mesophases. <i>Journal of Synchrotron Radiation</i> , 2002 , 9, 333-41	2.4	33
8	Controlling membrane cholesterol content. A role for polyunsaturated (docosahexaenoate) phospholipids. <i>Biochemistry</i> , 2002 , 41, 12509-19	3.2	70
7	Membrane protein crystallization in meso: lipid type-tailoring of the cubic phase. <i>Biophysical Journal</i> , 2002 , 83, 3393-407	2.9	135
6	Molecular organization of cholesterol in polyunsaturated membranes: microdomain formation. <i>Biophysical Journal</i> , 2002 , 82, 285-98	2.9	132
5	Biophysical and transfection studies of the diC(14)-amidine/DNA complex. <i>Biophysical Journal</i> , 2002 , 82, 3105-17	2.9	30
4	Crystallization screens: compatibility with the lipidic cubic phase for in meso crystallization of membrane proteins. <i>Biophysical Journal</i> , 2001 , 81, 225-42	2.9	82
3	Evidence of entropic contribution to HydrationForces between membranes Part II. Temperature dependence of the HydrationForce: a small angle neutron scattering study. <i>Journal of Molecular Structure</i> , 1996 , 383, 117-124	3.4	17
2	MicroED structure of the human adenosine receptor determined from a single nanocrystal in LCP		4
1	Structural Insights into Cholesterol Interactions with G-Protein-Coupled Receptors231-253		2