Raymond C Stevens

List of Publications by Year
in descending order

414 papers	55,422 citations	1118 115 h-index	1594 222 g-index
430 all docs	430 docs citations	430 times ranked	39937 citing authors

#	Article	IF	Citations
1	A new visual design language for biological structures in a cell. Structure, 2022, , .	1.6	2
2	Auto-segmentation and time-dependent systematic analysis of mesoscale cellular structure in Î²-cells during insulin secretion. PLoS ONE, 2022, 17, e0265567.	1.1	5
3	Structural insight into apelin receptor-G protein stoichiometry. Nature Structural and Molecular Biology, 2022, 29, 688-697.	3.6	14
4	Structure-Based Design of Melanocortin 4 Receptor Ligands Based on the SHU-9119-hMC4R Cocrystal Structure. Journal of Medicinal Chemistry, 2021, 64, 357-369.	2.9	12
5	Live-cell imaging of glucose-induced metabolic coupling of Î² and Î±Âcell metabolism in health and typeÂ2 diabetes. Communications Biology, 2021, 4, 594.	2.0	19
6	Assessment of scoring functions to rank the quality of 3D subtomogram clusters from cryo-electron tomography. Journal of Structural Biology, 2021, 213, 107727.	1.3	2
7	Structural insights into hormone recognition by the human glucose-dependent insulinotropic polypeptide receptor. ELife, 2021, 10, .	2.8	30
8	Bayesian metamodeling of complex biological systems across varying representations. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	19
9	Biased Signaling Pathways in Î²₂-Adrenergic Receptor Characterized by ¹⁹F-NMR. , 2021, , 179-183.		0
10	Allosteric Coupling of Drug Binding and Intracellular Signaling in the A2A Adenosine Receptor. , 2021, , 184-196.		0
11	Pursuing High-Resolution Structures of Nicotinic Acetylcholine Receptors: Lessons Learned from Five Decades. Molecules, 2021, 26, 5753.	1.7	8
12	Rational Remodeling of Atypical Scaffolds for the Design of Photoswitchable Cannabinoid Receptor Tools. Journal of Medicinal Chemistry, 2021, 64, 13752-13765.	2.9	9
13	Small-scale approach for precrystallization screening in GPCR X-ray crystallography. Nature Protocols, 2020, 15, 144-160.	5.5	8
14	An orthogonal seryl-tRNA synthetase/tRNA pair for noncanonical amino acid mutagenesis in Escherichia coli. Bioorganic and Medicinal Chemistry, 2020, 28, 115662.	1.4	10
15	Visualizing insulin vesicle neighborhoods in Î² cells by cryoâ€“electron tomography. Science Advances, 2020, 6, .	4.7	27
16	Visualizing subcellular rearrangements in intact Î² cells using soft x-ray tomography. Science Advances, 2020, 6, .	4.7	36
17	Neural Network Segmentation of Cell Ultrastructure Using Incomplete Annotation. , 2020, , .		3
18	Synthesis of site-specific antibody-drug conjugates by ADP-ribosyl cyclases. Science Advances, 2020, 6, eaba6752.	4.7	24

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19	Full-length human GLP-1 receptor structure without orthosteric ligands. Nature Communications, 2020, 11, 1272.	5.8	83
20	Biased Signaling of the G-Protein-Coupled Receptor Î²2AR Is Governed by Conformational Exchange Kinetics. Structure, 2020, 28, 371-377.e3.	1.6	36
21	Determination of the melanocortin-4 receptor structure identifies Ca ²⁺ as a cofactor for ligand binding. Science, 2020, 368, 428-433.	6.0	89
22	Probing the CB₁ Cannabinoid Receptor Binding Pocket with AM6538, a High-Affinity Irreversible Antagonist. Molecular Pharmacology, 2019, 96, 619-628.	1.0	4
23	An online resource for GPCR structure determination and analysis. Nature Methods, 2019, 16, 151-162.	9.0	108
24	The structure-based traceless specific fluorescence labeling of the smoothened receptor. Organic and Biomolecular Chemistry, 2019, 17, 6136-6142.	1.5	5
25	A Single Reactive Noncanonical Amino Acid Is Able to Dramatically Stabilize Protein Structure. ACS Chemical Biology, 2019, 14, 1150-1153.	1.6	15
26	Accelerating the Throughput of Affinity Mass Spectrometry-Based Ligand Screening toward a G Protein-Coupled Receptor. Analytical Chemistry, 2019, 91, 8162-8169.	3.2	25
27	Structural basis of ligand recognition at the human MT1 melatonin receptor. Nature, 2019, 569, 284-288.	13.7	140
28	XFEL structures of the human MT2 melatonin receptor reveal the basis of subtype selectivity. Nature, 2019, 569, 289-292.	13.7	106
29	The lipid phase preference of the adenosine A_{2A} receptor depends on its ligand binding state. Chemical Communications, 2019, 55, 5724-5727.	2.2	10
30	Advancing Chemokine GPCR Structure Based Drug Discovery. Structure, 2019, 27, 405-408.	1.6	26
31	Mesoscale Architecture of Beta Cells Upon Glucose and Ex-4 Stimulation. Biophysical Journal, 2019, 116, 431a.	0.2	0
32	Human substance P receptor binding mode of the antagonist drug aprepitant by NMR and crystallography. Nature Communications, 2019, 10, 638.	5.8	43
33	Towards a Model of the Human Pancreatic Beta Cell. Biophysical Journal, 2019, 116, 451a.	0.2	0
34	De Novo Structural Pattern Mining in Cellular Electron Cryotomograms. Structure, 2019, 27, 679-691.e14.	1.6	40
35	Molecular Mechanism for Ligand Recognition and Subtype Selectivity of Î±2C Adrenergic Receptor. Cell Reports, 2019, 29, 2936-2943.e4.	2.9	17
36	Elucidating the active Î´-opioid receptor crystal structure with peptide and small-molecule agonists. Science Advances, 2019, 5, eaax9115.	4.7	81

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37	Structural Basis of the Diversity of Adrenergic Receptors. Cell Reports, 2019, 29, 2929-2935.e4.	2.9	30
38	Crystal Structure of the Human Cannabinoid Receptor CB2. Cell, 2019, 176, 459-467.e13.	13.5	268
39	Crystal structure of misoprostol bound to the labor inducer prostaglandin E2 receptor. Nature Chemical Biology, 2019, 15, 11-17.	3.9	32
40	Emerging structural biology of lipid G proteinâ€coupled receptors. Protein Science, 2019, 28, 292-304.	3.1	46
41	Common activation mechanism of class A GPCRs. ELife, 2019, 8, .	2.8	339
42	High-throughput identification of G protein-coupled receptor modulators through affinity mass spectrometry screening. Chemical Science, 2018, 9, 3192-3199.	3.7	33
43	Structural basis of ligand binding modes at the neuropeptide Y Y1 receptor. Nature, 2018, 556, 520-524.	13.7	100
44	5-HT2C Receptor Structures Reveal the Structural Basis of GPCR Polypharmacology. Cell, 2018, 172, 719-730.e14.	13.5	185
45	Structural Connection between Activation Microswitch and Allosteric Sodium Site in GPCR Signaling. Structure, 2018, 26, 259-269.e5.	1.6	134
46	Allosteric Coupling of Drug Binding and Intracellular Signaling in the A2A Adenosine Receptor. Cell, 2018, 172, 68-80.e12.	13.5	173
47	Structure of the glucagon receptor in complex with a glucagon analogue. Nature, 2018, 553, 106-110.	13.7	109
48	Structure of the Nanobody-Stabilized Active State of the Kappa Opioid Receptor. Cell, 2018, 172, 55-67.e15.	13.5	299
49	Chemical Diversity in the G Protein-Coupled Receptor Superfamily. Trends in Pharmacological Sciences, 2018, 39, 494-512.	4.0	67
50	Opportunities and Challenges in Building a Spatiotemporal Multi-scale Model of the Human Pancreatic Î² Cell. Cell, 2018, 173, 11-19.	13.5	179
51	Identification of natural products as novel ligands for the human 5-HT2C receptor. Biophysics Reports, 2018, 4, 50-61.	0.2	23
52	Facile chemoenzymatic synthesis of a novel stable mimic of NAD⁺. Chemical Science, 2018, 9, 8337-8342.	3.7	15
53	A _{2A} adenosine receptor functional states characterized by ¹⁹ F-NMR. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12733-12738.	3.3	96
54	Structural basis for signal recognition and transduction by platelet-activating-factor receptor. Nature Structural and Molecular Biology, 2018, 25, 488-495.	3.6	58

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55	Salvianolic acids from antithrombotic Traditional Chinese Medicine Danshen are antagonists of human P2Y1 and P2Y12 receptors. Scientific Reports, 2018, 8, 8084.	1.6	20
56	Computational design of thermostabilizing point mutations for G protein-coupled receptors. ELife, 2018, 7, .	2.8	60
57	Crystal structure of the Frizzled 4 receptor in a ligand-free state. Nature, 2018, 560, 666-670.	13.7	77
58	Extrinsic Tryptophans as NMR Probes of Allosteric Coupling in Membrane Proteins: Application to the A_{2A} Adenosine Receptor. Journal of the American Chemical Society, 2018, 140, 8228-8235.	6.6	41
59	Globally Monitoring Allosteric Coupling in the A_{2A} Adenosine Receptor by NMR in Solution. FASEB Journal, 2018, 32, 533.99.	0.2	0
60	Towards Generating Spatiotemporal Multiscale Models of Human Pancreatic Beta Cells. Diabetes, 2018, 67, .	0.3	0
61	Generation of an Orthogonal Proteinâ€“Protein Interface with a Noncanonical Amino Acid. Journal of the American Chemical Society, 2017, 139, 5728-5731.	6.6	18
62	A structurally guided dissection-then-evolution strategy for ligand optimization of smoothened receptor. MedChemComm, 2017, 8, 1332-1336.	3.5	9
63	Structure of the full-length glucagon class B G-protein-coupled receptor. Nature, 2017, 546, 259-264.	13.7	179
64	Human GLP-1 receptor transmembrane domain structure in complex with allosteric modulators. Nature, 2017, 546, 312-315.	13.7	192
65	Crystal structure of a multi-domain human smoothened receptor in complex with a super stabilizing ligand. Nature Communications, 2017, 8, 15383.	5.8	81
66	Structural Basis for Apelin Control of the Human Apelin Receptor. Structure, 2017, 25, 858-866.e4.	1.6	96
67	Structure of CC Chemokine Receptor 5 with a Potent Chemokine Antagonist Reveals Mechanisms of Chemokine Recognition and Molecular Mimicry by HIV. Immunity, 2017, 46, 1005-1017.e5.	6.6	148
68	Structure-Based Discovery of New Antagonist and Biased Agonist Chemotypes for the Kappa Opioid Receptor. Journal of Medicinal Chemistry, 2017, 60, 3070-3081.	2.9	42
69	Structural basis for selectivity and diversity in angiotensin II receptors. Nature, 2017, 544, 327-332.	13.7	174
70	How Ligands Illuminate GPCR Molecular Pharmacology. Cell, 2017, 170, 414-427.	13.5	419
71	Structural insights into the extracellular recognition of the human serotonin 2B receptor by an antibody. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8223-8228.	3.3	54
72	Identification of Phosphorylation Codes for Arrestin Recruitment by G Protein-Coupled Receptors. Cell, 2017, 170, 457-469.e13.	13.5	344

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73	Dynamic Strategic Bond Analysis Yields a Ten-Step Synthesis of 20-nor-Salvinorin A, a Potent Î¹-OR Agonist. ACS Central Science, 2017, 3, 1329-1336.	5.3	34
74	Extending the Structural View of Class B GPCRs. Trends in Biochemical Sciences, 2017, 42, 946-960.	3.7	109
75	Structure and Function of Peptide-Binding G Protein-Coupled Receptors. Journal of Molecular Biology, 2017, 429, 2726-2745.	2.0	54
76	Crystal structures of agonist-bound human cannabinoid receptor CB1. Nature, 2017, 547, 468-471.	13.7	379
77	Structure of CC chemokine receptor 2 with orthosteric and allosteric antagonists. Nature, 2016, 540, 458-461.	13.7	220
78	Biochemical Characterization and Structure Determination of the Class C TAS1R Subfamily of Chemosensory Receptors. Biophysical Journal, 2016, 110, 395a.	0.2	0
79	In vitro expression and analysis of the 826 human G protein-coupled receptors. Protein and Cell, 2016, 7, 325-337.	4.8	53
80	The Molecular Mechanism of P2Y₁ Receptor Activation. Angewandte Chemie, 2016, 128, 10487-10491.	1.6	2
81	The Molecular Mechanism of P2Y₁ Receptor Activation. Angewandte Chemie - International Edition, 2016, 55, 10331-10335.	7.2	49
82	An electrostatic mechanism for Ca2+-mediated regulation of gap junction channels. Nature Communications, 2016, 7, 8770.	5.8	119
83	Î² 2 -Adrenergic Receptor Conformational Response to Fusion Protein in the Third Intracellular Loop. Structure, 2016, 24, 2190-2197.	1.6	43
84	Native phasing of x-ray free-electron laser data for a G proteinâ€“coupled receptor. Science Advances, 2016, 2, e1600292.	4.7	97
85	X-ray laser diffraction for structure determination of the rhodopsin-arrestin complex. Scientific Data, 2016, 3, 160021.	2.4	51
86	Crystal Structure of the Human Cannabinoid Receptor CB1. Cell, 2016, 167, 750-762.e14.	13.5	468
87	Structural Studies of the Human Kappa Opioid Receptor Active State Conformations. Biophysical Journal, 2016, 110, 38a-39a.	0.2	1
88	Structural Determinants of Binding the Seven-transmembrane Domain of the Glucagon-like Peptide-1 Receptor (GLP-1R). Journal of Biological Chemistry, 2016, 291, 12991-13004.	1.6	48
89	Conformational Dynamics of a G Protein-Coupled Receptor at the Single-Molecule Level. Biophysical Journal, 2015, 108, 350a.	0.2	0
90	Inâ€Membrane Chemical Modification (IMCM) for Siteâ€Specific Chromophore Labeling of GPCRs. Angewandte Chemie - International Edition, 2015, 54, 15246-15249.	7.2	23

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91	Exploring the potential impact of an expanded genetic code on protein function. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6961-6966.	3.3	69
92	Generic GPCR residue numbers â€“ aligning topology maps while minding the gaps. Trends in Pharmacological Sciences, 2015, 36, 22-31.	4.0	387
93	Trapping a transition state in a computationally designed protein bottle. Science, 2015, 347, 863-867.	6.0	36
94	Structural basis for bifunctional peptide recognition at human Î´-opioid receptor. Nature Structural and Molecular Biology, 2015, 22, 265-268.	3.6	151
95	The importance of ligands for G protein-coupled receptor stability. Trends in Biochemical Sciences, 2015, 40, 79-87.	3.7	65
96	Crystal structure of the chemokine receptor CXCR4 in complex with a viral chemokine. Science, 2015, 347, 1117-1122.	6.0	325
97	Crystal Structure of Antagonist Bound Human Lysophosphatidic Acid Receptor 1. Cell, 2015, 161, 1633-1643.	13.5	169
98	Single Amino Acid Variation Underlies Species-Specific Sensitivity to Amphibian Skin-Derived Opioid-like Peptides. Chemistry and Biology, 2015, 22, 764-775.	6.2	14
99	Conformational states of the full-length glucagon receptor. Nature Communications, 2015, 6, 7859.	5.8	110
100	Crystal structure of rhodopsin bound to arrestin by femtosecond X-ray laser. Nature, 2015, 523, 561-567.	13.7	683
101	Modeling ligand recognition at the P2Y12 receptor in light of X-ray structural information. Journal of Computer-Aided Molecular Design, 2015, 29, 737-756.	1.3	42
102	Structure of the Angiotensin Receptor Revealed by Serial Femtosecond Crystallography. Cell, 2015, 161, 833-844.	13.5	315
103	Sodium Ion Binding Pocket Mutations and Adenosine A_{2A}Receptor Function. Molecular Pharmacology, 2015, 87, 305-313.	1.0	79
104	Two disparate ligand-binding sites in the human P2Y1 receptor. Nature, 2015, 520, 317-321.	13.7	305
105	Nucleotides Acting at P2Y Receptors: Connecting Structure and Function. Molecular Pharmacology, 2015, 88, 220-230.	1.0	86
106	The Importance of Ligand-Receptor Conformational Pairs in Stabilization: Spotlight on the N/OFQ G Protein-Coupled Receptor. Structure, 2015, 23, 2291-2299.	1.6	64
107	Single-molecule view of basal activity and activation mechanisms of the G protein-coupled receptor Î²₂ AR. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14254-14259.	3.3	87
108	NMR structure and dynamics of the agonist dynorphin peptide bound to the human kappa opioid receptor. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11852-11857.	3.3	80

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109	Design, synthesis, pharmacological characterization of a fluorescent agonist of the P2Y 14 receptor. Bioorganic and Medicinal Chemistry Letters, 2015, 25, 4733-4739.	1.0	22
110	Structural Basis for Ligand Recognition and Functional Selectivity at Angiotensin Receptor. Journal of Biological Chemistry, 2015, 290, 29127-29139.	1.6	145
111	Exploring a 2-Naphthoic Acid Template for the Structure-Based Design of P2Y₁₄ Receptor Antagonist Molecular Probes. ACS Chemical Biology, 2014, 9, 2833-2842.	1.6	38
112	Constitutive phospholipid scramblase activity of a G protein-coupled receptor. Nature Communications, 2014, 5, 5115.	5.8	112
113	Structure of a Class C GPCR Metabotropic Glutamate Receptor 1 Bound to an Allosteric Modulator. Science, 2014, 344, 58-64.	6.0	476
114	Lipidic cubic phase injector facilitates membrane protein serial femtosecond crystallography. Nature Communications, 2014, 5, 3309.	5.8	505
115	Structure of the human P2Y12 receptor in complex with an antithrombotic drug. Nature, 2014, 509, 115-118.	13.7	330
116	Allosteric sodium in class A GPCR signaling. Trends in Biochemical Sciences, 2014, 39, 233-244.	3.7	417
117	The N-Terminal Sequence of Tyrosine Hydroxylase Is a Conformationally Versatile Motif That Binds 14-3-3 Proteins and Membranes. Journal of Molecular Biology, 2014, 426, 150-168.	2.0	29
118	Insights into the structure of class B GPCRs. Trends in Pharmacological Sciences, 2014, 35, 12-22.	4.0	218
119	Molecular control of Î´-opioid receptor signalling. Nature, 2014, 506, 191-196.	13.7	432
120	Structural basis for Smoothened receptor modulation and chemoresistance to anticancer drugs. Nature Communications, 2014, 5, 4355.	5.8	208
121	Advances in GPCR Modeling Evaluated by the GPCR Dock 2013 Assessment: Meeting New Challenges. Structure, 2014, 22, 1120-1139.	1.6	149
122	Agonist-bound structure of the human P2Y12 receptor. Nature, 2014, 509, 119-122.	13.7	279
123	THE SEVEN TRANSMEMBRANE SUPERFAMILY. , 2014, , .		0
124	Coordinating the impact of structural genomics on the human Î±-helical transmembrane proteome. Nature Structural and Molecular Biology, 2013, 20, 135-138.	3.6	64
125	Structure of the human glucagon class B G-protein-coupled receptor. Nature, 2013, 499, 444-449.	13.7	352
126	The Role of a Sodium Ion Binding Site in the Allosteric Modulation of the A2A Adenosine G Protein-Coupled Receptor. Structure, 2013, 21, 2175-2185.	1.6	118

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127	Fluorine-19 NMR of integral membrane proteins illustrated with studies of GPCRs. Current Opinion in Structural Biology, 2013, 23, 740-747.	2.6	81
128	Chemotype-selective Modes of Action of Î¼-Opioid Receptor Agonists. Journal of Biological Chemistry, 2013, 288, 34470-34483.	1.6	55
129	Structure-Based Ligand Discovery Targeting Orthosteric and Allosteric Pockets of Dopamine Receptors. Molecular Pharmacology, 2013, 84, 794-807.	1.0	78
130	Genetically Encoded Chemical Probes in Cells Reveal the Binding Path of Urocortin-I to CRF Class B GPCR. Cell, 2013, 155, 1258-1269.	13.5	159
131	Asia growth in membrane protein structure. Current Opinion in Structural Biology, 2013, 23, 481-482.	2.6	0
132	Serial Femtosecond Crystallography of G Proteinâ€“Coupled Receptors. Science, 2013, 342, 1521-1524.	6.0	424
133	Î²₂â€Adrenergic Receptor Activation by Agonists Studied with ¹⁹Fâ€...NMR Spectroscopy. Angewandte Chemie - International Edition, 2013, 52, 10762-10765.	7.2	71
134	Structure of the CCR5 Chemokine Receptorâ€“HIV Entry Inhibitor Maraviroc Complex. Science, 2013, 341, 1387-1390.	6.0	606
135	The GPCR Network: a large-scale collaboration to determine human GPCR structure and function. Nature Reviews Drug Discovery, 2013, 12, 25-34.	21.5	252
136	Opportunities for functional selectivity in GPCR antibodies. Biochemical Pharmacology, 2013, 85, 147-152.	2.0	40
137	Structure-Function of the G Proteinâ€“Coupled Receptor Superfamily. Annual Review of Pharmacology and Toxicology, 2013, 53, 531-556.	4.2	907
138	Î²₂â€Adrenergic Receptor Solutions for Structural Biology Analyzed with Microscale NMR Diffusion Measurements. Angewandte Chemie - International Edition, 2013, 52, 331-335.	7.2	21
139	Structural Features for Functional Selectivity at Serotonin Receptors. Science, 2013, 340, 615-619.	6.0	600
140	Structural Basis for Molecular Recognition at Serotonin Receptors. Science, 2013, 340, 610-614.	6.0	454
141	Structure of the human smoothened receptor bound to an antitumour agent. Nature, 2013, 497, 338-343.	13.7	415
142	Identification of Fibroblast Growth Factor Receptor 3 (FGFR3) as a Protein Receptor for Botulinum Neurotoxin Serotype A (BoNT/A). PLoS Pathogens, 2013, 9, e1003369.	2.1	70
143	Sphingosine-1-Phosphate and Its Receptors: Structure, Signaling, and Influence. Annual Review of Biochemistry, 2013, 82, 637-662.	5.0	184
144	Engineered nanostructured Î²-sheet peptides protect membrane proteins. Nature Methods, 2013, 10, 759-761.	9.0	110

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145	Rational Design of Fatty Acid Amide Hydrolase Inhibitors That Act by Covalently Bonding to Two Active Site Residues. Journal of the American Chemical Society, 2013, 135, 6289-6299.	6.6	30
146	Steroid-based facial amphiphiles for stabilization and crystallization of membrane proteins. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E1203-11.	3.3	127
147	A Novel Approach to Quantify G-Protein-Coupled Receptor Dimerization Equilibrium Using Bioluminescence Resonance Energy Transfer. Methods in Molecular Biology, 2013, 1013, 93-127.	0.4	15
148	Crystal Structure of a Voltage-gated K+ Channel Pore Module in a Closed State in Lipid Membranes. Journal of Biological Chemistry, 2012, 287, 43063-43070.	1.6	21
149	Structural Basis for Allosteric Regulation of GPCRs by Sodium Ions. Science, 2012, 337, 232-236.	6.0	860
150	Crystal Structure of a Lipid G Proteinâ€“Coupled Receptor. Science, 2012, 335, 851-855.	6.0	600
151	Diversity and modularity of G protein-coupled receptor structures. Trends in Pharmacological Sciences, 2012, 33, 17-27.	4.0	403
152	Synthesis and Properties of Dodecyl Trehaloside Detergents for Membrane Protein Studies. Langmuir, 2012, 28, 11173-11181.	1.6	22
153	Biased Signaling Pathways in Î² ₂ -Adrenergic Receptor Characterized by ¹⁹ F-NMR. Science, 2012, 335, 1106-1110.	6.0	618
154	Structure of the nociceptin/orphanin FQ receptor in complex with a peptide mimetic. Nature, 2012, 485, 395-399.	13.7	430
155	Structure of the human Î¼-opioid receptor in complex with JDTic. Nature, 2012, 485, 327-332.	13.7	797
156	Optimization of Adenosine 5â€²-Carboxamide Derivatives as Adenosine Receptor Agonists Using Structure-Based Ligand Design and Fragment Screening. Journal of Medicinal Chemistry, 2012, 55, 4297-4308.	2.9	57
157	Agonists for 13 Trace Amine-Associated Receptors Provide Insight into the Molecular Basis of Odor Selectivity. ACS Chemical Biology, 2012, 7, 1184-1189.	1.6	79
158	Evaluation of Molecular Modeling of Agonist Binding in Light of the Crystallographic Structure of an Agonist-Bound A2A Adenosine Receptor. Journal of Medicinal Chemistry, 2012, 55, 538-552.	2.9	36
159	Fusion Partner Toolchest for the Stabilization and Crystallization of G Protein-Coupled Receptors. Structure, 2012, 20, 967-976.	1.6	367
160	Fluoride-Mediated Capture of a Noncovalent Bound State of a Reversible Covalent Enzyme Inhibitor: X-ray Crystallographic Analysis of an Exceptionally Potent Î±-Ketoheterocycle Inhibitor of Fatty Acid Amide Hydrolase. Journal of the American Chemical Society, 2011, 133, 4092-4100.	6.6	33
161	Development of an Automated High Throughput LCP-FRAP Assay to Guide Membrane Protein Crystallization in Lipid Mesophases. Crystal Growth and Design, 2011, 11, 1193-1201.	1.4	49
162	Reversible Competitive Î±-Ketoheterocycle Inhibitors of Fatty Acid Amide Hydrolase Containing Additional Conformational Constraints in the Acyl Side Chain: Orally Active, Long-Acting Analgesics. Journal of Medicinal Chemistry, 2011, 54, 2805-2822.	2.9	48

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163	Crystal Structure-Based Virtual Screening for Fragment-like Ligands of the Human Histamine H₁ Receptor. Journal of Medicinal Chemistry, 2011, 54, 8195-8206.	2.9	189
164	GPCR stabilization using the bicelle-like architecture of mixed sterol-detergent micelles. Methods, 2011, 55, 310-317.	1.9	80
165	A roadmap to membrane protein structures. Methods, 2011, 55, 271-272.	1.9	2
166	Evaluation of orally administered PEGylated phenylalanine ammonia lyase in mice for the treatment of Phenylketonuria. Molecular Genetics and Metabolism, 2011, 104, 249-254.	0.5	41
167	Structure of an Agonist-Bound Human A _{2A} Adenosine Receptor. Science, 2011, 332, 322-327.	6.0	783
168	The Crystal Structure of the Î±-Neurexin-1 Extracellular Region Reveals a Hinge Point for Mediating Synaptic Adhesion and Function. Structure, 2011, 19, 767-778.	1.6	56
169	Status of GPCR Modeling and Docking as Reflected by Community-wide GPCR Dock 2010 Assessment. Structure, 2011, 19, 1108-1126.	1.6	269
170	Ligand-Dependent Perturbation of the Conformational Ensemble for the GPCR Î²2 Adrenergic Receptor Revealed by HDX. Structure, 2011, 19, 1424-1432.	1.6	129
171	Trapping Small Caffeine in a Large GPCR Pocket. Structure, 2011, 19, 1204-1207.	1.6	5
172	Structure of the human histamine H1 receptor complex with doxepin. Nature, 2011, 475, 65-70.	13.7	727
173	Structural Characterization of Three Novel Hydroxamate-Based Zinc Chelating Inhibitors of the Clostridium botulinum Serotype A Neurotoxin Light Chain Metalloprotease Reveals a Compact Binding Site Resulting from 60/70 Loop Flexibility. Biochemistry, 2011, 50, 4019-4028.	1.2	28
174	Purification, Modeling, and Analysis of Botulinum Neurotoxin Subtype A5 (BoNT/A5) from Clostridium botulinum Strain A661222. Applied and Environmental Microbiology, 2011, 77, 4217-4222.	1.4	34
175	Chaperone-Like Therapy with Tetrahydrobiopterin in Clinical Trials for Phenylketonuria: Is Genotype a Predictor of Response?. JIMD Reports, 2011, 5, 59-70.	0.7	14
176	Structure-Based Discovery of Novel Chemotypes for Adenosine A_{2A} Receptor Antagonists. Journal of Medicinal Chemistry, 2010, 53, 1799-1809.	2.9	231
177	Growth and excitement in membrane protein structural biology. Current Opinion in Structural Biology, 2010, 20, 399-400.	2.6	5
178	RAMP-ing up Class-B GPCR ECD Structural Coverage. Structure, 2010, 18, 1067-1068.	1.6	15
179	FoldGPCR: Structure prediction protocol for the transmembrane domain of G proteinâ€coupled receptors from class A. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2189-2201.	1.5	33
180	Ligand Binding and Subtype Selectivity of the Human A2A Adenosine Receptor. Journal of Biological Chemistry, 2010, 285, 13032-13044.	1.6	83

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