Raymond C Stevens

List of Publications by Year in Descending Order

403 papers	46,656 citations	109 h-index	208 g-index
430 ext. papers	51,580 ext. citations	12.7 avg, IF	7.25 L-index

#	Paper	IF	Citations
403	Auto-segmentation and time-dependent systematic analysis of mesoscale cellular structure in cells during insulin secretion.. *PLoS ONE*, **2022**, 17, e0265567	3.7	1
402	Live-cell imaging of glucose-induced metabolic coupling of and cell metabolism in health and type 2 diabetes. *Communications Biology*, **2021**, 4, 594	6.7	3
401	Assessment of scoring functions to rank the quality of 3D subtomogram clusters from cryo-electron tomography. *Journal of Structural Biology*, **2021**, 213, 107727	3.4	1
400	Structural insights into hormone recognition by the human glucose-dependent insulinotropic polypeptide receptor. *ELife*, **2021**, 10,	8.9	8
399	Structure-Based Design of Melanocortin 4 Receptor Ligands Based on the SHU-9119-hMC4R Cocrystal Structure *Journal of Medicinal Chemistry*, **2021**, 64, 357-369	8.3	4
398	Bayesian metamodeling of complex biological systems across varying representations. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	3
397	Biased Signaling Pathways in -Adrenergic Receptor Characterized by 19F-NMR **2021**, 179-183		
396	Allosteric Coupling of Drug Binding and Intracellular Signaling in the A2A Adenosine Receptor **2021** , 184-196		
395	Pursuing High-Resolution Structures of Nicotinic Acetylcholine Receptors: Lessons Learned from Five Decades. *Molecules*, **2021**, 26,	4.8	2
394	Rational Remodeling of Atypical Scaffolds for the Design of Photoswitchable Cannabinoid Receptor Tools. *Journal of Medicinal Chemistry*, **2021**, 64, 13752-13765	8.3	1
393	Visualizing insulin vesicle neighborhoods in cells by cryo-electron tomography. *Science Advances*, **2020**, 6,	14.3	5
392	Visualizing subcellular rearrangements in intact cells using soft x-ray tomography. *Science Advances*, **2020**, 6,	14.3	10
391	Neural Network Segmentation of Cell Ultrastructure Using Incomplete Annotation **2020**,		2
390	Synthesis of site-specific antibody-drug conjugates by ADP-ribosyl cyclases. *Science Advances*, **2020**, 6, eaba6752	14.3	13
389	Full-length human GLP-1 receptor structure without orthosteric ligands. *Nature Communications*, **2020**, 11, 1272	17.4	42
388	Biased Signaling of the G-Protein-Coupled Receptor AR Is Governed by Conformational Exchange Kinetics. *Structure*, **2020**, 28, 371-377.e3	5.2	18
387	Small-scale approach for precrystallization screening in GPCR X-ray crystallography. *Nature Protocols*, **2020**, 15, 144-160	18.8	4

386	An orthogonal seryl-tRNA synthetase/tRNA pair for noncanonical amino acid mutagenesis in Escherichia coli. *Bioorganic and Medicinal Chemistry*, **2020**, 28, 115662	3.4	3
385	Determination of the melanocortin-4 receptor structure identifies Ca as a cofactor for ligand binding. *Science*, **2020**, 368, 428-433	33.3	46
384	Probing the CB Cannabinoid Receptor Binding Pocket with AM6538, a High-Affinity Irreversible Antagonist. *Molecular Pharmacology*, **2019**, 96, 619-628	4.3	3
383	An online resource for GPCR structure determination and analysis. *Nature Methods*, **2019**, 16, 151-162	21.6	71
382	The structure-based traceless specific fluorescence labeling of the smoothened receptor. *Organic and Biomolecular Chemistry*, **2019**, 17, 6136-6142	3.9	3
381	A Single Reactive Noncanonical Amino Acid Is Able to Dramatically Stabilize Protein Structure. *ACS Chemical Biology*, **2019**, 14, 1150-1153	4.9	9
380	Accelerating the Throughput of Affinity Mass Spectrometry-Based Ligand Screening toward a G Protein-Coupled Receptor. *Analytical Chemistry*, **2019**, 91, 8162-8169	7.8	15
379	Structural basis of ligand recognition at the human MT melatonin receptor. *Nature*, **2019**, 569, 284-288	50.4	98
378	XFEL structures of the human MT melatonin receptor reveal the basis of subtype selectivity. *Nature* , **2019**, 569, 289-292	50.4	77
377	The lipid phase preference of the adenosine A receptor depends on its ligand binding state. *Chemical Communications*, **2019**, 55, 5724-5727	5.8	6
376	Advancing Chemokine GPCR Structure Based Drug Discovery. *Structure*, **2019**, 27, 405-408	5.2	11
375	Human substance P receptor binding mode of the antagonist drug aprepitant by NMR and crystallography. *Nature Communications*, **2019**, 10, 638	17.4	23
374	Common activation mechanism of class A GPCRs. *ELife*, **2019**, 8,	8.9	117
373	De Novo Structural Pattern Mining in Cellular Electron Cryotomograms. *Structure*, **2019**, 27, 679-691.e14	5.2	25
372	Molecular Mechanism for Ligand Recognition and Subtype Selectivity of Adrenergic Receptor. *Cell Reports*, **2019**, 29, 2936-2943.e4	10.6	5
371	Elucidating the active pioid receptor crystal structure with peptide and small-molecule agonists. *Science Advances*, **2019**, 5, eaax9115	14.3	38
370	Structural Basis of the Diversity of Adrenergic Receptors. *Cell Reports*, **2019**, 29, 2929-2935.e4	10.6	13
369	Crystal Structure of the Human Cannabinoid Receptor CB2. *Cell*, **2019**, 176, 459-467.e13	56.2	175

368	Crystal structure of misoprostol bound to the labor inducer prostaglandin E receptor. *Nature Chemical Biology*, **2019**, 15, 11-17	11.7	23
367	Emerging structural biology of lipid G protein-coupled receptors. *Protein Science*, **2019**, 28, 292-304	6.3	33
366	High-throughput identification of G protein-coupled receptor modulators through affinity mass spectrometry screening. *Chemical Science*, **2018**, 9, 3192-3199	9.4	23
365	Structural basis of ligand binding modes at the neuropeptide Y Y receptor. *Nature*, **2018**, 556, 520-524	50.4	75
364	5-HT Receptor Structures Reveal the Structural Basis of GPCR Polypharmacology. *Cell*, **2018**, 172, 719-736.e14	36.2	123
363	Structural Connection between Activation Microswitch and Allosteric Sodium Site in GPCR Signaling. *Structure*, **2018**, 26, 259-269.e5	5.2	77
362	Allosteric Coupling of Drug Binding and Intracellular Signaling in the A Adenosine Receptor. *Cell*, **2018**, 172, 68-80.e12	56.2	119
361	Structure of the glucagon receptor in complex with a glucagon analogue. *Nature*, **2018**, 553, 106-110	50.4	76
360	Structure of the Nanobody-Stabilized Active State of the Kappa Opioid Receptor. *Cell*, **2018**, 172, 55-67.e15	36.2	205
359	Chemical Diversity in the G Protein-Coupled Receptor Superfamily. *Trends in Pharmacological Sciences*, **2018**, 39, 494-512	13.2	54
358	Opportunities and Challenges in Building a Spatiotemporal Multi-scale Model of the Human Pancreatic β Cell. *Cell*, **2018**, 173, 11-19	56.2	39
357	Identification of natural products as novel ligands for the human 5-HT receptor. *Biophysics Reports*, **2018**, 4, 50-61	3.5	15
356	Crystal structure of the Frizzled 4 receptor in a ligand-free state. *Nature*, **2018**, 560, 666-670	50.4	51
355	Extrinsic Tryptophans as NMR Probes of Allosteric Coupling in Membrane Proteins: Application to the A Adenosine Receptor. *Journal of the American Chemical Society*, **2018**, 140, 8228-8235	16.4	24
354	Globally Monitoring Allosteric Coupling in the A2A Adenosine Receptor by NMR in Solution. *FASEB Journal*, **2018**, 32, 533.99	0.9	
353	Towards Generating Spatiotemporal Multiscale Models of Human Pancreatic Beta Cells. *Diabetes*, **2018**, 67, 2171-P	0.9	
352	Facile chemoenzymatic synthesis of a novel stable mimic of NAD. *Chemical Science*, **2018**, 9, 8337-8342	9.4	9
351	A adenosine receptor functional states characterized by F-NMR. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 12733-12738	11.5	56

350	Structural basis for signal recognition and transduction by platelet-activating-factor receptor. *Nature Structural and Molecular Biology*, **2018**, 25, 488-495	17.6	37
349	Salvianolic acids from antithrombotic Traditional Chinese Medicine Danshen are antagonists of human P2Y and P2Y receptors. *Scientific Reports*, **2018**, 8, 8084	4.9	13
348	Computational design of thermostabilizing point mutations for G protein-coupled receptors. *ELife*, **2018**, 7,	8.9	40
347	Generation of an Orthogonal Protein-Protein Interface with a Noncanonical Amino Acid. *Journal of the American Chemical Society*, **2017**, 139, 5728-5731	16.4	13
346	A structurally guided dissection-then-evolution strategy for ligand optimization of smoothened receptor. *MedChemComm*, **2017**, 8, 1332-1336	5	7
345	Structure of the full-length glucagon class B G-protein-coupled receptor. *Nature*, **2017**, 546, 259-264	50.4	141
344	Human GLP-1 receptor transmembrane domain structure in complex with allosteric modulators. *Nature*, **2017**, 546, 312-315	50.4	143
343	Crystal structure of a multi-domain human smoothened receptor in complex with a super stabilizing ligand. *Nature Communications*, **2017**, 8, 15383	17.4	62
342	Structural Basis for Apelin Control of the Human Apelin Receptor. *Structure*, **2017**, 25, 858-866.e4	5.2	74
341	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	32.3	106
340	Structure-Based Discovery of New Antagonist and Biased Agonist Chemotypes for the Kappa Opioid Receptor. *Journal of Medicinal Chemistry*, **2017**, 60, 3070-3081	8.3	35
339	Structural basis for selectivity and diversity in angiotensin II receptors. *Nature*, **2017**, 544, 327-332	50.4	128
338	How Ligands Illuminate GPCR Molecular Pharmacology. *Cell*, **2017**, 170, 414-427	56.2	276
337	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	11.5	43
336	Identification of Phosphorylation Codes for Arrestin Recruitment by G Protein-Coupled Receptors. *Cell*, **2017**, 170, 457-469.e13	56.2	225
335	Dynamic Strategic Bond Analysis Yields a Ten-Step Synthesis of 20-nor-Salvinorin A, a Potent KOR Agonist. *ACS Central Science*, **2017**, 3, 1329-1336	16.8	23
334	Extending the Structural View of Class B GPCRs. *Trends in Biochemical Sciences*, **2017**, 42, 946-960	10.3	75
333	Structure and Function of Peptide-Binding G Protein-Coupled Receptors. *Journal of Molecular Biology*, **2017**, 429, 2726-2745	6.5	41

332	Crystal structures of agonist-bound human cannabinoid receptor CB. *Nature*, **2017**, 547, 468-471	50.4	270
331	An electrostatic mechanism for Ca(2+)-mediated regulation of gap junction channels. *Nature Communications*, **2016**, 7, 8770	17.4	83
330	Adrenergic Receptor Conformational Response to Fusion Protein in the Third Intracellular Loop. *Structure*, **2016**, 24, 2190-2197	5.2	37
329	Native phasing of x-ray free-electron laser data for a G protein-coupled receptor. *Science Advances*, **2016**, 2, e1600292	14.3	85
328	X-ray laser diffraction for structure determination of the rhodopsin-arrestin complex. *Scientific Data*, **2016**, 3, 160021	8.2	40
327	Crystal Structure of the Human Cannabinoid Receptor CB. *Cell*, **2016**, 167, 750-762.e14	56.2	323
326	Structural Determinants of Binding the Seven-transmembrane Domain of the Glucagon-like Peptide-1 Receptor (GLP-1R). *Journal of Biological Chemistry*, **2016**, 291, 12991-3004	5.4	39
325	Structure of CC chemokine receptor 2 with orthosteric and allosteric antagonists. *Nature*, **2016**, 540, 458-461	50.4	168
324	In vitro expression and analysis of the 826 human G protein-coupled receptors. *Protein and Cell*, **2016**, 7, 325-37	7.2	38
323	The Molecular Mechanism of P2Y1 Receptor Activation. *Angewandte Chemie*, **2016**, 128, 10487-10491	3.6	0
322	The Molecular Mechanism of P2Y1 Receptor Activation. *Angewandte Chemie - International Edition*, **2016**, 55, 10331-5	16.4	41
321	Structural biology. Crystal structure of the chemokine receptor CXCR4 in complex with a viral chemokine. *Science*, **2015**, 347, 1117-22	33.3	262
320	Crystal Structure of Antagonist Bound Human Lysophosphatidic Acid Receptor 1. *Cell*, **2015**, 161, 1633-43	56.2	129
319	Single Amino Acid Variation Underlies Species-Specific Sensitivity to Amphibian Skin-Derived Opioid-like Peptides. *Chemistry and Biology*, **2015**, 22, 764-75		11
318	Conformational states of the full-length glucagon receptor. *Nature Communications*, **2015**, 6, 7859	17.4	86
317	Crystal structure of rhodopsin bound to arrestin by femtosecond X-ray laser. *Nature*, **2015**, 523, 561-7	50.4	572
316	Modeling ligand recognition at the P2Y12 receptor in light of X-ray structural information. *Journal of Computer-Aided Molecular Design*, **2015**, 29, 737-56	4.2	34
315	Structure of the Angiotensin receptor revealed by serial femtosecond crystallography. *Cell*, **2015**, 161, 833-44	56.2	262

314	Sodium ion binding pocket mutations and adenosine A2A receptor function. *Molecular Pharmacology*, **2015**, 87, 305-13	4.3	60
313	Two disparate ligand-binding sites in the human P2Y1 receptor. *Nature*, **2015**, 520, 317-21	50.4	239
312	Nucleotides Acting at P2Y Receptors: Connecting Structure and Function. *Molecular Pharmacology*, **2015**, 88, 220-30	4.3	74
311	The Importance of Ligand-Receptor Conformational Pairs in Stabilization: Spotlight on the N/OFQ G Protein-Coupled Receptor. *Structure*, **2015**, 23, 2291-2299	5.2	53
310	Single-molecule view of basal activity and activation mechanisms of the G protein-coupled receptor β2AR. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 14254-9	11.5	65
309	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, 11852-7	11.5	60
308	Design, synthesis, pharmacological characterization of a fluorescent agonist of the P2Y1 receptor. *Bioorganic and Medicinal Chemistry Letters*, **2015**, 25, 4733-4739	2.9	14
307	Structural Basis for Ligand Recognition and Functional Selectivity at Angiotensin Receptor. *Journal of Biological Chemistry*, **2015**, 290, 29127-39	5.4	111
306	In-Membrane Chemical Modification (IMCM) for Site-Specific Chromophore Labeling of GPCRs. *Angewandte Chemie*, **2015**, 127, 15461-15464	3.6	2
305	In-Membrane Chemical Modification (IMCM) for Site-Specific Chromophore Labeling of GPCRs. *Angewandte Chemie - International Edition*, **2015**, 54, 15246-9	16.4	9
304	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, 6961-6	11.5	56
303	Generic GPCR residue numbers - aligning topology maps while minding the gaps. *Trends in Pharmacological Sciences*, **2015**, 36, 22-31	13.2	259
302	Transition states. Trapping a transition state in a computationally designed protein bottle. *Science*, **2015**, 347, 863-867	33.3	31
301	Structural basis for bifunctional peptide recognition at human δ-opioid receptor. *Nature Structural and Molecular Biology*, **2015**, 22, 265-8	17.6	133
300	The importance of ligands for G protein-coupled receptor stability. *Trends in Biochemical Sciences*, **2015**, 40, 79-87	10.3	53
299	Structure of a class C GPCR metabotropic glutamate receptor 1 bound to an allosteric modulator. *Science*, **2014**, 344, 58-64	33.3	406
298	Lipidic cubic phase injector facilitates membrane protein serial femtosecond crystallography. *Nature Communications*, **2014**, 5, 3309	17.4	416
297	Structure of the human P2Y12 receptor in complex with an antithrombotic drug. *Nature*, **2014**, 509, 115-8	50.4	272

296	Allosteric sodium in class A GPCR signaling. *Trends in Biochemical Sciences*, **2014**, 39, 233-44	10.3	314
295	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, 150-68	6.5	24
294	Insights into the structure of class B GPCRs. *Trends in Pharmacological Sciences*, **2014**, 35, 12-22	13.2	172
293	Molecular control of δ-opioid receptor signalling. *Nature*, **2014**, 506, 191-6	50.4	355
292	Structural basis for Smoothened receptor modulation and chemoresistance to anticancer drugs. *Nature Communications*, **2014**, 5, 4355	17.4	175
291	Advances in GPCR modeling evaluated by the GPCR Dock 2013 assessment: meeting new challenges. *Structure*, **2014**, 22, 1120-1139	5.2	136
290	Agonist-bound structure of the human P2Y12 receptor. *Nature*, **2014**, 509, 119-22	50.4	222
289	Exploring a 2-naphthoic acid template for the structure-based design of P2Y14 receptor antagonist molecular probes. *ACS Chemical Biology*, **2014**, 9, 2833-42	4.9	30
288	Constitutive phospholipid scramblase activity of a G protein-coupled receptor. *Nature Communications*, **2014**, 5, 5115	17.4	78
287	Coordinating the impact of structural genomics on the human α-helical transmembrane proteome. *Nature Structural and Molecular Biology*, **2013**, 20, 135-8	17.6	57
286	Structure of the human glucagon class B G-protein-coupled receptor. *Nature*, **2013**, 499, 444-9	50.4	312
285	The role of a sodium ion binding site in the allosteric modulation of the A(2A) adenosine G protein-coupled receptor. *Structure*, **2013**, 21, 2175-85	5.2	98
284	Fluorine-19 NMR of integral membrane proteins illustrated with studies of GPCRs. *Current Opinion in Structural Biology*, **2013**, 23, 740-747	8.1	63
283	Chemotype-selective modes of action of δ-opioid receptor agonists. *Journal of Biological Chemistry*, **2013**, 288, 34470-83	5.4	45
282	Structure-based ligand discovery targeting orthosteric and allosteric pockets of dopamine receptors. *Molecular Pharmacology*, **2013**, 84, 794-807	4.3	69
281	Genetically encoded chemical probes in cells reveal the binding path of urocortin-I to CRF class B GPCR. *Cell*, **2013**, 155, 1258-69	56.2	131
280	Serial femtosecond crystallography of G protein-coupled receptors. *Science*, **2013**, 342, 1521-4	33.3	367
279	β-adrenergic receptor activation by agonists studied with ^{19}F NMR spectroscopy. *Angewandte Chemie - International Edition*, **2013**, 52, 10762-5	16.4	60

278	Structure of the CCR5 chemokine receptor-HIV entry inhibitor maraviroc complex. *Science*, **2013**, 341, 1387-90	33.3	505
277	The GPCR Network: a large-scale collaboration to determine human GPCR structure and function. *Nature Reviews Drug Discovery*, **2013**, 12, 25-34	64.1	207
276	Opportunities for functional selectivity in GPCR antibodies. *Biochemical Pharmacology*, **2013**, 85, 147-52	6	34
275	Structure-function of the G protein-coupled receptor superfamily. *Annual Review of Pharmacology and Toxicology*, **2013**, 53, 531-56	17.9	758
274	β-Adrenergic Receptor Solutions for Structural Biology Analyzed with Microscale NMR Diffusion Measurements. *Angewandte Chemie*, **2013**, 125, 349-353	3.6	1
273	β-Adrenergic receptor solutions for structural biology analyzed with microscale NMR diffusion measurements. *Angewandte Chemie - International Edition*, **2013**, 52, 331-5	16.4	20
272	Structural features for functional selectivity at serotonin receptors. *Science*, **2013**, 340, 615-9	33.3	492
271	Structural basis for molecular recognition at serotonin receptors. *Science*, **2013**, 340, 610-4	33.3	370
270	Structure of the human smoothened receptor bound to an antitumour agent. *Nature*, **2013**, 497, 338-43	50.4	375
269	Identification of fibroblast growth factor receptor 3 (FGFR3) as a protein receptor for botulinum neurotoxin serotype A (BoNT/A). *PLoS Pathogens*, **2013**, 9, e1003369	7.6	55
268	Sphingosine-1-phosphate and its receptors: structure, signaling, and influence. *Annual Review of Biochemistry*, **2013**, 82, 637-62	29.1	154
267	Engineered nanostructured β-sheet peptides protect membrane proteins. *Nature Methods*, **2013**, 10, 759-61	21.6	93
266	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, 6289-99	16.4	28
265	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	11.5	111
264	β-Adrenergic Receptor Activation by Agonists Studied with 19F NMR Spectroscopy. *Angewandte Chemie*, **2013**, 125, 10962-10965	3.6	11
263	A novel approach to quantify G-protein-coupled receptor dimerization equilibrium using bioluminescence resonance energy transfer. *Methods in Molecular Biology*, **2013**, 1013, 93-127	1.4	10
262	Fusion partner toolchest for the stabilization and crystallization of G protein-coupled receptors. *Structure*, **2012**, 20, 967-76	5.2	272
261	Crystal structure of a voltage-gated K+ channel pore module in a closed state in lipid membranes. *Journal of Biological Chemistry*, **2012**, 287, 43063-70	5.4	19

260	Structural basis for allosteric regulation of GPCRs by sodium ions. *Science*, **2012**, 337, 232-6	33.3	714
259	Crystal structure of a lipid G protein-coupled receptor. *Science*, **2012**, 335, 851-5	33.3	538
258	Diversity and modularity of G protein-coupled receptor structures. *Trends in Pharmacological Sciences*, **2012**, 33, 17-27	13.2	348
257	Synthesis and properties of dodecyl trehaloside detergents for membrane protein studies. *Langmuir*, **2012**, 28, 11173-81	4	17
256	Biased signaling pathways in β-adrenergic receptor characterized by 19F-NMR. *Science*, **2012**, 335, 1106-10	33.3	523
255	Structure of the nociceptin/orphanin FQ receptor in complex with a peptide mimetic. *Nature*, **2012**, 485, 395-9	50.4	383
254	Structure of the human δ-opioid receptor in complex with JDTic. *Nature*, **2012**, 485, 327-32	50.4	695
253	Optimization of adenosine 5'-carboxamide derivatives as adenosine receptor agonists using structure-based ligand design and fragment screening. *Journal of Medicinal Chemistry*, **2012**, 55, 4297-308	8.3	55
252	Agonists for 13 trace amine-associated receptors provide insight into the molecular basis of odor selectivity. *ACS Chemical Biology*, **2012**, 7, 1184-9	4.9	69
251	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, 538-52	8.3	36
250	Chaperone-like therapy with tetrahydrobiopterin in clinical trials for phenylketonuria: is genotype a predictor of response?. *JIMD Reports*, **2012**, 5, 59-70	1.9	8
249	Reversible competitive α-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, 2805-22	8.3	46
248	Crystal structure-based virtual screening for fragment-like ligands of the human histamine H(1) receptor. *Journal of Medicinal Chemistry*, **2011**, 54, 8195-206	8.3	171
247	GPCR stabilization using the bicelle-like architecture of mixed sterol-detergent micelles. *Methods*, **2011**, 55, 310-7	4.6	66
246	Evaluation of orally administered PEGylated phenylalanine ammonia lyase in mice for the treatment of Phenylketonuria. *Molecular Genetics and Metabolism*, **2011**, 104, 249-54	3.7	34
245	Structure of an agonist-bound human A2A adenosine receptor. *Science*, **2011**, 332, 322-7	33.3	706
244	The crystal structure of the β-neurexin-1 extracellular region reveals a hinge point for mediating synaptic adhesion and function. *Structure*, **2011**, 19, 767-78	5.2	56
243	Status of GPCR modeling and docking as reflected by community-wide GPCR Dock 2010 assessment. *Structure*, **2011**, 19, 1108-26	5.2	243

242	Ligand-dependent perturbation of the conformational ensemble for the GPCR β adrenergic receptor revealed by HDX. *Structure*, **2011**, 19, 1424-32	5.2	111
241	Trapping small caffeine in a large GPCR pocket. *Structure*, **2011**, 19, 1204-7	5.2	5
240	Structure of the human histamine H1 receptor complex with doxepin. *Nature*, **2011**, 475, 65-70	50.4	630
239	Fluoride-mediated capture of a noncovalent bound state of a reversible covalent enzyme inhibitor: X-ray crystallographic analysis of an exceptionally potent α-ketoheterocycle inhibitor of fatty acid amide hydrolase. *Journal of the American Chemical Society*, **2011**, 133, 4092-100	16.4	31
238	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	3.5	45
237	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, 4019-28	3.2	25
236	Purification, modeling, and analysis of botulinum neurotoxin subtype A5 (BoNT/A5) from Clostridium botulinum strain A661222. *Applied and Environmental Microbiology*, **2011**, 77, 4217-22	4.8	31
235	Ligand binding and subtype selectivity of the human A(2A) adenosine receptor: identification and characterization of essential amino acid residues. *Journal of Biological Chemistry*, **2010**, 285, 13032-44	5.4	77
234	LCP-Tm: an assay to measure and understand stability of membrane proteins in a membrane environment. *Biophysical Journal*, **2010**, 98, 1539-48	2.9	55
233	Dynamics of the beta2-adrenergic G-protein coupled receptor revealed by hydrogen-deuterium exchange. *Analytical Chemistry*, **2010**, 82, 1100-8	7.8	102
232	Design, synthesis, and properties of branch-chained maltoside detergents for stabilization and crystallization of integral membrane proteins: human connexin 26. *Langmuir*, **2010**, 26, 8690-6	4	32
231	Structure of the human dopamine D3 receptor in complex with a D2/D3 selective antagonist. *Science*, **2010**, 330, 1091-5	33.3	938
230	Structures of the CXCR4 chemokine GPCR with small-molecule and cyclic peptide antagonists. *Science*, **2010**, 330, 1066-71	33.3	1432
229	A single-domain llama antibody potently inhibits the enzymatic activity of botulinum neurotoxin by binding to the non-catalytic alpha-exosite binding region. *Journal of Molecular Biology*, **2010**, 397, 1106-18	6.5	66
228	Crystal structure of the botulinum neurotoxin type G binding domain: insight into cell surface binding. *Journal of Molecular Biology*, **2010**, 397, 1287-97	6.5	32
227	Crystal structure of fatty acid amide hydrolase bound to the carbamate inhibitor URB597: discovery of a deacylating water molecule and insight into enzyme inactivation. *Journal of Molecular Biology*, **2010**, 400, 743-54	6.5	81
226	Converting an injectable protein therapeutic into an oral form: phenylalanine ammonia lyase for phenylketonuria. *Molecular Genetics and Metabolism*, **2010**, 99, 4-9	3.7	46
225	Recent progress in the structure determination of GPCRs, a membrane protein family with high potential as pharmaceutical targets. *Methods in Molecular Biology*, **2010**, 654, 141-68	1.4	49

224	G Protein-Coupled Receptor Structures **2010**, 129-138		
223	Rescue of misfolded proteins and stabilization by small molecules. *Methods in Molecular Biology*, **2010**, 648, 313-24	1.4	10
222	Conserved binding mode of human beta2 adrenergic receptor inverse agonists and antagonist revealed by X-ray crystallography. *Journal of the American Chemical Society*, **2010**, 132, 11443-5	16.4	297
221	X-ray crystallographic analysis of alpha-ketoheterocycle inhibitors bound to a humanized variant of fatty acid amide hydrolase. *Journal of Medicinal Chemistry*, **2010**, 53, 230-40	8.3	49
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