

# Raymond C Stevens

## List of Publications by Citations

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403  
papers

46,656  
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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	High-resolution crystal structure of an engineered human beta2-adrenergic G protein-coupled receptor. <i>Science</i> , <b>2007</b> , 318, 1258-65	33.3	2776
402	The 2.6 angstrom crystal structure of a human A2A adenosine receptor bound to an antagonist. <i>Science</i> , <b>2008</b> , 322, 1211-7	33.3	1549
401	Structures of the CXCR4 chemokine GPCR with small-molecule and cyclic peptide antagonists. <i>Science</i> , <b>2010</b> , 330, 1066-71	33.3	1432
400	GPCR engineering yields high-resolution structural insights into beta2-adrenergic receptor function. <i>Science</i> , <b>2007</b> , 318, 1266-73	33.3	1173
399	Influenza neuraminidase inhibitors possessing a novel hydrophobic interaction in the enzyme active site: design, synthesis, and structural analysis of carbocyclic sialic acid analogues with potent anti-influenza activity. <i>Journal of the American Chemical Society</i> , <b>1997</b> , 119, 681-90	16.4	952
398	Structure of the human dopamine D3 receptor in complex with a D2/D3 selective antagonist. <i>Science</i> , <b>2010</b> , 330, 1091-5	33.3	938
397	A specific cholesterol binding site is established by the 2.8 A structure of the human beta2-adrenergic receptor. <i>Structure</i> , <b>2008</b> , 16, 897-905	5.2	794
396	Structure-function of the G protein-coupled receptor superfamily. <i>Annual Review of Pharmacology and Toxicology</i> , <b>2013</b> , 53, 531-56	17.9	758
395	Structural basis for allosteric regulation of GPCRs by sodium ions. <i>Science</i> , <b>2012</b> , 337, 232-6	33.3	714
394	Structure of an agonist-bound human A2A adenosine receptor. <i>Science</i> , <b>2011</b> , 332, 322-7	33.3	706
393	Structure of the human $\mu$ opioid receptor in complex with JDTic. <i>Nature</i> , <b>2012</b> , 485, 327-32	50.4	695
392	Protein production and purification. <i>Nature Methods</i> , <b>2008</b> , 5, 135-46	21.6	655
391	Structure of the human histamine H1 receptor complex with doxepin. <i>Nature</i> , <b>2011</b> , 475, 65-70	50.4	630
390	Crystal structure of botulinum neurotoxin type A and implications for toxicity. <i>Nature Structural Biology</i> , <b>1998</b> , 5, 898-902		601
389	Crystal structure of rhodopsin bound to arrestin by femtosecond X-ray laser. <i>Nature</i> , <b>2015</b> , 523, 561-7	50.4	572
388	Crystal structure of a lipid G protein-coupled receptor. <i>Science</i> , <b>2012</b> , 335, 851-5	33.3	538
387	Biased signaling pathways in $\beta$ -adrenergic receptor characterized by 19F-NMR. <i>Science</i> , <b>2012</b> , 335, 1106-10	33.3	523

386	Structure of the CCR5 chemokine receptor-HIV entry inhibitor maraviroc complex. <i>Science</i> , <b>2013</b> , 341, 1387-90	33.3	505
385	Structural insights into the evolution of an antibody combining site. <i>Science</i> , <b>1997</b> , 276, 1665-9	33.3	500
384	Structural features for functional selectivity at serotonin receptors. <i>Science</i> , <b>2013</b> , 340, 615-9	33.3	492
383	Structural adaptations in a membrane enzyme that terminates endocannabinoid signaling. <i>Science</i> , <b>2002</b> , 298, 1793-6	33.3	428
382	Lipidic cubic phase injector facilitates membrane protein serial femtosecond crystallography. <i>Nature Communications</i> , <b>2014</b> , 5, 3309	17.4	416
381	Structure of a class C GPCR metabotropic glutamate receptor 1 bound to an allosteric modulator. <i>Science</i> , <b>2014</b> , 344, 58-64	33.3	406
380	Structure of the nociceptin/orphanin FQ receptor in complex with a peptide mimetic. <i>Nature</i> , <b>2012</b> , 485, 395-9	50.4	383
379	Structural genomics of the <i>Thermotoga maritima</i> proteome implemented in a high-throughput structure determination pipeline. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2002</b> , 99, 11664-9	11.5	381
378	Structure of the human smoothed receptor bound to an antitumour agent. <i>Nature</i> , <b>2013</b> , 497, 338-43	50.4	375
377	Structural basis for molecular recognition at serotonin receptors. <i>Science</i> , <b>2013</b> , 340, 610-4	33.3	370
376	Serial femtosecond crystallography of G protein-coupled receptors. <i>Science</i> , <b>2013</b> , 342, 1521-4	33.3	367
375	Molecular control of $\mu$ opioid receptor signalling. <i>Nature</i> , <b>2014</b> , 506, 191-6	50.4	355
374	Discovery and characterization of a highly selective FAAH inhibitor that reduces inflammatory pain. <i>Chemistry and Biology</i> , <b>2009</b> , 16, 411-20		354
373	Ultrasensitive magnetic biosensor for homogeneous immunoassay. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2000</b> , 97, 14268-72	11.5	354
372	Diversity and modularity of G protein-coupled receptor structures. <i>Trends in Pharmacological Sciences</i> , <b>2012</b> , 33, 17-27	13.2	348
371	Microscale fluorescent thermal stability assay for membrane proteins. <i>Structure</i> , <b>2008</b> , 16, 351-9	5.2	332
370	Crystal Structure of the Human Cannabinoid Receptor CB. <i>Cell</i> , <b>2016</b> , 167, 750-762.e14	56.2	323
369	Allosteric sodium in class A GPCR signaling. <i>Trends in Biochemical Sciences</i> , <b>2014</b> , 39, 233-44	10.3	314

368	Structure of the human glucagon class B G-protein-coupled receptor. <i>Nature</i> , <b>2013</b> , 499, 444-9	50.4	312
367	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> , <b>2010</b> , 132, 11443-5	16.4	297
366	Severe acute respiratory syndrome coronavirus papain-like protease: structure of a viral deubiquitinating enzyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 5717-22	11.5	295
365	Cholera toxin binding affinity and specificity for gangliosides determined by surface plasmon resonance. <i>Biochemistry</i> , <b>1996</b> , 35, 6375-84	3.2	285
364	Sequence homology and structural analysis of the clostridial neurotoxins. <i>Journal of Molecular Biology</i> , <b>1999</b> , 291, 1091-104	6.5	284
363	How Ligands Illuminate GPCR Molecular Pharmacology. <i>Cell</i> , <b>2017</b> , 170, 414-427	56.2	276
362	Structure-activity relationship studies of novel carbocyclic influenza neuraminidase inhibitors. <i>Journal of Medicinal Chemistry</i> , <b>1998</b> , 41, 2451-60	8.3	276
361	Structure of the human P2Y12 receptor in complex with an antithrombotic drug. <i>Nature</i> , <b>2014</b> , 509, 115-8	50.4	272
360	Fusion partner toolchest for the stabilization and crystallization of G protein-coupled receptors. <i>Structure</i> , <b>2012</b> , 20, 967-76	5.2	272
359	Crystal structures of agonist-bound human cannabinoid receptor CB. <i>Nature</i> , <b>2017</b> , 547, 468-471	50.4	270
358	Structural biology. Crystal structure of the chemokine receptor CXCR4 in complex with a viral chemokine. <i>Science</i> , <b>2015</b> , 347, 1117-22	33.3	262
357	Structure of the Angiotensin receptor revealed by serial femtosecond crystallography. <i>Cell</i> , <b>2015</b> , 161, 833-44	56.2	262
356	Generic GPCR residue numbers - aligning topology maps while minding the gaps. <i>Trends in Pharmacological Sciences</i> , <b>2015</b> , 36, 22-31	13.2	259
355	Status of GPCR modeling and docking as reflected by community-wide GPCR Dock 2010 assessment. <i>Structure</i> , <b>2011</b> , 19, 1108-26	5.2	243
354	Two disparate ligand-binding sites in the human P2Y1 receptor. <i>Nature</i> , <b>2015</b> , 520, 317-21	50.4	239
353	Community-wide assessment of GPCR structure modelling and ligand docking: GPCR Dock 2008. <i>Nature Reviews Drug Discovery</i> , <b>2009</b> , 8, 455-63	64.1	236
352	Identification of Phosphorylation Codes for Arrestin Recruitment by G Protein-Coupled Receptors. <i>Cell</i> , <b>2017</b> , 170, 457-469.e13	56.2	225
351	Agonist-bound structure of the human P2Y12 receptor. <i>Nature</i> , <b>2014</b> , 509, 119-22	50.4	222

350	Crystal structure of tyrosine hydroxylase at 2.3 Å and its implications for inherited neurodegenerative diseases. <i>Nature Structural Biology</i> , <b>1997</b> , 4, 578-85		218
349	Structure-based discovery of novel chemotypes for adenosine A(2A) receptor antagonists. <i>Journal of Medicinal Chemistry</i> , <b>2010</b> , 53, 1799-809	8.3	211
348	A 'litmus test' for molecular recognition using artificial membranes. <i>Chemistry and Biology</i> , <b>1996</b> , 3, 113-20		210
347	The GPCR Network: a large-scale collaboration to determine human GPCR structure and function. <i>Nature Reviews Drug Discovery</i> , <b>2013</b> , 12, 25-34	64.1	207
346	Structure of the Nanobody-Stabilized Active State of the Kappa Opioid Receptor. <i>Cell</i> , <b>2018</b> , 172, 55-67.e15	8.6	205
345	High-throughput protein crystallization. <i>Current Opinion in Structural Biology</i> , <b>2000</b> , 10, 558-63	8.1	192
344	Crystal structure of the anti-viral APOBEC3G catalytic domain and functional implications. <i>Nature</i> , <b>2008</b> , 456, 121-4	50.4	190
343	Structural basis of autoregulation of phenylalanine hydroxylase. <i>Nature Structural Biology</i> , <b>1999</b> , 6, 442-8		188
342	Predicting the emergence of antibiotic resistance by directed evolution and structural analysis. <i>Nature Structural Biology</i> , <b>2001</b> , 8, 238-42		184
341	Design of high-throughput methods of protein production for structural biology. <i>Structure</i> , <b>2000</b> , 8, R173-85	17.8	179
340	Global efforts in structural genomics. <i>Science</i> , <b>2001</b> , 294, 89-92	33.3	176
339	Structural basis for Smoothed receptor modulation and chemoresistance to anticancer drugs. <i>Nature Communications</i> , <b>2014</b> , 5, 4355	17.4	175
338	Crystal Structure of the Human Cannabinoid Receptor CB2. <i>Cell</i> , <b>2019</b> , 176, 459-467.e13	56.2	175
337	Insights into the structure of class B GPCRs. <i>Trends in Pharmacological Sciences</i> , <b>2014</b> , 35, 12-22	13.2	172
336	Crystal structure-based virtual screening for fragment-like ligands of the human histamine H(1) receptor. <i>Journal of Medicinal Chemistry</i> , <b>2011</b> , 54, 8195-206	8.3	171
335	Structure of CC chemokine receptor 2 with orthosteric and allosteric antagonists. <i>Nature</i> , <b>2016</b> , 540, 458-461	50.4	168
334	Structural basis of cell surface receptor recognition by botulinum neurotoxin B. <i>Nature</i> , <b>2006</b> , 444, 1096-100	10.0	167
333	Discovery of new GPCR biology: one receptor structure at a time. <i>Structure</i> , <b>2009</b> , 17, 8-14	5.2	165

332	An approach to rapid protein crystallization using nanodroplets. <i>Journal of Applied Crystallography</i> , <b>2002</b> , 35, 278-281	3.8	164
331	Charge-Induced Chromatic Transition of Amino Acid-Derivatized Polydiacetylene Liposomes. <i>Langmuir</i> , <b>1998</b> , 14, 1974-1976	4	164
330	Immunological origins of binding and catalysis in a Diels-Alderase antibody. <i>Science</i> , <b>1998</b> , 279, 1929-33	33.3	156
329	Sphingosine-1-phosphate and its receptors: structure, signaling, and influence. <i>Annual Review of Biochemistry</i> , <b>2013</b> , 82, 637-62	29.1	154
328	Molecular evolution of antibody cross-reactivity for two subtypes of type A botulinum neurotoxin. <i>Nature Biotechnology</i> , <b>2007</b> , 25, 107-16	44.5	151
327	Structural Insight into the Aromatic Amino Acid Hydroxylases and Their Disease-Related Mutant Forms. <i>Chemical Reviews</i> , <b>1999</b> , 99, 2137-2160	68.1	151
326	Crystal structure of the catalytic domain of human phenylalanine hydroxylase reveals the structural basis for phenylketonuria. <i>Nature Structural Biology</i> , <b>1997</b> , 4, 995-1000		148
325	Structural basis of severe acute respiratory syndrome coronavirus ADP-ribose-1''-phosphate dephosphorylation by a conserved domain of nsP3. <i>Structure</i> , <b>2005</b> , 13, 1665-75	5.2	148
324	Modulating artificial membrane morphology: pH-induced chromatic transition and nanostructural transformation of a bolaamphiphilic conjugated polymer from blue helical ribbons to red nanofibers. <i>Journal of the American Chemical Society</i> , <b>2001</b> , 123, 3205-13	16.4	144
323	Human GLP-1 receptor transmembrane domain structure in complex with allosteric modulators. <i>Nature</i> , <b>2017</b> , 546, 312-315	50.4	143
322	Structure of the full-length glucagon class B G-protein-coupled receptor. <i>Nature</i> , <b>2017</b> , 546, 259-264	50.4	141
321	Proteomics analysis unravels the functional repertoire of coronavirus nonstructural protein 3. <i>Journal of Virology</i> , <b>2008</b> , 82, 5279-94	6.6	141
320	Correction of kinetic and stability defects by tetrahydrobiopterin in phenylketonuria patients with certain phenylalanine hydroxylase mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2004</b> , 101, 16903-8	11.5	140
319	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> , <b>2009</b> , 6 Suppl 5, S587-97	4.1	138
318	Crystal structure of botulinum neurotoxin type A in complex with the cell surface co-receptor GT1b-insight into the toxin-neuron interaction. <i>PLoS Pathogens</i> , <b>2008</b> , 4, e1000129	7.6	138
317	Rapid refinement of crystallographic protein construct definition employing enhanced hydrogen/deuterium exchange MS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2004</b> , 101, 751-6	11.5	137
316	Three-dimensional structure of human tryptophan hydroxylase and its implications for the biosynthesis of the neurotransmitters serotonin and melatonin. <i>Biochemistry</i> , <b>2002</b> , 41, 12569-74	3.2	137
315	Automation of X-ray crystallography. <i>Nature Structural Biology</i> , <b>2000</b> , 7 Suppl, 973-7		137

314	Advances in GPCR modeling evaluated by the GPCR Dock 2013 assessment: meeting new challenges. <i>Structure</i> , <b>2014</b> , 22, 1120-1139	5.2	136
313	Structural basis for bifunctional peptide recognition at human $\mu$ opioid receptor. <i>Nature Structural and Molecular Biology</i> , <b>2015</b> , 22, 265-8	17.6	133
312	Molecular genetics of tetrahydrobiopterin-responsive phenylalanine hydroxylase deficiency. <i>Human Mutation</i> , <b>2008</b> , 29, 167-75	4.7	132
311	Genetically encoded chemical probes in cells reveal the binding path of urocortin-I to CRF class B GPCR. <i>Cell</i> , <b>2013</b> , 155, 1258-69	56.2	131
310	Crystal Structure of Antagonist Bound Human Lysophosphatidic Acid Receptor 1. <i>Cell</i> , <b>2015</b> , 161, 1633-43	36.2	129
309	Structural basis for selectivity and diversity in angiotensin II receptors. <i>Nature</i> , <b>2017</b> , 544, 327-332	50.4	128
308	Structural consequences of effector binding to the T state of aspartate carbamoyltransferase: crystal structures of the unligated and ATP- and CTP-complexed enzymes at 2.6-A resolution. <i>Biochemistry</i> , <b>1990</b> , 29, 7691-701	3.2	128
307	Crystal structure of tyrosine hydroxylase with bound cofactor analogue and iron at 2.3 A resolution: self-hydroxylation of Phe300 and the pterin-binding site. <i>Biochemistry</i> , <b>1998</b> , 37, 13437-45	3.2	125
306	Structure of tetrameric human phenylalanine hydroxylase and its implications for phenylketonuria. <i>Journal of Biological Chemistry</i> , <b>1998</b> , 273, 16962-7	5.4	125
305	5-HT Receptor Structures Reveal the Structural Basis of GPCR Polypharmacology. <i>Cell</i> , <b>2018</b> , 172, 719-736	36.14	123
304	Structure-guided inhibitor design for human FAAH by interspecies active site conversion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 12820-4	11.5	120
303	Allosteric Coupling of Drug Binding and Intracellular Signaling in the A Adenosine Receptor. <i>Cell</i> , <b>2018</b> , 172, 68-80.e12	56.2	119
302	Coupling of an induced fit enzyme to polydiacetylene thin films: Colorimetric detection of glucose. <i>Advanced Materials</i> , <b>1997</b> , 9, 481-483	24	119
301	The structural basis of phenylketonuria. <i>Molecular Genetics and Metabolism</i> , <b>1999</b> , 68, 103-25	3.7	118
300	Common activation mechanism of class A GPCRs. <i>ELife</i> , <b>2019</b> , 8,	8.9	117
299	PAHdb 2003: what a locus-specific knowledgebase can do. <i>Human Mutation</i> , <b>2003</b> , 21, 333-44	4.7	115
298	Structural Basis for Ligand Recognition and Functional Selectivity at Angiotensin Receptor. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 29127-39	5.4	111
297	Steroid-based facial amphiphiles for stabilization and crystallization of membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, E1203-11	11.5	111

296	Ligand-dependent perturbation of the conformational ensemble for the GPCR $\beta$ adrenergic receptor revealed by HDX. <i>Structure</i> , <b>2011</b> , 19, 1424-32	5.2	111
295	Concept of the H( $\pi$ )-H( $\pi$ ) interaction. A low-temperature neutron diffraction study of cis-[IrH(OH)(PMe <sub>3</sub> ) <sub>4</sub> ]PF <sub>6</sub> . <i>Journal of the Chemical Society Dalton Transactions</i> , <b>1990</b> , 1429-1432		110
294	Stabilization of the human beta2-adrenergic receptor TM4-TM3-TM5 helix interface by mutagenesis of Glu122(3.41), a critical residue in GPCR structure. <i>Journal of Molecular Biology</i> , <b>2008</b> , 376, 1305-19	6.5	108
293	A structural perspective of the sequence variability within botulinum neurotoxin subtypes A1-A4. <i>Journal of Molecular Biology</i> , <b>2006</b> , 362, 733-42	6.5	108
292	Biophysical characterization of the stability of the 150-kilodalton botulinum toxin, the nontoxic component, and the 900-kilodalton botulinum toxin complex species. <i>Infection and Immunity</i> , <b>1998</b> , 66, 2420-5	3.7	107
291	Structure of CC Chemokine Receptor 5 with a Potent Chemokine Antagonist Reveals Mechanisms of Chemokine Recognition and Molecular Mimicry by HIV. <i>Immunity</i> , <b>2017</b> , 46, 1005-1017.e5	32.3	106
290	Time-controlled microfluidic seeding in nL-volume droplets to separate nucleation and growth stages of protein crystallization. <i>Angewandte Chemie - International Edition</i> , <b>2006</b> , 45, 8156-60	16.4	105
289	The genesis of high-throughput structure-based drug discovery using protein crystallography. <i>Current Opinion in Chemical Biology</i> , <b>2002</b> , 6, 704-10	9.7	104
288	Structural plasticity and the evolution of antibody affinity and specificity. <i>Journal of Molecular Biology</i> , <b>2003</b> , 330, 651-6	6.5	104
287	Ribonucleocapsid formation of severe acute respiratory syndrome coronavirus through molecular action of the N-terminal domain of N protein. <i>Journal of Virology</i> , <b>2007</b> , 81, 3913-21	6.6	103
286	Dynamics of the beta2-adrenergic G-protein coupled receptor revealed by hydrogen-deuterium exchange. <i>Analytical Chemistry</i> , <b>2010</b> , 82, 1100-8	7.8	102
285	Cocrystal structure of synaptobrevin-II bound to botulinum neurotoxin type B at 2.0 Å resolution. <i>Nature Structural Biology</i> , <b>2000</b> , 7, 687-92		102
284	Blue-fluorescent antibodies. <i>Science</i> , <b>2000</b> , 290, 307-13	33.3	102
283	Crystal structure and site-specific mutagenesis of pterin-bound human phenylalanine hydroxylase. <i>Biochemistry</i> , <b>2000</b> , 39, 2208-17	3.2	102
282	Crystal structures of aspartate carbamoyltransferase ligated with phosphonoacetamide, malonate, and CTP or ATP at 2.8-Å resolution and neutral pH. <i>Biochemistry</i> , <b>1990</b> , 29, 7702-15	3.2	99
281	Structural basis of ligand recognition at the human MT melatonin receptor. <i>Nature</i> , <b>2019</b> , 569, 284-288	50.4	98
280	The role of a sodium ion binding site in the allosteric modulation of the A(2A) adenosine G protein-coupled receptor. <i>Structure</i> , <b>2013</b> , 21, 2175-85	5.2	98
279	The interplay between binding energy and catalysis in the evolution of a catalytic antibody. <i>Nature</i> , <b>1997</b> , 389, 271-5	50.4	95



278	Crystal structure of nonstructural protein 10 from the severe acute respiratory syndrome coronavirus reveals a novel fold with two zinc-binding motifs. <i>Journal of Virology</i> , <b>2006</b> , 80, 7894-901	6.6	94
277	Engineered nanostructured sheet peptides protect membrane proteins. <i>Nature Methods</i> , <b>2013</b> , 10, 759-61	21.6	93
276	Automated sample mounting and alignment system for biological crystallography at a synchrotron source. <i>Structure</i> , <b>2004</b> , 12, 537-45	5.2	93
275	Mechanisms underlying responsiveness to tetrahydrobiopterin in mild phenylketonuria mutations. <i>Human Mutation</i> , <b>2004</b> , 24, 388-99	4.7	91
274	Protein biophysical properties that correlate with crystallization success in <i>Thermotoga maritima</i> : maximum clustering strategy for structural genomics. <i>Journal of Molecular Biology</i> , <b>2004</b> , 344, 977-91	6.5	91
273	Preclinical evaluation of multiple species of PEGylated recombinant phenylalanine ammonia lyase for the treatment of phenylketonuria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 20894-9	11.5	89
272	Designing facial amphiphiles for the stabilization of integral membrane proteins. <i>Angewandte Chemie - International Edition</i> , <b>2007</b> , 46, 7023-5	16.4	89
271	Conformational states of the full-length glucagon receptor. <i>Nature Communications</i> , <b>2015</b> , 6, 7859	17.4	86
270	Native phasing of x-ray free-electron laser data for a G protein-coupled receptor. <i>Science Advances</i> , <b>2016</b> , 2, e1600292	14.3	85
269	An electrostatic mechanism for Ca(2+)-mediated regulation of gap junction channels. <i>Nature Communications</i> , <b>2016</b> , 7, 8770	17.4	83
268	Amino Acid Terminated Polydiacetylene Lipid Microstructures: Morphology and Chromatic Transition. <i>Langmuir</i> , <b>2000</b> , 16, 5333-5342	4	83
267	Crystal structure of fatty acid amide hydrolase bound to the carbamate inhibitor URB597: discovery of a deacylating water molecule and insight into enzyme inactivation. <i>Journal of Molecular Biology</i> , <b>2010</b> , 400, 743-54	6.5	81
266	Binding and inactivation mechanism of a humanized fatty acid amide hydrolase by alpha-ketoheterocycle inhibitors revealed from cocrystal structures. <i>Journal of the American Chemical Society</i> , <b>2009</b> , 131, 10497-506	16.4	80
265	Constitutive phospholipid scramblase activity of a G protein-coupled receptor. <i>Nature Communications</i> , <b>2014</b> , 5, 5115	17.4	78
264	XFEL structures of the human MT melatonin receptor reveal the basis of subtype selectivity. <i>Nature</i> , <b>2019</b> , 569, 289-292	50.4	77
263	Structural Connection between Activation Microswitch and Allosteric Sodium Site in GPCR Signaling. <i>Structure</i> , <b>2018</b> , 26, 259-269.e5	5.2	77
262	Ligand binding and subtype selectivity of the human A(2A) adenosine receptor: identification and characterization of essential amino acid residues. <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 13032-44	5.4	77
261	Expression and purification of the <i>Saccharomyces cerevisiae</i> alpha-factor receptor (Ste2p), a 7-transmembrane-segment G protein-coupled receptor. <i>Journal of Biological Chemistry</i> , <b>1997</b> , 272, 15553-61	5.4	77

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- 258 Structural basis of ligand binding modes at the neuropeptide YY receptor. *Nature*, **2018**, 556, 520-524 50.4 75
- 257 Extending the Structural View of Class B GPCRs. *Trends in Biochemical Sciences*, **2017**, 42, 946-960 10.3 75
- 256 Structural Basis for Apelin Control of the Human Apelin Receptor. *Structure*, **2017**, 25, 858-866.e4 5.2 74
- 255 Nucleotides Acting at P2Y Receptors: Connecting Structure and Function. *Molecular Pharmacology*, **2015**, 88, 220-30 4.3 74
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