

# Gebhard Fx X Schertler

## List of Publications by Year in descending order

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121  
papers

15,738  
citations

38742

50  
h-index

24258

110  
g-index

129  
all docs

129  
docs citations

129  
times ranked

10738  
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal structure of the human $\beta_2$ adrenergic G-protein-coupled receptor. Nature, 2007, 450, 383-387.	27.8	1,832
2	Structure of a $\beta_1$ -adrenergic G-protein-coupled receptor. Nature, 2008, 454, 486-491.	27.8	1,334
3	Molecular signatures of G-protein-coupled receptors. Nature, 2013, 494, 185-194.	27.8	1,298
4	Projection structure of rhodopsin. Nature, 1993, 362, 770-772.	27.8	877
5	Structure of Bovine Rhodopsin in a Trigonal Crystal Form. Journal of Molecular Biology, 2004, 343, 1409-1438.	4.2	720
6	An alpha-carbon template for the transmembrane helices in the rhodopsin family of G-protein-coupled receptors   Edited by R. Huber. Journal of Molecular Biology, 1997, 272, 144-164.	4.2	642
7	The structural basis for agonist and partial agonist action on a $\beta_1$ -adrenergic receptor. Nature, 2011, 469, 241-244.	27.8	592
8	Structure of the $\mu$ -opioid receptor-Gi protein complex. Nature, 2018, 558, 547-552.	27.8	527
9	Arrangement of rhodopsin transmembrane $\pm$ -helices. Nature, 1997, 389, 203-206.	27.8	486
10	The structural basis of agonist-induced activation in constitutively active rhodopsin. Nature, 2011, 471, 656-660.	27.8	444
11	A three-dimensional movie of structural changes in bacteriorhodopsin. Science, 2016, 354, 1552-1557.	12.6	350
12	Electron crystallography reveals the structure of metarhodopsin I. EMBO Journal, 2004, 23, 3609-3620.	7.8	300
13	Low resolution structure of bovine rhodopsin determined by electron cryo-microscopy. Biophysical Journal, 1995, 68, 1776-1786.	0.5	298
14	Retinal isomerization in bacteriorhodopsin captured by a femtosecond x-ray laser. Science, 2018, 361, .	12.6	285
15	Tracking G-protein-coupled receptor activation using genetically encoded infrared probes. Nature, 2010, 464, 1386-1389.	27.8	245
16	Diverse activation pathways in class A GPCRs converge near the G-protein-coupling region. Nature, 2016, 536, 484-487.	27.8	245
17	Projection structure of frog rhodopsin in two crystal forms.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 11578-11582.	7.1	226
18	Stabilized G protein binding site in the structure of constitutively active metarhodopsin-II. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 119-124.	7.1	226

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19	Crystal Structure of a Thermally Stable Rhodopsin Mutant. <i>Journal of Molecular Biology</i> , 2007, 372, 1179-1188.	4.2	218
20	New G-protein-coupled receptor crystal structures: insights and limitations. <i>Trends in Pharmacological Sciences</i> , 2008, 29, 79-83.	8.7	217
21	Serial millisecond crystallography for routine room-temperature structure determination at synchrotrons. <i>Nature Communications</i> , 2017, 8, 542.	12.8	203
22	Lipidic cubic phase serial millisecond crystallography using synchrotron radiation. <i>IUCr</i> , 2015, 2, 168-176.	2.2	196
23	Two distinct conformations of helix 6 observed in antagonist-bound structures of a $\beta_1$ -adrenergic receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 8228-8232.	7.1	172
24	Engineering G protein-coupled receptors to facilitate their structure determination. <i>Current Opinion in Structural Biology</i> , 2009, 19, 386-395.	5.7	169
25	The 2.1 Å... Resolution Structure of Cyanopindolol-Bound $\beta_1$ -Adrenoceptor Identifies an Intramembrane Na <sup>+</sup> Ion that Stabilises the Ligand-Free Receptor. <i>PLoS ONE</i> , 2014, 9, e92727.	2.5	157
26	Development of an antibody fragment that stabilizes GPCR/G-protein complexes. <i>Nature Communications</i> , 2018, 9, 3712.	12.8	157
27	Orthorhombic Crystal Form of Bacteriorhodopsin Nucleated on Benzamidine Diffracting to 3.6 Å... Resolution. <i>Journal of Molecular Biology</i> , 1993, 234, 156-164.	4.2	156
28	Backbone NMR reveals allosteric signal transduction networks in the $\beta_1$ -adrenergic receptor. <i>Nature</i> , 2016, 530, 237-241.	27.8	155
29	Femtosecond-to-millisecond structural changes in a light-driven sodium pump. <i>Nature</i> , 2020, 583, 314-318.	27.8	115
30	Protein crystallography microdiffraction. <i>Current Opinion in Structural Biology</i> , 2005, 15, 556-562.	5.7	107
31	Overproduction of membrane proteins. <i>Current Opinion in Structural Biology</i> , 1992, 2, 534-544.	5.7	103
32	Characterisation of an improved two-dimensional p22121 crystal from bovine rhodopsin. <i>Journal of Molecular Biology</i> , 1998, 282, 991-1003.	4.2	103
33	Structural basis for recognition of synaptic vesicle protein 2C by botulinum neurotoxin A. <i>Nature</i> , 2014, 505, 108-111.	27.8	103
34	Development and crystallization of a minimal thermostabilised G protein-coupled receptor. <i>Protein Expression and Purification</i> , 2009, 65, 204-213.	1.3	90
35	Structure of rhodopsin and the metarhodopsin I photointermediate. <i>Current Opinion in Structural Biology</i> , 2005, 15, 408-415.	5.7	88
36	Distinct G protein-coupled receptor phosphorylation motifs modulate arrestin affinity and activation and global conformation. <i>Nature Communications</i> , 2019, 10, 1261.	12.8	86

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37	Expression and purification of truncated, non-glycosylated turkey beta-adrenergic receptors for crystallization. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2003, 1610, 133-140.	2.6	82
38	Insights into congenital stationary night blindness based on the structure of G90D rhodopsin. <i>EMBO Reports</i> , 2013, 14, 520-526.	4.5	79
39	Femtosecond X-ray diffraction from two-dimensional protein crystals. <i>IUCr</i> , 2014, 1, 95-100.	2.2	78
40	Protein crystallography with a micrometre-sized synchrotron-radiation beam. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 158-166.	2.5	77
41	Three-dimensional structure of an invertebrate rhodopsin and basis for ordered alignment in the photoreceptor membrane 1   Edited by D. Rees. <i>Journal of Molecular Biology</i> , 2001, 314, 455-463.	4.2	73
42	Three-dimensional mass density mapping of cellular ultrastructure byptychographic X-ray nanotomography. <i>Journal of Structural Biology</i> , 2015, 192, 461-469.	2.8	72
43	Lipidic cubic phase injector is a viable crystal delivery system for time-resolved serial crystallography. <i>Nature Communications</i> , 2016, 7, 12314.	12.8	71
44	Projection Structure of an Invertebrate Rhodopsin. <i>Journal of Structural Biology</i> , 1996, 117, 36-44.	2.8	65
45	Crystal structure of rhodopsin in complex with a mini-G $\alpha$ sheds light on the principles of G protein selectivity. <i>Science Advances</i> , 2018, 4, eaat7052.	10.3	65
46	Structure of rhodopsin. <i>Eye</i> , 1998, 12, 504-510.	2.1	62
47	Two Alternative Conformations of a Voltage-Gated Sodium Channel. <i>Journal of Molecular Biology</i> , 2013, 425, 4074-4088.	4.2	59
48	Probing G $\alpha$ 1 protein activation at single amino acid resolution. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 686-694.	8.2	58
49	Crystals of Native and Modified Bovine Rhodopsins and Their Heavy Atom Derivatives. <i>Journal of Molecular Biology</i> , 2004, 343, 1439-1450.	4.2	55
50	Structure of the Ligand-blocked Periplasmic Entrance of the Bacterial Multidrug Efflux Protein TolC. <i>Journal of Molecular Biology</i> , 2004, 342, 697-702.	4.2	53
51	Recoverin Binds Exclusively to an Amphipathic Peptide at the N Terminus of Rhodopsin Kinase, Inhibiting Rhodopsin Phosphorylation without Affecting Catalytic Activity of the Kinase. <i>Journal of Biological Chemistry</i> , 2006, 281, 19426-19432.	3.4	53
52	Conformational Selection in a Protein-Protein Interaction Revealed by Dynamic Pathway Analysis. <i>Cell Reports</i> , 2016, 14, 32-42.	6.4	52
53	Cryo-EM structure of the rhodopsin-G $\alpha$ 1 $\beta$ 3 complex reveals binding of the rhodopsin C-terminal tail to the g $\beta$ 2 subunit. <i>ELife</i> , 2019, 8, .	6.0	52
54	Crystal structure of jumping spider rhodopsin-1 as a light sensitive GPCR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14547-14556.	7.1	48

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55	The Three-dimensional Structure of Bovine Rhodopsin Determined by Electron Cryomicroscopy. <i>Journal of Biological Chemistry</i> , 2003, 278, 50217-50225.	3.4	43
56	Conserved activation pathways in G-protein-coupled receptors. <i>Biochemical Society Transactions</i> , 2012, 40, 383-388.	3.4	43
57	Dynamics and mechanism of a light-driven chloride pump. <i>Science</i> , 2022, 375, 845-851.	12.6	43
58	Membrane protein structural biology using X-ray free electron lasers. <i>Current Opinion in Structural Biology</i> , 2015, 33, 115-125.	5.7	42
59	Perspective: Opportunities for ultrafast science at SwissFEL. <i>Structural Dynamics</i> , 2017, 4, 061602.	2.3	40
60	Molecular architecture of a retinal cGMP-gated channel: the arrangement of the cytoplasmic domains. <i>EMBO Journal</i> , 2002, 21, 2087-2094.	7.8	39
61	Production of GPCR and GPCR complexes for structure determination. <i>Current Opinion in Structural Biology</i> , 2013, 23, 381-392.	5.7	37
62	Conformational activation of visual rhodopsin in native disc membranes. <i>Science Signaling</i> , 2015, 8, ra26.	3.6	37
63	Rhodopsin Photoproducts in 2D Crystals. <i>Journal of Molecular Biology</i> , 2004, 338, 597-609.	4.2	36
64	Structural basis of the activation of the CC chemokine receptor 5 by a chemokine agonist. <i>Science Advances</i> , 2021, 7, .	10.3	36
65	GPCR structure, function, drug discovery and crystallography: report from Academia-Industry International Conference (UK Royal Society) Chicheley Hall, 1 <sup>st</sup> 2 September 2014. <i>Naunyn-Schmiedeberg's Archives of Pharmacology</i> , 2015, 388, 883-903.	3.0	34
66	Structural role of the T94I rhodopsin mutation in congenital stationary night blindness. <i>EMBO Reports</i> , 2016, 17, 1431-1440.	4.5	34
67	Ligand channel in pharmacologically stabilized rhodopsin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3640-3645.	7.1	34
68	Constitutively active rhodopsin mutants causing night blindness are effectively phosphorylated by GRKs but differ in arrestin-1 binding. <i>Cellular Signalling</i> , 2013, 25, 2155-2162.	3.6	32
69	7 Å... resolution in protein two-dimensional-crystal X-ray diffraction at Linac Coherent Light Source. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2014, 369, 20130500.	4.0	32
70	The counterionâ€‘retinylidene Schiff base interaction of an invertebrate rhodopsin rearranges upon light activation. <i>Communications Biology</i> , 2019, 2, 180.	4.4	31
71	A graph-based approach identifies dynamic H-bond communication networks in spike protein S of SARS-CoV-2. <i>Journal of Structural Biology</i> , 2020, 212, 107617.	2.8	26
72	The rhodopsin story continued. <i>Nature</i> , 2008, 453, 292-293.	27.8	25

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73	Molecular mechanism of phosphorylation-dependent arrestin activation. <i>Current Opinion in Structural Biology</i> , 2014, 29, 143-151.	5.7	25
74	Advances in long-wavelength native phasing at X-ray free-electron lasers. <i>IUCr</i> , 2020, 7, 965-975.	2.2	25
75	Crystallization Scale Preparation of a Stable GPCR Signaling Complex between Constitutively Active Rhodopsin and G-Protein. <i>PLoS ONE</i> , 2014, 9, e98714.	2.5	24
76	Time-resolved structural studies with serial crystallography: A new light on retinal proteins. <i>Structural Dynamics</i> , 2015, 2, 041718.	2.3	22
77	[7] Preparation and analysis of two-dimensional crystals of rhodopsin. <i>Methods in Enzymology</i> , 2000, 315, 91-107.	1.0	19
78	Convergent evolution of tertiary structure in rhodopsin visual proteins from vertebrates and box jellyfish. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 6201-6206.	7.1	19
79	The Two-Photon Reversible Reaction of the Bistable Jumping Spider Rhodopsin-1. <i>Biophysical Journal</i> , 2019, 116, 1248-1258.	0.5	18
80	X-ray diffraction of heavy-atom labelled two-dimensional crystals of rhodopsin identifies the position of cysteine 140 in helix 3 and cysteine 316 in helix 8. <i>Journal of Molecular Biology</i> , 2002, 316, 693-709.	4.2	17
81	Preparation of an Activated Rhodopsin/Transducin Complex Using a Constitutively Active Mutant of Rhodopsin. <i>Biochemistry</i> , 2011, 50, 10399-10407.	2.5	16
82	The structure of the native CNGA1/CNGB1 CNG channel from bovine retinal rods. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 32-39.	8.2	14
83	Adaptation of pineal expressed teleost exo-rod opsin to non-image forming photoreception through enhanced Meta II decay. <i>Cellular and Molecular Life Sciences</i> , 2011, 68, 3713-3723.	5.4	13
84	Batch crystallization of rhodopsin for structural dynamics using an X-ray free-electron laser. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 856-860.	0.8	12
85	GPCR Activation States Induced by Nanobodies and Mini-G Proteins Compared by NMR Spectroscopy. <i>Molecules</i> , 2020, 25, 5984.	3.8	12
86	Projection structure of a transcriptional regulator, HupR, determined by electron cryo-microscopy. <i>Journal of Molecular Biology</i> , 2000, 296, 863-871.	4.2	11
87	Complete Reversible Refolding of a G-Protein Coupled Receptor on a Solid Support. <i>PLoS ONE</i> , 2016, 11, e0151582.	2.5	11
88	A set of common movements within GPCR-G-protein complexes from variability analysis of cryo-EM datasets. <i>Journal of Structural Biology</i> , 2021, 213, 107699.	2.8	11
89	C-Graphs Tool with Graphical User Interface to Dissect Conserved Hydrogen-Bond Networks: Applications to Visual Rhodopsins. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 5692-5707.	5.4	11
90	Rhodopsin Photointermediates in Two-Dimensional Crystals at Physiological Temperatures. <i>Biochemistry</i> , 2006, 45, 4974-4982.	2.5	10

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91	Structural basis of the partially open central gate in the human CNGA1/CNGB1 channel explained by additional density for calmodulin in cryo-EM map. <i>Journal of Structural Biology</i> , 2022, 214, 107828.	2.8	10
92	Structure of $\beta_2$ -Adrenergic Receptors. <i>Methods in Enzymology</i> , 2013, 520, 117-151.	1.0	9
93	New Insights into Arrestin Recruitment to GPCRs. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4949.	4.1	9
94	High-mass MALDI-MS unravels ligand-mediated G protein-coupling selectivity to GPCRs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	9
95	Efficient production of a functional G protein-coupled receptor in <i>E. coli</i> for structural studies. <i>Journal of Biomolecular NMR</i> , 2021, 75, 25-38.	2.8	9
96	Soluble dimeric prion protein ligand activates Adgrg6 receptor but does not rescue early signs of demyelination in PrP-deficient mice. <i>PLoS ONE</i> , 2020, 15, e0242137.	2.5	9
97	Arrestin-1 engineering facilitates complex stabilization with native rhodopsin. <i>Scientific Reports</i> , 2019, 9, 439.	3.3	8
98	Spial: analysis of subtype-specific features in multiple sequence alignments of proteins. <i>Bioinformatics</i> , 2010, 26, 2906-2907.	4.1	7
99	The role of water molecules in phototransduction of retinal proteins and G protein-coupled receptors. <i>Faraday Discussions</i> , 2018, 207, 27-37.	3.2	7
100	Ligands Stabilize Specific GPCR Conformations: But How?. <i>Structure</i> , 2012, 20, 1289-1290.	3.3	6
101	Retinal proteins - You can teach an old dog new tricks. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, 531-532.	1.0	6
102	Rhodopsin on Tracks: New Ways to Go in Signaling. <i>Structure</i> , 2015, 23, 606-608.	3.3	5
103	Photocrosslinking between nucleic acids and proteins: general discussion. <i>Faraday Discussions</i> , 2018, 207, 283-306.	3.2	5
104	Immobilization of arrestin-3 on different biosensor platforms for evaluating GPCR binding. <i>Physical Chemistry Chemical Physics</i> , 2020, 22, 24086-24096.	2.8	5
105	Exploring the signaling space of a GPCR using bivalent ligands with a rigid oligoproline backbone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	5
106	4D Biology for health and disease-workshop report. <i>New Biotechnology</i> , 2011, 28, 291-293.	4.4	2
107	Addendum to Three-dimensional mass density mapping of cellular ultrastructure by ptychographic X-ray nanotomography. <i>Struct. Biol.</i> 192 (2015) 461-469. <i>Journal of Structural Biology</i> , 2016, 193, 83.	2.8	2
108	Imaging of retina cellular and subcellular structures using ptychographic hard X-ray tomography. <i>Journal of Cell Science</i> , 2021, 134, .	2.0	2

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109	Membranes. Current Opinion in Structural Biology, 2011, 21, 495-496.	5.7	1
110	Large scale expression and purification of the rat 5-HT2c receptor. Protein Expression and Purification, 2015, 106, 1-9.	1.3	1
111	Comprehensive Analysis of the Role of Arrestin Residues in Receptor Binding. , 2017, , 83-102.		1
112	The greasy world of membrane proteins. Trends in Cell Biology, 1995, 5, 290-291.	7.9	0
113	Electron Crystallographic Studies of Rhodopsin. Phase Transitions, 2002, 75, 1-10.	1.3	0
114	Electrons and X-Rays Reveal the Structure of Rhodopsin: A Prototypical G Protein-Coupled Receptor-Implications for Colour Vision. , 2003, , 3-13.		0
115	Crystal Structures of the Î²2-Adrenergic Receptor. NATO Science for Peace and Security Series A: Chemistry and Biology, 2009, , 217-230.	0.5	0
116	Protein crystallization: robotics, procedures and developments. Acta Crystallographica Section A: Foundations and Advances, 2009, 65, s158-s159.	0.3	0
117	G Proteinâ€“Coupled Receptor Activation Based on X-ray Structural Studies. , 2013, , 877-881.		0
118	Title is missing!. , 2020, 15, e0242137.		0
119	Title is missing!. , 2020, 15, e0242137.		0
120	Title is missing!. , 2020, 15, e0242137.		0
121	Title is missing!. , 2020, 15, e0242137.		0