

# 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	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
2	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
3	Dynamics and mechanism of a light-driven chloride pump. <i>Science</i> , 2022, 375, 845-851.	12.6	43
4	Structural basis of the activation of the CC chemokine receptor 5 by a chemokine agonist. <i>Science Advances</i> , 2021, 7, .	10.3	36
5	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
6	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
7	Imaging of retina cellular and subcellular structures using ptychographic hard X-ray tomography. <i>Journal of Cell Science</i> , 2021, 134, .	2.0	2
8	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
9	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
10	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
11	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
12	New Insights into Arrestin Recruitment to GPCRs. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4949.	4.1	9
13	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
14	GPCR Activation States Induced by Nanobodies and Mini-G Proteins Compared by NMR Spectroscopy. <i>Molecules</i> , 2020, 25, 5984.	3.8	12
15	Femtosecond-to-millisecond structural changes in a light-driven sodium pump. <i>Nature</i> , 2020, 583, 314-318.	27.8	115
16	Advances in long-wavelength native phasing at X-ray free-electron lasers. <i>IUCr</i> , 2020, 7, 965-975.	2.2	25
17	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
18	Title is missing!. , 2020, 15, e0242137.		0

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19	Title is missing!. , 2020, 15, e0242137.		0
20	Title is missing!. , 2020, 15, e0242137.		0
21	Title is missing!. , 2020, 15, e0242137.		0
22	Crystal structure of jumping spider rhodopsin-1 as a light sensitive GPCR. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14547-14556.	7.1	48
23	The counterionâ€“retinylidene Schiff base interaction of an invertebrate rhodopsin rearranges upon light activation. Communications Biology, 2019, 2, 180.	4.4	31
24	Arrestin-1 engineering facilitates complex stabilization with native rhodopsin. Scientific Reports, 2019, 9, 439.	3.3	8
25	Distinct G protein-coupled receptor phosphorylation motifs modulate arrestin affinity and activation and global conformation. Nature Communications, 2019, 10, 1261.	12.8	86
26	The Two-Photon Reversible Reaction of the Bistable Jumping Spider Rhodopsin-1. Biophysical Journal, 2019, 116, 1248-1258.	0.5	18
27	Cryo-EM structure of the rhodopsin-GÎ±i-Î²3 complex reveals binding of the rhodopsin C-terminal tail to the gÎ²2 subunit. ELife, 2019, 8, .	6.0	52
28	Photocrosslinking between nucleic acids and proteins: general discussion. Faraday Discussions, 2018, 207, 283-306.	3.2	5
29	Ligand channel in pharmacologically stabilized rhodopsin. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3640-3645.	7.1	34
30	The role of water molecules in phototransduction of retinal proteins and G protein-coupled receptors. Faraday Discussions, 2018, 207, 27-37.	3.2	7
31	Development of an antibody fragment that stabilizes GPCR/G-protein complexes. Nature Communications, 2018, 9, 3712.	12.8	157
32	Crystal structure of rhodopsin in complex with a mini-G <sub>o</sub> sheds light on the principles of G protein selectivity. Science Advances, 2018, 4, eaat7052.	10.3	65
33	Convergent evolution of tertiary structure in rhodopsin visual proteins from vertebrates and box jellyfish. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 6201-6206.	7.1	19
34	Retinal isomerization in bacteriorhodopsin captured by a femtosecond x-ray laser. Science, 2018, 361, .	12.6	285
35	Structure of the Î¼-opioid receptorâ€“Gi protein complex. Nature, 2018, 558, 547-552.	27.8	527
36	Serial millisecond crystallography for routine room-temperature structure determination at synchrotrons. Nature Communications, 2017, 8, 542.	12.8	203

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37	Perspective: Opportunities for ultrafast science at SwissFEL. <i>Structural Dynamics</i> , 2017, 4, 061602.	2.3	40
38	Comprehensive Analysis of the Role of Arrestin Residues in Receptor Binding. , 2017, , 83-102.		1
39	Complete Reversible Refolding of a G-Protein Coupled Receptor on a Solid Support. <i>PLoS ONE</i> , 2016, 11, e0151582.	2.5	11
40	A three-dimensional movie of structural changes in bacteriorhodopsin. <i>Science</i> , 2016, 354, 1552-1557.	12.6	350
41	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
42	Addendum to "Three-dimensional mass density mapping of cellular ultrastructure by ptychographic X-ray nanotomography". <i>J. Struct. Biol.</i> 192 (2015) 461-469. <i>Journal of Structural Biology</i> , 2016, 193, 83.	2.8	2
43	Diverse activation pathways in class A GPCRs converge near the G-protein-coupling region. <i>Nature</i> , 2016, 536, 484-487.	27.8	245
44	Structural role of the T94I rhodopsin mutation in congenital stationary night blindness. <i>EMBO Reports</i> , 2016, 17, 1431-1440.	4.5	34
45	Conformational Selection in a Protein-Protein Interaction Revealed by Dynamic Pathway Analysis. <i>Cell Reports</i> , 2016, 14, 32-42.	6.4	52
46	Backbone NMR reveals allosteric signal transduction networks in the $\beta$ 21-adrenergic receptor. <i>Nature</i> , 2016, 530, 237-241.	27.8	155
47	Time-resolved structural studies with serial crystallography: A new light on retinal proteins. <i>Structural Dynamics</i> , 2015, 2, 041718.	2.3	22
48	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
49	Lipidic cubic phase serial millisecond crystallography using synchrotron radiation. <i>IUCr</i> , 2015, 2, 168-176.	2.2	196
50	Conformational activation of visual rhodopsin in native disc membranes. <i>Science Signaling</i> , 2015, 8, ra26.	3.6	37
51	Rhodopsin on Tracks: New Ways to Go in Signaling. <i>Structure</i> , 2015, 23, 606-608.	3.3	5
52	GPCR structure, function, drug discovery and crystallography: report from Academia-Industry International Conference (UK Royal Society) Chicheley Hall, 1-2 September 2014. <i>Naunyn-Schmiedeberg's Archives of Pharmacology</i> , 2015, 388, 883-903.	3.0	34
53	Three-dimensional mass density mapping of cellular ultrastructure by ptychographic X-ray nanotomography. <i>Journal of Structural Biology</i> , 2015, 192, 461-469.	2.8	72
54	Probing G $\alpha$ i1 protein activation at single amino acid resolution. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 686-694.	8.2	58

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55	Membrane protein structural biology using X-ray free electron lasers. <i>Current Opinion in Structural Biology</i> , 2015, 33, 115-125.	5.7	42
56	Large scale expression and purification of the rat 5-HT <sub>2c</sub> receptor. <i>Protein Expression and Purification</i> , 2015, 106, 1-9.	1.3	1
57	The 2.1 Å... Resolution Structure of Cyanopindolol-Bound $\beta_2$ -Adrenoceptor Identifies an Intramembrane Na <sup>+</sup> Ion that Stabilises the Ligand-Free Receptor. <i>PLoS ONE</i> , 2014, 9, e92727.	2.5	157
58	Femtosecond X-ray diffraction from two-dimensional protein crystals. <i>IUCr</i> , 2014, 1, 95-100.	2.2	78
59	Molecular mechanism of phosphorylation-dependent arrestin activation. <i>Current Opinion in Structural Biology</i> , 2014, 29, 143-151.	5.7	25
60	Retinal proteins – You can teach an old dog new tricks. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, 531-532.	1.0	6
61	Structural basis for recognition of synaptic vesicle protein 2C by botulinum neurotoxin A. <i>Nature</i> , 2014, 505, 108-111.	27.8	103
62	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
63	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
64	Production of GPCR and GPCR complexes for structure determination. <i>Current Opinion in Structural Biology</i> , 2013, 23, 381-392.	5.7	37
65	Two Alternative Conformations of a Voltage-Gated Sodium Channel. <i>Journal of Molecular Biology</i> , 2013, 425, 4074-4088.	4.2	59
66	Molecular signatures of G-protein-coupled receptors. <i>Nature</i> , 2013, 494, 185-194.	27.8	1,298
67	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
68	Structure of $\beta_2$ -Adrenergic Receptors. <i>Methods in Enzymology</i> , 2013, 520, 117-151.	1.0	9
69	Insights into congenital stationary night blindness based on the structure of G90D rhodopsin. <i>EMBO Reports</i> , 2013, 14, 520-526.	4.5	79
70	G Protein–Coupled Receptor Activation Based on X-ray Structural Studies. , 2013, , 877-881.		0
71	Stabilized G protein binding site in the structure of constitutively active metarhodopsin-II. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 119-124.	7.1	226
72	Ligands Stabilize Specific GPCR Conformations: But How?. <i>Structure</i> , 2012, 20, 1289-1290.	3.3	6

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73	Conserved activation pathways in G-protein-coupled receptors. <i>Biochemical Society Transactions</i> , 2012, 40, 383-388.	3.4	43
74	Preparation of an Activated Rhodopsin/Transducin Complex Using a Constitutively Active Mutant of Rhodopsin. <i>Biochemistry</i> , 2011, 50, 10399-10407.	2.5	16
75	The structural basis for agonist and partial agonist action on a $\beta_2$ -adrenergic receptor. <i>Nature</i> , 2011, 469, 241-244.	27.8	592
76	The structural basis of agonist-induced activation in constitutively active rhodopsin. <i>Nature</i> , 2011, 471, 656-660.	27.8	444
77	Membranes. <i>Current Opinion in Structural Biology</i> , 2011, 21, 495-496.	5.7	1
78	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
79	â€œ4D Biology for health and diseaseâ€workshop report. <i>New Biotechnology</i> , 2011, 28, 291-293.	4.4	2
80	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
81	Tracking G-protein-coupled receptor activation using genetically encoded infrared probes. <i>Nature</i> , 2010, 464, 1386-1389.	27.8	245
82	Spial: analysis of subtype-specific features in multiple sequence alignments of proteins. <i>Bioinformatics</i> , 2010, 26, 2906-2907.	4.1	7
83	Engineering G protein-coupled receptors to facilitate their structure determination. <i>Current Opinion in Structural Biology</i> , 2009, 19, 386-395.	5.7	169
84	Development and crystallization of a minimal thermostabilised G protein-coupled receptor. <i>Protein Expression and Purification</i> , 2009, 65, 204-213.	1.3	90
85	Crystal Structures of the $\beta_2$ -Adrenergic Receptor. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2009, , 217-230.	0.5	0
86	Protein crystallization: robotics, procedures and developments. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2009, 65, s158-s159.	0.3	0
87	Protein crystallography with a micrometre-sized synchrotron-radiation beam. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 158-166.	2.5	77
88	Structure of a $\beta_1$ -adrenergic G-protein-coupled receptor. <i>Nature</i> , 2008, 454, 486-491.	27.8	1,334
89	The rhodopsin story continued. <i>Nature</i> , 2008, 453, 292-293.	27.8	25
90	New G-protein-coupled receptor crystal structures: insights and limitations. <i>Trends in Pharmacological Sciences</i> , 2008, 29, 79-83.	8.7	217

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91	Crystal Structure of a Thermally Stable Rhodopsin Mutant. <i>Journal of Molecular Biology</i> , 2007, 372, 1179-1188.	4.2	218
92	Crystal structure of the human $\beta_2$ adrenergic G-protein-coupled receptor. <i>Nature</i> , 2007, 450, 383-387.	27.8	1,832
93	Rhodopsin Photointermediates in Two-Dimensional Crystals at Physiological Temperatures. <i>Biochemistry</i> , 2006, 45, 4974-4982.	2.5	10
94	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
95	Structure of rhodopsin and the metarhodopsin I photointermediate. <i>Current Opinion in Structural Biology</i> , 2005, 15, 408-415.	5.7	88
96	Protein crystallography microdiffraction. <i>Current Opinion in Structural Biology</i> , 2005, 15, 556-562.	5.7	107
97	Electron crystallography reveals the structure of metarhodopsin I. <i>EMBO Journal</i> , 2004, 23, 3609-3620.	7.8	300
98	Rhodopsin Photoproducts in 2D Crystals. <i>Journal of Molecular Biology</i> , 2004, 338, 597-609.	4.2	36
99	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
100	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
101	Structure of Bovine Rhodopsin in a Trigonal Crystal Form. <i>Journal of Molecular Biology</i> , 2004, 343, 1409-1438.	4.2	720
102	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
103	The Three-dimensional Structure of Bovine Rhodopsin Determined by Electron Cryomicroscopy. <i>Journal of Biological Chemistry</i> , 2003, 278, 50217-50225.	3.4	43
104	Electrons and X-Rays Reveal the Structure of Rhodopsin: A Prototypical G Protein-Coupled Receptor-Implications for Colour Vision. , 2003, , 3-13.		0
105	Electron Crystallographic Studies of Rhodopsin. <i>Phase Transitions</i> , 2002, 75, 1-10.	1.3	0
106	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
107	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
108	Three-dimensional structure of an invertebrate rhodopsin and basis for ordered alignment in the photoreceptor membrane 1 1 Edited by D. Rees. <i>Journal of Molecular Biology</i> , 2001, 314, 455-463.	4.2	73

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109	[7] Preparation and analysis of two-dimensional crystals of rhodopsin. <i>Methods in Enzymology</i> , 2000, 315, 91-107.	1.0	19
110	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
111	Characterisation of an improved two-dimensional p22121 crystal from bovine rhodopsin. <i>Journal of Molecular Biology</i> , 1998, 282, 991-1003.	4.2	103
112	Structure of rhodopsin. <i>Eye</i> , 1998, 12, 504-510.	2.1	62
113	An alpha-carbon template for the transmembrane helices in the rhodopsin family of G-protein-coupled receptors 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1997, 272, 144-164.	4.2	642
114	Arrangement of rhodopsin transmembrane $\alpha$ -helices. <i>Nature</i> , 1997, 389, 203-206.	27.8	486
115	Projection Structure of an Invertebrate Rhodopsin. <i>Journal of Structural Biology</i> , 1996, 117, 36-44.	2.8	65
116	Projection structure of frog rhodopsin in two crystal forms.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 11578-11582.	7.1	226
117	The greasy world of membrane proteins. <i>Trends in Cell Biology</i> , 1995, 5, 290-291.	7.9	0
118	Low resolution structure of bovine rhodopsin determined by electron cryo-microscopy. <i>Biophysical Journal</i> , 1995, 68, 1776-1786.	0.5	298
119	Projection structure of rhodopsin. <i>Nature</i> , 1993, 362, 770-772.	27.8	877
120	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
121	Overproduction of membrane proteins. <i>Current Opinion in Structural Biology</i> , 1992, 2, 534-544.	5.7	103