

# Gunnar F. Schröder

## List of Publications by Year in descending order

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71  
papers

7,444  
citations

101543

36  
h-index

110387

64  
g-index

78  
all docs

78  
docs citations

78  
times ranked

10441  
citing authors

#	ARTICLE	IF	CITATIONS
1	Major tail proteins of bacteriophages of the order Caudovirales. <i>Journal of Biological Chemistry</i> , 2022, 298, 101472.	3.4	37
2	High-Resolution Cryo-EM Structure of the Cardiac Actomyosin Complex. <i>Structure</i> , 2021, 29, 50-60.e4.	3.3	41
3	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. <i>Nature Methods</i> , 2021, 18, 156-164.	19.0	73
4	Clustering polymorphs of tau and IAPP fibrils with the CHEP algorithm. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 160, 16-25.	2.9	10
5	Amyloid-type Protein Aggregation and Prion-like Properties of Amyloids. <i>Chemical Reviews</i> , 2021, 121, 8285-8307.	47.7	98
6	Endo-lysosomal A $\beta$ concentration and pH trigger formation of A $\beta$ oligomers that potently induce Tau missorting. <i>Nature Communications</i> , 2021, 12, 4634.	12.8	59
7	Challenges in sample preparation and structure determination of amyloids by cryo-EM. <i>Journal of Biological Chemistry</i> , 2021, 297, 100938.	3.4	20
8	The <i>Uppsala APP</i> deletion causes early onset autosomal dominant Alzheimer's disease by altering APP processing and increasing amyloid $\beta$ fibril formation. <i>Science Translational Medicine</i> , 2021, 13, .	12.4	23
9	Conformational heterogeneity coupled with $\beta$ -fibril formation of a scaffold protein involved in chronic mental illnesses. <i>Translational Psychiatry</i> , 2021, 11, 639.	4.8	9
10	Engineering and application of a biosensor with focused ligand specificity. <i>Nature Communications</i> , 2020, 11, 4851.	12.8	56
11	Atomistic structure and dynamics of the human MHC-I peptide-loading complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20597-20606.	7.1	40
12	Architecture of the flexible tail tube of bacteriophage SPP1. <i>Nature Communications</i> , 2020, 11, 5759.	12.8	37
13	Cryo-EM structure of islet amyloid polypeptide fibrils reveals similarities with amyloid- $\beta$ fibrils. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 660-667.	8.2	120
14	Integrating cryo-EM and NMR data. <i>Current Opinion in Structural Biology</i> , 2020, 61, 173-181.	5.7	23
15	Atomic structure of PI3-kinase SH3 amyloid fibrils by cryo-electron microscopy. <i>Nature Communications</i> , 2019, 10, 3754.	12.8	32
16	$\beta$ -Synuclein-derived lipoparticles in the study of $\beta$ -Synuclein amyloid fibril formation. <i>Chemistry and Physics of Lipids</i> , 2019, 220, 57-65.	3.2	9
17	Integrated NMR, Fluorescence, and Molecular Dynamics Benchmark Study of Protein Mechanics and Hydrodynamics. <i>Journal of Physical Chemistry B</i> , 2019, 123, 1453-1480.	2.6	29
18	Clustering cryo-EM images of helical protein polymers for helical reconstructions. <i>Ultramicroscopy</i> , 2019, 203, 132-138.	1.9	9

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19	N-Terminal Domains of Cardiac Myosin Binding Protein C Cooperatively Activate the Thin Filament. <i>Structure</i> , 2018, 26, 1604-1611.e4.	3.3	57
20	Ca <sup>2+</sup> -induced movement of tropomyosin on native cardiac thin filaments revealed by cryoelectron microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 6782-6787.	7.1	63
21	Conformational Heterogeneity in a Fully Complementary DNA Three-Way Junction with a GC-Rich Branchpoint. <i>Biochemistry</i> , 2017, 56, 4985-4991.	2.5	12
22	Fibril structure of amyloid- $\beta$ (1-42) by cryo-electron microscopy. <i>Science</i> , 2017, 358, 116-119.	12.6	801
23	Protein structure refinement with adaptively restrained homologous replicas. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 302-313.	2.6	10
24	Archaeal flagellin combines a bacterial type IV pilin domain with an Ig-like domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10352-10357.	7.1	49
25	The pathway to GTPase activation of elongation factor SelB on the ribosome. <i>Nature</i> , 2016, 540, 80-85.	27.8	93
26	$\beta$ -Hairpin of Islet Amyloid Polypeptide Bound to an Aggregation Inhibitor. <i>Scientific Reports</i> , 2016, 6, 33474.	3.3	34
27	Near-Atomic Resolution for One State of F-Actin. <i>Structure</i> , 2015, 23, 173-182.	3.3	121
28	Archaeal actin from a hyperthermophile forms a single-stranded filament. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9340-9345.	7.1	22
29	Improving the visualization of cryo-EM density reconstructions. <i>Journal of Structural Biology</i> , 2015, 191, 207-213.	2.8	17
30	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015, 23, 1156-1167.	3.3	159
31	Hybrid methods for macromolecular structure determination: experiment with expectations. <i>Current Opinion in Structural Biology</i> , 2015, 31, 20-27.	5.7	37
32	Coupling an Ensemble of Homologues Improves Refinement of Protein Homology Models. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 5578-5582.	5.3	4
33	Deformable elastic network refinement for low-resolution macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2241-2255.	2.5	29
34	Unified Polymerization Mechanism for the Assembly of ASC-Dependent Inflammasomes. <i>Cell</i> , 2014, 156, 1193-1206.	28.9	1,035
35	Ligand-induced structural changes in the cyclic nucleotide-modulated potassium channel MloK1. <i>Nature Communications</i> , 2014, 5, 3106.	12.8	59
36	Rapid and Stable Transfer RNA Translocation through the Ribosome Ensured by Specific Contact Mechanisms. <i>Biophysical Journal</i> , 2014, 106, 493a.	0.5	0

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37	Ribosomal Kinetics and Concerted Motions from Nanoseconds to Seconds. <i>Biophysical Journal</i> , 2014, 106, 250a.	0.5	0
38	Cryo-Electron Microscopy of Potassium Channel Membrane Proteins. <i>Microscopy and Microanalysis</i> , 2014, 20, 1206-1207.	0.4	0
39	Mechanisms for Efficient tRNA Translocation through the Ribosome. <i>Biophysical Journal</i> , 2013, 104, 16a.	0.5	0
40	Energy barriers and driving forces in tRNA translocation through the ribosome. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1390-1396.	8.2	150
41	Structural Polymorphism of F-Actin is Coupled with its Mechanical Properties. <i>Biophysical Journal</i> , 2013, 104, 644a-645a.	0.5	0
42	Rate Estimates from Sampling Sparse Transitions: tRNA Motion Limits Transitions between Ribosomal Translocation Intermediates. <i>Biophysical Journal</i> , 2013, 104, 663a.	0.5	0
43	The Crystal Structures of the Eukaryotic Chaperonin CCT Reveal Its Functional Partitioning. <i>Structure</i> , 2013, 21, 540-549.	3.3	59
44	Visualizing GroEL/ES in the Act of Encapsulating a Folding Protein. <i>Cell</i> , 2013, 153, 1354-1365.	28.9	102
45	Cross-validation in cryo-EM based structural modeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 8930-8935.	7.1	42
46	Small-angle X-ray Scattering of Apolipoprotein A-IV Reveals the Importance of Its Termini for Structural Stability. <i>Journal of Biological Chemistry</i> , 2013, 288, 4854-4866.	3.4	10
47	Symmetry-free cryo-EM structures of the chaperonin TRiC along its ATPase-driven conformational cycle. <i>EMBO Journal</i> , 2012, 31, 720-730.	7.8	80
48	Remodeling of Actin Filaments by Cofilin. <i>Biophysical Journal</i> , 2012, 102, 238a.	0.5	0
49	Filaments from <i>Ignicoccus hospitalis</i> Show Diversity of Packing in Proteins Containing N-Terminal Type IV Pilin Helices. <i>Journal of Molecular Biology</i> , 2012, 422, 274-281.	4.2	40
50	Dynamic, Energetic, and Kinetic Determinants of Ribosomal Translocation: Microsecond All-Atom Simulations of Hybrid Cryoem/X-Ray Structural Substates. <i>Biophysical Journal</i> , 2012, 102, 67a.	0.5	0
51	Branchpoint Expansion in a Fully Complementary Three-Way DNA Junction. <i>Journal of the American Chemical Society</i> , 2012, 134, 6280-6285.	13.7	44
52	A grid-enabled web service for low-resolution crystal structure refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 261-267.	2.5	17
53	Improving the Accuracy of Macromolecular Structure Refinement at 7 Å Resolution. <i>Structure</i> , 2012, 20, 957-966.	3.3	37
54	Real-space refinement with DireX: From global fitting to side-chain improvements. <i>Biopolymers</i> , 2012, 97, 687-697.	2.4	52

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55	Application of DEN refinement and automated model building to a difficult case of molecular-replacement phasing: the structure of a putative succinyl-diaminopimelate desuccinylase from <i>Corynebacterium glutamicum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 391-403.	2.5	26
56	Global Structure of Forked DNA in Solution Revealed by High-Resolution Single-Molecule FRET. <i>Journal of the American Chemical Society</i> , 2011, 133, 1188-1191.	13.7	36
57	Structure of Myxovirus Resistance Protein A Reveals Intra- and Intermolecular Domain Interactions Required for the Antiviral Function. <i>Immunity</i> , 2011, 35, 514-525.	14.3	188
58	Remodeling of actin filaments by ADF/cofilin proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20568-20572.	7.1	194
59	The refined structure of functional unit h of keyhole limpet hemocyanin (KLH) reveals disulfide bridges. <i>IUBMB Life</i> , 2011, 63, 183-187.	3.4	23
60	A Spring-loaded Release Mechanism Regulates Domain Movement and Catalysis in Phosphoglycerate Kinase. <i>Journal of Biological Chemistry</i> , 2011, 286, 14040-14048.	3.4	53
61	Structural polymorphism in F-actin. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1318-1323.	8.2	170
62	Mechanism of folding chamber closure in a group II chaperonin. <i>Nature</i> , 2010, 463, 379-383.	27.8	196
63	Super-resolution biomolecular crystallography with low-resolution data. <i>Nature</i> , 2010, 464, 1218-1222.	27.8	267
64	Recognition Dynamics Up to Microseconds Revealed from an RDC-Derived Ubiquitin Ensemble in Solution. <i>Science</i> , 2008, 320, 1471-1475.	12.6	963
65	Single-molecule FRET measures bends and kinks in DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 18337-18342.	7.1	172
66	Combining Efficient Conformational Sampling with a Deformable Elastic Network Model Facilitates Structure Refinement at Low Resolution. <i>Structure</i> , 2007, 15, 1630-1641.	3.3	213
67	Detecting protein-induced folding of the U4 snRNA kink-turn by single-molecule multiparameter FRET measurements. <i>Rna</i> , 2005, 11, 1545-1554.	3.5	46
68	Simulation of Fluorescence Anisotropy Experiments: Probing Protein Dynamics. <i>Biophysical Journal</i> , 2005, 89, 3757-3770.	0.5	128
69	FRETsg: Biomolecular structure model building from multiple FRET experiments. <i>Computer Physics Communications</i> , 2004, 158, 150-157.	7.5	20
70	Maximum likelihood trajectories from single molecule fluorescence resonance energy transfer experiments. <i>Journal of Chemical Physics</i> , 2003, 119, 9920-9924.	3.0	62
71	Single-molecule fluorescence resonance energy transfer reveals a dynamic equilibrium between closed and open conformations of syntaxin 1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15516-15521.	7.1	268