

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	Unified Polymerization Mechanism for the Assembly of ASC-Dependent Inflammasomes. <i>Cell</i> , 2014, 156, 1193-1206.	28.9	1,035
2	Recognition Dynamics Up to Microseconds Revealed from an RDC-Derived Ubiquitin Ensemble in Solution. <i>Science</i> , 2008, 320, 1471-1475.	12.6	963
3	Fibril structure of amyloid- β (1-42) by cryo-electron microscopy. <i>Science</i> , 2017, 358, 116-119.	12.6	801
4	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
5	Super-resolution biomolecular crystallography with low-resolution data. <i>Nature</i> , 2010, 464, 1218-1222.	27.8	267
6	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
7	Mechanism of folding chamber closure in a group II chaperonin. <i>Nature</i> , 2010, 463, 379-383.	27.8	196
8	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
9	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
10	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
11	Structural polymorphism in F-actin. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1318-1323.	8.2	170
12	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015, 23, 1156-1167.	3.3	159
13	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
14	Simulation of Fluorescence Anisotropy Experiments: Probing Protein Dynamics. <i>Biophysical Journal</i> , 2005, 89, 3757-3770.	0.5	128
15	Near-Atomic Resolution for One State of F-Actin. <i>Structure</i> , 2015, 23, 173-182.	3.3	121
16	Cryo-EM structure of islet amyloid polypeptide fibrils reveals similarities with amyloid- β fibrils. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 660-667.	8.2	120
17	Visualizing GroEL/ES in the Act of Encapsulating a Folding Protein. <i>Cell</i> , 2013, 153, 1354-1365.	28.9	102
18	Amyloid-type Protein Aggregation and Prion-like Properties of Amyloids. <i>Chemical Reviews</i> , 2021, 121, 8285-8307.	47.7	98

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19	The pathway to GTPase activation of elongation factor SelB on the ribosome. <i>Nature</i> , 2016, 540, 80-85.	27.8	93
20	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
21	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. <i>Nature Methods</i> , 2021, 18, 156-164.	19.0	73
22	Ca ²⁺ -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
23	Maximum likelihood trajectories from single molecule fluorescence resonance energy transfer experiments. <i>Journal of Chemical Physics</i> , 2003, 119, 9920-9924.	3.0	62
24	The Crystal Structures of the Eukaryotic Chaperonin CCT Reveal Its Functional Partitioning. <i>Structure</i> , 2013, 21, 540-549.	3.3	59
25	Ligand-induced structural changes in the cyclic nucleotide-modulated potassium channel MloK1. <i>Nature Communications</i> , 2014, 5, 3106.	12.8	59
26	Endo-lysosomal A β concentration and pH trigger formation of A β oligomers that potently induce Tau missorting. <i>Nature Communications</i> , 2021, 12, 4634.	12.8	59
27	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
28	Engineering and application of a biosensor with focused ligand specificity. <i>Nature Communications</i> , 2020, 11, 4851.	12.8	56
29	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
30	Real-space refinement with DireX: From global fitting to side-chain improvements. <i>Biopolymers</i> , 2012, 97, 687-697.	2.4	52
31	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
32	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
33	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
34	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
35	High-Resolution Cryo-EM Structure of the Cardiac Actomyosin Complex. <i>Structure</i> , 2021, 29, 50-60.e4.	3.3	41
36	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

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37	Atomistic structure and dynamics of the human MHC-I peptide-loading complex. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 20597-20606.	7.1	40
38	Improving the Accuracy of Macromolecular Structure Refinement at 7Å... Resolution. Structure, 2012, 20, 957-966.	3.3	37
39	Hybrid methods for macromolecular structure determination: experiment with expectations. Current Opinion in Structural Biology, 2015, 31, 20-27.	5.7	37
40	Architecture of the flexible tail tube of bacteriophage SPP1. Nature Communications, 2020, 11, 5759.	12.8	37
41	Major tail proteins of bacteriophages of the order Caudovirales. Journal of Biological Chemistry, 2022, 298, 101472.	3.4	37
42	Global Structure of Forked DNA in Solution Revealed by High-Resolution Single-Molecule FRET. Journal of the American Chemical Society, 2011, 133, 1188-1191.	13.7	36
43	Î²-Hairpin of Islet Amyloid Polypeptide Bound to an Aggregation Inhibitor. Scientific Reports, 2016, 6, 33474.	3.3	34
44	Atomic structure of PI3-kinase SH3 amyloid fibrils by cryo-electron microscopy. Nature Communications, 2019, 10, 3754.	12.8	32
45	Deformable elastic network refinement for low-resolution macromolecular crystallography. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2241-2255.	2.5	29
46	Integrated NMR, Fluorescence, and Molecular Dynamics Benchmark Study of Protein Mechanics and Hydrodynamics. Journal of Physical Chemistry B, 2019, 123, 1453-1480.	2.6	29
47	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> . Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 391-403.	2.5	26
48	The refined structure of functional unit h of keyhole limpet hemocyanin (KLH1â€h) reveals disulfide bridges. IUBMB Life, 2011, 63, 183-187.	3.4	23
49	Integrating cryo-EM and NMR data. Current Opinion in Structural Biology, 2020, 61, 173-181.	5.7	23
50	The <i>Uppsala APP</i> deletion causes early onset autosomal dominant Alzheimerâ€™s disease by altering APP processing and increasing amyloid Î² fibril formation. Science Translational Medicine, 2021, 13, .	12.4	23
51	Archaeal actin from a hyperthermophile forms a single-stranded filament. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9340-9345.	7.1	22
52	FRETsg: Biomolecular structure model building from multiple FRET experiments. Computer Physics Communications, 2004, 158, 150-157.	7.5	20
53	Challenges in sample preparation and structure determination of amyloids by cryo-EM. Journal of Biological Chemistry, 2021, 297, 100938.	3.4	20
54	A grid-enabled web service for low-resolution crystal structure refinement. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 261-267.	2.5	17

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55	Improving the visualization of cryo-EM density reconstructions. <i>Journal of Structural Biology</i> , 2015, 191, 207-213.	2.8	17
56	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
57	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
58	Protein structure refinement with adaptively restrained homologous replicas. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 302-313.	2.6	10
59	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
60	Î±-Synuclein-derived lipoparticles in the study of Î±-Synuclein amyloid fibril formation. <i>Chemistry and Physics of Lipids</i> , 2019, 220, 57-65.	3.2	9
61	Clustering cryo-EM images of helical protein polymers for helical reconstructions. <i>Ultramicroscopy</i> , 2019, 203, 132-138.	1.9	9
62	Conformational heterogeneity coupled with Î²-fibril formation of a scaffold protein involved in chronic mental illnesses. <i>Translational Psychiatry</i> , 2021, 11, 639.	4.8	9
63	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
64	Remodeling of Actin Filaments by Cofilin. <i>Biophysical Journal</i> , 2012, 102, 238a.	0.5	0
65	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
66	Mechanisms for Efficient tRNA Translocation through the Ribosome. <i>Biophysical Journal</i> , 2013, 104, 16a.	0.5	0
67	Structural Polymorphism of F-Actin is Coupled with its Mechanical Properties. <i>Biophysical Journal</i> , 2013, 104, 644a-645a.	0.5	0
68	Rate Estimates from Sampling Sparse Transitions: tRNA Motion Limits Transitions between Ribosomal Translocation Intermediates. <i>Biophysical Journal</i> , 2013, 104, 663a.	0.5	0
69	Rapid and Stable Transfer RNA Translocation through the Ribosome Ensured by Specific Contact Mechanisms. <i>Biophysical Journal</i> , 2014, 106, 493a.	0.5	0
70	Ribosomal Kinetics and Concerted Motions from Nanoseconds to Seconds. <i>Biophysical Journal</i> , 2014, 106, 250a.	0.5	0
71	Cryo-Electron Microscopy of Potassium Channel Membrane Proteins. <i>Microscopy and Microanalysis</i> , 2014, 20, 1206-1207.	0.4	0