

Marius Schmidt

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

84
papers

3,453
citations

29
h-index

57
g-index

92
ext. papers

3,974
ext. citations

7.4
avg, IF

5.22
L-index

#	Paper	IF	Citations
84	Co-flow injection for serial crystallography at X-ray free-electron lasers.. <i>Journal of Applied Crystallography</i> , 2022 , 55, 1-13	3.8	3
83	Transient state measurements on proteins by time-resolved crystallography.. <i>Current Opinion in Structural Biology</i> , 2022 , 74, 102376	8.1	0
82	Few-fs resolution of a photoactive protein traversing a conical intersection. <i>Nature</i> , 2021 , 599, 697-701	50.4	9
81	Macromolecular movies, storybooks written by nature.. <i>Biophysical Reviews</i> , 2021 , 13, 1191-1197	3.7	0
80	Early-stage dynamics of chloride ion-pumping rhodopsin revealed by a femtosecond X-ray laser. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	14
79	X-ray-Based Techniques to Study the Nano-Bio Interface. <i>ACS Nano</i> , 2021 , 15, 3754-3807	16.7	18
78	High-resolution crystal structures of transient intermediates in the phytochrome photocycle. <i>Structure</i> , 2021 , 29, 743-754.e4	5.2	8
77	The three-dimensional structure of <i>Drosophila melanogaster</i> (6-4) photolyase at room temperature. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021 , 77, 1001-1009	5.5	0
76	Synchronous RNA conformational changes trigger ordered phase transitions in crystals. <i>Nature Communications</i> , 2021 , 12, 1762	17.4	12
75	Observation of substrate diffusion and ligand binding in enzyme crystals using high-repetition-rate mix-and-inject serial crystallography. <i>IUCrJ</i> , 2021 , 8, 878-895	4.7	9
74	Single-particle imaging by x-ray free-electron lasers-How many snapshots are needed?. <i>Structural Dynamics</i> , 2020 , 7, 024102	3.2	13
73	Reaction Initiation in Enzyme Crystals by Diffusion of Substrate. <i>Crystals</i> , 2020 , 10, 116	2.3	15
72	The primary structural photoresponse of phytochrome proteins captured by a femtosecond X-ray laser. <i>ELife</i> , 2020 , 9,	8.9	37
71	Time-resolved serial femtosecond crystallography at the European XFEL. <i>Nature Methods</i> , 2020 , 17, 73-78	21.6	50
70	Time-Resolved Macromolecular Crystallography at Pulsed X-ray Sources. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	23
69	Protein and RNA dynamical fingerprinting. <i>Nature Communications</i> , 2019 , 10, 1026	17.4	35
68	Trapping of a Putative Intermediate in the Cytochrome Nitrite Reductase (ccNiR)-Catalyzed Reduction of Nitrite: Implications for the ccNiR Reaction Mechanism. <i>Journal of the American Chemical Society</i> , 2019 , 141, 13358-13371	16.4	10

67	High-resolution crystal structures of a myxobacterial phytochrome at cryo and room temperatures. <i>Structural Dynamics</i> , 2019 , 6, 054701	3.2	14
66	Membrane protein megahertz crystallography at the European XFEL. <i>Nature Communications</i> , 2019 , 10, 5021	17.4	29
65	Evaluation of serial crystallographic structure determination within megahertz pulse trains. <i>Structural Dynamics</i> , 2019 , 6, 064702	3.2	14
64	Enzyme intermediates captured "on the fly" by mix-and-inject serial crystallography. <i>BMC Biology</i> , 2018 , 16, 59	7.3	73
63	Structural basis for light control of cell development revealed by crystal structures of a myxobacterial phytochrome. <i>IUCrJ</i> , 2018 , 5, 619-634	4.7	20
62	Towards Molecular Movies of Enzymes 2018 , 357-376		
61	Megahertz serial crystallography. <i>Nature Communications</i> , 2018 , 9, 4025	17.4	104
60	Structural enzymology using X-ray free electron lasers. <i>Structural Dynamics</i> , 2017 , 4, 044003	3.2	75
59	A short history of structure based research on the photocycle of photoactive yellow protein. <i>Structural Dynamics</i> , 2017 , 4, 032201	3.2	16
58	Watching Proteins Function with Time-resolved X-ray Crystallography. <i>Journal Physics D: Applied Physics</i> , 2017 , 50,	3	34
57	Conformational landscape of a virus by single-particle X-ray scattering. <i>Nature Methods</i> , 2017 , 14, 877-881	11.6	45
56	Time-Resolved Macromolecular Crystallography at Modern X-Ray Sources. <i>Methods in Molecular Biology</i> , 2017 , 1607, 273-294	1.4	9
55	The room temperature crystal structure of a bacterial phytochrome determined by serial femtosecond crystallography. <i>Scientific Reports</i> , 2016 , 6, 35279	4.9	29
54	Photocycle populations with femtosecond excitation of crystalline photoactive yellow protein. <i>Chemical Physics Letters</i> , 2016 , 654, 63-71	2.5	25
53	Macromolecular diffractive imaging using imperfect crystals. <i>Nature</i> , 2016 , 530, 202-6	50.4	101
52	Femtosecond structural dynamics drives the trans/cis isomerization in photoactive yellow protein. <i>Science</i> , 2016 , 352, 725-9	33.3	276
51	Towards time-resolved serial crystallography in a microfluidic device. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 823-30	1.1	27
50	Room temperature structures beyond 1.5 Å by serial femtosecond crystallography. <i>Structural Dynamics</i> , 2015 , 2, 041708	3.2	9

49	Simulations on time-resolved structure determination of uncrystallized biomolecules in the presence of shot noise. <i>Structural Dynamics</i> , 2015 , 2, 024103	3.2	3
48	Time-Resolved Crystallography at X-ray Free Electron Lasers and Synchrotron Light Sources. <i>Synchrotron Radiation News</i> , 2015 , 28, 25-30	0.6	7
47	Reply to 'contradictions in X-ray structures of intermediates in the photocycle of photoactive yellow protein'. <i>Nature Chemistry</i> , 2014 , 6, 259-60	17.6	20
46	Enzyme transient state kinetics in crystal and solution from the perspective of a time-resolved crystallographer. <i>Structural Dynamics</i> , 2014 , 1, 024701	3.2	7
45	Signal to noise considerations for single crystal femtosecond time resolved crystallography of the Photoactive Yellow Protein. <i>Faraday Discussions</i> , 2014 , 171, 439-55	3.6	14
44	Time-resolved serial crystallography captures high-resolution intermediates of photoactive yellow protein. <i>Science</i> , 2014 , 346, 1242-6	33.3	33 ⁸
43	Deducing fast electron density changes in randomly orientated uncrystallized biomolecules in a pump-probe experiment. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2014 , 369, 20130332	5.8	18
42	Field-enhanced magnetic moment in ellipsoidal nano-hematite. <i>Materials Research Express</i> , 2014 , 1, 026114	1.4	7
41	Volume-conserving trans-cis isomerization pathways in photoactive yellow protein visualized by picosecond X-ray crystallography. <i>Nature Chemistry</i> , 2013 , 5, 212-20	17.6	13 ⁸
40	Spectroscopic studies of model photo-receptors: validation of a nanosecond time-resolved micro-spectrophotometer design using photoactive yellow protein and Φ phycoerythrocyanin. <i>International Journal of Molecular Sciences</i> , 2013 , 14, 18881-98	6.3	9
39	Protein energy landscapes determined by five-dimensional crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013 , 69, 2534-42		42
38	Extraction of Fast Changes in the Structure of a Disordered Ensemble of Photoexcited Biomolecules. <i>Advances in Condensed Matter Physics</i> , 2013 , 2013, 1-5	1	5
37	Mix and Inject: Reaction Initiation by Diffusion for Time-Resolved Macromolecular Crystallography. <i>Advances in Condensed Matter Physics</i> , 2013 , 2013, 1-10	1	80
36	The kinetic dose limit in room-temperature time-resolved macromolecular crystallography. <i>Journal of Synchrotron Radiation</i> , 2012 , 19, 264-73	2.4	15
35	Colloidal crystallization and structural changes in suspensions of silica/magnetite core-shell nanoparticles. <i>Langmuir</i> , 2012 , 28, 14777-83	4	42
34	pH dependence of the photoactive yellow protein photocycle investigated by time-resolved crystallography. <i>Biophysical Journal</i> , 2012 , 102, 325-32	2.9	34
33	Laue crystal structure of <i>Shewanella oneidensis</i> cytochrome c nitrite reductase from a high-yield expression system. <i>Journal of Biological Inorganic Chemistry</i> , 2012 , 17, 647-62	3.7	42
32	Reconstructing an icosahedral virus from single-particle diffraction experiments. <i>Optics Express</i> , 2011 , 19, 17318-35	3.3	44

31	Interaction of nitric oxide with catalase: structural and kinetic analysis. <i>Biochemistry</i> , 2011 , 50, 4491-503	3.2	64
30	Five-dimensional crystallography. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2010 , 66, 198-206		29
29	Protein dynamics of a beta-sheet protein. <i>European Biophysics Journal</i> , 2009 , 38, 687-700	1.9	12
28	New software for the singular value decomposition of time-resolved crystallographic data. <i>Journal of Applied Crystallography</i> , 2009 , 42, 734-740	3.8	10
27	Structure Based Kinetics by Time-Resolved X-ray Crystallography 2008 , 201-241		14
26	Structural basis for the photochemistry of alpha-phycoerythrocyanin. <i>Biochemistry</i> , 2007 , 46, 416-23	3.2	38
25	A physical picture of protein dynamics and conformational changes. <i>Journal of Biological Physics</i> , 2007 , 33, 371-87	1.6	18
24	Protein dynamics on different timescales. <i>Journal of Non-Crystalline Solids</i> , 2006 , 352, 4371-4378	3.9	11
23	Local protein flexibility as a prerequisite for reversible chromophore isomerization in alpha-phycoerythrocyanin. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006 , 1764, 55-62	4	20
22	Ligand migration and protein fluctuations in myoglobin mutant L29W. <i>Biochemistry</i> , 2005 , 44, 5095-105	3.2	40
21	A structural pathway for signaling in the E46Q mutant of photoactive yellow protein. <i>Structure</i> , 2005 , 13, 55-63	5.2	69
20	Protein-ligand interaction probed by time-resolved crystallography. <i>Methods in Molecular Biology</i> , 2005 , 305, 115-54	1.4	27
19	Ligand migration pathway and protein dynamics in myoglobin: a time-resolved crystallographic study on L29W MbCO. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 11704-9	11.5	146
18	Visualizing reaction pathways in photoactive yellow protein from nanoseconds to seconds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 7145-50	11.5	233
17	Analysis of experimental time-resolved crystallographic data by singular value decomposition. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 860-71		38
16	Protein kinetics: structures of intermediates and reaction mechanism from time-resolved x-ray data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 4799-804	11.5	77
15	Application of singular value decomposition to the analysis of time-resolved macromolecular x-ray data. <i>Biophysical Journal</i> , 2003 , 84, 2112-29	2.9	111
14	Protein conformational relaxation and ligand migration in myoglobin: a nanosecond to millisecond molecular movie from time-resolved Laue X-ray diffraction. <i>Biochemistry</i> , 2001 , 40, 13802-15	3.2	296

13	Extraction of accurate structure-factor amplitudes from Laue data: wavelength normalization with wiggler and undulator X-ray sources. <i>Journal of Synchrotron Radiation</i> , 2000 , 7, 236-44	2.4	27
12	New techniques in fast time-resolved structure determination. <i>Cellular and Molecular Biology</i> , 2000 , 46, 895-913	1.1	7
11	Manipulating the coordination number of the ferric iron within the cambialistic superoxide dismutase of <i>Propionibacterium shermanii</i> by changing the pH-value A crystallographic analysis. <i>FEBS Journal</i> , 1999 , 262, 117-27		23
10	The structure of the azide coordinated superoxide dismutase of <i>Propionibacterium shermanii</i> investigated by X-ray structure analysis, extended X-ray absorption fine structure, Mössbauer and electron paramagnetic resonance spectroscopy. <i>Inorganica Chimica Acta</i> , 1998 , 275-276, 65-72	2.7	7
9	pH-dependent inhibition by azide and fluoride of the iron superoxide dismutase from <i>Propionibacterium shermanii</i> . <i>Biochemical Journal</i> , 1998 , 331 (Pt 2), 403-7	3.8	20
8	Effect of Lys175 mutation on structure function properties of <i>Propionibacterium shermanii</i> superoxide dismutase. <i>Protein Engineering, Design and Selection</i> , 1997 , 10, 1067-70	1.9	5
7	X-ray structure of the cambialistic superoxide dismutase from <i>Propionibacterium shermanii</i> active with Fe or Mn. <i>Journal of Biological Inorganic Chemistry</i> , 1996 , 1, 532-541	3.7	57
6	Density distributions in the water shell of myoglobin. <i>International Journal of Quantum Chemistry</i> , 1996 , 59, 263-269	2.1	4
5	EXAFS investigation of the active site of iron superoxide dismutase of <i>Escherichia coli</i> and <i>Propionibacterium shermanii</i> . <i>European Biophysics Journal</i> , 1996 , 24, 243-50	1.9	4
4	The hydration shell of myoglobin. <i>European Biophysics Journal</i> , 1992 , 21, 313-20	1.9	20
3	Direct Observation of the Mechanism of Antibiotic Resistance by Mix-and-Inject at the European XFEL		1
2	Single-femtosecond atomic-resolution observation of a protein traversing a conical intersection		1
1	Enzyme Intermediates Captured On-the-fly By Mix-and-Inject Serial Crystallography		1