Marius Schmidt

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Time-resolved serial crystallography captures high-resolution intermediates of photoactive yellow protein. Science, 2014, 346, 1242-1246.	12.6	418
2	Femtosecond structural dynamics drives the trans/cis isomerization in photoactive yellow protein. Science, 2016, 352, 725-729.	12.6	348
3	Protein Conformational Relaxation and Ligand Migration in Myoglobin:  A Nanosecond to Millisecond Molecular Movie from Time-Resolved Laue X-ray Diffraction. Biochemistry, 2001, 40, 13802-13815.	2.5	329
4	From The Cover: Visualizing reaction pathways in photoactive yellow protein from nanoseconds to seconds. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 7145-7150.	7.1	256
5	Volume-conserving trans–cis isomerization pathways in photoactive yellow protein visualized by picosecond X-ray crystallography. Nature Chemistry, 2013, 5, 212-220.	13.6	178
6	Ligand migration pathway and protein dynamics in myoglobin: A time-resolved crystallographic study on L29W MbCO. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 11704-11709.	7.1	153
7	Megahertz serial crystallography. Nature Communications, 2018, 9, 4025.	12.8	147
8	Application of Singular Value Decomposition to the Analysis of Time-Resolved Macromolecular X-Ray Data. Biophysical Journal, 2003, 84, 2112-2129.	0.5	146
9	Macromolecular diffractive imaging using imperfect crystals. Nature, 2016, 530, 202-206.	27.8	123
10	Enzyme intermediates captured "on the fly―by mix-and-inject serial crystallography. BMC Biology, 2018, 16, 59.	3.8	117
11	Time-resolved serial femtosecond crystallography at the European XFEL. Nature Methods, 2020, 17, 73-78.	19.0	110
12	Mix and Inject: Reaction Initiation by Diffusion for Time-Resolved Macromolecular Crystallography. Advances in Condensed Matter Physics, 2013, 2013, 1-10.	1.1	105
13	Structural enzymology using X-ray free electron lasers. Structural Dynamics, 2017, 4, 044003.	2.3	92
14	Protein kinetics: Structures of intermediates and reaction mechanism from time-resolved x-ray data. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 4799-4804.	7.1	88
15	The primary structural photoresponse of phytochrome proteins captured by a femtosecond X-ray laser. ELife, 2020, 9, .	6.0	78
16	Interaction of Nitric Oxide with Catalase: Structural and Kinetic Analysis. Biochemistry, 2011, 50, 4491-4503.	2.5	75
17	A Structural Pathway for Signaling in the E46Q Mutant of Photoactive Yellow Protein. Structure, 2005, 13, 55-63.	3.3	73
18	Protein and RNA dynamical fingerprinting. Nature Communications, 2019, 10, 1026.	12.8	72

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19	X-ray structure of the cambialistic superoxide dismutase from Propionibacterium shermanii active with Fe or Mn. Journal of Biological Inorganic Chemistry, 1996, 1, 532-541.	2.6	60
20	Conformational landscape of a virus by single-particle X-ray scattering. Nature Methods, 2017, 14, 877-881.	19.0	60
21	X-ray-Based Techniques to Study the Nano–Bio Interface. ACS Nano, 2021, 15, 3754-3807.	14.6	60
22	Protein energy landscapes determined by five-dimensional crystallography. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2534-2542.	2.5	56
23	Analysis of experimental time-resolved crystallographic data by singular value decomposition. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 860-871.	2.5	50
24	Laue crystal structure of Shewanella oneidensis cytochrome c nitrite reductase from a high-yield expression system. Journal of Biological Inorganic Chemistry, 2012, 17, 647-662.	2.6	50
25	Membrane protein megahertz crystallography at the European XFEL. Nature Communications, 2019, 10, 5021.	12.8	47
26	Reconstructing an icosahedral virus from single-particle diffraction experiments. Optics Express, 2011, 19, 17318.	3.4	46
27	Colloidal Crystallization and Structural Changes in Suspensions of Silica/Magnetite Core–Shell Nanoparticles. Langmuir, 2012, 28, 14777-14783.	3.5	46
28	Watching proteins function with time-resolved x-ray crystallography. Journal Physics D: Applied Physics, 2017, 50, 373001.	2.8	46
29	Observation of substrate diffusion and ligand binding in enzyme crystals using high-repetition-rate mix-and-inject serial crystallography. IUCrJ, 2021, 8, 878-895.	2.2	44
30	Ligand Migration and Protein Fluctuations in Myoglobin Mutant L29Wâ€,‡. Biochemistry, 2005, 44, 5095-5105.	2.5	41
31	Structural Basis for the Photochemistry of α-Phycoerythrocyaninâ€,‡. Biochemistry, 2007, 46, 416-423.	2.5	41
32	Time-Resolved Macromolecular Crystallography at Pulsed X-ray Sources. International Journal of Molecular Sciences, 2019, 20, 1401.	4.1	41
33	Early-stage dynamics of chloride ion–pumping rhodopsin revealed by a femtosecond X-ray laser. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	41
34	Five-dimensional crystallography. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, 198-206.	0.3	40
35	pH Dependence of the Photoactive Yellow Protein Photocycle Investigated by Time-Resolved Crystallography. Biophysical Journal, 2012, 102, 325-332.	0.5	40
36	The room temperature crystal structure of a bacterial phytochrome determined by serial femtosecond crystallography. Scientific Reports, 2016, 6, 35279.	3.3	39

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37	Reaction Initiation in Enzyme Crystals by Diffusion of Substrate. Crystals, 2020, 10, 116.	2.2	34
38	Structural basis for light control of cell development revealed by crystal structures of a myxobacterial phytochrome. IUCrJ, 2018, 5, 619-634.	2.2	33
39	Few-fs resolution of a photoactive protein traversing a conical intersection. Nature, 2021, 599, 697-701.	27.8	33
40	Photocycle populations with femtosecond excitation of crystalline photoactive yellow protein. Chemical Physics Letters, 2016, 654, 63-71.	2.6	32
41	High-resolution crystal structures of transient intermediates in the phytochrome photocycle. Structure, 2021, 29, 743-754.e4.	3.3	31
42	Extraction of accurate structure-factor amplitudes from Laue data: wavelength normalization with wiggler and undulator X-ray sources. Journal of Synchrotron Radiation, 2000, 7, 236-244.	2.4	30
43	Protein–Ligand Interaction Probed by Time-Resolved Crystallography. , 2005, 305, 115-154.		29
44	Towards time-resolved serial crystallography in a microfluidic device. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 823-830.	0.8	29
45	Evaluation of serial crystallographic structure determination within megahertz pulse trains. Structural Dynamics, 2019, 6, 064702.	2.3	26
46	Single-particle imaging by x-ray free-electron lasers—How many snapshots are needed?. Structural Dynamics, 2020, 7, 024102.	2.3	26
47	Local protein flexibility as a prerequisite for reversible chromophore isomerization in α-phycoerythrocyanin. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2006, 1764, 55-62.	2.3	24
48	Manipulating the coordination mumber of the ferric iron within the cambialistic superoxide dismutase of Propionibacterium shermanii by changing the pH-value . A crystallographic analysis. FEBS Journal, 1999, 262, 117-127.	0.2	23
49	Reply to 'Contradictions in X-ray structures of intermediates in the photocycle of photoactive yellow protein'. Nature Chemistry, 2014, 6, 259-260.	13.6	23
50	The hydration shell of myoglobin. European Biophysics Journal, 1992, 21, 313-20.	2.2	21
51	pH-dependent inhibition by azide and fluoride of the iron superoxide dismutase from Propionibacterium shermanii. Biochemical Journal, 1998, 331, 403-407.	3.7	21
52	A short history of structure based research on the photocycle of photoactive yellow protein. Structural Dynamics, 2017, 4, 032201.	2.3	21
53	A Physical Picture of Protein Dynamics and Conformational Changes. Journal of Biological Physics, 2007, 33, 371-387.	1.5	20
54	The kinetic dose limit in room-temperature time-resolved macromolecular crystallography. Journal of Synchrotron Radiation, 2012, 19, 264-273.	2.4	19

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55	Signal to noise considerations for single crystal femtosecond time resolved crystallography of the Photoactive Yellow Protein. Faraday Discussions, 2014, 171, 439-455.	3.2	19
56	High-resolution crystal structures of a myxobacterial phytochrome at cryo and room temperatures. Structural Dynamics, 2019, 6, 054701.	2.3	19
57	Deducing fast electron density changes in randomly orientated uncrystallized biomolecules in a pump‰probe experiment. Philosophical Transactions of the Royal Society B: Biological Sciences, 2014, 369, 20130332.	4.0	18
58	Structure Based Kinetics by Time-Resolved X-ray Crystallography. Biological and Medical Physics Series, 2008, , 201-241.	0.4	17
59	Trapping of a Putative Intermediate in the Cytochrome <i>c</i> Nitrite Reductase (ccNiR)-Catalyzed Reduction of Nitrite: Implications for the ccNiR Reaction Mechanism. Journal of the American Chemical Society, 2019, 141, 13358-13371.	13.7	17
60	Synchronous RNA conformational changes trigger ordered phase transitions in crystals. Nature Communications, 2021, 12, 1762.	12.8	17
61	Transient state measurements on proteins by time-resolved crystallography. Current Opinion in Structural Biology, 2022, 74, 102376.	5.7	17
62	Time-Resolved Macromolecular Crystallography at Modern X-Ray Sources. Methods in Molecular Biology, 2017, 1607, 273-294.	0.9	15
63	New software for the singular value decomposition of time-resolved crystallographic data. Journal of Applied Crystallography, 2009, 42, 734-740.	4.5	13
64	Protein dynamics on different timescales. Journal of Non-Crystalline Solids, 2006, 352, 4371-4378.	3.1	12
65	Protein dynamics of a β-sheet protein. European Biophysics Journal, 2009, 38, 687-700.	2.2	12
66	Co-flow injection for serial crystallography at X-ray free-electron lasers. Journal of Applied Crystallography, 2022, 55, 1-13.	4.5	12
67	Time-Resolved Crystallography at X-ray Free Electron Lasers and Synchrotron Light Sources. Synchrotron Radiation News, 2015, 28, 25-30.	0.8	11
68	Effect of Lys175 mutation on structure function properties of Propionibacterium shermanii superoxide dismutase. Protein Engineering, Design and Selection, 1997, 10, 1067-1070.	2.1	10
69	Enzyme transient state kinetics in crystal and solution from the perspective of a time-resolved crystallographer. Structural Dynamics, 2014, 1, 024701.	2.3	10
70	The structure of the azide coordinated superoxide dismutase of Propionibacterium shermanii investigated by X-ray structure analysis, extended X-ray absorption fine structure, MA¶ssbauer and electron paramagnetic resonance spectroscopy. Inorganica Chimica Acta, 1998, 275-276, 65-72.	2.4	9
71	Spectroscopic Studies of Model Photo-Receptors: Validation of a Nanosecond Time-Resolved Micro-Spectrophotometer Design Using Photoactive Yellow Protein and α-Phycoerythrocyanin. International Journal of Molecular Sciences, 2013, 14, 18881-18898.	4.1	9
72	Field-enhanced magnetic moment in ellipsoidal nano-hematite. Materials Research Express, 2014, 1, 026114.	1.6	9

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73	Room temperature structures beyond 1.5 à by serial femtosecond crystallography. Structural Dynamics, 2015, 2, 041708.	2.3	9
74	New techniques in fast time-resolved structure determination. Cellular and Molecular Biology, 2000, 46, 895-913.	0.9	9
75	Macromolecular movies, storybooks written by nature. Biophysical Reviews, 2021, 13, 1191-1197.	3.2	8
76	EXAFS investigation of the active site of iron superoxide dismutase of Escherichia coli and Propionibacterium shermanii. European Biophysics Journal, 1996, 24, 243-50.	2.2	7
77	The three-dimensional structure of <i>Drosophila melanogaster</i> (6–4) photolyase at room temperature. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1001-1009.	2.3	7
78	Density distributions in the water shell of myoglobin. International Journal of Quantum Chemistry, 1996, 59, 263-269.	2.0	5
79	Extraction of Fast Changes in the Structure of a Disordered Ensemble of Photoexcited Biomolecules. Advances in Condensed Matter Physics, 2013, 2013, 1-5.	1.1	5
80	Simulations on time-resolved structure determination of uncrystallized biomolecules in the presence of shot noise. Structural Dynamics, 2015, 2, 024103.	2.3	4
81	Towards Molecular Movies of Enzymes. , 2018, , 357-376.		1
82	Structural Dynamics of Photoactive Yellow Protein Investigated by Time Resolved Serial Femtosecond Crystallography. Biophysical Journal, 2016, 110, 374a-375a.	0.5	0