

Vukica Srajer

List of Publications by Year in descending order

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42
papers

3,809
citations

186265

28
h-index

276875

41
g-index

43
all docs

43
docs citations

43
times ranked

3083
citing authors

#	ARTICLE	IF	CITATIONS
1	High-resolution crystal structures of transient intermediates in the phytochrome photocycle. <i>Structure</i> , 2021, 29, 743-754.e4.	3.3	31
2	High-resolution crystal structures of a myxobacterial phytochrome at cryo and room temperatures. <i>Structural Dynamics</i> , 2019, 6, 054701.	2.3	19
3	Watching proteins function with time-resolved x-ray crystallography. <i>Journal Physics D: Applied Physics</i> , 2017, 50, 373001.	2.8	46
4	Electric-field-stimulated protein mechanics. <i>Nature</i> , 2016, 540, 400-405.	27.8	166
5	Graphene-based microfluidics for serial crystallography. <i>Lab on A Chip</i> , 2016, 16, 3082-3096.	6.0	48
6	Femtosecond structural dynamics drives the trans/cis isomerization in photoactive yellow protein. <i>Science</i> , 2016, 352, 725-729.	12.6	348
7	Towards time-resolved serial crystallography in a microfluidic device. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 823-830.	0.8	29
8	<i>In situ</i> serial Laue diffraction on a microfluidic crystallization device. <i>Journal of Applied Crystallography</i> , 2014, 47, 1975-1982.	4.5	29
9	Signal to noise considerations for single crystal femtosecond time resolved crystallography of the Photoactive Yellow Protein. <i>Faraday Discussions</i> , 2014, 171, 439-455.	3.2	19
10	Time-resolved serial crystallography captures high-resolution intermediates of photoactive yellow protein. <i>Science</i> , 2014, 346, 1242-1246.	12.6	418
11	Reply to 'Contradictions in X-ray structures of intermediates in the photocycle of photoactive yellow protein'. <i>Nature Chemistry</i> , 2014, 6, 259-260.	13.6	23
12	Time-Resolved Macromolecular Crystallography in Practice at BioCARS, Advanced Photon Source: From Data Collection to Structures of Intermediates. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2014, , 237-251.	0.5	1
13	Volume-conserving trans \leftrightarrow cis isomerization pathways in photoactive yellow protein visualized by picosecond X-ray crystallography. <i>Nature Chemistry</i> , 2013, 5, 212-220.	13.6	178
14	Resolution of structural heterogeneity in dynamic crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 946-959.	2.5	32
15	Functional Consequences of the Open Distal Pocket of Dehaloperoxidase-Hemoglobin Observed by Time-Resolved X-ray Crystallography. <i>Biochemistry</i> , 2013, 52, 7943-7950.	2.5	3
16	Protein energy landscapes determined by five-dimensional crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2534-2542.	2.5	56
17	Cooperative macromolecular device revealed by meta-analysis of static and time-resolved structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 107-112.	7.1	42
18	pH Dependence of the Photoactive Yellow Protein Photocycle Investigated by Time-Resolved Crystallography. <i>Biophysical Journal</i> , 2012, 102, 325-332.	0.5	40

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19	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, 647-662.	2.6	50
20	Five-dimensional crystallography. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2010, 66, 198-206.	0.3	40
21	Ligand Migration and Cavities within Scapharca Dimeric Hbl: Studies by Time-Resolved Crystallography, Xe Binding, and Computational Analysis. <i>Structure</i> , 2009, 17, 1494-1504.	3.3	60
22	Time-Resolved X-Ray Crystallography of Heme Proteins. <i>Methods in Enzymology</i> , 2008, 437, 379-395.	1.0	17
23	Time-Resolved Crystallographic Studies of the Heme Domain of the Oxygen Sensor FixL: Structural Dynamics of Ligand Rebinding and Their Relation to Signal Transduction. <i>Biochemistry</i> , 2007, 46, 4706-4715.	2.5	45
24	Allosteric action in real time: Time-resolved crystallographic studies of a cooperative dimeric hemoglobin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 7649-7654.	7.1	89
25	A Structural Pathway for Signaling in the E46Q Mutant of Photoactive Yellow Protein. <i>Structure</i> , 2005, 13, 55-63.	3.3	73
26	Protein-Ligand Interaction Probed by Time-Resolved Crystallography. , 2005, 305, 115-154.		29
27	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, 11704-11709.	7.1	153
28	From The Cover: 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, 7145-7150.	7.1	256
29	Structural Heterogeneity of Cryotrapped Intermediates in the Bacterial Blue Light Photoreceptor, Photoactive Yellow Protein. <i>Photochemistry and Photobiology</i> , 2004, 80, 7.	2.5	26
30	Time-resolved crystallographic studies of light-induced structural changes in the photosynthetic reaction center. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 5982-5987.	7.1	65
31	Chromophore Conformation and the Evolution of Tertiary Structural Changes in Photoactive Yellow Protein. <i>Structure</i> , 2004, 12, 1039-1045.	3.3	65
32	Immobilization of Scapharca Hbl crystals improves data quality in time-resolved crystallographic experiments. <i>Micron</i> , 2004, 35, 107-108.	2.2	8
33	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, 4799-4804.	7.1	88
34	Structural Heterogeneity of Cryotrapped Intermediates in the Bacterial Blue Light Photoreceptor, Photoactive Yellow Protein. <i>Photochemistry and Photobiology</i> , 2004, 80, 7-14.	2.5	3
35	Time-resolved capabilities at the advanced photon source. <i>Synchrotron Radiation News</i> , 2003, 16, 21-33.	0.8	1
36	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, 13802-13815.	2.5	329

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37	A Molecular Movie at 1.8 Å... Resolution Displays the Photocycle of Photoactive Yellow Protein, a Eubacterial Blue-Light Receptor, from Nanoseconds to Seconds. <i>Biochemistry</i> , 2001, 40, 13788-13801.	2.5	190
38	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, 236-244.	2.4	30
39	Laue crystallography: coming of age. <i>Journal of Synchrotron Radiation</i> , 1999, 6, 891-917.	2.4	122
40	Initial Trajectory of Carbon Monoxide after Photodissociation from Myoglobin at Cryogenic Temperatures. <i>Biochemistry</i> , 1997, 36, 12087-12100.	2.5	67
41	Structure of a Protein Photocycle Intermediate by Millisecond Time-Resolved Crystallography. <i>Science</i> , 1997, 275, 1471-1475.	12.6	445
42	Optical monitoring of protein crystals in time-resolved x-ray experiments: Microspectrophotometer design and performance. <i>Review of Scientific Instruments</i> , 1994, 65, 1506-1511.	1.3	29