Tobias Weinert

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Structural basis of the radical pair state in photolyases and cryptochromes. Chemical Communications, 2022, 58, 4889-4892.	4.1	9
2	Dynamics and mechanism of a light-driven chloride pump. Science, 2022, 375, 845-851.	12.6	43
3	<i>In Vivo</i> Photocontrol of Microtubule Dynamics and Integrity, Migration and Mitosis, by the Potent GFP-Imaging-Compatible Photoswitchable Reagents SBTubA4P and SBTub2M. Journal of the American Chemical Society, 2022, 144, 5614-5628.	13.7	24
4	A Robust, GFP-Orthogonal Photoswitchable Inhibitor Scaffold Extends Optical Control over the Microtubule Cytoskeleton. Cell Chemical Biology, 2021, 28, 228-241.e6.	5.2	43
5	Pink-beam serial femtosecond crystallography for accurate structure-factor determination at an X-ray free-electron laser. IUCrJ, 2021, 8, 905-920.	2.2	11
6	Femtosecond-to-millisecond structural changes in a light-driven sodium pump. Nature, 2020, 583, 314-318.	27.8	115
7	Membrane Protein Preparation for Serial Crystallography Using High-Viscosity Injectors: Rhodopsin as an Example. Methods in Molecular Biology, 2020, 2127, 321-338.	0.9	2
8	Advances in long-wavelength native phasing at X-ray free-electron lasers. IUCrJ, 2020, 7, 965-975.	2.2	25
9	Structural Basis for Allosteric Ligand Recognition in the Human CC Chemokine Receptor 7. Cell, 2019, 178, 1222-1230.e10.	28.9	81
10	Proton uptake mechanism in bacteriorhodopsin captured by serial synchrotron crystallography. Science, 2019, 365, 61-65.	12.6	117
11	Improving High Viscosity Extrusion of Microcrystals for Time-resolved Serial Femtosecond Crystallography at X-ray Lasers. Journal of Visualized Experiments, 2019, , .	0.3	14
12	Crystal structure of rhodopsin in complex with a mini-G _o sheds light on the principles of G protein selectivity. Science Advances, 2018, 4, eaat7052.	10.3	65
13	CLASP Suppresses Microtubule Catastrophes through a Single TOG Domain. Developmental Cell, 2018, 46, 40-58.e8.	7.0	110
14	In situ serial crystallography for rapid de novo membrane protein structure determination. Communications Biology, 2018, 1, 124.	4.4	27
15	Retinal isomerization in bacteriorhodopsin captured by a femtosecond x-ray laser. Science, 2018, 361, .	12.6	285
16	Structure of the Full-length VEGFR-1 Extracellular Domain in Complex with VEGF-A. Structure, 2017, 25, 341-352.	3.3	77
17	Serial millisecond crystallography for routine room-temperature structure determination at synchrotrons. Nature Communications, 2017, 8, 542.	12.8	203
18	Role of the nucleotidyl cyclase helical domain in catalytically active dimer formation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9821-E9828.	7.1	35

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19	DM9 Domain Containing Protein Functions As a Pattern Recognition Receptor with Broad Microbial Recognition Spectrum. Frontiers in Immunology, 2017, 8, 1607.	4.8	43
20	Data-collection strategy for challenging native SAD phasing. Acta Crystallographica Section D: Structural Biology, 2016, 72, 421-429.	2.3	42
21	<i>In meso in situ</i> serial X-ray crystallography of soluble and membrane proteins at cryogenic temperatures. Acta Crystallographica Section D: Structural Biology, 2016, 72, 93-112.	2.3	91
22	Structural basis of enzymatic benzene ring reduction. Nature Chemical Biology, 2015, 11, 586-591.	8.0	52
23	Fast native-SAD phasing for routine macromolecular structure determination. Nature Methods, 2015, 12, 131-133.	19.0	120
24	PRIGo: a new multi-axis goniometer for macromolecular crystallography. Journal of Synchrotron Radiation, 2015, 22, 895-900.	2.4	52
25	Structure of a methyl-coenzyme M reductase from Black Sea mats that oxidize methane anaerobically. Nature, 2012, 481, 98-101.	27.8	152
26	Structure and Mechanism of the Diiron Benzoyl-Coenzyme A Epoxidase BoxB. Journal of Biological Chemistry, 2011, 286, 29241-29248.	3.4	30