Till Rudack

List of Publications by Year
in descending order

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Version: 2024-02-01

28 papers	2,382 citations	361413 20 h-index	501196 28 g-index
33 all docs	33 docs citations	33 times ranked	3435 citing authors

#	Article	IF	Citations
1	Allosteric control of Ubp6 and the proteasome via a bidirectional switch. Nature Communications, 2022, 13, 838.	12.8	15
2	The Ras dimer structure. Chemical Science, 2021, 12, 8178-8189.	7.4	16
3	Structural insights into photosystem II assembly. Nature Plants, 2021, 7, 524-538.	9.3	102
4	Time-resolved spectroscopic and electrophysiological data reveal insights in the gating mechanism of anion channelrhodopsin. Communications Biology, 2021, 4, 578.	4.4	13
5	Structural basis for VIPP1 oligomerization and maintenance of thylakoid membrane integrity. Cell, 2021, 184, 3643-3659.e23.	28.9	76
6	Lamprey Parapinopsin (â€œUVLamPâ€): a Bistable UVâ€Sensitive Optogenetic Switch for Ultrafast Control of GPCR Pathways. ChemBioChem, 2020, 21, 612-617.	2.6	30
7	The Effect of (â^')-Epigallocatechin-3-Gallate on the Amyloid-Î² Secondary Structure. Biophysical Journal, 2020, 119, 349-359.	0.5	18
8	Insights into the assembly and activation of the microtubule nucleator Î³-TuRC. Nature, 2020, 578, 467-471.	27.8	106
9	GTP Hydrolysis Without an Active Site Base: A Unifying Mechanism for Ras and Related GTPases. Journal of the American Chemical Society, 2019, 141, 10684-10701.	13.7	44
10	Design of an Ultrafast G Protein Switch Based on a Mouse Melanopsin Variant. ChemBioChem, 2019, 20, 1766-1771.	2.6	6
11	Cryo-EM structures of the archaeal PAN-proteasome reveal an around-the-ring ATPase cycle. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 534-539.	7.1	65
12	In Situ Structure of Neuronal C9orf72 Poly-GA Aggregates Reveals Proteasome Recruitment. Cell, 2018, 172, 696-705.e12.	28.9	311
13	PyContact: Rapid, Customizable, and Visual Analysis of Noncovalent Interactions in MD Simulations. Biophysical Journal, 2018, 114, 577-583.	0.5	80
14	NAMD goes quantum: an integrative suite for hybrid simulations. Nature Methods, 2018, 15, 351-354.	19.0	149
15	Expanded Coverage of the 26S Proteasome Conformational Landscape Reveals Mechanisms of Peptidase Gating. Cell Reports, 2018, 24, 1301-1315.e5.	6.4	108
16	Monitoring transient events in infrared spectra using local mode analysis. Proteins: Structure, Function and Bioinformatics, 2018, 86, 1013-1019.	2.6	1
17	Local Mode Analysis: Decoding IR Spectra by Visualizing Molecular Details. Journal of Physical Chemistry B, 2017, 121, 3483-3492.	2.6	6
18	Structural insights into the functional cycle of the ATPase module of the 26S proteasome. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1305-1310.	7.1	151

#	Article	IF	Citations
19	Computational Methodologies for Real-Space Structural Refinement of Large Macromolecular Complexes. Annual Review of Biophysics, 2016, 45, 253-278.	10.0	67
20	QwikMDâ€‰â€”â€‰Integrative Molecular Dynamics Toolkit for Novices and Experts. Scientific Reports, 2016, 6, 26536.	3.3	153
21	Structure of the human 26S proteasome at a resolution of 3.9 Ã…. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7816-7821.	7.1	174
22	Molecular dynamics simulations of large macromolecular complexes. Current Opinion in Structural Biology, 2015, 31, 64-74.	5.7	347
23	Catalysis of GTP Hydrolysis by Small GTPases at Atomic Detail by Integration of X-ray Crystallography, Experimental, and Theoretical IR Spectroscopy. Journal of Biological Chemistry, 2015, 290, 24079-24090.	3.4	20
24	Detailed Structure of the H₂PO₄^{â€“}â€“Guanosine Diphosphate Intermediate in Ras-GAP Decoded from FTIR Experiments by Biomolecular Simulations. Journal of the American Chemical Society, 2012, 134, 20041-20044.	13.7	33
25	Ras and GTPase-activating protein (GAP) drive GTP into a precatalytic state as revealed by combining FTIR and biomolecular simulations. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15295-15300.	7.1	75
26	Exploring the Multidimensional Free Energy Surface of Phosphoester Hydrolysis with Constrained QM/MM Dynamics. Journal of Chemical Theory and Computation, 2012, 8, 3596-3604.	5.3	23
27	The Role of Magnesium for Geometry and Charge in GTP Hydrolysis, Revealed by Quantum Mechanics/Molecular Mechanics Simulations. Biophysical Journal, 2012, 103, 293-302.	0.5	46
28	N-Ras Forms Dimers at POPC Membranes. Biophysical Journal, 2012, 103, 1585-1593.	0.5	133