

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	Molecular dynamics simulations of large macromolecular complexes. <i>Current Opinion in Structural Biology</i> , 2015, 31, 64-74.	5.7	347
2	In Situ Structure of Neuronal C9orf72 Poly-GA Aggregates Reveals Proteasome Recruitment. <i>Cell</i> , 2018, 172, 696-705.e12.	28.9	311
3	Structure of the human 26S proteasome at a resolution of 3.9 Å... <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 7816-7821.	7.1	174
4	QwikMD—Integrative Molecular Dynamics Toolkit for Novices and Experts. <i>Scientific Reports</i> , 2016, 6, 26536.	3.3	153
5	Structural insights into the functional cycle of the ATPase module of the 26S proteasome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1305-1310.	7.1	151
6	NAMD goes quantum: an integrative suite for hybrid simulations. <i>Nature Methods</i> , 2018, 15, 351-354.	19.0	149
7	N-Ras Forms Dimers at POPC Membranes. <i>Biophysical Journal</i> , 2012, 103, 1585-1593.	0.5	133
8	Expanded Coverage of the 26S Proteasome Conformational Landscape Reveals Mechanisms of Peptidase Gating. <i>Cell Reports</i> , 2018, 24, 1301-1315.e5.	6.4	108
9	Insights into the assembly and activation of the microtubule nucleator $\hat{\gamma}$ -TuRC. <i>Nature</i> , 2020, 578, 467-471.	27.8	106
10	Structural insights into photosystem II assembly. <i>Nature Plants</i> , 2021, 7, 524-538.	9.3	102
11	PyContact: Rapid, Customizable, and Visual Analysis of Noncovalent Interactions in MD Simulations. <i>Biophysical Journal</i> , 2018, 114, 577-583.	0.5	80
12	Structural basis for VIPP1 oligomerization and maintenance of thylakoid membrane integrity. <i>Cell</i> , 2021, 184, 3643-3659.e23.	28.9	76
13	Ras and GTPase-activating protein (GAP) drive GTP into a precatalytic state as revealed by combining FTIR and biomolecular simulations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15295-15300.	7.1	75
14	Computational Methodologies for Real-Space Structural Refinement of Large Macromolecular Complexes. <i>Annual Review of Biophysics</i> , 2016, 45, 253-278.	10.0	67
15	Cryo-EM structures of the archaeal PAN-proteasome reveal an around-the-ring ATPase cycle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 534-539.	7.1	65
16	The Role of Magnesium for Geometry and Charge in GTP Hydrolysis, Revealed by Quantum Mechanics/Molecular Mechanics Simulations. <i>Biophysical Journal</i> , 2012, 103, 293-302.	0.5	46
17	GTP Hydrolysis Without an Active Site Base: A Unifying Mechanism for Ras and Related GTPases. <i>Journal of the American Chemical Society</i> , 2019, 141, 10684-10701.	13.7	44
18	Detailed Structure of the H ₂ PO ₄ [−] “Guanosine Diphosphate Intermediate in Ras-GAP Decoded from FTIR Experiments by Biomolecular Simulations. <i>Journal of the American Chemical Society</i> , 2012, 134, 20041-20044.	13.7	33

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19	Lamprey Parapinopsin (â€œUVLamPâ€): a Bistable UVâ€Sensitive Optogenetic Switch for Ultrafast Control of GPCR Pathways. <i>ChemBioChem</i> , 2020, 21, 612-617.	2.6	30
20	Exploring the Multidimensional Free Energy Surface of Phosphoester Hydrolysis with Constrained QM/MM Dynamics. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 3596-3604.	5.3	23
21	Catalysis of GTP Hydrolysis by Small GTPases at Atomic Detail by Integration of X-ray Crystallography, Experimental, and Theoretical IR Spectroscopy. <i>Journal of Biological Chemistry</i> , 2015, 290, 24079-24090.	3.4	20
22	The Effect of (âˆ™)-Epigallocatechin-3-Gallate on the Amyloid-Î² Secondary Structure. <i>Biophysical Journal</i> , 2020, 119, 349-359.	0.5	18
23	The Ras dimer structure. <i>Chemical Science</i> , 2021, 12, 8178-8189.	7.4	16
24	Allosteric control of Ubp6 and the proteasome via a bidirectional switch. <i>Nature Communications</i> , 2022, 13, 838.	12.8	15
25	Time-resolved spectroscopic and electrophysiological data reveal insights in the gating mechanism of anion channelrhodopsin. <i>Communications Biology</i> , 2021, 4, 578.	4.4	13
26	Local Mode Analysis: Decoding IR Spectra by Visualizing Molecular Details. <i>Journal of Physical Chemistry B</i> , 2017, 121, 3483-3492.	2.6	6
27	Design of an Ultrafast G Protein Switch Based on a Mouse Melanopsin Variant. <i>ChemBioChem</i> , 2019, 20, 1766-1771.	2.6	6
28	Monitoring transient events in infrared spectra using local mode analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 1013-1019.	2.6	1