Helmut GrubmÃ¼ller

List of Publications by Year
in descending order

154 papers	16,822 citations	26630 56 h-index	17105 122 g-index

176 all docs	176 docs citations	176 times ranked	18600 citing authors

#	Article	IF	Citations
1	Folding of VemP into translation-arresting secondary structure is driven by the ribosome exit tunnel. Nucleic Acids Research, 2022, 50, 2258-2269.	14.5	8
2	GROMACS in the Cloud: A Global Supercomputer to Speed Up Alchemical Drug Design. Journal of Chemical Information and Modeling, 2022, 62, 1691-1711.	5.4	37
3	Effects of cryo-EM cooling on structural ensembles. Nature Communications, 2022, 13, 1709.	12.8	33
4	Bending-torsional elasticity and energetics of the plus-end microtubule tip. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2115516119.	7.1	7
5	Estimating ruggedness of free-energy landscapes of small globular proteins from principal component analysis of molecular dynamics trajectories. Physical Review E, 2022, 105, 044404.	2.1	6
6	Intersubunit Coupling Enables Fast CO₂-Fixation by Reductive Carboxylases. ACS Central Science, 2022, 8, 1091-1101.	11.3	10
7	A CUDA fast multipole method with highly efficient M2L far field evaluation. International Journal of High Performance Computing Applications, 2021, 35, 97-117.	3.7	3
8	ATPâ€“Magnesium Coordination: Protein Structure-Based Force Field Evaluation and Corrections. Journal of Chemical Theory and Computation, 2021, 17, 1922-1930.	5.3	19
9	Choice of fluorophore affects dynamic DNA nanostructures. Nucleic Acids Research, 2021, 49, 4186-4195.	14.5	20
10	Per|Mut: Spatially Resolved Hydration Entropies from Atomistic Simulations. Journal of Chemical Theory and Computation, 2021, 17, 2090-2098.	5.3	13
11	Spatiotemporal Resolution of Conformational Changes in Biomolecules by Combining Pulsed Electronâ€“Electron Double Resonance Spectroscopy with Microsecond Freeze-Hyperquenching. Journal of the American Chemical Society, 2021, 143, 6981-6989.	13.7	33
12	Tight docking of membranes before fusion represents a metastable state with unique properties. Nature Communications, 2021, 12, 3606.	12.8	20
13	GROMACS implementation of free energy calculations with non-pairwise Variationally derived Intermediates. Computer Physics Communications, 2021, 264, 107931.	7.5	7
14	Structural and mechanistic basis for translation inhibition by macrolide and ketolide antibiotics. Nature Communications, 2021, 12, 4466.	12.8	43
15	Spatially resolved free-energy contributions ofÂnative fold and molten-globule-like Crambin. Biophysical Journal, 2021, 120, 3470-3482.	0.5	10
16	Time-Lagged Independent Component Analysis of Random Walks and Protein Dynamics. Journal of Chemical Theory and Computation, 2021, 17, 5766-5776.	5.3	27
17	Implementation of a Bayesian secondary structure estimation method for the SESCA circular dichroism analysis package. Computer Physics Communications, 2021, 266, 108022.	7.5	6
18	How proteins open fusion pores: insights from molecular simulations. European Biophysics Journal, 2021, 50, 279-293.	2.2	17

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19	Small-sample limit of the Bennett acceptance ratio method and the variationally derived intermediates. Physical Review E, 2021, 104, 054133.	2.1	2
20	Atomistic Simulations of the Human Proteasome Inhibited by a Covalent Ligand. , 2021, , 47-57.		0
21	tRNA Dissociation from EF-Tu after GTP Hydrolysis: Primary Steps and Antibiotic Inhibition. Biophysical Journal, 2020, 118, 151-161.	0.5	19
22	Computing Spatially Resolved Rotational Hydration Entropies from Atomistic Simulations. Journal of Chemical Theory and Computation, 2020, 16, 108-118.	5.3	15
23	A GPU-Accelerated Fast Multipole Method for GROMACS: Performance and Accuracy. Journal of Chemical Theory and Computation, 2020, 16, 6938-6949.	5.3	68
24	Sequential Water and Headgroup Merger: Membrane Poration Paths and Energetics from MD Simulations. Biophysical Journal, 2020, 119, 2418-2430.	0.5	8
25	How accurate is circular dichroism-based model validation?. European Biophysics Journal, 2020, 49, 497-510.	2.2	10
26	Microtubule instability driven by longitudinal and lateral strain propagation. PLoS Computational Biology, 2020, 16, e1008132.	3.2	15
27	Variationally derived intermediates for correlated free-energy estimates between intermediate states. Physical Review E, 2020, 102, 043312.	2.1	3
28	Determining Free-Energy Differences Through Variationally Derived Intermediates. Journal of Chemical Theory and Computation, 2020, 16, 3504-3512.	5.3	15
29	Probing the Accuracy of Explicit Solvent Constant pH Molecular Dynamics Simulations for Peptides. Journal of Chemical Theory and Computation, 2020, 16, 2561-2569.	5.3	13
30	GROMEX: A Scalable and Versatile Fast Multipole Method for Biomolecular Simulation. Lecture Notes in Computational Science and Engineering, 2020, , 517-543.	0.3	2
31	Microtubule instability driven by longitudinal and lateral strain propagation. , 2020, 16, e1008132.		0
32	Microtubule instability driven by longitudinal and lateral strain propagation. , 2020, 16, e1008132.		0
33	Microtubule instability driven by longitudinal and lateral strain propagation. , 2020, 16, e1008132.		0
34	Microtubule instability driven by longitudinal and lateral strain propagation. , 2020, 16, e1008132.		0
35	Microtubule instability driven by longitudinal and lateral strain propagation. , 2020, 16, e1008132.		0
36	Microtubule instability driven by longitudinal and lateral strain propagation. , 2020, 16, e1008132.		0

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37	SESCA: Predicting Circular Dichroism Spectra from Protein Molecular Structures. Journal of Chemical Theory and Computation, 2019, 15, 5087-5102.	5.3	54
38	More bang for your buck: Improved use of GPU nodes for GROMACS 2018. Journal of Computational Chemistry, 2019, 40, 2418-2431.	3.3	286
39	Thermodynamic control of â˜1 programmed ribosomal frameshifting. Nature Communications, 2019, 10, 4598.	12.8	34
40	Sharing Data from Molecular Simulations. Journal of Chemical Information and Modeling, 2019, 59, 4093-4099.	5.4	26
41	Heterogeneous and rate-dependent streptavidinâ€“biotin unbinding revealed by high-speed force spectroscopy and atomistic simulations. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 6594-6601.	7.1	95
42	Active role of elongation factor G in maintaining the mRNA reading frame during translation. Science Advances, 2019, 5, eaax8030.	10.3	38
43	Automated cryo-EM structure refinement using correlation-driven molecular dynamics. ELife, 2019, 8, .	6.0	83
44	Molecular simulations of the ribosome and associated translation factors. Current Opinion in Structural Biology, 2018, 49, 27-35.	5.7	33
45	Structure determination from single molecule X-ray scattering with three photons per image. Nature Communications, 2018, 9, 2375.	12.8	34
46	The 2018 biomembrane curvature and remodeling roadmap. Journal Physics D: Applied Physics, 2018, 51, 343001.	2.8	212
47	Transient Secondary and Tertiary Structure Formation Kinetics in the Intrinsically Disordered State of Î±â€Synuclein from Atomistic Simulations. ChemPhysChem, 2018, 19, 2507-2511.	2.1	17
48	Microtubule assembly governed by tubulin allosteric gain in flexibility and lattice induced fit. ELife, 2018, 7, .	6.0	42
49	Engineering fatty acid synthases for directed polyketide production. Nature Chemical Biology, 2017, 13, 363-365.	8.0	63
50	Mechanochemical Energy Transduction during the Main Rotary Step in the Synthesis Cycle of F₁-ATPase. Journal of the American Chemical Society, 2017, 139, 4025-4034.	13.7	23
51	Accurate Three States Model for Amino Acids with Two Chemically Coupled Titrating Sites in Explicit Solvent Atomistic Constant pH Simulations and pK_a Calculations. Journal of Chemical Theory and Computation, 2017, 13, 147-160.	5.3	27
52	Structural Basis for Polyproline-Mediated Ribosome Stalling and Rescue by the Translation Elongation Factor EF-P. Molecular Cell, 2017, 68, 515-527.e6.	9.7	118
53	CHARMM36m: an improved force field for folded and intrinsically disordered proteins. Nature Methods, 2017, 14, 71-73.	19.0	3,959
54	Cationic and Anionic Impact on the Electronic Structure of Liquid Water. Journal of Physical Chemistry Letters, 2017, 8, 3759-3764.	4.6	26

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55	The Low Barrier Hydrogen Bond in the Photoactive Yellow Protein: A Vacuum Artifact Absent in the Crystal and Solution. Journal of the American Chemical Society, 2016, 138, 16620-16631.	13.7	18
56	A combined cryo-EM and molecular dynamics approach reveals the mechanism of ErmBL-mediated translation arrest. Nature Communications, 2016, 7, 12026.	12.8	103
57	Phi29 Connector-DNA Interactions Govern DNA Crunching and Rotation, Supporting the Check-Valve Model. Biophysical Journal, 2016, 110, 455-469.	0.5	10
58	The pathway to GTPase activation of elongation factor SelB on the ribosome. Nature, 2016, 540, 80-85.	27.8	93
59	Exploiting Lipid Permutation Symmetry to Compute Membrane Remodeling Free Energies. Physical Review Letters, 2016, 117, 188102.	7.8	27
60	A Quantitative Model for cAMP Binding to the Binding Domain of MloK1. Biophysical Journal, 2016, 111, 1668-1678.	0.5	4
61	BASDet: Bayesian approach(es) for structure determination from single molecule X-ray diffraction images. Computer Physics Communications, 2016, 201, 159-166.	7.5	2
62	Charge-Neutral Constant pH Molecular Dynamics Simulations Using a Parsimonious Proton Buffer. Journal of Chemical Theory and Computation, 2016, 12, 1040-1051.	5.3	44
63	NuSol â€" Numerical solver for the 3D stationary nuclear SchrÃ¶dinger equation. Computer Physics Communications, 2016, 198, 169-178.	7.5	28
64	Best bang for your buck: GPU nodes for <scp>GROMACS</scp> biomolecular simulations. Journal of Computational Chemistry, 2015, 36, 1990-2008.	3.3	195
65	<scp>PspF</scp>â€binding domain <scp>PspA</scp>_{1â€"144} and the <scp>PspA</scp>Â·<scp>F</scp> complex: New insights into the coiledâ€"coilâ€dependent regulation of <scp>AAA</scp>+ proteins. Molecular Microbiology, 2015, 98, 743-759.	2.5	33
66	TatBC-Independent TatA/Tat Substrate Interactions Contribute to Transport Efficiency. PLoS ONE, 2015, 10, e0119761.	2.5	20
67	Binding Affinities Controlled by Shifting Conformational Equilibria: Opportunities and Limitations. Biophysical Journal, 2015, 108, 2585-2590.	0.5	10
68	Lipid Binding Defects and Perturbed Synaptogenic Activity of a Collybistin R290H Mutant That Causes Epilepsy and Intellectual Disability. Journal of Biological Chemistry, 2015, 290, 8256-8270.	3.4	32
69	MD Simulations and FRET Reveal an Environment-Sensitive Conformational Plasticity of Importin-Î². Biophysical Journal, 2015, 109, 277-286.	0.5	23
70	do_x3dna: a tool to analyze structural fluctuations of dsDNA or dsRNA from molecular dynamics simulations. Bioinformatics, 2015, 31, 2583-2585.	4.1	59
71	Hydrophobic mismatch sorts SNARE proteins into distinct membrane domains. Nature Communications, 2015, 6, 5984.	12.8	130
72	Structural Ensembles of Intrinsically Disordered Proteins Depend Strongly on Force Field: A Comparison to Experiment. Journal of Chemical Theory and Computation, 2015, 11, 5513-5524.	5.3	368

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73	Dynamic contact network between ribosomal subunits enables rapid large-scale rotation during spontaneous translocation. Nucleic Acids Research, 2015, 43, 6747-6760.	14.5	36
74	Bayesian orientation estimate and structure information from sparse single-molecule x-ray diffraction images. Physical Review E, 2014, 90, 022714.	2.1	12
75	AMBER-DYES: Characterization of Charge Fluctuations and Force Field Parameterization of Fluorescent Dyes for Molecular Dynamics Simulations. Journal of Chemical Theory and Computation, 2014, 10, 5505-5512.	5.3	44
76	Expansion of the fusion stalk and its implication for biological membrane fusion. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11043-11048.	7.1	99
77	Free Energy Landscape of Rim-Pore Expansion in Membrane Fusion. Biophysical Journal, 2014, 107, 2287-2295.	0.5	30
78	Anomalous Surface Diffusion of Protons on Lipid Membranes. Biophysical Journal, 2014, 107, 76-87.	0.5	55
79	Elastic Properties and Heterogeneous Stiffness of the Phi29 Motor Connector Channel. Biophysical Journal, 2014, 106, 1338-1348.	0.5	21
80	Force Distribution Analysis of Mechanochemically Reactive Dimethylcyclobutene. ChemPhysChem, 2013, 14, 2687-2697.	2.1	15
81	Energy barriers and driving forces in tRNA translocation through the ribosome. Nature Structural and Molecular Biology, 2013, 20, 1390-1396.	8.2	150
82	Structural Determinants and Mechanism of Mammalian CRM1 Allostery. Structure, 2013, 21, 1350-1360.	3.3	17
83	g_contacts: Fast contact search in bio-molecular ensemble data. Computer Physics Communications, 2013, 184, 2856-2859.	7.5	37
84	Proteins in the gas phase. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2013, 3, 408-425.	14.6	49
85	Structural basis for cooperativity of CRM1 export complex formation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 960-965.	7.1	64
86	Quantitative Assessment of Protein Interaction with Methyl-Lysine Analogues by Hybrid Computational and Experimental Approaches. ACS Chemical Biology, 2012, 7, 150-154.	3.4	42
87	Universal Relaxation Governs the Nonequilibrium Elasticity of Biomolecules. Physical Review Letters, 2012, 109, 118304.	7.8	12
88	Exploring Protein Dynamics Space: The Dynasome as the Missing Link between Protein Structure and Function. PLoS ONE, 2012, 7, e33931.	2.5	83
89	How SNARE molecules mediate membrane fusion: Recent insights from molecular simulations. Current Opinion in Structural Biology, 2012, 22, 187-196.	5.7	121
90	Linearâ€scaling softâ€core scheme for alchemical free energy calculations. Journal of Computational Chemistry, 2012, 33, 25-33.	3.3	37

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91	Line-Tension Controlled Mechanism for Influenza Fusion. PLoS ONE, 2012, 7, e38302.	2.5	63
92	Constant pH Molecular Dynamics in Explicit Solvent with Î»-Dynamics. Journal of Chemical Theory and Computation, 2011, 7, 1962-1978.	5.3	163
93	Estimating the Orientational Entropy of Water at Protein Interfaces. Biophysical Journal, 2011, 100, 613a.	0.5	4
94	Velocity-Dependent Mechanical Unfolding of Bacteriorhodopsin Is Governed by a Dynamic Interaction Network. Biophysical Journal, 2011, 100, 1109-1119.	0.5	17
95	Keep It Flexible: Driving Macromolecular Rotary Motions in Atomistic Simulations with GROMACS. Journal of Chemical Theory and Computation, 2011, 7, 1381-1393.	5.3	42
96	Determining equilibrium constants for dimerization reactions from molecular dynamics simulations. Journal of Computational Chemistry, 2011, 32, 1919-1928.	3.3	69
97	Caught in the Act: Visualization of SNAREâ€Mediated Fusion Events in Molecular Detail. ChemBioChem, 2011, 12, 1049-1055.	2.6	134
98	Towards computional specificity screening of DNA-binding proteins. Nucleic Acids Research, 2011, 39, 8281-8290.	14.5	20
99	Torsional elasticity and energetics of F ₁ -ATPase. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7408-7413.	7.1	46
100	Structural Heterogeneity and Quantitative FRET Efficiency Distributions of Polyprolines through a Hybrid Atomistic Simulation and Monte Carlo Approach. PLoS ONE, 2011, 6, e19791.	2.5	108
101	Quantitative Structural Analysis of Importin-Î² Flexibility: Paradigm for Solenoid Protein Structures. Structure, 2010, 18, 1171-1183.	3.3	89
102	A â€œForce Bufferâ€•Protecting Immunoglobulin Titin. Angewandte Chemie - International Edition, 2010, 49, 3528-3531.	13.8	23
103	Estimating Absolute Configurational Entropies of Macromolecules: The Minimally Coupled Subspace Approach. PLoS ONE, 2010, 5, e9179.	2.5	57
104	Molecular Basis of the Light-driven Switching of the Photochromic Fluorescent Protein Padron. Journal of Biological Chemistry, 2010, 285, 14603-14609.	3.4	65
105	Primary Changes of the Mechanical Properties of Southern Bean Mosaic Virus upon Calcium Removal. Biophysical Journal, 2010, 98, 687-695.	0.5	25
106	An Unusual Hydrophobic Core Confers Extreme Flexibility to HEAT Repeat Proteins. Biophysical Journal, 2010, 99, 1596-1603.	0.5	66
107	Adaptive anisotropic kernels for nonparametric estimation of absolute configurational entropies in high-dimensional configuration spaces. Physical Review E, 2009, 80, 011913.	2.1	21
108	Kinase-activity-independent functions of atypical protein kinase C in Drosophila. Journal of Cell Science, 2009, 122, 3759-3771.	2.0	67

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109	Primary Steps of pHâ€Dependent Insulin Aggregation Kinetics are Governed by Conformational Flexibility. ChemBioChem, 2009, 10, 1816-1822.	2.6	39
110	Inside Cover: Primary Steps of pH-Dependent Insulin Aggregation Kinetics are Governed by Conformational Flexibility (ChemBioChem 11/2009). ChemBioChem, 2009, 10, 1742-1742.	2.6	1
111	Accuracy and convergence of free energy differences calculated from nonequilibrium switching processes. Journal of Computational Chemistry, 2009, 30, 447-456.	3.3	81
112	Dynamics and Energetics of Permeation Through Aquaporins. What Do We Learn from Molecular Dynamics Simulations?. Handbook of Experimental Pharmacology, 2009, , 57-76.	1.8	92
113	Mechanical Properties of the Icosahedral Shell of Southern Bean Mosaic Virus: A Molecular Dynamics Study. Biophysical Journal, 2009, 96, 1350-1363.	0.5	117
114	Urea Impedes the Hydrophobic Collapse of Partially Unfolded Proteins. Biophysical Journal, 2009, 96, 3744-3752.	0.5	69
115	Molecular Determinants of Snurportin 1 Ligand Affinity and Structural Response upon Binding. Biophysical Journal, 2009, 97, 581-589.	0.5	7
116	Full correlation analysis of conformational protein dynamics. Proteins: Structure, Function and Bioinformatics, 2008, 70, 1294-1312.	2.6	122
117	Importin-Î²: Structural and Dynamic Determinants of a Molecular Spring. Structure, 2008, 16, 906-915.	3.3	49
118	Kinetics, Statistics, and Energetics of Lipid Membrane Electroporation Studied by Molecular Dynamics Simulations. Biophysical Journal, 2008, 95, 1837-1850.	0.5	280
119	Recognition Dynamics Up to Microseconds Revealed from an RDC-Derived Ubiquitin Ensemble in Solution. Science, 2008, 320, 1471-1475.	12.6	963
120	Polar or Apolarâ€"The Role of Polarity for Urea-Induced Protein Denaturation. PLoS Computational Biology, 2008, 4, e1000221.	3.2	65
121	Chromophore Protonation State Controls Photoswitching of the Fluoroprotein asFP595. PLoS Computational Biology, 2008, 4, e1000034.	3.2	98
122	Estimation of absolute solvent and solvation shell entropies via permutation reduction. Journal of Chemical Physics, 2007, 126, 014102.	3.0	43
123	Fluctuations of primary ubiquitin folding intermediates in a force clamp. Journal of Structural Biology, 2007, 157, 557-569.	2.8	28
124	Photoswitching of the Fluorescent Protein asFP595: Mechanism, Proton Pathways, and Absorption Spectra. Angewandte Chemie - International Edition, 2007, 46, 530-536.	13.8	95
125	Elastic Properties of Photoswitchable Azobenzene Polymers from Molecular Dynamics Simulations. Angewandte Chemie - International Edition, 2007, 46, 2232-2237.	13.8	46
126	Speeding up parallel GROMACS on high-latency networks. Journal of Computational Chemistry, 2007, 28, 2075-2084.	3.3	107

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127	Collective Langevin dynamics of conformational motions in proteins. Journal of Chemical Physics, 2006, 124, 214903.	3.0	114
128	Molecular Anatomy of a Trafficking Organelle. Cell, 2006, 127, 831-846.	28.9	1,985
129	A Highly Strained Nuclear Conformation of the Exportin Cse1p Revealed by Molecular Dynamics Simulations. Structure, 2006, 14, 1469-1478.	3.3	27
130	Flooding inGROMACS: Accelerated barrier crossings in molecular dynamics. Journal of Computational Chemistry, 2006, 27, 1693-1702.	3.3	63
131	The dynamics and energetics of water permeation and proton exclusion in aquaporins. Current Opinion in Structural Biology, 2005, 15, 176-183.	5.7	263
132	Molecular Dynamics Simulations of Protein G Challenge NMR-Derived Correlated Backbone Motions. Angewandte Chemie - International Edition, 2005, 44, 3394-3399.	13.8	25
133	Generalized correlation for biomolecular dynamics. Proteins: Structure, Function and Bioinformatics, 2005, 62, 1053-1061.	2.6	380
134	Structure and mechanism of the reversible photoswitch of a fluorescent protein. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 13070-13074.	7.1	253
135	Mechanically Induced Titin Kinase Activation Studied by Force-Probe Molecular Dynamics Simulations. Biophysical Journal, 2005, 88, 790-804.	0.5	195
136	Multistep Binding of Divalent Cations to Phospholipid Bilayers: A Molecular Dynamics Study. Angewandte Chemie - International Edition, 2004, 43, 1021-1024.	13.8	173
137	Cover Picture: Multistep Binding of Divalent Cations to Phospholipid Bilayers: A Molecular Dynamics Study (Angew. Chem. Int. Ed. 8/2004). Angewandte Chemie - International Edition, 2004, 43, 911-911.	13.8	0
138	The Structure of the Aquaporin-1 Water Channel: A Comparison between Cryo-electron Microscopy and X-ray Crystallography. Journal of Molecular Biology, 2003, 325, 485-493.	4.2	51
139	The Mechanism of Proton Exclusion in the Aquaporin-1 Water Channel. Journal of Molecular Biology, 2003, 333, 279-293.	4.2	257
140	Conformational Dynamics of the F1-ATPase Î²-Subunit: A Molecular Dynamics Study. Biophysical Journal, 2003, 85, 1482-1491.	0.5	38
141	Mechanical Coupling via the Membrane Fusion SNARE Protein Syntaxin 1A: A Molecular Dynamics Study. Biophysical Journal, 2003, 84, 1527-1547.	0.5	66
142	Maximum likelihood trajectories from single molecule fluorescence resonance energy transfer experiments. Journal of Chemical Physics, 2003, 119, 9920-9924.	3.0	62
143	What happens if the room at the bottom runs out? A close look at small water pores. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 7421-7422.	7.1	10
144	Predicting unimolecular chemical reactions: Chemical flooding. Journal of Chemical Physics, 2002, 116, 897-905.	3.0	63

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145	Water Permeation through Gramicidin A: Desformylation and the Double Helix: A Molecular Dynamics Study. Biophysical Journal, 2002, 82, 2934-2942.	0.5	89
146	Membrane fusion. Current Opinion in Cell Biology, 2002, 14, 488-495.	5.4	181
147	Structure and Function of Water Channels. Current Opinion in Structural Biology, 2002, 12, 509-515.	5.7	246
148	Essential dynamics of reversible peptide folding: memory-free conformational dynamics governed by internal hydrogen bonds. Journal of Molecular Biology, 2001, 309, 299-313.	4.2	126
149	A refined structure of human aquaporin-1. FEBS Letters, 2001, 504, 206-211.	2.8	120
150	Kraftspektroskopie von einzelnen BiomolekÃ¼len: Biologische MakromolekÃ¼le besser begreifen â€“ mit EinzelmolekÃ¼lâ€Kraftmessungen und Computersimulationen. Physik Journal, 2001, 57, 55-61.	0.1	4
151	Dynamic Force Spectroscopy of Molecular Adhesion Bonds. Physical Review Letters, 2000, 84, 6126-6129.	7.8	152
152	The Fold of Human Aquaporin 1. Journal of Molecular Biology, 2000, 300, 987-994.	4.2	34
153	Multiple time step algorithms for molecular dynamics simulations of proteins: How good are they?. Journal of Computational Chemistry, 1998, 19, 1534-1552.	3.3	33
154	Predicting slow structural transitions in macromolecular systems: Conformational flooding. Physical Review E, 1995, 52, 2893-2906.	2.1	573