

Matthias Buck

List of Publications by Year in descending order

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90
papers

5,107
citations

126858

33
h-index

88593

70
g-index

127
all docs

127
docs citations

127
times ranked

5091
citing authors

#	ARTICLE	IF	CITATIONS
1	Trifluoroethanol and colleagues: cosolvents come of age. Recent studies with peptides and proteins. Quarterly Reviews of Biophysics, 1998, 31, 297-355.	2.4	760
2	Importance of the CMAP Correction to the CHARMM22 Protein Force Field: Dynamics of Hen Lysozyme. Biophysical Journal, 2006, 90, L36-L38.	0.2	321
3	Structural and Dynamical Properties of a Denatured Protein. Heteronuclear 3D NMR Experiments and Theoretical Simulations of Lysozyme in 8 M Urea. Biochemistry, 1997, 36, 8977-8991.	1.2	296
4	A partially folded state of hen egg white lysozyme in trifluoroethanol: structural characterization and implications for protein folding. Biochemistry, 1993, 32, 669-678.	1.2	284
5	Structural Determinants of Protein Dynamics: Analysis of 15N NMR Relaxation Measurements for Main-Chain and Side-Chain Nuclei of Hen Egg White Lysozyme. Biochemistry, 1995, 34, 4041-4055.	1.2	211
6	Hydrogen exchange in native and denatured states of hen egg-white lysozyme. Proteins: Structure, Function and Bioinformatics, 1992, 14, 237-248.	1.5	170
7	Toward a Description of the Conformations of Denatured States of Proteins. Comparison of a Random Coil Model with NMR Measurements. The Journal of Physical Chemistry, 1996, 100, 2661-2666.	2.9	160
8	A refined solution structure of hen lysozyme determined using residual dipolar coupling data. Protein Science, 2001, 10, 677-688.	3.1	159
9	Characterization of Conformational Preferences in a Partly Folded Protein by Heteronuclear NMR Spectroscopy: Assignment and Secondary Structure Analysis of Hen Egg-White Lysozyme in Trifluoroethanol. Biochemistry, 1995, 34, 13219-13232.	1.2	151
10	Plexin structures are coming: opportunities for multilevel investigations of semaphorin guidance receptors, their cell signaling mechanisms, and functions. Cellular and Molecular Life Sciences, 2012, 69, 3765-3805.	2.4	145
11	EPHA2 Is Associated with Age-Related Cortical Cataract in Mice and Humans. PLoS Genetics, 2009, 5, e1000584.	1.5	140
12	Binding of Rac1, Rnd1, and RhoD to a Novel Rho GTPase Interaction Motif Destabilizes Dimerization of the Plexin-B1 Effector Domain. Journal of Biological Chemistry, 2007, 282, 37215-37224.	1.6	123
13	Conformational Properties of Four Peptides Spanning the Sequence of Hen Lysozyme. Journal of Molecular Biology, 1995, 252, 483-491.	2.0	121
14	Ligand recognition by class Eph receptors: crystal structures of the EphA2 ligand-binding domain and the EphA2/ephrinA1 complex. EMBO Reports, 2009, 10, 722-728.	2.0	106
15	Amide Hydrogen Exchange in a Highly Denatured State. Journal of Molecular Biology, 1994, 237, 247-254.	2.0	103
16	Main-chain Dynamics of a Partially Folded Protein: 15N NMR Relaxation Measurements of Hen Egg White Lysozyme Denatured in Trifluoroethanol. Journal of Molecular Biology, 1996, 257, 669-683.	2.0	96
17	Acceleration of the folding of hen lysozyme by trifluoroethanol. Journal of Molecular Biology, 1997, 265, 112-117.	2.0	86
18	Structure and Function of the Intracellular Region of the Plexin-B1 Transmembrane Receptor. Journal of Biological Chemistry, 2009, 284, 35962-35972.	1.6	81

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19	Hydrogen Bond Energetics: A Simulation and Statistical Analysis of N-Methyl Acetamide (NMA), Water, and Human Lysozyme. <i>Journal of Physical Chemistry B</i> , 2001, 105, 11000-11015.	1.2	79
20	Computational Modeling Reveals that Signaling Lipids Modulate the Orientation of K-Ras4A at the Membrane Reflecting Protein Topology. <i>Structure</i> , 2017, 25, 679-689.e2.	1.6	76
21	NMR Structure of a Heterodimeric SAM:SAM Complex: Characterization and Manipulation of EphA2 Binding Reveal New Cellular Functions of SHIP2. <i>Structure</i> , 2012, 20, 41-55.	1.6	56
22	A α -Tubulin Maintains a Dynamic Protein-Membrane Complex: Molecular Dynamics Simulations of C-Raf RBD-CRD Bound to K-Ras4B at an Anionic Membrane. <i>ACS Central Science</i> , 2018, 4, 298-305.	5.3	54
23	Internal and Overall Peptide Group Motion in Proteins: Molecular Dynamics Simulations for Lysozyme Compared with Results from X-ray and NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 1999, 121, 9645-9658.	6.6	52
24	A Two-State Allosteric Model for Autoinhibition Rationalizes WASP Signal Integration and Targeting. <i>Journal of Molecular Biology</i> , 2004, 338, 271-285.	2.0	51
25	Compensatory and Long-Range Changes in Picosecond-Nanosecond Main-Chain Dynamics upon Complex Formation: ^{15}N Relaxation Analysis of the Free and Bound States of the Ubiquitin-like Domain of Human Plexin-B1 and the Small GTPase Rac1. <i>Journal of Molecular Biology</i> , 2008, 377, 1474-1487.	2.0	50
26	APOL1 variants change C-terminal conformational dynamics and binding to SNARE protein VAMP8. <i>JCI Insight</i> , 2017, 2, .	2.3	48
27	K-Ras G-domain binding with signaling lipid phosphatidylinositol (4,5)-phosphate (PIP2): membrane association, protein orientation, and function. <i>Journal of Biological Chemistry</i> , 2019, 294, 7068-7084.	1.6	47
28	Neuropilin-1 assists SARS-CoV-2 infection by stimulating the separation of Spike protein S1 and S2. <i>Biophysical Journal</i> , 2021, 120, 2828-2837.	0.2	44
29	Insights into Oncogenic Mutations of Plexin-B1 Based on the Solution Structure of the Rho GTPase Binding Domain. <i>Structure</i> , 2008, 16, 246-258.	1.6	41
30	Backbone Dynamics of the Ribonuclease Binase Active Site Area Using Multinuclear (^{15}N and ^{13}C) NMR Relaxation and Computational Molecular Dynamics. <i>Biochemistry</i> , 2002, 41, 2655-2666.	1.2	40
31	Molecular profiling of the plexinome in melanoma and pancreatic cancer. <i>Human Mutation</i> , 2009, 30, 1167-1174.	1.1	40
32	A Metastable Contact and Structural Disorder in the Estrogen Receptor Transactivation Domain. <i>Structure</i> , 2019, 27, 229-240.e4.	1.6	39
33	Raf promotes dimerization of the Ras G-domain with increased allosteric connections. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	39
34	Structural Basis of Rnd1 Binding to Plexin Rho GTPase Binding Domains (RBDs). <i>Journal of Biological Chemistry</i> , 2011, 286, 26093-26106.	1.6	36
35	A role of the SAM domain in EphA2 receptor activation. <i>Scientific Reports</i> , 2017, 7, 45084.	1.6	36
36	Thermodynamic characterization of two homologous protein complexes: Associations of the semaphorin receptor plexin-B1 RhoGTPase binding domain with Rnd1 and active Rac1. <i>Protein Science</i> , 2009, 18, 1060-1071.	3.1	34

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37	Dissociation of a Dynamic Protein Complex Studied by All-Atom Molecular Simulations. <i>Biophysical Journal</i> , 2016, 110, 877-886.	0.2	34
38	Integrated Computational Approach to the Analysis of NMR Relaxation in Proteins: Application to psâns Main Chain ¹⁵Nâ”’¹H and Global Dynamics of the Rho GTPase Binding Domain of Plexin-B1. <i>Journal of Physical Chemistry B</i> , 2011, 115, 376-388.	1.2	32
39	NMR identification of a conserved Drp1 cardiolipin-binding motif essential for stress-induced mitochondrial fission. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	31
40	Combining NMR and Molecular Dynamics Studies for Insights into the Allostery of Small GTPaseâ€Protein Interactions. <i>Methods in Molecular Biology</i> , 2012, 796, 235-259.	0.4	31
41	When Monomers Are Preferred: A Strategy for the Identification and Disruption of Weakly Oligomerized Proteins. <i>Structure</i> , 2005, 13, 7-15.	1.6	30
42	Modeling Transmembrane Domain Dimers/Trimers of Plexin Receptors: Implications for Mechanisms of Signal Transmission across the Membrane. <i>PLoS ONE</i> , 2015, 10, e0121513.	1.1	30
43	Analysis of ¹⁵Nâ€“¹H NMR Relaxation in Proteins by a Combined Experimental and Molecular Dynamics Simulation Approach: Picosecondâ€Nanosecond Dynamics of the Rho GTPase Binding Domain of Plexin-B1 in the Dimeric State Indicates Allosteric Pathways. <i>Journal of Physical Chemistry B</i> , 2013, 117, 174-184.	1.2	28
44	Molecular Simulations of a Dynamic Protein Complex: Role of Salt-Bridges and Polar Interactions in Configurational Transitions. <i>Biophysical Journal</i> , 2013, 105, 2412-2417.	0.2	27
45	LAR-RPTP Clustering Is Modulated by Competitive Binding between Synaptic Adhesion Partners and Heparan Sulfate. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 327.	1.4	25
46	Molecular Dynamics Simulations Reveal Isoform Specific Contact Dynamics between the Plexin Rho GTPase Binding Domain (RBD) and Small Rho GTPases Rac1 and Rnd1. <i>Journal of Physical Chemistry B</i> , 2017, 121, 1485-1498.	1.2	24
47	Prediction, refinement, and persistency of transmembrane helix dimers in lipid bilayers using implicit and explicit solvent/lipid representations: Microsecond molecular dynamics simulations of ErbB1/B2 and EphA1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 365-376.	1.5	23
48	Modified Potential Functions Result in Enhanced Predictions of a Protein Complex by All-Atom Molecular Dynamics Simulations, Confirming a Stepwise Association Process for Native Proteinâ€Protein Interactions. <i>Journal of Chemical Theory and Computation</i> , 2019, 15, 4318-4331.	2.3	23
49	HBD-2 binds SARS-CoV-2 RBD and blocks viral entry: Strategy to combat COVID-19. <i>IScience</i> , 2022, 25, 103856.	1.9	23
50	Letter to the Editor: 1H, 15N and 13C Resonance assignments and secondary structure determination reveal that the minimal Rac1 GTPase binding domain of plexin-B1 has a ubiquitin fold. <i>Journal of Biomolecular NMR</i> , 2005, 31, 369-370.	1.6	22
51	G Protein Î²2 Subunit-derived Peptides for Inhibition and Induction of G Protein Pathways. <i>Journal of Biological Chemistry</i> , 2005, 280, 23945-23959.	1.6	21
52	Equilibrium Unfolding Studies of Horse Muscle Acylphosphatase. <i>FEBS Journal</i> , 1994, 225, 811-817.	0.2	20
53	Structure and Dynamics Analysis on Plexin-B1 Rho GTPase Binding Domain as a Monomer and Dimer. <i>Journal of Physical Chemistry B</i> , 2014, 118, 7302-7311.	1.2	20
54	The RNA-Binding Site of Poliovirus 3C Protein Doubles as a Phosphoinositide-Binding Domain. <i>Structure</i> , 2017, 25, 1875-1886.e7.	1.6	20

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55	Global Disruption of the WASP Autoinhibited Structure on Cdc42 Binding. Ligand Displacement as a Novel Method for Monitoring Amide Hydrogen Exchange. <i>Biochemistry</i> , 2001, 40, 14115-14122.	1.2	19
56	Cyclase-associated protein 1 (CAP1) is a prenyl-binding partner of Rap1 GTPase. <i>Journal of Biological Chemistry</i> , 2018, 293, 7659-7673.	1.6	19
57	The cytoplasmic domain of neuropilin-1 regulates focal adhesion turnover. <i>FEBS Letters</i> , 2013, 587, 3392-3399.	1.3	16
58	Binding and Function of Phosphotyrosines of the Ephrin A2 (EphA2) Receptor Using Synthetic Sterile Motif (SAM) Domains. <i>Journal of Biological Chemistry</i> , 2014, 289, 19694-19703.	1.6	16
59	Acceptable Protein and Solvent Behavior in Primary Hydration Shell Simulations of Hen Lysozyme. <i>Biophysical Journal</i> , 2007, 92, L49-L51.	0.2	13
60	A Direct Coupling between Global and Internal Motions in a Single Domain Protein? MD Investigation of Extreme Scenarios. <i>Biophysical Journal</i> , 2011, 101, 196-204.	0.2	13
61	K-Ras at Anionic Membranes: Orientation, Orientation, Orientation. <i>Recent Simulations and Experiments. Biophysical Journal</i> , 2016, 110, 1033-1035.	0.2	13
62	Computational Design of Myristoylated Cell-Penetrating Peptides Targeting Oncogenic K-Ras.G12D at the Effector-Binding Membrane Interface. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 306-315.	2.5	12
63	STRUCTURAL BIOLOGY: Flipping a Switch. <i>Science</i> , 2001, 291, 2329-2330.	6.0	12
64	Translocation of Human Defensin Type 3 through a Neutrally Charged Lipid Membrane: A Free Energy Study. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11883-11894.	1.2	11
65	Conformational Clamping by a Membrane Ligand Activates the EphA2 Receptor. <i>Journal of Molecular Biology</i> , 2021, 433, 167144.	2.0	10
66	Conformational Entropy from Mobile Bond Vectors in Proteins: A Viewpoint that Unifies NMR Relaxation Theory and Molecular Dynamics Simulation Approaches. <i>Journal of Physical Chemistry B</i> , 2020, 124, 9323-9334.	1.2	9
67	Plexin-Bs enhance their GAP activity with a novel activation switch loop generating a cooperative enzyme. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 1101-1112.	2.4	9
68	Interactions between semaphorins and plexin-neuropilin receptor complexes in the membranes of live cells. <i>Journal of Biological Chemistry</i> , 2021, 297, 100965.	1.6	9
69	Structural and Functional Insights into the Transmembrane Domain Association of Eph Receptors. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8593.	1.8	9
70	Computational studies of the principle of dynamic-change-driven protein interactions. <i>Structure</i> , 2022, , .	1.6	8
71	Crystallography. <i>Structure</i> , 2003, 11, 735-736.	1.6	7
72	Local Ordering at the N-H Sites of the Rho GTPase Binding Domain of Plexin-B1: Impact of Dimerization. <i>Journal of Physical Chemistry B</i> , 2019, 123, 8019-8033.	1.2	6

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73	¹ H, ¹⁵ N, ¹³ C assignments for the activated form of the small Rho-GTPase Rac1. Journal of Biomolecular NMR, 2006, 36, 51-51.	1.6	4
74	Refinement of the primary hydration shell model for molecular dynamics simulations of large proteins. Journal of Computational Chemistry, 2009, 30, 2635-2644.	1.5	4
75	Optimization and stabilization of Rho small GTPase proteins for solution NMR studies. Small GTPases, 2011, 2, 295-304.	0.7	3
76	Backbone assignment and secondary structure of Rnd1, an unusual Rho family small GTPase. Biomolecular NMR Assignments, 2013, 7, 121-128.	0.4	3
77	Beyond history and a roll: The list of the most well-studied human protein structures and overall trends in the protein data bank. Protein Science, 2021, 30, 745-760.	3.1	3
78	The Relationship between APOL1 Structure and Function: Clinical Implications. Kidney360, 2021, 2, 134-140.	0.9	3
79	Tripping a Switch: PDZ-RhoGEF-Grb2-RGS-Bound GTPase. Structure, 2008, 16, 1439-1441.	1.6	2
80	Characterizing Plexin GTPase Interactions Using Gel Filtration, Surface Plasmon Resonance Spectrometry, and Isothermal Titration Calorimetry. Methods in Molecular Biology, 2017, 1493, 89-105.	0.4	2
81	Two Hands Grip Better Than One for Tight Binding and Specificity: How a Phage Endolysin Fits into the Cell Wall of Its Host. Structure, 2019, 27, 1350-1352.	1.6	2
82	Membrane Proteins The Plexin Family of Transmembrane Receptors. , 2021, , 594-610.		2
83	Keys to Amyloid City: Computation and NMR Reveal Potential TDP-43 ALS Intermediates. Biophysical Journal, 2018, 115, 1625-1627.	0.2	1
84	Biophysica: A New International Open Access Journal to Integrate Across the Modern Biophysical Sciences and Engineering. Biophysica, 2021, 1, 73-74.	0.6	1
85	Understanding the Structural Basis of EphA2 Dimerization, Membrane Interactions and Its Implications in Cancer Progression. FASEB Journal, 2021, 35, .	0.2	0
86	Raf promotes dimerization of the Ras GTPase domain with increased allosteric connections. FASEB Journal, 2021, 35, .	0.2	0
87	Letting go: Deep computational modeling insights into pH-dependent calcium affinity. Journal of Biological Chemistry, 2021, 297, 100974.	1.6	0
88	Biochemical and mutational analysis of intracellular regions of the Plexin-B1 guidance receptor as a RasGAP. FASEB Journal, 2012, 26, 975.3.	0.2	0
89	First Year of Biophysica. Biophysica, 2022, 2, 89-90.	0.6	0
90	Understanding the Structural Basis of EphA1 and EphA2 Homodimerization, Membrane Proximal Domain Interactions and its Implications for Cancer. FASEB Journal, 2022, 36, .	0.2	0