Matthias Buck

List of Publications by Year
in descending order

90 papers	5,107 citations	126907 33 h-index	88630 70 g-index
127 all docs	127 docs citations	127 times ranked	5091 citing authors

#	Article	IF	Citations
1	HBD-2 binds SARS-CoV-2 RBD and blocks viral entry: Strategy to combat COVID-19. IScience, 2022, 25, 103856.	4.1	23
2	First Year of Biophysica. Biophysica, 2022, 2, 89-90.	1.4	0
3	Computational studies of the principle of dynamic-change-driven protein interactions. Structure, 2022, , .	3.3	8
4	Understanding the Structural Basis of Epha1 and Epha2 Homoâ€Dimerization, Membrane Proximal Domain Interactions and its Implications for Cancer. FASEB Journal, 2022, 36, .	0.5	0
5	Plexin-Bs enhance their GAP activity with a novel activation switch loop generating a cooperative enzyme. Cellular and Molecular Life Sciences, 2021, 78, 1101-1112.	5.4	9
6	Membrane Proteins | The Plexin Family of Transmembrane Receptors. , 2021, , 594-610.		2
7	Beyond history and â€œon a rollâ€: The list of the most wellâ€studied human protein structures and overall trends in the protein data bank. Protein Science, 2021, 30, 745-760.	7.6	3
8	Raf promotes dimerization of the Ras G-domain with increased allosteric connections. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	39
9	Biophysicaâ€”A New International Open Access Journal to Integrate Across the Modern Biophysical Sciences and Engineering. Biophysica, 2021, 1, 73-74.	1.4	1
10	Understanding the Structural Basis of Epha2â€dimerization, â€membrane Interactions and Its Implications in Cancer Progression. FASEB Journal, 2021, 35, .	0.5	0
11	Raf promotes dimerization of the Ras Gâ€domain with increased allosteric connections. FASEB Journal, 2021, 35, .	0.5	0
12	Neuropilin-1 assists SARS-CoV-2 infection by stimulating the separation of Spike protein S1 andÂS2. Biophysical Journal, 2021, 120, 2828-2837.	0.5	44
13	NMR identification of a conserved Drp1 cardiolipin-binding motif essential for stress-induced mitochondrial fission. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	31
14	Letting go: Deep computational modeling insights into pH-dependent calcium affinity. Journal of Biological Chemistry, 2021, 297, 100974.	3.4	0
15	Interactions between semaphorins and plexinâ€“neuropilin receptor complexes in the membranes of live cells. Journal of Biological Chemistry, 2021, 297, 100965.	3.4	9
16	Structural and Functional Insights into the Transmembrane Domain Association of Eph Receptors. International Journal of Molecular Sciences, 2021, 22, 8593.	4.1	9
17	Conformational Clamping by a Membrane Ligand Activates the EphA2 Receptor. Journal of Molecular Biology, 2021, 433, 167144.	4.2	10
18	The Relationship between APOL1 Structure and Function: Clinical Implications. Kidney360, 2021, 2, 134-140.	2.1	3

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19	Computational Design of Myristoylated Cell-Penetrating Peptides Targeting Oncogenic K-Ras.G12D at the Effector-Binding Membrane Interface. Journal of Chemical Information and Modeling, 2020, 60, 306-315.	5.4	12
20	Conformational Entropy from Mobile Bond Vectors in Proteins: A Viewpoint that Unifies NMR Relaxation Theory and Molecular Dynamics Simulation Approaches. Journal of Physical Chemistry B, 2020, 124, 9323-9334.	2.6	9
21	Local Ordering at the Nâ€“H Sites of the Rho GTPase Binding Domain of Plexin-B1: Impact of Dimerization. Journal of Physical Chemistry B, 2019, 123, 8019-8033.	2.6	6
22	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.	3.3	2
23	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. Journal of Chemical Theory and Computation, 2019, 15, 4318-4331.	5.3	23
24	K-Ras G-domain binding with signaling lipid phosphatidylinositol (4,5)-phosphate (PIP2): membrane association, protein orientation, and function. Journal of Biological Chemistry, 2019, 294, 7068-7084.	3.4	47
25	A Metastable Contact and Structural Disorder in the Estrogen Receptor Transactivation Domain. Structure, 2019, 27, 229-240.e4.	3.3	39
26	Cyclase-associated protein 1 (CAP1) is a prenyl-binding partner of Rap1 GTPase. Journal of Biological Chemistry, 2018, 293, 7659-7673.	3.4	19
27	A â€œTug of Warâ€•Maintains a Dynamic Proteinâ€“Membrane Complex: Molecular Dynamics Simulations of C-Raf RBD-CRD Bound to K-Ras4B at an Anionic Membrane. ACS Central Science, 2018, 4, 298-305.	11.3	54
28	Translocation of Human Î² Defensin Type 3 through a Neutrally Charged Lipid Membrane: A Free Energy Study. Journal of Physical Chemistry B, 2018, 122, 11883-11894.	2.6	11
29	Keys to Amyloid City: Computation and NMR Reveal Potential TDP-43 ALS Intermediates. Biophysical Journal, 2018, 115, 1625-1627.	0.5	1
30	Molecular Dynamics Simulations Reveal Isoform Specific Contact Dynamics between the Plexin Rho GTPase Binding Domain (RBD) and Small Rho GTPases Rac1 and Rnd1. Journal of Physical Chemistry B, 2017, 121, 1485-1498.	2.6	24
31	A role of the SAM domain in EphA2 receptor activation. Scientific Reports, 2017, 7, 45084.	3.3	36
32	Computational Modeling Reveals that Signaling Lipids Modulate the Orientation of K-Ras4A at the Membrane Reflecting Protein Topology. Structure, 2017, 25, 679-689.e2.	3.3	76
33	Characterizing Plexin GTPase Interactions Using Gel Filtration, Surface Plasmon Resonance Spectrometry, and Isothermal Titration Calorimetry. Methods in Molecular Biology, 2017, 1493, 89-105.	0.9	2
34	The RNA-Binding Site of Poliovirus 3C Protein Doubles as a Phosphoinositide-Binding Domain. Structure, 2017, 25, 1875-1886.e7.	3.3	20
35	LAR-RPTP Clustering Is Modulated by Competitive Binding between Synaptic Adhesion Partners and Heparan Sulfate. Frontiers in Molecular Neuroscience, 2017, 10, 327.	2.9	25
36	APOL1 variants change C-terminal conformational dynamics and binding to SNARE protein VAMP8. JCI Insight, 2017, 2, .	5.0	48

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37	Dissociation of a Dynamic Protein Complex Studied by All-Atom Molecular Simulations. Biophysical Journal, 2016, 110, 877-886.	0.5	34
38	K-Ras at Anionic Membranes: Orientation, Orientationâ€¦Orientation. Recent Simulations and Experiments. Biophysical Journal, 2016, 110, 1033-1035.	0.5	13
39	Modeling Transmembrane Domain Dimers/Trimers of Plexin Receptors: Implications for Mechanisms of Signal Transmission across the Membrane. PLoS ONE, 2015, 10, e0121513.	2.5	30
40	Binding and Function of Phosphotyrosines of the Ephrin A2 (EphA2) Receptor Using Synthetic Sterile Î± Motif (SAM) Domains. Journal of Biological Chemistry, 2014, 289, 19694-19703.	3.4	16
41	Structure and Dynamics Analysis on Plexin-B1 Rho GTPase Binding Domain as a Monomer and Dimer. Journal of Physical Chemistry B, 2014, 118, 7302-7311.	2.6	20
42	The cytoplasmic domain of neuropilinâ€1 regulates focal adhesion turnover. FEBS Letters, 2013, 587, 3392-3399.	2.8	16
43	Molecular Simulations of a Dynamic Protein Complex: Role of Salt-Bridges and Polar Interactions in Configurational Transitions. Biophysical Journal, 2013, 105, 2412-2417.	0.5	27
44	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. Journal of Physical Chemistry B, 2013, 117, 174-184.	2.6	28
45	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. Proteins: Structure, Function and Bioinformatics, 2013, 81, 365-376.	2.6	23
46	Backbone assignment and secondary structure of Rnd1, an unusual Rho family small GTPase. Biomolecular NMR Assignments, 2013, 7, 121-128.	0.8	3
47	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.	5.4	145
48	NMR Structure of a Heterodimeric SAM:SAM Complex: Characterization and Manipulation of EphA2 Binding Reveal New Cellular Functions of SHIP2. Structure, 2012, 20, 41-55.	3.3	56
49	Combining NMR and Molecular Dynamics Studies for Insights into the Allostery of Small GTPaseâ€“Protein Interactions. Methods in Molecular Biology, 2012, 796, 235-259.	0.9	31
50	Biochemical and mutational analysis of intracellular regions of the Plexinâ€B1 guidance receptor as a Râ€RasGAP. FASEB Journal, 2012, 26, 975.3.	0.5	0
51	A Direct Coupling between Global and Internal Motions in a Single Domain Protein? MD Investigation of Extreme Scenarios. Biophysical Journal, 2011, 101, 196-204.	0.5	13
52	Integrated Computational Approach to the Analysis of NMR Relaxation in Proteins: Application to psâ^ns Main Chain ¹⁵Nâ^’¹H and Global Dynamics of the Rho GTPase Binding Domain of Plexin-B1. Journal of Physical Chemistry B, 2011, 115, 376-388.	2.6	32
53	Structural Basis of Rnd1 Binding to Plexin Rho GTPase Binding Domains (RBDs). Journal of Biological Chemistry, 2011, 286, 26093-26106.	3.4	36
54	Optimization and stabilization of Rho small GTPase proteins for solution NMR studies. Small GTPases, 2011, 2, 295-304.	1.6	3

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55	Structure and Function of the Intracellular Region of the Plexin-B1 Transmembrane Receptor. Journal of Biological Chemistry, 2009, 284, 35962-35972.	3.4	81
56	Molecular profiling of the Ã¢Â€ÂœplexinomeÃ¢Â€Â•in melanoma and pancreatic cancer. Human Mutation, 2009, 30, 1167-1174.	2.5	40
57	Refinement of the primary hydration shell model for molecular dynamics simulations of large proteins. Journal of Computational Chemistry, 2009, 30, 2635-2644.	3.3	4
58	Thermodynamic characterization of two homologous protein complexes: Associations of the semaphorin receptor plexinâ€B1 RhoGTPase binding domain with Rnd1 and active Rac1. Protein Science, 2009, 18, 1060-1071.	7.6	34
59	Ligand recognition by Aâ€class Eph receptors: crystal structures of the EphA2 ligandâ€binding domain and the EphA2/ephrinâ€A1 complex. EMBO Reports, 2009, 10, 722-728.	4.5	106
60	EPHA2 Is Associated with Age-Related Cortical Cataract in Mice and Humans. PLoS Genetics, 2009, 5, e1000584.	3.5	140
61	Insights into Oncogenic Mutations of Plexin-B1 Based on the Solution Structure of the Rho GTPase Binding Domain. Structure, 2008, 16, 246-258.	3.3	41
62	Tripping a Switch: PDZRhoGEF rgRGS-Bound Gα13. Structure, 2008, 16, 1439-1441.	3.3	2
63	Compensatory and Long-Range Changes in Picosecondâ€“Nanosecond Main-Chain Dynamics upon Complex Formation: 15N Relaxation Analysis of the Free and Bound States of the Ubiquitin-like Domain of Human Plexin-B1 and the Small GTPase Rac1. Journal of Molecular Biology, 2008, 377, 1474-1487.	4.2	50
64	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.	3.4	123
65	Acceptable Protein and Solvent Behavior in Primary Hydration Shell Simulations of Hen Lysozyme. Biophysical Journal, 2007, 92, L49-L51.	0.5	13
66	Importance of the CMAP Correction to the CHARMM22 Protein Force Field: Dynamics of Hen Lysozyme. Biophysical Journal, 2006, 90, L36-L38.	0.5	321
67	1H, 15N, 13C assignments for the activated form of the small Rho-GTPase Rac1. Journal of Biomolecular NMR, 2006, 36, 51-51.	2.8	4
68	When Monomers Are Preferred: A Strategy for the Identification and Disruption of Weakly Oligomerized Proteins. Structure, 2005, 13, 7-15.	3.3	30
69	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. Journal of Biomolecular NMR, 2005, 31, 369-370.	2.8	22
70	G Protein Î²2 Subunit-derived Peptides for Inhibition and Induction of G Protein Pathways. Journal of Biological Chemistry, 2005, 280, 23945-23959.	3.4	21
71	A Two-State Allosteric Model for Autoinhibition Rationalizes WASP Signal Integration and Targeting. Journal of Molecular Biology, 2004, 338, 271-285.	4.2	51
72	Crystallography. Structure, 2003, 11, 735-736.	3.3	7

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73	Backbone Dynamics of the Ribonuclease Binase Active Site Area Using Multinuclear (15N and13CO) NMR Relaxation and Computational Molecular Dynamicsâ€. Biochemistry, 2002, 41, 2655-2666.	2.5	40
74	Hydrogen Bond Energetics:Â A Simulation and Statistical Analysis ofN-Methyl Acetamide (NMA), Water, and Human Lysozymeâ€. Journal of Physical Chemistry B, 2001, 105, 11000-11015.	2.6	79
75	Global Disruption of the WASP Autoinhibited Structure on Cdc42 Binding. Ligand Displacement as a Novel Method for Monitoring Amide Hydrogen Exchange. Biochemistry, 2001, 40, 14115-14122.	2.5	19
76	A refined solution structure of hen lysozyme determined using residual dipolar coupling data. Protein Science, 2001, 10, 677-688.	7.6	159
77	STRUCTURAL BIOLOGY: Flipping a Switch. Science, 2001, 291, 2329-2330.	12.6	12
78	Internal and Overall Peptide Group Motion in Proteins:â€‰ Molecular Dynamics Simulations for Lysozyme Compared with Results from X-ray and NMR Spectroscopy. Journal of the American Chemical Society, 1999, 121, 9645-9658.	13.7	52
79	Trifluoroethanol and colleagues: cosolvents come of age. Recent studies with peptides and proteins. Quarterly Reviews of Biophysics, 1998, 31, 297-355.	5.7	760
80	Structural and Dynamical Properties of a Denatured Protein. Heteronuclear 3D NMR Experiments and Theoretical Simulations of Lysozyme in 8 M Ureaâ€. Biochemistry, 1997, 36, 8977-8991.	2.5	296
81	Acceleration of the folding of hen lysozyme by trifluoroethanol. Journal of Molecular Biology, 1997, 265, 112-117.	4.2	86
82	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.	4.2	96
83	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
84	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.	2.5	151
85	Conformational Properties of Four Peptides Spanning the Sequence of Hen Lysozyme. Journal of Molecular Biology, 1995, 252, 483-491.	4.2	121
86	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.	2.5	211
87	Equilibrium Unfolding Studies of Horse Muscle Acylphosphatase. FEBS Journal, 1994, 225, 811-817.	0.2	20
88	Amide Hydrogen Exchange in a Highly Denatured State. Journal of Molecular Biology, 1994, 237, 247-254.	4.2	103
89	A partially folded state of hen egg white lysozyme in trifluoroethanol: structural characterization and implications for protein folding. Biochemistry, 1993, 32, 669-678.	2.5	284
90	Hydrogen exchange in native and denatured states of hen egg-white lysozyme. Proteins: Structure, Function and Bioinformatics, 1992, 14, 237-248.	2.6	170