

Matthias Buck

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88
papers

4,305
citations

30
h-index

65
g-index

127
ext. papers

4,745
ext. citations

4.9
avg, IF

5.66
L-index

#	Paper	IF	Citations
88	Trifluoroethanol and colleagues: cosolvents come of age. Recent studies with peptides and proteins. <i>Quarterly Reviews of Biophysics</i> , 1998 , 31, 297-355	7	687
87	Structural and dynamical properties of a denatured protein. Heteronuclear 3D NMR experiments and theoretical simulations of lysozyme in 8 M urea. <i>Biochemistry</i> , 1997 , 36, 8977-91	3.2	271
86	A partially folded state of hen egg white lysozyme in trifluoroethanol: structural characterization and implications for protein folding. <i>Biochemistry</i> , 1993 , 32, 669-78	3.2	264
85	Importance of the CMAP correction to the CHARMM22 protein force field: dynamics of hen lysozyme. <i>Biophysical Journal</i> , 2006 , 90, L36-8	2.9	263
84	Structural determinants of protein dynamics: analysis of 15N NMR relaxation measurements for main-chain and side-chain nuclei of hen egg white lysozyme. <i>Biochemistry</i> , 1995 , 34, 4041-55	3.2	197
83	Hydrogen exchange in native and denatured states of hen egg-white lysozyme. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992 , 14, 237-48	4.2	151
82	Toward a Description of the Conformations of Denatured States of Proteins. Comparison of a Random Coil Model with NMR Measurements. <i>The Journal of Physical Chemistry</i> , 1996 , 100, 2661-2666		148
81	A refined solution structure of hen lysozyme determined using residual dipolar coupling data. <i>Protein Science</i> , 2001 , 10, 677-88	6.3	141
80	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. <i>Biochemistry</i> , 1995 , 34, 13219-32	3.2	141
79	Plexin structures are coming: opportunities for multilevel investigations of semaphorin guidance receptors, their cell signaling mechanisms, and functions. <i>Cellular and Molecular Life Sciences</i> , 2012 , 69, 3765-805	10.3	119
78	EPHA2 is associated with age-related cortical cataract in mice and humans. <i>PLoS Genetics</i> , 2009 , 5, e1000584		114
77	Conformational properties of four peptides spanning the sequence of hen lysozyme. <i>Journal of Molecular Biology</i> , 1995 , 252, 483-91	6.5	112
76	Binding of Rac1, Rnd1, and RhoD to a novel Rho GTPase interaction motif destabilizes dimerization of the plexin-B1 effector domain. <i>Journal of Biological Chemistry</i> , 2007 , 282, 37215-24	5.4	101
75	Main-chain dynamics of a partially folded protein: 15N NMR relaxation measurements of hen egg white lysozyme denatured in trifluoroethanol. <i>Journal of Molecular Biology</i> , 1996 , 257, 669-83	6.5	93
74	Amide hydrogen exchange in a highly denatured state. Hen egg-white lysozyme in urea. <i>Journal of Molecular Biology</i> , 1994 , 237, 247-54	6.5	93
73	Ligand recognition by A-class Eph receptors: crystal structures of the EphA2 ligand-binding domain and the EphA2/ephrin-A1 complex. <i>EMBO Reports</i> , 2009 , 10, 722-8	6.5	90
72	Acceleration of the folding of hen lysozyme by trifluoroethanol. <i>Journal of Molecular Biology</i> , 1997 , 265, 112-7	6.5	84

71	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	3.4	73
70	Structure and function of the intracellular region of the plexin-b1 transmembrane receptor. <i>Journal of Biological Chemistry</i> , 2009 , 284, 35962-72	5.4	71
69	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	5.2	58
68	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	16.4	51
67	A two-state allosteric model for autoinhibition rationalizes WASP signal integration and targeting. <i>Journal of Molecular Biology</i> , 2004 , 338, 271-85	6.5	49
66	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	5.2	47
65	Compensatory and long-range changes in picosecond-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. <i>Journal of Molecular Biology</i> , 2008 , 377, 1474-87	6.5	43
64	A "Tug of War" 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	16.8	40
63	Backbone dynamics of the ribonuclease binase active site area using multinuclear ((15)N and (13)CO) NMR relaxation and computational molecular dynamics. <i>Biochemistry</i> , 2002 , 41, 2655-66	3.2	39
62	Insights into oncogenic mutations of plexin-B1 based on the solution structure of the Rho GTPase binding domain. <i>Structure</i> , 2008 , 16, 246-58	5.2	35
61	Molecular profiling of the "plexinome" in melanoma and pancreatic cancer. <i>Human Mutation</i> , 2009 , 30, 1167-74	4.7	34
60	Structural basis of Rnd1 binding to plexin Rho GTPase binding domains (RBDs). <i>Journal of Biological Chemistry</i> , 2011 , 286, 26093-106	5.4	33
59	A Metastable Contact and Structural Disorder in the Estrogen Receptor Transactivation Domain. <i>Structure</i> , 2019 , 27, 229-240.e4	5.2	31
58	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	5.4	30
57	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, 1060-71	6.3	30
56	APOL1 variants change C-terminal conformational dynamics and binding to SNARE protein VAMP8. <i>JCI Insight</i> , 2017 , 2,	9.9	30
55	When monomers are preferred: a strategy for the identification and disruption of weakly oligomerized proteins. <i>Structure</i> , 2005 , 13, 7-15	5.2	29
54	A role of the SAM domain in EphA2 receptor activation. <i>Scientific Reports</i> , 2017 , 7, 45084	4.9	28

53	Dissociation of a Dynamic Protein Complex Studied by All-Atom Molecular Simulations. <i>Biophysical Journal</i> , 2016 , 110, 877-86	2.9	25
52	Molecular simulations of a dynamic protein complex: role of salt-bridges and polar interactions in configurational transitions. <i>Biophysical Journal</i> , 2013 , 105, 2412-7	2.9	24
51	Integrated computational approach to the analysis of NMR relaxation in proteins: application to ps-ns main chain 15N-1H and global dynamics of the Rho GTPase binding domain of plexin-B1. <i>Journal of Physical Chemistry B</i> , 2011 , 115, 376-88	3.4	24
50	Combining NMR and molecular dynamics studies for insights into the allostery of small GTPase-protein interactions. <i>Methods in Molecular Biology</i> , 2012 , 796, 235-59	1.4	23
49	Analysis of 15N-1H NMR relaxation in proteins by a combined experimental and molecular dynamics simulation approach: picosecond-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, 174-84	3.4	21
48	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, 365-76	4.2	21
47	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, 369-70	3	21
46	G protein beta2 subunit-derived peptides for inhibition and induction of G protein pathways. Examination of voltage-gated Ca2+ and G protein inwardly rectifying K+ channels. <i>Journal of Biological Chemistry</i> , 2005 , 280, 23945-59	5.4	20
45	Modeling transmembrane domain dimers/trimers of plexin receptors: implications for mechanisms of signal transmission across the membrane. <i>PLoS ONE</i> , 2015 , 10, e0121513	3.7	20
44	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	2.9	19
43	LAR-RPTP Clustering Is Modulated by Competitive Binding between Synaptic Adhesion Partners and Heparan Sulfate. <i>Frontiers in Molecular Neuroscience</i> , 2017 , 10, 327	6.1	18
42	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, 14115-22	3.2	18
41	Equilibrium unfolding studies of horse muscle acylphosphatase. <i>FEBS Journal</i> , 1994 , 225, 811-7		18
40	The RNA-Binding Site of Poliovirus 3C Protein Doubles as a Phosphoinositide-Binding Domain. <i>Structure</i> , 2017 , 25, 1875-1886.e7	5.2	14
39	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,	11.5	14
38	K-Ras at Anionic Membranes: Orientation, Orientation Orientation. Recent Simulations and Experiments. <i>Biophysical Journal</i> , 2016 , 110, 1033-5	2.9	13
37	The cytoplasmic domain of neuropilin-1 regulates focal adhesion turnover. <i>FEBS Letters</i> , 2013 , 587, 3392-8	3.9	13
36	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	2.9	12

35	Acceptable protein and solvent behavior in primary hydration shell simulations of hen lysozyme. <i>Biophysical Journal</i> , 2007 , 92, L49-51	2.9	12
34	Modified Potential Functions Result in Enhanced Predictions of a Protein Complex by All-Atom Molecular Dynamics Simulations, Confirming a Stepwise Association Process for Native Protein-Protein Interactions. <i>Journal of Chemical Theory and Computation</i> , 2019 , 15, 4318-4331	6.4	11
33	Cyclase-associated protein 1 (CAP1) is a prenyl-binding partner of Rap1 GTPase. <i>Journal of Biological Chemistry</i> , 2018 , 293, 7659-7673	5.4	11
32	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, 7302-11	3.4	11
31	Structural biology. Flipping a switch. <i>Science</i> , 2001 , 291, 2329-30	33.3	11
30	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	3.4	10
29	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, 19694-703	5.4	10
28	Translocation of Human α -Defensin Type 3 through a Neutrally Charged Lipid Membrane: A Free Energy Study. <i>Journal of Physical Chemistry B</i> , 2018 , 122, 11883-11894	3.4	8
27	Molecular dynamics simulations and functional studies reveal that hBD-2 binds SARS-CoV-2 spike RBD and blocks viral entry into ACE2 expressing cells 2021 ,		7
26	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	6.1	6
25	Neuropilin-1 Assists SARS-CoV-2 Infection by Stimulating the Separation of Spike Protein Domains S1 and S2 2021 ,		5
24	Refinement of the primary hydration shell model for molecular dynamics simulations of large proteins. <i>Journal of Computational Chemistry</i> , 2009 , 30, 2635-44	3.5	4
23	¹ H, ¹⁵ N, ¹³ C assignments for the activated form of the small Rho-GTPase Rac1. <i>Journal of Biomolecular NMR</i> , 2006 , 36 Suppl 1, 51	3	4
22	Backbone assignment and secondary structure of Rnd1, an unusual Rho family small GTPase. <i>Biomolecular NMR Assignments</i> , 2013 , 7, 121-8	0.7	3
21	Optimization and stabilization of Rho small GTPase proteins for solution NMR studies: The case of Rnd1. <i>Small GTPases</i> , 2011 , 2, 295-304	2.7	3
20	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,	11.5	3
19	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	10.3	3
18	Conformational Clamping by a Membrane Ligand Activates the EphA2 Receptor. <i>Journal of Molecular Biology</i> , 2021 , 433, 167144	6.5	3

17	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	3.4	2
16	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	3.4	2
15	Structural and Functional Insights into the Transmembrane Domain Association of Eph Receptors. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	2
14	Two Hands Grip Better Than One for Tight Binding and Specificity: How a Phage Endolysin Fits into the Cell Wall of Its Host. <i>Structure</i> , 2019 , 27, 1350-1352	5.2	1
13	Characterizing Plexin GTPase Interactions Using Gel Filtration, Surface Plasmon Resonance Spectrometry, and Isothermal Titration Calorimetry. <i>Methods in Molecular Biology</i> , 2017 , 1493, 89-105	1.4	1
12	HBD-2 binds SARS-CoV-2 RBD and blocks viral entry: Strategy to combat COVID-19.. <i>iScience</i> , 2022 , 103866		1
11	The Relationship between APOL1 Structure and Function: Clinical Implications.. <i>Kidney360</i> , 2021 , 2, 134-140		1
10	Modified Potential Functions Result in Enhanced Predictions of a Protein Complex by All-Atom MD Simulations, Confirming a Step-wise Association Process for Native PPIs		1
9	K-Ras G-domain binding with signaling lipid phosphoinositides: PIP2 association, orientation, function		1
8	Beyond history and "on a roll": The list of the most well-studied human protein structures and overall trends in the protein data bank. <i>Protein Science</i> , 2021 , 30, 745-760	6.3	1
7	Conformational clamping by a membrane ligand activates the EphA2 receptor		1
6	Interactions between semaphorins and plexin-neuropilin receptor complexes in the membranes of live cells. <i>Journal of Biological Chemistry</i> , 2021 , 297, 100965	5.4	1
5	Tripping a switch: PDZRhoGEF rgRGS-bound Galpha13. <i>Structure</i> , 2008 , 16, 1439-41	5.2	0
4	Membrane Proteins The Plexin Family of Transmembrane Receptors 2021 , 594-610		0
3	Keys to Amyloid City: Computation and NMR Reveal Potential TDP-43 ALS Intermediates. <i>Biophysical Journal</i> , 2018 , 115, 1625-1627	2.9	0
2	Biochemical and mutational analysis of intracellular regions of the Plexin-B1 guidance receptor as a R-RasGAP. <i>FASEB Journal</i> , 2012 , 26, 975.3	0.9	
1	Letting go: Deep computational modeling insights into pH-dependent calcium affinity. <i>Journal of Biological Chemistry</i> , 2021 , 297, 100974	5.4	