Matthias Buck

List of Publications by Year in Descending Order

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	HBD-2 binds SARS-CoV-2 RBD and blocks viral entry: Strategy to combat COVID-19.. *IScience*, **2022**, 103856	5.1	1
87	The Relationship between APOL1 Structure and Function: Clinical Implications.. *Kidney360*, **2021**, 2, 134-140	1.8	1
86	Beyond history and "on 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	6.3	1
85	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,	11.5	14
84	Neuropilin-1 assists SARS-CoV-2 infection by stimulating the separation of Spike protein S1 and S2. *Biophysical Journal*, **2021**, 120, 2828-2837	2.9	19
83	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,	11.5	3
82	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	10.3	3
81	Membrane Proteins | The Plexin Family of Transmembrane Receptors **2021**, 594-610		0
80	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
79	Letting go: Deep computational modeling insights into pH-dependent calcium affinity. *Journal of Biological Chemistry*, **2021**, 297, 100974	5.4	
78	Interactions between semaphorins and plexin-neuropilin receptor complexes in the membranes of live cells. *Journal of Biological Chemistry*, **2021**, 297, 100965	5.4	1
77	Structural and Functional Insights into the Transmembrane Domain Association of Eph Receptors. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	2
76	Conformational Clamping by a Membrane Ligand Activates the EphA2 Receptor. *Journal of Molecular Biology*, **2021**, 433, 167144	6.5	3
75	Neuropilin-1 Assists SARS-CoV-2 Infection by Stimulating the Separation of Spike Protein Domains S1 and S2 **2021**,		5
74	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	6.1	6
73	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	3.4	2
72	Local Ordering at the N-H Sites of the Rho GTPase Binding Domain of Plexin-B1: Impact of Dimerization. *Journal of Physical Chemistry B*, **2019**, 123, 8019-8033	3.4	2

71	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	5.2	1
70	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. *Journal of Chemical Theory and Computation*, **2019**, 15, 4318-4331	6.4	11
69	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	5.4	30
68	A Metastable Contact and Structural Disorder in the Estrogen Receptor Transactivation Domain. *Structure*, **2019**, 27, 229-240.e4	5.2	31
67	Cyclase-associated protein 1 (CAP1) is a prenyl-binding partner of Rap1 GTPase. *Journal of Biological Chemistry*, **2018**, 293, 7659-7673	5.4	11
66	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. *ACS Central Science*, **2018**, 4, 298-305	16.8	40
65	Translocation of Human Defensin Type 3 through a Neutrally Charged Lipid Membrane: A Free Energy Study. *Journal of Physical Chemistry B*, **2018**, 122, 11883-11894	3.4	8
64	Keys to Amyloid City: Computation and NMR Reveal Potential TDP-43 ALS Intermediates. *Biophysical Journal*, **2018**, 115, 1625-1627	2.9	0
63	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	3.4	10
62	A role of the SAM domain in EphA2 receptor activation. *Scientific Reports*, **2017**, 7, 45084	4.9	28
61	Computational Modeling Reveals that Signaling Lipids Modulate the Orientation of K-Ras4A at the Membrane Reflecting Protein Topology. *Structure*, **2017**, 25, 679-689.e2	5.2	58
60	Characterizing Plexin GTPase Interactions Using Gel Filtration, Surface Plasmon Resonance Spectrometry, and Isothermal Titration Calorimetry. *Methods in Molecular Biology*, **2017**, 1493, 89-105	1.4	1
59	The RNA-Binding Site of Poliovirus 3C Protein Doubles as a Phosphoinositide-Binding Domain. *Structure*, **2017**, 25, 1875-1886.e7	5.2	14
58	LAR-RPTP Clustering Is Modulated by Competitive Binding between Synaptic Adhesion Partners and Heparan Sulfate. *Frontiers in Molecular Neuroscience*, **2017**, 10, 327	6.1	18
57	APOL1 variants change C-terminal conformational dynamics and binding to SNARE protein VAMP8. *JCI Insight*, **2017**, 2,	9.9	30
56	K-Ras at Anionic Membranes: Orientation, Orientation Orientation. Recent Simulations and Experiments. *Biophysical Journal*, **2016**, 110, 1033-5	2.9	13
55	Dissociation of a Dynamic Protein Complex Studied by All-Atom Molecular Simulations. *Biophysical Journal*, **2016**, 110, 877-86	2.9	25
54	Modeling transmembrane domain dimers/trimers of plexin receptors: implications for mechanisms of signal transmission across the membrane. *PLoS ONE*, **2015**, 10, e0121513	3.7	20

53	Structure and dynamics analysis on plexin-B1 Rho GTPase binding domain as a monomer and dimer. *Journal of Physical Chemistry B*, **2014**, 118, 7302-11	3.4	11
52	Binding and function of phosphotyrosines of the Ephrin A2 (EphA2) receptor using synthetic sterile motif (SAM) domains. *Journal of Biological Chemistry*, **2014**, 289, 19694-703	5.4	10
51	The cytoplasmic domain of neuropilin-1 regulates focal adhesion turnover. *FEBS Letters*, **2013**, 587, 3392-98	3.8	13
50	Molecular simulations of a dynamic protein complex: role of salt-bridges and polar interactions in configurational transitions. *Biophysical Journal*, **2013**, 105, 2412-7	2.9	24
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. *Journal of Physical Chemistry B*, **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. *Proteins: Structure, Function and Bioinformatics*, **2013**, 81, 365-76	4.2	21
47	Backbone assignment and secondary structure of Rnd1, an unusual Rho family small GTPase. *Biomolecular NMR Assignments*, **2013**, 7, 121-8	0.7	3
46	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	5.2	47
45	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, 3765-805	10.3	119
44	Combining NMR and molecular dynamics studies for insights into the allostery of small GTPase-protein interactions. *Methods in Molecular Biology*, **2012**, 796, 235-59	1.4	23
43	Biochemical and mutational analysis of intracellular regions of the Plexin-B1 guidance receptor as a R-RasGAP. *FASEB Journal*, **2012**, 26, 975.3	0.9	
42	A direct coupling between global and internal motions in a single domain protein? MD investigation of extreme scenarios. *Biophysical Journal*, **2011**, 101, 196-204	2.9	12
41	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. *Journal of Physical Chemistry B*, **2011**, 115, 376-88	3.4	24
40	Structural basis of Rnd1 binding to plexin Rho GTPase binding domains (RBDs). *Journal of Biological Chemistry*, **2011**, 286, 26093-106	5.4	33
39	Optimization and stabilization of Rho small GTPase proteins for solution NMR studies: The case of Rnd1. *Small GTPases*, **2011**, 2, 295-304	2.7	3
38	Structure and function of the intracellular region of the plexin-b1 transmembrane receptor. *Journal of Biological Chemistry*, **2009**, 284, 35962-72	5.4	71
37	Molecular profiling of the "plexinome" in melanoma and pancreatic cancer. *Human Mutation*, **2009**, 30, 1167-74	4.7	34
36	Refinement of the primary hydration shell model for molecular dynamics simulations of large proteins. *Journal of Computational Chemistry*, **2009**, 30, 2635-44	3.5	4

35	Thermodynamic characterization of two homologous protein complexes: associations of the semaphorin receptor plexin-B1 RhoGTPase binding domain with Rnd1 and active Rac1. *Protein Science*, **2009**, 18, 1060-71	6.3	30
34	Ligand recognition by A-class Eph receptors: crystal structures of the EphA2 ligand-binding domain and the EphA2/ephrin-A1 complex. *EMBO Reports*, **2009**, 10, 722-8	6.5	90
33	EPHA2 is associated with age-related cortical cataract in mice and humans. *PLoS Genetics*, **2009**, 5, e1000584	6	114
32	Insights into oncogenic mutations of plexin-B1 based on the solution structure of the Rho GTPase binding domain. *Structure*, **2008**, 16, 246-58	5.2	35
31	Tripping a switch: PDZRhoGEF rgRGS-bound Galpha13. *Structure*, **2008**, 16, 1439-41	5.2	0
30	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. *Journal of Molecular Biology*, **2008**, 377, 1474-87	6.5	43
29	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, 37215-24	5.4	101
28	Acceptable protein and solvent behavior in primary hydration shell simulations of hen lysozyme. *Biophysical Journal*, **2007**, 92, L49-51	2.9	12
27	Importance of the CMAP correction to the CHARMM22 protein force field: dynamics of hen lysozyme. *Biophysical Journal*, **2006**, 90, L36-8	2.9	263
26	1H, 15N, 13C assignments for the activated form of the small Rho-GTPase Rac1. *Journal of Biomolecular NMR*, **2006**, 36 Suppl 1, 51	3	4
25	When monomers are preferred: a strategy for the identification and disruption of weakly oligomerized proteins. *Structure*, **2005**, 13, 7-15	5.2	29
24	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, 369-70	3	21
23	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. *Journal of Biological Chemistry*, **2005**, 280, 23945-59	5.4	20
22	A two-state allosteric model for autoinhibition rationalizes WASP signal integration and targeting. *Journal of Molecular Biology*, **2004**, 338, 271-85	6.5	49
21	Backbone dynamics of the ribonuclease binase active site area using multinuclear ((15)N and (13)CO) NMR relaxation and computational molecular dynamics. *Biochemistry*, **2002**, 41, 2655-66	3.2	39
20	A refined solution structure of hen lysozyme determined using residual dipolar coupling data. *Protein Science*, **2001**, 10, 677-88	6.3	141
19	Hydrogen Bond Energetics: A Simulation and Statistical Analysis of N-Methyl Acetamide (NMA), Water, and Human Lysozyme *Journal of Physical Chemistry B*, **2001**, 105, 11000-11015	3.4	73
18	Global disruption of the WASP autoinhibited structure on Cdc42 binding. Ligand displacement as a novel method for monitoring amide hydrogen exchange. *Biochemistry*, **2001**, 40, 14115-22	3.2	18

17	Structural biology. Flipping a switch. *Science*, **2001**, 291, 2329-30	33.3	11
16	Internal and Overall Peptide Group Motion in Proteins: Molecular Dynamics Simulations for Lysozyme Compared with Results from X-ray and NMR Spectroscopy. *Journal of the American Chemical Society*, **1999**, 121, 9645-9658	16.4	51
15	Trifluoroethanol and colleagues: cosolvents come of age. Recent studies with peptides and proteins. *Quarterly Reviews of Biophysics*, **1998**, 31, 297-355	7	687
14	Structural and dynamical properties of a denatured protein. Heteronuclear 3D NMR experiments and theoretical simulations of lysozyme in 8 M urea. *Biochemistry*, **1997**, 36, 8977-91	3.2	271
13	Acceleration of the folding of hen lysozyme by trifluoroethanol. *Journal of Molecular Biology*, **1997**, 265, 112-7	6.5	84
12	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, 669-83	6.5	93
11	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		148
10	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, 13219-32	3.2	141
9	Conformational properties of four peptides spanning the sequence of hen lysozyme. *Journal of Molecular Biology*, **1995**, 252, 483-91	6.5	112
8	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, 4041-55	3.2	197
7	Equilibrium unfolding studies of horse muscle acylphosphatase. *FEBS Journal*, **1994**, 225, 811-7		18
6	Amide hydrogen exchange in a highly denatured state. Hen egg-white lysozyme in urea. *Journal of Molecular Biology*, **1994**, 237, 247-54	6.5	93
5	A partially folded state of hen egg white lysozyme in trifluoroethanol: structural characterization and implications for protein folding. *Biochemistry*, **1993**, 32, 669-78	3.2	264
4	Hydrogen exchange in native and denatured states of hen egg-white lysozyme. *Proteins: Structure, Function and Bioinformatics*, **1992**, 14, 237-48	4.2	151
3	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
2	K-Ras G-domain binding with signaling lipid phosphoinositides: PIP2 association, orientation, function		1
1	Conformational clamping by a membrane ligand activates the EphA2 receptor		1