

# Matthias Buck

## List of Publications by Year in descending order

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90  
papers

5,107  
citations

126907

33  
h-index

88630

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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.  | 5.7 | 760       |
| 2  | Importance of the CMAP Correction to the CHARMM22 Protein Force Field: Dynamics of Hen Lysozyme. Biophysical Journal, 2006, 90, L36-L38.   | 0.5 | 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.   | 2.5 | 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.   | 2.5 | 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.  | 2.5 | 211       |
| 6  | Hydrogen exchange in native and denatured states of hen egg-white lysozyme. Proteins: Structure, Function and Bioinformatics, 1992, 14, 237-248.   | 2.6 | 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.  | 7.6 | 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. | 2.5 | 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.                       | 5.4 | 145       |
| 11 | EPHA2 Is Associated with Age-Related Cortical Cataract in Mice and Humans. PLoS Genetics, 2009, 5, e1000584.   | 3.5 | 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.   | 3.4 | 123       |
| 13 | Conformational Properties of Four Peptides Spanning the Sequence of Hen Lysozyme. Journal of Molecular Biology, 1995, 252, 483-491.  | 4.2 | 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.  | 4.5 | 106       |
| 15 | Amide Hydrogen Exchange in a Highly Denatured State. Journal of Molecular Biology, 1994, 237, 247-254.   | 4.2 | 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.  | 4.2 | 96        |
| 17 | Acceleration of the folding of hen lysozyme by trifluoroethanol. Journal of Molecular Biology, 1997, 265, 112-117.   | 4.2 | 86        |
| 18 | Structure and Function of the Intracellular Region of the Plexin-B1 Transmembrane Receptor. Journal of Biological Chemistry, 2009, 284, 35962-35972.   | 3.4 | 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.   | 2.6  | 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.   | 3.3  | 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.   | 3.3  | 56        |
| 22 | A $\alpha$ -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.  | 11.3 | 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.  | 13.7 | 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.  | 4.2  | 51        |
| 25 | Compensatory and Long-Range Changes in Picosecond-Nanosecond Main-Chain Dynamics upon Complex Formation: $^{15}\text{N}$ 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. | 4.2  | 50        |
| 26 | APOL1 variants change C-terminal conformational dynamics and binding to SNARE protein VAMP8. <i>JCI Insight</i> , 2017, 2, .   | 5.0  | 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.   | 3.4  | 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.   | 0.5  | 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.   | 3.3  | 41        |
| 30 | Backbone Dynamics of the Ribonuclease Binase Active Site Area Using Multinuclear ( $^{15}\text{N}$ and $^{13}\text{C}$ ) NMR Relaxation and Computational Molecular Dynamics. <i>Biochemistry</i> , 2002, 41, 2655-2666.   | 2.5  | 40        |
| 31 | Molecular profiling of the plexinome in melanoma and pancreatic cancer. <i>Human Mutation</i> , 2009, 30, 1167-1174.   | 2.5  | 40        |
| 32 | A Metastable Contact and Structural Disorder in the Estrogen Receptor Transactivation Domain. <i>Structure</i> , 2019, 27, 229-240.e4.   | 3.3  | 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, .   | 7.1  | 39        |
| 34 | Structural Basis of Rnd1 Binding to Plexin Rho GTPase Binding Domains (RBDs). <i>Journal of Biological Chemistry</i> , 2011, 286, 26093-26106.   | 3.4  | 36        |
| 35 | A role of the SAM domain in EphA2 receptor activation. <i>Scientific Reports</i> , 2017, 7, 45084.   | 3.3  | 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.  | 7.6  | 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.  | 0.5 | 34        |
| 38 | Integrated Computational Approach to the Analysis of NMR Relaxation in Proteins: Application to psâns Main Chain <sup>15</sup>Nâ”’<sup>1</sup>H and Global Dynamics of the Rho GTPase Binding Domain of Plexin-B1. <i>Journal of Physical Chemistry B</i> , 2011, 115, 376-388.  | 2.6 | 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, .   | 7.1 | 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.   | 0.9 | 31        |
| 41 | When Monomers Are Preferred: A Strategy for the Identification and Disruption of Weakly Oligomerized Proteins. <i>Structure</i> , 2005, 13, 7-15.  | 3.3 | 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.  | 2.5 | 30        |
| 43 | Analysis of <sup>15</sup>Nâ€”<sup>1</sup>H 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. | 2.6 | 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.   | 0.5 | 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.  | 2.9 | 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.   | 2.6 | 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.  | 2.6 | 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.   | 5.3 | 23        |
| 49 | HBD-2 binds SARS-CoV-2 RBD and blocks viral entry: Strategy to combat COVID-19. <i>IScience</i> , 2022, 25, 103856.  | 4.1 | 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.  | 2.8 | 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.  | 3.4 | 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.  | 2.6 | 20        |
| 54 | The RNA-Binding Site of Poliovirus 3C Protein Doubles as a Phosphoinositide-Binding Domain. <i>Structure</i> , 2017, 25, 1875-1886.e7.   | 3.3 | 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.                       | 2.5  | 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.   | 3.4  | 19        |
| 57 | The cytoplasmic domain of neuropilin-1 regulates focal adhesion turnover. <i>FEBS Letters</i> , 2013, 587, 3392-3399.  | 2.8  | 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.                                 | 3.4  | 16        |
| 59 | Acceptable Protein and Solvent Behavior in Primary Hydration Shell Simulations of Hen Lysozyme. <i>Biophysical Journal</i> , 2007, 92, L49-L51.  | 0.5  | 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.  | 0.5  | 13        |
| 61 | K-Ras at Anionic Membranes: Orientation, Orientation, Orientation. <i>Recent Simulations and Experiments. Biophysical Journal</i> , 2016, 110, 1033-1035.  | 0.5  | 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.      | 5.4  | 12        |
| 63 | STRUCTURAL BIOLOGY: Flipping a Switch. <i>Science</i> , 2001, 291, 2329-2330.  | 12.6 | 12        |
| 64 | Translocation of Human $\beta$ 2 Defensin Type 3 through a Neutrally Charged Lipid Membrane: A Free Energy Study. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11883-11894.                                       | 2.6  | 11        |
| 65 | Conformational Clamping by a Membrane Ligand Activates the EphA2 Receptor. <i>Journal of Molecular Biology</i> , 2021, 433, 167144.  | 4.2  | 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. | 2.6  | 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.   | 5.4  | 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.  | 3.4  | 9         |
| 69 | Structural and Functional Insights into the Transmembrane Domain Association of Eph Receptors. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8593.  | 4.1  | 9         |
| 70 | Computational studies of the principle of dynamic-change-driven protein interactions. <i>Structure</i> , 2022, , .   | 3.3  | 8         |
| 71 | Crystallography. <i>Structure</i> , 2003, 11, 735-736.   | 3.3  | 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.  | 2.6  | 6         |

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|----|---|-----|-----------|
| 73 | <sup>1</sup> H, <sup>15</sup> N, <sup>13</sup> C assignments for the activated form of the small Rho-GTPase Rac1. Journal of Biomolecular NMR, 2006, 36, 51-51.                                 | 2.8 | 4         |
| 74 | 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         |
| 75 | Optimization and stabilization of Rho small GTPase proteins for solution NMR studies. Small GTPases, 2011, 2, 295-304.  | 1.6 | 3         |
| 76 | Backbone assignment and secondary structure of Rnd1, an unusual Rho family small GTPase. Biomolecular NMR Assignments, 2013, 7, 121-128.  | 0.8 | 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.                          | 7.6 | 3         |
| 78 | The Relationship between APOL1 Structure and Function: Clinical Implications. Kidney360, 2021, 2, 134-140.  | 2.1 | 3         |
| 79 | Tripping a Switch: PDZRhoGEF rgRGS-Bound G13. Structure, 2008, 16, 1439-1441.   | 3.3 | 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. | 0.9 | 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.                                    | 3.3 | 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.   | 0.5 | 1         |
| 84 | Biophysica: A New International Open Access Journal to Integrate Across the Modern Biophysical Sciences and Engineering. Biophysica, 2021, 1, 73-74.  | 1.4 | 1         |
| 85 | Understanding the Structural Basis of Epha2 dimerization, membrane Interactions and Its Implications in Cancer Progression. FASEB Journal, 2021, 35, .  | 0.5 | 0         |
| 86 | Raf promotes dimerization of the Ras G domain with increased allosteric connections. FASEB Journal, 2021, 35, .   | 0.5 | 0         |
| 87 | Letting go: Deep computational modeling insights into pH-dependent calcium affinity. Journal of Biological Chemistry, 2021, 297, 100974.  | 3.4 | 0         |
| 88 | Biochemical and mutational analysis of intracellular regions of the Plexin-B1 guidance receptor as a RasGAP. FASEB Journal, 2012, 26, 975.3.  | 0.5 | 0         |
| 89 | First Year of Biophysica. Biophysica, 2022, 2, 89-90.   | 1.4 | 0         |
| 90 | Understanding the Structural Basis of Epha1 and Epha2 Homodimerization, Membrane Proximal Domain Interactions and its Implications for Cancer. FASEB Journal, 2022, 36, .                       | 0.5 | 0         |