

Chad A Brautigam

List of Publications by Year in descending order

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116
papers

8,020
citations

50276

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56724

83
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130
docs citations

130
times ranked

11334
citing authors

#	ARTICLE	IF	CITATIONS
1	A Protein Semisynthesis-Based Strategy to Investigate the Functional Impact of Linker Histone Serine ADP-Ribosylation. <i>ACS Chemical Biology</i> , 2022, 17, 810-815.	3.4	7
2	The feasibility of determining kinetic constants from isothermal titration calorimetry data. <i>Biophysical Journal</i> , 2022, , .	0.5	3
3	Measuring the KD of Protein-Ligand Interactions Using Microscale Thermophoresis. <i>Methods in Molecular Biology</i> , 2021, 2263, 161-181.	0.9	3
4	Mechanism of karyopherin- $\beta 2$ binding and nuclear import of ALS variants FUS(P525L) and FUS(R495X). <i>Scientific Reports</i> , 2021, 11, 3754.	3.3	35
5	A multi-laboratory benchmark study of isothermal titration calorimetry (ITC) using Ca ²⁺ and Mg ²⁺ binding to EDTA. <i>European Biophysics Journal</i> , 2021, 50, 429-451.	2.2	12
6	Reproducibility and accuracy of microscale thermophoresis in the NanoTemper Monolith: a multi laboratory benchmark study. <i>European Biophysics Journal</i> , 2021, 50, 411-427.	2.2	13
7	Inhibition of bacterial FMN transferase: A potential avenue for countering antimicrobial resistance. <i>Protein Science</i> , 2021, , .	7.6	2
8	Fast and Robust Quantification of Detergent Micellization Thermodynamics from Isothermal Titration Calorimetry. <i>Analytical Chemistry</i> , 2020, 92, 1154-1161.	6.5	13
9	Biophysical and Biochemical Characterization of TP0037, a <i>sdhA</i> -Lactate Dehydrogenase, Supports an Acetogenic Energy Conservation Pathway in <i>Treponema pallidum</i> . <i>MBio</i> , 2020, 11, .	4.1	4
10	Using modern approaches to sedimentation velocity to detect conformational changes in proteins. <i>European Biophysics Journal</i> , 2020, 49, 729-743.	2.2	7
11	Tissue-Specific Regulation of the Wnt/ β -Catenin Pathway by PAGE4 Inhibition of Tankyrase. <i>Cell Reports</i> , 2020, 32, 107922.	6.4	7
12	Recognition of nuclear export signals by CRM1 carrying the oncogenic E571K mutation. <i>Molecular Biology of the Cell</i> , 2020, 31, 1879-1891.	2.1	22
13	Genetic and structural studies of RABL3 reveal an essential role in lymphoid development and function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 8563-8572.	7.1	10
14	Molecular Size Analysis of Recombinant Importin-histone Complexes Using Analytical Ultracentrifugation. <i>Bio-protocol</i> , 2020, 10, e3625.	0.4	1
15	Enhanced Sample Handling for Analytical Ultracentrifugation with 3D-Printed Centerpieces. <i>Analytical Chemistry</i> , 2019, 91, 5866-5873.	6.5	16
16	Importin-9 wraps around the H2A-H2B core to act as nuclear importer and histone chaperone. <i>ELife</i> , 2019, 8, .	6.0	47
17	Cryo-EM analyses reveal the common mechanism and diversification in the activation of RET by different ligands. <i>ELife</i> , 2019, 8, .	6.0	37
18	Fucosylated Molecules Competitively Interfere with Cholera Toxin Binding to Host Cells. <i>ACS Infectious Diseases</i> , 2018, 4, 758-770.	3.8	42

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19	Crystal structures of MglB-2 (TPO684), a topologically variant <i>glucose</i> -binding protein from <i>Treponema pallidum</i> , reveal a ligand-induced conformational change. <i>Protein Science</i> , 2018, 27, 880-885.	7.6	4
20	RIM C2B Domains Target Presynaptic Active Zone Functions to PIP2-Containing Membranes. <i>Neuron</i> , 2018, 98, 335-349.e7.	8.1	52
21	Using two-site binding models to analyze microscale thermophoresis data. <i>Analytical Biochemistry</i> , 2018, 540-541, 64-75.	2.4	27
22	Direct regulation of p190RhoGEF by activated Rho and Rac GTPases. <i>Journal of Structural Biology</i> , 2018, 202, 13-24.	2.8	12
23	Biophysical insights into a highly selective <i>arginine</i> -binding lipoprotein of a pathogenic treponeme. <i>Protein Science</i> , 2018, 27, 2037-2050.	7.6	0
24	Design principles of a microtubule polymerase. <i>ELife</i> , 2018, 7, .	6.0	45
25	An isolated CLASP TOG domain suppresses microtubule catastrophe and promotes rescue. <i>Molecular Biology of the Cell</i> , 2018, 29, 1359-1375.	2.1	36
26	Functional clues from the crystal structure of an orphan periplasmic <i>glucose</i> -binding protein from <i>Treponema pallidum</i> . <i>Protein Science</i> , 2017, 26, 847-856.	7.6	7
27	Mechanistic insight into TRIP13-catalyzed Mad2 structural transition and spindle checkpoint silencing. <i>Nature Communications</i> , 2017, 8, 1956.	12.8	38
28	Structural basis of arrestin-3 activation and signaling. <i>Nature Communications</i> , 2017, 8, 1427.	12.8	92
29	Rac1 GTPase activates the WAVE regulatory complex through two distinct binding sites. <i>ELife</i> , 2017, 6, .	6.0	129
30	SAV1 promotes Hippo kinase activation through antagonizing the PP2A phosphatase STRIPAK. <i>ELife</i> , 2017, 6, .	6.0	100
31	Autoinhibition of Munc18-1 modulates synaptobrevin binding and helps to enable Munc13-dependent regulation of membrane fusion. <i>ELife</i> , 2017, 6, .	6.0	80
32	Structure analyses reveal a regulated oligomerization mechanism of the PlexinD1/GIPC/myosin VI complex. <i>ELife</i> , 2017, 6, .	6.0	44
33	Reconciling isothermal titration calorimetry analyses of interactions between complexin and truncated SNARE complexes. <i>ELife</i> , 2017, 6, .	6.0	11
34	The Tp0684 (MglB-2) Lipoprotein of <i>Treponema pallidum</i> : A Glucose-Binding Protein with Divergent Topology. <i>PLoS ONE</i> , 2016, 11, e0161022.	2.5	14
35	Integration and global analysis of isothermal titration calorimetry data for studying macromolecular interactions. <i>Nature Protocols</i> , 2016, 11, 882-894.	12.0	225
36	Molecular insights into the enzymatic diversity of <i>flavin</i> -trafficking protein (Ftp; formerly ApbE) in flavoprotein biogenesis in the bacterial periplasm. <i>MicrobiologyOpen</i> , 2016, 5, 21-38.	3.0	28

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37	Structure and ligand-binding mechanism of the human OX1 and OX2 orexin receptors. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 293-299.	8.2	114
38	On the acquisition and analysis of microscale thermophoresis data. <i>Analytical Biochemistry</i> , 2016, 496, 79-93.	2.4	130
39	The human SKA complex drives the metaphase-anaphase cell cycle transition by recruiting protein phosphatase 1 to kinetochores. <i>ELife</i> , 2016, 5, .	6.0	64
40	Calculations and Publication-Quality Illustrations for Analytical Ultracentrifugation Data. <i>Methods in Enzymology</i> , 2015, 562, 109-133.	1.0	414
41	The Cdc20-binding Phe Box of the Spindle Checkpoint Protein BubR1 Maintains the Mitotic Checkpoint Complex During Mitosis. <i>Journal of Biological Chemistry</i> , 2015, 290, 2431-2443.	3.4	56
42	Fitting two- and three-site binding models to isothermal titration calorimetric data. <i>Methods</i> , 2015, 76, 124-136.	3.8	66
43	Biocalorimetry. <i>Methods</i> , 2015, 76, 1-2.	3.8	9
44	High-precision, automated integration of multiple isothermal titration calorimetric thermograms: New features of NITPIC. <i>Methods</i> , 2015, 76, 87-98.	3.8	155
45	Evidence for Posttranslational Protein Flavinylation in the Syphilis Spirochete <i>Treponema pallidum</i> : Structural and Biochemical Insights from the Catalytic Core of a Periplasmic Flavin-Trafficking Protein. <i>MBio</i> , 2015, 6, e00519-15.	4.1	32
46	Secondary PDZ domain-binding site on class B plexins enhances the affinity for PDZ α -RhoGEF. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14852-14857.	7.1	19
47	A <i>Moraxella catarrhalis</i> Two-Component Signal Transduction System Necessary for Growth in Liquid Media Affects Production of Two Lysozyme Inhibitors. <i>Infection and Immunity</i> , 2015, 83, 146-160.	2.2	6
48	Insights into the potential function and membrane organization of the <i>TP0435</i> (<i>Tp17</i>) lipoprotein from <i>Treponema pallidum</i> derived from structural and biophysical analyses. <i>Protein Science</i> , 2015, 24, 11-19.	7.6	15
49	A Multilaboratory Comparison of Calibration Accuracy and the Performance of External References in Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2015, 10, e0126420.	2.5	71
50	Structural determinants of nuclear export signal orientation in binding to exportin CRM1. <i>ELife</i> , 2015, 4, .	6.0	79
51	<i>Haemophilus ducreyi</i> Hfq Contributes to Virulence Gene Regulation as Cells Enter Stationary Phase. <i>MBio</i> , 2014, 5, e01081-13.	4.1	42
52	Sequence, biophysical, and structural analyses of the PstS lipoprotein (BB0215) from <i>Borrelia burgdorferi</i> reveal a likely binding component of an ABC-type phosphate transporter. <i>Protein Science</i> , 2014, 23, 200-212.	7.6	21
53	Identification of a core sequence for the binding of BosR to the <i>rpoS</i> promoter region in <i>Borrelia burgdorferi</i> . <i>Microbiology (United Kingdom)</i> , 2014, 160, 851-862.	1.8	17
54	Identification of an Outer Membrane Lipoprotein Involved in Nasopharyngeal Colonization by <i>Moraxella catarrhalis</i> in an Animal Model. <i>Infection and Immunity</i> , 2014, 82, 2287-2299.	2.2	8

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55	Measurement of the temperature of the resting rotor in analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2014, 458, 37-39.	2.4	14
56	The Cytosolic DNA Sensor cGAS Forms an Oligomeric Complex with DNA and Undergoes Switch-like Conformational Changes in the Activation Loop. <i>Cell Reports</i> , 2014, 6, 421-430.	6.4	351
57	A tethered delivery mechanism explains the catalytic action of a microtubule polymerase. <i>ELife</i> , 2014, 3, e03069.	6.0	94
58	Structural Basis for Autoactivation of Human Mst2 Kinase and Its Regulation by RASSF5. <i>Structure</i> , 2013, 21, 1757-1768.	3.3	82
59	Improving the thermal, radial, and temporal accuracy of the analytical ultracentrifuge through external references. <i>Analytical Biochemistry</i> , 2013, 440, 81-95.	2.4	60
60	Recorded scan times can limit the accuracy of sedimentation coefficients in analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2013, 437, 104-108.	2.4	102
61	Overview of Current Methods in Sedimentation Velocity and Sedimentation Equilibrium Analytical Ultracentrifugation. <i>Current Protocols in Protein Science</i> , 2013, 71, Unit20.12.	2.8	154
62	Multi-Signal Sedimentation Velocity Analysis with Mass Conservation for Determining the Stoichiometry of Protein Complexes. <i>PLoS ONE</i> , 2013, 8, e62694.	2.5	18
63	Evidence for an ABC-Type Riboflavin Transporter System in Pathogenic Spirochetes. <i>MBio</i> , 2013, 4, e00615-12.	4.1	38
64	The TP0796 Lipoprotein of <i>Treponema pallidum</i> Is a Bimetal-dependent FAD Pyrophosphatase with a Potential Role in Flavin Homeostasis. <i>Journal of Biological Chemistry</i> , 2013, 288, 11106-11121.	3.4	29
65	The <i>Haemophilus ducreyi</i> Fis Protein Is Involved in Controlling Expression of the <i>ispB-ispA2</i> Operon and Other Virulence Factors. <i>Infection and Immunity</i> , 2013, 81, 4160-4170.	2.2	4
66	Purification, crystallization and preliminary X-ray analysis of TP0435 (Tp17) from the syphilis spirochete <i>Treponema pallidum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 453-455.	0.7	4
67	<i>Trypanosoma brucei</i> S-Adenosylmethionine Decarboxylase N Terminus Is Essential for Allosteric Activation by the Regulatory Subunit Prozyme. <i>Journal of Biological Chemistry</i> , 2013, 288, 5232-5240.	3.4	16
68	Structure of the human cohesin inhibitor Wapl. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11355-11360.	7.1	62
69	Structural basis for activation and non-canonical catalysis of the Rap GTPase activating protein domain of plexin. <i>ELife</i> , 2013, 2, e01279.	6.0	66
70	Structural and Biochemical Characterization of Human Mitochondrial Branched-chain α -Ketoacid Dehydrogenase Phosphatase. <i>Journal of Biological Chemistry</i> , 2012, 287, 9178-9192.	3.4	19
71	Structural and Molecular Characterization of Iron-sensing Hemerythrin-like Domain within F-box and Leucine-rich Repeat Protein 5 (FBXL5). <i>Journal of Biological Chemistry</i> , 2012, 287, 7357-7365.	3.4	59
72	Biophysical and Bioinformatic Analyses Implicate the <i>Treponema pallidum</i> Tp34 Lipoprotein (Tp0971) in Transition Metal Homeostasis. <i>Journal of Bacteriology</i> , 2012, 194, 6771-6781.	2.2	17

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73	A TOG:±Î²-tubulin Complex Structure Reveals Conformation-Based Mechanisms for a Microtubule Polymerase. <i>Science</i> , 2012, 337, 857-860.	12.6	226
74	Multivalent di-nucleosome recognition enables the Rpd3S histone deacetylase complex to tolerate decreased H3K36 methylation levels. <i>EMBO Journal</i> , 2012, 31, 3564-3574.	7.8	49
75	Structural, Bioinformatic, and In Vivo Analyses of Two <i>Treponema pallidum</i> Lipoproteins Reveal a Unique TRAP Transporter. <i>Journal of Molecular Biology</i> , 2012, 416, 678-696.	4.2	30
76	Structural and Thermodynamic Characterization of the Interaction between Two Periplasmic <i>Treponema pallidum</i> Lipoproteins that are Components of a TPR-Protein-Associated TRAP Transporter (TPAT). <i>Journal of Molecular Biology</i> , 2012, 420, 70-86.	4.2	27
77	Ubiquitin-Induced Oligomerization of the RNA Sensors RIG-I and MDA5 Activates Antiviral Innate Immune Response. <i>Immunity</i> , 2012, 36, 959-973.	14.3	337
78	Requirements for Efficient Correction of Î²F508 CFTR Revealed by Analyses of Evolved Sequences. <i>Cell</i> , 2012, 148, 164-174.	28.9	243
79	High-Precision Isothermal Titration Calorimetry with Automated Peak-Shape Analysis. <i>Analytical Chemistry</i> , 2012, 84, 5066-5073.	6.5	440
80	Using Lamm-Equation modeling of sedimentation velocity data to determine the kinetic and thermodynamic properties of macromolecular interactions. <i>Methods</i> , 2011, 54, 4-15.	3.8	40
81	Evaluating the stoichiometry of macromolecular complexes using multisignal sedimentation velocity. <i>Methods</i> , 2011, 54, 39-55.	3.8	30
82	Structural and Thermodynamic Basis for Weak Interactions between Dihydrolipoamide Dehydrogenase and Subunit-binding Domain of the Branched-chain Î±-Ketoacid Dehydrogenase Complex. <i>Journal of Biological Chemistry</i> , 2011, 286, 23476-23488.	3.4	23
83	Arp2/3 complex is bound and activated by two WASP proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E472-9.	7.1	180
84	Identification of Gene Products Involved in the Oxidative Stress Response of <i>Moraxella catarrhalis</i> . <i>Infection and Immunity</i> , 2011, 79, 745-755.	2.2	35
85	Mechanism of actin filament nucleation by the bacterial effector VopL. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1068-1074.	8.2	56
86	Determination of protein complex stoichiometry through multisignal sedimentation velocity experiments. <i>Analytical Biochemistry</i> , 2010, 407, 89-103.	2.4	39
87	Characterization of the CpxRA Regulon in <i>Haemophilus ducreyi</i> . <i>Infection and Immunity</i> , 2010, 78, 4779-4791.	2.2	37
88	Kinetic and Structural Insights into the Mechanism of AMPylation by VopS Fic Domain. <i>Journal of Biological Chemistry</i> , 2010, 285, 20155-20163.	3.4	77
89	<i>S. aureus</i> MscL Is a Pentamer In Vivo but of Variable Stoichiometries In Vitro: Implications for Detergent-Solubilized Membrane Proteins. <i>PLoS Biology</i> , 2010, 8, e1000555.	5.6	60
90	Structural and Mutational Analysis of Functional Differentiation between Synaptotagmins-1 and -7. <i>PLoS ONE</i> , 2010, 5, e12544.	2.5	28

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91	Subunit and Catalytic Component Stoichiometries of an in Vitro Reconstituted Human Pyruvate Dehydrogenase Complex. <i>Journal of Biological Chemistry</i> , 2009, 284, 13086-13098.	3.4	57
92	Localization and Structure of the Ankyrin-binding Site on β 2-Spectrin. <i>Journal of Biological Chemistry</i> , 2009, 284, 6982-6987.	3.4	59
93	Identification of a bacteriocin and its cognate immunity factor expressed by <i>Moraxella catarrhalis</i> . <i>BMC Microbiology</i> , 2009, 9, 207.	3.3	8
94	Bifunctional NMN Adenylyltransferase/ADP-Ribose Pyrophosphatase: Structure and Function in Bacterial NAD Metabolism. <i>Structure</i> , 2008, 16, 196-209.	3.3	30
95	Hierarchical Regulation of WASP/WAVE Proteins. <i>Molecular Cell</i> , 2008, 32, 426-438.	9.7	188
96	Changes at the KinA PAS-A Dimerization Interface Influence Histidine Kinase Function. <i>Biochemistry</i> , 2008, 47, 4051-4064.	2.5	59
97	<i>Moraxella catarrhalis</i> Expresses an Unusual Hfq Protein. <i>Infection and Immunity</i> , 2008, 76, 2520-2530.	2.2	28
98	<i>Moraxella catarrhalis</i> Synthesizes an Autotransporter That Is an Acid Phosphatase. <i>Journal of Bacteriology</i> , 2008, 190, 1459-1472.	2.2	13
99	Structural Analysis of <i>Xanthomonas</i> XopD Provides Insights into Substrate Specificity of Ubiquitin-like Protein Proteases. <i>Journal of Biological Chemistry</i> , 2007, 282, 6773-6782.	3.4	71
100	Crystal Structure of the Tp34 (TP0971) Lipoprotein of <i>Treponema pallidum</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 5944-5958.	3.4	46
101	Structural and Biochemical Basis for Polyamine Binding to the Tp0655 Lipoprotein of <i>Treponema pallidum</i> : Putative Role for Tp0655 (TpPotD) as a Polyamine Receptor. <i>Journal of Molecular Biology</i> , 2007, 373, 681-694.	4.2	37
102	Structural basis of histone demethylation by LSD1 revealed by suicide inactivation. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 535-539.	8.2	170
103	A Proximal Arginine R206 Participates in Switching of the <i>Bradyrhizobium japonicum</i> FixL Oxygen Sensor. <i>Journal of Molecular Biology</i> , 2006, 360, 80-89.	4.2	33
104	A synchronized substrate-gating mechanism revealed by cubic-core structure of the bovine branched-chain α -ketoacid dehydrogenase complex. <i>EMBO Journal</i> , 2006, 25, 5983-5994.	7.8	44
105	A Versatile Conformational Switch Regulates Reactivity in Human Branched-Chain α -Ketoacid Dehydrogenase. <i>Structure</i> , 2006, 14, 287-298.	3.3	46
106	Structural Insight into Interactions between Dihydrolipoamide Dehydrogenase (E3) and E3 Binding Protein of Human Pyruvate Dehydrogenase Complex. <i>Structure</i> , 2006, 14, 611-621.	3.3	90
107	The PnrA (Tp0319; TmpC) Lipoprotein Represents a New Family of Bacterial Purine Nucleoside Receptor Encoded within an ATP-binding Cassette (ABC)-like Operon in <i>Treponema pallidum</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 8072-8081.	3.4	53
108	Side chain and backbone contributions of Phe508 to CFTR folding. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 10-16.	8.2	173

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109	Crystal Structure of Human Dihydropyrimidinase: NAD ⁺ /NADH Binding and the Structural Basis of Disease-causing Mutations. <i>Journal of Molecular Biology</i> , 2005, 350, 543-552.	4.2	110
110	Structure of the photolyase-like domain of cryptochrome 1 from <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12142-12147.	7.1	267
111	Structural Evidence That the 32-Kilodalton Lipoprotein (Tp32) of <i>Treponema pallidum</i> Is an I-Methionine-binding Protein. <i>Journal of Biological Chemistry</i> , 2004, 279, 55644-55650.	3.4	36
112	Tetramerization and ATP Binding by a Protein Comprising the A, B, and C Domains of Rat Synapsin I. <i>Journal of Biological Chemistry</i> , 2004, 279, 11948-11956.	3.4	31
113	Structural elucidation of the binding and inhibitory properties of lanthanide (III) ions at the 3'-5' exonucleolytic active site of the Klenow fragment. <i>Chemistry and Biology</i> , 1999, 6, 901-908.	6.0	34
114	Structures of Normal Single-Stranded DNA and Deoxyribo-3'-S-phosphorothiolates Bound to the 3'-5' Exonucleolytic Active Site of DNA Polymerase I from <i>Escherichia coli</i> . <i>Biochemistry</i> , 1999, 38, 696-704.	2.5	77
115	Structural and functional insights provided by crystal structures of DNA polymerases and their substrate complexes. <i>Current Opinion in Structural Biology</i> , 1998, 8, 54-63.	5.7	353
116	Structural principles for the inhibition of the 3'-5' exonuclease activity of <i>Escherichia coli</i> DNA polymerase I by phosphorothioates. <i>Journal of Molecular Biology</i> , 1998, 277, 363-377.	4.2	197