

Christopher M Johnson

List of Publications by Year in descending order

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69
papers

4,945
citations

87888

38
h-index

95266

68
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71
all docs

71
docs citations

71
times ranked

6074
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular mechanisms underlying the role of the centriolar CEP164-TTBK2 complex in ciliopathies. <i>Structure</i> , 2022, 30, 114-128.e9.	3.3	11
2	Target-induced clustering activates Trim-Away of pathogens and proteins. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 278-289.	8.2	44
3	Signalling lymphocyte activation molecule family member 9 is found on select subsets of antigen-presenting cells and promotes resistance to <i>Salmonella</i> infection. <i>Immunology</i> , 2020, 159, 393-403.	4.4	7
4	CCDC61/VFL3 Is a Paralog of SAS6 and Promotes Ciliary Functions. <i>Structure</i> , 2020, 28, 674-689.e11.	3.3	16
5	Effect of structural stability on endolysosomal degradation and cell reactivity of major shrimp allergen tropomyosin. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2020, 75, 2909-2919.	5.7	25
6	Membrane characteristics tune activities of endosomal and autophagic human VPS34 complexes. <i>ELife</i> , 2020, 9, .	6.0	34
7	Structural insights into the critical DNA damage sensors DNA-PKcs, ATM and ATR. <i>Progress in Biophysics and Molecular Biology</i> , 2019, 147, 4-16.	2.9	23
8	Methionine in a protein hydrophobic core drives tight interactions required for assembly of spider silk. <i>Nature Communications</i> , 2019, 10, 4378.	12.8	23
9	Direct binding of CEP85 to STIL ensures robust PLK4 activation and efficient centriole assembly. <i>Nature Communications</i> , 2018, 9, 1731.	12.8	32
10	RNA-directed activation of cytoplasmic dynein-1 in reconstituted transport RNPs. <i>ELife</i> , 2018, 7, .	6.0	72
11	Intracellular antibody signalling is regulated by phosphorylation of the Fc receptor TRIM21. <i>ELife</i> , 2018, 7, .	6.0	57
12	Protein Folding, Energy Landscapes and Downhill Protein Folding Scenarios. , 2018, , 1-19.		2
13	The Ciliopathy-Associated Cep104 Protein Interacts with Tubulin and Nek1 Kinase. <i>Structure</i> , 2017, 25, 146-156.	3.3	36
14	Structures of closed and open conformations of dimeric human ATM. <i>Science Advances</i> , 2017, 3, e1700933.	10.3	91
15	Conservation of folding and association within a family of spidroin N-terminal domains. <i>Scientific Reports</i> , 2017, 7, 16789.	3.3	10
16	Exploration of Protein Unfolding by Modelling Calorimetry Data from Reheating. <i>Scientific Reports</i> , 2017, 7, 16321.	3.3	39
17	Tor forms a dimer through an N-terminal helical solenoid with a complex topology. <i>Nature Communications</i> , 2016, 7, 11016.	12.8	76
18	Wnt Signalosome Assembly by DEP Domain Swapping of Dishevelled. <i>Molecular Cell</i> , 2016, 64, 92-104.	9.7	125

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19	Characterization of Atg38 and NRBF2, a fifth subunit of the autophagic Vps34/PIK3C3 complex. <i>Autophagy</i> , 2016, 12, 2129-2144.	9.1	52
20	Fold stability during endolysosomal acidification is a key factor for allergenicity and immunogenicity of the major birch pollen allergen. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 137, 1525-1534.	2.9	69
21	An ancient Pygo-dependent Wnt enhanceosome integrated by Chip/LDB-SSDP. <i>ELife</i> , 2015, 4, .	6.0	49
22	CTNNB1 facilitates the association of CWC15 with CDC5L and is required to maintain the abundance of the Prp19 spliceosomal complex. <i>Nucleic Acids Research</i> , 2015, 43, 7058-7069.	14.5	19
23	Ubiquitination of the Dishevelled DIX domain blocks its head-to-tail polymerization. <i>Nature Communications</i> , 2015, 6, 6718.	12.8	50
24	Microsecond Folding and Domain Motions of a Spider Silk Protein Structural Switch. <i>Journal of the American Chemical Society</i> , 2014, 136, 17136-17144.	13.7	39
25	Structural and mutational analysis reveals that CTNNB1 binds NLSs in a manner distinct from that of its closest armadillo-related, karyopherin β . <i>FEBS Letters</i> , 2014, 588, 21-27.	2.8	5
26	Novel microscale approaches for easy, rapid determination of protein stability in academic and commercial settings. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 2241-2250.	2.3	76
27	Structure of the SAS-6 cartwheel hub from <i>Leishmania major</i> . <i>ELife</i> , 2014, 3, e01812.	6.0	54
28	Bacterial actin MreB forms antiparallel double filaments. <i>ELife</i> , 2014, 3, e02634.	6.0	153
29	The hepatitis B virus preS1 domain hijacks host trafficking proteins by motif mimicry. <i>Nature Chemical Biology</i> , 2013, 9, 540-547.	8.0	29
30	The N-terminal domains of spider silk proteins assemble ultrafast and protected from charge screening. <i>Nature Communications</i> , 2013, 4, 2815.	12.8	65
31	Don't waste good methods on bad buffers and ambiguous data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E331-E332.	7.1	6
32	Differential scanning calorimetry as a tool for protein folding and stability. <i>Archives of Biochemistry and Biophysics</i> , 2013, 531, 100-109.	3.0	289
33	Bicaudal-D uses a parallel, homodimeric coiled coil with heterotypic registry to coordinate recruitment of cargos to dynein. <i>Genes and Development</i> , 2013, 27, 1233-1246.	5.9	79
34	Crystal structures of the CPAP/STIL complex reveal its role in centriole assembly and human microcephaly. <i>ELife</i> , 2013, 2, e01071.	6.0	90
35	Backbone-Driven Collapse in Unfolded Protein Chains. <i>Journal of Molecular Biology</i> , 2011, 409, 250-262.	4.2	95
36	Intrinsic Motions in the N-Terminal Domain of an Ionotropic Glutamate Receptor Detected by Fluorescence Correlation Spectroscopy. <i>Journal of Molecular Biology</i> , 2011, 414, 96-105.	4.2	17

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37	Folding of the Pit1 homeodomain near the speed limit. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 569-573.	7.1	53
38	Structures of SAS-6 Suggest Its Organization in Centrioles. Science, 2011, 331, 1196-1199.	12.6	284
39	The human peripheral subunit's binding domain folds rapidly while overcoming repulsive Coulomb forces. Protein Science, 2010, 19, 1704-1713.	7.6	3
40	Bacterial actin MreB assembles in complex with cell shape protein RodZ. EMBO Journal, 2010, 29, 1081-1090.	7.8	144
41	Engineering a two-helix bundle protein for folding studies. Protein Engineering, Design and Selection, 2010, 23, 357-364.	2.1	7
42	Allosteric Remodelling of the Histone H3 Binding Pocket in the Pygo2 PHD Finger Triggered by Its Binding to the B9L/BCL9 Co-Factor. Journal of Molecular Biology, 2010, 401, 969-984.	4.2	43
43	Direct observation of ultrafast folding and denatured state dynamics in single protein molecules. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18569-18574.	7.1	109
44	Downhill versus Barrier-Limited Folding of BBL 2: Mechanistic Insights from Kinetics of Folding Monitored by Independent Tryptophan Probes. Journal of Molecular Biology, 2009, 387, 975-985.	4.2	28
45	The Folding Mechanism of BBL: Plasticity of Transition-State Structure Observed within an Ultrafast Folding Protein Family. Journal of Molecular Biology, 2009, 390, 1060-1073.	4.2	31
46	Conservation of Transition State Structure in Fast Folding Peripheral Subunit-Binding Domains. Journal of Molecular Biology, 2008, 383, 224-237.	4.2	20
47	Moving towards High-Resolution Descriptions of the Molecular Interactions and Structural Rearrangements of the Human Hepatitis B Core Protein. Journal of Molecular Biology, 2008, 384, 1301-1313.	4.2	27
48	Demonstration by burst-phase analysis of a robust folding intermediate in the FF domain. Protein Engineering, Design and Selection, 2008, 21, 207-214.	2.1	9
49	The helix turn helix motif as an ultrafast independently folding domain: The pathway of folding of Engrailed homeodomain. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 9272-9277.	7.1	71
50	Analysis of 'downhill' protein folding. Nature, 2007, 445, E14-E15.	27.8	44
51	The Transition State for Folding of a Peripheral Subunit-binding Domain Contains Robust and Ionic-strength Dependent Characteristics. Journal of Molecular Biology, 2006, 356, 1237-1247.	4.2	24
52	Effects of Heme on the Structure of the Denatured State and Folding Kinetics of Cytochrome b562. Journal of Molecular Biology, 2005, 346, 331-344.	4.2	33
53	Simulation and Experiment at High Temperatures: Ultrafast Folding of a Thermophilic Protein by Nucleation-condensation. Journal of Molecular Biology, 2005, 347, 855-870.	4.2	49
54	Ultra-fast Barrier-limited Folding in the Peripheral Subunit-binding Domain Family. Journal of Molecular Biology, 2005, 353, 427-446.	4.2	99

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55	Demonstration of a low-energy on-pathway intermediate in a fast-folding protein by kinetics, protein engineering, and simulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 6450-6455.	7.1	98
56	The complete folding pathway of a protein from nanoseconds to microseconds. <i>Nature</i> , 2003, 421, 863-867.	27.8	449
57	Loss of a metal-binding site in gelsolin leads to familial amyloidosis—Finnish type. <i>Nature Structural Biology</i> , 2002, 9, 112-116.	9.7	67
58	Heat does not come in different colours: entropy—enthalpy compensation, free energy windows, quantum confinement, pressure perturbation calorimetry, solvation and the multiple causes of heat capacity effects in biomolecular interactions. <i>Biophysical Chemistry</i> , 2001, 93, 215-230.	2.8	308
59	Structural Consequences of α -toc-type Heme Conversion in Oxidized <i>Escherichia coli</i> Cytochrome <i>b</i> ₅₆₂ . <i>Biochemistry</i> , 2000, 39, 1499-1514.	2.5	46
60	Design of highly stable functional GroEL minichaperones. <i>Protein Science</i> , 1999, 8, 2186-2193.	7.6	73
61	Folding intermediates of wild-type and mutants of barnase. II. correlation of changes in equilibrium amide exchange kinetics with the population of the folding intermediate. <i>Journal of Molecular Biology</i> , 1998, 276, 647-656.	4.2	33
62	Thermodynamics of the interaction of barnase and barstar: changes in free energy versus changes in enthalpy on mutation 1. Edited by J. Karn. <i>Journal of Molecular Biology</i> , 1997, 267, 696-706.	4.2	125
63	Thermodynamics of denaturation of mutants of barnase with disulfide crosslinks. <i>Journal of Molecular Biology</i> , 1997, 268, 198-208.	4.2	34
64	Folding and stability of a fibronectin type III domain of human tenascin. <i>Journal of Molecular Biology</i> , 1997, 270, 771-778.	4.2	111
65	Protein Stability as a Function of Denaturant Concentration: The Thermal Stability of Barnase in the Presence of Urea. <i>Biochemistry</i> , 1995, 34, 6795-6804.	2.5	151
66	Extrapolation to water of kinetic and equilibrium data for the unfolding of barnase in urea solutions. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 1089-1095.	2.1	71
67	The A-State of Barnase. <i>Biochemistry</i> , 1994, 33, 11189-11199.	2.5	32
68	Effect of cavity-creating mutations in the hydrophobic core of chymotrypsin inhibitor 2. <i>Biochemistry</i> , 1993, 32, 11259-11269.	2.5	294
69	A comparison of the reactivity and stability of wild type and His388 Gln mutant phosphoglycerate kinase from yeast. <i>FEBS Journal</i> , 1991, 202, 1157-1164.	0.2	13