

Christopher E Berndsen

List of Publications by Year in descending order

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43
papers

2,170
citations

430874

18
h-index

361022

35
g-index

53
all docs

53
docs citations

53
times ranked

3292
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural and functional analysis of the human coneâ€rod homeobox transcription factor. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1584-1593.	2.6	4
2	The <i>BAM7</i> gene in <i>Zea mays</i> encodes a protein with similar structural and catalytic properties to <i>Arabidopsis</i> BAM2. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 560-570.	2.3	4
3	Dynamic gating of substrate binding in Î²-â€mylase2 from <i>Arabidopsis thaliana</i> . <i>FASEB Journal</i> , 2022, 36, .	0.5	0
4	Teaching data management and literacy to support courseâ€embedded research projects. <i>FASEB Journal</i> , 2021, 35, .	0.5	0
5	Solution structure and assembly of Î²-â€mylase 2 from <i>Arabidopsis thaliana</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 357-365.	2.3	9
6	Resilience of BST-2/Tetherin structure to single amino acid substitutions. <i>PeerJ</i> , 2019, 7, e7043.	2.0	2
7	Structural and Functional Characterization of the <i>Leishmania donovani</i> Ufmâ€ylation Pathway. <i>FASEB Journal</i> , 2019, 33, 465.3.	0.5	0
8	Managing course embedded research projects of any size using the Open Science Framework. <i>FASEB Journal</i> , 2019, 33, 617.3.	0.5	0
9	Glutathionylation Inhibits the Catalytic Activity of <i>Arabidopsis</i> Î²-â€mylase3 but Not That of Paralog Î²-â€mylase1. <i>Biochemistry</i> , 2018, 57, 711-721.	2.5	11
10	Quaternary Structure, Salt Sensitivity, and Allosteric Regulation of Î²-â€MYLASE2 From <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1176.	3.6	12
11	A Tetrameric Î²-â€mylase2 (BAM2) From <i>Arabidopsis thaliana</i> : Using Mutagenesis To Interrogate Its Structure, Sigmoidal Kinetics, And Requirement For KCl. <i>FASEB Journal</i> , 2018, 32, 528.3.	0.5	0
12	Structural comparison of the <i>Arabidopsis thaliana</i> family of Î²-â€mylases. <i>FASEB Journal</i> , 2018, 32, 792.12.	0.5	0
13	In silico modeling of epigenetic-induced changes in photoreceptor cis-regulatory elements. <i>Molecular Vision</i> , 2018, 24, 218-230.	1.1	4
14	Deregulated Ca ²⁺ cycling underlies the development of arrhythmia and heart disease due to mutant obscurin. <i>Science Advances</i> , 2017, 3, e1603081.	10.3	33
15	<i>Arabidopsis</i> Î²-â€mylase2 Is a K ⁺ -Requiring, Catalytic Tetramer with Sigmoidal Kinetics. <i>Plant Physiology</i> , 2017, 175, 1525-1535.	4.8	27
16	Novel insights into the interaction of UBA5 with UFM1 via a UFM1-interacting sequence. <i>Scientific Reports</i> , 2017, 7, 508.	3.3	27
17	Bending of the BSTâ€2 coiledâ€coil during viral budding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 2081-2087.	2.6	6
18	Novel obscurins mediate cardiomyocyte adhesion and size via the PI3K/AKT/mTOR signaling pathway. <i>Journal of Molecular and Cellular Cardiology</i> , 2017, 111, 27-39.	1.9	26

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19	A novel FLNC frameshift and an OBSCN variant in a family with distal muscular dystrophy. PLoS ONE, 2017, 12, e0186642.	2.5	29
20	Connecting common genetic polymorphisms to protein function: A modular project sequence for lecture or lab. Biochemistry and Molecular Biology Education, 2016, 44, 526-536.	1.2	1
21	Characterization of the structure and catalytic activity of <i>Legionella pneumophila</i> VipF. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1422-1430.	2.6	5
22	Trans -Binding Mechanism of Ubiquitin-like Protein Activation Revealed by a UBA5-UFM1 Complex. Cell Reports, 2016, 16, 3113-3120.	6.4	44
23	The Disulfide Bonds within BST-2 Enhance Tensile Strength during Viral Tethering. Biochemistry, 2016, 55, 940-947.	2.5	8
24	The Vps27/Hrs/STAM (VHS) Domain of the Signal-transducing Adaptor Molecule (STAM) Directs Associated Molecule with the SH3 Domain of STAM (AMSH) Specificity to Longer Ubiquitin Chains and Dictates the Position of Cleavage. Journal of Biological Chemistry, 2016, 291, 2033-2042.	3.4	9
25	Positioning of Cysteine Residues within the N-terminal Portion of the BST-2/Tetherin Ectodomain Is Important for Functional Dimerization of BST-2. Journal of Biological Chemistry, 2015, 290, 3740-3751.	3.4	9
26	Chemical shift assignments for <i>S. cerevisiae</i> Ubc13. Biomolecular NMR Assignments, 2015, 9, 407-410.	0.8	4
27	New insights into ubiquitin E3 ligase mechanism. Nature Structural and Molecular Biology, 2014, 21, 301-307.	8.2	521
28	A conserved asparagine has a structural role in ubiquitin-conjugating enzymes. Nature Chemical Biology, 2013, 9, 154-156.	8.0	60
29	Architectural Organization of the Metabolic Regulatory Enzyme Ghrelin O-Acyltransferase. Journal of Biological Chemistry, 2013, 288, 32211-32228.	3.4	59
30	RNF4-Dependent Hybrid SUMO-Ubiquitin Chains are Signals for RAP80 and thereby Mediate the Recruitment of BRCA1 to Sites of DNA Damage. FASEB Journal, 2013, 27, 782.7.	0.5	0
31	RNF4-Dependent Hybrid SUMO-Ubiquitin Chains Are Signals for RAP80 and Thereby Mediate the Recruitment of BRCA1 to Sites of DNA Damage. Science Signaling, 2012, 5, ra88.	3.6	158
32	The Size and Conservation of a Coiled-coil Structure in the Ectodomain of Human BST-2/Tetherin Is Dispensable for Inhibition of HIV-1 Virion Release. Journal of Biological Chemistry, 2012, 287, 44278-44288.	3.4	19
33	A spectrophotometric assay for conjugation of ubiquitin and ubiquitin-like proteins. Analytical Biochemistry, 2011, 418, 102-110.	2.4	89
34	Structural Insights into the Assembly and Function of the SAGA Deubiquitinating Module. Science, 2010, 328, 1025-1029.	12.6	190
35	Molecular functions of the histone acetyltransferase chaperone complex Rtt109-Vps75. Nature Structural and Molecular Biology, 2008, 15, 948-956.	8.2	104
36	Catalysis and substrate selection by histone/protein lysine acetyltransferases. Current Opinion in Structural Biology, 2008, 18, 682-689.	5.7	194

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37	Histone H3-K56 Acetylation Is Catalyzed by Histone Chaperone-Dependent Complexes. <i>Molecular Cell</i> , 2007, 25, 703-712.	9.7	268
38	Catalytic Mechanism of a MYST Family Histone Acetyltransferase. <i>Biochemistry</i> , 2007, 46, 623-629.	2.5	114
39	Nucleosome Recognition by the Piccolo NuA4 Histone Acetyltransferase Complex. <i>Biochemistry</i> , 2007, 46, 2091-2099.	2.5	34
40	Structure of Arabidopsis thaliana At1g77540 Protein, a Minimal Acetyltransferase from the COG2388 Family. <i>Biochemistry</i> , 2006, 45, 14325-14336.	2.5	13
41	Assays for mechanistic investigations of protein/histone acetyltransferases. <i>Methods</i> , 2005, 36, 321-331.	3.8	70
42	Unwrapping Enzyme Kinetics. <i>CourseSource</i> , 0, 7, .	0.0	2
43	Hiding the Vegetables: Teaching Programming to Chemists as a Professional Skill. <i>ACS Symposium Series</i> , 0, , 29-41.	0.5	0