

Joseph S Brunzelle

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

36
papers

1,023
citations

16
h-index

31
g-index

38
ext. papers

1,351
ext. citations

11.1
avg, IF

3.94
L-index

#	Paper	IF	Citations
36	The histone H3.1 variant regulates TONSOKU-mediated DNA repair during replication.. <i>Science</i> , 2022 , 375, 1281-1286	33.3	1
35	Structural basis of binding and inhibition of ornithine decarboxylase by 1-amino-oxy-3-aminopropane. <i>Biochemical Journal</i> , 2021 , 478, 4137-4149	3.8	2
34	Lysine 53 Acetylation of Cytochrome in Prostate Cancer: Warburg Metabolism and Evasion of Apoptosis. <i>Cells</i> , 2021 , 10,	7.9	8
33	Mn coordinates Cap-0-RNA to align substrates for efficient 2F-methyl transfer by SARS-CoV-2 nsp16. <i>Science Signaling</i> , 2021 , 14,	8.8	2
32	Structure of an AMPK complex in an inactive, ATP-bound state. <i>Science</i> , 2021 , 373, 413-419	33.3	5
31	Structural basis of Fusarium myosin I inhibition by phenamacril. <i>PLoS Pathogens</i> , 2020 , 16, e1008323	7.6	9
30	Structure-Based Design and Evaluation of Peptidomimetic Inhibitors Against the Human Norovirus Protease. <i>FASEB Journal</i> , 2020 , 34, 1-1	0.9	
29	High-resolution structures of the SARS-CoV-2 2F-methyltransferase reveal strategies for structure-based inhibitor design. <i>Science Signaling</i> , 2020 , 13,	8.8	76
28	Structures of AMP-activated protein kinase bound to novel pharmacological activators in phosphorylated, non-phosphorylated, and nucleotide-free states. <i>Journal of Biological Chemistry</i> , 2019 , 294, 953-967	5.4	13
27	Functional insights into the interplay between DNA interaction and metal coordination in ferric uptake regulators. <i>Scientific Reports</i> , 2018 , 8, 7140	4.9	11
26	Structure and Conformational Dynamics of a COMPASS Histone H3K4 Methyltransferase Complex. <i>Cell</i> , 2018 , 174, 1117-1126.e12	56.2	50
25	Targeting Aspartate Transcarbamoylase in Staphylococcus aureus: A Novel Therapeutic Approach for Sepsis. <i>FASEB Journal</i> , 2018 , 32, 797.12	0.9	0
24	Elucidation of a 2.3 Å Resolution Norovirus GII.4 Protease Structure by X-Ray Crystallography. <i>FASEB Journal</i> , 2018 , 32, 526.47	0.9	
23	Novel Aldo-Keto Reductases for the Biocatalytic Conversion of 3-Hydroxybutanal to 1,3-Butanediol: Structural and Biochemical Studies. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	21
22	Acetylation of PCNA Sliding Surface by Eco1 Promotes Genome Stability through Homologous Recombination. <i>Molecular Cell</i> , 2017 , 65, 78-90	17.6	28
21	Structural Basis of TPR-Mediated Oligomerization and Activation of Oncogenic Fusion Kinases. <i>Structure</i> , 2017 , 25, 867-877.e3	5.2	9
20	Molecular basis for the methylation specificity of ATXR5 for histone H3. <i>Nucleic Acids Research</i> , 2017 , 45, 6375-6387	20.1	15

19	A D53 repression motif induces oligomerization of TOPLESS corepressors and promotes assembly of a corepressor-nucleosome complex. <i>Science Advances</i> , 2017 , 3, e1601217	14.3	40
18	Phosphorylation of Cytochrome c Threonine 28 Regulates Electron Transport Chain Activity in Kidney: IMPLICATIONS FOR AMP KINASE. <i>Journal of Biological Chemistry</i> , 2017 , 292, 64-79	5.4	36
17	Ligand Binding Enhances Millisecond Conformational Exchange in Xylanase B2 from <i>Streptomyces lividans</i> . <i>Biochemistry</i> , 2016 , 55, 4184-96	3.2	16
16	The L33F darunavir resistance mutation acts as a molecular anchor reducing the flexibility of the HIV-1 protease 30s and 80s loops. <i>Biochemistry and Biophysics Reports</i> , 2015 , 2, 160-165	2.2	5
15	Structural basis for recognition of diverse transcriptional repressors by the TOPLESS family of corepressors. <i>Science Advances</i> , 2015 , 1, e1500107	14.3	86
14	Structural and functional study of D-glucuronyl C5-epimerase. <i>Journal of Biological Chemistry</i> , 2015 , 290, 4620-4630	5.4	28
13	Structural basis of JAZ repression of MYC transcription factors in jasmonate signalling. <i>Nature</i> , 2015 , 525, 269-73	50.4	175
12	The Tetrahymena telomerase p75-p45-p19 subcomplex is a unique CST complex. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 1023-6	17.6	28
11	A phosphorylation switch on RbBP5 regulates histone H3 Lys4 methylation. <i>Genes and Development</i> , 2015 , 29, 123-8	12.6	30
10	Selective methylation of histone H3 variant H3.1 regulates heterochromatin replication. <i>Science</i> , 2014 , 343, 1249-53	33.3	119
9	Molecular basis for DPY-30 association to COMPASS-like and NURF complexes. <i>Structure</i> , 2014 , 22, 1821-1830	18.30	27
8	Agonist ligands mediate the transcriptional response of nuclear receptor heterodimers through distinct stoichiometric assemblies with coactivators. <i>Journal of Biological Chemistry</i> , 2014 , 289, 24771-8	5.4	12
7	Higher Desolvation Energy Reduces Molecular Recognition in Multi-Drug Resistant HIV-1 Protease. <i>Biology</i> , 2012 , 1, 81-93	4.9	9
6	Molecular Mechanisms of Lysine Methylation. <i>FASEB Journal</i> , 2010 , 24, 78.3	0.9	
5	Chaperones of F1-ATPase. <i>Journal of Biological Chemistry</i> , 2009 , 284, 17138-17146	5.4	23
4	Structure of the two-site beta-d-xylosidase from <i>Selenomonas ruminantium</i> in complex with 1,3-bis[tris(hydroxymethyl)methylamino]propane. <i>Archives of Biochemistry and Biophysics</i> , 2008 , 474, 157-66	4.1	45
3	Crystal structure of <i>Bacillus subtilis</i> YdaF protein: a putative ribosomal N-acetyltransferase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 57, 850-3	4.2	8
2	Crystal structures of the catalytic domain of human protein kinase associated with apoptosis and tumor suppression. <i>Nature Structural Biology</i> , 2001 , 8, 899-907		85

1 Mn²⁺ coordinates Cap-0-RNA to align substrates for efficient 2'-O-methyl transfer by SARS-CoV-2 nsp16

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