

# Joseph S Brunzelle

## List of Publications by Citations

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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	Structural basis of JAZ repression of MYC transcription factors in jasmonate signalling. <i>Nature</i> , <b>2015</b> , 525, 269-73	50.4	175
35	Selective methylation of histone H3 variant H3.1 regulates heterochromatin replication. <i>Science</i> , <b>2014</b> , 343, 1249-53	33.3	119
34	Structural basis for recognition of diverse transcriptional repressors by the TOPLESS family of corepressors. <i>Science Advances</i> , <b>2015</b> , 1, e1500107	14.3	86
33	Crystal structures of the catalytic domain of human protein kinase associated with apoptosis and tumor suppression. <i>Nature Structural Biology</i> , <b>2001</b> , 8, 899-907		85
32	High-resolution structures of the SARS-CoV-2 2F-methyltransferase reveal strategies for structure-based inhibitor design. <i>Science Signaling</i> , <b>2020</b> , 13,	8.8	76
31	Structure and Conformational Dynamics of a COMPASS Histone H3K4 Methyltransferase Complex. <i>Cell</i> , <b>2018</b> , 174, 1117-1126.e12	56.2	50
30	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> , <b>2008</b> , 474, 157-66	4.1	45
29	A D53 repression motif induces oligomerization of TOPLESS corepressors and promotes assembly of a corepressor-nucleosome complex. <i>Science Advances</i> , <b>2017</b> , 3, e1601217	14.3	40
28	Phosphorylation of Cytochrome c Threonine 28 Regulates Electron Transport Chain Activity in Kidney: IMPLICATIONS FOR AMP KINASE. <i>Journal of Biological Chemistry</i> , <b>2017</b> , 292, 64-79	5.4	36
27	A phosphorylation switch on RbBP5 regulates histone H3 Lys4 methylation. <i>Genes and Development</i> , <b>2015</b> , 29, 123-8	12.6	30
26	Acetylation of PCNA Sliding Surface by Eco1 Promotes Genome Stability through Homologous Recombination. <i>Molecular Cell</i> , <b>2017</b> , 65, 78-90	17.6	28
25	Structural and functional study of D-glucuronyl C5-epimerase. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 4620-4630	5.4	28
24	The Tetrahymena telomerase p75-p45-p19 subcomplex is a unique CST complex. <i>Nature Structural and Molecular Biology</i> , <b>2015</b> , 22, 1023-6	17.6	28
23	Molecular basis for DPY-30 association to COMPASS-like and NURF complexes. <i>Structure</i> , <b>2014</b> , 22, 1821-1830	18.30	27
22	Chaperones of F1-ATPase. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 17138-17146	5.4	23
21	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> , <b>2017</b> , 83,	4.8	21
20	Ligand Binding Enhances Millisecond Conformational Exchange in Xylanase B2 from <i>Streptomyces lividans</i> . <i>Biochemistry</i> , <b>2016</b> , 55, 4184-96	3.2	16

19	Molecular basis for the methylation specificity of ATXR5 for histone H3. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, 6375-6387	20.1	15
18	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> , <b>2019</b> , 294, 953-967	5.4	13
17	Agonist ligands mediate the transcriptional response of nuclear receptor heterodimers through distinct stoichiometric assemblies with coactivators. <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 24771-8	5.4	12
16	Functional insights into the interplay between DNA interaction and metal coordination in ferric uptake regulators. <i>Scientific Reports</i> , <b>2018</b> , 8, 7140	4.9	11
15	Structural Basis of TPR-Mediated Oligomerization and Activation of Oncogenic Fusion Kinases. <i>Structure</i> , <b>2017</b> , 25, 867-877.e3	5.2	9
14	Structural basis of Fusarium myosin I inhibition by phenamacril. <i>PLoS Pathogens</i> , <b>2020</b> , 16, e1008323	7.6	9
13	Higher Desolvation Energy Reduces Molecular Recognition in Multi-Drug Resistant HIV-1 Protease. <i>Biology</i> , <b>2012</b> , 1, 81-93	4.9	9
12	Crystal structure of Bacillus subtilis YdaF protein: a putative ribosomal N-acetyltransferase. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2004</b> , 57, 850-3	4.2	8
11	Lysine 53 Acetylation of Cytochrome in Prostate Cancer: Warburg Metabolism and Evasion of Apoptosis. <i>Cells</i> , <b>2021</b> , 10,	7.9	8
10	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> , <b>2015</b> , 2, 160-165	2.2	5
9	Structure of an AMPK complex in an inactive, ATP-bound state. <i>Science</i> , <b>2021</b> , 373, 413-419	33.3	5
8	Structural basis of binding and inhibition of ornithine decarboxylase by 1-amino-oxy-3-aminopropane. <i>Biochemical Journal</i> , <b>2021</b> , 478, 4137-4149	3.8	2
7	Mn coordinates Cap-0-RNA to align substrates for efficient 2'-methyl transfer by SARS-CoV-2 nsp16. <i>Science Signaling</i> , <b>2021</b> , 14,	8.8	2
6	Mn <sup>2+</sup> coordinates Cap-0-RNA to align substrates for efficient 2'-O-methyl transfer by SARS-CoV-2 nsp16		1
5	The histone H3.1 variant regulates TONSOKU-mediated DNA repair during replication.. <i>Science</i> , <b>2022</b> , 375, 1281-1286	33.3	1
4	Targeting Aspartate Transcarbamoylase in Staphylococcus aureus: A Novel Therapeutic Approach for Sepsis. <i>FASEB Journal</i> , <b>2018</b> , 32, 797.12	0.9	0
3	Structure-Based Design and Evaluation of Peptidomimetic Inhibitors Against the Human Norovirus Protease. <i>FASEB Journal</i> , <b>2020</b> , 34, 1-1	0.9	
2	Elucidation of a 2.3 Å Resolution Norovirus GII.4 Protease Structure by X-Ray Crystallography. <i>FASEB Journal</i> , <b>2018</b> , 32, 526.47	0.9	

1 Molecular Mechanisms of Lysine Methylation. *FASEB Journal*, **2010**, 24, 78.3

0.9