

# Joshua S Chappie

## List of Publications by Year in descending order

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Version: 2024-02-01

30  
papers

2,563  
citations

567281

15  
h-index

454955

30  
g-index

37  
all docs

37  
docs citations

37  
times ranked

3648  
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal structure of the potato leafroll virus coat protein and implications for viral assembly. <i>Journal of Structural Biology</i> , 2022, 214, 107811.	2.8	4
2	Bacteriophage $\lambda$ RexA and RexB functions assist the transition from lysogeny to lytic growth. <i>Molecular Microbiology</i> , 2021, 116, 1044-1063.	2.5	8
3	AraC-type regulators HilC and RtsA are directly controlled by an intestinal fatty acid to regulate <i>Salmonella</i> invasion. <i>Molecular Microbiology</i> , 2021, 116, 1464-1475.	2.5	8
4	The N-terminal domain of <i>Staphylothermus marinus</i> McrB shares structural homology with PUA-like RNA binding proteins. <i>Journal of Structural Biology</i> , 2020, 211, 107572.	2.8	4
5	Structural asymmetry governs the assembly and GTPase activity of McrBC restriction complexes. <i>Nature Communications</i> , 2020, 11, 5907.	12.8	7
6	Diffusible Signal Factors Act through AraC-Type Transcriptional Regulators as Chemical Cues To Repress Virulence of Enteric Pathogens. <i>Infection and Immunity</i> , 2020, 88, .	2.2	24
7	Cyclin N-Terminal Domain-Containing-1 Coordinates Meiotic Crossover Formation with Cell-Cycle Progression in a Cyclin-Independent Manner. <i>Cell Reports</i> , 2020, 32, 107858.	6.4	20
8	The full-length structure of <i>Thermus scotoductus</i> OLD defines the ATP hydrolysis properties and catalytic mechanism of Class 1 OLD family nucleases. <i>Nucleic Acids Research</i> , 2020, 48, 2762-2776.	14.5	17
9	The structure of the <i>Thermococcus gammatolerans</i> McrB N-terminal domain reveals a new mode of substrate recognition and specificity among McrB homologs. <i>Journal of Biological Chemistry</i> , 2020, 295, 743-756.	3.4	13
10	Structural and functional characterization of the dominant negative P $\alpha$ -loop lysine mutation in the dynamin superfamily protein Vps1. <i>Protein Science</i> , 2020, 29, 1416-1428.	7.6	6
11	Phylogenetic Analysis and Structural Modeling of SARS-CoV-2 Spike Protein Reveals an Evolutionary Distinct and Proteolytically Sensitive Activation Loop. <i>Journal of Molecular Biology</i> , 2020, 432, 3309-3325.	4.2	406
12	The structure of the <i>Thermococcus gammatolerans</i> McrB N-terminal domain reveals a new mode of substrate recognition and specificity among McrB homologs. <i>Journal of Biological Chemistry</i> , 2020, 295, 743-756.	3.4	7
13	Structural characterization of Class 2 OLD family nucleases supports a two-metal catalysis mechanism for cleavage. <i>Nucleic Acids Research</i> , 2019, 47, 9448-9463.	14.5	36
14	The structural biology of the dynamin-related proteins: New insights into a diverse, multitasking family. <i>Traffic</i> , 2019, 20, 717-740.	2.7	31
15	Endopeptidase Regulation as a Novel Function of the Zur-Dependent Zinc Starvation Response. <i>MBio</i> , 2019, 10, .	4.1	31
16	A structural mechanism for phosphorylation-dependent inactivation of the AP2 complex. <i>ELife</i> , 2019, 8, .	6.0	15
17	Structures of the fungal dynamin-related protein Vps1 reveal a unique, open helical architecture. <i>Journal of Cell Biology</i> , 2018, 217, 3608-3624.	5.2	12
18	The crystal structure of the <i>Helicobacter pylori</i> LlaJL.R1 N-terminal domain provides a model for site-specific DNA binding. <i>Journal of Biological Chemistry</i> , 2018, 293, 11758-11771.	3.4	6

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19	A Dynamin Mutant Defines a Superconstricted Prefission State. <i>Cell Reports</i> , 2014, 8, 734-742.	6.4	83
20	Building a fission machine – structural insights into dynamin assembly and activation. <i>Journal of Cell Science</i> , 2013, 126, 2773-84.	2.0	63
21	The Amino Acid Linker between the Endonuclease and Helicase Domains of Adeno-Associated Virus Type 5 Rep Plays a Critical Role in DNA-Dependent Oligomerization. <i>Journal of Virology</i> , 2012, 86, 3337-3346.	3.4	15
22	A Pseudoatomic Model of the Dynamin Polymer Identifies a Hydrolysis-Dependent Powerstroke. <i>Cell</i> , 2011, 147, 209-222.	28.9	189
23	G domain dimerization controls dynamin's assembly-stimulated GTPase activity. <i>Nature</i> , 2010, 465, 435-440.	27.8	264
24	Helical Crystallization of Soluble and Membrane Binding Proteins. <i>Methods in Enzymology</i> , 2010, 481, 45-62.	1.0	9
25	An Intramolecular Signaling Element that Modulates Dynamin Function In Vitro and In Vivo. <i>Molecular Biology of the Cell</i> , 2009, 20, 3561-3571.	2.1	76
26	Similarities and Differences between Frozen-Hydrated, Rigor Acto-S1 Complexes of Insect Flight and Chicken Skeletal Muscles. <i>Journal of Molecular Biology</i> , 2008, 381, 519-528.	4.2	7
27	The dynamin middle domain is critical for tetramerization and higher-order self-assembly. <i>EMBO Journal</i> , 2007, 26, 559-566.	7.8	164
28	The Conserved KMN Network Constitutes the Core Microtubule-Binding Site of the Kinetochores. <i>Cell</i> , 2006, 127, 983-997.	28.9	887
29	The Structure of a Eukaryotic Nicotinic Acid Phosphoribosyltransferase Reveals Structural Heterogeneity among Type II PRTases. <i>Structure</i> , 2005, 13, 1385-1396.	3.3	35
30	Electrostatic Tuning of Ion Conductance in Potassium Channels. <i>Biochemistry</i> , 2003, 42, 9263-9268.	2.5	115