

# Stephen H Mclaughlin

## List of Publications by Year in descending order

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54  
papers

3,718  
citations

159358

30  
h-index

161609

54  
g-index

68  
all docs

68  
docs citations

68  
times ranked

5464  
citing authors

#	ARTICLE	IF	CITATIONS
1	Synthetic Genetic Polymers Capable of Heredity and Evolution. <i>Science</i> , 2012, 336, 341-344.	6.0	635
2	Stimulation of the weak ATPase activity of human Hsp90 by a client protein 1 Edited by G. von Heijne. <i>Journal of Molecular Biology</i> , 2002, 315, 787-798.	2.0	240
3	Atomic structure of the APC/C and its mechanism of protein ubiquitination. <i>Nature</i> , 2015, 522, 450-454.	13.7	208
4	Structural Basis for the Recognition of Histone H4 by the Histone-Chaperone RbAp46. <i>Structure</i> , 2008, 16, 1077-1085.	1.6	192
5	Molecular architecture and mechanism of the anaphase-promoting complex. <i>Nature</i> , 2014, 513, 388-393.	13.7	180
6	The Co-chaperone p23 Arrests the Hsp90 ATPase Cycle to Trap Client Proteins. <i>Journal of Molecular Biology</i> , 2006, 356, 746-758.	2.0	179
7	Structures of PI4KIII <sup>2</sup> complexes show simultaneous recruitment of Rab11 and its effectors. <i>Science</i> , 2014, 344, 1035-1038.	6.0	131
8	SPATA2 Links CYLD to LUBAC, Activates CYLD, and Controls LUBAC Signaling. <i>Molecular Cell</i> , 2016, 63, 990-1005.	4.5	130
9	Structure of the inner kinetochore CCAN complex assembled onto a centromeric nucleosome. <i>Nature</i> , 2019, 574, 278-282.	13.7	113
10	Molecular recognition in procollagen chain assembly. <i>Matrix Biology</i> , 1998, 16, 369-377.	1.5	106
11	Independent ATPase Activity of Hsp90 Subunits Creates a Flexible Assembly Platform. <i>Journal of Molecular Biology</i> , 2004, 344, 813-826.	2.0	95
12	Biochemical and Structural Studies of the Interaction of Cdc37 with Hsp90. <i>Journal of Molecular Biology</i> , 2004, 340, 891-907.	2.0	82
13	The chromosome passenger complex is required for fidelity of chromosome transmission and cytokinesis in meiosis of mouse oocytes. <i>Journal of Cell Science</i> , 2010, 123, 4292-4300.	1.2	77
14	The N-terminal acetylation of Sir3 stabilizes its binding to the nucleosome core particle. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1119-1121.	3.6	72
15	RNA-directed activation of cytoplasmic dynein-1 in reconstituted transport RNPs. <i>ELife</i> , 2018, 7, .	2.8	72
16	Evolution of oligomeric state through allosteric pathways that mimic ligand binding. <i>Science</i> , 2014, 346, 1254-346.	6.0	62
17	Intracellular antibody signalling is regulated by phosphorylation of the Fc receptor TRIM21. <i>ELife</i> , 2018, 7, .	2.8	57
18	Structure of KAP1 tripartite motif identifies molecular interfaces required for retroelement silencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15042-15051.	3.3	57

#	ARTICLE	IF	CITATIONS
19	Structure of the SAS-6 cartwheel hub from <i>Leishmania major</i> . <i>ELife</i> , 2014, 3, e01812.	2.8	54
20	Structural basis for P <sup>an3</sup> binding to P <sup>an2</sup> and its function in mRNA recruitment and deadenylation. <i>EMBO Journal</i> , 2014, 33, 1514-1526.	3.5	50
21	Thiol-independent interaction of protein disulphide isomerase with type X collagen during intra-cellular folding and assembly. <i>Biochemical Journal</i> , 1998, 331, 793-800.	1.7	49
22	Mechanistic Studies on Hsp90 Inhibition by Ansamycin Derivatives. <i>Journal of Molecular Biology</i> , 2007, 372, 287-297.	2.0	49
23	Conformational Dynamics of the Molecular Chaperone Hsp90 in Complexes with a Co-chaperone and Anticancer Drugs. <i>Journal of Molecular Biology</i> , 2007, 372, 1189-1203.	2.0	44
24	Target-induced clustering activates Trim-Away of pathogens and proteins. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 278-289.	3.6	44
25	Structural Analysis of the Interaction between the Bacterial Cell Division Proteins FtsQ and FtsB. <i>MBio</i> , 2018, 9, .	1.8	40
26	Structure of the human inner kinetochore bound to a centromeric CENP-A nucleosome. <i>Science</i> , 2022, 376, 844-852.	6.0	40
27	[38] Protein disulfide-isomerase. <i>Methods in Enzymology</i> , 1995, 251, 397-406.	0.4	39
28	An oligomeric state-dependent switch in the ER enzyme FICD regulates AMPylation and deAMPylation of BiP. <i>EMBO Journal</i> , 2019, 38, e102177.	3.5	39
29	Crenactin forms actin-like double helical filaments regulated by arcadin-2. <i>ELife</i> , 2016, 5, .	2.8	39
30	Differential Binding of RhoA, RhoB, and RhoC to Protein Kinase C-Related Kinase (PRK) Isoforms PRK1, PRK2, and PRK3: PRKs Have the Highest Affinity for RhoB. <i>Biochemistry</i> , 2013, 52, 7999-8011.	1.2	37
31	The Soluble Periplasmic Domains of <i>Escherichia coli</i> Cell Division Proteins FtsQ/FtsB/FtsL Form a Trimeric Complex with Submicromolar Affinity. <i>Journal of Biological Chemistry</i> , 2015, 290, 21498-21509.	1.6	37
32	The Ciliopathy-Associated Cep104 Protein Interacts with Tubulin and Nek1 Kinase. <i>Structure</i> , 2017, 25, 146-156.	1.6	36
33	Structure of the DOCK2~ELMO1 complex provides insights into regulation of the auto-inhibited state. <i>Nature Communications</i> , 2020, 11, 3464.	5.8	34
34	Direct binding of CEP85 to STIL ensures robust PLK4 activation and efficient centriole assembly. <i>Nature Communications</i> , 2018, 9, 1731.	5.8	32
35	A tri-ionic anchor mechanism drives Ube2N-specific recruitment and K63-chain ubiquitination in TRIM ligases. <i>Nature Communications</i> , 2019, 10, 4502.	5.8	32
36	The structure of bactofilin filaments reveals their mode of membrane binding and lack of polarity. <i>Nature Microbiology</i> , 2019, 4, 2357-2368.	5.9	30

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37	Structural Insights into Arl1-Mediated Targeting of the Arf-GEF BIG1 to the trans-Golgi. <i>Cell Reports</i> , 2016, 16, 839-850.	2.9	29
38	Electrostatic Interactions Involving the Extreme C Terminus of Nuclear Export Factor CRM1 Modulate Its Affinity for Cargo. <i>Journal of Biological Chemistry</i> , 2011, 286, 29325-29335.	1.6	26
39	Structural Characterization of the <i>Chaetomium thermophilum</i> TREX-2 Complex and its Interaction with the mRNA Nuclear Export Factor Mex67:Mtr2. <i>Structure</i> , 2015, 23, 1246-1257.	1.6	26
40	Molecular mechanism of Mad1 kinetochore targeting by phosphorylated Bub1. <i>EMBO Reports</i> , 2021, 22, e52242.	2.0	26
41	Architecture of the CBF3 centromere complex of the budding yeast kinetochore. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 1103-1110.	3.6	23
42	Structural basis for the dimerization of Nab2 generated by RNA binding provides insight into its contribution to both poly(A) tail length determination and transcript compaction in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2017, 45, 1529-1538.	6.5	22
43	Folding and Assembly of Type X Collagen Mutants That Cause Metaphyseal Chondrodysplasia-type Schmid. <i>Journal of Biological Chemistry</i> , 1999, 274, 7570-7575.	1.6	21
44	Folding and stability of the ligand-binding domain of the glucocorticoid receptor. <i>Protein Science</i> , 2002, 11, 1926-1936.	3.1	20
45	CCDC61/VFL3 Is a Paralog of SAS6 and Promotes Ciliary Functions. <i>Structure</i> , 2020, 28, 674-689.e11.	1.6	16
46	Mutational Analysis Reveals a Single Binding Interface between RhoA and Its Effector, PRK1. <i>Biochemistry</i> , 2011, 50, 2860-2869.	1.2	14
47	Crystal structure of the $\epsilon$ -ring associated cell division protein ZapC from <i>Escherichia coli</i> . <i>FEBS Letters</i> , 2015, 589, 3822-3828.	1.3	13
48	The G-Protein Rab5A Activates VPS34 Complex II, a Class III PI3K, by a Dual Regulatory Mechanism. <i>Biophysical Journal</i> , 2020, 119, 2205-2218.	0.2	13
49	Reproducibility and accuracy of microscale thermophoresis in the NanoTemper Monolith: a multi laboratory benchmark study. <i>European Biophysics Journal</i> , 2021, 50, 411-427.	1.2	13
50	Engineering mono- and multi-valent inhibitors on a modular scaffold. <i>Chemical Science</i> , 2021, 12, 880-895.	3.7	7
51	Bipartite binding and partial inhibition links DEPTOR and mTOR in a mutually antagonistic embrace. <i>ELife</i> , 2021, 10, .	2.8	5
52	Diffuse transition state structure for the unfolding of a leucine-rich repeat protein. <i>Physical Chemistry Chemical Physics</i> , 2014, 16, 6448.	1.3	4
53	Equilibrium Binding Model for CpG DNA-Dependent Dimerization of Toll-like Receptor 9 Ectodomain. <i>Biochemistry</i> , 2020, 59, 4155-4162.	1.2	3
54	Cloning and expression of active domains of human protein disulphide isomerase. <i>Biochemical Society Transactions</i> , 1995, 23, 69S-69S.	1.6	1