J Mark Skehel

List of Publications by Year in descending order

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			136740	1	138251	
58	4,207		32		58	
papers	citations		h-index	h-index g		
67	67		67		6873	
all docs	docs citations		times ranked		citing authors	

#	Article	IF	CITATIONS
1	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. Nature Methods, 2019, 16, 595-602.	9.0	452
2	Atomic structure of the entire mammalian mitochondrial complex I. Nature, 2016, 538, 406-410.	13.7	427
3	Human CNS barrier-forming organoids with cerebrospinal fluid production. Science, 2020, 369, .	6.0	244
4	Mechanism and Regulation of DNA-Protein Crosslink Repair by the DNA-Dependent Metalloprotease SPRTN. Molecular Cell, 2016, 64, 688-703.	4.5	189
5	Molecular basis of APC/C regulation by the spindle assembly checkpoint. Nature, 2016, 536, 431-436.	13.7	178
6	CK2 Phospho-Dependent Binding of R2TP Complex to TEL2 Is Essential for mTOR and SMG1 Stability. Molecular Cell, 2010, 39, 839-850.	4.5	175
7	Molecular mechanism of APC/C activation by mitotic phosphorylation. Nature, 2016, 533, 260-264.	13.7	159
8	Structures of Respiratory Supercomplex I+III2 Reveal Functional and Conformational Crosstalk. Molecular Cell, 2019, 75, 1131-1146.e6.	4.5	148
9	Structure of a human 48 <i>S</i> translational initiation complex. Science, 2020, 369, 1220-1227.	6.0	138
10	Architecture of eukaryotic mRNA 3′-end processing machinery. Science, 2017, 358, 1056-1059.	6.0	124
11	Cryo-EM Structure of the Fork Protection Complex Bound to CMG at a Replication Fork. Molecular Cell, 2020, 78, 926-940.e13.	4.5	111
12	PRMT5-Dependent Methylation of the TIP60 Coactivator RUVBL1 Is a Key Regulator of Homologous Recombination. Molecular Cell, 2017, 65, 900-916.e7.	4.5	106
13	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. Analytical Chemistry, 2019, 91, 6953-6961.	3.2	100
14	Human PrimPol is a highly error-prone polymerase regulated by single-stranded DNA binding proteins. Nucleic Acids Research, 2015, 43, 1056-1068.	6.5	93
15	Architecture of the mycobacterial type VII secretion system. Nature, 2019, 576, 321-325.	13.7	89
16	POLE3-POLE4 Is a Histone H3-H4 Chaperone that Maintains Chromatin Integrity during DNA Replication. Molecular Cell, 2018, 72, 112-126.e5.	4.5	87
17	Trivalent RING Assembly on Retroviral Capsids Activates TRIM5ÂUbiquitination and Innate Immune Signaling. Cell Host and Microbe, 2018, 24, 761-775.e6.	5.1	82
18	Structure of the Fanconi anaemia monoubiquitin ligase complex. Nature, 2019, 575, 234-237.	13.7	80

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19	The ATPase Inhibitor Protein from Bovine Heart Mitochondria: The Minimal Inhibitory Sequenceâ€. Biochemistry, 1996, 35, 15618-15625.	1.2	79
20	The F1Fo-ATPase Complex from Bovine Heart Mitochondria:Â The Molar Ratio of the Subunits in the Stalk Region Linking the F1 and FoDomains. Biochemistry, 1996, 35, 12640-12646.	1.2	76
21	Phosphorylation-Dependent PIH1D1 Interactions Define Substrate Specificity of the R2TP Cochaperone Complex. Cell Reports, 2014, 7, 19-26.	2.9	74
22	Activation of the Endonuclease that Defines mRNA 3′ Ends Requires Incorporation into an 8-Subunit Core Cleavage and Polyadenylation Factor Complex. Molecular Cell, 2019, 73, 1217-1231.e11.	4.5	70
23	Protein CoAlation: a redox-regulated protein modification by coenzyme A in mammalian cells. Biochemical Journal, 2017, 474, 2489-2508.	1.7	65
24	Protein CoAlation and antioxidant function of coenzyme A in prokaryotic cells. Biochemical Journal, 2018, 475, 1909-1937.	1.7	60
25	RPAP3 provides a flexible scaffold for coupling HSP90 to the human R2TP co-chaperone complex. Nature Communications, 2018, 9, 1501.	5.8	54
26	Mechanistic Insights into Autoinhibition of the Oncogenic Chromatin Remodeler ALC1. Molecular Cell, 2017, 68, 847-859.e7.	4.5	53
27	Structure of the <i>Escherichia coli</i> ProQ RNA-binding protein. Rna, 2017, 23, 696-711.	1.6	50
28	A bipartite structural organization defines the SERINC family of HIV-1 restriction factors. Nature Structural and Molecular Biology, 2020, 27, 78-83.	3.6	50
29	Structural basis for VPS34 kinase activation by Rab1 and Rab5 on membranes. Nature Communications, 2021, 12, 1564.	5.8	50
30	The Structure of the R2TP Complex Defines a Platform for Recruiting Diverse Client Proteins to the HSP90 Molecular Chaperone System. Structure, 2017, 25, 1145-1152.e4.	1.6	48
31	Covalent Aurora A regulation by the metabolic integrator coenzyme A. Redox Biology, 2020, 28, 101318.	3.9	45
32	Inter-membrane association of the Sec and BAM translocons for bacterial outer-membrane biogenesis. ELife, 2020, 9, .	2.8	39
33	Arginine methylation of the c-Jun coactivator RACO-1 is required for c-Jun/AP-1 activation. EMBO Journal, 2013, 32, 1556-1567.	3.5	34
34	Shulin packages axonemal outer dynein arms for ciliary targeting. Science, 2021, 371, 910-916.	6.0	31
35	The Atypical MAP Kinase ErkB Transmits Distinct Chemotactic Signals through a Core Signaling Module. Developmental Cell, 2019, 48, 491-505.e9.	3.1	28
36	The accessory Sec system (SecY2A2) in Streptococcus pneumoniae is involved in export of pneumolysin toxin, adhesion and biofilm formation. Microbes and Infection, 2017, 19, 402-412.	1.0	23

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37	High-fidelity DNA replication in Mycobacterium tuberculosis relies on a trinuclear zinc center. Nature Communications, 2017, 8, 855.	5.8	23
38	A key metabolic integrator, coenzyme A, modulates the activity of peroxiredoxin 5 via covalent modification. Molecular and Cellular Biochemistry, 2019, 461, 91-102.	1.4	22
39	Structure of the TELO2-TTI1-TTI2 complex and its function in TOR recruitment to the R2TP chaperone. Cell Reports, 2021, 36, 109317.	2.9	20
40	Mechanistic Insights into Regulation of the ALC1 Remodeler by the Nucleosome Acidic Patch. Cell Reports, 2020, 33, 108529.	2.9	20
41	CTNNBL1 facilitates the association of CWC15 with CDC5L and is required to maintain the abundance of the Prp19 spliceosomal complex. Nucleic Acids Research, 2015, 43, 7058-7069.	6.5	19
42	Repurposed floxacins targeting RSK4 prevent chemoresistance and metastasis in lung and bladder cancer. Science Translational Medicine, 2021, 13, .	5.8	19
43	Crystal structure of the N-terminal domain of human Timeless and its interaction with Tipin. Nucleic Acids Research, 2017, 45, 5555-5563.	6.5	18
44	Regulation of metastasis suppressor NME1 by a key metabolic cofactor coenzyme A. Redox Biology, 2021, 44, 101978.	3.9	17
45	Arginine methylation and ubiquitylation crosstalk controls DNA end-resection and homologous recombination repair. Nature Communications, 2021, 12, 6313.	5.8	16
46	Structural Organization and Dynamics of Homodimeric Cytohesin Family Arf GTPase Exchange Factors in Solution and on Membranes. Structure, 2019, 27, 1782-1797.e7.	1.6	14
47	Electrospray ionization mass spectrometric analysis of subunits of NADH:ubiquinone oxidoreductase (complex I) from bovine heart mitochondria. Biochemical Society Transactions, 1994, 22, 551-555.	1.6	13
48	A NuRD Complex from Xenopus laevis Eggs Is Essential for DNA Replication during Early Embryogenesis. Cell Reports, 2018, 22, 2265-2278.	2.9	11
49	Phosphorylation-dependent BRD4 dimerization and implications for therapeutic inhibition of BET family proteins. Communications Biology, 2021, 4, 1273.	2.0	10
50	Redox Regulation of the Quorum-sensing Transcription Factor AgrA by Coenzyme A. Antioxidants, 2021, 10, 841.	2.2	9
51	Mpe1 senses the binding of pre-mRNA and controls 3′ end processing by CPF. Molecular Cell, 2022, 82, 2490-2504.e12.	4.5	9
52	Extensive Anti-CoA Immunostaining in Alzheimer's Disease and Covalent Modification of Tau by a Key Cellular Metabolite Coenzyme A. Frontiers in Cellular Neuroscience, 2021, 15, 739425.	1.8	8
53	Analysis of disulphide bond linkage between CoA and protein cysteine thiols during sporulation and in spores of <i>Bacillus</i>	0.7	6
54	Profiling the Site of Protein CoAlation and Coenzyme A Stabilization Interactions. Antioxidants, 2022, 11, 1362.	2.2	6

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55	Bipartite binding and partial inhibition links DEPTOR and mTOR in a mutually antagonistic embrace. ELife, 2021, 10, .	2.8	5
56	Multidimensional Dynamics of the Proteome in the Neurodegenerative and Aging Mammalian Brain. Molecular and Cellular Proteomics, 2022, 21, 100192.	2.5	5
57	Controlled Ligand Exchange Between Ruthenium Organometallic Cofactor Precursors and a NaÃ ⁻ ve Protein Scaffold Generates Artificial Metalloenzymes Catalysing Transfer Hydrogenation. Angewandte Chemie - International Edition, 2021, 60, 10919-10927.	7.2	3
58	Controlled Ligand Exchange Between Ruthenium Organometallic Cofactor Precursors and a Na $\tilde{A}^{\scriptscriptstyleT}$ ve Protein Scaffold Generates Artificial Metalloenzymes Catalysing Transfer Hydrogenation. Angewandte Chemie, 2021, 133, 11014-11022.	1.6	0