

Kevin D Corbett

List of Publications by Year in descending order

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69
papers

5,284
citations

117453

34
h-index

118652

62
g-index

88
all docs

88
docs citations

88
times ranked

8044
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 Infection Depends on Cellular Heparan Sulfate and ACE2. <i>Cell</i> , 2020, 183, 1043-1057.e15.	13.5	860
2	Structure, Molecular Mechanisms, and Evolutionary Relationships in DNA Topoisomerases. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2004, 33, 95-118.	18.3	379
3	The SARS-CoV-2 nucleocapsid phosphoprotein forms mutually exclusive condensates with RNA and the membrane-associated M protein. <i>Nature Communications</i> , 2021, 12, 502.	5.8	307
4	Architecture and self-assembly of the SARS-CoV-2 nucleocapsid protein. <i>Protein Science</i> , 2020, 29, 1890-1901.	3.1	218
5	Elimination of Toxic Microsatellite Repeat Expansion RNA by RNA-Targeting Cas9. <i>Cell</i> , 2017, 170, 899-912.e10.	13.5	213
6	Identification of H3K4me1-associated proteins at mammalian enhancers. <i>Nature Genetics</i> , 2018, 50, 73-82.	9.4	177
7	The C-terminal domain of DNA gyrase A adopts a DNA-bending \hat{A} -pinwheel fold. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7293-7298.	3.3	148
8	Structure and Mechanism of a Cyclic Trinucleotide-Activated Bacterial Endonuclease Mediating Bacteriophage Immunity. <i>Molecular Cell</i> , 2020, 77, 723-733.e6.	4.5	148
9	The Structural Basis for Substrate Specificity in DNA Topoisomerase IV. <i>Journal of Molecular Biology</i> , 2005, 351, 545-561.	2.0	147
10	TRIP13 is a protein-remodeling AAA+ ATPase that catalyzes MAD2 conformation switching. <i>ELife</i> , 2015, 4, .	2.8	137
11	Structural basis for receptor recognition by New World hemorrhagic fever arenaviruses. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 438-444.	3.6	125
12	Dynamic reorganization of the genome shapes the recombination landscape in meiotic prophase. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 164-174.	3.6	123
13	The Monopolin Complex Crosslinks Kinetochore Components to Regulate Chromosome-Microtubule Attachments. <i>Cell</i> , 2010, 142, 556-567.	13.5	119
14	HORMA Domain Proteins and a Trip13-like ATPase Regulate Bacterial cGAS-like Enzymes to Mediate Bacteriophage Immunity. <i>Molecular Cell</i> , 2020, 77, 709-722.e7.	4.5	116
15	The Chromosome Axis Controls Meiotic Events through a Hierarchical Assembly of HORMA Domain Proteins. <i>Developmental Cell</i> , 2014, 31, 487-502.	3.1	108
16	The multifaceted roles of the HORMA domain in cellular signaling. <i>Journal of Cell Biology</i> , 2015, 211, 745-755.	2.3	106
17	A conserved filamentous assembly underlies the structure of the meiotic chromosome axis. <i>ELife</i> , 2019, 8, .	2.8	100
18	Structure of the topoisomerase VI-B subunit: implications for type II topoisomerase mechanism and evolution. <i>EMBO Journal</i> , 2003, 22, 151-163.	3.5	98

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19	Molecular organization of mammalian meiotic chromosome axis revealed by expansion STORM microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 18423-18428.	3.3	89
20	Holoenzyme assembly and ATP-mediated conformational dynamics of topoisomerase VI. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 611-619.	3.6	86
21	The many faces of Ras: recognition of small GTP-binding proteins. <i>Trends in Biochemical Sciences</i> , 2001, 26, 710-716.	3.7	80
22	Stable RAGE-Heparan Sulfate Complexes Are Essential for Signal Transduction. <i>ACS Chemical Biology</i> , 2013, 8, 1611-1620.	1.6	71
23	Structural Dissection of ATP Turnover in the Prototypical GHL ATPase TopoVI. <i>Structure</i> , 2005, 13, 873-882.	1.6	69
24	The <sc>AAA</sc> + <sc>ATP</sc> ase <sc>TRIP</sc> 13 remodels <sc>HORMA</sc> domains through N-terminal engagement and unfolding. <i>EMBO Journal</i> , 2017, 36, 2419-2434.	3.5	69
25	Structure of M11L: A myxoma virus structural homolog of the apoptosis inhibitor, Bcl-2. <i>Protein Science</i> , 2007, 16, 695-703.	3.1	68
26	Sister kinetochores are mechanically fused during meiosis I in yeast. <i>Science</i> , 2014, 346, 248-251.	6.0	68
27	Conformational dynamics of the Hop1 HORMA domain reveal a common mechanism with the spindle checkpoint protein Mad2. <i>Nucleic Acids Research</i> , 2018, 46, 279-292.	6.5	68
28	Blocking Zika virus vertical transmission. <i>Scientific Reports</i> , 2018, 8, 1218.	1.6	55
29	Dephosphorylation of the Ndc80 Tail Stabilizes Kinetochores-Microtubule Attachments via the Ska Complex. <i>Developmental Cell</i> , 2017, 41, 424-437.e4.	3.1	54
30	Structure of the ATP-binding domain of <i>Plasmodium falciparum</i> Hsp90. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2738-2744.	1.5	52
31	Structural and Computational Characterization of the SHV-1 β -Lactamase- β -Lactamase Inhibitor Protein Interface. <i>Journal of Biological Chemistry</i> , 2006, 281, 26745-26753.	1.6	46
32	Molecular Architecture of the Yeast Monopolin Complex. <i>Cell Reports</i> , 2012, 1, 583-589.	2.9	46
33	A tripartite mechanism catalyzes Mad2-Cdc20 assembly at unattached kinetochores. <i>Science</i> , 2021, 371, 64-67.	6.0	45
34	How Do Type II Topoisomerases Use ATP Hydrolysis to Simplify DNA Topology beyond Equilibrium? Investigating the Relaxation Reaction of Nonsupercoiling Type II Topoisomerases. <i>Journal of Molecular Biology</i> , 2009, 385, 1397-1408.	2.0	43
35	Sit4p/PP6 regulates ER-to-Golgi traffic by controlling the dephosphorylation of COPII coat subunits. <i>Molecular Biology of the Cell</i> , 2013, 24, 2727-2738.	0.9	43
36	TRIP13 and APC15 drive mitotic exit by turnover of interphase- and unattached kinetochores-produced MCC. <i>Nature Communications</i> , 2018, 9, 4354.	5.8	39

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37	Architecture and Dynamics of Meiotic Chromosomes. <i>Annual Review of Genetics</i> , 2021, 55, 497-526.	3.2	38
38	Structural Basis for SARS-CoV-2 Nucleocapsid Protein Recognition by Single-Domain Antibodies. <i>Frontiers in Immunology</i> , 2021, 12, 719037.	2.2	35
39	Emerging Roles for Plant Topoisomerase VI. <i>Chemistry and Biology</i> , 2003, 10, 107-111.	6.2	32
40	Structural basis for topoisomerase VI inhibition by the anti-Hsp90 drug radicicol. <i>Nucleic Acids Research</i> , 2006, 34, 4269-4277.	6.5	32
41	Structure, assembly and reading of centromeric chromatin. <i>Current Opinion in Genetics and Development</i> , 2012, 22, 139-147.	1.5	31
42	Recruitment of a SUMO isopeptidase to rDNA stabilizes silencing complexes by opposing SUMO targeted ubiquitin ligase activity. <i>Genes and Development</i> , 2017, 31, 802-815.	2.7	31
43	Molecular Mechanisms of Spindle Assembly Checkpoint Activation and Silencing. <i>Progress in Molecular and Subcellular Biology</i> , 2017, 56, 429-455.	0.9	31
44	±-Tubulin acetylation from the inside out. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19515-19516.	3.3	26
45	The conserved XPF:ERCC1-like Zip2:Spo16 complex controls meiotic crossover formation through structure-specific DNA binding. <i>Nucleic Acids Research</i> , 2019, 47, 2365-2376.	6.5	24
46	Evolutionary Dynamics and Molecular Mechanisms of HORMA Domain Protein Signaling. <i>Annual Review of Biochemistry</i> , 2022, 91, 541-569.	5.0	23
47	Control of bacterial immune signaling by a WYL domain transcription factor. <i>Nucleic Acids Research</i> , 2022, 50, 5239-5250.	6.5	23
48	Structure of the <i>Saccharomyces cerevisiae</i> Hrr25:Mam1 monopolin subcomplex reveals a novel kinase regulator. <i>EMBO Journal</i> , 2016, 35, 2139-2151.	3.5	22
49	Proteomics-based screening of the endothelial heparan sulfate interactome reveals that C-type lectin 14a (CLEC14A) is a heparin-binding protein. <i>Journal of Biological Chemistry</i> , 2020, 295, 2804-2821.	1.6	18
50	The molecular basis of monopolin recruitment to the kinetochore. <i>Chromosoma</i> , 2019, 128, 331-354.	1.0	17
51	Responses to 10 common criticisms of anti-racism action in STEM. <i>PLoS Computational Biology</i> , 2021, 17, e1009141.	1.5	16
52	Two pathways drive meiotic chromosome axis assembly in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2022, 50, 4545-4556.	6.5	15
53	A Rho-like small GTPase of <i>Entamoeba histolytica</i> contains an unusual amino acid residue in a conserved GDP-stabilization region and is not a substrate for C3 exoenzyme. <i>Experimental Parasitology</i> , 2002, 101, 107-110.	0.5	14
54	Effects of preoperative and postoperative resistance exercise interventions on recovery of physical function in patients undergoing abdominal surgery for cancer: a systematic review of randomised controlled trials. <i>BMJ Open Sport and Exercise Medicine</i> , 2018, 4, e000331.	1.4	13

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55	A Chemical and Enzymatic Approach to Study Site-Specific Sumoylation. PLoS ONE, 2015, 10, e0143810.	1.1	10
56	Phosphoregulation of HORMA domain protein HIM-3 promotes asymmetric synaptonemal complex disassembly in meiotic prophase in <i>Caenorhabditis elegans</i> . PLoS Genetics, 2020, 16, e1008968.	1.5	8
57	The odds and implications of coinheritance of hemophilia A and B. Research and Practice in Thrombosis and Haemostasis, 2020, 4, 931-935.	1.0	3
58	The budding yeast RWD protein Csm1 scaffolds diverse protein complexes through a conserved structural mechanism. Protein Science, 2018, 27, 2094-2100.	3.1	2
59	p31 ^{comet} and TRIP13 recycle Rev7 to regulate DNA repair. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 27761-27763.	3.3	2
60	Structure and activity of a bacterial defense-associated 3'→5' exonuclease. Protein Science, 2022, 31, .	3.1	2
61	A new piece in the kinetochore jigsaw puzzle. Journal of Cell Biology, 2014, 206, 457-459.	2.3	1
62	Electron counting takes microED to the next level. Nature Methods, 2022, 19, 652-653.	9.0	1
63	A new phase in meiotic cell division. Nature, 2021, 592, 32-33.	13.7	0
64	Title is missing!. , 2020, 16, e1008968.		0
65	Title is missing!. , 2020, 16, e1008968.		0
66	Title is missing!. , 2020, 16, e1008968.		0
67	Title is missing!. , 2020, 16, e1008968.		0
68	Title is missing!. , 2020, 16, e1008968.		0
69	Title is missing!. , 2020, 16, e1008968.		0