

# Kevin D Corbett

## List of Publications by Citations

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72  
papers

3,436  
citations

33  
h-index

58  
g-index

88  
ext. papers

4,548  
ext. citations

14.2  
avg, IF

5.71  
L-index

#	Paper	IF	Citations
72	SARS-CoV-2 Infection Depends on Cellular Heparan Sulfate and ACE2. <i>Cell</i> , <b>2020</b> , 183, 1043-1057.e15	56.2	454
71	Structure, molecular mechanisms, and evolutionary relationships in DNA topoisomerases. <i>Annual Review of Biophysics and Biomolecular Structure</i> , <b>2004</b> , 33, 95-118		333
70	Elimination of Toxic Microsatellite Repeat Expansion RNA by RNA-Targeting Cas9. <i>Cell</i> , <b>2017</b> , 170, 899-917.e10	17.5	155
69	The structural basis for substrate specificity in DNA topoisomerase IV. <i>Journal of Molecular Biology</i> , <b>2005</b> , 351, 545-61	6.5	133
68	The C-terminal domain of DNA gyrase A adopts a DNA-bending beta-pinwheel fold. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2004</b> , 101, 7293-8	11.5	131
67	Architecture and self-assembly of the SARS-CoV-2 nucleocapsid protein. <i>Protein Science</i> , <b>2020</b> , 29, 1890-1901	13.9	117
66	Structural basis for receptor recognition by New World hemorrhagic fever arenaviruses. <i>Nature Structural and Molecular Biology</i> , <b>2010</b> , 17, 438-44	17.6	105
65	TRIP13 is a protein-remodeling AAA+ ATPase that catalyzes MAD2 conformation switching. <i>ELife</i> , <b>2015</b> , 4,	8.9	103
64	The SARS-CoV-2 nucleocapsid phosphoprotein forms mutually exclusive condensates with RNA and the membrane-associated M protein. <i>Nature Communications</i> , <b>2021</b> , 12, 502	17.4	101
63	The monopolin complex crosslinks kinetochore components to regulate chromosome-microtubule attachments. <i>Cell</i> , <b>2010</b> , 142, 556-67	56.2	99
62	Identification of H3K4me1-associated proteins at mammalian enhancers. <i>Nature Genetics</i> , <b>2018</b> , 50, 73-83	26.3	96
61	Structure of the topoisomerase VI-B subunit: implications for type II topoisomerase mechanism and evolution. <i>EMBO Journal</i> , <b>2003</b> , 22, 151-63	13	82
60	The many faces of Ras: recognition of small GTP-binding proteins. <i>Trends in Biochemical Sciences</i> , <b>2001</b> , 26, 710-6	10.3	77
59	The chromosome axis controls meiotic events through a hierarchical assembly of HORMA domain proteins. <i>Developmental Cell</i> , <b>2014</b> , 31, 487-502	10.2	75
58	The multifaceted roles of the HORMA domain in cellular signaling. <i>Journal of Cell Biology</i> , <b>2015</b> , 211, 745-55	7.3	72
57	Dynamic reorganization of the genome shapes the recombination landscape in meiotic prophase. <i>Nature Structural and Molecular Biology</i> , <b>2019</b> , 26, 164-174	17.6	72
56	Structure of M11L: A myxoma virus structural homolog of the apoptosis inhibitor, Bcl-2. <i>Protein Science</i> , <b>2007</b> , 16, 695-703	6.3	66

55	Holoenzyme assembly and ATP-mediated conformational dynamics of topoisomerase VI. <i>Nature Structural and Molecular Biology</i> , <b>2007</b> , 14, 611-9	17.6	64
54	Structural dissection of ATP turnover in the prototypical GHL ATPase TopoVI. <i>Structure</i> , <b>2005</b> , 13, 873-82	5.2	63
53	A conserved filamentous assembly underlies the structure of the meiotic chromosome axis. <i>ELife</i> , <b>2019</b> , 8,	8.9	60
52	Stable RAGE-heparan sulfate complexes are essential for signal transduction. <i>ACS Chemical Biology</i> , <b>2013</b> , 8, 1611-20	4.9	57
51	Sister kinetochores are mechanically fused during meiosis I in yeast. <i>Science</i> , <b>2014</b> , 346, 248-51	33.3	56
50	Structure and Mechanism of a Cyclic Trinucleotide-Activated Bacterial Endonuclease Mediating Bacteriophage Immunity. <i>Molecular Cell</i> , <b>2020</b> , 77, 723-733.e6	17.6	56
49	The AAA+ ATPase TRIP13 remodels HORMA domains through N-terminal engagement and unfolding. <i>EMBO Journal</i> , <b>2017</b> , 36, 2419-2434	13	50
48	HORMA Domain Proteins and a Trip13-like ATPase Regulate Bacterial cGAS-like Enzymes to Mediate Bacteriophage Immunity. <i>Molecular Cell</i> , <b>2020</b> , 77, 709-722.e7	17.6	50
47	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> , <b>2019</b> , 116, 18423-18428	11.5	49
46	Structure of the ATP-binding domain of Plasmodium falciparum Hsp90. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2010</b> , 78, 2738-44	4.2	43
45	Structural and computational characterization of the SHV-1 beta-lactamase-beta-lactamase inhibitor protein interface. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 26745-53	5.4	42
44	Blocking Zika virus vertical transmission. <i>Scientific Reports</i> , <b>2018</b> , 8, 1218	4.9	41
43	Conformational dynamics of the Hop1 HORMA domain reveal a common mechanism with the spindle checkpoint protein Mad2. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 279-292	20.1	39
42	Dephosphorylation of the Ndc80 Tail Stabilizes Kinetochores-Microtubule Attachments via the Ska Complex. <i>Developmental Cell</i> , <b>2017</b> , 41, 424-437.e4	10.2	38
41	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> , <b>2009</b> , 385, 1397-408	6.5	38
40	Molecular architecture of the yeast monopolin complex. <i>Cell Reports</i> , <b>2012</b> , 1, 583-9	10.6	36
39	Sit4p/PP6 regulates ER-to-Golgi traffic by controlling the dephosphorylation of COPII coat subunits. <i>Molecular Biology of the Cell</i> , <b>2013</b> , 24, 2727-38	3.5	32
38	Structural basis for topoisomerase VI inhibition by the anti-Hsp90 drug radicicol. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, 4269-77	20.1	28

37	TRIP13 and APC15 drive mitotic exit by turnover of interphase- and unattached kinetochore-produced MCC. <i>Nature Communications</i> , <b>2018</b> , 9, 4354	17.4	28
36	Emerging roles for plant topoisomerase VI. <i>Chemistry and Biology</i> , <b>2003</b> , 10, 107-11		27
35	Recruitment of a SUMO isopeptidase to rDNA stabilizes silencing complexes by opposing SUMO targeted ubiquitin ligase activity. <i>Genes and Development</i> , <b>2017</b> , 31, 802-815	12.6	26
34	Structure, assembly and reading of centromeric chromatin. <i>Current Opinion in Genetics and Development</i> , <b>2012</b> , 22, 139-47	4.9	25
33	βTubulin acetylation from the inside out. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 19515-6	11.5	22
32	Molecular Mechanisms of Spindle Assembly Checkpoint Activation and Silencing. <i>Progress in Molecular and Subcellular Biology</i> , <b>2017</b> , 56, 429-455	3	21
31	Architecture and self-assembly of the SARS-CoV-2 nucleocapsid protein <b>2020</b> ,		21
30	Structure of the <i>Saccharomyces cerevisiae</i> Hrr25:Mam1 monopolin subcomplex reveals a novel kinase regulator. <i>EMBO Journal</i> , <b>2016</b> , 35, 2139-2151	13	15
29	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> , <b>2002</b> , 101, 107-10	2.1	13
28	The conserved XPF:ERCC1-like Zip2:Spo16 complex controls meiotic crossover formation through structure-specific DNA binding. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 2365-2376	20.1	13
27	The molecular basis of monopolin recruitment to the kinetochore. <i>Chromosoma</i> , <b>2019</b> , 128, 331-354	2.8	12
26	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> , <b>2018</b> , 4, e000331	3.4	11
25	A tripartite mechanism catalyzes Mad2-Cdc20 assembly at unattached kinetochores. <i>Science</i> , <b>2021</b> , 371, 64-67	33.3	11
24	The SARS-CoV-2 Nucleocapsid phosphoprotein forms mutually exclusive condensates with RNA and the membrane-associated M protein <b>2020</b> ,		10
23	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> , <b>2020</b> , 295, 2804-2821	5.4	9
22	Structural Basis for SARS-CoV-2 Nucleocapsid Protein Recognition by Single-Domain Antibodies. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 719037	8.4	9
21	A Chemical and Enzymatic Approach to Study Site-Specific Sumoylation. <i>PLoS ONE</i> , <b>2015</b> , 10, e0143810	3.7	8
20	Architecture and Dynamics of Meiotic Chromosomes. <i>Annual Review of Genetics</i> , <b>2021</b> , 55, 497-526	14.5	7

19	Phosphoregulation of HORMA domain protein HIM-3 promotes asymmetric synaptonemal complex disassembly in meiotic prophase in <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , <b>2020</b> , 16, e1008968	6	6
18	Evolutionary Dynamics and Molecular Mechanisms of HORMA Domain Protein Signaling.. <i>Annual Review of Biochemistry</i> , <b>2022</b> ,	29.1	4
17	Structure and mechanism of a cyclic trinucleotide-activated bacterial endonuclease mediating bacteriophage immunity		3
16	A Cytoskeletal Vortex Drives Phage Nucleus Rotation During Jumbo Phage Replication in <i>E. coli</i>		2
15	A cohesin-independent mechanism modulates recombination activity along meiotic chromosomes		2
14	HORMA domain proteins and a Pch2-like ATPase regulate bacterial cGAS-like enzymes to mediate bacteriophage immunity		2
13	A new piece in the kinetochore jigsaw puzzle. <i>Journal of Cell Biology</i> , <b>2014</b> , 206, 457-9	7.3	1
12	Structure of Zip2:Spo16, a conserved XPF:ERCC1-like complex critical for meiotic crossover formation		1
11	A conserved mechanism for meiotic chromosome organization through self-assembly of a filamentous chromosome axis core		1
10	The odds and implications of coinheritance of hemophilia A and B. <i>Research and Practice in Thrombosis and Haemostasis</i> , <b>2020</b> , 4, 931-935	5.1	1
9	The budding-yeast RWD protein Csm1 scaffolds diverse protein complexes through a conserved structural mechanism. <i>Protein Science</i> , <b>2018</b> , 27, 2094-2100	6.3	1
8	Two pathways drive meiotic chromosome axis assembly in <i>Saccharomyces cerevisiae</i> .. <i>Nucleic Acids Research</i> , <b>2022</b> ,	20.1	1
7	p31 and TRIP13 recycle Rev7 to regulate DNA repair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 27761-27763	11.5	0
6	Phosphoregulation of HORMA domain protein HIM-3 promotes asymmetric synaptonemal complex disassembly in meiotic prophase in <i>Caenorhabditis elegans</i> <b>2020</b> , 16, e1008968		
5	Phosphoregulation of HORMA domain protein HIM-3 promotes asymmetric synaptonemal complex disassembly in meiotic prophase in <i>Caenorhabditis elegans</i> <b>2020</b> , 16, e1008968		
4	Phosphoregulation of HORMA domain protein HIM-3 promotes asymmetric synaptonemal complex disassembly in meiotic prophase in <i>Caenorhabditis elegans</i> <b>2020</b> , 16, e1008968		
3	Phosphoregulation of HORMA domain protein HIM-3 promotes asymmetric synaptonemal complex disassembly in meiotic prophase in <i>Caenorhabditis elegans</i> <b>2020</b> , 16, e1008968		
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Phosphoregulation of HORMA domain protein HIM-3 promotes asymmetric synaptonemal complex disassembly in meiotic prophase in *Caenorhabditis elegans* **2020**, 16, e1008968