Kevin D Corbett

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/408811/kevin-d-corbett-publications-by-year.pdf
Version: 2024-04-25

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	Evolutionary Dynamics and Molecular Mechanisms of HORMA Domain Protein Signaling.. *Annual Review of Biochemistry*, **2022**,	29.1	4
71	Two pathways drive meiotic chromosome axis assembly in Saccharomyces cerevisiae.. *Nucleic Acids Research*, **2022**,	20.1	1
70	Structural Basis for SARS-CoV-2 Nucleocapsid Protein Recognition by Single-Domain Antibodies. *Frontiers in Immunology*, **2021**, 12, 719037	8.4	9
69	The SARS-CoV-2 nucleocapsid phosphoprotein forms mutually exclusive condensates with RNA and the membrane-associated M protein. *Nature Communications*, **2021**, 12, 502	17.4	101
68	Architecture and Dynamics of Meiotic Chromosomes. *Annual Review of Genetics*, **2021**, 55, 497-526	14.5	7
67	A tripartite mechanism catalyzes Mad2-Cdc20 assembly at unattached kinetochores. *Science*, **2021**, 371, 64-67	33.3	11
66	Architecture and self-assembly of the SARS-CoV-2 nucleocapsid protein. *Protein Science*, **2020**, 29, 1890-1901	6.3	117
65	Phosphoregulation of HORMA domain protein HIM-3 promotes asymmetric synaptonemal complex disassembly in meiotic prophase in Caenorhabditis elegans. *PLoS Genetics*, **2020**, 16, e1008968	6	6
64	Proteomics-based screening of the endothelial heparan sulfate interactome reveals that C-type lectin 14a (CLEC14A) is a heparin-binding protein. *Journal of Biological Chemistry*, **2020**, 295, 2804-2821	5.4	9
63	Architecture and self-assembly of the SARS-CoV-2 nucleocapsid protein **2020**,		21
62	The SARS-CoV-2 Nucleocapsid phosphoprotein forms mutually exclusive condensates with RNA and the membrane-associated M protein **2020**,		10
61	HORMA Domain Proteins and a Trip13-like ATPase Regulate Bacterial cGAS-like Enzymes to Mediate Bacteriophage Immunity. *Molecular Cell*, **2020**, 77, 709-722.e7	17.6	50
60	Structure and Mechanism of a Cyclic Trinucleotide-Activated Bacterial Endonuclease Mediating Bacteriophage Immunity. *Molecular Cell*, **2020**, 77, 723-733.e6	17.6	56
59	The odds and implications of coinheritance of hemophilia A and B. *Research and Practice in Thrombosis and Haemostasis*, **2020**, 4, 931-935	5.1	1
58	p31 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	11.5	0
57	SARS-CoV-2 Infection Depends on Cellular Heparan Sulfate and ACE2. *Cell*, **2020**, 183, 1043-1057.e15	56.2	454
56	Phosphoregulation of HORMA domain protein HIM-3 promotes asymmetric synaptonemal complex disassembly in meiotic prophase in Caenorhabditis elegans **2020**, 16, e1008968		

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55	Phosphoregulation of HORMA domain protein HIM-3 promotes asymmetric synaptonemal complex disassembly in meiotic prophase in Caenorhabditis elegans **2020**, 16, e1008968		
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51	Phosphoregulation of HORMA domain protein HIM-3 promotes asymmetric synaptonemal complex disassembly in meiotic prophase in Caenorhabditis elegans **2020**, 16, e1008968		
50	Molecular organization of mammalian meiotic chromosome axis revealed by expansion STORM microscopy. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 18423-18428	11.5	49
49	The molecular basis of monopolin recruitment to the kinetochore. *Chromosoma*, **2019**, 128, 331-354	2.8	12
48	A conserved filamentous assembly underlies the structure of the meiotic chromosome axis. *ELife*, **2019**, 8,	8.9	60
47	Dynamic reorganization of the genome shapes the recombination landscape in meiotic prophase. *Nature Structural and Molecular Biology*, **2019**, 26, 164-174	17.6	72
46	The conserved XPF:ERCC1-like Zip2:Spo16 complex controls meiotic crossover formation through structure-specific DNA binding. *Nucleic Acids Research*, **2019**, 47, 2365-2376	20.1	13
45	Conformational dynamics of the Hop1 HORMA domain reveal a common mechanism with the spindle checkpoint protein Mad2. *Nucleic Acids Research*, **2018**, 46, 279-292	20.1	39
44	Blocking Zika virus vertical transmission. *Scientific Reports*, **2018**, 8, 1218	4.9	41
43	Identification of H3K4me1-associated proteins at mammalian enhancers. *Nature Genetics*, **2018**, 50, 73-83	36.3	96
42	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. *BMJ Open Sport and Exercise Medicine*, **2018**, 4, e000331	3.4	11
41	The budding-yeast RWD protein Csm1 scaffolds diverse protein complexes through a conserved structural mechanism. *Protein Science*, **2018**, 27, 2094-2100	6.3	1
40	TRIP13 and APC15 drive mitotic exit by turnover of interphase- and unattached kinetochore-produced MCC. *Nature Communications*, **2018**, 9, 4354	17.4	28
39	Recruitment of a SUMO isopeptidase to rDNA stabilizes silencing complexes by opposing SUMO targeted ubiquitin ligase activity. *Genes and Development*, **2017**, 31, 802-815	12.6	26
38	Dephosphorylation of the Ndc80 Tail Stabilizes Kinetochore-Microtubule Attachments via the Ska Complex. *Developmental Cell*, **2017**, 41, 424-437.e4	10.2	38

37	Elimination of Toxic Microsatellite Repeat Expansion RNA by RNA-Targeting Cas9. *Cell*, **2017**, 170, 899-912.e10	56.2	155
36	The AAA+ ATPase TRIP13 remodels HORMA domains through N-terminal engagement and unfolding. *EMBO Journal*, **2017**, 36, 2419-2434	13	50
35	Molecular Mechanisms of Spindle Assembly Checkpoint Activation and Silencing. *Progress in Molecular and Subcellular Biology*, **2017**, 56, 429-455	3	21
34	Structure of the Saccharomyces cerevisiae Hrr25:Mam1 monopolin subcomplex reveals a novel kinase regulator. *EMBO Journal*, **2016**, 35, 2139-2151	13	15
33	The multifaceted roles of the HORMA domain in cellular signaling. *Journal of Cell Biology*, **2015**, 211, 745-55	7.3	72
32	A Chemical and Enzymatic Approach to Study Site-Specific Sumoylation. *PLoS ONE*, **2015**, 10, e0143810	3.7	8
31	TRIP13 is a protein-remodeling AAA+ ATPase that catalyzes MAD2 conformation switching. *ELife*, **2015**, 4,	8.9	103
30	The chromosome axis controls meiotic events through a hierarchical assembly of HORMA domain proteins. *Developmental Cell*, **2014**, 31, 487-502	10.2	75
29	Sister kinetochores are mechanically fused during meiosis I in yeast. *Science*, **2014**, 346, 248-51	33.3	56
28	A new piece in the kinetochore jigsaw puzzle. *Journal of Cell Biology*, **2014**, 206, 457-9	7.3	1
27	Stable RAGE-heparan sulfate complexes are essential for signal transduction. *ACS Chemical Biology*, **2013**, 8, 1611-20	4.9	57
26	Sit4p/PP6 regulates ER-to-Golgi traffic by controlling the dephosphorylation of COPII coat subunits. *Molecular Biology of the Cell*, **2013**, 24, 2727-38	3.5	32
25	□Tubulin acetylation from the inside out. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 19515-6	11.5	22
24	Molecular architecture of the yeast monopolin complex. *Cell Reports*, **2012**, 1, 583-9	10.6	36
23	Structure, assembly and reading of centromeric chromatin. *Current Opinion in Genetics and Development*, **2012**, 22, 139-47	4.9	25
22	Structural basis for receptor recognition by New World hemorrhagic fever arenaviruses. *Nature Structural and Molecular Biology*, **2010**, 17, 438-44	17.6	105
21	The monopolin complex crosslinks kinetochore components to regulate chromosome-microtubule attachments. *Cell*, **2010**, 142, 556-67	56.2	99
20	Structure of the ATP-binding domain of Plasmodium falciparum Hsp90. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 2738-44	4.2	43

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19	How do type II topoisomerases use ATP hydrolysis to simplify DNA topology beyond equilibrium? Investigating the relaxation reaction of nonsupercoiling type II topoisomerases. *Journal of Molecular Biology*, **2009**, 385, 1397-408	6.5	38
18	Holoenzyme assembly and ATP-mediated conformational dynamics of topoisomerase VI. *Nature Structural and Molecular Biology*, **2007**, 14, 611-9	17.6	64
17	Structure of M11L: A myxoma virus structural homolog of the apoptosis inhibitor, Bcl-2. *Protein Science*, **2007**, 16, 695-703	6.3	66
16	Structural basis for topoisomerase VI inhibition by the anti-Hsp90 drug radicicol. *Nucleic Acids Research*, **2006**, 34, 4269-77	20.1	28
15	Structural and computational characterization of the SHV-1 beta-lactamase-beta-lactamase inhibitor protein interface. *Journal of Biological Chemistry*, **2006**, 281, 26745-53	5.4	42
14	The structural basis for substrate specificity in DNA topoisomerase IV. *Journal of Molecular Biology*, **2005**, 351, 545-61	6.5	133
13	Structural dissection of ATP turnover in the prototypical GHL ATPase TopoVI. *Structure*, **2005**, 13, 873-82	5.2	63
12	The C-terminal domain of DNA gyrase A adopts a DNA-bending beta-pinwheel fold. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 7293-8	11.5	131
11	Structure, molecular mechanisms, and evolutionary relationships in DNA topoisomerases. *Annual Review of Biophysics and Biomolecular Structure*, **2004**, 33, 95-118		333
10	Structure of the topoisomerase VI-B subunit: implications for type II topoisomerase mechanism and evolution. *EMBO Journal*, **2003**, 22, 151-63	13	82
9	Emerging roles for plant topoisomerase VI. *Chemistry and Biology*, **2003**, 10, 107-11		27
8	A Rho-like small GTPase of Entamoeba histolytica contains an unusual amino acid residue in a conserved GDP-stabilization region and is not a substrate for C3 exoenzyme. *Experimental Parasitology*, **2002**, 101, 107-10	2.1	13
7	The many faces of Ras: recognition of small GTP-binding proteins. *Trends in Biochemical Sciences*, **2001**, 26, 710-6	10.3	77
6	A Cytoskeletal Vortex Drives Phage Nucleus Rotation During Jumbo Phage Replication in E. coli		2
5	A cohesin-independent mechanism modulates recombination activity along meiotic chromosomes		2
4	Structure of Zip2:Spo16, a conserved XPF:ERCC1-like complex critical for meiotic crossover formation		1
3	A conserved mechanism for meiotic chromosome organization through self-assembly of a filamentous chromosome axis core		1
2	HORMA domain proteins and a Pch2-like ATPase regulate bacterial cGAS-like enzymes to mediate bacteriophage immunity		2

1	Structure and mechanism of a cyclic trinucleotide-activated bacterial endonuclease mediating bacteriophage immunity	3