Kevin D Corbett

List of Publications by Year in descending order

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KEVIN D CODBETT

#	Article	IF	CITATIONS
1	SARS-CoV-2 Infection Depends on Cellular Heparan Sulfate and ACE2. Cell, 2020, 183, 1043-1057.e15.	28.9	860
2	Structure, Molecular Mechanisms, and Evolutionary Relationships in DNA Topoisomerases. Annual Review of Biophysics and Biomolecular Structure, 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. Nature Communications, 2021, 12, 502.	12.8	307
4	Architecture and selfâ€assembly of the <scp>SARS oV</scp> â€2 nucleocapsid protein. Protein Science, 2020, 29, 1890-1901.	7.6	218
5	Elimination of Toxic Microsatellite Repeat Expansion RNA by RNA-Targeting Cas9. Cell, 2017, 170, 899-912.e10.	28.9	213
6	Identification of H3K4me1-associated proteins at mammalian enhancers. Nature Genetics, 2018, 50, 73-82.	21.4	177
7	The C-terminal domain of DNA gyrase A adopts a DNA-bending Â-pinwheel fold. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7293-7298.	7.1	148
8	Structure and Mechanism of a Cyclic Trinucleotide-Activated Bacterial Endonuclease Mediating Bacteriophage Immunity. Molecular Cell, 2020, 77, 723-733.e6.	9.7	148
9	The Structural Basis for Substrate Specificity in DNA Topoisomerase IV. Journal of Molecular Biology, 2005, 351, 545-561.	4.2	147
10	TRIP13 is a protein-remodeling AAA+ ATPase that catalyzes MAD2 conformation switching. ELife, 2015, 4, .	6.0	137
11	Structural basis for receptor recognition by New World hemorrhagic fever arenaviruses. Nature Structural and Molecular Biology, 2010, 17, 438-444.	8.2	125
12	Dynamic reorganization of the genome shapes the recombination landscape in meiotic prophase. Nature Structural and Molecular Biology, 2019, 26, 164-174.	8.2	123
13	The Monopolin Complex Crosslinks Kinetochore Components to Regulate Chromosome-Microtubule Attachments. Cell, 2010, 142, 556-567.	28.9	119
14	HORMA Domain Proteins and a Trip13-like ATPase Regulate Bacterial cGAS-like Enzymes to Mediate Bacteriophage Immunity. Molecular Cell, 2020, 77, 709-722.e7.	9.7	116
15	The Chromosome Axis Controls Meiotic Events through a Hierarchical Assembly of HORMA Domain Proteins. Developmental Cell, 2014, 31, 487-502.	7.0	108
16	The multifaceted roles of the HORMA domain in cellular signaling. Journal of Cell Biology, 2015, 211, 745-755.	5.2	106
17	A conserved filamentous assembly underlies the structure of the meiotic chromosome axis. ELife, 2019, 8, .	6.0	100
18	Structure of the topoisomerase VI-B subunit: implications for type II topoisomerase mechanism and evolution. EMBO Journal, 2003, 22, 151-163.	7.8	98

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19	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.	7.1	89
20	Holoenzyme assembly and ATP-mediated conformational dynamics of topoisomerase VI. Nature Structural and Molecular Biology, 2007, 14, 611-619.	8.2	86
21	The many faces of Ras: recognition of small GTP-binding proteins. Trends in Biochemical Sciences, 2001, 26, 710-716.	7.5	80
22	Stable RAGE-Heparan Sulfate Complexes Are Essential for Signal Transduction. ACS Chemical Biology, 2013, 8, 1611-1620.	3.4	71
23	Structural Dissection of ATP Turnover in the Prototypical GHL ATPase TopoVI. Structure, 2005, 13, 873-882.	3.3	69
24	The <scp>AAA</scp> + <scp>ATP</scp> ase <scp>TRIP</scp> 13 remodels <scp>HORMA</scp> domains through Nâ€ŧerminal engagement and unfolding. EMBO Journal, 2017, 36, 2419-2434.	7.8	69
25	Structure of M11L: A myxoma virus structural homolog of the apoptosis inhibitor, Bcl-2. Protein Science, 2007, 16, 695-703.	7.6	68
26	Sister kinetochores are mechanically fused during meiosis I in yeast. Science, 2014, 346, 248-251.	12.6	68
27	Conformational dynamics of the Hop1 HORMA domain reveal a common mechanism with the spindle checkpoint protein Mad2. Nucleic Acids Research, 2018, 46, 279-292.	14.5	68
28	Blocking Zika virus vertical transmission. Scientific Reports, 2018, 8, 1218.	3.3	55
29	Dephosphorylation of the Ndc80 Tail Stabilizes Kinetochore-Microtubule Attachments via the Ska Complex. Developmental Cell, 2017, 41, 424-437.e4.	7.0	54
30	Structure of the ATPâ€binding domain of <i>Plasmodium falciparum</i> Hsp90. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2738-2744.	2.6	52
31	Structural and Computational Characterization of the SHV-1 β-Lactamase-β-Lactamase Inhibitor Protein Interface. Journal of Biological Chemistry, 2006, 281, 26745-26753.	3.4	46
32	Molecular Architecture of the Yeast Monopolin Complex. Cell Reports, 2012, 1, 583-589.	6.4	46
33	A tripartite mechanism catalyzes Mad2-Cdc20 assembly at unattached kinetochores. Science, 2021, 371, 64-67.	12.6	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. Journal of Molecular Biology, 2009, 385, 1397-1408.	4.2	43
35	Sit4p/PP6 regulates ER-to-Golgi traffic by controlling the dephosphorylation of COPII coat subunits. Molecular Biology of the Cell, 2013, 24, 2727-2738.	2.1	43
36	TRIP13 and APC15 drive mitotic exit by turnover of interphase- and unattached kinetochore-produced MCC. Nature Communications, 2018, 9, 4354.	12.8	39

KEVIN D CORBETT

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37	Architecture and Dynamics of Meiotic Chromosomes. Annual Review of Genetics, 2021, 55, 497-526.	7.6	38
38	Structural Basis for SARS-CoV-2 Nucleocapsid Protein Recognition by Single-Domain Antibodies. Frontiers in Immunology, 2021, 12, 719037.	4.8	35
39	Emerging Roles for Plant Topoisomerase VI. Chemistry and Biology, 2003, 10, 107-111.	6.0	32
40	Structural basis for topoisomerase VI inhibition by the anti-Hsp90 drug radicicol. Nucleic Acids Research, 2006, 34, 4269-4277.	14.5	32
41	Structure, assembly and reading of centromeric chromatin. Current Opinion in Genetics and Development, 2012, 22, 139-147.	3.3	31
42	Recruitment of a SUMO isopeptidase to rDNA stabilizes silencing complexes by opposing SUMO targeted ubiquitin ligase activity. Genes and Development, 2017, 31, 802-815.	5.9	31
43	Molecular Mechanisms of Spindle Assembly Checkpoint Activation and Silencing. Progress in Molecular and Subcellular Biology, 2017, 56, 429-455.	1.6	31
44	α-Tubulin acetylation from the inside out. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 19515-19516.	7.1	26
45	The conserved XPF:ERCC1-like Zip2:Spo16 complex controls meiotic crossover formation through structure-specific DNA binding. Nucleic Acids Research, 2019, 47, 2365-2376.	14.5	24
46	Evolutionary Dynamics and Molecular Mechanisms of HORMA Domain Protein Signaling. Annual Review of Biochemistry, 2022, 91, 541-569.	11.1	23
47	Control of bacterial immune signaling by a WYL domain transcription factor. Nucleic Acids Research, 2022, 50, 5239-5250.	14.5	23
48	Structure of the <i>Saccharomyces cerevisiae</i> Hrr25:Mam1 monopolin subcomplex reveals a novel kinase regulator. EMBO Journal, 2016, 35, 2139-2151.	7.8	22
49	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.	3.4	18
50	The molecular basis of monopolin recruitment to the kinetochore. Chromosoma, 2019, 128, 331-354.	2.2	17
51	Responses to 10 common criticisms of anti-racism action in STEMM. PLoS Computational Biology, 2021, 17, e1009141.	3.2	16
52	Two pathways drive meiotic chromosome axis assembly in <i>Saccharomyces cerevisiae</i> . Nucleic Acids Research, 2022, 50, 4545-4556.	14.5	15
53	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, 107-110.	1.2	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. BMJ Open Sport and Exercise Medicine, 2018, 4, e000331.	2.9	13

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55	A Chemical and Enzymatic Approach to Study Site-Specific Sumoylation. PLoS ONE, 2015, 10, e0143810.	2.5	10
56	Phosphoregulation of HORMA domain protein HIM-3 promotes asymmetric synaptonemal complex disassembly in meiotic prophase in Caenorhabditis elegans. PLoS Genetics, 2020, 16, e1008968.	3.5	8
57	The odds and implications of coinheritance of hemophilia A and B. Research and Practice in Thrombosis and Haemostasis, 2020, 4, 931-935.	2.3	3
58	The buddingâ€yeast RWD protein Csm1 scaffolds diverse protein complexes through a conserved structural mechanism. Protein Science, 2018, 27, 2094-2100.	7.6	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.	7.1	2
60	Structure and activity of a bacterial defenseâ€associated 3′â€5′ exonuclease. Protein Science, 2022, 31, .	7.6	2
61	A new piece in the kinetochore jigsaw puzzle. Journal of Cell Biology, 2014, 206, 457-459.	5.2	1
62	Electron counting takes microED to the next level. Nature Methods, 2022, 19, 652-653.	19.0	1
63	A new phase in meiotic cell division. Nature, 2021, 592, 32-33.	27.8	Ο
64	Title is missing!. , 2020, 16, e1008968.		0
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