Hongtao Yu

List of Publications by Year in descending order

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45213 36203 9,449 96 51 90 citations h-index g-index papers 112 112 112 9558 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Noncoding RNA NORAD Regulates Genomic Stability by Sequestering PUMILIO Proteins. Cell, 2016, 164, 69-80.	13.5	723
2	Human cohesin compacts DNA by loop extrusion. Science, 2019, 366, 1345-1349.	6.0	513
3	Direct Binding of CDC20 Protein Family Members Activates the Anaphase-Promoting Complex in Mitosis and G1. Molecular Cell, 1998, 2, 163-171.	4.5	466
4	Mad2-Independent Inhibition of APCCdc20 by the Mitotic Checkpoint Protein BubR1. Developmental Cell, 2001, 1, 227-237.	3.1	383
5	Regulation of APC–Cdc20 by the spindle checkpoint. Current Opinion in Cell Biology, 2002, 14, 706-714.	2.6	320
6	PP2A Is Required for Centromeric Localization of Sgo1 and Proper Chromosome Segregation. Developmental Cell, 2006, 10, 575-585.	3.1	320
7	Cdc20: A WD40 Activator for a Cell Cycle Degradation Machine. Molecular Cell, 2007, 27, 3-16.	4.5	313
8	The Mad2 Spindle Checkpoint Protein Undergoes Similar Major Conformational Changes Upon Binding to Either Mad1 or Cdc20. Molecular Cell, 2002, 9, 59-71.	4.5	290
9	The Mad2 spindle checkpoint protein has two distinct natively folded states. Nature Structural and Molecular Biology, 2004, 11, 338-345.	3.6	263
10	Phosphorylation of Cdc20 by Bub1 Provides a Catalytic Mechanism for APC/C Inhibition by the Spindle Checkpoint. Molecular Cell, 2004, 16, 387-397.	4.5	257
11	Synergistic blockade of mitotic exit by two chemical inhibitors of the APC/C. Nature, 2014, 514, 646-649.	13.7	212
12	Mitotic transcription and waves of gene reactivation during mitotic exit. Science, 2017, 358, 119-122.	6.0	201
13	Structure of the Mad2 spindle assembly checkpoint protein and its interaction with Cdc20. Nature Structural Biology, 2000, 7, 224-229.	9.7	181
14	Conformation-specific binding of p31comet antagonizes the function of Mad2 in the spindle checkpoint. EMBO Journal, 2004, 23, 3133-3143.	3.5	177
15	Kinetochore attachment sensed by competitive Mps1 and microtubule binding to Ndc80C. Science, 2015, 348, 1260-1264.	6.0	175
16	p31comet Blocks Mad2 Activation through Structural Mimicry. Cell, 2007, 131, 744-755.	13.5	172
17	Cryo-EM structure of the human cohesin-NIPBL-DNA complex. Science, 2020, 368, 1454-1459.	6.0	171
18	Phosphorylation-enabled binding of SGO1–PP2A to cohesin protects sororin and centromeric cohesion during mitosis. Nature Cell Biology, 2013, 15, 40-49.	4.6	167

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19	Prolonged activation of innate immune pathways by a polyvalent STING agonist. Nature Biomedical Engineering, 2021, 5, 455-466.	11.6	157
20	Scc2 Is a Potent Activator of Cohesin's ATPase that Promotes Loading by Binding Scc1 without Pds5. Molecular Cell, 2018, 70, 1134-1148.e7.	4.5	141
21	Mitotic Transcription Installs Sgo1 at Centromeres to Coordinate Chromosome Segregation. Molecular Cell, 2015, 59, 426-436.	4.5	139
22	A sequential multi-target Mps1 phosphorylation cascade promotes spindle checkpoint signaling. ELife, 2017, 6, .	2.8	134
23	Protein Metamorphosis: The Two-State Behavior of Mad2. Structure, 2008, 16, 1616-1625.	1.6	133
24	Structure of cohesin subcomplex pinpoints direct shugoshin-Wapl antagonism in centromeric cohesion. Nature Structural and Molecular Biology, 2014, 21, 864-870.	3.6	131
25	Tracking spindle checkpoint signals from kinetochores to APC/C. Trends in Biochemical Sciences, 2013, 38, 302-311.	3.7	124
26	Activation mechanism of the insulin receptor revealed by cryo-EM structure of the fully liganded receptor–ligand complex. ELife, 2019, 8, .	2.8	123
27	Phospho-H2A and Cohesin Specify Distinct Tension-Regulated Sgo1 Pools at Kinetochores and Inner Centromeres. Current Biology, 2013, 23, 1927-1933.	1.8	120
28	Structural insights into the TRIM family of ubiquitin E3 ligases. Cell Research, 2014, 24, 762-765.	5.7	118
29	Structural basis of the activation of type 1 insulin-like growth factor receptor. Nature Communications, 2019, 10, 4567.	5.8	117
30	Multiple assembly mechanisms anchor the KMN spindle checkpoint platform at human mitotic kinetochores. Journal of Cell Biology, 2015, 208, 181-196.	2.3	116
31	Structural Basis and IP6 Requirement for Pds5-Dependent Cohesin Dynamics. Molecular Cell, 2016, 62, 248-259.	4.5	106
32	Crystal structure of the cohesin loader Scc2 and insight into cohesinopathy. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12444-12449.	3.3	104
33	The Smc complexes in DNA damage response. Cell and Bioscience, 2012, 2, 5.	2.1	102
34	The Bubl–Plk1 kinase complex promotes spindle checkpoint signalling through Cdc20 phosphorylation. Nature Communications, 2016, 7, 10818.	5.8	100
35	Structural activation of Mad2 in the mitotic spindle checkpoint: the two-state Mad2 model versus the Mad2 template model. Journal of Cell Biology, 2006, 173, 153-157.	2.3	97
36	Structure and Substrate Recruitment of the Human Spindle Checkpoint Kinase Bub1. Molecular Cell, 2008, 32, 394-405.	4.5	91

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37	Structure of human Mad1 C-terminal domain reveals its involvement in kinetochore targeting. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6549-6554.	3.3	91
38	Mitotic Checkpoint Regulators Control Insulin Signaling and Metabolic Homeostasis. Cell, 2016, 166, 567-581.	13.5	89
39	Insights into Mad2 Regulation in the Spindle Checkpoint Revealed by the Crystal Structure of the Symmetric Mad2 Dimer. PLoS Biology, 2008, 6, e50.	2.6	86
40	Mutual regulation between the spindle checkpoint and APC/C. Seminars in Cell and Developmental Biology, 2011, 22, 551-558.	2.3	79
41	Ska3 Phosphorylated by Cdk1 Binds Ndc80 and Recruits Ska to Kinetochores to Promote Mitotic Progression. Current Biology, 2017, 27, 1477-1484.e4.	1.8	78
42	Scc1 sumoylation by Mms21 promotes sister chromatid recombination through counteracting Wapl. Genes and Development, 2012, 26, 1473-1485.	2.7	72
43	The kinase activity of the Ser/Thr kinase BUB1 promotes TGF-Î ² signaling. Science Signaling, 2015, 8, ra1.	1.6	72
44	Mitotic regulators and the SHP2-MAPK pathway promote IR endocytosis and feedback regulation of insulin signaling. Nature Communications, 2019, 10, 1473.	5.8	71
45	Insulin receptor endocytosis in the pathophysiology of insulin resistance. Experimental and Molecular Medicine, 2020, 52, 911-920.	3.2	71
46	Structural basis of cohesin cleavage by separase. Nature, 2016, 532, 131-134.	13.7	67
47	PUMILIO hyperactivity drives premature aging of Norad-deficient mice. ELife, 2019, 8, .	2.8	65
48	The human SKA complex drives the metaphase-anaphase cell cycle transition by recruiting protein phosphatase 1 to kinetochores. ELife, $2016, 5, .$	2.8	64
49	Structure of the human cohesin inhibitor Wapl. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11355-11360.	3.3	62
50	Structure of guanine-nucleotide-exchange factor human Mss4 and identification of its Rab-interacting surface. Nature, 1995, 376, 788-791.	13.7	60
51	Structure of human GABAB receptor in an inactive state. Nature, 2020, 584, 304-309.	13.7	59
52	MCM2–7-dependent cohesin loading during S phase promotes sister-chromatid cohesion. ELife, 2018, 7,	2.8	57
53	The Cdc20-binding Phe Box of the Spindle Checkpoint Protein BubR1 Maintains the Mitotic Checkpoint Complex During Mitosis. Journal of Biological Chemistry, 2015, 290, 2431-2443.	1.6	56
54	Familial STAG2 germline mutation defines a new human cohesinopathy. Npj Genomic Medicine, 2017, 2, 7.	1.7	56

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55	The BUB3-BUB1 Complex Promotes Telomere DNA Replication. Molecular Cell, 2018, 70, 395-407.e4.	4.5	54
56	Structural basis of tubulin detyrosination by vasohibins. Nature Structural and Molecular Biology, 2019, 26, 583-591.	3 . 6	50
57	Defining pathways of spindle checkpoint silencing: functional redundancy between Cdc20 ubiquitination and p31 ^{comet} . Molecular Biology of the Cell, 2011, 22, 4227-4235.	0.9	47
58	Structural Insight into DNA-Dependent Activation of Human Metalloprotease Spartan. Cell Reports, 2019, 26, 3336-3346.e4.	2.9	42
59	Interaction of the Warsaw breakage syndrome DNA helicase DDX11 with the replication fork-protection factor Timeless promotes sister chromatid cohesion. PLoS Genetics, 2018, 14, e1007622.	1.5	40
60	Genomeâ€wide si RNA screen reveals coupling between mitotic apoptosis and adaptation. EMBO Journal, 2014, 33, 1960-1976.	3 . 5	39
61	Mechanistic insight into TRIP13-catalyzed Mad2 structural transition and spindle checkpoint silencing. Nature Communications, 2017, 8, 1956.	5. 8	38
62	The Transcription Factor TFII-I Promotes DNA Translesion Synthesis and Genomic Stability. PLoS Genetics, 2014, 10, e1004419.	1.5	37
63	Control of APC/C-dependent ubiquitin chain elongation by reversible phosphorylation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 1540-1545.	3.3	36
64	Structure of an intermediate conformer of the spindle checkpoint protein Mad2. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11252-11257.	3.3	31
65	Substrate-Specific Activation of the Mitotic Kinase Bub1 through Intramolecular Autophosphorylation and Kinetochore Targeting. Structure, 2014, 22, 1616-1627.	1.6	29
66	Releasing the cohesin ring: A rigid scaffold model for opening the DNA exit gate by Pds5 and Wapl. BioEssays, 2017, 39, 1600207.	1.2	28
67	Functional Analysis of the Spindle-Checkpoint Proteins Using an In Vitro Ubiquitination Assay. , 2004, 281, 227-242.		27
68	Sumoylation promotes optimal APC/C activation and timely anaphase. ELife, 2018, 7, .	2.8	26
69	Regulation of sister chromatid cohesion during the mitotic cell cycle. Science China Life Sciences, 2015, 58, 1089-1098.	2.3	24
70	Cryo-EM structure of VASH1-SVBP bound to microtubules. ELife, 2020, 9, .	2.8	23
71	The chromatin remodeler RSF1 controls centromeric histone modifications to coordinate chromosome segregation. Nature Communications, 2018, 9, 3848.	5. 8	20
72	Shaping of the 3D genome by the ATPase machine cohesin. Experimental and Molecular Medicine, 2020, 52, 1891-1897.	3.2	19

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73	TP53 promotes lineage commitment of human embryonic stem cells through ciliogenesis and sonic hedgehog signaling. Cell Reports, 2022, 38, 110395.	2.9	17
74	Chk1: A Double Agent in Cell Cycle Checkpoints. Developmental Cell, 2007, 12, 167-168.	3.1	13
75	Opposing Functions of the N-terminal Acetyltransferases Naa50 and NatA in Sister-chromatid Cohesion. Journal of Biological Chemistry, 2016, 291, 19079-19091.	1.6	12
76	Mps1 regulates spindle morphology through MCRS1 to promote chromosome alignment. Molecular Biology of the Cell, 2019, 30, 1060-1068.	0.9	11
77	Spindle Checkpoint Regulators in Insulin Signaling. Frontiers in Cell and Developmental Biology, 2018, 6, 161.	1.8	10
78	Cryo-EM structures of human p97 double hexamer capture potentiated ATPase-competent state. Cell Discovery, 2022, 8, 19.	3.1	10
79	Magic Acts with the Cohesin Ring. Molecular Cell, 2016, 61, 489-491.	4.5	9
80	A Protective Chaperone for the Kinetochore Adaptor Bub3. Developmental Cell, 2014, 28, 223-224.	3.1	6
81	Partner switching for Ran during the mitosis dance. Journal of Molecular Cell Biology, 2018, 10, 89-90.	1.5	6
82	Cyclin A Turns on Bora to Light the Path to Mitosis. Developmental Cell, 2018, 45, 542-543.	3.1	4
83	A Method for SUMO Modification of Proteins in vitro. Bio-protocol, 2018, 8, .	0.2	4
84	Tango between Ubiquitin Ligase and Deubiquitinase Keeps Cyclin A Tag Free. Molecular Cell, 2011, 42, 409-410.	4.5	3
85	PP2A as a mercenary for warring kinases in the egg. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 17245-17246.	3.3	2
86	Chromosome Biology: Wapl Spreads Its Wings. Current Biology, 2013, 23, R923-R925.	1.8	2
87	Biochemical and Functional Assays of Human Cohesin-Releasing Factor Wapl. Methods in Molecular Biology, 2017, 1515, 37-53.	0.4	2
88	The complexity of life and death decisions in mitosis. Molecular and Cellular Oncology, 2015, 2, e969658.	0.3	1
89	CENP-T bears the load in mitosis. Nature Cell Biology, 2018, 20, 1335-1337.	4.6	1
90	Molecular Mechanism of the Spindle Checkpoint. FASEB Journal, 2007, 21, A209.	0.2	1

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91	A mad partner for Shugoshin in meiosis. EMBO Journal, 2011, 30, 2759-2761.	3.5	0
92	The SMC5/6 Complex Maintains Telomere Length in ALT Cancer Cells through Sumoylation of Telomereâ€Binding Proteins. FASEB Journal, 2007, 21, A655.	0.2	0
93	Scc1 sumoylation by Mms21 promotes sister chromatid recombination through counteracting Wapl. FASEB Journal, 2012, 26, 539.5.	0.2	0
94	Structure of Human Mad1 Câ€terminal Domain Reveals Its Kinetochoreâ€Targeting Function. FASEB Journal, 2012, 26, 934.3.	0.2	0
95	NIP45 Promotes Telomere Targeting to PML Bodies in ALT Cells. FASEB Journal, 2012, 26, 933.6.	0.2	0
96	Functional redundancy between Cdc20 ubiquitination and p31 comet. FASEB Journal, 2012, 26, .	0.2	0