

# Hongtao Yu

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

95  
papers

7,072  
citations

47  
h-index

84  
g-index

112  
ext. papers

8,574  
ext. citations

14.2  
avg, IF

6.34  
L-index

#	Paper	IF	Citations
95	TP53 promotes lineage commitment of human embryonic stem cells through ciliogenesis and sonic hedgehog signaling.. <i>Cell Reports</i> , <b>2022</b> , 38, 110395	10.6	1
94	Cryo-EM structures of human p97 double hexamer capture potentiated ATPase-competent state.. <i>Cell Discovery</i> , <b>2022</b> , 8, 19	22.3	0
93	Prolonged activation of innate immune pathways by a polyvalent STING agonist. <i>Nature Biomedical Engineering</i> , <b>2021</b> , 5, 455-466	19	49
92	Shaping of the 3D genome by the ATPase machine cohesin. <i>Experimental and Molecular Medicine</i> , <b>2020</b> , 52, 1891-1897	12.8	7
91	Cryo-EM structure of the human cohesin-NIPBL-DNA complex. <i>Science</i> , <b>2020</b> , 368, 1454-1459	33.3	71
90	Insulin receptor endocytosis in the pathophysiology of insulin resistance. <i>Experimental and Molecular Medicine</i> , <b>2020</b> , 52, 911-920	12.8	19
89	Structure of human GABA receptor in an inactive state. <i>Nature</i> , <b>2020</b> , 584, 304-309	50.4	32
88	Cryo-EM structure of VASH1-SVBP bound to microtubules. <i>ELife</i> , <b>2020</b> , 9,	8.9	12
87	Structural basis of tubulin detyrosination by vasohibins. <i>Nature Structural and Molecular Biology</i> , <b>2019</b> , 26, 583-591	17.6	31
86	Structural Insight into DNA-Dependent Activation of Human Metalloprotease Spartan. <i>Cell Reports</i> , <b>2019</b> , 26, 3336-3346.e4	10.6	27
85	Mitotic regulators and the SHP2-MAPK pathway promote IR endocytosis and feedback regulation of insulin signaling. <i>Nature Communications</i> , <b>2019</b> , 10, 1473	17.4	35
84	Structural basis of the activation of type 1 insulin-like growth factor receptor. <i>Nature Communications</i> , <b>2019</b> , 10, 4567	17.4	56
83	PUMILIO hyperactivity drives premature aging of -deficient mice. <i>ELife</i> , <b>2019</b> , 8,	8.9	40
82	Activation mechanism of the insulin receptor revealed by cryo-EM structure of the fully liganded receptor-ligand complex. <i>ELife</i> , <b>2019</b> , 8,	8.9	65
81	Mps1 regulates spindle morphology through MCRS1 to promote chromosome alignment. <i>Molecular Biology of the Cell</i> , <b>2019</b> , 30, 1060-1068	3.5	5
80	Human cohesin compacts DNA by loop extrusion. <i>Science</i> , <b>2019</b> , 366, 1345-1349	33.3	270
79	Partner switching for Ran during the mitosis dance. <i>Journal of Molecular Cell Biology</i> , <b>2018</b> , 10, 89-90	6.3	5

78	The BUB3-BUB1 Complex Promotes Telomere DNA Replication. <i>Molecular Cell</i> , <b>2018</b> , 70, 395-407.e4	17.6	34
77	Cyclin A Turns on Bora to Light the Path to Mitosis. <i>Developmental Cell</i> , <b>2018</b> , 45, 542-543	10.2	2
76	A Method for SUMO Modification of Proteins. <i>Bio-protocol</i> , <b>2018</b> , 8,	0.9	4
75	Sumoylation promotes optimal APC/C Activation and Timely Anaphase. <i>ELife</i> , <b>2018</b> , 7,	8.9	19
74	CENP-T bears the load in mitosis. <i>Nature Cell Biology</i> , <b>2018</b> , 20, 1335-1337	23.4	0
73	Spindle Checkpoint Regulators in Insulin Signaling. <i>Frontiers in Cell and Developmental Biology</i> , <b>2018</b> , 6, 161	5.7	5
72	The chromatin remodeler RSF1 controls centromeric histone modifications to coordinate chromosome segregation. <i>Nature Communications</i> , <b>2018</b> , 9, 3848	17.4	10
71	Interaction of the Warsaw breakage syndrome DNA helicase DDX11 with the replication fork-protection factor Timeless promotes sister chromatid cohesion. <i>PLoS Genetics</i> , <b>2018</b> , 14, e1007622 <sup>6</sup>		24
70	Scc2 Is a Potent Activator of Cohesin's ATPase that Promotes Loading by Binding Scc1 without Pds5. <i>Molecular Cell</i> , <b>2018</b> , 70, 1134-1148.e7	17.6	71
69	MCM2-7-dependent cohesin loading during S phase promotes sister-chromatid cohesion. <i>ELife</i> , <b>2018</b> , 7,	8.9	35
68	Releasing the cohesin ring: A rigid scaffold model for opening the DNA exit gate by Pds5 and Wapl. <i>BioEssays</i> , <b>2017</b> , 39, 1600207	4.1	21
67	Ska3 Phosphorylated by Cdk1 Binds Ndc80 and Recruits Ska to Kinetochores to Promote Mitotic Progression. <i>Current Biology</i> , <b>2017</b> , 27, 1477-1484.e4	6.3	50
66	Familial germline mutation defines a new human cohesinopathy. <i>Npj Genomic Medicine</i> , <b>2017</b> , 2, 7	6.2	37
65	Mitotic transcription and waves of gene reactivation during mitotic exit. <i>Science</i> , <b>2017</b> , 358, 119-122	33.3	112
64	Mechanistic insight into TRIP13-catalyzed Mad2 structural transition and spindle checkpoint silencing. <i>Nature Communications</i> , <b>2017</b> , 8, 1956	17.4	23
63	Biochemical and Functional Assays of Human Cohesin-Releasing Factor Wapl. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1515, 37-53	1.4	2
62	A sequential multi-target Mps1 phosphorylation cascade promotes spindle checkpoint signaling. <i>ELife</i> , <b>2017</b> , 6,	8.9	84
61	Opposing Functions of the N-terminal Acetyltransferases Naa50 and NatA in Sister-chromatid Cohesion. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 19079-91	5.4	7

60	Crystal structure of the cohesin loader Scc2 and insight into cohesinopathy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 12444-12449	11.5	61
59	Control of APC/C-dependent ubiquitin chain elongation by reversible phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 1540-5	11.5	31
58	Magic Acts with the Cohesin Ring. <i>Molecular Cell</i> , <b>2016</b> , 61, 489-491	17.6	6
57	Structural Basis and IP6 Requirement for Pds5-Dependent Cohesin Dynamics. <i>Molecular Cell</i> , <b>2016</b> , 62, 248-259	17.6	78
56	Noncoding RNA NORAD Regulates Genomic Stability by Sequestering PUMILIO Proteins. <i>Cell</i> , <b>2016</b> , 164, 69-80	56.2	496
55	The human SKA complex drives the metaphase-anaphase cell cycle transition by recruiting protein phosphatase 1 to kinetochores. <i>ELife</i> , <b>2016</b> , 5,	8.9	53
54	Mitotic Checkpoint Regulators Control Insulin Signaling and Metabolic Homeostasis. <i>Cell</i> , <b>2016</b> , 166, 567-581	56.2	60
53	The Bub1-Plk1 kinase complex promotes spindle checkpoint signalling through Cdc20 phosphorylation. <i>Nature Communications</i> , <b>2016</b> , 7, 10818	17.4	71
52	Structural basis of cohesin cleavage by separase. <i>Nature</i> , <b>2016</b> , 532, 131-4	50.4	48
51	Multiple assembly mechanisms anchor the KMN spindle checkpoint platform at human mitotic kinetochores. <i>Journal of Cell Biology</i> , <b>2015</b> , 208, 181-96	7.3	89
50	The Cdc20-binding Phe box of the spindle checkpoint protein BubR1 maintains the mitotic checkpoint complex during mitosis. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 2431-43	5.4	42
49	Mitotic Transcription Installs Sgo1 at Centromeres to Coordinate Chromosome Segregation. <i>Molecular Cell</i> , <b>2015</b> , 59, 426-36	17.6	108
48	Structure of an intermediate conformer of the spindle checkpoint protein Mad2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 11252-7	11.5	24
47	The kinase activity of the Ser/Thr kinase BUB1 promotes TGF- $\beta$ signaling. <i>Science Signaling</i> , <b>2015</b> , 8, ra1	8.8	50
46	CELL DIVISION CYCLE. Kinetochore attachment sensed by competitive Mps1 and microtubule binding to Ndc80C. <i>Science</i> , <b>2015</b> , 348, 1260-4	33.3	138
45	The complexity of life and death decisions in mitosis. <i>Molecular and Cellular Oncology</i> , <b>2015</b> , 2, e969658	1.2	1
44	Regulation of sister chromatid cohesion during the mitotic cell cycle. <i>Science China Life Sciences</i> , <b>2015</b> , 58, 1089-98	8.5	17
43	Genome-wide siRNA screen reveals coupling between mitotic apoptosis and adaptation. <i>EMBO Journal</i> , <b>2014</b> , 33, 1960-76	13	36

42	Synergistic blockade of mitotic exit by two chemical inhibitors of the APC/C. <i>Nature</i> , <b>2014</b> , 514, 646-9	50.4	165
41	A protective chaperone for the kinetochore adaptor Bub3. <i>Developmental Cell</i> , <b>2014</b> , 28, 223-4	10.2	3
40	Structural insights into the TRIM family of ubiquitin E3 ligases. <i>Cell Research</i> , <b>2014</b> , 24, 762-5	24.7	82
39	The transcription factor TFII-I promotes DNA translesion synthesis and genomic stability. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004419	6	32
38	Structure of cohesin subcomplex pinpoints direct shugoshin-Wapl antagonism in centromeric cohesion. <i>Nature Structural and Molecular Biology</i> , <b>2014</b> , 21, 864-70	17.6	104
37	Substrate-specific activation of the mitotic kinase Bub1 through intramolecular autophosphorylation and kinetochore targeting. <i>Structure</i> , <b>2014</b> , 22, 1616-27	5.2	23
36	Phospho-H2A and cohesin specify distinct tension-regulated Sgo1 pools at kinetochores and inner centromeres. <i>Current Biology</i> , <b>2013</b> , 23, 1927-33	6.3	98
35	Chromosome biology: Wapl spreads its wings. <i>Current Biology</i> , <b>2013</b> , 23, R923-5	6.3	2
34	Phosphorylation-enabled binding of SGO1-PP2A to cohesin protects sororin and centromeric cohesion during mitosis. <i>Nature Cell Biology</i> , <b>2013</b> , 15, 40-9	23.4	137
33	Tracking spindle checkpoint signals from kinetochores to APC/C. <i>Trends in Biochemical Sciences</i> , <b>2013</b> , 38, 302-11	10.3	108
32	Structure of the human cohesin inhibitor Wapl. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 11355-60	11.5	48
31	The Smc complexes in DNA damage response. <i>Cell and Bioscience</i> , <b>2012</b> , 2, 5	9.8	82
30	Scc1 sumoylation by Mms21 promotes sister chromatid recombination through counteracting Wapl. <i>Genes and Development</i> , <b>2012</b> , 26, 1473-85	12.6	66
29	Structure of human Mad1 C-terminal domain reveals its involvement in kinetochore targeting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 6549-54	11.5	74
28	Scc1 sumoylation by Mms21 promotes sister chromatid recombination through counteracting Wapl. <i>FASEB Journal</i> , <b>2012</b> , 26, 539.5	0.9	
27	Structure of Human Mad1 C-terminal Domain Reveals Its Kinetochore-Targeting Function. <i>FASEB Journal</i> , <b>2012</b> , 26, 934.3	0.9	
26	NIP45 Promotes Telomere Targeting to PML Bodies in ALT Cells. <i>FASEB Journal</i> , <b>2012</b> , 26, 933.6	0.9	
25	Tango between ubiquitin ligase and deubiquitinase keeps cyclin A tag free. <i>Molecular Cell</i> , <b>2011</b> , 42, 409-106	10.6	3

24	Mutual regulation between the spindle checkpoint and APC/C. <i>Seminars in Cell and Developmental Biology</i> , <b>2011</b> , 22, 551-8	7.5	74
23	Defining pathways of spindle checkpoint silencing: functional redundancy between Cdc20 ubiquitination and p31(comet). <i>Molecular Biology of the Cell</i> , <b>2011</b> , 22, 4227-35	3.5	45
22	A mad partner for Shugoshin in meiosis. <i>EMBO Journal</i> , <b>2011</b> , 30, 2759-61	13	
21	Protein metamorphosis: the two-state behavior of Mad2. <i>Structure</i> , <b>2008</b> , 16, 1616-25	5.2	114
20	Structure and substrate recruitment of the human spindle checkpoint kinase Bub1. <i>Molecular Cell</i> , <b>2008</b> , 32, 394-405	17.6	72
19	Insights into mad2 regulation in the spindle checkpoint revealed by the crystal structure of the symmetric mad2 dimer. <i>PLoS Biology</i> , <b>2008</b> , 6, e50	9.7	71
18	PP2A as a mercenary for warring kinases in the egg. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 17245-6	11.5	2
17	p31comet blocks Mad2 activation through structural mimicry. <i>Cell</i> , <b>2007</b> , 131, 744-55	56.2	157
16	Chk1: a double agent in cell cycle checkpoints. <i>Developmental Cell</i> , <b>2007</b> , 12, 167-8	10.2	12
15	Cdc20: a WD40 activator for a cell cycle degradation machine. <i>Molecular Cell</i> , <b>2007</b> , 27, 3-16	17.6	264
14	Molecular Mechanism of the Spindle Checkpoint. <i>FASEB Journal</i> , <b>2007</b> , 21, A209	0.9	
13	The SMC5/6 Complex Maintains Telomere Length in ALT Cancer Cells through Sumoylation of Telomere-Binding Proteins. <i>FASEB Journal</i> , <b>2007</b> , 21, A655	0.9	
12	Structural activation of Mad2 in the mitotic spindle checkpoint: the two-state Mad2 model versus the Mad2 template model. <i>Journal of Cell Biology</i> , <b>2006</b> , 173, 153-7	7.3	86
11	PP2A is required for centromeric localization of Sgo1 and proper chromosome segregation. <i>Developmental Cell</i> , <b>2006</b> , 10, 575-85	10.2	279
10	Functional analysis of the spindle-checkpoint proteins using an in vitro ubiquitination assay. <i>Methods in Molecular Biology</i> , <b>2004</b> , 281, 227-42	1.4	26
9	Conformation-specific binding of p31(comet) antagonizes the function of Mad2 in the spindle checkpoint. <i>EMBO Journal</i> , <b>2004</b> , 23, 3133-43	13	167
8	The Mad2 spindle checkpoint protein has two distinct natively folded states. <i>Nature Structural and Molecular Biology</i> , <b>2004</b> , 11, 338-45	17.6	234
7	Phosphorylation of Cdc20 by Bub1 provides a catalytic mechanism for APC/C inhibition by the spindle checkpoint. <i>Molecular Cell</i> , <b>2004</b> , 16, 387-97	17.6	213

6	Regulation of APC-Cdc20 by the spindle checkpoint. <i>Current Opinion in Cell Biology</i> , <b>2002</b> , 14, 706-14	9	298
5	The Mad2 spindle checkpoint protein undergoes similar major conformational changes upon binding to either Mad1 or Cdc20. <i>Molecular Cell</i> , <b>2002</b> , 9, 59-71	17.6	260
4	Mad2-Independent inhibition of APC-Cdc20 by the mitotic checkpoint protein BubR1. <i>Developmental Cell</i> , <b>2001</b> , 1, 227-37	10.2	359
3	Structure of the Mad2 spindle assembly checkpoint protein and its interaction with Cdc20. <i>Nature Structural Biology</i> , <b>2000</b> , 7, 224-9		151
2	Direct binding of CDC20 protein family members activates the anaphase-promoting complex in mitosis and G1. <i>Molecular Cell</i> , <b>1998</b> , 2, 163-71	17.6	430
1	Structure of guanine-nucleotide-exchange factor human Mss4 and identification of its Rab-interacting surface. <i>Nature</i> , <b>1995</b> , 376, 788-91	50.4	54