

# Yong Xiong

## List of Publications by Year in descending order

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72  
papers

3,338  
citations

172386  
29  
h-index

168321  
53  
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77  
all docs

77  
docs citations

77  
times ranked

6133  
citing authors

#	ARTICLE	IF	CITATIONS
1	Accelerating Novel Candidate Gene Discovery in Neurogenetic Disorders via Whole-Exome Sequencing of Prescreened Multiplex Consanguineous Families. <i>Cell Reports</i> , 2015, 10, 148-161.	2.9	375
2	Nonstructural Protein 1 of SARS-CoV-2 Is a Potent Pathogenicity Factor Redirecting Host Protein Synthesis Machinery toward Viral RNA. <i>Molecular Cell</i> , 2020, 80, 1055-1066.e6.	4.5	152
3	Functional landscape of SARS-CoV-2 cellular restriction. <i>Molecular Cell</i> , 2021, 81, 2656-2668.e8.	4.5	137
4	Mechanism of allosteric activation of SAMHD1 by dGTP. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1304-1309.	3.6	135
5	IFT27, encoding a small GTPase component of IFT particles, is mutated in a consanguineous family with Bardet-Biedl syndrome. <i>Human Molecular Genetics</i> , 2014, 23, 3307-3315.	1.4	134
6	Mechanism of transfer RNA maturation by CCA-adding enzyme without using an oligonucleotide template. <i>Nature</i> , 2004, 430, 640-645.	13.7	120
7	Structural basis of cellular dNTP regulation by SAMHD1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4305-14.	3.3	113
8	Structural Insight into HIV-1 Restriction by MxB. <i>Cell Host and Microbe</i> , 2014, 16, 627-638.	5.1	106
9	Structural Insight into the Human Immunodeficiency Virus Vif SOCS Box and Its Role in Human E3 Ubiquitin Ligase Assembly. <i>Journal of Virology</i> , 2008, 82, 8656-8663.	1.5	104
10	Transposon molecular domestication and the evolution of the RAG recombinase. <i>Nature</i> , 2019, 569, 79-84.	13.7	100
11	Neu-Laxova Syndrome, an Inborn Error of Serine Metabolism, Is Caused by Mutations in PHGDH. <i>American Journal of Human Genetics</i> , 2014, 94, 898-904.	2.6	93
12	SAMHD1 suppresses innate immune responses to viral infections and inflammatory stimuli by inhibiting the NF- $\kappa$ B and interferon pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3798-E3807.	3.3	88
13	Structural basis of HIV-1 Vpu-mediated BST2 antagonism via hijacking of the clathrin adaptor protein complex 1. <i>ELife</i> , 2014, 3, e02362.	2.8	88
14	SAMHD1-mediated HIV-1 restriction in cells does not involve ribonuclease activity. <i>Nature Medicine</i> , 2016, 22, 1072-1074.	15.2	85
15	A story with a good ending: tRNA 3'-end maturation by CCA-adding enzymes. <i>Current Opinion in Structural Biology</i> , 2006, 16, 12-17.	2.6	75
16	Impaired dNTPase Activity of SAMHD1 by Phosphomimetic Mutation of Thr-592. <i>Journal of Biological Chemistry</i> , 2015, 290, 26352-26359.	1.6	75
17	A Single Amino Acid Difference in Human APOBEC3H Variants Determines HIV-1 Vif Sensitivity. <i>Journal of Virology</i> , 2010, 84, 1902-1911.	1.5	71
18	Mechanisms of activation and inhibition of Zika virus NS2B-NS3 protease. <i>Cell Research</i> , 2016, 26, 1260-1263.	5.7	71

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19	Structural Basis for Ligand Binding to the Guanidine-I Riboswitch. <i>Structure</i> , 2017, 25, 195-202.	1.6	62
20	Insights into Cullin-RING E3 Ubiquitin Ligase Recruitment: Structure of the VHL-EloBC-Cul2 Complex. <i>Structure</i> , 2015, 23, 441-449.	1.6	59
21	FEZ1 Is Recruited to a Conserved Cofactor Site on Capsid to Promote HIV-1 Trafficking. <i>Cell Reports</i> , 2019, 28, 2373-2385.e7.	2.9	55
22	Mutations in ASPH Cause Facial Dysmorphism, Lens Dislocation, Anterior-Segment Abnormalities, and Spontaneous Filtering Blebs, or Traboulsi Syndrome. <i>American Journal of Human Genetics</i> , 2014, 94, 755-759.	2.6	50
23	Cullin-RING E3 Ubiquitin Ligases: Bridges to Destruction. <i>Sub-Cellular Biochemistry</i> , 2017, 83, 323-347.	1.0	45
24	HIV suppression by host restriction factors and viral immune evasion. <i>Current Opinion in Structural Biology</i> , 2015, 31, 106-114.	2.6	44
25	Selective inactivation of hypomethylating agents by SAMHD1 provides a rationale for therapeutic stratification in AML. <i>Nature Communications</i> , 2019, 10, 3475.	5.8	43
26	Coronavirus Nsp1: Immune Response Suppression and Protein Expression Inhibition. <i>Frontiers in Microbiology</i> , 2021, 12, 752214.	1.5	43
27	MxB Restricts HIV-1 by Targeting the Tri-hexamer Interface of the Viral Capsid. <i>Structure</i> , 2019, 27, 1234-1245.e5.	1.6	36
28	Core Binding Factor Beta Plays a Critical Role by Facilitating the Assembly of the Vif-Cullin 5 E3 Ubiquitin Ligase. <i>Journal of Virology</i> , 2014, 88, 3309-3319.	1.5	35
29	FBXO32, encoding a member of the SCF complex, is mutated in dilated cardiomyopathy. <i>Genome Biology</i> , 2016, 17, 2.	3.8	35
30	Sorting sub-150-nm liposomes of distinct sizes by DNA-brick-assisted centrifugation. <i>Nature Chemistry</i> , 2021, 13, 335-342.	6.6	34
31	TRIM15 is a focal adhesion protein that regulates focal adhesion disassembly. <i>Journal of Cell Science</i> , 2014, 127, 3928-42.	1.2	31
32	Crystal structure of E. coli apolipoprotein N-acyl transferase. <i>Nature Communications</i> , 2017, 8, 15948.	5.8	31
33	Cryo-EM structure of an active central apparatus. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 472-482.	3.6	31
34	The structural basis for cancer drug interactions with the catalytic and allosteric sites of SAMHD1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10022-E10031.	3.3	30
35	Modular HIV-1 Capsid Assemblies Reveal Diverse Host-Capsid Recognition Mechanisms. <i>Cell Host and Microbe</i> , 2019, 26, 203-216.e6.	5.1	29
36	Structural insight into T cell coinhibition by PD-1H (VISTA). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 1648-1657.	3.3	29

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37	Study of Mendelian forms of Crohn's disease in Saudi Arabia reveals novel risk loci and alleles. <i>Gut</i> , 2014, 63, 1831-1832.	6.1	28
38	Structural basis for GTP-induced dimerization and antiviral function of guanylate-binding proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	28
39	A snapshot of HIV-1 capsid-host interactions. <i>Current Research in Structural Biology</i> , 2020, 2, 222-228.	1.1	26
40	SAMHD1 Impairs HIV-1 Gene Expression and Negatively Modulates Reactivation of Viral Latency in CD4 <sup>+</sup> T Cells. <i>Journal of Virology</i> , 2018, 92, .	1.5	25
41	Insights into DNA substrate selection by APOBEC3G from structural, biochemical, and functional studies. <i>PLoS ONE</i> , 2018, 13, e0195048.	1.1	25
42	Relative Resistance of HLA-B to Downregulation by Naturally Occurring HIV-1 Nef Sequences. <i>MBio</i> , 2016, 7, e01516-15.	1.8	23
43	A deubiquitylase with an unusually high-affinity ubiquitin-binding domain from the scrub typhus pathogen <i>Orientia tsutsugamushi</i> . <i>Nature Communications</i> , 2020, 11, 2343.	5.8	22
44	Electron Density Sharpening as a General Technique in Crystallographic Studies. <i>Journal of Molecular Biology</i> , 2014, 426, 980-993.	2.0	21
45	Structural basis of antagonism of human APOBEC3F by HIV-1 Vif. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 1176-1183.	3.6	21
46	From electron microscopy to X-ray crystallography: molecular-replacement case studies. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 76-82.	2.5	18
47	The SAM domain of mouse SAMHD1 is critical for its activation and regulation. <i>Nature Communications</i> , 2018, 9, 411.	5.8	18
48	Nuclear Import of HIV-1. <i>Viruses</i> , 2021, 13, 2242.	1.5	18
49	Structural Basis for tRNA Mimicry by a Bacterial $\gamma$ RNA. <i>Structure</i> , 2018, 26, 1635-1644.e3.	1.6	17
50	A Conserved Acidic-Cluster Motif in SERINC5 Confers Partial Resistance to Antagonism by HIV-1 Nef. <i>Journal of Virology</i> , 2020, 94, .	1.5	16
51	DNA-Origami NanoTrap for Studying the Selective Barriers Formed by Phenylalanine-Glycine-Rich Nucleoporins. <i>Journal of the American Chemical Society</i> , 2021, 143, 12294-12303.	6.6	15
52	A Cyclin-Binding Motif in Human SAMHD1 Is Required for Its HIV-1 Restriction, dNTPase Activity, Tetramer Formation, and Efficient Phosphorylation. <i>Journal of Virology</i> , 2018, 92, .	1.5	14
53	The dNTPase activity of SAMHD1 is important for its suppression of innate immune responses in differentiated monocytic cells. <i>Journal of Biological Chemistry</i> , 2020, 295, 1575-1586.	1.6	14
54	Multifaceted HIV-1 Vif interactions with human E3 ubiquitin ligase and APOBEC3s. <i>FEBS Journal</i> , 2021, 288, 3407-3417.	2.2	14

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55	A local-optimization refinement algorithm in single particle analysis for macromolecular complex with multiple rigid modules. <i>Protein and Cell</i> , 2016, 7, 46-62.	4.8	13
56	Endocytic activity of HIV-1 Vpu: Phosphoserine-dependent interactions with clathrin adaptors. <i>Traffic</i> , 2017, 18, 545-561.	1.3	13
57	Monospecific and bispecific monoclonal SARS-CoV-2 neutralizing antibodies that maintain potency against B.1.617. <i>Nature Communications</i> , 2022, 13, 1638.	5.8	11
58	Phosphoserine acidic cluster motifs bind distinct basic regions on the $\beta$ subunits of clathrin adaptor protein complexes. <i>Journal of Biological Chemistry</i> , 2018, 293, 15678-15690.	1.6	10
59	Computational insights into the membrane fusion mechanism of SARS-CoV-2 at the cellular level. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5019-5028.	1.9	10
60	APOBEC3A Loop 1 Is a Determinant for Single-Stranded DNA Binding and Deamination. <i>Biochemistry</i> , 2019, 58, 3838-3847.	1.2	9
61	A Noncanonical Basic Motif of Epstein-Barr Virus ZEBRA Protein Facilitates Recognition of Methylated DNA, High-Affinity DNA Binding, and Lytic Activation. <i>Journal of Virology</i> , 2019, 93, .	1.5	9
62	The Polar Region of the HIV-1 Envelope Protein Determines Viral Fusion and Infectivity by Stabilizing the gp120-gp41 Association. <i>Journal of Virology</i> , 2019, 93, .	1.5	9
63	Differences between intrinsic and acquired nucleoside analogue resistance in acute myeloid leukaemia cells. <i>Journal of Experimental and Clinical Cancer Research</i> , 2021, 40, 317.	3.5	9
64	Crystal structure of a guanine nucleotide exchange factor encoded by the scrub typhus pathogen <i>Orientia tsutsugamushi</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30380-30390.	3.3	7
65	Structural and functional characterization explains loss of dNTPase activity of the cancer-specific R366C/H mutant SAMHD1 proteins. <i>Journal of Biological Chemistry</i> , 2021, 297, 101170.	1.6	7
66	Importance of homo-dimerization of Fanconi-associated nuclease 1 in DNA flap cleavage. <i>DNA Repair</i> , 2018, 64, 53-58.	1.3	6
67	A threonine zipper that mediates protein-protein interactions: Structure and prediction. <i>Protein Science</i> , 2018, 27, 1969-1977.	3.1	5
68	Nodal modulator (NOMO) is required to sustain endoplasmic reticulum morphology. <i>Journal of Biological Chemistry</i> , 2021, 297, 100937.	1.6	4
69	Maedi-visna virus Vif protein uses motifs distinct from HIV-1 Vif to bind zinc and the cofactor required for A3 degradation. <i>Journal of Biological Chemistry</i> , 2021, 296, 100045.	1.6	2
70	Two Tales (Tails) of SAMHD1 Destruction by Vpx. <i>Cell Host and Microbe</i> , 2015, 17, 425-427.	5.1	0
71	The Role of UAF1 in the Fanconi Anemia Pathway Regulation of Homologous Recombination-Mediated Genome Maintenance. <i>Blood</i> , 2016, 128, 1041-1041.	0.6	0
72	Structure of a Synaptic $\gamma$ Resolvase Tetramer Covalently Linked to Two Cleaved DNAs. <i>Journal of hand surgery Asian-Pacific volume, The</i> , 2020, , 447-452.	0.2	0