

# Yong Xiong

## List of Publications by Year in descending order

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Version: 2024-02-01

72  
papers

3,338  
citations

172386  
29  
h-index

168321  
53  
g-index

77  
all docs

77  
docs citations

77  
times ranked

6133  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Cryo-EM structure of an active central apparatus. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 472-482.	3.6	31
3	Multifaceted HIV-1 Vif interactions with human E3 ubiquitin ligase and APOBEC3s. <i>FEBS Journal</i> , 2021, 288, 3407-3417.	2.2	14
4	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
5	Sorting sub-150-nm liposomes of distinct sizes by DNA-brick-assisted centrifugation. <i>Nature Chemistry</i> , 2021, 13, 335-342.	6.6	34
6	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
7	Functional landscape of SARS-CoV-2 cellular restriction. <i>Molecular Cell</i> , 2021, 81, 2656-2668.e8.	4.5	137
8	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
9	Nodal modulator (NOMO) is required to sustain endoplasmic reticulum morphology. <i>Journal of Biological Chemistry</i> , 2021, 297, 100937.	1.6	4
10	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
11	Coronavirus Nsp1: Immune Response Suppression and Protein Expression Inhibition. <i>Frontiers in Microbiology</i> , 2021, 12, 752214.	1.5	43
12	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
13	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
14	Nuclear Import of HIV-1. <i>Viruses</i> , 2021, 13, 2242.	1.5	18
15	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
16	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
17	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
18	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

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19	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
20	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
21	A snapshot of HIV-1 capsidâ€“host interactions. <i>Current Research in Structural Biology</i> , 2020, 2, 222-228.	1.1	26
22	Structure of a Synaptic Î³ Resolvase Tetramer Covalently Linked to Two Cleaved DNAs. <i>Journal of Hand Surgery Asian-Pacific volume, The</i> , 2020, , 447-452.	0.2	0
23	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
24	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
25	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
26	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
27	APOBEC3A Loop 1 Is a Determinant for Single-Stranded DNA Binding and Deamination. <i>Biochemistry</i> , 2019, 58, 3838-3847.	1.2	9
28	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
29	Transposon molecular domestication and the evolution of the RAG recombinase. <i>Nature</i> , 2019, 569, 79-84.	13.7	100
30	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
31	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
32	Importance of homo-dimerization of Fanconi-associated nuclease 1 in DNA flap cleavage. <i>DNA Repair</i> , 2018, 64, 53-58.	1.3	6
33	The SAM domain of mouse SAMHD1 is critical for its activation and regulation. <i>Nature Communications</i> , 2018, 9, 411.	5.8	18
34	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
35	SAMHD1 suppresses innate immune responses to viral infections and inflammatory stimuli by inhibiting the NF-Î³B 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
36	A threonine zipper that mediates proteinâ€“protein interactions: Structure and prediction. <i>Protein Science</i> , 2018, 27, 1969-1977.	3.1	5

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37	The structural basis for cancer drug interactions with the catalytic and allosteric sites of SAMHD1. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10022-E10031.	3.3	30
38	Structural Basis for tRNA Mimicry by a Bacterial Y RNA. Structure, 2018, 26, 1635-1644.e3.	1.6	17
39	SAMHD1 Impairs HIV-1 Gene Expression and Negatively Modulates Reactivation of Viral Latency in CD4 <sup>+</sup> T Cells. Journal of Virology, 2018, 92, .	1.5	25
40	Phosphoserine acidic cluster motifs bind distinct basic regions on the $\beta$ subunits of clathrin adaptor protein complexes. Journal of Biological Chemistry, 2018, 293, 15678-15690.	1.6	10
41	Insights into DNA substrate selection by APOBEC3G from structural, biochemical, and functional studies. PLoS ONE, 2018, 13, e0195048.	1.1	25
42	Cullin-RING E3 Ubiquitin Ligases: Bridges to Destruction. Sub-Cellular Biochemistry, 2017, 83, 323-347.	1.0	45
43	Endocytic activity of HIV-1 Vpu: Phosphoserine-dependent interactions with clathrin adaptors. Traffic, 2017, 18, 545-561.	1.3	13
44	Structural Basis for Ligand Binding to the Guanidine-I Riboswitch. Structure, 2017, 25, 195-202.	1.6	62
45	Crystal structure of E. coli apolipoprotein N-acyl transferase. Nature Communications, 2017, 8, 15948.	5.8	31
46	SAMHD1-mediated HIV-1 restriction in cells does not involve ribonuclease activity. Nature Medicine, 2016, 22, 1072-1074.	15.2	85
47	Mechanisms of activation and inhibition of Zika virus NS2B-NS3 protease. Cell Research, 2016, 26, 1260-1263.	5.7	71
48	FBXO32, encoding a member of the SCF complex, is mutated in dilated cardiomyopathy. Genome Biology, 2016, 17, 2.	3.8	35
49	Relative Resistance of HLA-B to Downregulation by Naturally Occurring HIV-1 Nef Sequences. MBio, 2016, 7, e01516-15.	1.8	23
50	A local-optimization refinement algorithm in single particle analysis for macromolecular complex with multiple rigid modules. Protein and Cell, 2016, 7, 46-62.	4.8	13
51	The Role of UAF1 in the Fanconi Anemia Pathway Regulation of Homologous Recombination-Mediated Genome Maintenance. Blood, 2016, 128, 1041-1041.	0.6	0
52	Insights into Cullin-RING E3 Ubiquitin Ligase Recruitment: Structure of the VHL-EloBC-Cul2 Complex. Structure, 2015, 23, 441-449.	1.6	59
53	Accelerating Novel Candidate Gene Discovery in Neurogenetic Disorders via Whole-Exome Sequencing of Prescreened Multiplex Consanguineous Families. Cell Reports, 2015, 10, 148-161.	2.9	375
54	HIV suppression by host restriction factors and viral immune evasion. Current Opinion in Structural Biology, 2015, 31, 106-114.	2.6	44

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55	Two Tales (Tails) of SAMHD1 Destruction by Vpx. <i>Cell Host and Microbe</i> , 2015, 17, 425-427.	5.1	0
56	Impaired dNTPase Activity of SAMHD1 by Phosphomimetic Mutation of Thr-592. <i>Journal of Biological Chemistry</i> , 2015, 290, 26352-26359.	1.6	75
57	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
58	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
59	TRIM15 is a focal adhesion protein that regulates focal adhesion disassembly. <i>Journal of Cell Science</i> , 2014, 127, 3928-42.	1.2	31
60	Structural Insight into HIV-1 Restriction by MxB. <i>Cell Host and Microbe</i> , 2014, 16, 627-638.	5.1	106
61	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
62	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
63	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
64	Electron Density Sharpening as a General Technique in Crystallographic Studies. <i>Journal of Molecular Biology</i> , 2014, 426, 980-993.	2.0	21
65	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
66	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
67	Mechanism of allosteric activation of SAMHD1 by dGTP. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1304-1309.	3.6	135
68	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
69	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
70	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
71	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
72	Mechanism of transfer RNA maturation by CCA-adding enzyme without using an oligonucleotide template. <i>Nature</i> , 2004, 430, 640-645.	13.7	120