

Yong Xiong

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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.

73 papers	2,181 citations	24 h-index	45 g-index
77 ext. papers	2,844 ext. citations	11.4 avg, IF	4.95 L-index

#	Paper	IF	Citations
73	Accelerating novel candidate gene discovery in neurogenetic disorders via whole-exome sequencing of prescreened multiplex consanguineous families. <i>Cell Reports</i> , 2015 , 10, 148-61	10.6	262
72	Mechanism of transfer RNA maturation by CCA-adding enzyme without using an oligonucleotide template. <i>Nature</i> , 2004 , 430, 640-5	50.4	105
71	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, 3307-15	5.6	103
70	Mechanism of allosteric activation of SAMHD1 by dGTP. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 1304-9	17.6	103
69	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, 8656-63	6.6	94
68	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	11.5	87
67	Structural insight into HIV-1 restriction by MxB. <i>Cell Host and Microbe</i> , 2014 , 16, 627-638	23.4	80
66	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	11	68
65	Structural basis of HIV-1 Vpu-mediated BST2 antagonism via hijacking of the clathrin adaptor protein complex 1. <i>ELife</i> , 2014 , 3, e02362	8.9	67
64	A single amino acid difference in human APOBEC3H variants determines HIV-1 Vif sensitivity. <i>Journal of Virology</i> , 2010 , 84, 1902-11	6.6	66
63	A story with a good ending: tRNA 3Xend maturation by CCA-adding enzymes. <i>Current Opinion in Structural Biology</i> , 2006 , 16, 12-7	8.1	65
62	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	17.6	65
61	Transposon molecular domestication and the evolution of the RAG recombinase. <i>Nature</i> , 2019 , 569, 79-84	50.4	64
60	Impaired dNTPase activity of SAMHD1 by phosphomimetic mutation of Thr-592. <i>Journal of Biological Chemistry</i> , 2015 , 290, 26352-9	5.4	63
59	SAMHD1-mediated HIV-1 restriction in cells does not involve ribonuclease activity. <i>Nature Medicine</i> , 2016 , 22, 1072-1074	50.5	63
58	Mechanisms of activation and inhibition of Zika virus NS2B-NS3 protease. <i>Cell Research</i> , 2016 , 26, 1260-1263	17.7	59
57	SAMHD1 suppresses innate immune responses to viral infections and inflammatory stimuli by inhibiting the NF- κ B and interferon pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E3798-E3807	11.5	52

56	Functional landscape of SARS-CoV-2 cellular restriction. <i>Molecular Cell</i> , 2021 , 81, 2656-2668.e8	17.6	47
55	Structural Basis for Ligand Binding to the Guanidine-I Riboswitch. <i>Structure</i> , 2017 , 25, 195-202	5.2	43
54	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, 755-9 ¹¹		4 ¹
53	Insights into Cullin-RING E3 ubiquitin ligase recruitment: structure of the VHL-EloBC-Cul2 complex. <i>Structure</i> , 2015 , 23, 441-449	5.2	40
52	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, 3309-19	6.6	32
51	HIV suppression by host restriction factors and viral immune evasion. <i>Current Opinion in Structural Biology</i> , 2015 , 31, 106-14	8.1	31
50	FEZ1 Is Recruited to a Conserved Cofactor Site on Capsid to Promote HIV-1 Trafficking. <i>Cell Reports</i> , 2019 , 28, 2373-2385.e7	10.6	31
49	Crystal structure of E. coli apolipoprotein N-acyl transferase. <i>Nature Communications</i> , 2017 , 8, 15948	17.4	24
48	FBXO32, encoding a member of the SCF complex, is mutated in dilated cardiomyopathy. <i>Genome Biology</i> , 2016 , 17, 2	18.3	23
47	Study of Mendelian forms of Crohn's disease in Saudi Arabia reveals novel risk loci and alleles. <i>Gut</i> , 2014 , 63, 1831-2	19.2	23
46	Cullin-RING E3 Ubiquitin Ligases: Bridges to Destruction. <i>Sub-Cellular Biochemistry</i> , 2017 , 83, 323-347	5.5	21
45	Insights into DNA substrate selection by APOBEC3G from structural, biochemical, and functional studies. <i>PLoS ONE</i> , 2018 , 13, e0195048	3.7	21
44	MxB Restricts HIV-1 by Targeting the Tri-hexamer Interface of the Viral Capsid. <i>Structure</i> , 2019 , 27, 1234-1245.e5		1245.e5
43	TRIM15 is a focal adhesion protein that regulates focal adhesion disassembly. <i>Journal of Cell Science</i> , 2014 , 127, 3928-42	5.3	19
42	Electron density sharpening as a general technique in crystallographic studies. <i>Journal of Molecular Biology</i> , 2014 , 426, 980-93	6.5	18
41	From electron microscopy to X-ray crystallography: molecular-replacement case studies. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008 , 64, 76-82		18
40	SAMHD1 Impairs HIV-1 Gene Expression and Negatively Modulates Reactivation of Viral Latency in CD4 T Cells. <i>Journal of Virology</i> , 2018 , 92,	6.6	18
39	Modular HIV-1 Capsid Assemblies Reveal Diverse Host-Capsid Recognition Mechanisms. <i>Cell Host and Microbe</i> , 2019 , 26, 203-216.e6	23.4	16

38	Selective inactivation of hypomethylating agents by SAMHD1 provides a rationale for therapeutic stratification in AML. <i>Nature Communications</i> , 2019 , 10, 3475	17.4	16
37	Relative Resistance of HLA-B to Downregulation by Naturally Occurring HIV-1 Nef Sequences. <i>MBio</i> , 2016 , 7, e01516-15	7.8	15
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	11.5	15
35	Structural basis of antagonism of human APOBEC3F by HIV-1 Vif. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 1176-1183	17.6	15
34	The SAM domain of mouse SAMHD1 is critical for its activation and regulation. <i>Nature Communications</i> , 2018 , 9, 411	17.4	14
33	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	11.5	14
32	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,	6.6	11
31	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	7.2	11
30	A Conserved Acidic-Cluster Motif in SERINC5 Confers Partial Resistance to Antagonism by HIV-1 Nef. <i>Journal of Virology</i> , 2020 , 94,	6.6	10
29	Endocytic activity of HIV-1 Vpu: Phosphoserine-dependent interactions with clathrin adaptors. <i>Traffic</i> , 2017 , 18, 545-561	5.7	9
28	Multifaceted HIV-1 Vif interactions with human E3 ubiquitin ligase and APOBEC3s. <i>FEBS Journal</i> , 2021 , 288, 3407-3417	5.7	9
27	Phosphoserine acidic cluster motifs bind distinct basic regions on the β subunits of clathrin adaptor protein complexes. <i>Journal of Biological Chemistry</i> , 2018 , 293, 15678-15690	5.4	8
26	Sorting sub-150-nm liposomes of distinct sizes by DNA-brick-assisted centrifugation. <i>Nature Chemistry</i> , 2021 , 13, 335-342	17.6	8
25	Structural Basis for tRNA Mimicry by a Bacterial Y RNA. <i>Structure</i> , 2018 , 26, 1635-1644.e3	5.2	8
24	Coronavirus Nsp1: Immune Response Suppression and Protein Expression Inhibition. <i>Frontiers in Microbiology</i> , 2021 , 12, 752214	5.7	7
23	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	17.4	6
22	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	5.4	6
21	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,	6.6	5

20	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	16.4	5
19	Importance of homo-dimerization of Fanconi-associated nuclease 1 in DNA flap cleavage. <i>DNA Repair</i> , 2018 , 64, 53-58	4.3	4
18	A snapshot of HIV-1 capsid-host interactions. <i>Current Research in Structural Biology</i> , 2020 , 2, 222-228	2.8	4
17	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,	11.5	4
16	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,	6.6	4
15	Cryo-EM structure of an active central apparatus.. <i>Nature Structural and Molecular Biology</i> , 2022 , 29, 472-482	14.8	4
14	APOBEC3A Loop 1 Is a Determinant for Single-Stranded DNA Binding and Deamination. <i>Biochemistry</i> , 2019 , 58, 3838-3847	3.2	3
13	A DNA-origami nuclear pore mimic reveals nuclear entry mechanisms of HIV-1 capsid		3
12	A threonine zipper that mediates protein-protein interactions: Structure and prediction. <i>Protein Science</i> , 2018 , 27, 1969-1977	6.3	2
11	Monospecific and bispecific monoclonal SARS-CoV-2 neutralizing antibodies that maintain potency against B.1.617.. <i>Nature Communications</i> , 2022 , 13, 1638	17.4	2
10	Nuclear Import of HIV-1. <i>Viruses</i> , 2021 , 13,	6.2	1
9	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	12.8	1
8	Crystal structure of a guanine nucleotide exchange factor encoded by the scrub typhus pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 30380-30390	11.5	1
7	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	5.4	1
6	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	5.4	1
5	Nodal modulator (NOMO) is required to sustain endoplasmic reticulum morphology. <i>Journal of Biological Chemistry</i> , 2021 , 297, 100937	5.4	0
4	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	6.8	0
3	Two tales (tails) of SAMHD1 destruction by Vpx. <i>Cell Host and Microbe</i> , 2015 , 17, 425-7	23.4	

- 2 Structure of a Synaptic γ -Resolvase Tetramer Covalently Linked to Two Cleaved DNAs. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 447-452 0.5
- 1 The Role of UAF1 in the Fanconi Anemia Pathway Regulation of Homologous Recombination-Mediated Genome Maintenance. *Blood*, **2016**, 128, 1041-1041 2.2