

# Haiyang Hu

## List of Publications by Year in descending order

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Version: 2024-02-01

27  
papers

2,072  
citations

430442

18  
h-index

525886

27  
g-index

33  
all docs

33  
docs citations

33  
times ranked

4219  
citing authors

#	ARTICLE	IF	CITATIONS
1	UXT attenuates the CGAS-STING1 signaling by targeting STING1 for autophagic degradation. <i>Autophagy</i> , 2023, 19, 440-456.	4.3	15
2	Mice deficient in UXT exhibit retinitis pigmentosa-like features via aberrant autophagy activation. <i>Autophagy</i> , 2021, 17, 1873-1888.	4.3	12
3	RNF111-facilitated neddylation potentiates cGAS-mediated antiviral innate immune response. <i>PLoS Pathogens</i> , 2021, 17, e1009401.	2.1	27
4	Variation of microRNA expression in the human placenta driven by population identity and sex of the newborn. <i>BMC Genomics</i> , 2021, 22, 286.	1.2	8
5	STING inhibitors target the cyclic dinucleotide binding pocket. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	84
6	WZ66, a novel acetyl-CoA carboxylase inhibitor, alleviates nonalcoholic steatohepatitis (NASH) in mice. <i>Acta Pharmacologica Sinica</i> , 2020, 41, 336-347.	2.8	17
7	Coordinated changes of gut microbiome and lipidome differentiates nonalcoholic steatohepatitis (NASH) from isolated steatosis. <i>Liver International</i> , 2020, 40, 622-637.	1.9	32
8	NSUN5 Facilitates Viral RNA Recognition by RIG-I Receptor. <i>Journal of Immunology</i> , 2020, 205, 3408-3418.	0.4	2
9	Sa1628 “ Coordinated Changes of Gut Microbiome and Lipidome Differentiates Nonalcoholic Steatohepatitis (NASH) from Isolated Steatosis. <i>Gastroenterology</i> , 2019, 156, S-1260.	0.6	0
10	Chitosan Oligosaccharide Ameliorates Nonalcoholic Fatty Liver Disease (NAFLD) in Diet-Induced Obese Mice. <i>Marine Drugs</i> , 2019, 17, 391.	2.2	43
11	JNK1 Induces Notch1 Expression to Regulate Genes Governing Photoreceptor Production. <i>Cells</i> , 2019, 8, 970.	1.8	5
12	Recently Evolved Tumor Suppressor Transcript TP73-AS1 Functions as Sponge of Human-Specific miR-941. <i>Molecular Biology and Evolution</i> , 2018, 35, 1063-1077.	3.5	21
13	Constrained vertebrate evolution by pleiotropic genes. <i>Nature Ecology and Evolution</i> , 2017, 1, 1722-1730.	3.4	72
14	Disruption of an Evolutionarily Novel Synaptic Expression Pattern in Autism. <i>PLoS Biology</i> , 2016, 14, e1002558.	2.6	73
15	Transcript and protein expression decoupling reveals RNA binding proteins and miRNAs as potential modulators of human aging. <i>Genome Biology</i> , 2015, 16, 41.	3.8	82
16	Deep sequencing reveals a novel class of bidirectional promoters associated with neuronal genes. <i>BMC Genomics</i> , 2014, 15, 457.	1.2	20
17	PROMiRNA: a new miRNA promoter recognition method uncovers the complex regulation of intronic miRNAs. <i>Genome Biology</i> , 2013, 14, R84.	13.9	104
18	Birth and expression evolution of mammalian microRNA genes. <i>Genome Research</i> , 2013, 23, 34-45.	2.4	252

#	ARTICLE	IF	CITATIONS
19	Evolution of the human-specific microRNA miR-941. <i>Nature Communications</i> , 2012, 3, 1145.	5.8	103
20	Mechanisms of Dietary Response in Mice and Primates: A Role for EGR1 in Regulating the Reaction to Human-Specific Nutritional Content. <i>PLoS ONE</i> , 2012, 7, e43915.	1.1	3
21	Ab initio identification of transcription start sites in the Rhesus macaque genome by histone modification and RNA-Seq. <i>Nucleic Acids Research</i> , 2011, 39, 1408-1418.	6.5	19
22	Widespread expression of piRNA-like molecules in somatic tissues. <i>Nucleic Acids Research</i> , 2011, 39, 6596-6607.	6.5	182
23	MicroRNA-Driven Developmental Remodeling in the Brain Distinguishes Humans from Other Primates. <i>PLoS Biology</i> , 2011, 9, e1001214.	2.6	198
24	MicroRNA Expression and Regulation in Human, Chimpanzee, and Macaque Brains. <i>PLoS Genetics</i> , 2011, 7, e1002327.	1.5	126
25	Comprehensive survey of human brain microRNA by deep sequencing. <i>BMC Genomics</i> , 2010, 11, 409.	1.2	142
26	MicroRNA, mRNA, and protein expression link development and aging in human and macaque brain. <i>Genome Research</i> , 2010, 20, 1207-1218.	2.4	283
27	Sequence features associated with microRNA strand selection in humans and flies. <i>BMC Genomics</i> , 2009, 10, 413.	1.2	139