

# Hong Qu

## List of Publications by Year in descending order

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39  
papers

740  
citations

623734

14  
h-index

552781

26  
g-index

41  
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41  
docs citations

41  
times ranked

1301  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide circular RNA (circRNA) and mRNA profiling identify a circMET-miR-410-3p regulatory motif for cell growth in colorectal cancer. <i>Genomics</i> , 2022, 114, 351-360.	2.9	11
2	A stop-gain mutation in GXYLT1 promotes metastasis of colorectal cancer via the MAPK pathway. <i>Cell Death and Disease</i> , 2022, 13, 395.	6.3	5
3	circExp database: an online transcriptome platform for human circRNA expressions in cancers. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	3.0	4
4	Possible mechanism and potential application of anti-opioid effect of diazepam-binding inhibitor. <i>Life Sciences</i> , 2021, 265, 118836.	4.3	0
5	Online database for brain cancer-implicated genes: exploring the subtype-specific mechanisms of brain cancer. <i>BMC Genomics</i> , 2021, 22, 458.	2.8	7
6	circVAR database: genome-wide archive of genetic variants for human circular RNAs. <i>BMC Genomics</i> , 2020, 21, 750.	2.8	7
7	Comparative analysis of rare <i>EDAR</i> mutations and tooth agenesis pattern in <i>EDAR</i> and <i>EDA</i> -associated nonsyndromic oligodontia. <i>Human Mutation</i> , 2020, 41, 1957-1966.	2.5	12
8	A novel EDA1 missense mutation in X-linked hypohidrotic ectodermal dysplasia. <i>Medicine (United States)</i> , 2020, 99, 1000000.	1.0	5
9	A novel inhibitor of nuclear factor kappa-B kinase subunit gamma mutation identified in an incontinentia pigmenti patient with syndromic tooth agenesis. <i>Archives of Oral Biology</i> , 2019, 101, 100-107.	1.8	7
10	dbEMT 2.0: An updated database for epithelial-mesenchymal transition genes with experimentally verified information and precalculated regulation information for cancer metastasis. <i>Journal of Genetics and Genomics</i> , 2019, 46, 595-597.	3.9	56
11	Identification of novel mouse and rat CB1R isoforms and in silico modeling of human CB1R for peripheral cannabinoid therapeutics. <i>Acta Pharmacologica Sinica</i> , 2019, 40, 387-397.	6.1	14
12	CIGene: a literature-based online resource for cancer initiation genes. <i>BMC Genomics</i> , 2018, 19, 552.	2.8	1
13	dbLGL: an online leukemia gene and literature database for the retrospective comparison of adult and childhood leukemia genetics with literature evidence. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	3
14	Systematic review of next-generation sequencing simulators: computational tools, features and perspectives. <i>Briefings in Functional Genomics</i> , 2017, 16, elw012.	2.7	28
15	CMGene: A literature-based database and knowledge resource for cancer metastasis genes. <i>Journal of Genetics and Genomics</i> , 2017, 44, 277-279.	3.9	8
16	Discovery of new cellulases from the metagenome by a metagenomics-guided strategy. <i>Biotechnology for Biofuels</i> , 2016, 9, 138.	6.2	74
17	A gene browser of colorectal cancer with literature evidence and pre-computed regulatory information to identify key tumor suppressors and oncogenes. <i>Scientific Reports</i> , 2016, 6, 30624.	3.3	3
18	Induction of anti-EGFR immune response with mimotopes identified from a phage display peptide library by panitumumab. <i>Oncotarget</i> , 2016, 7, 75293-75306.	1.8	12

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19	Expression of epithelial-mesenchymal transition-related genes increases with copy number in multiple cancer types. <i>Oncotarget</i> , 2016, 7, 24688-24699.	1.8	17
20	GCGene: a gene resource for gastric cancer with literature evidence. <i>Oncotarget</i> , 2016, 7, 33983-33993.	1.8	1
21	dbEMT: an epithelial-mesenchymal transition associated gene resource. <i>Scientific Reports</i> , 2015, 5, 11459.	3.3	117
22	An evidence-based knowledgebase of metastasis suppressors to identify key pathways relevant to cancer metastasis. <i>Scientific Reports</i> , 2015, 5, 15478.	3.3	19
23	METSP: A Maximum-Entropy Classifier Based Text Mining Tool for Transporter-Substrate Identification with Semistructured Text. <i>BioMed Research International</i> , 2015, 2015, 1-7.	1.9	3
24	Cellular Metabolic Network Analysis: Discovering Important Reactions in <i>Treponema pallidum</i> . <i>BioMed Research International</i> , 2015, 2015, 1-8.	1.9	5
25	Validation of the Memorial Sloan-Kettering Cancer Center Nomogram to Predict Overall Survival After Curative Colectomy in a Chinese Colon Cancer Population. <i>Annals of Surgical Oncology</i> , 2015, 22, 3881-3887.	1.5	17
26	Pedican: an online gene resource for pediatric cancers with literature evidence. <i>Scientific Reports</i> , 2015, 5, 11435.	3.3	8
27	Computational analysis of AnmK-like kinase: New insights into the cell wall metabolism of fungi. <i>Journal of Theoretical Biology</i> , 2015, 379, 59-65.	1.7	9
28	Species Differences in Cannabinoid Receptor 2 and Receptor Responses to Cocaine Self-Administration in Mice and Rats. <i>Neuropsychopharmacology</i> , 2015, 40, 1037-1051.	5.4	110
29	A systems biology approach to identify intelligence quotient score-related genomic regions and pathways relevant to potential therapeutic treatments. <i>Scientific Reports</i> , 2014, 4, 4176.	3.3	15
30	Human Transporter Database: Comprehensive Knowledge and Discovery Tools in the Human Transporter Genes. <i>PLoS ONE</i> , 2014, 9, e88883.	2.5	24
31	EDdb: A web resource for eating disorder and its application to identify an extended adipocytokine signaling pathway related to eating disorder. <i>Science China Life Sciences</i> , 2013, 56, 1086-1096.	4.9	36
32	IQdb: an intelligence quotient score-associated gene resource for human intelligence. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat063.	3.0	15
33	TSdb: A database of transporter substrates linking metabolic pathways and transporter systems on a genome scale via their shared substrates. <i>Science China Life Sciences</i> , 2011, 54, 60-64.	4.9	25
34	High similarity of phylogenetic profiles of rate-limiting enzymes with inhibitory relation in Human, Mouse, Rat, budding Yeast and E. coli. <i>BMC Genomics</i> , 2011, 12, S10.	2.8	11
35	PathLocdb: a comprehensive database for the subcellular localization of metabolic pathways and its application to multiple localization analysis. <i>BMC Genomics</i> , 2010, 11, S13.	2.8	21
36	Human liver rate-limiting enzymes influence metabolic flux via branch points and inhibitors. <i>BMC Genomics</i> , 2009, 10, S31.	2.8	21

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37	Emergence in swarming pervasive computing and Chaos Analysis. , 2006, , .		5
38	Biochemical characterization of the protein encoded by rice osRACD gene*. Progress in Natural Science: Materials International, 2004, 14, 332-337.	4.4	1
39	Active regionsâ€™ setting of the extracellular ligandbinding domain of human interleukin-6 receptor. Science Bulletin, 2000, 45, 1182-1187.	1.7	3