

# Huaqin Pan

## List of Publications by Year in descending order

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33  
papers

25,769  
citations

279487

23  
h-index

433756

31  
g-index

33  
all docs

33  
docs citations

33  
times ranked

29215  
citing authors

#	ARTICLE	IF	CITATIONS
1	Linking complex disease and exposure data—insights from an environmental and occupational health study. <i>Journal of Exposure Science and Environmental Epidemiology</i> , 2022, , .	1.8	0
2	Using the PhenX Toolkit to Select Standard Measurement Protocols for Your Research Study. <i>Current Protocols</i> , 2021, 1, e149.	1.3	16
3	An assessment of environmental health measures in the Deepwater Horizon Research Consortia. <i>Current Opinion in Toxicology</i> , 2019, 16, 75-82.	2.6	3
4	Comprehensive anatomic ontologies for lung development: A comparison of alveolar formation and maturation within mouse and human lung. <i>Journal of Biomedical Semantics</i> , 2019, 10, 18.	0.9	45
5	Using the PhenX Toolkit to Add Standard Measures to a Study. <i>Current Protocols in Human Genetics</i> , 2015, 86, 1.21.1-1.21.17.	3.5	33
6	Sample and data sharing: Observations from a central data repository. <i>Clinical Biochemistry</i> , 2014, 47, 252-257.	0.8	7
7	“What’s in the NIDDK CDR?” public query tools for the NIDDK central data repository. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bas058.	1.4	6
8	Using PhenX measures to identify opportunities for cross-study analysis. <i>Human Mutation</i> , 2012, 33, 849-857.	1.1	27
9	Using the PhenX Toolkit to Add Standard Measures to a Study. <i>Current Protocols in Human Genetics</i> , 2011, 71, Unit1.21.	3.5	17
10	The NIDDK Central Repository at 8 years—Ambition, Revision, Use and Impact. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar043-bar043.	1.4	15
11	The PhenX Toolkit: Get the Most From Your Measures. <i>American Journal of Epidemiology</i> , 2011, 174, 253-260.	1.6	610
12	Identification of Quantitative Trait Loci Underlying Proteome Variation in Human Lymphoblastoid Cells. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1383-1399.	2.5	37
13	Transcriptome analysis reveals new insight into appressorium formation and function in the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Genome Biology</i> , 2008, 9, R85.	13.9	169
14	The role of transposable element clusters in genome evolution and loss of synteny in the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Genome Biology</i> , 2006, 7, R16.	13.9	81
15	Global gene expression during nitrogen starvation in the rice blast fungus, <i>Magnaporthe grisea</i> . <i>Fungal Genetics and Biology</i> , 2006, 43, 605-617.	0.9	109
16	The genome sequence of the rice blast fungus <i>Magnaporthe grisea</i> . <i>Nature</i> , 2005, 434, 980-986.	13.7	1,447
17	The Î±- and Î²-subunits of the Human UDP-N-acetylglucosamine:Lysosomal Enzyme Phosphotransferase Are Encoded by a Single cDNA. <i>Journal of Biological Chemistry</i> , 2005, 280, 36141-36149.	1.6	108
18	Novel G-protein-coupled receptor-like proteins in the plant pathogenic fungus <i>Magnaporthe grisea</i> . <i>Genome Biology</i> , 2005, 6, R24.	13.9	182

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19	Gene Discovery and Gene Expression in the Rice Blast Fungus, <i>Magnaporthe grisea</i> : Analysis of Expressed Sequence Tags. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 1337-1347.	1.4	83
20	Regions of Microsynteny in <i>Magnaporthe grisea</i> and <i>Neurospora crassa</i> . <i>Fungal Genetics and Biology</i> , 2001, 33, 137-143.	0.9	33
21	Identification of lysine decarboxylase as a mammalian cell growth inhibitor in <i>Eikenella corrodens</i> : possible role in periodontal disease. <i>Microbial Pathogenesis</i> , 2001, 30, 179-192.	1.3	19
22	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	13.7	21,074
23	Analysis of the Cat Eye Syndrome Critical Region in Humans and the Region of Conserved Synteny in Mice: A Search for Candidate Genes at or near the Human Chromosome 22 Pericentromere. <i>Genome Research</i> , 2001, 11, 1053-1070.	2.4	99
24	A transcription map of the minimally deleted region from 13q14 in B-cell chronic lymphocytic leukemia as defined by large scale sequencing of the 650â€‰kb critical region. <i>Oncogene</i> , 2000, 19, 5772-5780.	2.6	15
25	The Human Homolog of Insect-Derived Growth Factor, <i>CECR1</i> , Is a Candidate Gene for Features of Cat Eye Syndrome. <i>Genomics</i> , 2000, 64, 277-285.	1.3	64
26	Duplications on Human Chromosome 22 Reveal a Novel Ret Finger Protein-Like Gene Family with Sense and Endogenous Antisense Transcripts. <i>Genome Research</i> , 1999, 9, 803-814.	2.4	32
27	The DNA sequence of human chromosome 22. <i>Nature</i> , 1999, 402, 489-495.	13.7	1,086
28	TOM1Genes Map to Human Chromosome 22q13.1 and Mouse Chromosome 8C1 and Encode Proteins Similar to the Endosomal Proteins HGS and STAM. <i>Genomics</i> , 1999, 57, 380-388.	1.3	26
29	Characterization of the human synaptogyrin gene family. <i>Human Genetics</i> , 1998, 103, 131-141.	1.8	54
30	Characterization of the human NIPSNAP1 gene from 22q12: a member of a novel gene family. <i>Gene</i> , 1998, 212, 13-20.	1.0	48
31	Structure of the Promoter and Genomic Organization of the Human $\beta$ -Adaptin Gene ( <i>BAM22</i> ) from Chromosome 22q12. <i>Genomics</i> , 1996, 36, 112-117.	1.3	27
32	Sequence and Analysis of the Human ABL Gene, the BCR Gene, and Regions Involved in the Philadelphia Chromosomal Translocation. <i>Genomics</i> , 1995, 27, 67-82.	1.3	196
33	Correlation Analysis of Variables From the Atherosclerosis Risk in Communities Study. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	1