

# Jingjing Li

## List of Publications by Year in descending order

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Version: 2024-02-01

34  
papers

2,142  
citations

304743

22  
h-index

395702

33  
g-index

36  
all docs

36  
docs citations

36  
times ranked

5038  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide identification of the genetic basis of amyotrophic lateral sclerosis. <i>Neuron</i> , 2022, 110, 992-1008.e11.	8.1	51
2	PML Body Component Sp100A Restricts Wild-Type Herpes Simplex Virus 1 Infection. <i>Journal of Virology</i> , 2022, 96, e0027922.	3.4	5
3	Exome sequencing identifies genetic variants in anophthalmia and micropthalmia. <i>American Journal of Medical Genetics, Part A</i> , 2022, 188, 2376-2388.	1.2	2
4	A panoramic view of proteomics and multiomics in precision health. <i>IScience</i> , 2021, 24, 102925.	4.1	4
5	A Deep Learning Framework Identifies Pathogenic Noncoding Somatic Mutations from Personal Prostate Cancer Genomes. <i>Cancer Research</i> , 2020, 80, 4644-4654.	0.9	9
6	A Genome-Wide Analysis of Clinical Chorioamnionitis among Preterm Infants. <i>American Journal of Perinatology</i> , 2019, 36, 1453-1458.	1.4	4
7	The contributions of genetics to premature birth. <i>Pediatric Research</i> , 2019, 85, 416-417.	2.3	7
8	Gene-Environment Interaction in the Era of Precision Medicine. <i>Cell</i> , 2019, 177, 38-44.	28.9	73
9	Understanding health disparities. <i>Journal of Perinatology</i> , 2019, 39, 354-358.	2.0	14
10	Decoding the Genomics of Abdominal Aortic Aneurysm. <i>Cell</i> , 2018, 174, 1361-1372.e10.	28.9	68
11	Natural Selection Has Differentiated the Progesterone Receptor among Human Populations. <i>American Journal of Human Genetics</i> , 2018, 103, 45-57.	6.2	30
12	In vitro comparison of two titanium dental implant surface treatments: 3Mâ„¢,â„¢ESPEâ„¢,â„¢ MDIs versus Ankylosâ„¢. <i>International Journal of Implant Dentistry</i> , 2017, 3, 27.	2.7	6
13	Fetal de novo mutations and preterm birth. <i>PLoS Genetics</i> , 2017, 13, e1006689.	3.5	30
14	The genetic predisposition to bronchopulmonary dysplasia. <i>Current Opinion in Pediatrics</i> , 2016, 28, 318-323.	2.0	34
15	Exome Sequencing of Neonatal Blood Spots and the Identification of Genes Implicated in Bronchopulmonary Dysplasia. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015, 192, 589-596.	5.6	76
16	Identification of Human Neuronal Protein Complexes Reveals Biochemical Activities and Convergent Mechanisms of Action in Autism Spectrum Disorders. <i>Cell Systems</i> , 2015, 1, 361-374.	6.2	42
17	Integrated systems analysis reveals a molecular network underlying autism spectrum disorders. <i>Molecular Systems Biology</i> , 2014, 10, 774.	7.2	138
18	Identifying mRNA sequence elements for target recognition by human Argonaute proteins. <i>Genome Research</i> , 2014, 24, 775-785.	5.5	34

#	ARTICLE	IF	CITATIONS
19	Principles of regulatory information conservation between mouse and human. <i>Nature</i> , 2014, 515, 371-375.	27.8	259
20	Extensive Variation in Chromatin States Across Humans. <i>Science</i> , 2013, 342, 750-752.	12.6	338
21	SH3 interactome conserves general function over specific form. <i>Molecular Systems Biology</i> , 2013, 9, 652.	7.2	61
22	miRNA regulatory variation in human evolution. <i>Trends in Genetics</i> , 2013, 29, 116-124.	6.7	34
23	Evidence for Positive Selection on a Number of MicroRNA Regulatory Interactions during Recent Human Evolution. <i>PLoS Genetics</i> , 2012, 8, e1002578.	3.5	63
24	PhenoM: a database of morphological phenotypes caused by mutation of essential genes in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2012, 40, D687-D694.	14.5	13
25	Systematic exploration of essential yeast gene function with temperature-sensitive mutants. <i>Nature Biotechnology</i> , 2011, 29, 361-367.	17.5	352
26	Integrating high-throughput genetic interaction mapping and high-content screening to explore yeast spindle morphogenesis. <i>Journal of Cell Biology</i> , 2010, 188, 69-81.	5.2	100
27	Revisiting the Contribution of cis-Elements to Expression Divergence between Duplicated Genes: The Role of Chromatin Structure. <i>Molecular Biology and Evolution</i> , 2010, 27, 1461-1466.	8.9	8
28	Gene Expression Variability within and between Human Populations and Implications toward Disease Susceptibility. <i>PLoS Computational Biology</i> , 2010, 6, e1000910.	3.2	85
29	The Cellular Robustness by Genetic Redundancy in Budding Yeast. <i>PLoS Genetics</i> , 2010, 6, e1001187.	3.5	58
30	Evolution of an X-Linked Primate-Specific Micro RNA Cluster. <i>Molecular Biology and Evolution</i> , 2010, 27, 671-683.	8.9	64
31	Exploiting the determinants of stochastic gene expression in <i>Saccharomyces cerevisiae</i> for genome-wide prediction of expression noise. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10472-10477.	7.1	30
32	Learned Random-Walk Kernels and Empirical-Map Kernels for Protein Sequence Classification. <i>Journal of Computational Biology</i> , 2009, 16, 457-474.	1.6	2
33	A PROBABILISTIC FRAMEWORK TO IMPROVE MICRORNA TARGET PREDICTION BY INCORPORATING PROTEOMICS DATA. <i>Journal of Bioinformatics and Computational Biology</i> , 2009, 07, 955-972.	0.8	17
34	Preferential regulation of duplicated genes by microRNAs in mammals. <i>Genome Biology</i> , 2008, 9, R132.	9.6	31