Jun Z Li

List of Publications by Year
in descending order

46	14,762	159585 30	206112 48
papers	citations	h-index	g-index

60	60	60	32337
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). Autophagy, 2016, 12, 1-222.	9.1	4,701
2	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	21.4	2,067
3	Worldwide Human Relationships Inferred from Genome-Wide Patterns of Variation. Science, 2008, 319, 1100-1104.	12.6	1,774
4	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	21.4	1,191
5	An Abundance of Rare Functional Variants in 202 Drug Target Genes Sequenced in 14,002 People. Science, 2012, 337, 100-104.	12.6	626
6	Landscape of Intercellular Crosstalk in Healthy and NASH Liver Revealed by Single-Cell Secretome Gene Analysis. Molecular Cell, 2019, 75, 644-660.e5.	9.7	488
7	Circadian patterns of gene expression in the human brain and disruption in major depressive disorder. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 9950-9955.	7.1	477
8	A Comprehensive Roadmap of Murine Spermatogenesis Defined by Single-Cell RNA-Seq. Developmental Cell, 2018, 46, 651-667.e10.	7.0	346
9	Effect of agonal and postmortem factors on gene expression profile: quality control in microarray analyses of postmortem human brain. Biological Psychiatry, 2004, 55, 346-352.	1.3	294
10	Genome-wide association and meta-analysis of bipolar disorder in individuals of European ancestry. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 7501-7506.	7.1	274
11	Critical limitations of consensus clustering in class discovery. Scientific Reports, 2014, 4, 6207.	3.3	248
12	Systematic changes in gene expression in postmortem human brains associated with tissue pH and terminal medical conditions. Human Molecular Genetics, 2004, 13, 609-616.	2.9	237
13	Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma. Nature Genetics, 2014, 46, 1126-1130.	21.4	212
14	Mutation in ATG5 reduces autophagy and leads to ataxia with developmental delay. ELife, 2016, 5, .	6.0	161
15	Single-Cell RNA Sequencing of Human, Macaque, and Mouse Testes Uncovers Conserved and Divergent Features of Mammalian Spermatogenesis. Developmental Cell, 2020, 54, 529-547.e12.	7.0	150
16	Genetics of Combined Pituitary Hormone Deficiency: Roadmap into the Genome Era. Endocrine Reviews, 2016, 37, 636-675.	20.1	147
17	Mutations in VPS13D lead to a new recessive ataxia with spasticity and mitochondrial defects. Annals of Neurology, 2018, 83, 1075-1088.	5.3	122
18	Extremely rare variants reveal patterns of germline mutation rate heterogeneity in humans. Nature Communications, 2018, 9, 3753.	12.8	121

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19	Methodological considerations for gene expression profiling of human brain. Journal of Neuroscience Methods, 2007, 163, 295-309.	2.5	111
20	Genome-wide association study and meta-analysis of intraocular pressure. Human Genetics, 2014, 133, 41-57.	3.8	93
21	Recommendations to enhance rigor and reproducibility in biomedical research. GigaScience, 2020, 9, .	6.4	83
22	Inference of cell type content from human brain transcriptomic datasets illuminates the effects of age, manner of death, dissection, and psychiatric diagnosis. PLoS ONE, 2018, 13, e0200003.	2.5	65
23	Chromosome 1q21.2 and additional loci influence risk of spontaneous coronary artery dissection and myocardial infarction. Nature Communications, 2020, 11, 4432.	12.8	60
24	Individual Identifiability Predicts Population Identifiability in Forensic Microsatellite Markers. Current Biology, 2016, 26, 935-942.	3.9	59
25	The influence of genomic context on mutation patterns in the human genome inferred from rare variants. Genome Research, 2013, 23, 1974-1984.	5.5	51
26	Fibroblast growth factor 9 is a novel modulator of negative affect. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11953-11958.	7.1	49
27	Linkage disequilibrium matches forensic genetic records to disjoint genomic marker sets. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 5671-5676.	7.1	49
28	Cancer classification in the genomic era: five contemporary problems. Human Genomics, 2015, 9, 27.	2.9	48
29	Genetic Analysis of a Rat Model of Aerobic Capacity and Metabolic Fitness. PLoS ONE, 2013, 8, e77588.	2.5	44
30	Statistical Detection of Relatives Typed with Disjoint Forensic and Biomedical Loci. Cell, 2018, 175, 848-858.e6.	28.9	37
31	Mesenchymal VEGFA induces aberrant differentiation in heterotopic ossification. Bone Research, 2019, 7, 36.	11.4	37
32	Genomic Estimates of Aneuploid Content in Glioblastoma Multiforme and Improved Classification. Clinical Cancer Research, 2012, 18, 5595-5605.	7.0	34
33	Homozygous splice mutation in CWF19L1 in a Turkish family with recessive ataxia syndrome. Neurology, 2014, 83, 2175-2182.	1.1	34
34	Genetic investigation of fibromuscular dysplasia identifies risk loci and shared genetics with common cardiovascular diseases. Nature Communications, 2021, 12, 6031.	12.8	34
35	TCF21+ mesenchymal cells contribute to testis somatic cell development, homeostasis, and regeneration in mice. Nature Communications, 2021, 12, 3876.	12.8	27
36	<scp>HESX</scp>1 mutations in patients with congenital hypopituitarism: variable phenotypes with the same genotype. Clinical Endocrinology, 2016, 85, 408-414.	2.4	24

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37	Extended regions of suspected mis-assembly in the rat reference genome. Scientific Data, 2019, 6, 39.	5.3	24
38	Regulation of meiotic progression by Sertoli-cell androgen signaling. Molecular Biology of the Cell, 2020, 31, 2841-2862.	2.1	24
39	Cellular heterogeneity of human fallopian tubes in normal and hydrosalpinx disease states identified using scRNA-seq. Developmental Cell, 2022, 57, 914-929.e7.	7.0	19
40	The phenotypic spectrum associated with OTX2 mutations in humans. European Journal of Endocrinology, 2021, 185, 121-135.	3.7	15
41	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. Molecular Psychiatry, 2021, 26, 5239-5250.	7.9	15
42	Murine models of IDH-wild-type glioblastoma exhibit spatial segregation of tumor initiation and manifestation during evolution. Nature Communications, 2020, 11, 3669.	12.8	14
43	Sensitized mutagenesis screen in Factor V Leiden mice identifies thrombosis suppressor loci. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9659-9664.	7.1	13
44	Selection-, age-, and exercise-dependence of skeletal muscle gene expression patterns in a rat model of metabolic fitness. Physiological Genomics, 2016, 48, 816-825.	2.3	12
45	Circadian rhythms and mood: Opportunities for multiâ€level analyses in genomics and neuroscience. BioEssays, 2014, 36, 305-315.	2.5	10
46	Multiethnic PDX models predict a possible immune signature associated with TNBC of African ancestry. Breast Cancer Research and Treatment, 2021, 186, 391-401.	2.5	7