

Jun Z Li

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/826331/publications.pdf>

Version: 2024-02-01

46
papers

14,762
citations

159585

30
h-index

206112

48
g-index

60
all docs

60
docs citations

60
times ranked

32337
citing authors

#	ARTICLE	IF	CITATIONS
1	Cellular heterogeneity of human fallopian tubes in normal and hydrosalpinx disease states identified using scRNA-seq. <i>Developmental Cell</i> , 2022, 57, 914-929.e7.	7.0	19
2	Multiethnic PDX models predict a possible immune signature associated with TNBC of African ancestry. <i>Breast Cancer Research and Treatment</i> , 2021, 186, 391-401.	2.5	7
3	TCF21+ mesenchymal cells contribute to testis somatic cell development, homeostasis, and regeneration in mice. <i>Nature Communications</i> , 2021, 12, 3876.	12.8	27
4	The phenotypic spectrum associated with OTX2 mutations in humans. <i>European Journal of Endocrinology</i> , 2021, 185, 121-135.	3.7	15
5	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. <i>Molecular Psychiatry</i> , 2021, 26, 5239-5250.	7.9	15
6	Genetic investigation of fibromuscular dysplasia identifies risk loci and shared genetics with common cardiovascular diseases. <i>Nature Communications</i> , 2021, 12, 6031.	12.8	34
7	Regulation of meiotic progression by Sertoli-cell androgen signaling. <i>Molecular Biology of the Cell</i> , 2020, 31, 2841-2862.	2.1	24
8	Murine models of IDH-wild-type glioblastoma exhibit spatial segregation of tumor initiation and manifestation during evolution. <i>Nature Communications</i> , 2020, 11, 3669.	12.8	14
9	Chromosome 1q21.2 and additional loci influence risk of spontaneous coronary artery dissection and myocardial infarction. <i>Nature Communications</i> , 2020, 11, 4432.	12.8	60
10	Recommendations to enhance rigor and reproducibility in biomedical research. <i>GigaScience</i> , 2020, 9, .	6.4	83
11	Single-Cell RNA Sequencing of Human, Macaque, and Mouse Testes Uncovers Conserved and Divergent Features of Mammalian Spermatogenesis. <i>Developmental Cell</i> , 2020, 54, 529-547.e12.	7.0	150
12	Landscape of Intercellular Crosstalk in Healthy and NASH Liver Revealed by Single-Cell Secretome Gene Analysis. <i>Molecular Cell</i> , 2019, 75, 644-660.e5.	9.7	488
13	Genome-wide association study identifies 30 loci associated with bipolar disorder. <i>Nature Genetics</i> , 2019, 51, 793-803.	21.4	1,191
14	Extended regions of suspected mis-assembly in the rat reference genome. <i>Scientific Data</i> , 2019, 6, 39.	5.3	24
15	Mesenchymal VEGFA induces aberrant differentiation in heterotopic ossification. <i>Bone Research</i> , 2019, 7, 36.	11.4	37
16	Mutations in <i>VPS13D</i> lead to a new recessive ataxia with spasticity and mitochondrial defects. <i>Annals of Neurology</i> , 2018, 83, 1075-1088.	5.3	122
17	Statistical Detection of Relatives Typed with Disjoint Forensic and Biomedical Loci. <i>Cell</i> , 2018, 175, 848-858.e6.	28.9	37
18	Extremely rare variants reveal patterns of germline mutation rate heterogeneity in humans. <i>Nature Communications</i> , 2018, 9, 3753.	12.8	121

#	ARTICLE	IF	CITATIONS
19	Inference of cell type content from human brain transcriptomic datasets illuminates the effects of age, manner of death, dissection, and psychiatric diagnosis. <i>PLoS ONE</i> , 2018, 13, e0200003.	2.5	65
20	A Comprehensive Roadmap of Murine Spermatogenesis Defined by Single-Cell RNA-Seq. <i>Developmental Cell</i> , 2018, 46, 651-667.e10.	7.0	346
21	Linkage disequilibrium matches forensic genetic records to disjoint genomic marker sets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 5671-5676.	7.1	49
22	Sensitized mutagenesis screen in Factor V Leiden mice identifies thrombosis suppressor loci. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 9659-9664.	7.1	13
23	<i>HESX1</i> mutations in patients with congenital hypopituitarism: variable phenotypes with the same genotype. <i>Clinical Endocrinology</i> , 2016, 85, 408-414.	2.4	24
24	Selection-, age-, and exercise-dependence of skeletal muscle gene expression patterns in a rat model of metabolic fitness. <i>Physiological Genomics</i> , 2016, 48, 816-825.	2.3	12
25	Individual Identifiability Predicts Population Identifiability in Forensic Microsatellite Markers. <i>Current Biology</i> , 2016, 26, 935-942.	3.9	59
26	Genetics of Combined Pituitary Hormone Deficiency: Roadmap into the Genome Era. <i>Endocrine Reviews</i> , 2016, 37, 636-675.	20.1	147
27	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). <i>Autophagy</i> , 2016, 12, 1-222.	9.1	4,701
28	Mutation in <i>ATG5</i> reduces autophagy and leads to ataxia with developmental delay. <i>ELife</i> , 2016, 5, .	6.0	161
29	Cancer classification in the genomic era: five contemporary problems. <i>Human Genomics</i> , 2015, 9, 27.	2.9	48
30	Fibroblast growth factor 9 is a novel modulator of negative affect. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11953-11958.	7.1	49
31	Homozygous splice mutation in <i>CWF19L1</i> in a Turkish family with recessive ataxia syndrome. <i>Neurology</i> , 2014, 83, 2175-2182.	1.1	34
32	Circadian rhythms and mood: Opportunities for multi-level analyses in genomics and neuroscience. <i>BioEssays</i> , 2014, 36, 305-315.	2.5	10
33	Genome-wide association study and meta-analysis of intraocular pressure. <i>Human Genetics</i> , 2014, 133, 41-57.	3.8	93
34	Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma. <i>Nature Genetics</i> , 2014, 46, 1126-1130.	21.4	212
35	Critical limitations of consensus clustering in class discovery. <i>Scientific Reports</i> , 2014, 4, 6207.	3.3	248
36	The influence of genomic context on mutation patterns in the human genome inferred from rare variants. <i>Genome Research</i> , 2013, 23, 1974-1984.	5.5	51

#	ARTICLE	IF	CITATIONS
37	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. <i>Nature Genetics</i> , 2013, 45, 984-994.	21.4	2,067
38	Circadian patterns of gene expression in the human brain and disruption in major depressive disorder. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 9950-9955.	7.1	477
39	Genetic Analysis of a Rat Model of Aerobic Capacity and Metabolic Fitness. <i>PLoS ONE</i> , 2013, 8, e77588.	2.5	44
40	Genomic Estimates of Aneuploid Content in Glioblastoma Multiforme and Improved Classification. <i>Clinical Cancer Research</i> , 2012, 18, 5595-5605.	7.0	34
41	An Abundance of Rare Functional Variants in 202 Drug Target Genes Sequenced in 14,002 People. <i>Science</i> , 2012, 337, 100-104.	12.6	626
42	Genome-wide association and meta-analysis of bipolar disorder in individuals of European ancestry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 7501-7506.	7.1	274
43	Worldwide Human Relationships Inferred from Genome-Wide Patterns of Variation. <i>Science</i> , 2008, 319, 1100-1104.	12.6	1,774
44	Methodological considerations for gene expression profiling of human brain. <i>Journal of Neuroscience Methods</i> , 2007, 163, 295-309.	2.5	111
45	Systematic changes in gene expression in postmortem human brains associated with tissue pH and terminal medical conditions. <i>Human Molecular Genetics</i> , 2004, 13, 609-616.	2.9	237
46	Effect of agonal and postmortem factors on gene expression profile: quality control in microarray analyses of postmortem human brain. <i>Biological Psychiatry</i> , 2004, 55, 346-352.	1.3	294