Jean Monlong

List of Publications by Year
in descending order

33 papers	20,777 citations	304743 22 h-index	395702 33 g-index
38 all docs	38 docs citations	38 times ranked	41787 citing authors

#	Article	IF	Citations
1	The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585.	21.4	6,815
2	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	12.6	4,659
3	Genetic effects on gene expression across human tissues. Nature, 2017, 550, 204-213.	27.8	3,500
4	Transcriptome and genome sequencing uncovers functional variation in humans. Nature, 2013, 501, 506-511.	27.8	1,857
5	The human transcriptome across tissues and individuals. Science, 2015, 348, 660-665.	12.6	1,127
6	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. Nature Biotechnology, 2020, 38, 1044-1053.	17.5	344
7	High Rate of Recurrent De Novo Mutations in Developmental and Epileptic Encephalopathies. American Journal of Human Genetics, 2017, 101, 664-685.	6.2	337
8	Single-cell RNA-seq reveals that glioblastoma recapitulates a normal neurodevelopmental hierarchy. Nature Communications, 2020, 11, 3406.	12.8	300
9	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	21.4	275
10	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	12.6	252
11	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. Genome Research, 2014, 24, 212-226.	5.5	175
12	Genotyping structural variants in pangenome graphs using the vg toolkit. Genome Biology, 2020, 21, 35.	8.8	150
13	Stalled developmental programs at the root of pediatric brain tumors. Nature Genetics, 2019, 51, 1702-1713.	21.4	136
14	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. Science, 2021, 374, abg8871.	12.6	132
15	Identification of genetic variants associated with alternative splicing using sQTLseekeR. Nature Communications, 2014, 5, 4698.	12.8	121
16	Ultrarapid Nanopore Genome Sequencing in a Critical Care Setting. New England Journal of Medicine, 2022, 386, 700-702.	27.0	116
17	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. Nature Communications, 2015, 6, 5903.	12.8	73
18	Global characterization of copy number variants in epilepsy patients from whole genome sequencing. PLoS Genetics, 2018, 14, e1007285.	3.5	50

#	Article	IF	Citations
19	Overdiagnosis from non-progressive cancer detected by screening mammography: stochastic simulation study with calibration to population based registry data. BMJ: British Medical Journal, 2011, 343, d7017-d7017.	2.3	49
20	Accelerated identification of disease-causing variants with ultra-rapid nanopore genome sequencing. Nature Biotechnology, 2022, 40, 1035-1041.	17.5	45
21	Loss of chromosome Y leads to down regulation of KDM5D and KDM6C epigenetic modifiers in clear cell renal cell carcinoma. Scientific Reports, 2017, 7, 44876.	3.3	42
22	Human copy number variants are enriched in regions of low mappability. Nucleic Acids Research, 2018, 46, 7236-7249.	14.5	36
23	Genome-wide microhomologies enable precise template-free editing of biologically relevant deletion mutations. Nature Communications, 2019, 10, 4856.	12.8	22
24	A Preclinical Trial and Molecularly Annotated Patient Cohort Identify Predictive Biomarkers in Homologous Recombinationâ€“deficient Pancreatic Cancer. Clinical Cancer Research, 2020, 26, 5462-5476.	7.0	20
25	Invasive growth associated with cold-inducible RNA-binding protein expression drives recurrence of surgically resected brain metastases. Neuro-Oncology, 2021, 23, 1470-1480.	1.2	18
26	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	14
27	Glioblastoma scRNA-seq shows treatment-induced, immune-dependent increase in mesenchymal cancer cells and structural variants in distal neural stem cells. Neuro-Oncology, 2022, 24, 1494-1508.	1.2	11
28	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	5
29	AnÂinternationalÂvirtualÂhackathon toÂbuildÂtools for theÂanalysis ofÂstructuralÂvariants withinÂspeciesÂranging fromÂcoronaviruses toÂvertebrates. F1000Research, 2021, 10, 246.	1.6	3
30	Ultra-Rapid Nanopore Whole Genome Genetic Diagnosis of Dilated Cardiomyopathy in an Adolescent With Cardiogenic Shock. Circulation Genomic and Precision Medicine, 2022, 15, CIRCGEN121003591.	3.6	3
31	AnÂinternationalÂvirtualÂhackathon toÂbuildÂtools for theÂanalysis ofÂstructuralÂvariants withinÂspeciesÂranging fromÂcoronaviruses toÂvertebrates. F1000Research, 2021, 10, 246.	1.6	2
32	Inferring Copy Number from Triple-Negative Breast Cancer Patient Derived Xenograft scRNAseq Data Using scCNA. Methods in Molecular Biology, 2021, 2381, 285-303.	0.9	2
33	Abstract 2177: Sensitive single cell copy number profiling using a novel microfluidic droplet based platform. , 2018, , .		1