

Jean Monlong

List of Publications by Year in descending order

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Version: 2024-02-01

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	Ultrarapid Nanopore Genome Sequencing in a Critical Care Setting. <i>New England Journal of Medicine</i> , 2022, 386, 700-702.	27.0	116
2	Ultra-Rapid Nanopore Whole Genome Genetic Diagnosis of Dilated Cardiomyopathy in an Adolescent With Cardiogenic Shock. <i>Circulation Genomic and Precision Medicine</i> , 2022, 15, CIRCGEN121003591.	3.6	3
3	Accelerated identification of disease-causing variants with ultra-rapid nanopore genome sequencing. <i>Nature Biotechnology</i> , 2022, 40, 1035-1041.	17.5	45
4	Glioblastoma scRNA-seq shows treatment-induced, immune-dependent increase in mesenchymal cancer cells and structural variants in distal neural stem cells. <i>Neuro-Oncology</i> , 2022, 24, 1494-1508.	1.2	11
5	An international virtual hackathon to build tools for the analysis of structural variants within species ranging from coronaviruses to vertebrates. <i>F1000Research</i> , 2021, 10, 246.	1.6	3
6	An international virtual hackathon to build tools for the analysis of structural variants within species ranging from coronaviruses to vertebrates. <i>F1000Research</i> , 2021, 10, 246.	1.6	2
7	Invasive growth associated with cold-inducible RNA-binding protein expression drives recurrence of surgically resected brain metastases. <i>Neuro-Oncology</i> , 2021, 23, 1470-1480.	1.2	18
8	Inferring Copy Number from Triple-Negative Breast Cancer Patient Derived Xenograft scRNAseq Data Using scCNA. <i>Methods in Molecular Biology</i> , 2021, 2381, 285-303.	0.9	2
9	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. <i>Science</i> , 2021, 374, abg8871.	12.6	132
10	A Preclinical Trial and Molecularly Annotated Patient Cohort Identify Predictive Biomarkers in Homologous Recombination-deficient Pancreatic Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 5462-5476.	7.0	20
11	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. <i>Nature Biotechnology</i> , 2020, 38, 1044-1053.	17.5	344
12	Single-cell RNA-seq reveals that glioblastoma recapitulates a normal neurodevelopmental hierarchy. <i>Nature Communications</i> , 2020, 11, 3406.	12.8	300
13	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , 2020, 52, 306-319.	21.4	275
14	Genotyping structural variants in pangenome graphs using the vg toolkit. <i>Genome Biology</i> , 2020, 21, 35.	8.8	150
15	Genome-wide microhomologies enable precise template-free editing of biologically relevant deletion mutations. <i>Nature Communications</i> , 2019, 10, 4856.	12.8	22
16	Stalled developmental programs at the root of pediatric brain tumors. <i>Nature Genetics</i> , 2019, 51, 1702-1713.	21.4	136
17	A strategy for building and using a human reference pangenome. <i>F1000Research</i> , 2019, 8, 1751.	1.6	5
18	A strategy for building and using a human reference pangenome. <i>F1000Research</i> , 2019, 8, 1751.	1.6	14

#	ARTICLE	IF	CITATIONS
19	Human copy number variants are enriched in regions of low mappability. <i>Nucleic Acids Research</i> , 2018, 46, 7236-7249.	14.5	36
20	Global characterization of copy number variants in epilepsy patients from whole genome sequencing. <i>PLoS Genetics</i> , 2018, 14, e1007285.	3.5	50
21	Abstract 2177: Sensitive single cell copy number profiling using a novel microfluidic droplet based platform. , 2018, , .		1
22	Loss of chromosome Y leads to down regulation of KDM5D and KDM6C epigenetic modifiers in clear cell renal cell carcinoma. <i>Scientific Reports</i> , 2017, 7, 44876.	3.3	42
23	High Rate of Recurrent De Novo Mutations in Developmental and Epileptic Encephalopathies. <i>American Journal of Human Genetics</i> , 2017, 101, 664-685.	6.2	337
24	Genetic effects on gene expression across human tissues. <i>Nature</i> , 2017, 550, 204-213.	27.8	3,500
25	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. <i>Nature Communications</i> , 2015, 6, 5903.	12.8	73
26	The human transcriptome across tissues and individuals. <i>Science</i> , 2015, 348, 660-665.	12.6	1,127
27	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. <i>Science</i> , 2015, 348, 648-660.	12.6	4,659
28	Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , 2015, 348, 666-669.	12.6	252
29	Identification of genetic variants associated with alternative splicing using sQTLseeker. <i>Nature Communications</i> , 2014, 5, 4698.	12.8	121
30	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. <i>Genome Research</i> , 2014, 24, 212-226.	5.5	175
31	Transcriptome and genome sequencing uncovers functional variation in humans. <i>Nature</i> , 2013, 501, 506-511.	27.8	1,857
32	The Genotype-Tissue Expression (GTEx) project. <i>Nature Genetics</i> , 2013, 45, 580-585.	21.4	6,815
33	Overdiagnosis from non-progressive cancer detected by screening mammography: stochastic simulation study with calibration to population based registry data. <i>BMJ: British Medical Journal</i> , 2011, 343, d7017-d7017.	2.3	49