

Imad Abugessaisa

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

4,164
citations

361413

20
h-index

395702

33
g-index

43
all docs

43
docs citations

43
times ranked

9110
citing authors

#	ARTICLE	IF	CITATIONS
1	Inducing human retinal pigment epithelium-like cells from somatic tissue. <i>Stem Cell Reports</i> , 2022, 17, 289-306.	4.8	3
2	SkewC: Identifying cells with skewed gene body coverage in single-cell RNA sequencing data. <i>IScience</i> , 2022, 25, 103777.	4.1	4
3	FANTOM enters 20th year: expansion of transcriptomic atlases and functional annotation of non-coding RNAs. <i>Nucleic Acids Research</i> , 2021, 49, D892-D898.	14.5	57
4	A robust machine learning framework to identify signatures for frailty: a nested case-control study in four aging European cohorts. <i>GeroScience</i> , 2021, 43, 1317-1329.	4.6	31
5	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	12.8	11
6	The choice of negative control antisense oligonucleotides dramatically impacts downstream analysis depending on the cellular background. <i>BMC Genomic Data</i> , 2021, 22, 33.	1.7	0
7	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	5.5	109
8	Comparative transcriptomics of primary cells in vertebrates. <i>Genome Research</i> , 2020, 30, 951-961.	5.5	29
9	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution. <i>Nature Communications</i> , 2019, 10, 360.	12.8	102
10	refTSS: A Reference Data Set for Human and Mouse Transcription Start Sites. <i>Journal of Molecular Biology</i> , 2019, 431, 2407-2422.	4.2	72
11	Update of the FANTOM web resource: expansion to provide additional transcriptome atlases. <i>Nucleic Acids Research</i> , 2019, 47, D752-D758.	14.5	172
12	Incidence and risk factors for adalimumab and infliximab anti-drug antibodies in rheumatoid arthritis: A European retrospective multicohort analysis. <i>Seminars in Arthritis and Rheumatism</i> , 2019, 48, 967-975.	3.4	46
13	SCPortalen: human and mouse single-cell centric database. <i>Nucleic Acids Research</i> , 2018, 46, D781-D787.	14.5	48
14	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204.	27.8	898
15	The FANTOM5 Computation Ecosystem: Genomic Information Hub for Promoters and Active Enhancers. <i>Methods in Molecular Biology</i> , 2017, 1611, 199-217.	0.9	23
16	Genome Annotation. <i>Methods in Molecular Biology</i> , 2017, 1525, 107-121.	0.9	3
17	Linking FANTOM5 CAGE peaks to annotations with CAGEScan. <i>Scientific Data</i> , 2017, 4, 170147.	5.3	29
18	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878.	17.5	456

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19	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , 2017, 4, 170112.	5.3	195
20	FANTOM5 CAGE profiles of human and mouse reprocessed for GRCh38 and GRCm38 genome assemblies. <i>Scientific Data</i> , 2017, 4, 170107.	5.3	68
21	Monitoring transcription initiation activities in rat and dog. <i>Scientific Data</i> , 2017, 4, 170173.	5.3	6
22	Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. <i>Nucleic Acids Research</i> , 2017, 45, D737-D743.	14.5	116
23	Transcription start site profiling of 15 anatomical regions of the <i>Macaca mulatta</i> central nervous system. <i>Scientific Data</i> , 2017, 4, 170163.	5.3	4
24	FANTOM5 transcriptome catalog of cellular states based on Semantic MediaWiki. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw105.	3.0	64
25	Laboratory biomarkers and frailty: presentation of the FRAILOMIC initiative. <i>Clinical Chemistry and Laboratory Medicine</i> , 2015, 53, e253-5.	2.3	17
26	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , 2015, 347, 1010-1014.	12.6	517
27	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015, 16, 22.	8.8	687
28	Data integration in the era of omics: current and future challenges. <i>BMC Systems Biology</i> , 2014, 8, 11.	3.0	300
29	STATegra EMS: an Experiment Management System for complex next-generation omics experiments. <i>BMC Systems Biology</i> , 2014, 8, S9.	3.0	19
30	Systems Medicine: from molecular features and models to the clinic in COPD. <i>Journal of Translational Medicine</i> , 2014, 12, S4.	4.4	23
31	Accelerating Translational Research by Clinically Driven Development of an Informatics Platform—A Case Study. <i>PLoS ONE</i> , 2014, 9, e104382.	2.5	10
32	Implementation of the CDC translational informatics platform - from genetic variants to the national Swedish Rheumatology Quality Register. <i>Journal of Translational Medicine</i> , 2013, 11, 85.	4.4	8
33	Pediatric systems medicine: evaluating needs and opportunities using congenital heart block as a case study. <i>Pediatric Research</i> , 2013, 73, 508-513.	2.3	8
34	Geospatial metadata extraction from product description document applying methods from ontology engineering. <i>International Journal of Metadata, Semantics and Ontologies</i> , 2010, 5, 321.	0.2	6