Imad Abugessaisa

List of Publications by Year
in descending order

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	An atlas of human long non-coding RNAs with accurate 5â€² ends. Nature, 2017, 543, 199-204.	27.8	898
2	Gateways to the FANTOM5 promoter level mammalian expression atlas. Genome Biology, 2015, 16, 22.	8.8	687
3	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. Science, 2015, 347, 1010-1014.	12.6	517
4	An integrated expression atlas of miRNAs and their promoters in human and mouse. Nature Biotechnology, 2017, 35, 872-878.	17.5	456
5	Data integration in the era of omics: current and future challenges. BMC Systems Biology, 2014, 8, I1.	3.0	300
6	FANTOM5 CAGE profiles of human and mouse samples. Scientific Data, 2017, 4, 170112.	5.3	195
7	Update of the FANTOM web resource: expansion to provide additional transcriptome atlases. Nucleic Acids Research, 2019, 47, D752-D758.	14.5	172
8	Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. Nucleic Acids Research, 2017, 45, D737-D743.	14.5	116
9	Functional annotation of human long noncoding RNAs via molecular phenotyping. Genome Research, 2020, 30, 1060-1072.	5.5	109
10	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution. Nature Communications, 2019, 10, 360.	12.8	102
11	refTSS: A Reference Data Set for Human and Mouse Transcription Start Sites. Journal of Molecular Biology, 2019, 431, 2407-2422.	4.2	72
12	FANTOM5 CAGE profiles of human and mouse reprocessed for GRCh38 and GRCm38 genome assemblies. Scientific Data, 2017, 4, 170107.	5.3	68
13	FANTOM5 transcriptome catalog of cellular states based on Semantic MediaWiki. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw105.	3.0	64
14	FANTOM enters 20th year: expansion of transcriptomic atlases and functional annotation of non-coding RNAs. Nucleic Acids Research, 2021, 49, D892-D898.	14.5	57
15	SCPortalen: human and mouse single-cell centric database. Nucleic Acids Research, 2018, 46, D781-D787.	14.5	48
16	Incidence and risk factors for adalimumab and infliximab anti-drug antibodies in rheumatoid arthritis: A European retrospective multicohort analysis. Seminars in Arthritis and Rheumatism, 2019, 48, 967-975.	3.4	46
17	A robust machine learning framework to identify signatures for frailty: a nested case-control study in four aging European cohorts. GeroScience, 2021, 43, 1317-1329.	4.6	31
18	Linking FANTOM5 CAGE peaks to annotations with CAGEscan. Scientific Data, 2017, 4, 170147.	5.3	29

#	Article	IF	Citations
19	Comparative transcriptomics of primary cells in vertebrates. Genome Research, 2020, 30, 951-961.	5.5	29
20	Systems Medicine: from molecular features and models to the clinic in COPD. Journal of Translational Medicine, 2014, 12, S4.	4.4	23
21	The FANTOM5 Computation Ecosystem: Genomic Information Hub for Promoters and Active Enhancers. Methods in Molecular Biology, 2017, 1611, 199-217.	0.9	23
22	STATegra EMS: an Experiment Management System for complex next-generation omics experiments. BMC Systems Biology, 2014, 8, S9.	3.0	19
23	Laboratory biomarkers and frailty: presentation of the FRAILOMIC initiative. Clinical Chemistry and Laboratory Medicine, 2015, 53, e253-5.	2.3	17
24	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	12.8	11
25	Accelerating Translational Research by Clinically Driven Development of an Informatics Platform—A Case Study. PLoS ONE, 2014, 9, e104382.	2.5	10
26	Implementation of the CDC translational informatics platform - from genetic variants to the national Swedish Rheumatology Quality Register. Journal of Translational Medicine, 2013, 11, 85.	4.4	8
27	Pediatric systems medicine: evaluating needs and opportunities using congenital heart block as a case study. Pediatric Research, 2013, 73, 508-513.	2.3	8
28	Geospatial metadata extraction from product description document applying methods from ontology engineering. International Journal of Metadata, Semantics and Ontologies, 2010, 5, 321.	0.2	6
29	Monitoring transcription initiation activities in rat and dog. Scientific Data, 2017, 4, 170173.	5.3	6
30	Transcription start site profiling of 15 anatomical regions of the Macaca mulatta central nervous system. Scientific Data, 2017, 4, 170163.	5.3	4
31	SkewC: Identifying cells with skewed gene body coverage in single-cell RNA sequencing data. IScience, 2022, 25, 103777.	4.1	4
32	Genome Annotation. Methods in Molecular Biology, 2017, 1525, 107-121.	0.9	3
33	Inducing human retinal pigment epithelium-like cells from somatic tissue. Stem Cell Reports, 2022, 17, 289-306.	4.8	3
34	The choice of negative control antisense oligonucleotides dramatically impacts downstream analysis depending on the cellular background. BMC Genomic Data, 2021, 22, 33.	1.7	0