Tejaswini Mishra

List of Publications by Year
in descending order

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23 papers	4,671 citations	471509 17 h-index	642732 23 g-index
25 all docs	25 docs citations	25 times ranked	10157 citing authors

#	Article	IF	Citations
1	Real-time alerting system for COVID-19 and other stress events using wearable data. Nature Medicine, 2022, 28, 175-184.	30.7	69
2	NASA GeneLab RNA-seq consensus pipeline: Standardized processing of short-read RNA-seq data. IScience, 2021, 24, 102361.	4.1	20
3	Mammalian and Invertebrate Models as Complementary Tools for Gaining Mechanistic Insight on Muscle Responses to Spaceflight. International Journal of Molecular Sciences, 2021, 22, 9470.	4.1	12
4	Deep longitudinal multiomics profiling reveals two biological seasonal patterns in California. Nature Communications, 2020, 11, 4933.	12.8	36
5	Pre-symptomatic detection of COVID-19 from smartwatch data. Nature Biomedical Engineering, 2020, 4, 1208-1220.	22.5	304
6	Cell-free DNA (cfDNA) and Exosome Profiling from a Year-Long Human Spaceflight Reveals Circulating Biomarkers. IScience, 2020, 23, 101844.	4.1	31
7	Longitudinal multi-omics of hostâ€“microbe dynamics in prediabetes. Nature, 2019, 569, 663-671.	27.8	391
8	A longitudinal big data approach for precision health. Nature Medicine, 2019, 25, 792-804.	30.7	329
9	The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight. Science, 2019, 364, .	12.6	576
10	Distinct transcriptomic and exomic abnormalities within myelodysplastic syndrome marrow cells. Leukemia and Lymphoma, 2018, 59, 2952-2962.	1.3	16
11	Integrative Personal Omics Profiles during Periods of Weight Gain and Loss. Cell Systems, 2018, 6, 157-170.e8.	6.2	183
12	SBR-Blood: systems biology repository for hematopoietic cells. Nucleic Acids Research, 2016, 44, D925-D931.	14.5	4
13	Dynamics of GATA1 binding and expression response in a GATA1-induced erythroid differentiation system. Genomics Data, 2015, 4, 1-7.	1.3	10
14	A Dynamic Intron Retention Program in the Mammalian Megakaryocyte and Erythrocyte Lineages. Blood, 2015, 126, 2380-2380.	1.4	1
15	Divergent functions of hematopoietic transcription factors in lineage priming and differentiation during erythro-megakaryopoiesis. Genome Research, 2014, 24, 1932-1944.	5.5	88
16	Dynamic shifts in occupancy by TAL1 are guided by GATA factors and drive large-scale reprogramming of gene expression during hematopoiesis. Genome Research, 2014, 24, 1945-1962.	5.5	71
17	Principles of regulatory information conservation between mouse and human. Nature, 2014, 515, 371-375.	27.8	259
18	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	27.8	1,444

#	ARTICLE	IF	CITATIONS
19	Lineage and species-specific long noncoding RNAs during erythro-megakaryocytic development. Blood, 2014, 123, 1927-1937.	1.4	169
20	A Comprehensive and High-Resolution Genome-wide Response of p53 to Stress. Cell Reports, 2014, 8, 514-527.	6.4	56
21	Identification of Biologically Relevant Enhancers in Human Erythroid Cells. Journal of Biological Chemistry, 2013, 288, 8433-8444.	3.4	49
22	An encyclopedia of mouse DNA elements (Mouse ENCODE). Genome Biology, 2012, 13, 418.	9.6	410
23	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. Genome Research, 2011, 21, 1659-1671.	5.5	110