# Tejaswini Mishra

List of Publications by Year
in descending order

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

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364. | 27.8 | 1,444 |
| 2 | The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight. Science, 2019, 364, . | 12.6 | 576 |
| 3 | An encyclopedia of mouse DNA elements (Mouse ENCODE). Genome Biology, 2012, 13, 418. | 9.6 | 410 |
| 4 | Longitudinal multi-omics of host–microbe dynamics in prediabetes. Nature, 2019, 569, 663-671. | 27.8 | 391 |
| 5 | A longitudinal big data approach for precision health. Nature Medicine, 2019, 25, 792-804. | 30.7 | 329 |
| 6 | Pre-symptomatic detection of COVID-19 from smartwatch data. Nature Biomedical Engineering, 2020, 4, 1208-1220. | 22.5 | 304 |
| 7 | Principles of regulatory information conservation between mouse and human. Nature, 2014, 515, 371-375. | 27.8 | 259 |
| 8 | Integrative Personal Omics Profiles during Periods of Weight Gain and Loss. Cell Systems, 2018, 6, 157-170.e8. | 6.2 | 183 |
| 9 | Lineage and species-specific long noncoding RNAs during erythro-megakaryocytic development. Blood, 2014, 123, 1927-1937. | 1.4 | 169 |
| 10 | Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. Genome Research, 2011, 21, 1659-1671. | 5.5 | 110 |
| 11 | Divergent functions of hematopoietic transcription factors in lineage priming and differentiation during erythro-megakaryopoiesis. Genome Research, 2014, 24, 1932-1944. | 5.5 | 88 |
| 12 | 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 |
| 13 | Real-time alerting system for COVID-19 and other stress events using wearable data. Nature Medicine, 2022, 28, 175-184. | 30.7 | 69 |
| 14 | A Comprehensive and High-Resolution Genome-wide Response of p53 to Stress. Cell Reports, 2014, 8, 514-527. | 6.4 | 56 |
| 15 | Identification of Biologically Relevant Enhancers in Human Erythroid Cells. Journal of Biological Chemistry, 2013, 288, 8433-8444. | 3.4 | 49 |
| 16 | Deep longitudinal multiomics profiling reveals two biological seasonal patterns in California. Nature Communications, 2020, 11, 4933. | 12.8 | 36 |
| 17 | Cell-free DNA (cfDNA) and Exosome Profiling from a Year-Long Human Spaceflight Reveals Circulating Biomarkers. IScience, 2020, 23, 101844. | 4.1 | 31 |
| 18 | NASA GeneLab RNA-seq consensus pipeline: Standardized processing of short-read RNA-seq data. IScience, 2021, 24, 102361. | 4.1 | 20 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 19 | Distinct transcriptomic and exomic abnormalities within myelodysplastic syndrome marrow cells. Leukemia and Lymphoma, 2018, 59, 2952-2962. | 1.3 | 16 |
| 20 | 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 |
| 21 | Dynamics of GATA1 binding and expression response in a GATA1-induced erythroid differentiation system. Genomics Data, 2015, 4, 1-7. | 1.3 | 10 |
| 22 | SBR-Blood: systems biology repository for hematopoietic cells. Nucleic Acids Research, 2016, 44, D925-D931. | 14.5 | 4 |
| 23 | A Dynamic Intron Retention Program in the Mammalian Megakaryocyte and Erythrocyte Lineages. Blood, 2015, 126, 2380-2380. | 1.4 | 1 |