

Simone Ecker

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

2,191
citations

566801

15
h-index

839053

18
g-index

24
all docs

24
docs citations

24
times ranked

5953
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Genetic perturbation of PU.1 binding and chromatin looping at neutrophil enhancers associates with autoimmune disease. <i>Nature Communications</i> , 2021, 12, 2298. | 5.8 | 32 |
| 2 | Exaggerated IL-17A activity in human in vivo recall responses discriminates active tuberculosis from latent infection and cured disease. <i>Science Translational Medicine</i> , 2021, 13, . | 5.8 | 27 |
| 3 | Chemotherapy induces canalization of cell state in childhood B-cell precursor acute lymphoblastic leukemia. <i>Nature Cancer</i> , 2021, 2, 835-852. | 5.7 | 25 |
| 4 | GenomeChronicler: The Personal Genome Project UK Genomic Report Generator Pipeline. <i>Frontiers in Genetics</i> , 2020, 11, 518644. | 1.1 | 4 |
| 5 | The epigenetic clock: a molecular crystal ball for human aging?. <i>Aging</i> , 2019, 11, 833-835. | 1.4 | 19 |
| 6 | Epigenetic and Transcriptional Variability Shape Phenotypic Plasticity. <i>BioEssays</i> , 2018, 40, 1700148. | 1.2 | 71 |
| 7 | Personal Genome Project UK (PGP-UK): a research and citizen science hybrid project in support of personalized medicine. <i>BMC Medical Genomics</i> , 2018, 11, 108. | 0.7 | 34 |
| 8 | Increased DNA methylation variability in rheumatoid arthritis-discordant monozygotic twins. <i>Genome Medicine</i> , 2018, 10, 64. | 3.6 | 71 |
| 9 | Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. <i>Genome Biology</i> , 2017, 18, 18. | 3.8 | 97 |
| 10 | Epigenetic variation taking center stage in immunological research. <i>Epigenomics</i> , 2017, 9, 375-378. | 1.0 | 4 |
| 11 | Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. <i>Nature Communications</i> , 2016, 7, 13555. | 5.8 | 142 |
| 12 | Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. <i>Cell</i> , 2016, 167, 1398-1414.e24. | 13.5 | 573 |
| 13 | Whole-genome fingerprint of the DNA methylome during human B cell differentiation. <i>Nature Genetics</i> , 2015, 47, 746-756. | 9.4 | 278 |
| 14 | Higher gene expression variability in the more aggressive subtype of chronic lymphocytic leukemia. <i>Genome Medicine</i> , 2015, 7, 8. | 3.6 | 57 |
| 15 | Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. <i>Genome Research</i> , 2014, 24, 212-226. | 2.4 | 175 |
| 16 | The synthetic glucocorticoids prednisolone and dexamethasone regulate the same genes in acute lymphoblastic leukemia cells. <i>BMC Genomics</i> , 2014, 15, 662. | 1.2 | 20 |
| 17 | Characterization of Transcriptional Changes in ERG Rearrangement-Positive Prostate Cancer Identifies the Regulation of Metabolic Sensors Such as Neuropeptide Y. <i>PLoS ONE</i> , 2013, 8, e55207. | 1.1 | 32 |
| 18 | Epigenomic analysis detects widespread gene-body DNA hypomethylation in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2012, 44, 1236-1242. | 9.4 | 525 |