

Avik Datta

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3071334/publications.pdf>

Version: 2024-02-01

14
papers

3,387
citations

623734

14
h-index

996975

15
g-index

15
all docs

15
docs citations

15
times ranked

9101
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.	12.8	32
2	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. <i>Cell Reports</i> , 2018, 24, 2784-2794.	6.4	104
3	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. <i>Nature Medicine</i> , 2018, 24, 868-880.	30.7	157
4	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. <i>Genome Biology</i> , 2017, 18, 50.	8.8	71
5	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. <i>Nature Communications</i> , 2016, 7, 13555.	12.8	142
6	Decoding the DNA Methylome of Mantle Cell Lymphoma in the Light of the Entire B Cell Lineage. <i>Cancer Cell</i> , 2016, 30, 806-821.	16.8	103
7	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. <i>Cell</i> , 2016, 167, 1369-1384.e19.	28.9	863
8	Distinct Trends of DNA Methylation Patterning in the Innate and Adaptive Immune Systems. <i>Cell Reports</i> , 2016, 17, 2101-2111.	6.4	54
9	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. <i>Cell</i> , 2016, 167, 1398-1414.e24.	28.9	573
10	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. <i>Nature Genetics</i> , 2015, 47, 746-756.	21.4	278
11	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. <i>Genome Research</i> , 2015, 25, 478-487.	5.5	118
12	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	19.0	789
13	ANVAYA: A WORKFLOWS ENVIRONMENT FOR AUTOMATED GENOME ANALYSIS. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1250006.	0.8	2
14	Genome Sequences of <i>Salmonella enterica</i> Serovar Typhimurium, Choleraesuis, Dublin, and Gallinarum Strains of Well- Defined Virulence in Food-Producing Animals. <i>Journal of Bacteriology</i> , 2011, 193, 3162-3163.	2.2	61