

Gert Hulselmans

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

6,784
citations

516710

16
h-index

752698

20
g-index

31
all docs

31
docs citations

31
times ranked

11557
citing authors

#	ARTICLE	IF	CITATIONS
1	Decoding gene regulation in the fly brain. <i>Nature</i> , 2022, 601, 630-636.	27.8	102
2	Interpretation of allele-specific chromatin accessibility using cell state-aware deep learning. <i>Genome Research</i> , 2021, 31, 1082-1096.	5.5	34
3	Analysis of long and short enhancers in melanoma cell states. <i>ELife</i> , 2021, 10, .	6.0	18
4	Cross-species analysis of enhancer logic using deep learning. <i>Genome Research</i> , 2020, 30, 1815-1834.	5.5	65
5	Robust gene expression programs underlie recurrent cell states and phenotype switching in melanoma. <i>Nature Cell Biology</i> , 2020, 22, 986-998.	10.3	148
6	A scalable SCENIC workflow for single-cell gene regulatory network analysis. <i>Nature Protocols</i> , 2020, 15, 2247-2276.	12.0	553
7	Identification of genomic enhancers through spatial integration of single-cell transcriptomics and epigenomics. <i>Molecular Systems Biology</i> , 2020, 16, e9438.	7.2	60
8	cisTopic: cis-regulatory topic modeling on single-cell ATAC-seq data. <i>Nature Methods</i> , 2019, 16, 397-400.	19.0	322
9	The transcription factor Grainy head primes epithelial enhancers for spatiotemporal activation by displacing nucleosomes. <i>Nature Genetics</i> , 2018, 50, 1011-1020.	21.4	122
10	A Single-Cell Transcriptome Atlas of the Aging <i>Drosophila</i> Brain. <i>Cell</i> , 2018, 174, 982-998.e20.	28.9	616
11	SCENIC: single-cell regulatory network inference and clustering. <i>Nature Methods</i> , 2017, 14, 1083-1086.	19.0	3,086
12	Conserved Transcription Factors Steer Growth-Related Genomic Programs in <i>Daphnia</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 1821-1842.	2.5	13
13	Multiplex enhancer-reporter assays uncover unsophisticated TP53 enhancer logic. <i>Genome Research</i> , 2016, 26, 882-895.	5.5	70
14	CD45 antigen negativity in T-lineage ALL correlates with <i>PTPRC</i> mutation and sensitivity to a selective JAK inhibitor. <i>British Journal of Haematology</i> , 2015, 171, 884-887.	2.5	4
15	Decoding the regulatory landscape of melanoma reveals TEADS as regulators of the invasive cell state. <i>Nature Communications</i> , 2015, 6, 6683.	12.8	365
16	Identification of Lineage-Specific Cis-Regulatory Modules Associated with Variation in Transcription Factor Binding and Chromatin Activity Using Ornstein-Uhlenbeck Models. <i>Molecular Biology and Evolution</i> , 2015, 32, 2441-2455.	8.9	11
17	i-cisTarget 2015 update: generalized cis-regulatory enrichment analysis in human, mouse and fly. <i>Nucleic Acids Research</i> , 2015, 43, W57-W64.	14.5	169
18	Mapping Gene Regulatory Networks in <i>Drosophila</i> Eye Development by Large-Scale Transcriptome Perturbations and Motif Inference. <i>Cell Reports</i> , 2014, 9, 2290-2303.	6.4	85

#	ARTICLE	IF	CITATIONS
19	iRegulon: From a Gene List to a Gene Regulatory Network Using Large Motif and Track Collections. PLoS Computational Biology, 2014, 10, e1003731.	3.2	787
20	Comprehensive Analysis of Transcriptome Variation Uncovers Known and Novel Driver Events in T-Cell Acute Lymphoblastic Leukemia. PLoS Genetics, 2013, 9, e1003997.	3.5	110
21	Whole Transcriptome Sequencing In Refractory T-Cell Acute Lymphoblastic Leukemia. Blood, 2013, 122, 350-350.	1.4	0