

Jelena M Telenius

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

1,744
citations

516710

16
h-index

677142

22
g-index

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34
docs citations

34
times ranked

2645
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamic Runx1 chromatin boundaries affect gene expression in hematopoietic development. <i>Nature Communications</i> , 2022, 13, 773.	12.8	10
2	The chromatin remodeller ATRX facilitates diverse nuclear processes, in a stochastic manner, in both heterochromatin and euchromatin. <i>Nature Communications</i> , 2022, 13, .	12.8	20
3	High-resolution targeted 3C interrogation of cis-regulatory element organization at genome-wide scale. <i>Nature Communications</i> , 2021, 12, 531.	12.8	32
4	Enhancers predominantly regulate gene expression during differentiation via transcription initiation. <i>Molecular Cell</i> , 2021, 81, 983-997.e7.	9.7	27
5	A gain-of-function single nucleotide variant creates a new promoter which acts as an orientation-dependent enhancer-blocker. <i>Nature Communications</i> , 2021, 12, 3806.	12.8	18
6	Reactivation of a developmentally silenced embryonic globin gene. <i>Nature Communications</i> , 2021, 12, 4439.	12.8	19
7	DeepC: predicting 3D genome folding using megabase-scale transfer learning. <i>Nature Methods</i> , 2020, 17, 1118-1124.	19.0	109
8	Dynamics of the 4D genome during in vivo lineage specification and differentiation. <i>Nature Communications</i> , 2020, 11, 2722.	12.8	79
9	A Dynamic Folded Hairpin Conformation Is Associated with $\hat{\iota}$ -Globin Activation in Erythroid Cells. <i>Cell Reports</i> , 2020, 30, 2125-2135.e5.	6.4	38
10	DOT1L inhibition reveals a distinct subset of enhancers dependent on H3K79 methylation. <i>Nature Communications</i> , 2019, 10, 2803.	12.8	99
11	Reconstruction of the Global Neural Crest Gene Regulatory Network In Vivo. <i>Developmental Cell</i> , 2019, 51, 255-276.e7.	7.0	108
12	A revised model for promoter competition based on multi-way chromatin interactions at the $\hat{\iota}$ -globin locus. <i>Nature Communications</i> , 2019, 10, 5412.	12.8	60
13	High-Throughput Genotyping of CRISPR/Cas Edited Cells in 96-Well Plates. <i>Methods and Protocols</i> , 2018, 1, 29.	2.0	6
14	A tissue-specific self-interacting chromatin domain forms independently of enhancer-promoter interactions. <i>Nature Communications</i> , 2018, 9, 3849.	12.8	62
15	Single-allele chromatin interactions identify regulatory hubs in dynamic compartmentalized domains. <i>Nature Genetics</i> , 2018, 50, 1744-1751.	21.4	150
16	How to Tackle Challenging CHIP-Seq, with Long-Range Cross-Linking, Using ATRX as an Example. <i>Methods in Molecular Biology</i> , 2018, 1832, 105-130.	0.9	7
17	Functional characterisation of cis-regulatory elements governing dynamic <i>Eomes</i> expression in the early mouse embryo. <i>Development (Cambridge)</i> , 2017, 144, 1249-1260.	2.5	32
18	DNA methylation of intragenic CpG islands depends on their transcriptional activity during differentiation and disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7526-E7535.	7.1	125

#	ARTICLE	IF	CITATIONS
19	Sasquatch: predicting the impact of regulatory SNPs on transcription factor binding from cell- and tissue-specific DNase footprints. <i>Genome Research</i> , 2017, 27, 1730-1742.	5.5	33
20	Editing an $\hat{\epsilon}$ -globin enhancer in primary human hematopoietic stem cells as a treatment for $\hat{\epsilon}^2$ -thalassemia. <i>Nature Communications</i> , 2017, 8, 424.	12.8	85
21	Genetic dissection of the $\hat{\epsilon}$ -globin super-enhancer in vivo. <i>Nature Genetics</i> , 2016, 48, 895-903.	21.4	308
22	Multiplexed analysis of chromosome conformation at vastly improved sensitivity. <i>Nature Methods</i> , 2016, 13, 74-80.	19.0	225