Jelena M Telenius

List of Publications by Year
in descending order

22 papers	1,744 citations	516710 16 h-index	677142 22 g-index
34 all docs	34 docs citations	34 times ranked	2645 citing authors

#	Article	IF	Citations
1	Genetic dissection of the α-globin super-enhancer in vivo. Nature Genetics, 2016, 48, 895-903.	21.4	308
2	Multiplexed analysis of chromosome conformation at vastly improved sensitivity. Nature Methods, 2016, 13, 74-80.	19.0	225
3	Single-allele chromatin interactions identify regulatory hubs in dynamic compartmentalized domains. Nature Genetics, 2018, 50, 1744-1751.	21.4	150
4	DNA methylation of intragenic CpG islands depends on their transcriptional activity during differentiation and disease. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7526-E7535.	7.1	125
5	DeepC: predicting 3D genome folding using megabase-scale transfer learning. Nature Methods, 2020, 17, 1118-1124.	19.0	109
6	Reconstruction of the Global Neural Crest Gene Regulatory Network InÂVivo. Developmental Cell, 2019, 51, 255-276.e7.	7.0	108
7	DOT1L inhibition reveals a distinct subset of enhancers dependent on H3K79 methylation. Nature Communications, 2019, 10, 2803.	12.8	99
8	Editing an α-globin enhancer in primary human hematopoietic stem cells as a treatment for β²-thalassemia. Nature Communications, 2017, 8, 424.	12.8	85
9	Dynamics of the 4D genome during in vivo lineage specification and differentiation. Nature Communications, 2020, 11, 2722.	12.8	79
10	A tissue-specific self-interacting chromatin domain forms independently of enhancer-promoter interactions. Nature Communications, 2018, 9, 3849.	12.8	62
11	A revised model for promoter competition based on multi-way chromatin interactions at the α-globin locus. Nature Communications, 2019, 10, 5412.	12.8	60
12	A Dynamic Folded Hairpin Conformation Is Associated with α-Globin Activation in Erythroid Cells. Cell Reports, 2020, 30, 2125-2135.e5.	6.4	38
13	Sasquatch: predicting the impact of regulatory SNPs on transcription factor binding from cell- and tissue-specific DNase footprints. Genome Research, 2017, 27, 1730-1742.	5.5	33
14	Functional characterisation of cis-regulatory elements governing dynamic *Eomes* expression in the early mouse embryo. Development (Cambridge), 2017, 144, 1249-1260.	2.5	32
15	High-resolution targeted 3C interrogation of cis-regulatory element organization at genome-wide scale. Nature Communications, 2021, 12, 531.	12.8	32
16	Enhancers predominantly regulate gene expression during differentiation via transcription initiation. Molecular Cell, 2021, 81, 983-997.e7.	9.7	27
17	The chromatin remodeller ATRX facilitates diverse nuclear processes, in a stochastic manner, in both heterochromatin and euchromatin. Nature Communications, 2022, 13, .	12.8	20
18	Reactivation of a developmentally silenced embryonic globin gene. Nature Communications, 2021, 12, 4439.	12.8	19

#	Article	IF	Citations
19	A gain-of-function single nucleotide variant creates a new promoter which acts as an orientation-dependent enhancer-blocker. Nature Communications, 2021, 12, 3806.	12.8	18
20	Dynamic Runx1 chromatin boundaries affect gene expression in hematopoietic development. Nature Communications, 2022, 13, 773.	12.8	10
21	How to Tackle Challenging ChIP-Seq, with Long-Range Cross-Linking, Using ATRX as an Example. Methods in Molecular Biology, 2018, 1832, 105-130.	0.9	7
22	High-Throughput Genotyping of CRISPR/Cas Edited Cells in 96-Well Plates. Methods and Protocols, 2018, 1, 29.	2.0	6