

# Mikhail Spivakov

## List of Publications by Year in descending order

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Version: 2024-02-01

44  
papers

7,760  
citations

136950

32  
h-index

243625

44  
g-index

60  
all docs

60  
docs citations

60  
times ranked

13902  
citing authors

#	ARTICLE	IF	CITATIONS
1	OA30â€¦Identification of causal genes and mechanisms by which genetic variation mediates juvenile idiopathic arthritis susceptibility using functional genomics and CRISPR-Cas9. <i>Rheumatology</i> , 2022, 61, .	1.9	0
2	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
3	TOP1 inhibition therapy protects against SARS-CoV-2-induced lethal inflammation. <i>Cell</i> , 2021, 184, 2618-2632.e17.	28.9	80
4	Transcriptional enhancers and their communication with gene promoters. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 6453-6485.	5.4	25
5	Detecting chromosomal interactions in Capture Hi-C data with CHiCAGO and companion tools. <i>Nature Protocols</i> , 2021, 16, 4144-4176.	12.0	21
6	Prioritisation of Candidate Genes Underpinning COVID-19 Host Genetic Traits Based on High-Resolution 3D Chromosomal Topology. <i>Frontiers in Genetics</i> , 2021, 12, 745672.	2.3	5
7	Cohesin-Dependent and -Independent Mechanisms Mediate Chromosomal Contacts between Promoters and Enhancers. <i>Cell Reports</i> , 2020, 32, 107929.	6.4	106
8	Silencers in the spotlight. <i>Nature Genetics</i> , 2020, 52, 244-245.	21.4	9
9	Functional effects of variation in transcription factor binding highlight long-range gene regulation by epromoters. <i>Nucleic Acids Research</i> , 2020, 48, 2866-2879.	14.5	15
10	Chicdiff: a computational pipeline for detecting differential chromosomal interactions in Capture Hi-C data. <i>Bioinformatics</i> , 2019, 35, 4764-4766.	4.1	20
11	Disease-relevant transcriptional signatures identified in individual smooth muscle cells from healthy mouse vessels. <i>Nature Communications</i> , 2018, 9, 4567.	12.8	219
12	Genome organization and chromatin analysis identify transcriptional downregulation of insulin-like growth factor signaling as a hallmark of aging in developing B cells. <i>Genome Biology</i> , 2018, 19, 126.	8.8	29
13	Promoter interactome of human embryonic stem cell-derived cardiomyocytes connects GWAS regions to cardiac gene networks. <i>Nature Communications</i> , 2018, 9, 2526.	12.8	48
14	Dynamic Rewiring of Promoter-Anchored Chromatin Loops during Adipocyte Differentiation. <i>Molecular Cell</i> , 2017, 66, 420-435.e5.	9.7	188
15	Lineage-specific dynamic and pre-established enhancerâ€¦promoter contacts cooperate in terminal differentiation. <i>Nature Genetics</i> , 2017, 49, 1522-1528.	21.4	255
16	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. <i>Nature Communications</i> , 2017, 8, 16058.	12.8	50
17	207â€¦Vascular smooth muscle cell heterogeneity and plasticity. <i>Heart</i> , 2017, 103, A138.2-A138.	2.9	0
18	Chromosome contacts in activated T cells identify autoimmune disease candidate genes. <i>Genome Biology</i> , 2017, 18, 165.	8.8	68

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19	Global reorganisation of cis-regulatory units upon lineage commitment of human embryonic stem cells. <i>ELife</i> , 2017, 6, .	6.0	130
20	Integrated genome-scale analysis of the transcriptional regulatory landscape in a blood stem/progenitor cell model. <i>Blood</i> , 2016, 127, e12-e23.	1.4	49
21	Two Mutually Exclusive Local Chromatin States Drive Efficient V(D)J Recombination. <i>Cell Reports</i> , 2016, 15, 2475-2487.	6.4	78
22	Integrating epigenomic data and 3D genomic structure with a new measure of chromatin assortativity. <i>Genome Biology</i> , 2016, 17, 152.	8.8	46
23	CHiCAGO: robust detection of DNA looping interactions in Capture Hi-C data. <i>Genome Biology</i> , 2016, 17, 127.	8.8	344
24	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
25	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	28.9	404
26	Defining cell type with chromatin profiling. <i>Nature Biotechnology</i> , 2016, 34, 1126-1128.	17.5	4
27	A novel phosphate-starvation response in fission yeast requires the endocytic function of Myosin I. <i>Journal of Cell Science</i> , 2015, 128, 3707-13.	2.0	2
28	Dynamic Reorganization of Extremely Long-Range Promoter-Promoter Interactions between Two States of Pluripotency. <i>Cell Stem Cell</i> , 2015, 17, 748-757.	11.1	179
29	Spatial separation of Xist RNA and polycomb proteins revealed by superresolution microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2235-2240.	7.1	91
30	Genomic and Phenotypic Characterization of a Wild Medaka Population: Towards the Establishment of an Isogenic Population Genetic Resource in Fish. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 433-445.	1.8	54
31	Spurious transcription factor binding: Non-functional or genetically redundant?. <i>BioEssays</i> , 2014, 36, 798-806.	2.5	80
32	A Comparison of Peak Callers Used for DNase-Seq Data. <i>PLoS ONE</i> , 2014, 9, e96303.	2.5	71
33	Genome-wide identification of Ikaros targets elucidates its contribution to mouse B-cell lineage specification and pre-B <sup>1</sup> cell differentiation. <i>Blood</i> , 2013, 121, 1769-1782.	1.4	102
34	Analysis of variation at transcription factor binding sites in <i>Drosophila</i> and humans. <i>Genome Biology</i> , 2012, 13, R49.	9.6	83
35	A Transcription Factor Collective Defines Cardiac Cell Fate and Reflects Lineage History. <i>Cell</i> , 2012, 148, 473-486.	28.9	239
36	Jarid2 is a PRC2 component in embryonic stem cells required for multi-lineage differentiation and recruitment of PRC1 and RNA Polymerase II to developmental regulators. <i>Nature Cell Biology</i> , 2010, 12, 618-624.	10.3	274

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37	Cohesins Functionally Associate with CTCF on Mammalian Chromosome Arms. <i>Cell</i> , 2008, 132, 422-433.	28.9	800
38	T cell receptor signaling controls Foxp3 expression via PI3K, Akt, and mTOR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 7797-7802.	7.1	747
39	Distinct Promoters Mediate the Regulation of Ebf1 Gene Expression by Interleukin-7 and Pax5. <i>Molecular and Cellular Biology</i> , 2007, 27, 579-594.	2.3	150
40	The impact of chromatin modifiers on the timing of locus replication in mouse embryonic stem cells. <i>Genome Biology</i> , 2007, 8, R169.	9.6	68
41	Epigenetic signatures of stem-cell identity. <i>Nature Reviews Genetics</i> , 2007, 8, 263-271.	16.3	352
42	Chromatin signatures of pluripotent cell lines. <i>Nature Cell Biology</i> , 2006, 8, 532-538.	10.3	1,213
43	A Dynamic Switch in the Replication Timing of Key Regulator Genes in Embryonic Stem Cells upon Neural Induction. <i>Cell Cycle</i> , 2004, 3, 1619-1624.	2.6	77
44	A dynamic switch in the replication timing of key regulator genes in embryonic stem cells upon neural induction. <i>Cell Cycle</i> , 2004, 3, 1645-50.	2.6	46