

Michael Y Tolstorukov

List of Publications by Year in descending order

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Version: 2024-02-01

12
papers

2,055
citations

840776

11
h-index

1199594

12
g-index

12
all docs

12
docs citations

12
times ranked

4624
citing authors

#	ARTICLE	IF	CITATIONS
1	Design and analysis of ChIP-seq experiments for DNA-binding proteins. <i>Nature Biotechnology</i> , 2008, 26, 1351-1359.	17.5	825
2	Comparative analysis of metazoan chromatin organization. <i>Nature</i> , 2014, 512, 449-452.	27.8	363
3	Histone demethylase KDM6A directly senses oxygen to control chromatin and cell fate. <i>Science</i> , 2019, 363, 1217-1222.	12.6	281
4	Swi/Snf chromatin remodeling/tumor suppressor complex establishes nucleosome occupancy at target promoters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10165-10170.	7.1	174
5	Histone Variant H2A.Bbd Is Associated with Active Transcription and mRNA Processing in Human Cells. <i>Molecular Cell</i> , 2012, 47, 596-607.	9.7	92
6	Widespread changes in nucleosome accessibility without changes in nucleosome occupancy during a rapid transcriptional induction. <i>Genes and Development</i> , 2017, 31, 451-462.	5.9	90
7	Comparative analysis of H2A.Z nucleosome organization in the human and yeast genomes. <i>Genome Research</i> , 2009, 19, 967-977.	5.5	88
8	Impact of chromatin structure on sequence variability in the human genome. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 510-515.	8.2	66
9	Chromatin restriction by the nucleosome remodeler Mi-2 β and functional interplay with lineage-specific transcription regulators control B-cell differentiation. <i>Genes and Development</i> , 2019, 33, 763-781.	5.9	26
10	Activation of Tumor-Cell STING Primes NK-Cell Therapy. <i>Cancer Immunology Research</i> , 2022, 10, 947-961.	3.4	22
11	Plasticity in the Absence of NOTCH Uncovers a RUNX2-Dependent Pathway in Small Cell Lung Cancer. <i>Cancer Research</i> , 2022, 82, 248-263.	0.9	17
12	Analysis of the primary structure of chromatin with next-generation sequencing. <i>Epigenomics</i> , 2010, 2, 187-197.	2.1	11