

Ilya E Vorontsov

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

3,608
citations

687363

13
h-index

642732

23
g-index

27
all docs

27
docs citations

27
times ranked

9183
citing authors

#	ARTICLE	IF	CITATIONS
1	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	27.8	1,838
2	HOCOMOCO: towards a complete collection of transcription factor binding models for human and mouse via large-scale ChIP-Seq analysis. <i>Nucleic Acids Research</i> , 2018, 46, D252-D259.	14.5	660
3	EpiFactors: a comprehensive database of human epigenetic factors and complexes. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav067.	3.0	226
4	HOCOMOCO: expansion and enhancement of the collection of transcription factor binding sites models. <i>Nucleic Acids Research</i> , 2016, 44, D116-D125.	14.5	215
5	HOCOMOCO: a comprehensive collection of human transcription factor binding sites models. <i>Nucleic Acids Research</i> , 2013, 41, D195-D202.	14.5	206
6	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	5.5	109
7	FROM BINDING MOTIFS IN CHIP-SEQ DATA TO IMPROVED MODELS OF TRANSCRIPTION FACTOR BINDING SITES. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1340004.	0.8	58
8	Landscape of allele-specific transcription factor binding in the human genome. <i>Nature Communications</i> , 2021, 12, 2751.	12.8	55
9	Jaccard index based similarity measure to compare transcription factor binding site models. <i>Algorithms for Molecular Biology</i> , 2013, 8, 23.	1.2	53
10	Insights gained from a comprehensive all-against-all transcription factor binding motif benchmarking study. <i>Genome Biology</i> , 2020, 21, 114.	8.8	39
11	PERFECTOS-APE - Predicting Regulatory Functional Effect of SNPs by Approximate P-value Estimation. , 2015, , .		28
12	Early B-cell factor 1 (EBF1) is critical for transcriptional control of SLAMF1 gene in human B cells. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 1259-1268.	1.9	20
13	Multiple single nucleotide polymorphisms in the first intron of the IL2RA gene affect transcription factor binding and enhancer activity. <i>Gene</i> , 2017, 602, 50-56.	2.2	19
14	Genome-wide map of human and mouse transcription factor binding sites aggregated from ChIP-Seq data. <i>BMC Research Notes</i> , 2018, 11, 756.	1.4	19
15	Negative selection maintains transcription factor binding motifs in human cancer. <i>BMC Genomics</i> , 2016, 17, 395.	2.8	16
16	The single nucleotide variant rs12722489 determines differential estrogen receptor binding and enhancer properties of an IL2RA intronic region. <i>PLoS ONE</i> , 2017, 12, e0172681.	2.5	10
17	In silico motif analysis suggests an interplay of transcriptional and translational control in mTOR response. <i>Translation</i> , 2013, 1, 18-24.	2.9	9
18	ANANASTRA: annotation and enrichment analysis of allele-specific transcription factor binding at SNPs. <i>Nucleic Acids Research</i> , 2022, 50, W51-W56.	14.5	7

#	ARTICLE	IF	CITATIONS
19	Enhanced C/EBP binding to GÂ-T mismatches facilitates fixation of CpG mutations in cancer and adult stem cells. Cell Reports, 2021, 35, 109221.	6.4	5
20	What Do Neighbors Tell About You: The Local Context of Cis-Regulatory Modules Complicates Prediction of Regulatory Variants. Frontiers in Genetics, 2019, 10, 1078.	2.3	3
21	A holistic view of mouse enhancer architectures reveals analogous pleiotropic effects and correlation with human disease. BMC Genomics, 2020, 21, 754.	2.8	3
22	Assessing Ribosome Distribution Along Transcripts with Polarity Scores and Regression Slope Estimates. Methods in Molecular Biology, 2021, 2252, 269-294.	0.9	1
23	Abstract 5206: Role of super-enhancers in HPV+ head and neck squamous cell carcinoma. , 2019, , .		0