

Yulia Medvedeva

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

5,893
citations

279798

23
h-index

289244

40
g-index

48
all docs

48
docs citations

48
times ranked

13370
citing authors

#	ARTICLE	IF	CITATIONS
1	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	27.8	1,838
2	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204.	27.8	898
3	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
4	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878.	17.5	456
5	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
6	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
7	Effects of cytosine methylation on transcription factor binding sites. <i>BMC Genomics</i> , 2014, 15, 119.	2.8	214
8	HOCOMOCO: a comprehensive collection of human transcription factor binding sites models. <i>Nucleic Acids Research</i> , 2013, 41, D195-D202.	14.5	206
9	Exploring Massive, Genome Scale Datasets with the GenometriCorr Package. <i>PLoS Computational Biology</i> , 2012, 8, e1002529.	3.2	167
10	Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. <i>Nucleic Acids Research</i> , 2017, 45, D737-D743.	14.5	116
11	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	5.5	109
12	Genome-Wide DNA Methylation Profiling Reveals Epigenetic Adaptation of Stickleback to Marine and Freshwater Conditions. <i>Molecular Biology and Evolution</i> , 2017, 34, 2203-2213.	8.9	105
13	RADICL-seq identifies general and cell type-specific principles of genome-wide RNA-chromatin interactions. <i>Nature Communications</i> , 2020, 11, 1018.	12.8	98
14	Promoter Analysis Reveals Globally Differential Regulation of Human Long Non-Coding RNA and Protein-Coding Genes. <i>PLoS ONE</i> , 2014, 9, e109443.	2.5	72
15	Intergenic, gene terminal, and intragenic CpG islands in the human genome. <i>BMC Genomics</i> , 2010, 11, 48.	2.8	67
16	Insights into the Transcriptional Architecture of Behavioral Plasticity in the Honey Bee <i>Apis mellifera</i> . <i>Scientific Reports</i> , 2015, 5, 11136.	3.3	59
17	Prediction of lncRNAs and their interactions with nucleic acids: benchmarking bioinformatics tools. <i>Briefings in Bioinformatics</i> , 2019, 20, 551-564.	6.5	47
18	CpG traffic lights are markers of regulatory regions in human genome. <i>BMC Genomics</i> , 2019, 20, 102.	2.8	43

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19	Differential Targeting of c-Maf, Bach-1, and Elmo-1 by microRNA-143 and microRNA-365 Promotes the Intracellular Growth of Mycobacterium tuberculosis in Alternatively IL-4/IL-13 Activated Macrophages. <i>Frontiers in Immunology</i> , 2019, 10, 421.	4.8	37
20	A novel method for improved accuracy of transcription factor binding site prediction. <i>Nucleic Acids Research</i> , 2018, 46, e72-e72.	14.5	35
21	Perinatal exposure to low dose 2,2,4,4-tetrabromodiphenyl ether (BDE-47) alters sperm DNA methylation in adult rats. <i>Reproductive Toxicology</i> , 2018, 75, 136-143.	2.9	33
22	Regional differences in gene expression and promoter usage in aged human brains. <i>Neurobiology of Aging</i> , 2013, 34, 1825-1836.	3.1	30
23	Peripubertal serum dioxin concentrations and subsequent sperm methylome profiles of young Russian adults. <i>Reproductive Toxicology</i> , 2018, 78, 40-49.	2.9	28
24	Heavy and light chain interrelations of MS-associated immunoglobulins probed by deep sequencing and rational variation. <i>Molecular Immunology</i> , 2014, 62, 305-314.	2.2	23
25	Practical Guidance in Genome-Wide RNA:DNA Triple Helix Prediction. <i>International Journal of Molecular Sciences</i> , 2020, 21, 830.	4.1	16
26	Preservation of methylated CpG dinucleotides in human CpG islands. <i>Biology Direct</i> , 2016, 11, 11.	4.6	15
27	Computational analysis of sense-antisense chimeric transcripts reveals their potential regulatory features and the landscape of expression in human cells. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab074.	3.2	12
28	Mutations and Binding Sites of Human Transcription Factors. <i>Frontiers in Genetics</i> , 2012, 3, 100.	2.3	11
29	ASSA: Fast identification of statistically significant interactions between long RNAs. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1840001.	0.8	10
30	Direct Interactions with Nascent Transcripts Is Potentially a Common Targeting Mechanism of Long Non-Coding RNAs. <i>Genes</i> , 2020, 11, 1483.	2.4	7
31	Integration of transcription coregulator complexes with sequence-specific DNA-binding factor interactomes. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194749.	1.9	6
32	Purine-rich low complexity regions are potential RNA binding hubs in the human genome. <i>F1000Research</i> , 2018, 7, 76.	1.6	5
33	DNA sequence features in the establishing of H3K27ac. <i>F1000Research</i> , 2018, 7, 165.	1.6	4
34	The gene regulation knowledge commons: the action area of GREEKC. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2022, 1865, 194768.	1.9	3
35	HiMoRNA: A Comprehensive Database of Human lncRNAs Involved in Genome-Wide Epigenetic Regulation. <i>Non-coding RNA</i> , 2022, 8, 18.	2.6	3
36	Genome-wide regulation of CpG methylation by ecCEBP1 in acute myeloid leukemia. <i>F1000Research</i> , 2021, 10, 204.	1.6	2

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37	Identification of self-consistent modulons from bacterial microarray expression data with the help of structured regulon gene sets. Journal of Biomolecular Structure and Dynamics, 2013, 31, 115-124.	3.5	1
38	Genome-wide regulation of CpG methylation by ecCEBPÎ± in acute myeloid leukemia. F1000Research, 2021, 10, 204.	1.6	1
39	MIREyA: a computational approach to detect miRNA-directed gene activation. F1000Research, 2021, 10, 249.	1.6	1
40	Improving prediction of core transcription factors for cell reprogramming and transdifferentiation. F1000Research, 0, 11, 38.	1.6	1
41	Experimental Design and Bioinformatic Analysis of DNA Methylation Data. Methods in Molecular Biology, 2018, 1766, 175-194.	0.9	0
42	A Catalogus Immune Muris of the mouse immune responses to diverse pathogens. Cell Death and Disease, 2021, 12, 798.	6.3	0
43	Methylation Patterns in Patients with High-Risk Myelodysplastic Syndromes and Secondary Acute Myeloid Leukemia Treated with Azacitidine (high-risk MDS 2009 protocol from CETLAM Group). Blood, 2015, 126, 1682-1682.	1.4	0