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List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

4,513
citations

516710

16
h-index

330143

37
g-index

44
all docs

44
docs citations

44
times ranked

8034
citing authors

#	ARTICLE	IF	CITATIONS
1	Databases on transcriptional regulation: TRANSFAC, TRRD and COMPEL. <i>Nucleic Acids Research</i> , 1998, 26, 362-367.	14.5	1,345
2	The Systems Biology Graphical Notation. <i>Nature Biotechnology</i> , 2009, 27, 735-741.	17.5	828
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	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	Reproducible computational biology experiments with SED-ML - The Simulation Experiment Description Markup Language. <i>BMC Systems Biology</i> , 2011, 5, 198.	3.0	211
6	GTRD: a database of transcription factor binding sites identified by ChIP-seq experiments. <i>Nucleic Acids Research</i> , 2017, 45, D61-D67.	14.5	206
7	GTRD: a database on gene transcription regulation – 2019 update. <i>Nucleic Acids Research</i> , 2019, 47, D100-D105.	14.5	181
8	<sc>SBML</sc> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	7.2	178
9	GTRD: an integrated view of transcription regulation. <i>Nucleic Acids Research</i> , 2021, 49, D104-D111.	14.5	137
10	MicroRNA Expression Profile in Human Macrophages in Response to <i>Leishmania major</i> Infection. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2478.	3.0	125
11	GeneNet: a gene network database and its automated visualization. <i>Bioinformatics</i> , 1998, 14, 529-537.	4.1	65
12	Landscape of allele-specific transcription factor binding in the human genome. <i>Nature Communications</i> , 2021, 12, 2751.	12.8	55
13	Transcription Regulatory Regions Database (TRRD): its status in 2000. <i>Nucleic Acids Research</i> , 2000, 28, 298-301.	14.5	47
14	Walking pathways with positive feedback loops reveal DNA methylation biomarkers of colorectal cancer. <i>BMC Bioinformatics</i> , 2019, 20, 119.	2.6	37
15	BioUML: an integrated environment for systems biology and collaborative analysis of biomedical data. <i>Nucleic Acids Research</i> , 2019, 47, W225-W233.	14.5	32
16	Transcription Regulatory Regions Database (TRRD): its status in 1999. <i>Nucleic Acids Research</i> , 1999, 27, 303-306.	14.5	27
17	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
18	Transcriptome Characteristics and X-Chromosome Inactivation Status in Cultured Rat Pluripotent Stem Cells. <i>Stem Cells and Development</i> , 2015, 24, 2912-2924.	2.1	18

#	ARTICLE	IF	CITATIONS
19	Model composition through model reduction: a combined model of CD95 and NF- κ B signaling pathways. <i>BMC Systems Biology</i> , 2013, 7, 13.	3.0	17
20	CYCLONET--an integrated database on cell cycle regulation and carcinogenesis. <i>Nucleic Acids Research</i> , 2007, 35, D550-D556.	14.5	16
21	A Modular Model of the Apoptosis Machinery. <i>Advances in Experimental Medicine and Biology</i> , 2012, 736, 235-245.	1.6	12
22	Computational master-regulator search reveals mTOR and PI3K pathways responsible for low sensitivity of NCI-H292 and A427 lung cancer cell lines to cytotoxic action of p53 activator Nutlin-3. <i>BMC Medical Genomics</i> , 2018, 11, 12.	1.5	11
23	BioUML--"towards a universal research platform. <i>Nucleic Acids Research</i> , 2022, 50, W124-W131.	14.5	10
24	A Modular Mathematical Model of Exercise-Induced Changes in Metabolism, Signaling, and Gene Expression in Human Skeletal Muscle. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10353.	4.1	8
25	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
26	Thoroughly Calibrated Modular Agent-Based Model of the Human Cardiovascular and Renal Systems for Blood Pressure Regulation in Health and Disease. <i>Frontiers in Physiology</i> , 2021, 12, 746300.	2.8	6
27	BioUML Genome Browser. <i>Virtual Biology</i> , 2013, 1, 15.	0.2	5
28	Multicompartmental Mathematical Model of SARS-CoV-2 Distribution in Human Organs and Their Treatment. <i>Mathematics</i> , 2022, 10, 1925.	2.2	5
29	Prediction of protein-DNA interactions of transcription factors linking proteomics and transcriptomics data. <i>EuPA Open Proteomics</i> , 2016, 13, 14-23.	2.5	4
30	Population size estimation for quality control of ChIP-Seq datasets. <i>PLoS ONE</i> , 2019, 14, e0221760.	2.5	4
31	Prediction of nonsmall cell lung cancer sensitivity to cisplatin and paclitaxel based on marker gene expression. <i>Molecular Biology</i> , 2011, 45, 600-607.	1.3	2
32	Genome-Wide Atlas of Promoter Expression Reveals Contribution of Transcribed Regulatory Elements to Genetic Control of Disuse-Mediated Atrophy of Skeletal Muscle. <i>Biology</i> , 2021, 10, 557.	2.8	2
33	BioUML plug-in for nonlinear parameter estimation using multiple experimental data. <i>Virtual Biology</i> , 2013, 1, 47.	0.2	2
34	BioUML: plugin for population-based modeling. <i>Virtual Biology</i> , 2014, 1, 7.	0.2	2
35	Modular Modeling of Biological Systems. <i>Virtual Biology</i> , 2013, 1, 30.	0.2	2
36	Patient-specific 1D model of the human cardiovascular system. , 2015, , .		1

#	ARTICLE	IF	CITATIONS
37	Meta-analysis of ChIP-seq Datasets Through the Rank Aggregation Approach. , 2020, , .		1
38	Modular Representation of Physiologically Based Pharmacokinetic Models: Nanoparticle Delivery to Solid Tumors in Mice as an Example. Mathematics, 2022, 10, 1176.	2.2	1
39	Advanced data curation in GTRD database: hierarchical dictionaries of cell types and experimental factors. , 2020, , .		0
40	Toolkit for ChIP-Seq based comparative analysis of the PWM methods for prediction of transcription factor binding sites. Virtual Biology, 2014, 1, 19.	0.2	0
41	Assessment of transcriptional importance of cell line-specific features based on GTRD and FANTOM5 data. PLoS ONE, 2020, 15, e0243332.	2.5	0