

Edgar Wingender

List of Publications by Year in descending order

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83
papers

7,112
citations

159585

30
h-index

69250

77
g-index

87
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87
docs citations

87
times ranked

9513
citing authors

#	ARTICLE	IF	CITATIONS
1	High-Throughput Profiling of Colorectal Cancer Liver Metastases Reveals Intra- and Inter-Patient Heterogeneity in the EGFR and WNT Pathways Associated with Clinical Outcome. <i>Cancers</i> , 2022, 14, 2084.	3.7	5
2	IGFBP2 Is a Potential Master Regulator Driving the Dysregulated Gene Network Responsible for Short Survival in Glioblastoma Multiforme. <i>Frontiers in Genetics</i> , 2021, 12, 670240.	2.3	8
3	Text mining-based word representations for biomedical data analysis and protein-protein interaction networks in machine learning tasks. <i>PLoS ONE</i> , 2021, 16, e0258623.	2.5	6
4	Constructing temporal regulatory cascades in the context of development and cell differentiation. <i>PLoS ONE</i> , 2020, 15, e0231326.	2.5	1
5	Transcription Factor Databases. , 2019, , 134-141.		0
6	Walking pathways with positive feedback loops reveal DNA methylation biomarkers of colorectal cancer. <i>BMC Bioinformatics</i> , 2019, 20, 119.	2.6	37
7	TFClass: expanding the classification of human transcription factors to their mammalian orthologs. <i>Nucleic Acids Research</i> , 2018, 46, D343-D347.	14.5	112
8	Removing Background Co-occurrences of Transcription Factor Binding Sites Greatly Improves the Prediction of Specific Transcription Factor Cooperations. <i>Frontiers in Genetics</i> , 2018, 9, 189.	2.3	8
9	Defined Engineered Human Myocardium With Advanced Maturation for Applications in Heart Failure Modeling and Repair. <i>Circulation</i> , 2017, 135, 1832-1847.	1.6	462
10	geneXplainR: An R interface for the geneXplain platform. <i>Journal of Open Source Software</i> , 2017, 2, 412.	4.6	3
11	Computational Detection of Stage-Specific Transcription Factor Clusters during Heart Development. <i>Frontiers in Genetics</i> , 2016, 7, 33.	2.3	11
12	Computational Identification of Key Regulators in Two Different Colorectal Cancer Cell Lines. <i>Frontiers in Genetics</i> , 2016, 7, 42.	2.3	10
13	NF-Y Binding Site Architecture Defines a C-Fos Targeted Promoter Class. <i>PLoS ONE</i> , 2016, 11, e0160803.	2.5	17
14	Identifying cell-specific microRNA transcriptional start sites. <i>Bioinformatics</i> , 2016, 32, 2403-2410.	4.1	18
15	Multi-omics "upstream analysis" of regulatory genomic regions helps identifying targets against methotrexate resistance of colon cancer. <i>EuPA Open Proteomics</i> , 2016, 13, 1-13.	2.5	31
16	PC-TraFF: identification of potentially collaborating transcription factors using pointwise mutual information. <i>BMC Bioinformatics</i> , 2015, 16, 400.	2.6	23
17	"Upstream Analysis": An Integrated Promoter-Pathway Analysis Approach to Causal Interpretation of Microarray Data. <i>Microarrays (Basel, Switzerland)</i> , 2015, 4, 270-286.	1.4	55
18	TFClass: a classification of human transcription factors and their rodent orthologs. <i>Nucleic Acids Research</i> , 2015, 43, D97-D102.	14.5	78

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19	Multiobjective triclustering of time-series transcriptome data reveals key genes of biological processes. <i>BMC Bioinformatics</i> , 2015, 16, 200.	2.6	19
20	EndoNet: an information resource about the intercellular signaling network. <i>BMC Systems Biology</i> , 2014, 8, 49.	3.0	10
21	Coexpression and coregulation analysis of time-series gene expression data in estrogen-induced breast cancer cell. <i>Algorithms for Molecular Biology</i> , 2013, 8, 9.	1.2	39
22	MatrixCatch - a novel tool for the recognition of composite regulatory elements in promoters. <i>BMC Bioinformatics</i> , 2013, 14, 241.	2.6	22
23	Inhomogeneous Parsimonious Markov Models. <i>Lecture Notes in Computer Science</i> , 2013, , 321-336.	1.3	3
24	TFClass: an expandable hierarchical classification of human transcription factors. <i>Nucleic Acids Research</i> , 2013, 41, D165-D170.	14.5	132
25	CRITERIA FOR AN UPDATED CLASSIFICATION OF HUMAN TRANSCRIPTION FACTOR DNA-BINDING DOMAINS. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1340007.	0.8	9
26	A Discriminative Approach for Unsupervised Clustering of DNA Sequence Motifs. <i>PLoS Computational Biology</i> , 2013, 9, e1002958.	3.2	12
27	The architecture of the gene regulatory networks of different tissues. <i>Bioinformatics</i> , 2012, 28, i509-i514.	4.1	24
28	Using potential master regulator sites and paralogous expansion to construct tissue-specific transcriptional networks. <i>BMC Systems Biology</i> , 2012, 6, S15.	3.0	5
29	The ontology-based answers (OBA) service: a connector for embedded usage of ontologies in applications. <i>Frontiers in Genetics</i> , 2012, 3, 197.	2.3	14
30	Advanced Computational Biology Methods Identify Molecular Switches for Malignancy in an EGF Mouse Model of Liver Cancer. <i>PLoS ONE</i> , 2011, 6, e17738.	2.5	17
31	Integration of gene expression data with prior knowledge for network analysis and validation. <i>BMC Research Notes</i> , 2011, 4, 520.	1.4	3
32	Molecular mechanistic associations of human diseases. <i>BMC Systems Biology</i> , 2010, 4, 124.	3.0	11
33	The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , 2010, 28, 935-942.	17.5	613
34	An approach to evaluate the topological significance of motifs and other patterns in regulatory networks. <i>BMC Systems Biology</i> , 2009, 3, 53.	3.0	12
35	The pairwise disconnectivity index as a new metric for the topological analysis of regulatory networks. <i>BMC Bioinformatics</i> , 2008, 9, 227.	2.6	33
36	The TRANSFAC project as an example of framework technology that supports the analysis of genomic regulation. <i>Briefings in Bioinformatics</i> , 2008, 9, 326-332.	6.5	390

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37	Building a knowledge base for systems pathology. Briefings in Bioinformatics, 2008, 9, 518-531.	6.5	14
38	EndoNet: an information resource about regulatory networks of cell-to-cell communication. Nucleic Acids Research, 2007, 36, D689-D694.	14.5	8
39	DEEP-A tool for differential expression effector prediction. Nucleic Acids Research, 2007, 35, W619-W624.	14.5	3
40	Integrative content-driven concepts for bioinformatics â€œbeyond the cellâ€• Journal of Biosciences, 2007, 32, 169-180.	1.1	11
41	TRANSPATH(R): an information resource for storing and visualizing signaling pathways and their pathological aberrations. Nucleic Acids Research, 2006, 34, D546-D551.	14.5	157
42	Evaluating phylogenetic footprinting for human-rodent comparisons. Bioinformatics, 2006, 22, 430-437.	4.1	28
43	Beyond microarrays: Finding key transcription factors controlling signal transduction pathways. BMC Bioinformatics, 2006, 7, S13.	2.6	78
44	TiProD: the Tissue-specific Promoter Database. Nucleic Acids Research, 2006, 34, D104-D107.	14.5	29
45	EndoNet: an information resource about endocrine networks. Nucleic Acids Research, 2006, 34, D540-D545.	14.5	11
46	Eukaryotic regulatory sequences. , 2005, , .		0
47	Construction of predictive promoter models on the example of antibacterial response of human epithelial cells. Theoretical Biology and Medical Modelling, 2005, 2, 2.	2.1	8
48	Deriving an ontology for human gene expression sources from the CYTOMER database on human organs and cell types. In Silico Biology, 2005, 5, 61-6.	0.9	8
49	Topology of mammalian transcription networks. Genome Informatics, 2005, 16, 270-8.	0.4	26
50	A Novel Computational Approach for the Prediction of Networked Transcription Factors of Aryl Hydrocarbon-Receptor-Regulated Genes. Molecular Pharmacology, 2004, 66, 1557-1572.	2.3	33
51	TRANSPATHâ€™A High Quality Database Focused on Signal Transduction. Comparative and Functional Genomics, 2004, 5, 163-168.	2.0	33
52	TRANSFAC, TRANSPATH and CYTOMER as starting points for an ontology of regulatory networks. In Silico Biology, 2004, 4, 55-61.	0.9	38
53	Consistent re-modeling of signaling pathways and its implementation in the TRANSPATH database. Genome Informatics, 2004, 15, 244-54.	0.4	14
54	Systematic DNA-binding domain classification of transcription factors. Genome Informatics, 2004, 15, 276-86.	0.4	27

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55	PRODORIC: prokaryotic database of gene regulation. <i>Nucleic Acids Research</i> , 2003, 31, 266-269.	14.5	220
56	TRANSPATH(R): an integrated database on signal transduction and a tool for array analysis. <i>Nucleic Acids Research</i> , 2003, 31, 97-100.	14.5	80
57	Composition-sensitive analysis of the human genome for regulatory signals. <i>In Silico Biology</i> , 2003, 3, 145-71.	0.9	19
58	TRANSCompel(R): a database on composite regulatory elements in eukaryotic genes. <i>Nucleic Acids Research</i> , 2002, 30, 332-334.	14.5	112
59	S/MARt DB: a database on scaffold/matrix attached regions. <i>Nucleic Acids Research</i> , 2002, 30, 372-374.	14.5	54
60	The TGF- β Smad network: introducing bioinformatic tools. <i>Trends in Genetics</i> , 2002, 18, 96-103.	6.7	32
61	Modeling regulatory pathways with the use of the TRANSFAC system. <i>Gene Function & Disease</i> , 2002, 3, 9-17.	0.3	2
62	Computer-assisted identification of cell cycle-related genes: new targets for E2F transcription factors. <i>Journal of Molecular Biology</i> , 2001, 309, 99-120.	4.2	165
63	Database-assisted promoter analysis. <i>Trends in Plant Science</i> , 2001, 6, 251-255.	8.8	44
64	Experimental analysis and computer prediction of CTF/NFI transcription factor DNA binding sites 1 1 Edited by M. Yaniv. <i>Journal of Molecular Biology</i> , 2000, 297, 833-848.	4.2	70
65	Recognition of NFATp/AP-1 composite elements within genes induced upon the activation of immune cells. <i>Journal of Molecular Biology</i> , 1999, 288, 353-376.	4.2	118
66	Activation of nuclear factor- κ B in macrophages by mycoplasmal lipopeptides. <i>European Journal of Immunology</i> , 1998, 28, 4207-4212.	2.9	36
67	Computer-Assisted Methods for the Identification and Characterization of Polymerase II Promoters. , 1998, 20, 25-40.		1
68	Parathyroid Hormone-related Protein Antagonizes the Action of Parathyroid Hormone on Adult Cardiomyocytes. <i>Journal of Biological Chemistry</i> , 1996, 271, 3074-3078.	3.4	17
69	Modellierung der Genregulation in Eukaryonten. <i>IT - Information Technology</i> , 1996, 38, 27-31.	0.9	0
70	Combining structural analysis of DNA with search routines for the detection of transcription regulatory elements. <i>Bioinformatics</i> , 1996, 12, 441-446.	4.1	29
71	A compilation of composite regulatory elements affecting gene transcription in vertebrates. <i>Nucleic Acids Research</i> , 1995, 23, 4097-4103.	14.5	96
72	MatInd and MatInspector: new fast and versatile tools for detection of consensus matches in nucleotide sequence data. <i>Nucleic Acids Research</i> , 1995, 23, 4878-4884.	14.5	2,535

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73	Recognition of regulatory regions in genomic sequences. Journal of Biotechnology, 1994, 35, 273-280.	3.8	67
74	The Human Immunodeficiency Virus Type 1 Encoded Vpu Protein is Phosphorylated by Casein Kinase-2 (CK-2) at Positions Ser52 and Ser56 within a Predicted α -Helix-Turn- α -Helix-Motif. Journal of Molecular Biology, 1994, 236, 16-25.	4.2	164
75	PARATHYROID HORMONE GENE EXPRESSION: IDENTIFICATION OF AN UPSTREAM ELEMENT INVOLVED IN DOWN-REGULATION BY VITAMIN D3. , 1991, , 306-307.		0
76	The promoter of the human parathyroid hormone gene contains a functional cyclic AMP-response element. Nucleic Acids Research, 1990, 18, 5677-5683.	14.5	29
77	Compilation of transcription regulating proteins. Nucleic Acids Research, 1988, 16, 1879-1902.	14.5	311
78	Transcription in Eukaryotesâ€”The Role of Transcription Complexes and Their Components. Angewandte Chemie International Edition in English, 1987, 26, 218-227.	4.4	9
79	Zinc ions are differentially required for the transcription of ribosomal 5S RNA and tRNA in a HeLa-cell extract. Nucleic Acids Research, 1984, 12, 8971-8985.	14.5	23
80	Faithful Transcription of Ribosomal 5-S RNA in vitro Depends on the Presence of Several Factors. FEBS Journal, 1983, 131, 189-194.	0.2	11
81	Modulation of the Nucleosome Structure by Histone Acetylation. FEBS Journal, 1980, 110, 143-152.	0.2	77
82	Computational Methods and Bioinformatic Tools. , 0, , 769-904.		0
83	Isolation and Analysis of Gene Regulatory Sequences. , 0, , .		2