

# Edgar Wingender

## List of Publications by Year in descending order

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Version: 2024-02-01

83  
papers

7,112  
citations

159585

30  
h-index

69250

77  
g-index

87  
all docs

87  
docs citations

87  
times ranked

9513  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , 2010, 28, 935-942.	17.5	613
3	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
4	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
5	Compilation of transcription regulating proteins. <i>Nucleic Acids Research</i> , 1988, 16, 1879-1902.	14.5	311
6	PRODORIC: prokaryotic database of gene regulation. <i>Nucleic Acids Research</i> , 2003, 31, 266-269.	14.5	220
7	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
8	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 $\alpha$ -Helix-Turn- $\beta$ -Helix-Motif. <i>Journal of Molecular Biology</i> , 1994, 236, 16-25.	4.2	164
9	TRANSPATH(R): an information resource for storing and visualizing signaling pathways and their pathological aberrations. <i>Nucleic Acids Research</i> , 2006, 34, D546-D551.	14.5	157
10	TFClass: an expandable hierarchical classification of human transcription factors. <i>Nucleic Acids Research</i> , 2013, 41, D165-D170.	14.5	132
11	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
12	TRANSCompel(R): a database on composite regulatory elements in eukaryotic genes. <i>Nucleic Acids Research</i> , 2002, 30, 332-334.	14.5	112
13	TFClass: expanding the classification of human transcription factors to their mammalian orthologs. <i>Nucleic Acids Research</i> , 2018, 46, D343-D347.	14.5	112
14	A compilation of composite regulatory elements affecting gene transcription in vertebrates. <i>Nucleic Acids Research</i> , 1995, 23, 4097-4103.	14.5	96
15	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
16	Beyond microarrays: Finding key transcription factors controlling signal transduction pathways. <i>BMC Bioinformatics</i> , 2006, 7, S13.	2.6	78
17	TFClass: a classification of human transcription factors and their rodent orthologs. <i>Nucleic Acids Research</i> , 2015, 43, D97-D102.	14.5	78
18	Modulation of the Nucleosome Structure by Histone Acetylation. <i>FEBS Journal</i> , 1980, 110, 143-152.	0.2	77

#	ARTICLE	IF	CITATIONS
19	Experimental analysis and computer prediction of CTF/NFI transcription factor DNA binding sites 1 1 Edited by M. Yaniv. Journal of Molecular Biology, 2000, 297, 833-848.	4.2	70
20	Recognition of regulatory regions in genomic sequences. Journal of Biotechnology, 1994, 35, 273-280.	3.8	67
21	“Upstream Analysis”: An Integrated Promoter-Pathway Analysis Approach to Causal Interpretation of Microarray Data. Microarrays (Basel, Switzerland), 2015, 4, 270-286.	1.4	55
22	S/MARt DB: a database on scaffold/matrix attached regions. Nucleic Acids Research, 2002, 30, 372-374.	14.5	54
23	Database-assisted promoter analysis. Trends in Plant Science, 2001, 6, 251-255.	8.8	44
24	Coexpression and coregulation analysis of time-series gene expression data in estrogen-induced breast cancer cell. Algorithms for Molecular Biology, 2013, 8, 9.	1.2	39
25	TRANSFAC, TRANSPATH and CYTOMER as starting points for an ontology of regulatory networks. In Silico Biology, 2004, 4, 55-61.	0.9	38
26	Walking pathways with positive feedback loops reveal DNA methylation biomarkers of colorectal cancer. BMC Bioinformatics, 2019, 20, 119.	2.6	37
27	Activation of nuclear factor- $\kappa$ B in macrophages by mycoplasmal lipopeptides. European Journal of Immunology, 1998, 28, 4207-4212.	2.9	36
28	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
29	TRANSPATH “A High Quality Database Focused on Signal Transduction. Comparative and Functional Genomics, 2004, 5, 163-168.	2.0	33
30	The pairwise disconnectivity index as a new metric for the topological analysis of regulatory networks. BMC Bioinformatics, 2008, 9, 227.	2.6	33
31	The TGF- $\beta$ “Smad network: introducing bioinformatic tools. Trends in Genetics, 2002, 18, 96-103.	6.7	32
32	Multi-omics “upstream analysis” of regulatory genomic regions helps identifying targets against methotrexate resistance of colon cancer. EuPA Open Proteomics, 2016, 13, 1-13.	2.5	31
33	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
34	Combining structural analysis of DNA with search routines for the detection of transcription regulatory elements. Bioinformatics, 1996, 12, 441-446.	4.1	29
35	TiProD: the Tissue-specific Promoter Database. Nucleic Acids Research, 2006, 34, D104-D107.	14.5	29
36	Evaluating phylogenetic footprinting for human-rodent comparisons. Bioinformatics, 2006, 22, 430-437.	4.1	28

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37	Systematic DNA-binding domain classification of transcription factors. <i>Genome Informatics</i> , 2004, 15, 276-86.	0.4	27
38	Topology of mammalian transcription networks. <i>Genome Informatics</i> , 2005, 16, 270-8.	0.4	26
39	The architecture of the gene regulatory networks of different tissues. <i>Bioinformatics</i> , 2012, 28, i509-i514.	4.1	24
40	Zinc ions are differentially required for the transcription of ribosomal 5S RNA and tRNA in a HeLa-cell extract. <i>Nucleic Acids Research</i> , 1984, 12, 8971-8985.	14.5	23
41	PC-TraFF: identification of potentially collaborating transcription factors using pointwise mutual information. <i>BMC Bioinformatics</i> , 2015, 16, 400.	2.6	23
42	MatrixCatch - a novel tool for the recognition of composite regulatory elements in promoters. <i>BMC Bioinformatics</i> , 2013, 14, 241.	2.6	22
43	Multiobjective triclustering of time-series transcriptome data reveals key genes of biological processes. <i>BMC Bioinformatics</i> , 2015, 16, 200.	2.6	19
44	Composition-sensitive analysis of the human genome for regulatory signals. <i>In Silico Biology</i> , 2003, 3, 145-71.	0.9	19
45	Identifying cell-specific microRNA transcriptional start sites. <i>Bioinformatics</i> , 2016, 32, 2403-2410.	4.1	18
46	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
47	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
48	NF-Y Binding Site Architecture Defines a C-Fos Targeted Promoter Class. <i>PLoS ONE</i> , 2016, 11, e0160803.	2.5	17
49	Building a knowledge base for systems pathology. <i>Briefings in Bioinformatics</i> , 2008, 9, 518-531.	6.5	14
50	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
51	Consistent re-modeling of signaling pathways and its implementation in the TRANSPATH database. <i>Genome Informatics</i> , 2004, 15, 244-54.	0.4	14
52	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
53	A Discriminative Approach for Unsupervised Clustering of DNA Sequence Motifs. <i>PLoS Computational Biology</i> , 2013, 9, e1002958.	3.2	12
54	Faithful Transcription of Ribosomal 5-S RNA in vitro Depends on the Presence of Several Factors. <i>FEBS Journal</i> , 1983, 131, 189-194.	0.2	11

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55	EndoNet: an information resource about endocrine networks. <i>Nucleic Acids Research</i> , 2006, 34, D540-D545.	14.5	11
56	Integrative content-driven concepts for bioinformatics â€œbeyond the cellâ€. <i>Journal of Biosciences</i> , 2007, 32, 169-180.	1.1	11
57	Molecular mechanistic associations of human diseases. <i>BMC Systems Biology</i> , 2010, 4, 124.	3.0	11
58	Computational Detection of Stage-Specific Transcription Factor Clusters during Heart Development. <i>Frontiers in Genetics</i> , 2016, 7, 33.	2.3	11
59	EndoNet: an information resource about the intercellular signaling network. <i>BMC Systems Biology</i> , 2014, 8, 49.	3.0	10
60	Computational Identification of Key Regulators in Two Different Colorectal Cancer Cell Lines. <i>Frontiers in Genetics</i> , 2016, 7, 42.	2.3	10
61	Transcription in Eukaryotesâ€”The Role of Transcription Complexes and Their Components. <i>Angewandte Chemie International Edition in English</i> , 1987, 26, 218-227.	4.4	9
62	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
63	Construction of predictive promoter models on the example of antibacterial response of human epithelial cells. <i>Theoretical Biology and Medical Modelling</i> , 2005, 2, 2.	2.1	8
64	EndoNet: an information resource about regulatory networks of cell-to-cell communication. <i>Nucleic Acids Research</i> , 2007, 36, D689-D694.	14.5	8
65	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
66	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
67	Deriving an ontology for human gene expression sources from the CYTOMER database on human organs and cell types. <i>In Silico Biology</i> , 2005, 5, 61-6.	0.9	8
68	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
69	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
70	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
71	DEEP-A tool for differential expression effector prediction. <i>Nucleic Acids Research</i> , 2007, 35, W619-W624.	14.5	3
72	Integration of gene expression data with prior knowledge for network analysis and validation. <i>BMC Research Notes</i> , 2011, 4, 520.	1.4	3

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73	Inhomogeneous Parsimonious Markov Models. Lecture Notes in Computer Science, 2013, , 321-336.	1.3	3
74	geneXplainR: An R interface for the geneXplain platform. Journal of Open Source Software, 2017, 2, 412.	4.6	3
75	Modeling regulatory pathways with the use of the TRANSFAC system. Gene Function & Disease, 2002, 3, 9-17.	0.3	2
76	Isolation and Analysis of Gene Regulatory Sequences. , 0, , .		2
77	Constructing temporal regulatory cascades in the context of development and cell differentiation. PLoS ONE, 2020, 15, e0231326.	2.5	1
78	Computer-Assisted Methods for the Identification and Characterization of Polymerase II Promoters. , 1998, 20, 25-40.		1
79	PARATHYROID HORMONE GENE EXPRESSION: IDENTIFICATION OF AN UPSTREAM ELEMENT INVOLVED IN DOWN-REGULATION BY VITAMIN D3. , 1991, , 306-307.		0
80	Modellierung der Genregulation in Eukaryonten. IT - Information Technology, 1996, 38, 27-31.	0.9	0
81	Computational Methods and Bioinformatic Tools. , 0, , 769-904.		0
82	Eukaryotic regulatory sequences. , 2005, , .		0
83	Transcription Factor Databases. , 2019, , 134-141.		0