Wyeth W Wasserman

List of Publications by Year
in descending order

160	22,244	26630	10158
papers	citations	56	140
		h-index	g-index

192	192	192	40728
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	JASPAR 2022: the 9th release of the open-access database of transcription factor binding profiles. Nucleic Acids Research, 2022, 50, D165-D173.	14.5	902
2	Linkage analysis identifies an isolated strabismus locus at 14q12 overlapping with FOXG1 syndrome region. Journal of Medical Genetics, 2022, 59, 46-55.	3.2	2
3	Knowledge Base of Inborn Errors of Metabolism (IEMbase): A Practical Approach. , 2022, , 1449-1455.		1
4	RevUP: an online scoring system for regulatory variants implicated in rare diseases. Bioinformatics, 2022, 38, 2664-2666.	4.1	0
5	Human complete NFAT1 deficiency causes a triad ofÂjoint contractures, osteochondromas, and B-cellÂmalignancy. Blood, 2022, 140, 1858-1874.	1.4	6
6	Exome sequencing enables diagnosis of X-linked hypohidrotic ectodermal dysplasia in patient with eosinophilic esophagitis and severe atopy. Allergy, Asthma and Clinical Immunology, 2021, 17, 9.	2.0	2
7	GeneBreaker: Variant simulation to improve the diagnosis of Mendelian rare genetic diseases. Human Mutation, 2021, 42, 346-358.	2.5	3
8	Human MiniPromoters for ocular-rAAV expression in ON bipolar, cone, corneal, endothelial, MÃ¼ller glial, and PAX6 cells. Gene Therapy, 2021, 28, 351-372.	4.5	18
9	Cross-species examination of X-chromosome inactivation highlights domains of escape from silencing. Epigenetics and Chromatin, 2021, 14, 12.	3.9	23
10	Demonstrating the utility of flexible sequence queries against indexed short reads with FlexTyper. PLoS Computational Biology, 2021, 17, e1008815.	3.2	0
11	Adult GAMT deficiency: A literature review and report of two siblings. Molecular Genetics and Metabolism Reports, 2021, 27, 100761.	1.1	6
12	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	12.8	11
13	Human progranulin-expressing mice as a novel tool for the development of progranulin-modulating therapeutics. Neurobiology of Disease, 2021, 153, 105314.	4.4	8
14	Secondary biogenic amine deficiencies: genetic etiology, therapeutic interventions, and clinical effects. Neurogenetics, 2021, 22, 251-262.	1.4	1
15	The genome atlas: navigating a new era of reference genomes. Trends in Genetics, 2021, 37, 807-818.	6.7	8
16	Biologically relevant transfer learning improves transcription factor binding prediction. Genome Biology, 2021, 22, 280.	8.8	24
17	JASPAR 2020: update of the open-access database of transcription factor binding profiles. Nucleic Acids Research, 2020, 48, D87-D92.	14.5	1,039
18	metPropagate: network-guided propagation of metabolomic information for prioritization of metabolic disease genes. Npj Genomic Medicine, 2020, 5, 25.	3.8	13

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19	The variability conundrum in neurometabolic degenerative diseases. Molecular Genetics and Metabolism, 2020, 131, 367-369.	1.1	3
20	Indigenous Genomic Databases: Pragmatic Considerations and Cultural Contexts. Frontiers in Public Health, 2020, 8, 111.	2.7	37
21	Multi-Omic Approach to Identify Phenotypic Modifiers Underlying Cerebral Demyelination in X-Linked Adrenoleukodystrophy. Frontiers in Cell and Developmental Biology, 2020, 8, 520.	3.7	14
22	ExpansionHunter Denovo: a computational method for locating known and novel repeat expansions in short-read sequencing data. Genome Biology, 2020, 21, 102.	8.8	114
23	Deregulated Regulators: Disease-Causing cis Variants in Transcription Factor Genes. Trends in Genetics, 2020, 36, 523-539.	6.7	26
24	Targeting AXL Kinase Sensitizes Acute Myeloid Leukemia Stem and Progenitor Cells to Venetoclax Treatment. Blood, 2020, 136, 20-20.	1.4	0
25	New MiniPromoter Ple345 (NEFL) Drives Strong and Specific Expression in Retinal Ganglion Cells of Mouse and Primate Retina. Human Gene Therapy, 2019, 30, 257-272.	2.7	21
26	Bi-allelic GOT2 Mutations Cause a Treatable Malate-Aspartate Shuttle-Related Encephalopathy. American Journal of Human Genetics, 2019, 105, 534-548.	6.2	46
27	TFEA.ChIP: a tool kit for transcription factor binding site enrichment analysis capitalizing on ChIP-seq datasets. Bioinformatics, 2019, 35, 5339-5340.	4.1	41
28	Identification of novel cerebellar developmental transcriptional regulators with motif activity analysis. BMC Genomics, 2019, 20, 718.	2.8	11
29	PLPHP deficiency: clinical, genetic, biochemical, and mechanistic insights. Brain, 2019, 142, 542-559.	7.6	67
30	Strabismus in Children With Intellectual Disability: Part of a Broader Motor Control Phenotype?. Pediatric Neurology, 2019, 100, 87-91.	2.1	4
31	Glutaminase Deficiency Caused by Short Tandem Repeat Expansion in GLS. New England Journal of Medicine, 2019, 380, 1433-1441.	27.0	71
32	Curation and bioinformatic analysis of strabismus genes supports functional heterogeneity and proposes candidate genes with connections to RASopathies. Gene, 2019, 697, 213-226.	2.2	5
33	Twenty-Seven Tamoxifen-Inducible iCre-Driver Mouse Strains for Eye and Brain, Including Seventeen Carrying a New Inducible-First Constitutive-Ready Allele. Genetics, 2019, 211, 1155-1177.	2.9	17
34	Gene expression models based on transcription factor binding events confer insight into functional cis-regulatory variants. Bioinformatics, 2019, 35, 2610-2617.	4.1	19
35	Development and user evaluation of a rare disease gene prioritization workflow based on cognitive ergonomics. Journal of the American Medical Informatics Association: JAMIA, 2019, 26, 124-133.	4.4	2
36	Atypical cerebral palsy: genomics analysis enables precision medicine. Genetics in Medicine, 2019, 21, 1621-1628.	2.4	47

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37	Introduction to Genomic Analysis Workshop: A catalyst for engaging life-science researchers in high throughput analysis. F1000Research, 2019, 8, 1221.	1.6	2
38	Genome sequencing reveals a novel genetic mechanism underlying dihydropyrimidine dehydrogenase deficiency: A novel missense variant c.1700G>A and a large intragenic inversion in DPYD spanning intron 8 to intron 12. Human Mutation, 2018, 39, 947-953.	2.5	6
39	Textâ€based phenotypic profiles incorporating biochemical phenotypes of inborn errors of metabolism improve phenomicsâ€based diagnosis. Journal of Inherited Metabolic Disease, 2018, 41, 555-562.	3.6	5
40	JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. Nucleic Acids Research, 2018, 46, D260-D266.	14.5	1,232
41	The role of the clinician in the multiâ€omics era: are you ready?. Journal of Inherited Metabolic Disease, 2018, 41, 571-582.	3.6	55
42	The SIN3A histone deacetylase complex is required for a complete transcriptional response to hypoxia. Nucleic Acids Research, 2018, 46, 120-133.	14.5	96
43	Improvement of Self-Injury With Dopamine and Serotonin Replacement Therapy in a Patient With a Hemizygous PAK3 Mutation: A New Therapeutic Strategy for Neuropsychiatric Features of an Intellectual Disability Syndrome. Journal of Child Neurology, 2018, 33, 106-113.	1.4	20
44	Integration of genomics and metabolomics for prioritization of rare disease variants: a 2018 literature review. Journal of Inherited Metabolic Disease, 2018, 41, 435-445.	3.6	35
45	Knowledge base and mini-expert platform for the diagnosis of inborn errors of metabolism. Genetics in Medicine, 2018, 20, 151-158.	2.4	67
46	The genotypic and phenotypic spectrum of MTO1 deficiency. Molecular Genetics and Metabolism, 2018, 123, 28-42.	1.1	24
47	Bone health and <scp>SATB2</scp>â€associated syndrome. Clinical Genetics, 2018, 93, 588-594.	2.0	18
48	Gain-of-function KCNJ6 Mutation in a Severe Hyperkinetic Movement Disorder Phenotype. Neuroscience, 2018, 384, 152-164.	2.3	18
49	c-Myc is a novel Leishmania virulence factor by proxy that targets the host miRNA system and is essential for survival in human macrophages. Journal of Biological Chemistry, 2018, 293, 12805-12819.	3.4	20
50	Human Enhancers Harboring Specific Sequence Composition, Activity, and Genome Organization Are Linked to the Immune Response. Genetics, 2018, 209, 1055-1071.	2.9	16
51	Genome-wide prediction of cis-regulatory regions using supervised deep learning methods. BMC Bioinformatics, 2018, 19, 202.	2.6	88
52	Computational Analysis of Transcriptional Regulation Sites at the HTT Gene Locus. Journal of Huntington's Disease, 2018, 7, 223-237.	1.9	2
53	MANTA2, update of the Mongo database for the analysis of transcription factor binding site alterations. Scientific Data, 2018, 5, 180141.	5.3	11
54	Sialic acid catabolism by N-acetylneuraminate pyruvate lyase is essential for muscle function. JCI Insight, 2018, 3, .	5.0	36

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55	Optic atrophy, cataracts, lipodystrophy/lipoatrophy, and peripheral neuropathy caused by a de novo OPA3 mutation. Journal of Physical Education and Sports Management, 2017, 3, a001156.	1.2	11
56	A girl with developmental delay, ataxia, cranial nerve palsies, severe respiratory problems in infancyâ€"Expanding NDST1 syndrome. American Journal of Medical Genetics, Part A, 2017, 173, 712-715.	1.2	14
57	Impact of next-generation sequencing on diagnosis and management of neurometabolic disorders: current advances and future perspectives. Expert Review of Molecular Diagnostics, 2017, 17, 307-309.	3.1	15
58	Identification of a large intronic transposal insertion in SLC17A5 causing sialic acid storage disease. Orphanet Journal of Rare Diseases, 2017, 12, 28.	2.7	14
59	A case of splenomegaly in CBL syndrome. European Journal of Medical Genetics, 2017, 60, 374-379.	1.3	10
60	Assessment of the ExAC data set for the presence of individuals with pathogenic genotypes implicated in severe Mendelian pediatric disorders. Genetics in Medicine, 2017, 19, 1300-1308.	2.4	58
61	A de novo mosaic mutation in SPAST with two novel alternative alleles and chromosomal copy number variant in a boy with spastic paraplegia and autism spectrum disorder. European Journal of Medical Genetics, 2017, 60, 548-552.	1.3	12
62	CuboCube: Student creation of a cancer genetics e-textbook using open-access software for social learning. PLoS Biology, 2017, 15, e2001192.	5.6	6
63	Identification of non-coding genetic variants in samples from hypoxemic respiratory disease patients that affect the transcriptional response to hypoxia. Nucleic Acids Research, 2016, 44, gkw811.	14.5	8
64	Further Validation of the SIGMAR1 c.151+1G>T Mutation as Cause of Distal Hereditary Motor Neuropathy. Child Neurology Open, 2016, 3, 2329048X1666991.	1.1	14
65	Exome Sequencing and the Management of Neurometabolic Disorders. New England Journal of Medicine, 2016, 374, 2246-2255.	27.0	254
66	DeepCAGE transcriptomics identify HOXD10 as transcription factor regulating lymphatic endothelial responses to VEGF-C. Journal of Cell Science, 2016, 129, 2573-85.	2.0	15
67	NANS-mediated synthesis of sialic acid is required for brain and skeletal development. Nature Genetics, 2016, 48, 777-784.	21.4	125
68	DNA Shape Features Improve Transcription Factor Binding Site Predictions InÂVivo. Cell Systems, 2016, 3, 278-286.e4.	6.2	119
69	YY1 binding association with sex-biased transcription revealed through X-linked transcript levels and allelic binding analyses. Scientific Reports, 2016, 6, 37324.	3.3	32
70	Evaluating the impact of single nucleotide variants on transcription factor binding. Nucleic Acids Research, 2016, 44, gkw691.	14.5	35
71	PAX6 MiniPromoters drive restricted expression from rAAV in the adult mouse retina. Molecular Therapy - Methods and Clinical Development, 2016, 3, 16051.	4.1	17
72	Mitochondrial Complex III Deficiency with Ketoacidosis and Hyperglycemia Mimicking Neonatal Diabetes. JIMD Reports, 2016, 31, 57-62.	1.5	5

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73	CAGEd-oPOSSUM: motif enrichment analysis from CAGE-derived TSSs. Bioinformatics, 2016, 32, 2858-2860.	4.1	13
74	rAAV-compatible MiniPromoters for restricted expression in the brain and eye. Molecular Brain, 2016, 9, 52.	2.6	69
75	Deep Feature Selection: Theory and Application to Identify Enhancers and Promoters. Journal of Computational Biology, 2016, 23, 322-336.	1.6	118
76	Secondary neurotransmitter deficiencies in epilepsy caused by voltage-gated sodium channelopathies: A potential treatment target?. Molecular Genetics and Metabolism, 2016, 117, 42-48.	1.1	40
77	Cytosolic phosphoenolpyruvate carboxykinase deficiency presenting with acute liver failure following gastroenteritis. Molecular Genetics and Metabolism, 2016, 118, 21-27.	1.1	23
78	JASPAR 2016: a major expansion and update of the open-access database of transcription factor binding profiles. Nucleic Acids Research, 2016, 44, D110-D115.	14.5	968
79	DNA methylation profiling in human Huntington's disease brain. Human Molecular Genetics, 2016, 25, 2013-2030.	2.9	56
80	De novo dominant variants affecting the motor domain of KIF1A are a cause of PEHO syndrome. European Journal of Human Genetics, 2016, 24, 949-953.	2.8	37
81	Dynamic software design for clinical exome and genome analyses: insights from bioinformaticians, clinical geneticists, and genetic counselors. Journal of the American Medical Informatics Association: JAMIA, 2016, 23, 257-268.	4.4	9
82	DeepCAGE Transcriptomics Reveal an Important Role of the Transcription Factor MAFB in the Lymphatic Endothelium. Cell Reports, 2015, 13, 1493-1504.	6.4	46
83	Defects in fatty acid amide hydrolase 2 in a male with neurologic and psychiatric symptoms. Orphanet Journal of Rare Diseases, 2015, 10, 38.	2.7	19
84	Cis-regulatory somatic mutations and gene-expression alteration in B-cell lymphomas. Genome Biology, 2015, 16, 84.	8.8	36
85	GeneYenta: A PhenotypeÂBased Rare Disease Case Matching Tool Based on Online Dating Algorithms for the Acceleration of Exome Interpretation. Human Mutation, 2015, 36, 432-438.	2.5	16
86	Identification of altered cis-regulatory elements in human disease. Trends in Genetics, 2015, 31, 67-76.	6.7	99
87	RMND1 deficiency associated with neonatal lactic acidosis, infantile onset renal failure, deafness, and multiorgan involvement. European Journal of Human Genetics, 2015, 23, 1301-1307.	2.8	28
88	Expansion of the QARS deficiency phenotype with report of a family with isolated supratentorial brain abnormalities. Neurogenetics, 2015, 16, 145-149.	1.4	11
89	The genotypic and phenotypic spectrum of PIGA deficiency. Orphanet Journal of Rare Diseases, 2015, 10, 23.	2.7	70
90	A SNP in the HTT promoter alters NF-ÎºB binding and is a bidirectional genetic modifier of Huntington disease. Nature Neuroscience, 2015, 18, 807-816.	14.8	113

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91	The identification of cis-regulatory elements: A review from a machine learning perspective. BioSystems, 2015, 138, 6-17.	2.0	51
92	Combined serial analysis of gene expression and transcription factor binding site prediction identifies novel-candidate-target genes of Nr2e1 in neocortex development. BMC Genomics, 2015, 16, 545.	2.8	9
93	Deep Feature Selection: Theory and Application to Identify Enhancers and Promoters. Lecture Notes in Computer Science, 2015, , 205-217.	1.3	32
94	Single point mutation in Rabenosyn-5 in a female with intractable seizures and evidence of defective endocytotic trafficking. Orphanet Journal of Rare Diseases, 2014, 9, 141.	2.7	26
95	FLAGS, frequently mutated genes in public exomes. BMC Medical Genomics, 2014, 7, 64.	1.5	108
96	Strabismus genetics across a spectrum of eye misalignment disorders. Clinical Genetics, 2014, 86, 103-111.	2.0	35
97	TFBSshape: a motif database for DNA shape features of transcription factor binding sites. Nucleic Acids Research, 2014, 42, D148-D155.	14.5	111
98	Spread of X-chromosome inactivation into autosomal sequences: role for DNA elements, chromatin features and chromosomal domains. Human Molecular Genetics, 2014, 23, 1211-1223.	2.9	60
99	JASPAR 2014: an extensively expanded and updated open-access database of transcription factor binding profiles. Nucleic Acids Research, 2014, 42, D142-D147.	14.5	915
100	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
101	Exome sequencing identifies mutations in <scp>KIF14</scp> as a novel cause of an autosomal recessive lethal fetal ciliopathy phenotype. Clinical Genetics, 2014, 86, 220-228.	2.0	92
102	Mitochondrial Carbonic Anhydrase VA Deficiency Resulting from CA5A Alterations Presents with Hyperammonemia in Early Childhood. American Journal of Human Genetics, 2014, 94, 453-461.	6.2	82
103	DNAJC13 mutations in Parkinson disease. Human Molecular Genetics, 2014, 23, 1794-1801.	2.9	258
104	Improving analysis of transcription factor binding sites within ChIP-Seq data based on topological motif enrichment. BMC Genomics, 2014, 15, 472.	2.8	47
105	On the identification of potential regulatory variants within genome wide association candidate SNP sets. BMC Medical Genomics, 2014, 7, 34.	1.5	43
106	Exome sequencing pilot study in children with carbamazepineâ€induced serious skin reactions. Clinical and Translational Allergy, 2014, 4, P119.	3.2	0
107	Non-targeted transcription factors motifs are a systemic component of ChIP-seq datasets. Genome Biology, 2014, 15, 412.	8.8	59
108	Usability study of clinical exome analysis software: Top lessons learned and recommendations. Journal of Biomedical Informatics, 2014, 51, 129-136.	4.3	15

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109	Targeted CNS delivery using human MiniPromoters and demonstrated compatibility with adeno-associated viral vectors. Molecular Therapy - Methods and Clinical Development, 2014, 1, 5.	4.1	44
110	Compensating for literature annotation bias when predicting novel drug-disease relationships through Medical Subject Heading Over-representation Profile (MeSHOP) similarity. BMC Medical Genomics, 2013, 6, S3.	1.5	10
111	The Next Generation of Transcription Factor Binding Site Prediction. PLoS Computational Biology, 2013, 9, e1003214.	3.2	160
112	Non-coding-regulatory regions of human brain genes delineated by bacterial artificial chromosome knock-in mice. BMC Biology, 2013, 11, 106.	3.8	4
113	Utilizing Social Media to Study Information-Seeking and Ethical Issues in Gene Therapy. Journal of Medical Internet Research, 2013, 15, e44.	4.3	20
114	Portal for Families Overcoming Neurodevelopmental Disorders (PFOND): Implementation of a Software Framework for Facilitated Community Website Creation by Nontechnical Volunteers. JMIR Research Protocols, 2013, 2, e25.	1.0	3
115	oPOSSUM-3: Advanced Analysis of Regulatory Motif Over-Representation Across Genes or ChIP-Seq Datasets. G3: Genes, Genomes, Genetics, 2012, 2, 987-1002.	1.8	293
116	The Transcription Factor Encyclopedia. Genome Biology, 2012, 13, R24.	9.6	103
117	Quantitative biomedical annotation using medical subject heading over-representation profiles (MeSHOPs). BMC Bioinformatics, 2012, 13, 249.	2.6	24
118	Inferring novel gene-disease associations using Medical Subject Heading Over-representation Profiles. Genome Medicine, 2012, 4, 75.	8.2	25
119	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. Nature, 2012, 486, 395-399.	27.8	1,778
120	Identification of cis-regulatory sequence variations in individual genome sequences. Genome Medicine, 2011, 3, 65.	8.2	17
121	VPS35 Mutations in Parkinson Disease. American Journal of Human Genetics, 2011, 89, 162-167.	6.2	747
122	MIR@NT@N: a framework integrating transcription factors, microRNAs and their targets to identify sub-network motifs in a meta-regulation network model. BMC Bioinformatics, 2011, 12, 67.	2.6	64
123	Towards resolving the transcription factor network controlling myelin gene expression. Nucleic Acids Research, 2011, 39, 7974-7991.	14.5	22
124	Validation of Skeletal Muscle cis-Regulatory Module Predictions Reveals Nucleotide Composition Bias in Functional Enhancers. PLoS Computational Biology, 2011, 7, e1002256.	3.2	8
125	Laboratory Animal Management Assistant (LAMA): a LIMS for active research colonies. Mammalian Genome, 2010, 21, 224-230.	2.2	10
126	Global mapping of binding sites for Nrf2 identifies novel targets in cell survival response through ChIP-Seq profiling and network analysis. Nucleic Acids Research, 2010, 38, 5718-5734.	14.5	653

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127	A regulatory toolbox of MiniPromoters to drive selective expression in the brain. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 16589-16594.	7.1	74
128	JASPAR 2010: the greatly expanded open-access database of transcription factor binding profiles. Nucleic Acids Research, 2010, 38, D105-D110.	14.5	529
129	The PAZAR database of gene regulatory information coupled to the ORCA toolkit for the study of regulatory sequences. Nucleic Acids Research, 2009, 37, D54-D60.	14.5	97
130	TFCat: the curated catalog of mouse and human transcription factors. Genome Biology, 2009, 10, R29.	9.6	193
131	Transcriptional repression of microRNA genes by PML-RARA increases expression of key cancer proteins in acute promyelocytic leukemia. Blood, 2009, 113, 412-421.	1.4	97
132	Dynamics of the yeast transcriptome during wine fermentation reveals a novel fermentation stress response. FEMS Yeast Research, 2008, 8, 35-52.	2.3	173
133	Identification of a set of genes showing regionally enriched expression in the mouse brain. BMC Neuroscience, 2008, 9, 66.	1.9	25
134	Mechanisms underlying p53 regulation of PIK3CA transcription in ovarian surface epithelium and in ovarian cancer. Journal of Cell Science, 2008, 121, 664-674.	2.0	72
135	In Silico Detection of Sequence Variations Modifying Transcriptional Regulation. PLoS Computational Biology, 2008, 4, e5.	3.2	94
136	Gene Characterization Index: Assessing the Depth of Gene Annotation. PLoS ONE, 2008, 3, e1440.	2.5	9
137	Discovery and Expansion of Gene Modules by Seeking Isolated Groups in a Random Graph Process. PLoS ONE, 2008, 3, e3358.	2.5	3
138	ORegAnno: an open-access community-driven resource for regulatory annotation. Nucleic Acids Research, 2007, 36, D107-D113.	14.5	227
139	oPOSSUM: integrated tools for analysis of regulatory motif over-representation. Nucleic Acids Research, 2007, 35, W245-W252.	14.5	148
140	PAZAR: a framework for collection and dissemination of cis-regulatory sequence annotation. Genome Biology, 2007, 8, R207.	9.6	89
141	A new generation of JASPAR, the open-access repository for transcription factor binding site profiles. Nucleic Acids Research, 2006, 34, D95-D97.	14.5	200
142	IDENTIFICATION OF OVER-REPRESENTED COMBINATIONS OF TRANSCRIPTION FACTOR BINDING SITES IN SETS OF CO-EXPRESSED GENES. , 2005, , .		1
143	The Gene Set Builder: collation, curation, and distribution of sets of genes. BMC Bioinformatics, 2005, 6, 305.	2.6	5
144	Prediction of Nuclear Hormone Receptor Response Elements. Molecular Endocrinology, 2005, 19, 595-606.	3.7	124

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145	oPOSSUM: identification of over-represented transcription factor binding sites in co-expressed genes. Nucleic Acids Research, 2005, 33, 3154-3164.	14.5	360
146	Regulog Analysis: Detection of Conserved Regulatory Networks Across Bacteria: Application to Staphylococcus aureus. Genome Research, 2004, 14, 1362-1373.	5.5	58
147	Decoding Human Regulatory Circuits. Genome Research, 2004, 14, 1967-1974.	5.5	86
148	JASPAR: an open-access database for eukaryotic transcription factor binding profiles. Nucleic Acids Research, 2004, 32, 91D-94.	14.5	1,451
149	ConSite: web-based prediction of regulatory elements using cross-species comparison. Nucleic Acids Research, 2004, 32, W249-W252.	14.5	388
150	MSCAN: identification of functional clusters of transcription factor binding sites. Nucleic Acids Research, 2004, 32, W195-W198.	14.5	52
151	Applied bioinformatics for the identification of regulatory elements. Nature Reviews Genetics, 2004, 5, 276-287.	16.3	1,032
152	Constrained Binding Site Diversity within Families of Transcription Factors Enhances Pattern Discovery Bioinformatics. Journal of Molecular Biology, 2004, 338, 207-215.	4.2	157
153	In silico identification of metazoan transcriptional regulatory regions. Die Naturwissenschaften, 2003, 90, 156-166.	1.6	31
154	Integrated analysis of yeast regulatory sequences for biologically linked clusters of genes. Functional and Integrative Genomics, 2003, 3, 125-134.	3.5	27
155	Identification of conserved regulatory elements by comparative genome analysis. Journal of Biology, 2003, 2, 13.	2.7	222
156	TFBS: Computational framework for transcription factor binding site analysis. Bioinformatics, 2002, 18, 1135-1136.	4.1	154
157	A Predictive Model for Regulatory Sequences Directing Liver-Specific Transcription. Genome Research, 2001, 11, 1559-1566.	5.5	179
158	GeneLynx: A Gene-Centric Portal to the Human Genome. Genome Research, 2001, 11, 2151-2157.	5.5	49
159	Human-mouse genome comparisons to locate regulatory sites. Nature Genetics, 2000, 26, 225-228.	21.4	440
160	Identification of regulatory regions which confer muscle-specific gene expression. Journal of Molecular Biology, 1998, 278, 167-181.	4.2	362