

Michael R Brent

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6553505/publications.pdf>

Version: 2024-02-01

84
papers

43,415
citations

81900

39
h-index

79698

73
g-index

88
all docs

88
docs citations

88
times ranked

61277
citing authors

#	ARTICLE	IF	CITATIONS
1	The Transcription Factor Pdr802 Regulates Titan Cell Formation and Pathogenicity of <i>Cryptococcus neoformans</i> . <i>MBio</i> , 2021, 12, .	4.1	11
2	Inferring TF activities and activity regulators from gene expression data with constraints from TF perturbation data. <i>Bioinformatics</i> , 2021, 37, 1234-1245.	4.1	18
3	Dual threshold optimization and network inference reveal convergent evidence from TF binding locations and TF perturbation responses. <i>Genome Research</i> , 2020, 30, 459-471.	5.5	24
4	Seven-Up Is a Novel Regulator of Insulin Signaling. <i>Genetics</i> , 2018, 208, 1643-1656.	2.9	14
5	NetProphet 2.0: mapping transcription factor networks by exploiting scalable data resources. <i>Bioinformatics</i> , 2018, 34, 249-257.	4.1	14
6	Unintended Side Effects of Transformation Are Very Rare in <i>Cryptococcus neoformans</i> . G3: Genes, Genomes, <i>Genetics</i> , 2018, 8, 815-822.	1.8	12
7	Model-based Transcriptome Engineering. , 2017, , .		0
8	Computational Analysis Reveals a Key Regulator of Cryptococcal Virulence and Determinant of Host Response. <i>MBio</i> , 2016, 7, e00313-16.	4.1	43
9	Past Roadblocks and New Opportunities in Transcription Factor Network Mapping. <i>Trends in Genetics</i> , 2016, 32, 736-750.	6.7	23
10	Model-based transcriptome engineering promotes a fermentative transcriptional state in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7428-E7437.	7.1	32
11	SpDamID: Marking DNA Bound by Protein Complexes Identifies Notch-Dimer Responsive Enhancers. <i>Molecular Cell</i> , 2015, 59, 685-697.	9.7	50
12	Model-driven mapping of transcriptional networks reveals the circuitry and dynamics of virulence regulation. <i>Genome Research</i> , 2015, 25, 690-700.	5.5	47
13	<i>Cryptococcus neoformans</i> Dual GDP-Mannose Transporters and Their Role in Biology and Virulence. <i>Eukaryotic Cell</i> , 2014, 13, 832-842.	3.4	23
14	Mapping functional transcription factor networks from gene expression data. <i>Genome Research</i> , 2013, 23, 1319-1328.	5.5	48
15	Role of Fat Body Lipogenesis in Protection against the Effects of Caloric Overload in <i>Drosophila</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 8028-8042.	3.4	104
16	Reduced DICER1 Elicits an Interferon Response in Endometrial Cancer Cells. <i>Molecular Cancer Research</i> , 2012, 10, 316-325.	3.4	15
17	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	27.8	15,516
18	GENCODE: The reference human genome annotation for The ENCODE Project. <i>Genome Research</i> , 2012, 22, 1760-1774.	5.5	4,217

#	ARTICLE	IF	CITATIONS
19	Abstract 2312: A genomics approach to determining the role of DICER1 in tumorigenesis: Interferon responses in the cancer cell. , 2012, , .		0
20	The developmental transcriptome of <i>Drosophila melanogaster</i> . <i>Nature</i> , 2011, 471, 473-479.	27.8	1,379
21	The transcriptional diversity of 25 <i>Drosophila</i> cell lines. <i>Genome Research</i> , 2011, 21, 301-314.	5.5	235
22	Toward an Integrated Model of Capsule Regulation in <i>Cryptococcus neoformans</i> . <i>PLoS Pathogens</i> , 2011, 7, e1002411.	4.7	82
23	A Quantitative Model of Glucose Signaling in Yeast Reveals an Incoherent Feed Forward Loop Leading to a Specific, Transient Pulse of Transcription. <i>Lecture Notes in Computer Science</i> , 2011, , 153-153.	1.3	0
24	Abstract 1173: A genomics approach to understanding DICER1's role in tumorigenesis. , 2011, , .		0
25	A quantitative model of glucose signaling in yeast reveals an incoherent feed forward loop leading to a specific, transient pulse of transcription. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 16743-16748.	7.1	37
26	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797.	12.6	1,124
27	The completion of the Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2009, 19, 2324-2333.	5.5	125
28	Benchmarking regulatory network reconstruction with GRENDL. <i>Bioinformatics</i> , 2009, 25, 801-807.	4.1	25
29	Constrained optimization for validation-guided conditional random field learning. , 2009, , .		1
30	Pairagon: a highly accurate, HMM-based cDNA-to-genome aligner. <i>Bioinformatics</i> , 2009, 25, 1587-1593.	4.1	6
31	Gradient-Based Feature Selection for Conditional Random Fields and its Applications in Computational Genetics. , 2009, , .		2
32	Steady progress and recent breakthroughs in the accuracy of automated genome annotation. <i>Nature Reviews Genetics</i> , 2008, 9, 62-73.	16.3	133
33	wuHMM: a robust algorithm to detect DNA copy number variation using long oligonucleotide microarray data. <i>Nucleic Acids Research</i> , 2008, 36, e41.	14.5	25
34	Using N ₂ ESCAN or TWINSKAN to Predict Gene Structures in Genomic DNA Sequences. <i>Current Protocols in Bioinformatics</i> , 2007, 20, Unit 4.8.	25.8	20
35	Targeted discovery of novel human exons by comparative genomics. <i>Genome Research</i> , 2007, 17, 1763-1773.	5.5	42
36	The Treeterbi and Parallel Treeterbi algorithms: efficient, optimal decoding for ordinary, generalized and pair HMMs. <i>Bioinformatics</i> , 2007, 23, 545-554.	4.1	9

#	ARTICLE	IF	CITATIONS
37	A tale of two templates: Automatically resolving double traces has many applications, including efficient PCR-based elucidation of alternative splices. <i>Genome Research</i> , 2007, 17, 212-218.	5.5	13
38	How does eukaryotic gene prediction work?. <i>Nature Biotechnology</i> , 2007, 25, 883-885.	17.5	30
39	Matrix and Steiner-triple-system smart pooling assays for high-performance transcription regulatory network mapping. <i>Nature Methods</i> , 2007, 4, 659-664.	19.0	62
40	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	27.8	4,709
41	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886
42	Using several pair-wise informant sequences for de novo prediction of alternatively spliced transcripts. <i>Genome Biology</i> , 2006, 7, S8.	9.6	6
43	Pairagon+N-SCAN_EST: a model-based gene annotation pipeline. <i>Genome Biology</i> , 2006, 7, S5.	9.6	15
44	Performance assessment of promoter predictions on ENCODE regions in the EGASP experiment. <i>Genome Biology</i> , 2006, 7, S3.	9.6	61
45	Using Multiple Alignments to Improve Gene Prediction. <i>Journal of Computational Biology</i> , 2006, 13, 379-393.	1.6	121
46	Using ESTs to improve the accuracy of de novo gene prediction. <i>BMC Bioinformatics</i> , 2006, 7, 327.	2.6	47
47	Iterative gene prediction and pseudogene removal improves genome annotation. <i>Genome Research</i> , 2006, 16, 678-685.	5.5	63
48	Molecular Properties of Adult Mouse Gastric and Intestinal Epithelial Progenitors in Their Niches. <i>Journal of Biological Chemistry</i> , 2006, 281, 11292-11300.	3.4	149
49	Gene finding in the chicken genome. <i>BMC Bioinformatics</i> , 2005, 6, 131.	2.6	34
50	Genome annotation past, present, and future: How to define an ORF at each locus. <i>Genome Research</i> , 2005, 15, 1777-1786.	5.5	110
51	Begin at the beginning: Predicting genes with 5' UTRs. <i>Genome Research</i> , 2005, 15, 742-747.	5.5	32
52	Closing in on the <i>C. elegans</i> ORFeome by cloning TWINSKAN predictions. <i>Genome Research</i> , 2005, 15, 577-582.	5.5	39
53	Using Multiple Alignments to Improve Gene Prediction. <i>Lecture Notes in Computer Science</i> , 2005, , 374-388.	1.3	8
54	The Genome of the Basidiomycetous Yeast and Human Pathogen <i>Cryptococcus neoformans</i> . <i>Science</i> , 2005, 307, 1321-1324.	12.6	664

#	ARTICLE	IF	CITATIONS
55	Identification of Rat Genes by TWINSKAN Gene Prediction, RT-PCR, and Direct Sequencing. <i>Genome Research</i> , 2004, 14, 665-671.	5.5	31
56	The Status, Quality, and Expansion of the NIH Full-Length cDNA Project: The Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2004, 14, 2121-2127.	5.5	486
57	Gene prediction and verification in a compact genome with numerous small introns. <i>Genome Research</i> , 2004, 14, 2330-2335.	5.5	41
58	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	27.8	1,943
59	Recent advances in gene structure prediction. <i>Current Opinion in Structural Biology</i> , 2004, 14, 264-272.	5.7	119
60	Recent advances in gene structure prediction. <i>Current Opinion in Structural Biology</i> , 2004, 14, 264-264.	5.7	0
61	Reexamining the Vocabulary Spurt.. <i>Developmental Psychology</i> , 2004, 40, 621-632.	1.6	180
62	Eval: a software package for analysis of genome annotations. <i>BMC Bioinformatics</i> , 2003, 4, 50.	2.6	56
63	The DNA sequence of human chromosome 7. <i>Nature</i> , 2003, 424, 157-164.	27.8	236
64	Comparison of mouse and human genomes followed by experimental verification yields an estimated 1,019 additional genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 1140-1145.	7.1	106
65	Leveraging the Mouse Genome for Gene Prediction in Human: From Whole-Genome Shotgun Reads to a Global Synteny Map. <i>Genome Research</i> , 2003, 13, 46-54.	5.5	88
66	The Genome Sequence of <i>Caenorhabditis briggsae</i> : A Platform for Comparative Genomics. <i>PLoS Biology</i> , 2003, 1, e45.	5.6	812
67	Using TWINSKAN to Predict Gene Structures in Genomic DNA Sequences. <i>Current Protocols in Bioinformatics</i> , 2003, 3, 4.8.1.	25.8	2
68	The Effects of Evolutionary Distance on TWINSKAN, an Algorithm for Pair-wise Comparative Gene Prediction. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2003, 68, 125-130.	1.1	7
69	Predicting full-length transcripts. <i>Trends in Biotechnology</i> , 2002, 20, 273-275.	9.3	8
70	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	27.8	6,319
71	The role of exposure to isolated words in early vocabulary development. <i>Cognition</i> , 2001, 81, B33-B44.	2.2	336
72	A Bayesian model for morpheme and paradigm identification. , 2001, , .		22

#	ARTICLE	IF	CITATIONS
73	An Efficient, Probabilistically Sound Algorithm for Segmentation and Word Discovery. Machine Learning, 1999, 34, 71-105.	5.4	183
74	Speech segmentation and word discovery: a computational perspective. Trends in Cognitive Sciences, 1999, 3, 294-301.	7.8	125
75	On the discovery of novel wordlike units from utterances: An artificial-language study with implications for native-language acquisition.. Journal of Experimental Psychology: General, 1999, 128, 165-185.	2.1	50
76	Syntactic categorization in early language acquisition: formalizing the role of distributional analysis. Cognition, 1997, 63, 121-170.	2.2	134
77	Toward a Unified Model of Lexical Acquisition and Lexical Access. Journal of Psycholinguistic Research, 1997, 26, 363-375.	1.3	29
78	Lexical categorization: Fitting template grammars by incremental MDL optimization. Lecture Notes in Computer Science, 1996, , 84-94.	1.3	2
79	Distributional regularity and phonotactic constraints are useful for segmentation. Cognition, 1996, 61, 93-125.	2.2	390
80	Advances in the computational study of language acquisition. Cognition, 1996, 61, 1-38.	2.2	92
81	Surface cues and robust inference as a basis for the early acquisition of subcategorization frames. Lingua, 1994, 92, 433-470.	1.0	12
82	Automatic acquisition of subcategorization frames from untagged text. , 1991, , .		54
83	Automatic acquisition of subcategorization frames from tagged text. , 1991, , .		39
84	A simplified theory of tense representations and constraints on their composition. , 1990, , .		6