Michael R Brent

List of Publications by Year
in descending order

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	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	27.8	15,516
2	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319
3	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
4	GENCODE: The reference human genome annotation for The ENCODE Project. Genome Research, 2012, 22, 1760-1774.	5.5	4,217
5	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	27.8	1,943
6	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	27.8	1,886
7	The developmental transcriptome of Drosophila melanogaster. Nature, 2011, 471, 473-479.	27.8	1,379
8	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. Science, 2010, 330, 1787-1797.	12.6	1,124
9	The Genome Sequence of Caenorhabditis briggsae: A Platform for Comparative Genomics. PLoS Biology, 2003, 1, e45.	5.6	812
10	The Genome of the Basidiomycetous Yeast and Human Pathogen <i>Cryptococcus neoformans</i>. Science, 2005, 307, 1321-1324.	12.6	664
11	The Status, Quality, and Expansion of the NIH Full-Length cDNA Project: The Mammalian Gene Collection (MGC). Genome Research, 2004, 14, 2121-2127.	5.5	486
12	Distributional regularity and phonotactic constraints are useful for segmentation. Cognition, 1996, 61, 93-125.	2.2	390
13	The role of exposure to isolated words in early vocabulary development. Cognition, 2001, 81, B33-B44.	2.2	336
14	The DNA sequence of human chromosome 7. Nature, 2003, 424, 157-164.	27.8	236
15	The transcriptional diversity of 25 <i>Drosophila</i> cell lines. Genome Research, 2011, 21, 301-314.	5.5	235
16	An Efficient, Probabilistically Sound Algorithm for Segmentation and Word Discovery. Machine Learning, 1999, 34, 71-105.	5.4	183
17	Reexamining the Vocabulary Spurt.. Developmental Psychology, 2004, 40, 621-632.	1.6	180
18	Molecular Properties of Adult Mouse Gastric and Intestinal Epithelial Progenitors in Their Niches. Journal of Biological Chemistry, 2006, 281, 11292-11300.	3.4	149

#	ARTICLE	IF	CITATIONS
19	Syntactic categorization in early language acquisition: formalizing the role of distributional analysis. Cognition, 1997, 63, 121-170.	2.2	134
20	Steady progress and recent breakthroughs in the accuracy of automated genome annotation. Nature Reviews Genetics, 2008, 9, 62-73.	16.3	133
21	Speech segmentation and word discovery: a computational perspective. Trends in Cognitive Sciences, 1999, 3, 294-301.	7.8	125
22	The completion of the Mammalian Gene Collection (MGC). Genome Research, 2009, 19, 2324-2333.	5.5	125
23	Using Multiple Alignments to Improve Gene Prediction. Journal of Computational Biology, 2006, 13, 379-393.	1.6	121
24	Recent advances in gene structure prediction. Current Opinion in Structural Biology, 2004, 14, 264-272.	5.7	119
25	Genome annotation past, present, and future: How to define an ORF at each locus. Genome Research, 2005, 15, 1777-1786.	5.5	110
26	Comparison of mouse and human genomes followed by experimental verification yields an estimated 1,019 additional genes. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1140-1145.	7.1	106
27	Role of Fat Body Lipogenesis in Protection against the Effects of Caloric Overload in Drosophila. Journal of Biological Chemistry, 2013, 288, 8028-8042.	3.4	104
28	Advances in the computational study of language acquisition. Cognition, 1996, 61, 1-38.	2.2	92
29	Leveraging the Mouse Genome for Gene Prediction in Human: From Whole-Genome Shotgun Reads to a Global Synteny Map. Genome Research, 2003, 13, 46-54.	5.5	88
30	Toward an Integrated Model of Capsule Regulation in Cryptococcus neoformans. PLoS Pathogens, 2011, 7, e1002411.	4.7	82
31	Iterative gene prediction and pseudogene removal improves genome annotation. Genome Research, 2006, 16, 678-685.	5.5	63
32	Matrix and Steiner-triple-system smart pooling assays for high-performance transcription regulatory network mapping. Nature Methods, 2007, 4, 659-664.	19.0	62
33	Performance assessment of promoter predictions on ENCODE regions in the EGASP experiment. Genome Biology, 2006, 7, S3.	9.6	61
34	Eval: a software package for analysis of genome annotations. BMC Bioinformatics, 2003, 4, 50.	2.6	56
35	Automatic acquisition of subcategorization frames from untagged text. , 1991, , .		54
36	SpDamID: Marking DNA Bound by Protein Complexes Identifies Notch-Dimer Responsive Enhancers. Molecular Cell, 2015, 59, 685-697.	9.7	50

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37	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
38	Mapping functional transcription factor networks from gene expression data. Genome Research, 2013, 23, 1319-1328.	5.5	48
39	Using ESTs to improve the accuracy of de novo gene prediction. BMC Bioinformatics, 2006, 7, 327.	2.6	47
40	Model-driven mapping of transcriptional networks reveals the circuitry and dynamics of virulence regulation. Genome Research, 2015, 25, 690-700.	5.5	47
41	Computational Analysis Reveals a Key Regulator of Cryptococcal Virulence and Determinant of Host Response. MBio, 2016, 7, e00313-16.	4.1	43
42	Targeted discovery of novel human exons by comparative genomics. Genome Research, 2007, 17, 1763-1773.	5.5	42
43	Gene prediction and verification in a compact genome with numerous small introns. Genome Research, 2004, 14, 2330-2335.	5.5	41
44	Closing in on the C. elegans ORFeome by cloning TWINSCAN predictions. Genome Research, 2005, 15, 577-582.	5.5	39
45	Automatic acquisition of subcategorization frames from tagged text. , 1991, , .		39
46	A quantitative model of glucose signaling in yeast reveals an incoherent feed forward loop leading to a specific, transient pulse of transcription. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 16743-16748.	7.1	37
47	Gene finding in the chicken genome. BMC Bioinformatics, 2005, 6, 131.	2.6	34
48	Begin at the beginning: Predicting genes with 5' UTRs. Genome Research, 2005, 15, 742-747.	5.5	32
49	Model-based transcriptome engineering promotes a fermentative transcriptional state in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E7428-E7437.	7.1	32
50	Identification of Rat Genes by TWINSCAN Gene Prediction, RT-PCR, and Direct Sequencing. Genome Research, 2004, 14, 665-671.	5.5	31
51	How does eukaryotic gene prediction work?. Nature Biotechnology, 2007, 25, 883-885.	17.5	30
52	Toward a Unified Model of Lexical Acquisition and Lexical Access. Journal of Psycholinguistic Research, 1997, 26, 363-375.	1.3	29
53	wuHMM: a robust algorithm to detect DNA copy number variation using long oligonucleotide microarray data. Nucleic Acids Research, 2008, 36, e41.	14.5	25
54	Benchmarking regulatory network reconstruction with GRENDEL. Bioinformatics, 2009, 25, 801-807.	4.1	25

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55	Dual threshold optimization and network inference reveal convergent evidence from TF binding locations and TF perturbation responses. Genome Research, 2020, 30, 459-471.	5.5	24
56	Cryptococcus neoformans Dual GDP-Mannose Transporters and Their Role in Biology and Virulence. Eukaryotic Cell, 2014, 13, 832-842.	3.4	23
57	Past Roadblocks and New Opportunities in Transcription Factor Network Mapping. Trends in Genetics, 2016, 32, 736-750.	6.7	23
58	A Bayesian model for morpheme and paradigm identification. , 2001, , .		22
59	Using Nâ€SCAN or TWINSCAN to Predict Gene Structures in Genomic DNA Sequences. Current Protocols in Bioinformatics, 2007, 20, Unit 4.8.	25.8	20
60	Inferring TF activities and activity regulators from gene expression data with constraints from TF perturbation data. Bioinformatics, 2021, 37, 1234-1245.	4.1	18
61	Pairagon+N-SCAN_EST: a model-based gene annotation pipeline. Genome Biology, 2006, 7, S5.	9.6	15
62	Reduced DICER1 Elicits an Interferon Response in Endometrial Cancer Cells. Molecular Cancer Research, 2012, 10, 316-325.	3.4	15
63	Seven-Up Is a Novel Regulator of Insulin Signaling. Genetics, 2018, 208, 1643-1656.	2.9	14
64	NetProphet 2.0: mapping transcription factor networks by exploiting scalable data resources. Bioinformatics, 2018, 34, 249-257.	4.1	14
65	A tale of two templates: Automatically resolving double traces has many applications, including efficient PCR-based elucidation of alternative splices. Genome Research, 2007, 17, 212-218.	5.5	13
66	Surface cues and robust inference as a basis for the early acquisition of subcategorization frames. Lingua, 1994, 92, 433-470.	1.0	12
67	Unintended Side Effects of Transformation Are Very Rare in <i>Cryptococcus neoformans</i>. G3: Genes, Genomes, Genetics, 2018, 8, 815-822.	1.8	12
68	The Transcription Factor Pdr802 Regulates Titan Cell Formation and Pathogenicity of Cryptococcus neoformans. MBio, 2021, 12, .	4.1	11
69	The Treeterbi and Parallel Treeterbi algorithms: efficient, optimal decoding for ordinary, generalized and pair HMMs. Bioinformatics, 2007, 23, 545-554.	4.1	9
70	Predicting full-length transcripts. Trends in Biotechnology, 2002, 20, 273-275.	9.3	8
71	Using Multiple Alignments to Improve Gene Prediction. Lecture Notes in Computer Science, 2005, , 374-388.	1.3	8
72	The Effects of Evolutionary Distance on TWINSCAN, an Algorithm for Pair-wise Comparative Gene Prediction. Cold Spring Harbor Symposia on Quantitative Biology, 2003, 68, 125-130.	1.1	7

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73	Using several pair-wise informant sequences for de novo prediction of alternatively spliced transcripts. Genome Biology, 2006, 7, S8.	9.6	6
74	Pairagon: a highly accurate, HMM-based cDNA-to-genome aligner. Bioinformatics, 2009, 25, 1587-1593.	4.1	6
75	A simplified theory of tense representations and constraints on their composition. , 1990, , .		6
76	Lexical categorization: Fitting template grammars by incremental MDL optimization. Lecture Notes in Computer Science, 1996, , 84-94.	1.3	2
77	Using TWINSCAN to Predict Gene Structures in Genomic DNA Sequences. Current Protocols in Bioinformatics, 2003, 3, 4.8.1.	25.8	2
78	Gradient-Based Feature Selection for Conditional Random Fields and its Applications in Computational Genetics. , 2009, , .		2
79	Constrained optimization for validation-guided conditional random field learning. , 2009, , .		1
80	Recent advances in gene structure prediction. Current Opinion in Structural Biology, 2004, 14, 264-264.	5.7	0
81	Model-based Transcriptome Engineering. , 2017, , .		0
82	A Quantitative Model of Glucose Signaling in Yeast Reveals an Incoherent Feed Forward Loop Leading to a Specific, Transient Pulse of Transcription. Lecture Notes in Computer Science, 2011, , 153-153.	1.3	0
83	Abstract 1173: A genomics approach to understanding DICER1's role in tumorigenesis. , 2011, , .		0
84	Abstract 2312: A genomics approach to determining the role of DICER1 in tumorigenesis: Interferon responses in the cancer cell. , 2012, , .		0