Martin Vingron

List of Publications by Year
in descending order

188 papers	22,327 citations	22099 59 h-index	9553 142 g-index
202 all docs	202 docs citations	202 times ranked	35802 citing authors

#	Article	IF	Citations
1	Minimum information about a microarray experiment (MIAME)â€"toward standards for microarray data. Nature Genetics, 2001, 29, 365-371.	9.4	3,750
2	A gene expression map of Arabidopsis thaliana development. Nature Genetics, 2005, 37, 501-506.	9.4	2,293
3	Comprehensive genomic profiles of small cell lung cancer. Nature, 2015, 524, 47-53.	13.7	1,634
4	A Global View of Gene Activity and Alternative Splicing by Deep Sequencing of the Human Transcriptome. Science, 2008, 321, 956-960.	6.0	1,164
5	Histone modification levels are predictive for gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2926-2931.	3.3	664
6	Formation of new chromatin domains determines pathogenicity of genomic duplications. Nature, 2016, 538, 265-269.	13.7	582
7	The Translational Landscape of the Human Heart. Cell, 2019, 178, 242-260.e29.	13.5	407
8	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
9	Homology of 54K protein of signal-recognition particle, docking protein and two E. coli proteins with putative GTPâ€"binding domains. Nature, 1989, 340, 478-482.	13.7	388
10	T cells become licensed in the lung to enter the central nervous system. Nature, 2012, 488, 675-679.	13.7	363
11	BLUEPRINT to decode the epigenetic signature written in blood. Nature Biotechnology, 2012, 30, 224-226.	9.4	323
12	Modeling Amino Acid Replacement. Journal of Computational Biology, 2000, 7, 761-776.	0.8	312
13	Plant nitric oxide synthase: a never-ending story?. Trends in Plant Science, 2006, 11, 524-525.	4.3	297
14	A trans-acting locus regulates an anti-viral expression network and type 1 diabetes risk. Nature, 2010, 467, 460-464.	13.7	271
15	Integrative genomic profiling of large-cell neuroendocrine carcinomas reveals distinct subtypes of high-grade neuroendocrine lung tumors. Nature Communications, 2018, 9, 1048.	5.8	254
16	Frequent mutations in chromatin-remodelling genes in pulmonary carcinoids. Nature Communications, 2014, 5, 3518.	5.8	239
17	CD74â€"NRG1 Fusions in Lung Adenocarcinoma. Cancer Discovery, 2014, 4, 415-422.	7.7	238
18	Sequence alignment and penalty choice. Journal of Molecular Biology, 1994, 235, 1-12.	2.0	228

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19	Haplotype-resolved sweet potato genome traces back its hexaploidization history. Nature Plants, 2017, 3, 696-703.	4.7	228
20	Functional dissection of the Sox9â€“Kcnj2 locus identifies nonessential and instructive roles of TAD architecture. Nature Genetics, 2019, 51, 1263-1271.	9.4	223
21	Transcription factor binding predictions using TRAP for the analysis of ChIP-seq data and regulatory SNPs. Nature Protocols, 2011, 6, 1860-1869.	5.5	220
22	Increase of functional diversity by alternative splicing. Trends in Genetics, 2003, 19, 124-128.	2.9	208
23	Gene expression screening in Xenopus identifies molecular pathways, predicts gene function and provides a global view of embryonic patterning. Mechanisms of Development, 1998, 77, 95-141.	1.7	198
24	Monitoring the Switch from Housekeeping to Pathogen Defense Metabolism in Arabidopsis thaliana Using cDNA Arrays. Journal of Biological Chemistry, 2002, 277, 10555-10561.	1.6	193
25	Identification and Classification of Differentially Expressed Genes in Renal Cell Carcinoma by Expression Profiling on a Global Human 31,500-Element cDNA Array. Genome Research, 2001, 11, 1861-1870.	2.4	184
26	Predicting transcription factor affinities to DNA from a biophysical model. Bioinformatics, 2007, 23, 134-141.	1.8	184
27	Polymer physics predicts the effects of structural variants on chromatin architecture. Nature Genetics, 2018, 50, 662-667.	9.4	179
28	SVIM: structural variant identification using mapped long reads. Bioinformatics, 2019, 35, 2907-2915.	1.8	173
29	Soluble epoxide hydrolase is a susceptibility factor for heart failure in a rat model of human disease. Nature Genetics, 2008, 40, 529-537.	9.4	163
30	New Evidence for Genome-Wide Duplications at the Origin of Vertebrates Using an Amphioxus Gene Set and Completed Animal Genomes. Genome Research, 2003, 13, 1056-1066.	2.4	157
31	Dynamic 3D chromatin architecture contributes to enhancer specificity and limb morphogenesis. Nature Genetics, 2018, 50, 1463-1473.	9.4	147
32	The SRF Target Gene Fhl2 Antagonizes RhoA/MAL-Dependent Activation of SRF. Molecular Cell, 2004, 16, 867-880.	4.5	137
33	The BTB and CNC Homology 1 (BACH1) Target Genes Are Involved in the Oxidative Stress Response and in Control of the Cell Cycle. Journal of Biological Chemistry, 2011, 286, 23521-23532.	1.6	136
34	A New Subfamily of Vertebrate Calpains Lacking a Calmodulin-Like Domain: Implications for Calpain Regulation and Evolution. Genomics, 1997, 45, 175-184.	1.3	134
35	Prediction of alternative isoforms from exon expression levels in RNA-Seq experiments. Nucleic Acids Research, 2010, 38, e112-e112.	6.5	134
36	Preformed chromatin topology assists transcriptional robustness of Shh during limb development. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 12390-12399.	3.3	131

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37	TIFâ€IA, the factor mediating growthâ€dependent control of ribosomal RNA synthesis, is the mammalian homolog of yeast Rrn3p. EMBO Reports, 2000, 1, 171-175.	2.0	128
38	Estimating Amino Acid Substitution Models: A Comparison of Dayhoff's Estimator, the Resolvent Approach and a Maximum Likelihood Method. Molecular Biology and Evolution, 2002, 19, 8-13.	3.5	123
39	Characterization of hundreds of regulatory landscapes in developing limbs reveals two regimes of chromatin folding. Genome Research, 2017, 27, 223-233.	2.4	123
40	Transcriptional profiling on all open reading frames ofSaccharomyces cerevisiae. , 1998, 14, 1209-1221.		118
41	Mapping translocation breakpoints by next-generation sequencing. Genome Research, 2008, 18, 1143-1149.	2.4	118
42	Motif recognition and alignment for many sequences by comparison of dot-matrices. Journal of Molecular Biology, 1991, 218, 33-43.	2.0	116
43	ChIP-exo signal associated with DNA-binding motifs provides insight into the genomic binding of the glucocorticoid receptor and cooperating transcription factors. Genome Research, 2015, 25, 825-835.	2.4	113
44	Genome-Wide Array Analysis of Normal and Malformed Human Hearts. Circulation, 2003, 107, 2467-2474.	1.6	109
45	Composition and dosage of a multipartite enhancer cluster control developmental expression of Ihh (Indian hedgehog). Nature Genetics, 2017, 49, 1539-1545.	9.4	107
46	Serial genomic inversions induce tissue-specific architectural stripes, gene misexpression and congenital malformations. Nature Cell Biology, 2019, 21, 305-310.	4.6	107
47	The Effect of Micrococcal Nuclease Digestion on Nucleosome Positioning Data. PLoS ONE, 2010, 5, e15754.	1.1	106
48	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. Cell Reports, 2018, 24, 2784-2794.	2.9	104
49	Paracrine control of oligodendrocyte differentiation by SRF-directed neuronal gene expression. Nature Neuroscience, 2009, 12, 418-427.	7.1	99
50	Determination of reliable regions in protein sequence alignments. Protein Engineering, Design and Selection, 1990, 3, 565-569.	1.0	89
51	Genome-wide Kinase-Chromatin Interactions Reveal the Regulatory Network of ERK Signaling in Human Embryonic Stem Cells. Molecular Cell, 2013, 50, 844-855.	4.5	88
52	Hi-C Identifies Complex Genomic Rearrangements and TAD-Shuffling in Developmental Diseases. American Journal of Human Genetics, 2020, 106, 872-884.	2.6	85
53	On the Power of Profiles for Transcription Factor Binding Site Detection. Statistical Applications in Genetics and Molecular Biology, 2003, 2, Article7.	0.2	80
54	Early vertebrate whole genome duplications were predated by a period of intense genome rearrangement. Genome Research, 2008, 18, 1582-1591.	2.4	80

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55	Translational regulation shapes the molecular landscape of complex disease phenotypes. Nature Communications, 2015, 6, 7200.	5.8	79
56	Esrrb Unlocks Silenced Enhancers for Reprogramming to Naive Pluripotency. Cell Stem Cell, 2018, 23, 266-275.e6.	5.2	79
57	Primer design for large scale sequencing. Nucleic Acids Research, 1998, 26, 3006-3012.	6.5	75
58	Normalization and quantification of differential expression in gene expression microarrays. Briefings in Bioinformatics, 2006, 7, 166-177.	3.2	69
59	Gene expression profile of mouse bone marrow stromal cells determined by cDNA microarray analysis. Cell and Tissue Research, 2003, 311, 227-237.	1.5	64
60	Gene expression in kidney cancer is associated with cytogenetic abnormalities, metastasis formation, and patient survival. Clinical Cancer Research, 2005, 11, 646-55.	3.2	64
61	Quantifying the effect of sequence variation on regulatory interactions. Human Mutation, 2010, 31, 477-483.	1.1	62
62	Methylation and deamination of CpGs generate p53-binding sites on a genomic scale. Trends in Genetics, 2009, 25, 63-66.	2.9	61
63	Genome-wide H4 K16 acetylation by SAS-I is deposited independently of transcription and histone exchange. Nucleic Acids Research, 2012, 40, 65-74.	6.5	60
64	Quantifying the local reliability of a sequence alignment. Protein Engineering, Design and Selection, 1996, 9, 127-132.	1.0	58
65	Genome-wide comparison of cyanobacterial transposable elements, potential genetic diversity indicators. Gene, 2011, 473, 139-149.	1.0	58
66	Role of the chromatin landscape and sequence in determining cell type-specific genomic glucocorticoid receptor binding and gene regulation. Nucleic Acids Research, 2017, 45, 1805-1819.	6.5	56
67	Nucleotide sequence of the glyceraldehyde-3-phosphate dehydrogenase gene from the mesophilic methanogenic archaebacteria Methanobacterium bryantii and Methanobacterium formicicum. Comparison with the respective gene structure of the closely related extreme thermophile Methanothermus fervidus. FEBS Journal, 1989, 179, 405-413.	0.2	55
68	SYSTERS, GeneNest, SpliceNest: exploring sequence space from genome to protein. Nucleic Acids Research, 2002, 30, 299-300.	6.5	54
69	Statistical Modeling of Transcription Factor Binding Affinities Predicts Regulatory Interactions. PLoS Computational Biology, 2008, 4, e1000039.	1.5	54
70	Sequence-dependent Nucleosome Positioning. Journal of Molecular Biology, 2009, 386, 1411-1422.	2.0	54
71	Natural variation of histone modification and its impact on gene expression in the rat genome. Genome Research, 2014, 24, 942-953.	2.4	53
72	A systems biological approach suggests that transcriptional feedback regulation by dualâ€specificity phosphataseâ€ƒ6 shapes extracellular signalâ€related kinase activity in RASâ€transformed fibroblasts. FEBS Journal, 2009, 276, 1024-1035.	2.2	52

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73	A naturally occuring insertion of a single amino acid rewires transcriptional regulation by glucocorticoid receptor isoforms. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17826-17831.	3.3	52
74	Control of replication initiation and heterochromatin formation in Saccharomyces cerevisiae by a regulator of meiotic gene expression. Genes and Development, 2005, 19, 1811-1822.	2.7	50
75	A Polyhedral Approach to RNA Sequence Structure Alignment. Journal of Computational Biology, 1998, 5, 517-530.	0.8	48
76	A polyhedral approach to sequence alignment problems. Discrete Applied Mathematics, 2000, 104, 143-186.	0.5	48
77	Sequences flanking the core-binding site modulate glucocorticoid receptor structure and activity. Nature Communications, 2016, 7, 12621.	5.8	48
78	SVIM-asm: structural variant detection from haploid and diploid genome assemblies. Bioinformatics, 2021, 36, 5519-5521.	1.8	47
79	CpG Deamination Creates Transcription Factorâ€“Binding Sites with High Efficiency. Genome Biology and Evolution, 2011, 3, 1304-1311.	1.1	45
80	CpG-depleted promoters harbor tissue-specific transcription factor binding signalsâ€”implications for motif overrepresentation analyses. Nucleic Acids Research, 2009, 37, 6305-6315.	6.5	44
81	Identification of novel fusion genes in lung cancer using breakpoint assembly of transcriptome sequencing data. Genome Biology, 2015, 16, 7.	3.8	44
82	GeneNest: automated generation and visualization of gene indices. Trends in Genetics, 2000, 16, 521-523.	2.9	43
83	Deeply conserved chordate noncoding sequences preserve genome synteny but do not drive gene duplicate retention. Genome Research, 2009, 19, 2036-2051.	2.4	43
84	Combinatorial Binding in Human and Mouse Embryonic Stem Cells Identifies Conserved Enhancers Active in Early Embryonic Development. PLoS Computational Biology, 2011, 7, e1002304.	1.5	43
85	Near-optimal sequence alignment. Current Opinion in Structural Biology, 1996, 6, 346-352.	2.6	42
86	SpliceNest: visualizing gene structure and alternative splicing based on EST clusters. Trends in Genetics, 2002, 18, 53-55.	2.9	42
87	The mole genome reveals regulatory rearrangements associated with adaptive intersexuality. Science, 2020, 370, 208-214.	6.0	41
88	Analysis of CREM-dependent gene expression during mouse spermatogenesis. Molecular and Cellular Endocrinology, 2003, 212, 29-39.	1.6	39
89	A DNA microarray for fission yeast: minimal changes in global gene expression after temperature shift. Yeast, 2004, 21, 25-39.	0.8	39
90	Finding Associations among Histone Modifications Using Sparse Partial Correlation Networks. PLoS Computational Biology, 2013, 9, e1003168.	1.5	39

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91	ssHMM: extracting intuitive sequence-structure motifs from high-throughput RNA-binding protein data. Nucleic Acids Research, 2017, 45, 11004-11018.	6.5	39
92	Linking aberrant chromatin features in chronic lymphocytic leukemia to transcription factor networks. Molecular Systems Biology, 2019, 15, e8339.	3.2	39
93	Protein sequence comparison: methods and significance. Protein Engineering, Design and Selection, 1991, 4, 375-383.	1.0	38
94	An entropic characterization of protein interaction networks and cellular robustness. Journal of the Royal Society Interface, 2006, 3, 843-850.	1.5	38
95	Epigenomic Co-localization and Co-evolution Reveal a Key Role for 5hmC as a Communication Hub in the Chromatin Network of ESCs. Cell Reports, 2016, 14, 1246-1257.	2.9	38
96	Epigenomic profiling of non-small cell lung cancer xenografts uncover LRP12 DNA methylation as predictive biomarker for carboplatin resistance. Genome Medicine, 2018, 10, 55.	3.6	37
97	Capn7: A highly divergent vertebrate calpain with a novel C-terminal domain. Mammalian Genome, 1999, 10, 318-321.	1.0	36
98	The KRAB-containing zinc-finger transcriptional regulator ZBRK1 activates SCA2 gene transcription through direct interaction with its gene product, ataxin-2. Human Molecular Genetics, 2011, 20, 104-114.	1.4	36
99	Inferring the paths of somatic evolution in cancer. Bioinformatics, 2014, 30, 2456-2463.	1.8	36
100	Towards Integration of Multiple Alignment and Phylogenetic Tree Construction. Journal of Computational Biology, 1997, 4, 23-34.	0.8	35
101	Transcriptional Autoregulatory Loops Are Highly Conserved in Vertebrate Evolution. PLoS ONE, 2008, 3, e3210.	1.1	35
102	Correlating Proteinâ€“DNA and Proteinâ€“Protein Interaction Networks. Journal of Molecular Biology, 2003, 333, 75-85.	2.0	34
103	Predicting the outcome of renal transplantation. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 255-262.	2.2	33
104	Genome-wide analysis of LXRÎ± activation reveals new transcriptional networks in human atherosclerotic foam cells. Nucleic Acids Research, 2013, 41, 3518-3531.	6.5	32
105	Evolution of DNA-Binding Sites of a Floral Master Regulatory Transcription Factor. Molecular Biology and Evolution, 2016, 33, 185-200.	3.5	32
106	Genome-scale design of PCR primers and long oligomers for DNA microarrays. Nucleic Acids Research, 2003, 31, 5576-5581.	6.5	31
107	Condition-specific target prediction from motifs and expression. Bioinformatics, 2014, 30, 1643-1650.	1.8	30
108	Genomic dissection of enhancers uncovers principles of combinatorial regulation and cell type-specific wiring of enhancerâ€“promoter contacts. Nucleic Acids Research, 2018, 46, 2868-2882.	6.5	30

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109	Computational aspects of expression data. Journal of Molecular Medicine, 1999, 77, 3-7.	1.7	29
110	Synthetic STARR-seq reveals how DNA shape and sequence modulate transcriptional output and noise. PLoS Genetics, 2018, 14, e1007793.	1.5	29
111	Conserved DNA sequence features underlie pervasive RNA polymerase pausing. Nucleic Acids Research, 2021, 49, 4402-4420.	6.5	29
112	histoneHMM: Differential analysis of histone modifications with broad genomic footprints. BMC Bioinformatics, 2015, 16, 60.	1.2	28
113	A calibrated diversity assay for nucleic acid libraries using DiStROâ€"a Diversity Standard of Random Oligonucleotides. Nucleic Acids Research, 2010, 38, e23-e23.	6.5	27
114	Synthetic sickness or lethality points at candidate combination therapy targets in glioblastoma. International Journal of Cancer, 2013, 133, 2123-2132.	2.3	27
115	Elucidating regulatory mechanisms downstream of a signaling pathway using informative experiments. Molecular Systems Biology, 2009, 5, 287.	3.2	26
116	CRUP: a comprehensive framework to predict condition-specific regulatory units. Genome Biology, 2019, 20, 227.	3.8	26
117	Enhanced cortical neural stem cell identity through short SMAD and WNT inhibition in human cerebral organoids facilitates emergence of outer radial glial cells. Nature Cell Biology, 2022, 24, 981-995.	4.6	26
118	Multiomic atlas with functional stratification and developmental dynamics of zebrafish cis-regulatory elements. Nature Genetics, 2022, 54, 1037-1050.	9.4	26
119	Comparative 3'UTR Analysis Allows Identification of Regulatory Clusters that Drive Eph/ephrin Expression in Cancer Cell Lines. PLoS ONE, 2008, 3, e2780.	1.1	25
120	Inference of interactions between chromatin modifiers and histone modifications: from ChIP-Seq data to chromatin-signaling. Nucleic Acids Research, 2014, 42, 13689-13695.	6.5	23
121	Ranbow: A fast and accurate method for polyploid haplotype reconstruction. PLoS Computational Biology, 2020, 16, e1007843.	1.5	23
122	Integer linear programming approaches for non-unique probe selection. Discrete Applied Mathematics, 2007, 155, 840-856.	0.5	22
123	Single-Cell Analysis Uncovers a Vast Diversity in Intracellular Viral Defective Interfering RNA Content Affecting the Large Cell-to-Cell Heterogeneity in Influenza A Virus Replication. Viruses, 2020, 12, 71.	1.5	22
124	Identification of highly specific localized sequence motifs in human ribosomal protein gene promoters. Gene, 2006, 365, 48-56.	1.0	20
125	Horizontal Gene Transfer in Aminoacyl-tRNA Synthetases Including Leucine-Specific Subtypes. Journal of Molecular Evolution, 2006, 63, 437-447.	0.8	20
126	Somatic neurofibromatosis type 1 (NF1) inactivation events in cutaneous neurofibromas of a single NF1 patient. European Journal of Human Genetics, 2015, 23, 870-873.	1.4	20

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127	Phylogenetic information improves homology detection. Proteins: Structure, Function and Bioinformatics, 2001, 45, 360-371.	1.5	19
128	Functional analysis and identification of cis-regulatory elements of human chromosome 21 gene promoters. Nucleic Acids Research, 2010, 38, 6112-6123.	6.5	19
129	Studying the Evolution of Promoter Sequences: A Waiting Time Problem. Journal of Computational Biology, 2010, 17, 1591-1606.	0.8	19
130	Reconstruction of gene regulatory network related to photosynthesis in Arabidopsis thaliana. Frontiers in Plant Science, 2014, 5, 273.	1.7	19
131	Integrating sequence, evolution and functional genomics in regulatory genomics. Genome Biology, 2009, 10, 202.	13.9	18
132	Reconstruction of gene networks using prior knowledge. BMC Systems Biology, 2015, 9, 84.	3.0	18
133	Effect of imputation on gene network reconstruction from single-cell RNA-seq data. Patterns, 2022, 3, 100414.	3.1	17
134	Detection of interacting transcription factors in human tissues using predicted DNA binding affinity. BMC Genomics, 2012, 13, S2.	1.2	16
135	The Deferred Path Heuristic for the Generalized Tree Alignment Problem. Journal of Computational Biology, 1997, 4, 415-431.	0.8	15
136	Prediction of cardiac transcription networks based on molecular data and complex clinical phenotypes. Molecular BioSystems, 2008, 4, 589.	2.9	15
137	Compound Poisson Approximation of the Number of Occurrences of a Position Frequency Matrix (PFM) on Both Strands. Journal of Computational Biology, 2008, 15, 547-564.	0.8	14
138	A MicroRNA Network Controls Legionella pneumophila Replication in Human Macrophages via LGALS8 and MX1. MBio, 2020, 11, .	1.8	14
139	Anisotropic expansion of hepatocyte lumina enforced by apical bulkheads. Journal of Cell Biology, 2021, 220, .	2.3	14
140	Evidence for Gene-Specific Rather Than Transcription Rateâ€“Dependent Histone H3 Exchange in Yeast Coding Regions. PLoS Computational Biology, 2009, 5, e1000282.	1.5	13
141	Genome-wide Chromatin Profiling ofLegionella pneumophilaâ€“Infected Human Macrophages Reveals Activation of the Probacterial Host Factor TNFAIP2. Journal of Infectious Diseases, 2016, 214, 454-463.	1.9	13
142	Predicting enhancers in mammalian genomes using supervised hidden Markov models. BMC Bioinformatics, 2019, 20, 157.	1.2	12
143	Assessing genome-wide dynamic changes in enhancer activity during early mESC differentiation by FAIRE-STARR-seq. Nucleic Acids Research, 2021, 49, 12178-12195.	6.5	12
144	Transcriptional profiling: is it worth the money?. Research in Microbiology, 2000, 151, 113-119.	1.0	11

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145	Effects of Long-Range Correlations in DNA on Sequence Alignment Score Statistics. Journal of Computational Biology, 2007, 14, 655-668.	0.8	11
146	A computational evaluation of over-representation of regulatory motifs in the promoter regions of differentially expressed genes. BMC Bioinformatics, 2010, 11, 267.	1.2	11
147	The Distance Precision Matrix: computing networks from non-linear relationships. Bioinformatics, 2019, 35, 1009-1017.	1.8	11
148	Weighted sequence graphs: boosting iterated dynamic programming using locally suboptimal solutions. Discrete Applied Mathematics, 2003, 127, 95-117.	0.5	9
149	Functional inference from non-random distributions of conserved predicted transcription factor binding sites. Bioinformatics, 2004, 20, i109-i115.	1.8	9
150	Introducing Knowledge into Differential Expression Analysis. Journal of Computational Biology, 2010, 17, 953-967.	0.8	9
151	An improved compound Poisson model for the number of motif hits in DNA sequences. Bioinformatics, 2017, 33, 3929-3937.	1.8	9
152	Classifying human promoters by occupancy patterns identifies recurring sequence elements, combinatorial binding, and spatial interactions. BMC Biology, 2018, 16, 138.	1.7	9
153	Haplotype Reconstruction for Diploid Populations. Human Heredity, 2005, 59, 144-156.	0.4	8
154	Incorporating evolution of transcription factor binding sites into annotated alignments. Journal of Biosciences, 2007, 32, 841-850.	0.5	8
155	Improved Prediction of Non-methylated Islands in Vertebrates Highlights Different Characteristic Sequence Patterns. PLoS Computational Biology, 2016, 12, e1005249.	1.5	8
156	coTRaCTE predicts co-occurring transcription factors within cell-type specific enhancers. PLoS Computational Biology, 2018, 14, e1006372.	1.5	8
157	The deferred path heuristic for the generalized tree alignment problem. , 1997, , .		7
158	Lethality and entropy of protein interaction networks. Genome Informatics, 2005, 16, 159-63.	0.4	7
159	Visualizing Cluster-specific Genes from Single-cell Transcriptomics Data Using Association Plots. Journal of Molecular Biology, 2022, 434, 167525.	2.0	7
160	Simultaneous alignment and annotation of cis-regulatory regions. Bioinformatics, 2007, 23, e44-e49.	1.8	6
161	R2KS: A Novel Measure for Comparing Gene Expression Based on Ranked Gene Lists. Journal of Computational Biology, 2012, 19, 766-775.	0.8	6
162	ModHMM: A Modular Supra-Bayesian Genome Segmentation Method. Journal of Computational Biology, 2020, 27, 442-457.	0.8	6

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163	Application of Bootstrap Techniques to Physical Mapping. Genomics, 2000, 69, 235-241.	1.3	5
164	A new statistical model to select target sequences bound by transcription factors. Genome Informatics, 2006, 17, 134-40.	0.4	5
165	About the interrelation of evolutionary rate and protein age. Genome Informatics, 2006, 17, 240-50.	0.4	5
166	A trans locus causes a ribosomopathy in hypertrophic hearts that affects mRNA translation in a protein length-dependent fashion. Genome Biology, 2021, 22, 191.	3.8	4
167	Position effects at the FGF8 locus are associated with femoral hypoplasia. American Journal of Human Genetics, 2021, 108, 1725-1734.	2.6	4
168	TADAâ€"a machine learning tool for functional annotation-based prioritisation of pathogenic CNVs. Genome Biology, 2022, 23, 67.	3.8	4
169	Alignment networks and electrical networks. Discrete Applied Mathematics, 1996, 71, 297-309.	0.5	3
170	P53 Binding Sites in Transposons. Frontiers in Genetics, 2012, 3, 40.	1.1	3
171	Contig Selection in Physical Mapping. Journal of Computational Biology, 2000, 7, 395-408.	0.8	2
172	DNA Motif Match Statistics Without Poisson Approximation. Journal of Computational Biology, 2019, 26, 846-865.	0.8	1
173	ISCB Honors 2021 Award Recipients Peer Bork, Barbara Engelhardt, Ben Raphael, Teresa Attwood. Bioinformatics, 2021, 37, i1-i6.	1.8	1
174	USING TRANSCRIPTION FACTOR BINDING SITE CO-OCCURRENCE TO PREDICT REGULATORY REGIONS. , 2007, , .		1
175	Annotating significant pairs of transcription factor binding sites in regulatory DNA. In Silico Biology, 2004, 4, 479-87.	0.4	1
176	Special RECOMB 2003 Issue. Journal of Computational Biology, 2004, 11, 213-213.	0.8	0
177	Corrigendum to â€œMammalian mitochondrial nitric oxide synthase: Characterization of a novel candidateâ€•[FEBS Lett. 580 (2006) 455-462]. FEBS Letters, 2007, 581, 2072-2073.	1.3	0
178	The BREW workshop series: a stimulating experience in PhD education. Briefings in Bioinformatics, 2008, 9, 250-253.	3.2	0
179	Maximum Similarity: A New Formulation of Phylogenetic Reconstruction. Journal of Computational Biology, 2009, 16, 887-896.	0.8	0
180	Special RECOMB 2008 Issue. Journal of Computational Biology, 2009, 16, 969-969.	0.8	0

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181	Statistical tools for discovering pseudo-periodicities in biological sequences. ESAIM - Probability and Statistics, 2001, 5, 171-181.	0.2	0
182	Quantifying the tissue-specific regulatory information within enhancer DNA sequences. NAR Genomics and Bioinformatics, 2021, 3, lqab095.	1.5	0
183	Bioinformatics research and education in Germany. In Silico Biology, 2002, 2, 169-71.	0.4	0
184	Michael Waterman's Contributions to Computational Biology and Bioinformatics. Journal of Computational Biology, 0, , .	0.8	0
185	2022 Outstanding Contributions to ISCB Award: Reinhard Schneider. Bioinformatics, 2022, 38, i7-i7.	1.8	0
186	2022 ISCB Innovator Award: NÃºria LÃ³pez-Bigas. Bioinformatics, 2022, 38, i5-i6.	1.8	0
187	2022 ISCB Overton Prize: Po-Ru Loh. Bioinformatics, 2022, 38, i3-i4.	1.8	0
188	2022 ISCB Accomplishments by a Senior Scientist Award: Ron Shamir. Bioinformatics, 2022, 38, i1-i2.	1.8	0