

# Martin Vingron

## List of Publications by Year in descending order

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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	Effect of imputation on gene network reconstruction from single-cell RNA-seq data. <i>Patterns</i> , 2022, 3, 100414.	3.1	17
2	TADA—a machine learning tool for functional annotation-based prioritisation of pathogenic CNVs. <i>Genome Biology</i> , 2022, 23, 67.	3.8	4
3	Visualizing Cluster-specific Genes from Single-cell Transcriptomics Data Using Association Plots. <i>Journal of Molecular Biology</i> , 2022, 434, 167525.	2.0	7
4	Enhanced cortical neural stem cell identity through short SMAD and WNT inhibition in human cerebral organoids facilitates emergence of outer radial glial cells. <i>Nature Cell Biology</i> , 2022, 24, 981-995.	4.6	26
5	2022 Outstanding Contributions to ISCB Award: Reinhard Schneider. <i>Bioinformatics</i> , 2022, 38, i7-i7.	1.8	0
6	2022 ISCB Innovator Award: Nària Lázpez-Bigas. <i>Bioinformatics</i> , 2022, 38, i5-i6.	1.8	0
7	2022 ISCB Overton Prize: Po-Ru Loh. <i>Bioinformatics</i> , 2022, 38, i3-i4.	1.8	0
8	2022 ISCB Accomplishments by a Senior Scientist Award: Ron Shamir. <i>Bioinformatics</i> , 2022, 38, i1-i2.	1.8	0
9	Multimic atlas with functional stratification and developmental dynamics of zebrafish cis-regulatory elements. <i>Nature Genetics</i> , 2022, 54, 1037-1050.	9.4	26
10	SVIM-asm: structural variant detection from haploid and diploid genome assemblies. <i>Bioinformatics</i> , 2021, 36, 5519-5521.	1.8	47
11	Conserved DNA sequence features underlie pervasive RNA polymerase pausing. <i>Nucleic Acids Research</i> , 2021, 49, 4402-4420.	6.5	29
12	A trans locus causes a ribosomopathy in hypertrophic hearts that affects mRNA translation in a protein length-dependent fashion. <i>Genome Biology</i> , 2021, 22, 191.	3.8	4
13	Anisotropic expansion of hepatocyte lumina enforced by apical bulkheads. <i>Journal of Cell Biology</i> , 2021, 220, .	2.3	14
14	ISCB Honors 2021 Award Recipients Peer Bork, Barbara Engelhardt, Ben Raphael, Teresa Attwood. <i>Bioinformatics</i> , 2021, 37, i1-i6.	1.8	1
15	Position effects at the FGF8 locus are associated with femoral hypoplasia. <i>American Journal of Human Genetics</i> , 2021, 108, 1725-1734.	2.6	4
16	Assessing genome-wide dynamic changes in enhancer activity during early mESC differentiation by FAIRE-STARR-seq. <i>Nucleic Acids Research</i> , 2021, 49, 12178-12195.	6.5	12
17	Quantifying the tissue-specific regulatory information within enhancer DNA sequences. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab095.	1.5	0
18	The mole genome reveals regulatory rearrangements associated with adaptive intersexuality. <i>Science</i> , 2020, 370, 208-214.	6.0	41

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19	Ranbow: A fast and accurate method for polyploid haplotype reconstruction. PLoS Computational Biology, 2020, 16, e1007843.	1.5	23
20	Hi-C Identifies Complex Genomic Rearrangements and TAD-Shuffling in Developmental Diseases. American Journal of Human Genetics, 2020, 106, 872-884.	2.6	85
21	ModHMM: A Modular Supra-Bayesian Genome Segmentation Method. Journal of Computational Biology, 2020, 27, 442-457.	0.8	6
22	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
23	A MicroRNA Network Controls <i>Legionella pneumophila</i> Replication in Human Macrophages via LGALS8 and MX1. MBio, 2020, 11, .	1.8	14
24	Functional dissection of the Sox9-Kcnj2 locus identifies nonessential and instructive roles of TAD architecture. Nature Genetics, 2019, 51, 1263-1271.	9.4	223
25	CRUP: a comprehensive framework to predict condition-specific regulatory units. Genome Biology, 2019, 20, 227.	3.8	26
26	DNA Motif Match Statistics Without Poisson Approximation. Journal of Computational Biology, 2019, 26, 846-865.	0.8	1
27	SVIM: structural variant identification using mapped long reads. Bioinformatics, 2019, 35, 2907-2915.	1.8	173
28	The Translational Landscape of the Human Heart. Cell, 2019, 178, 242-260.e29.	13.5	407
29	Preformed chromatin topology assists transcriptional robustness of <i>Shh</i> during limb development. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 12390-12399.	3.3	131
30	Linking aberrant chromatin features in chronic lymphocytic leukemia to transcription factor networks. Molecular Systems Biology, 2019, 15, e8339.	3.2	39
31	Predicting enhancers in mammalian genomes using supervised hidden Markov models. BMC Bioinformatics, 2019, 20, 157.	1.2	12
32	Serial genomic inversions induce tissue-specific architectural stripes, gene misexpression and congenital malformations. Nature Cell Biology, 2019, 21, 305-310.	4.6	107
33	The Distance Precision Matrix: computing networks from non-linear relationships. Bioinformatics, 2019, 35, 1009-1017.	1.8	11
34	Polymer physics predicts the effects of structural variants on chromatin architecture. Nature Genetics, 2018, 50, 662-667.	9.4	179
35	Genomic dissection of enhancers uncovers principles of combinatorial regulation and cell type-specific wiring of enhancer-promoter contacts. Nucleic Acids Research, 2018, 46, 2868-2882.	6.5	30
36	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

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37	Synthetic STARR-seq reveals how DNA shape and sequence modulate transcriptional output and noise. PLoS Genetics, 2018, 14, e1007793.	1.5	29
38	Classifying human promoters by occupancy patterns identifies recurring sequence elements, combinatorial binding, and spatial interactions. BMC Biology, 2018, 16, 138.	1.7	9
39	Dynamic 3D chromatin architecture contributes to enhancer specificity and limb morphogenesis. Nature Genetics, 2018, 50, 1463-1473.	9.4	147
40	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. Cell Reports, 2018, 24, 2784-2794.	2.9	104
41	coTRaCTE predicts co-occurring transcription factors within cell-type specific enhancers. PLoS Computational Biology, 2018, 14, e1006372.	1.5	8
42	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
43	Esrrb Unlocks Silenced Enhancers for Reprogramming to Naive Pluripotency. Cell Stem Cell, 2018, 23, 266-275.e6.	5.2	79
44	Characterization of hundreds of regulatory landscapes in developing limbs reveals two regimes of chromatin folding. Genome Research, 2017, 27, 223-233.	2.4	123
45	Haplotype-resolved sweet potato genome traces back its hexaploidization history. Nature Plants, 2017, 3, 696-703.	4.7	228
46	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
47	Composition and dosage of a multipartite enhancer cluster control developmental expression of <i>lh</i> (Indian hedgehog). Nature Genetics, 2017, 49, 1539-1545.	9.4	107
48	ssHMM: extracting intuitive sequence-structure motifs from high-throughput RNA-binding protein data. Nucleic Acids Research, 2017, 45, 11004-11018.	6.5	39
49	An improved compound Poisson model for the number of motif hits in DNA sequences. Bioinformatics, 2017, 33, 3929-3937.	1.8	9
50	Improved Prediction of Non-methylated Islands in Vertebrates Highlights Different Characteristic Sequence Patterns. PLoS Computational Biology, 2016, 12, e1005249.	1.5	8
51	Genome-wide Chromatin Profiling of <i>Legionella pneumophila</i> Infected Human Macrophages Reveals Activation of the Probacterial Host Factor TNFAIP2. Journal of Infectious Diseases, 2016, 214, 454-463.	1.9	13
52	Formation of new chromatin domains determines pathogenicity of genomic duplications. Nature, 2016, 538, 265-269.	13.7	582
53	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
54	Sequences flanking the core-binding site modulate glucocorticoid receptor structure and activity. Nature Communications, 2016, 7, 12621.	5.8	48

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55	Epigenomic Co-localization and Co-evolution Reveal a Key Role for 5hmC as a Communication Hub in the Chromatin Network of ESCs. <i>Cell Reports</i> , 2016, 14, 1246-1257.	2.9	38
56	Evolution of DNA-Binding Sites of a Floral Master Regulatory Transcription Factor. <i>Molecular Biology and Evolution</i> , 2016, 33, 185-200.	3.5	32
57	Reconstruction of gene networks using prior knowledge. <i>BMC Systems Biology</i> , 2015, 9, 84.	3.0	18
58	Translational regulation shapes the molecular landscape of complex disease phenotypes. <i>Nature Communications</i> , 2015, 6, 7200.	5.8	79
59	ChIP-exo signal associated with DNA-binding motifs provides insight into the genomic binding of the glucocorticoid receptor and cooperating transcription factors. <i>Genome Research</i> , 2015, 25, 825-835.	2.4	113
60	Comprehensive genomic profiles of small cell lung cancer. <i>Nature</i> , 2015, 524, 47-53.	13.7	1,634
61	histoneHMM: Differential analysis of histone modifications with broad genomic footprints. <i>BMC Bioinformatics</i> , 2015, 16, 60.	1.2	28
62	Identification of novel fusion genes in lung cancer using breakpoint assembly of transcriptome sequencing data. <i>Genome Biology</i> , 2015, 16, 7.	3.8	44
63	Somatic neurofibromatosis type 1 (NF1) inactivation events in cutaneous neurofibromas of a single NF1 patient. <i>European Journal of Human Genetics</i> , 2015, 23, 870-873.	1.4	20
64	Inference of interactions between chromatin modifiers and histone modifications: from ChIP-Seq data to chromatin-signaling. <i>Nucleic Acids Research</i> , 2014, 42, 13689-13695.	6.5	23
65	Reconstruction of gene regulatory network related to photosynthesis in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2014, 5, 273.	1.7	19
66	Inferring the paths of somatic evolution in cancer. <i>Bioinformatics</i> , 2014, 30, 2456-2463.	1.8	36
67	Frequent mutations in chromatin-remodelling genes in pulmonary carcinoids. <i>Nature Communications</i> , 2014, 5, 3518.	5.8	239
68	CD74-NRG1 Fusions in Lung Adenocarcinoma. <i>Cancer Discovery</i> , 2014, 4, 415-422.	7.7	238
69	Condition-specific target prediction from motifs and expression. <i>Bioinformatics</i> , 2014, 30, 1643-1650.	1.8	30
70	Natural variation of histone modification and its impact on gene expression in the rat genome. <i>Genome Research</i> , 2014, 24, 942-953.	2.4	53
71	Synthetic sickness or lethality points at candidate combination therapy targets in glioblastoma. <i>International Journal of Cancer</i> , 2013, 133, 2123-2132.	2.3	27
72	Genome-wide Kinase-Chromatin Interactions Reveal the Regulatory Network of ERK Signaling in Human Embryonic Stem Cells. <i>Molecular Cell</i> , 2013, 50, 844-855.	4.5	88

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73	Finding Associations among Histone Modifications Using Sparse Partial Correlation Networks. <i>PLoS Computational Biology</i> , 2013, 9, e1003168.	1.5	39
74	Genome-wide analysis of LXR $\pm$ activation reveals new transcriptional networks in human atherosclerotic foam cells. <i>Nucleic Acids Research</i> , 2013, 41, 3518-3531.	6.5	32
75	A naturally occurring insertion of a single amino acid rewires transcriptional regulation by glucocorticoid receptor isoforms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17826-17831.	3.3	52
76	Genome-wide H4 K16 acetylation by SAS-I is deposited independently of transcription and histone exchange. <i>Nucleic Acids Research</i> , 2012, 40, 65-74.	6.5	60
77	R2KS: A Novel Measure for Comparing Gene Expression Based on Ranked Gene Lists. <i>Journal of Computational Biology</i> , 2012, 19, 766-775.	0.8	6
78	Predicting the outcome of renal transplantation. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2012, 19, 255-262.	2.2	33
79	P53 Binding Sites in Transposons. <i>Frontiers in Genetics</i> , 2012, 3, 40.	1.1	3
80	T cells become licensed in the lung to enter the central nervous system. <i>Nature</i> , 2012, 488, 675-679.	13.7	363
81	Detection of interacting transcription factors in human tissues using predicted DNA binding affinity. <i>BMC Genomics</i> , 2012, 13, S2.	1.2	16
82	BLUEPRINT to decode the epigenetic signature written in blood. <i>Nature Biotechnology</i> , 2012, 30, 224-226.	9.4	323
83	Genome-wide comparison of cyanobacterial transposable elements, potential genetic diversity indicators. <i>Gene</i> , 2011, 473, 139-149.	1.0	58
84	Transcription factor binding predictions using TRAP for the analysis of ChIP-seq data and regulatory SNPs. <i>Nature Protocols</i> , 2011, 6, 1860-1869.	5.5	220
85	The KRAB-containing zinc-finger transcriptional regulator ZBRK1 activates SCA2 gene transcription through direct interaction with its gene product, ataxin-2. <i>Human Molecular Genetics</i> , 2011, 20, 104-114.	1.4	36
86	CpG Deamination Creates Transcription Factor $\alpha$ Binding Sites with High Efficiency. <i>Genome Biology and Evolution</i> , 2011, 3, 1304-1311.	1.1	45
87	The BTB and CNC Homology 1 (BACH1) Target Genes Are Involved in the Oxidative Stress Response and in Control of the Cell Cycle. <i>Journal of Biological Chemistry</i> , 2011, 286, 23521-23532.	1.6	136
88	Combinatorial Binding in Human and Mouse Embryonic Stem Cells Identifies Conserved Enhancers Active in Early Embryonic Development. <i>PLoS Computational Biology</i> , 2011, 7, e1002304.	1.5	43
89	A computational evaluation of over-representation of regulatory motifs in the promoter regions of differentially expressed genes. <i>BMC Bioinformatics</i> , 2010, 11, 267.	1.2	11
90	Quantifying the effect of sequence variation on regulatory interactions. <i>Human Mutation</i> , 2010, 31, 477-483.	1.1	62

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91	A trans-acting locus regulates an anti-viral expression network and type 1 diabetes risk. <i>Nature</i> , 2010, 467, 460-464.	13.7	271
92	Functional analysis and identification of cis-regulatory elements of human chromosome 21 gene promoters. <i>Nucleic Acids Research</i> , 2010, 38, 6112-6123.	6.5	19
93	A calibrated diversity assay for nucleic acid libraries using DiStRO—a Diversity Standard of Random Oligonucleotides. <i>Nucleic Acids Research</i> , 2010, 38, e23-e23.	6.5	27
94	Prediction of alternative isoforms from exon expression levels in RNA-Seq experiments. <i>Nucleic Acids Research</i> , 2010, 38, e112-e112.	6.5	134
95	Introducing Knowledge into Differential Expression Analysis. <i>Journal of Computational Biology</i> , 2010, 17, 953-967.	0.8	9
96	Histone modification levels are predictive for gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2926-2931.	3.3	664
97	Studying the Evolution of Promoter Sequences: A Waiting Time Problem. <i>Journal of Computational Biology</i> , 2010, 17, 1591-1606.	0.8	19
98	The Effect of Micrococcal Nuclease Digestion on Nucleosome Positioning Data. <i>PLoS ONE</i> , 2010, 5, e15754.	1.1	106
99	Maximum Similarity: A New Formulation of Phylogenetic Reconstruction. <i>Journal of Computational Biology</i> , 2009, 16, 887-896.	0.8	0
100	Special RECOMB 2008 Issue. <i>Journal of Computational Biology</i> , 2009, 16, 969-969.	0.8	0
101	Elucidating regulatory mechanisms downstream of a signaling pathway using informative experiments. <i>Molecular Systems Biology</i> , 2009, 5, 287.	3.2	26
102	Evidence for Gene-Specific Rather Than Transcription Rate-Dependent Histone H3 Exchange in Yeast Coding Regions. <i>PLoS Computational Biology</i> , 2009, 5, e1000282.	1.5	13
103	Deeply conserved chordate noncoding sequences preserve genome synteny but do not drive gene duplicate retention. <i>Genome Research</i> , 2009, 19, 2036-2051.	2.4	43
104	Methylation and deamination of CpGs generate p53-binding sites on a genomic scale. <i>Trends in Genetics</i> , 2009, 25, 63-66.	2.9	61
105	Paracrine control of oligodendrocyte differentiation by SRF-directed neuronal gene expression. <i>Nature Neuroscience</i> , 2009, 12, 418-427.	7.1	99
106	A systems biological approach suggests that transcriptional feedback regulation by dual-specificity phosphatase-6 shapes extracellular signal-related kinase activity in RAS-transformed fibroblasts. <i>FEBS Journal</i> , 2009, 276, 1024-1035.	2.2	52
107	Sequence-dependent Nucleosome Positioning. <i>Journal of Molecular Biology</i> , 2009, 386, 1411-1422.	2.0	54
108	Integrating sequence, evolution and functional genomics in regulatory genomics. <i>Genome Biology</i> , 2009, 10, 202.	13.9	18

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109	CpG-depleted promoters harbor tissue-specific transcription factor binding signalsâ€”implications for motif overrepresentation analyses. <i>Nucleic Acids Research</i> , 2009, 37, 6305-6315.	6.5	44
110	Soluble epoxide hydrolase is a susceptibility factor for heart failure in a rat model of human disease. <i>Nature Genetics</i> , 2008, 40, 529-537.	9.4	163
111	A Global View of Gene Activity and Alternative Splicing by Deep Sequencing of the Human Transcriptome. <i>Science</i> , 2008, 321, 956-960.	6.0	1,164
112	Compound Poisson Approximation of the Number of Occurrences of a Position Frequency Matrix (PFM) on Both Strands. <i>Journal of Computational Biology</i> , 2008, 15, 547-564.	0.8	14
113	Prediction of cardiac transcription networks based on molecular data and complex clinical phenotypes. <i>Molecular BioSystems</i> , 2008, 4, 589.	2.9	15
114	Mapping translocation breakpoints by next-generation sequencing. <i>Genome Research</i> , 2008, 18, 1143-1149.	2.4	118
115	Statistical Modeling of Transcription Factor Binding Affinities Predicts Regulatory Interactions. <i>PLoS Computational Biology</i> , 2008, 4, e1000039.	1.5	54
116	The BREW workshop series: a stimulating experience in PhD education. <i>Briefings in Bioinformatics</i> , 2008, 9, 250-253.	3.2	0
117	Early vertebrate whole genome duplications were predated by a period of intense genome rearrangement. <i>Genome Research</i> , 2008, 18, 1582-1591.	2.4	80
118	Comparative 3'UTR Analysis Allows Identification of Regulatory Clusters that Drive Eph/ephrin Expression in Cancer Cell Lines. <i>PLoS ONE</i> , 2008, 3, e2780.	1.1	25
119	Transcriptional Autoregulatory Loops Are Highly Conserved in Vertebrate Evolution. <i>PLoS ONE</i> , 2008, 3, e3210.	1.1	35
120	Simultaneous alignment and annotation of cis-regulatory regions. <i>Bioinformatics</i> , 2007, 23, e44-e49.	1.8	6
121	Predicting transcription factor affinities to DNA from a biophysical model. <i>Bioinformatics</i> , 2007, 23, 134-141.	1.8	184
122	Effects of Long-Range Correlations in DNA on Sequence Alignment Score Statistics. <i>Journal of Computational Biology</i> , 2007, 14, 655-668.	0.8	11
123	Corrigendum to â€œMammalian mitochondrial nitric oxide synthase: Characterization of a novel candidateâ€ [FEBS Lett. 580 (2006) 455-462]. <i>FEBS Letters</i> , 2007, 581, 2072-2073.	1.3	0
124	Integer linear programming approaches for non-unique probe selection. <i>Discrete Applied Mathematics</i> , 2007, 155, 840-856.	0.5	22
125	Incorporating evolution of transcription factor binding sites into annotated alignments. <i>Journal of Biosciences</i> , 2007, 32, 841-850.	0.5	8
126	USING TRANSCRIPTION FACTOR BINDING SITE CO-OCCURRENCE TO PREDICT REGULATORY REGIONS. , 2007, , .		1



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127	An entropic characterization of protein interaction networks and cellular robustness. <i>Journal of the Royal Society Interface</i> , 2006, 3, 843-850.	1.5	38
128	Identification of highly specific localized sequence motifs in human ribosomal protein gene promoters. <i>Gene</i> , 2006, 365, 48-56.	1.0	20
129	Plant nitric oxide synthase: a never-ending story?. <i>Trends in Plant Science</i> , 2006, 11, 524-525.	4.3	297
130	Normalization and quantification of differential expression in gene expression microarrays. <i>Briefings in Bioinformatics</i> , 2006, 7, 166-177.	3.2	69
131	Horizontal Gene Transfer in Aminoacyl-tRNA Synthetases Including Leucine-Specific Subtypes. <i>Journal of Molecular Evolution</i> , 2006, 63, 437-447.	0.8	20
132	A new statistical model to select target sequences bound by transcription factors. <i>Genome Informatics</i> , 2006, 17, 134-40.	0.4	5
133	About the interrelation of evolutionary rate and protein age. <i>Genome Informatics</i> , 2006, 17, 240-50.	0.4	5
134	A gene expression map of <i>Arabidopsis thaliana</i> development. <i>Nature Genetics</i> , 2005, 37, 501-506.	9.4	2,293
135	Haplotype Reconstruction for Diploid Populations. <i>Human Heredity</i> , 2005, 59, 144-156.	0.4	8
136	Control of replication initiation and heterochromatin formation in <i>Saccharomyces cerevisiae</i> by a regulator of meiotic gene expression. <i>Genes and Development</i> , 2005, 19, 1811-1822.	2.7	50
137	Gene expression in kidney cancer is associated with cytogenetic abnormalities, metastasis formation, and patient survival. <i>Clinical Cancer Research</i> , 2005, 11, 646-55.	3.2	64
138	Lethality and entropy of protein interaction networks. <i>Genome Informatics</i> , 2005, 16, 159-63.	0.4	7
139	Special RECOMB 2003 Issue. <i>Journal of Computational Biology</i> , 2004, 11, 213-213.	0.8	0
140	A DNA microarray for fission yeast: minimal changes in global gene expression after temperature shift. <i>Yeast</i> , 2004, 21, 25-39.	0.8	39
141	The SRF Target Gene Fhl2 Antagonizes RhoA/MAL-Dependent Activation of SRF. <i>Molecular Cell</i> , 2004, 16, 867-880.	4.5	137
142	Functional inference from non-random distributions of conserved predicted transcription factor binding sites. <i>Bioinformatics</i> , 2004, 20, i109-i115.	1.8	9
143	Annotating significant pairs of transcription factor binding sites in regulatory DNA. <i>In Silico Biology</i> , 2004, 4, 479-87.	0.4	1
144	Gene expression profile of mouse bone marrow stromal cells determined by cDNA microarray analysis. <i>Cell and Tissue Research</i> , 2003, 311, 227-237.	1.5	64

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145	Increase of functional diversity by alternative splicing. Trends in Genetics, 2003, 19, 124-128.	2.9	208
146	Weighted sequence graphs: boosting iterated dynamic programming using locally suboptimal solutions. Discrete Applied Mathematics, 2003, 127, 95-117.	0.5	9
147	Correlating Protein-DNA and Protein-Protein Interaction Networks. Journal of Molecular Biology, 2003, 333, 75-85.	2.0	34
148	Analysis of CREM-dependent gene expression during mouse spermatogenesis. Molecular and Cellular Endocrinology, 2003, 212, 29-39.	1.6	39
149	Genome-Wide Array Analysis of Normal and Malformed Human Hearts. Circulation, 2003, 107, 2467-2474.	1.6	109
150	On the Power of Profiles for Transcription Factor Binding Site Detection. Statistical Applications in Genetics and Molecular Biology, 2003, 2, Article7.	0.2	80
151	Genome-scale design of PCR primers and long oligomers for DNA microarrays. Nucleic Acids Research, 2003, 31, 5576-5581.	6.5	31
152	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
153	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
154	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
155	SYSTERS, GeneNest, SpliceNest: exploring sequence space from genome to protein. Nucleic Acids Research, 2002, 30, 299-300.	6.5	54
156	SpliceNest: visualizing gene structure and alternative splicing based on EST clusters. Trends in Genetics, 2002, 18, 53-55.	2.9	42
157	Bioinformatics research and education in Germany. In Silico Biology, 2002, 2, 169-71.	0.4	0
158	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
159	Phylogenetic information improves homology detection. Proteins: Structure, Function and Bioinformatics, 2001, 45, 360-371.	1.5	19
160	Minimum information about a microarray experiment (MIAME) toward standards for microarray data. Nature Genetics, 2001, 29, 365-371.	9.4	3,750
161	Statistical tools for discovering pseudo-periodicities in biological sequences. ESAIM - Probability and Statistics, 2001, 5, 171-181.	0.2	0
162	A polyhedral approach to sequence alignment problems. Discrete Applied Mathematics, 2000, 104, 143-186.	0.5	48

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163	GeneNest: automated generation and visualization of gene indices. Trends in Genetics, 2000, 16, 521-523.	2.9	43
164	TIF $\alpha$ , the factor mediating growth-dependent control of ribosomal RNA synthesis, is the mammalian homolog of yeast Rrn3p. EMBO Reports, 2000, 1, 171-175.	2.0	128
165	Contig Selection in Physical Mapping. Journal of Computational Biology, 2000, 7, 395-408.	0.8	2
166	Application of Bootstrap Techniques to Physical Mapping. Genomics, 2000, 69, 235-241.	1.3	5
167	Transcriptional profiling: is it worth the money?. Research in Microbiology, 2000, 151, 113-119.	1.0	11
168	Modeling Amino Acid Replacement. Journal of Computational Biology, 2000, 7, 761-776.	0.8	312
169	Capn7: A highly divergent vertebrate calpain with a novel C-terminal domain. Mammalian Genome, 1999, 10, 318-321.	1.0	36
170	Computational aspects of expression data. Journal of Molecular Medicine, 1999, 77, 3-7.	1.7	29
171	Transcriptional profiling on all open reading frames of <i>Saccharomyces cerevisiae</i> . , 1998, 14, 1209-1221.		118
172	Gene expression screening in <i>Xenopus</i> identifies molecular pathways, predicts gene function and provides a global view of embryonic patterning. Mechanisms of Development, 1998, 77, 95-141.	1.7	198
173	Primer design for large scale sequencing. Nucleic Acids Research, 1998, 26, 3006-3012.	6.5	75
174	A Polyhedral Approach to RNA Sequence Structure Alignment. Journal of Computational Biology, 1998, 5, 517-530.	0.8	48
175	The deferred path heuristic for the generalized tree alignment problem. , 1997, , .		7
176	Towards Integration of Multiple Alignment and Phylogenetic Tree Construction. Journal of Computational Biology, 1997, 4, 23-34.	0.8	35
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