

Kenta Nakai

List of Publications by Year in descending order

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Version: 2024-02-01

180
papers

18,779
citations

50566

48
h-index

14386

132
g-index

188
all docs

188
docs citations

188
times ranked

29133
citing authors

#	ARTICLE	IF	CITATIONS
1	Protein design via deep learning. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	33
2	scIMC: a platform for benchmarking comparison and visualization analysis of scRNA-seq data imputation methods. <i>Nucleic Acids Research</i> , 2022, 50, 4877-4899.	6.5	12
3	Predicting proteinâ€“peptide binding residues via interpretable deep learning. <i>Bioinformatics</i> , 2022, 38, 3351-3360.	1.8	24
4	Recent Advances in the Prediction of Subcellular Localization of Proteins and Related Topics. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	3
5	Signaling Pathway of Taurine-Induced Upregulation of TXNIP. <i>Metabolites</i> , 2022, 12, 636.	1.3	2
6	Qualitative differences in disease-associated MEK mutants reveal molecular signatures and aberrant signaling-crosstalk in cancer. <i>Nature Communications</i> , 2022, 13, .	5.8	10
7	OpenContami: a web-based application for detecting microbial contaminants in next-generation sequencing data. <i>Bioinformatics</i> , 2021, 37, 3021-3022.	1.8	4
8	A bacterial small RNA regulates the adaptation of <i>Helicobacter pylori</i> to the host environment. <i>Nature Communications</i> , 2021, 12, 2085.	5.8	31
9	Characterizing Promoter and Enhancer Sequences by a Deep Learning Method. <i>Frontiers in Genetics</i> , 2021, 12, 681259.	1.1	2
10	A semi-supervised deep learning approach for predicting the functional effects of genomic non-coding variations. <i>BMC Bioinformatics</i> , 2021, 22, 128.	1.2	4
11	Extreme value theory as a framework for understanding mutation frequency distribution in cancer genomes. <i>PLoS ONE</i> , 2021, 16, e0243595.	1.1	2
12	Existence and possible roles of independent non-CpG methylation in the mammalian brain. <i>DNA Research</i> , 2020, 27, .	1.5	10
13	A hypothetical trivalent epigenetic code that affects the nature of human ESCs. <i>PLoS ONE</i> , 2020, 15, e0238742.	1.1	2
14	Tools for the Recognition of Sorting Signals and the Prediction of Subcellular Localization of Proteins From Their Amino Acid Sequences. <i>Frontiers in Genetics</i> , 2020, 11, 607812.	1.1	17
15	HHEX promotes myeloid transformation in cooperation with mutant ASXL1. <i>Blood</i> , 2020, 136, 1670-1684.	0.6	11
16	Mutational diversity in mutY deficient <i>Helicobacter pylori</i> and its effect on adaptation to the gastric environment. <i>Biochemical and Biophysical Research Communications</i> , 2020, 525, 806-811.	1.0	6
17	RNA-sequencing reveals positional memory of multipotent mesenchymal stromal cells from oral and maxillofacial tissue transcriptomes. <i>BMC Genomics</i> , 2020, 21, 417.	1.2	11
18	Whole genome sequencing analysis identifies recurrent structural alterations in esophageal squamous cell carcinoma. <i>PeerJ</i> , 2020, 8, e9294.	0.9	12

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19	Prediction of Protein Localization. , 2019, , 53-59.		1
20	Prediction of Protein-Binding Sites in DNA Sequences. , 2019, , 447-451.		0
21	Broad Heterochromatic Domains Open in Gonocyte Development Prior to De Novo DNA Methylation. Developmental Cell, 2019, 51, 21-34.e5.	3.1	26
22	A systematic sequencing-based approach for microbial contaminant detection and functional inference. BMC Biology, 2019, 17, 72.	1.7	13
23	Information Science Should Take a Lead in Future Biomedical Research. Engineering, 2019, 5, 1155-1158.	3.2	3
24	Genomic analysis of pancreatic juice DNA assesses malignant risk of intraductal papillary mucinous neoplasm of pancreas. Cancer Medicine, 2019, 8, 4565-4573.	1.3	21
25	Analyzing the 3D chromatin organization coordinating with gene expression regulation in B-cell lymphoma. BMC Medical Genomics, 2019, 11, 127.	0.7	13
26	Homeobox Transcription Factor Hhex Promotes Myeloid Leukemia in Cooperation with Mutant ASXL1. Blood, 2019, 134, 2525-2525.	0.6	0
27	Generation of tumor antigen-specific murine CD8+ T cells with enhanced anti-tumor activity via highly efficient CRISPR/Cas9 genome editing. International Immunology, 2018, 30, 141-154.	1.8	9
28	DBTSS/DBKERO for integrated analysis of transcriptional regulation. Nucleic Acids Research, 2018, 46, D229-D238.	6.5	48
29	ANISEED 2017: extending the integrated ascidian database to the exploration and evolutionary comparison of genome-scale datasets. Nucleic Acids Research, 2018, 46, D718-D725.	6.5	90
30	Integrative analysis of gene expression and DNA methylation using unsupervised feature extraction for detecting candidate cancer biomarkers. Journal of Bioinformatics and Computational Biology, 2018, 16, 1850006.	0.3	11
31	Introduction to Selected Papers from GIW2018. Journal of Bioinformatics and Computational Biology, 2018, 16, 1802005.	0.3	0
32	Waves of chromatin modifications in mouse dendritic cells in response to LPS stimulation. Genome Biology, 2018, 19, 138.	3.8	19
33	TimeXNet Web: identifying cellular response networks from diverse omics time-course data. Bioinformatics, 2018, 34, 3764-3765.	1.8	0
34	Biomarker discovery by integrated joint non-negative matrix factorization and pathway signature analyses. Scientific Reports, 2018, 8, 9743.	1.6	25
35	Mutational Intratumor Heterogeneity is a Complex and Early Event in the Development of Adult T-cell Leukemia/Lymphoma. Neoplasia, 2018, 20, 883-893.	2.3	12
36	Genomic landscape of colitis-associated cancer indicates the impact of chronic inflammation and its stratification by mutations in the Wnt signaling. Oncotarget, 2018, 9, 969-981.	0.8	34

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37	Organism-Level Analysis of Vaccination Reveals Networks of Protection across Tissues. <i>Cell</i> , 2017, 171, 398-413.e21.	13.5	69
38	Differential landscape of non-CpG methylation in embryonic stem cells and neurons caused by DNMT3s. <i>Scientific Reports</i> , 2017, 7, 11295.	1.6	59
39	Targeted deletion of miRNAs and cis-regulatory modules associated with cone opsin genes in medaka. <i>Mechanisms of Development</i> , 2017, 145, S145-S146.	1.7	0
40	Multidisciplinary insight into clonal expansion of HTLV-1-infected cells in adult T-cell leukemia via modeling by deterministic finite automata coupled with high-throughput sequencing. <i>BMC Medical Genomics</i> , 2017, 10, 4.	0.7	10
41	Inferring clonal structure in HTLV-1-infected individuals: towards bridging the gap between analysis and visualization. <i>Human Genomics</i> , 2017, 11, 15.	1.4	7
42	Clonality of HTLV-1-infected T cells as a risk indicator for development and progression of adult T-cell leukemia. <i>Blood Advances</i> , 2017, 1, 1195-1205.	2.5	35
43	Modeling the cis-regulatory modules of genes expressed in developmental stages of <i>Drosophila melanogaster</i> . <i>PeerJ</i> , 2017, 5, e3389.	0.9	2
44	The Exon Junction Complex Controls the Efficient and Faithful Splicing of a Subset of Transcripts Involved in Mitotic Cell-Cycle Progression. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1153.	1.8	27
45	ZBTB16 as a Downstream Target Gene of Osterix Regulates Osteoblastogenesis of Human Multipotent Mesenchymal Stromal Cells. <i>Journal of Cellular Biochemistry</i> , 2016, 117, 2423-2434.	1.2	27
46	Stable feature selection based on the ensemble L1-norm support vector machine for biomarker discovery. <i>BMC Genomics</i> , 2016, 17, 1026.	1.2	28
47	Transcriptional regulation of a horizontally transferred gene from bacterium to chordate. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161712.	1.2	20
48	A study on the application of topic models to motif finding algorithms. <i>BMC Bioinformatics</i> , 2016, 17, 502.	1.2	4
49	Advances, practice, and clinical perspectives in high-throughput sequencing. <i>Oral Diseases</i> , 2016, 22, 353-364.	1.5	11
50	PAX6 Isoforms, along with Reprogramming Factors, Differentially Regulate the Induction of Cornea-specific Genes. <i>Scientific Reports</i> , 2016, 6, 20807.	1.6	39
51	OpenTein: a database of digital whole-slide images of stem cell-derived teratomas. <i>Nucleic Acids Research</i> , 2016, 44, D1000-D1004.	6.5	3
52	Genome-wide identification and characterization of transcription start sites and promoters in the tunicate <i>Ciona intestinalis</i> . <i>Genome Research</i> , 2016, 26, 140-150.	2.4	13
53	HitPredict version 4: comprehensive reliability scoring of physical protein-protein interactions from more than 100 species. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav117.	1.4	92
54	A Genetic Algorithm for Motif Finding Based on Statistical Significance. <i>Lecture Notes in Computer Science</i> , 2015, , 438-449.	1.0	5

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55	DBTSS as an integrative platform for transcriptome, epigenome and genome sequence variation data. <i>Nucleic Acids Research</i> , 2015, 43, D87-D91.	6.5	46
56	DBTMEE: a database of transcriptome in mouse early embryos. <i>Nucleic Acids Research</i> , 2015, 43, D771-D776.	6.5	71
57	Discovery of Intermediary Genes between Pathways Using Sparse Regression. <i>PLoS ONE</i> , 2015, 10, e0137222.	1.1	1
58	Computational Promoter Modeling Identifies the Modes of Transcriptional Regulation in Hematopoietic Stem Cells. <i>PLoS ONE</i> , 2014, 9, e93853.	1.1	8
59	A Set of Structural Features Defines the Cis-Regulatory Modules of Antenna-Expressed Genes in <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2014, 9, e104342.	1.1	2
60	Innate Immunity Interactome Dynamics. <i>Gene Regulation and Systems Biology</i> , 2014, 8, GRSB.S12850.	2.3	1
61	Development and validation of a new high-throughput method to investigate the clonality of HTLV-1-infected cells based on provirus integration sites. <i>Genome Medicine</i> , 2014, 6, 46.	3.6	56
62	Alterations in rRNA-mRNA Interaction during Plastid Evolution. <i>Molecular Biology and Evolution</i> , 2014, 31, 1728-1740.	3.5	3
63	Analysis of changes in transcription start site distribution by a classification approach. <i>Gene</i> , 2014, 537, 29-40.	1.0	12
64	TimeXNet: Identifying active gene sub-networks using time-course gene expression profiles. <i>BMC Systems Biology</i> , 2014, 8, S2.	3.0	12
65	Evaluation of Sequence Features from Intrinsically Disordered Regions for the Estimation of Protein Function. <i>PLoS ONE</i> , 2014, 9, e89890.	1.1	19
66	Identification of novel motif patterns to decipher the promoter architecture of co-expressed genes in <i>Arabidopsis thaliana</i> . <i>BMC Systems Biology</i> , 2013, 7, S10.	3.0	6
67	Characterization of the compact bicistronic microRNA precursor, miR-1/miR-133, expressed specifically in <i>Ciona</i> muscle tissues. <i>Gene Expression Patterns</i> , 2013, 13, 43-50.	0.3	19
68	Inferring the choreography of parental genomes during fertilization from ultralarge-scale whole-transcriptome analysis. <i>Genes and Development</i> , 2013, 27, 2736-2748.	2.7	86
69	Linking Transcriptional Changes over Time in Stimulated Dendritic Cells to Identify Gene Networks Activated during the Innate Immune Response. <i>PLoS Computational Biology</i> , 2013, 9, e1003323.	1.5	24
70	Impacts of the ENCODE Project. <i>Seibutsu Butsuri</i> , 2013, 53, 272-273.	0.0	0
71	A BIT-PARALLEL DYNAMIC PROGRAMMING ALGORITHM SUITABLE FOR DNA SEQUENCE ALIGNMENT. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1250002.	0.3	4
72	DBTSS: DataBase of Transcriptional Start Sites progress report in 2012. <i>Nucleic Acids Research</i> , 2012, 40, D150-D154.	6.5	112

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73	Genome-Wide Analysis of DNA Methylation and Expression of MicroRNAs in Breast Cancer Cells. International Journal of Molecular Sciences, 2012, 13, 8259-8272.	1.8	36
74	Sequence- and Species-Dependence of Proteasomal Processivity. ACS Chemical Biology, 2012, 7, 1444-1453.	1.6	50
75	T Cell Receptor Stimulation-Induced Epigenetic Changes and Foxp3 Expression Are Independent and Complementary Events Required for Treg Cell Development. Immunity, 2012, 37, 785-799.	6.6	621
76	Global gene expression of the inner cell mass and trophectoderm of the bovine blastocyst. BMC Developmental Biology, 2012, 12, 33.	2.1	79
77	Chemical composition is maintained in poorly conserved intrinsically disordered regions and suggests a means for their classification. Molecular BioSystems, 2012, 8, 3262.	2.9	48
78	Genome Structure, Functional Genomics, and Proteomics in Ascidians. , 2012, , 87-132.		2
79	Functional annotation of intrinsically disordered domains by their amino acid content using IDD Navigator. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2012, , 164-75.	0.7	3
80	RANK signaling induces interferon-stimulated genes in the fetal thymic stroma. Biochemical and Biophysical Research Communications, 2011, 408, 530-536.	1.0	13
81	A regression analysis of gene expression in ES cells reveals two gene classes that are significantly different in epigenetic patterns. BMC Bioinformatics, 2011, 12, S50.	1.2	18
82	Assessing the utility of gene co-expression stability in combination with correlation in the analysis of protein-protein interaction networks. BMC Genomics, 2011, 12, S19.	1.2	9
83	Profiling ascidian promoters as the primordial type of vertebrate promoter. BMC Genomics, 2011, 12, S7.	1.2	7
84	HitPredict: a database of quality assessed protein-protein interactions in nine species. Nucleic Acids Research, 2011, 39, D744-D749.	6.5	111
85	Genome-wide characterization of transcriptional start sites in humans by integrative transcriptome analysis. Genome Research, 2011, 21, 775-789.	2.4	122
86	Cross-validated methods for promoter/transcription start site mapping in SL trans-spliced genes, established using the Ciona intestinalis troponin I gene. Nucleic Acids Research, 2011, 39, 2638-2648.	6.5	5
87	Predicting promoter activities of primary human DNA sequences. Nucleic Acids Research, 2011, 39, e75-e75.	6.5	10
88	Seed-Set Construction by Equi-entropy Partitioning for Efficient and Sensitive Short-Read Mapping. Lecture Notes in Computer Science, 2011, , 151-162.	1.0	1
89	FUNCTIONAL ANNOTATION OF INTRINSICALLY DISORDERED DOMAINS BY THEIR AMINO ACID CONTENT USING IDD NAVIGATOR. , 2011, , .		1
90	3P303 Computational prediction of mitochondrial inner membrane proteins(Bioinformatics:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 67 T 2010, 50, S199.	0.0	0

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91	Positional variations among heterogeneous nucleosome maps give dynamical information on chromatin. <i>Chromosoma</i> , 2010, 119, 391-404.	1.0	8
92	InCoB2010 - 9th International Conference on Bioinformatics at Tokyo, Japan, September 26-28, 2010. <i>BMC Bioinformatics</i> , 2010, 11, S1.	1.2	3
93	Gradual transition from mosaic to global DNA methylation patterns during deuterostome evolution. <i>BMC Bioinformatics</i> , 2010, 11, S2.	1.2	20
94	Effects of Alu elements on global nucleosome positioning in the human genome. <i>BMC Genomics</i> , 2010, 11, 309.	1.2	46
95	Challenges of the next decade for the Asia Pacific region: 2010 International Conference in Bioinformatics (InCoB 2010). <i>BMC Genomics</i> , 2010, 11, S1.	1.2	14
96	Prediction of subcellular locations of proteins: Where to proceed?. <i>Proteomics</i> , 2010, 10, 3970-3983.	1.3	81
97	The Jmjd3-Irf4 axis regulates M2 macrophage polarization and host responses against helminth infection. <i>Nature Immunology</i> , 2010, 11, 936-944.	7.0	996
98	DBTSS provides a tissue specific dynamic view of Transcription Start Sites. <i>Nucleic Acids Research</i> , 2010, 38, D98-D104.	6.5	57
99	Modeling tissue-specific structural patterns in human and mouse promoters. <i>Nucleic Acids Research</i> , 2010, 38, 17-25.	6.5	73
100	Genomic cis-regulatory networks in the early <i>Ciona intestinalis</i> embryo. <i>Development (Cambridge)</i> , 2010, 137, 1613-1623.	1.2	61
101	Characterization of Transcription Start Sites of Putative Non-coding RNAs by Multifaceted Use of Massively Paralleled Sequencer. <i>DNA Research</i> , 2010, 17, 169-183.	1.5	4
102	Design and utility of CCN2 anchor peptide aptamers. <i>Biochimie</i> , 2010, 92, 1010-1015.	1.3	6
103	Pseudocounts for transcription factor binding sites. <i>Nucleic Acids Research</i> , 2009, 37, 939-944.	6.5	45
104	Massive transcriptional start site analysis of human genes in hypoxia cells. <i>Nucleic Acids Research</i> , 2009, 37, 2249-2263.	6.5	103
105	Comparative genomic analyses of <i>Streptococcus mutans</i> provide insights into chromosomal shuffling and species-specific content. <i>BMC Genomics</i> , 2009, 10, 358.	1.2	72
106	PrognosScan: a new database for meta-analysis of the prognostic value of genes. <i>BMC Medical Genomics</i> , 2009, 2, 18.	0.7	787
107	Spatial and temporal preferences for trans-splicing in <i>Ciona intestinalis</i> revealed by EST-based gene expression analysis. <i>Gene</i> , 2009, 430, 44-49.	1.0	4
108	AN ASSESSMENT OF PREDICTION ALGORITHMS FOR NUCLEOSOME POSITIONING. , 2009, , .		5

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109	An assessment of prediction algorithms for nucleosome positioning. <i>Genome Informatics</i> , 2009, 23, 169-78.	0.4	7
110	Genome-wide demethylation during neural differentiation of P19 embryonal carcinoma cells. <i>Journal of Human Genetics</i> , 2008, 53, 185-191.	1.1	16
111	Two different classes of co-occurring motif pairs found by a novel visualization method in human promoter regions. <i>BMC Genomics</i> , 2008, 9, 112.	1.2	6
112	Weak correlation between sequence conservation in promoter regions and in protein-coding regions of human-mouse orthologous gene pairs. <i>BMC Genomics</i> , 2008, 9, 152.	1.2	14
113	Retrotransposition as a Source of New Promoters. <i>Molecular Biology and Evolution</i> , 2008, 25, 1231-1238.	3.5	38
114	Comprehensive detection of human terminal oligo-pyrimidine (TOP) genes and analysis of their characteristics. <i>Nucleic Acids Research</i> , 2008, 36, 3707-3715.	6.5	103
115	Markov Chain-based Promoter Structure Modeling for Tissue-specific Expression Pattern Prediction. <i>DNA Research</i> , 2008, 15, 3-11.	1.5	7
116	DBTBS: a database of transcriptional regulation in <i>Bacillus subtilis</i> containing upstream intergenic conservation information. <i>Nucleic Acids Research</i> , 2008, 36, D93-D96.	6.5	339
117	Genome-wide Analysis of <i>Chlamydomonas reinhardtii</i> Gene Expression at the Late Stage of Infection. <i>DNA Research</i> , 2008, 15, 83-91.	1.5	5
118	USING SIMPLE RULES ON PRESENCE AND POSITIONING OF MOTIFS FOR PROMOTER STRUCTURE MODELING AND TISSUE-SPECIFIC EXPRESSION PREDICTION. , 2008, , .		1
119	A NOVEL STRATEGY TO SEARCH CONSERVED TRANSCRIPTION FACTOR BINDING SITES AMONG COEXPRESSING GENES IN HUMAN. , 2008, , .		0
120	Using simple rules on presence and positioning of motifs for promoter structure modeling and tissue-specific expression prediction. <i>Genome Informatics</i> , 2008, 21, 188-99.	0.4	2
121	ATTED-II: a database of co-expressed genes and cis elements for identifying co-regulated gene groups in <i>Arabidopsis</i> . <i>Nucleic Acids Research</i> , 2007, 35, D863-D869.	6.5	343
122	Melina II: a web tool for comparisons among several predictive algorithms to find potential motifs from promoter regions. <i>Nucleic Acids Research</i> , 2007, 35, W227-W231.	6.5	39
123	Distinct class of putative "non-conserved" promoters in humans: Comparative studies of alternative promoters of human and mouse genes. <i>Genome Research</i> , 2007, 17, 1005-1014.	2.4	29
124	THE JAPANESE SOCIETY OF BIOINFORMATICS (JSBi). <i>Asia Pacific Biotech News</i> , 2007, 11, 1056-1057.	0.5	0
125	DBTSS: database of transcription start sites, progress report 2008. <i>Nucleic Acids Research</i> , 2007, 36, D97-D101.	6.5	148
126	Intrinsic Promoter Activities of Primary DNA Sequences in the Human Genome. <i>DNA Research</i> , 2007, 14, 71-77.	1.5	5

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127	The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. <i>Nucleic Acids Research</i> , 2007, 36, D793-D799.	6.5	57
128	WOLF PSORT: protein localization predictor. <i>Nucleic Acids Research</i> , 2007, 35, W585-W587.	6.5	3,028
129	Computational Prediction of Subcellular Localization. , 2007, 390, 429-466.		41
130	S2d2-2 Comparative analysis of firmicute promoters(S2-d2: "Bioinformatics of Transcriptional) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 627 S129.	0.0	0
131	S2d2-3 Comparative analysis of mamalian transcriptomes(S2-d2: "Bioinformatics of Transcriptional) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 627	0.0	0
132	DBTSS: DataBase of Human Transcription Start Sites, progress report 2006. <i>Nucleic Acids Research</i> , 2006, 34, D86-D89.	6.5	87
133	Diverse DNA Methylation Statuses at Alternative Promoters of Human Genes in Various Tissues. <i>DNA Research</i> , 2006, 13, 155-167.	1.5	24
134	DBTGR: a database of tunicate promoters and their regulatory elements. <i>Nucleic Acids Research</i> , 2006, 34, D552-D555.	6.5	28
135	PROTEIN SUBCELLULAR LOCALIZATION PREDICTION WITH WOLF PSORT. , 2005, , .		84
136	Diversification of transcriptional modulation: Large-scale identification and characterization of putative alternative promoters of human genes. <i>Genome Research</i> , 2005, 16, 55-65.	2.4	433
137	Large-scale analysis of human alternative protein isoforms: pattern classification and correlation with subcellular localization signals. <i>Nucleic Acids Research</i> , 2005, 33, 2355-2363.	6.5	26
138	Genome-wide analysis reveals strong correlation between CpG islands with nearby transcription start sites of genes and their tissue specificity. <i>Gene</i> , 2005, 350, 129-136.	1.0	97
139	Prediction of Transcriptional Terminators in <i>Bacillus subtilis</i> and Related Species. <i>PLoS Computational Biology</i> , 2005, 1, e25.	1.5	158
140	Prediction of Transcriptional Terminators in <i>Bacillus subtilis</i> and Related Species. <i>PLoS Computational Biology</i> , 2005, preprint, e25.	1.5	1
141	Finding Optimal Pairs of Patterns. <i>Lecture Notes in Computer Science</i> , 2004, , 450-462.	1.0	8
142	Finding Optimal Pairs of Cooperative and Competing Patterns with Bounded Distance. <i>Lecture Notes in Computer Science</i> , 2004, , 32-46.	1.0	8
143	Sequence Comparison of Human and Mouse Genes Reveals a Homologous Block Structure in the Promoter Regions. <i>Genome Research</i> , 2004, 14, 1711-1718.	2.4	54
144	DBTSS, DataBase of Transcriptional Start Sites: progress report 2004. <i>Nucleic Acids Research</i> , 2004, 32, 78D-81.	6.5	120

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145	DBTBS: database of transcriptional regulation in <i>Bacillus subtilis</i> and its contribution to comparative genomics. <i>Nucleic Acids Research</i> , 2004, 32, 75D-77.	6.5	134
146	Cancer gene expression database (CGED): a database for gene expression profiling with accompanying clinical information of human cancer tissues. <i>Nucleic Acids Research</i> , 2004, 33, D533-D536.	6.5	38
147	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	2.6	290
148	Complete sequencing and characterization of 21,243 full-length human cDNAs. <i>Nature Genetics</i> , 2004, 36, 40-45.	9.4	796
149	An $O(N/\text{sup } 2)$ algorithm for discovering optimal Boolean pattern pairs. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2004, 1, 159-170.	1.9	10
150	Large-scale collection and characterization of promoters of human and mouse genes. <i>In Silico Biology</i> , 2004, 4, 429-44.	0.4	14
151	Small open reading frames in 5' untranslated regions of mRNAs. <i>Comptes Rendus - Biologies</i> , 2003, 326, 987-991.	0.1	19
152	PSORT-B: improving protein subcellular localization prediction for Gram-negative bacteria. <i>Nucleic Acids Research</i> , 2003, 31, 3613-3617.	6.5	383
153	MELINA: motif extraction from promoter regions of potentially co-regulated genes. <i>Bioinformatics</i> , 2003, 19, 423-424.	1.8	18
154	DBTSS: DataBase of human Transcriptional Start Sites and full-length cDNAs. <i>Nucleic Acids Research</i> , 2002, 30, 328-331.	6.5	188
155	Extensive feature detection of N-terminal protein sorting signals. <i>Bioinformatics</i> , 2002, 18, 298-305.	1.8	775
156	Oligo-capped cDNAs for promoter identification and annotation. <i>International Congress Series</i> , 2002, 1246, 233-239.	0.2	1
157	Sequence-based approach for identification of cell wall proteins in <i>Saccharomyces cerevisiae</i> . <i>Current Genetics</i> , 2002, 40, 311-316.	0.8	21
158	The Origin and Evolution of Eukaryotic Protein Kinases. <i>Journal of Genome Science and Technology</i> , 2002, 1, 83-104.	0.7	2
159	Prediction of co-regulated genes in <i>Bacillus subtilis</i> on the basis of upstream elements conserved across three closely related species. <i>Genome Biology</i> , 2001, 2, research0048.1.	13.9	15
160	Review: Prediction of in Vivo Fates of Proteins in the Era of Genomics and Proteomics. <i>Journal of Structural Biology</i> , 2001, 134, 103-116.	1.3	52
161	Differential display analysis of mutants for the transcription factor Pdr1p regulating multidrug resistance in the budding yeast. <i>FEBS Letters</i> , 2001, 505, 103-108.	1.3	11
162	Assessment of prediction accuracy of protein function from protein-protein interaction data. <i>Yeast</i> , 2001, 18, 523-531.	0.8	337

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163	A Novel Bacterial Gene-Finding System with Improved Accuracy in Locating Start Codons. DNA Research, 2001, 8, 97-106.	1.5	38
164	DBTBS: a database of Bacillus subtilis promoters and transcription factors. Nucleic Acids Research, 2001, 29, 278-280.	6.5	70
165	Assessment of prediction accuracy of protein function from protein-protein interaction data. , 2001, 18, 523.		9
166	An Alternative-Exon Database and Its Statistical Analysis. DNA and Cell Biology, 2000, 19, 739-756.	0.9	147
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