

Kenta Nakai

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

172
papers

15,279
citations

44
h-index

123
g-index

188
ext. papers

17,181
ext. citations

8.4
avg, IF

6.36
L-index

#	Paper	IF	Citations
172	A bacterial small RNA regulates the adaptation of <i>Helicobacter pylori</i> to the host environment. <i>Nature Communications</i> , 2021 , 12, 2085	17.4	14
171	Characterizing Promoter and Enhancer Sequences by a Deep Learning Method. <i>Frontiers in Genetics</i> , 2021 , 12, 681259	4.5	0
170	A semi-supervised deep learning approach for predicting the functional effects of genomic non-coding variations. <i>BMC Bioinformatics</i> , 2021 , 22, 128	3.6	0
169	Extreme value theory as a framework for understanding mutation frequency distribution in cancer genomes. <i>PLoS ONE</i> , 2021 , 16, e0243595	3.7	0
168	HHEX promotes myeloid transformation in cooperation with mutant ASXL1. <i>Blood</i> , 2020 , 136, 1670-1684	4.2	6
167	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	3.4	3
166	RNA-sequencing reveals positional memory of multipotent mesenchymal stromal cells from oral and maxillofacial tissue transcriptomes. <i>BMC Genomics</i> , 2020 , 21, 417	4.5	4
165	Whole genome sequencing analysis identifies recurrent structural alterations in esophageal squamous cell carcinoma. <i>PeerJ</i> , 2020 , 8, e9294	3.1	6
164	Existence and possible roles of independent non-CpG methylation in the mammalian brain. <i>DNA Research</i> , 2020 , 27,	4.5	4
163	A hypothetical trivalent epigenetic code that affects the nature of human ESCs. <i>PLoS ONE</i> , 2020 , 15, e0238742	3.7	1
162	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	4.5	5
161	Broad Heterochromatic Domains Open in Gonocyte Development Prior to De Novo DNA Methylation. <i>Developmental Cell</i> , 2019 , 51, 21-34.e5	10.2	17
160	A systematic sequencing-based approach for microbial contaminant detection and functional inference. <i>BMC Biology</i> , 2019 , 17, 72	7.3	8
159	Information Science Should Take a Lead in Future Biomedical Research. <i>Engineering</i> , 2019 , 5, 1155-1158	9.7	1
158	Genomic analysis of pancreatic juice DNA assesses malignant risk of intraductal papillary mucinous neoplasm of pancreas. <i>Cancer Medicine</i> , 2019 , 8, 4565-4573	4.8	10
157	Analyzing the 3D chromatin organization coordinating with gene expression regulation in B-cell lymphoma. <i>BMC Medical Genomics</i> , 2019 , 11, 127	3.7	8
156	Prediction of Protein Localization 2019 , 53-59		0

155	Prediction of Protein-Binding Sites in DNA Sequences 2019 , 447-451		
154	Homeobox Transcription Factor Hhex Promotes Myeloid Leukemia in Cooperation with Mutant ASXL1. <i>Blood</i> , 2019 , 134, 2525-2525	2.2	
153	Generation of tumor antigen-specific murine CD8+ T cells with enhanced anti-tumor activity via highly efficient CRISPR/Cas9 genome editing. <i>International Immunology</i> , 2018 , 30, 141-154	4.9	7
152	DBTSS/DBKERO for integrated analysis of transcriptional regulation. <i>Nucleic Acids Research</i> , 2018 , 46, D229-D238	20.1	37
151	ANISEED 2017: extending the integrated ascidian database to the exploration and evolutionary comparison of genome-scale datasets. <i>Nucleic Acids Research</i> , 2018 , 46, D718-D725	20.1	58
150	Integrative analysis of gene expression and DNA methylation using unsupervised feature extraction for detecting candidate cancer biomarkers. <i>Journal of Bioinformatics and Computational Biology</i> , 2018 , 16, 1850006	1	10
149	Biomarker discovery by integrated joint non-negative matrix factorization and pathway signature analyses. <i>Scientific Reports</i> , 2018 , 8, 9743	4.9	15
148	Mutational Intratumor Heterogeneity is a Complex and Early Event in the Development of Adult T-cell Leukemia/Lymphoma. <i>Neoplasia</i> , 2018 , 20, 883-893	6.4	7
147	Genomic landscape of colitis-associated cancer indicates the impact of chronic inflammation and its stratification by mutations in the Wnt signaling. <i>Oncotarget</i> , 2018 , 9, 969-981	3.3	23
146	Introduction to Selected Papers from GIW2018. <i>Journal of Bioinformatics and Computational Biology</i> , 2018 , 16, 1802005	1	
145	Waves of chromatin modifications in mouse dendritic cells in response to LPS stimulation. <i>Genome Biology</i> , 2018 , 19, 138	18.3	9
144	TimeXNet Web: identifying cellular response networks from diverse omics time-course data. <i>Bioinformatics</i> , 2018 , 34, 3764-3765	7.2	
143	Organism-Level Analysis of Vaccination Reveals Networks of Protection across Tissues. <i>Cell</i> , 2017 , 171, 398-413.e21	56.2	50
142	Inferring clonal structure in HTLV-1-infected individuals: towards bridging the gap between analysis and visualization. <i>Human Genomics</i> , 2017 , 11, 15	6.8	6
141	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	7.8	21
140	Differential landscape of non-CpG methylation in embryonic stem cells and neurons caused by DNMT3s. <i>Scientific Reports</i> , 2017 , 7, 11295	4.9	44
139	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	3.7	7
138	Modeling the -regulatory modules of genes expressed in developmental stages of. <i>PeerJ</i> , 2017 , 5, e33893.1	3.1	1

137	PAX6 Isoforms, along with Reprogramming Factors, Differentially Regulate the Induction of Cornea-specific Genes. <i>Scientific Reports</i> , 2016 , 6, 20807	4.9	34
136	OpenTein: a database of digital whole-slide images of stem cell-derived teratomas. <i>Nucleic Acids Research</i> , 2016 , 44, D1000-4	20.1	2
135	Genome-wide identification and characterization of transcription start sites and promoters in the tunicate <i>Ciona intestinalis</i> . <i>Genome Research</i> , 2016 , 26, 140-50	9.7	10
134	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,	6.3	17
133	ZBTB16 as a Downstream Target Gene of Osterix Regulates Osteoblastogenesis of Human Multipotent Mesenchymal Stromal Cells. <i>Journal of Cellular Biochemistry</i> , 2016 , 117, 2423-34	4.7	18
132	Stable feature selection based on the ensemble L -norm support vector machine for biomarker discovery. <i>BMC Genomics</i> , 2016 , 17, 1026	4.5	20
131	Transcriptional regulation of a horizontally transferred gene from bacterium to chordate. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016 , 283,	4.4	14
130	A study on the application of topic models to motif finding algorithms. <i>BMC Bioinformatics</i> , 2016 , 17, 502	3.6	4
129	Advances, practice, and clinical perspectives in high-throughput sequencing. <i>Oral Diseases</i> , 2016 , 22, 353-64	3.5	7
128	DBTMEE: a database of transcriptome in mouse early embryos. <i>Nucleic Acids Research</i> , 2015 , 43, D771-6	20.1	44
127	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,	5	63
126	A Genetic Algorithm for Motif Finding Based on Statistical Significance. <i>Lecture Notes in Computer Science</i> , 2015 , 438-449	0.9	5
125	DBTSS as an integrative platform for transcriptome, epigenome and genome sequence variation data. <i>Nucleic Acids Research</i> , 2015 , 43, D87-91	20.1	43
124	Discovery of Intermediary Genes between Pathways Using Sparse Regression. <i>PLoS ONE</i> , 2015 , 10, e0137222	3.7	1
123	Alterations in rRNA-mRNA interaction during plastid evolution. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1728-40	8.3	2
122	Analysis of changes in transcription start site distribution by a classification approach. <i>Gene</i> , 2014 , 537, 29-40	3.8	10
121	TimeXNet: identifying active gene sub-networks using time-course gene expression profiles. <i>BMC Systems Biology</i> , 2014 , 8 Suppl 4, S2	3.5	9
120	Computational promoter modeling identifies the modes of transcriptional regulation in hematopoietic stem cells. <i>PLoS ONE</i> , 2014 , 9, e93853	3.7	7

119	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	3.7	2
118	Innate immunity interactome dynamics. <i>Gene Regulation and Systems Biology</i> , 2014 , 8, 1-15	2	1
117	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	14.4	42
116	Evaluation of sequence features from intrinsically disordered regions for the estimation of protein function. <i>PLoS ONE</i> , 2014 , 9, e89890	3.7	17
115	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 Suppl 3, S10	3.5	6
114	Characterization of the compact bicistronic microRNA precursor, miR-1/miR-133, expressed specifically in Ciona muscle tissues. <i>Gene Expression Patterns</i> , 2013 , 13, 43-50	1.5	18
113	Inferring the choreography of parental genomes during fertilization from ultralarge-scale whole-transcriptome analysis. <i>Genes and Development</i> , 2013 , 27, 2736-48	12.6	64
112	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	5	21
111	Impacts of the ENCODE Project. <i>Seibutsu Butsuri</i> , 2013 , 53, 272-273	0	
110	Sequence- and species-dependence of proteasomal processivity. <i>ACS Chemical Biology</i> , 2012 , 7, 1444-53	4.9	40
109	T cell receptor stimulation-induced epigenetic changes and Foxp3 expression are independent and complementary events required for Treg cell development. <i>Immunity</i> , 2012 , 37, 785-99	32.3	494
108	Global gene expression of the inner cell mass and trophectoderm of the bovine blastocyst. <i>BMC Developmental Biology</i> , 2012 , 12, 33	3.1	61
107	Chemical composition is maintained in poorly conserved intrinsically disordered regions and suggests a means for their classification. <i>Molecular BioSystems</i> , 2012 , 8, 3262-73		34
106	A bit-parallel dynamic programming algorithm suitable for DNA sequence alignment. <i>Journal of Bioinformatics and Computational Biology</i> , 2012 , 10, 1250002	1	4
105	DBTSS: DataBase of Transcriptional Start Sites progress report in 2012. <i>Nucleic Acids Research</i> , 2012 , 40, D150-4	20.1	42
104	Genome-wide analysis of DNA methylation and expression of microRNAs in breast cancer cells. <i>International Journal of Molecular Sciences</i> , 2012 , 13, 8259-72	6.3	35
103	Genome Structure, Functional Genomics, and Proteomics in Ascidians 2012 , 87-132		2
102	Functional annotation of intrinsically disordered domains by their amino acid content using IDD Navigator. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2012 , 164-75	1.3	3

101	RANK signaling induces interferon-stimulated genes in the fetal thymic stroma. <i>Biochemical and Biophysical Research Communications</i> , 2011 , 408, 530-6	3.4	12
100	A regression analysis of gene expression in ES cells reveals two gene classes that are significantly different in epigenetic patterns. <i>BMC Bioinformatics</i> , 2011 , 12 Suppl 1, S50	3.6	17
99	Assessing the utility of gene co-expression stability in combination with correlation in the analysis of protein-protein interaction networks. <i>BMC Genomics</i> , 2011 , 12 Suppl 3, S19	4.5	7
98	Profiling ascidian promoters as the primordial type of vertebrate promoter. <i>BMC Genomics</i> , 2011 , 12 Suppl 3, S7	4.5	4
97	HitPredict: a database of quality assessed protein-protein interactions in nine species. <i>Nucleic Acids Research</i> , 2011 , 39, D744-9	20.1	74
96	Genome-wide characterization of transcriptional start sites in humans by integrative transcriptome analysis. <i>Genome Research</i> , 2011 , 21, 775-89	9.7	100
95	Cross-validated methods for promoter/transcription start site mapping in SL trans-spliced genes, established using the <i>Ciona intestinalis</i> troponin I gene. <i>Nucleic Acids Research</i> , 2011 , 39, 2638-48	20.1	5
94	Predicting promoter activities of primary human DNA sequences. <i>Nucleic Acids Research</i> , 2011 , 39, e75	20.1	8
93	Seed-Set Construction by Equi-entropy Partitioning for Efficient and Sensitive Short-Read Mapping. <i>Lecture Notes in Computer Science</i> , 2011 , 151-162	0.9	1
92	The Jmjd3-Irf4 axis regulates M2 macrophage polarization and host responses against helminth infection. <i>Nature Immunology</i> , 2010 , 11, 936-44	19.1	803
91	DBTSS provides a tissue specific dynamic view of Transcription Start Sites. <i>Nucleic Acids Research</i> , 2010 , 38, D98-104	20.1	46
90	Modeling tissue-specific structural patterns in human and mouse promoters. <i>Nucleic Acids Research</i> , 2010 , 38, 17-25	20.1	39
89	Genomic cis-regulatory networks in the early <i>Ciona intestinalis</i> embryo. <i>Development (Cambridge)</i> , 2010 , 137, 1613-23	6.6	54
88	Characterization of transcription start sites of putative non-coding RNAs by multifaceted use of massively paralleled sequencer. <i>DNA Research</i> , 2010 , 17, 169-83	4.5	3
87	Design and utility of CCN2 anchor peptide aptamers. <i>Biochimie</i> , 2010 , 92, 1010-5	4.6	6
86	3P303 Computational prediction of mitochondrial inner membrane proteins(Bioinformatics: Functional genomics, The 48th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2010 , 50, S199	0	
85	Positional variations among heterogeneous nucleosome maps give dynamical information on chromatin. <i>Chromosoma</i> , 2010 , 119, 391-404	2.8	6
84	InCoB2010 - 9th International Conference on Bioinformatics at Tokyo, Japan, September 26-28, 2010. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 7, S1	3.6	1

83	Gradual transition from mosaic to global DNA methylation patterns during deuterostome evolution. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 7, S2	3.6	16
82	Effects of Alu elements on global nucleosome positioning in the human genome. <i>BMC Genomics</i> , 2010 , 11, 309	4.5	39
81	Challenges of the next decade for the Asia Pacific region: 2010 International Conference in Bioinformatics (InCoB 2010). <i>BMC Genomics</i> , 2010 , 11 Suppl 4, S1	4.5	9
80	Prediction of subcellular locations of proteins: where to proceed?. <i>Proteomics</i> , 2010 , 10, 3970-83	4.8	66
79	Pseudocounts for transcription factor binding sites. <i>Nucleic Acids Research</i> , 2009 , 37, 939-44	20.1	36
78	Massive transcriptional start site analysis of human genes in hypoxia cells. <i>Nucleic Acids Research</i> , 2009 , 37, 2249-63	20.1	87
77	Comparative genomic analyses of <i>Streptococcus mutans</i> provide insights into chromosomal shuffling and species-specific content. <i>BMC Genomics</i> , 2009 , 10, 358	4.5	56
76	PrognoScan: a new database for meta-analysis of the prognostic value of genes. <i>BMC Medical Genomics</i> , 2009 , 2, 18	3.7	507
75	Spatial and temporal preferences for trans-splicing in <i>Ciona intestinalis</i> revealed by EST-based gene expression analysis. <i>Gene</i> , 2009 , 430, 44-9	3.8	4
74	AN ASSESSMENT OF PREDICTION ALGORITHMS FOR NUCLEOSOME POSITIONING 2009 ,		4
73	An assessment of prediction algorithms for nucleosome positioning. <i>Genome Informatics</i> , 2009 , 23, 169-78		7
72	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	4.5	6
71	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	4.5	11
70	Retrotransposition as a source of new promoters. <i>Molecular Biology and Evolution</i> , 2008 , 25, 1231-8	8.3	35
69	Comprehensive detection of human terminal oligo-pyrimidine (TOP) genes and analysis of their characteristics. <i>Nucleic Acids Research</i> , 2008 , 36, 3707-15	20.1	79
68	Markov chain-based promoter structure modeling for tissue-specific expression pattern prediction. <i>DNA Research</i> , 2008 , 15, 3-11	4.5	7
67	DBTBS: a database of transcriptional regulation in <i>Bacillus subtilis</i> containing upstream intergenic conservation information. <i>Nucleic Acids Research</i> , 2008 , 36, D93-6	20.1	290
66	Genome-wide analysis of <i>Chlamydomonas reinhardtii</i> gene expression at the late stage of infection. <i>DNA Research</i> , 2008 , 15, 83-91	4.5	4

65	USING SIMPLE RULES ON PRESENCE AND POSITIONING OF MOTIFS FOR PROMOTER STRUCTURE MODELING AND TISSUE-SPECIFIC EXPRESSION PREDICTION 2008 ,		1
64	Genome-wide demethylation during neural differentiation of P19 embryonal carcinoma cells. <i>Journal of Human Genetics</i> , 2008 , 53, 185-191	4-3	15
63	DBTSS: database of transcription start sites, progress report 2008. <i>Nucleic Acids Research</i> , 2008 , 36, D97-101	10-1	105
62	The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. <i>Nucleic Acids Research</i> , 2008 , 36, D793-9	20-1	52
61	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		2
60	WoLF PSORT: protein localization predictor. <i>Nucleic Acids Research</i> , 2007 , 35, W585-7	20-1	2146
59	ATTED-II: a database of co-expressed genes and cis elements for identifying co-regulated gene groups in Arabidopsis. <i>Nucleic Acids Research</i> , 2007 , 35, D863-9	20-1	319
58	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, W227-31	20-1	33
57	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, 1005-14	9-7	28
56	THE JAPANESE SOCIETY OF BIOINFORMATICS (JSBi). <i>Asia Pacific Biotech News</i> , 2007 , 11, 1056-1057	0	
55	Intrinsic promoter activities of primary DNA sequences in the human genome. <i>DNA Research</i> , 2007 , 14, 71-7	4-5	5
54	Computational prediction of subcellular localization. <i>Methods in Molecular Biology</i> , 2007 , 390, 429-66	1-4	35
53	DBTSS: DataBase of Human Transcription Start Sites, progress report 2006. <i>Nucleic Acids Research</i> , 2006 , 34, D86-9	20-1	84
52	Diverse DNA methylation statuses at alternative promoters of human genes in various tissues. <i>DNA Research</i> , 2006 , 13, 155-67	4-5	23
51	DBTGR: a database of tunicate promoters and their regulatory elements. <i>Nucleic Acids Research</i> , 2006 , 34, D552-5	20-1	27
50	S2d2-2 Comparative analysis of firmicute promoters(S2-d2: "Bioinformatics of Transcriptional Regulation",Symposia,Abstract,Meeting Program of EABS & BSJ 2006). <i>Seibutsu Butsuri</i> , 2006 , 46, S129	0	
49	S2d2-3 Comparative analysis of mamalian transcriptomes(S2-d2: "Bioinformatics of Transcriptional Regulation",Symposia,Abstract,Meeting Program of EABS & BSJ 2006). <i>Seibutsu Butsuri</i> , 2006 , 46, S129	0	
48	Diversification of transcriptional modulation: large-scale identification and characterization of putative alternative promoters of human genes. <i>Genome Research</i> , 2006 , 16, 55-65	9-7	354

47	Large-scale analysis of human alternative protein isoforms: pattern classification and correlation with subcellular localization signals. <i>Nucleic Acids Research</i> , 2005 , 33, 2355-63	20.1	21
46	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, 129-36	3.8	79
45	Prediction of transcriptional terminators in <i>Bacillus subtilis</i> and related species. <i>PLoS Computational Biology</i> , 2005 , 1, e25	5	140
44	Cancer gene expression database (CGED): a database for gene expression profiling with accompanying clinical information of human cancer tissues. <i>Nucleic Acids Research</i> , 2005 , 33, D533-6	20.1	36
43	Parameter Landscape Analysis for Common Motif Discovery Programs. <i>Lecture Notes in Computer Science</i> , 2005 , 79-87	0.9	2
42	PROTEIN SUBCELLULAR LOCALIZATION PREDICTION WITH WOLF PSORT 2005 ,		40
41	Prediction of Transcriptional Terminators in <i>Bacillus subtilis</i> and Related Species. <i>PLoS Computational Biology</i> , 2005 , preprint, e25	5	1
40	Finding Optimal Pairs of Patterns. <i>Lecture Notes in Computer Science</i> , 2004 , 450-462	0.9	8
39	Finding Optimal Pairs of Cooperative and Competing Patterns with Bounded Distance. <i>Lecture Notes in Computer Science</i> , 2004 , 32-46	0.9	8
38	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions. <i>Genome Research</i> , 2004 , 14, 1711-8	9.7	47
37	DBTSS, DataBase of Transcriptional Start Sites: progress report 2004. <i>Nucleic Acids Research</i> , 2004 , 32, D78-81	20.1	112
36	DBTBS: database of transcriptional regulation in <i>Bacillus subtilis</i> and its contribution to comparative genomics. <i>Nucleic Acids Research</i> , 2004 , 32, D75-7	20.1	117
35	Integrative annotation of 21,037 human genes validated by full-length cDNA clones. <i>PLoS Biology</i> , 2004 , 2, e162	9.7	255
34	Complete sequencing and characterization of 21,243 full-length human cDNAs. <i>Nature Genetics</i> , 2004 , 36, 40-5	36.3	695
33	An O(N ²) algorithm for discovering optimal Boolean pattern pairs. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2004 , 1, 159-70	3	9
32	Large-scale collection and characterization of promoters of human and mouse genes. <i>In Silico Biology</i> , 2004 , 4, 429-44	2	13
31	Melina: motif extraction from promoter regions of potentially co-regulated genes. <i>Bioinformatics</i> , 2003 , 19, 423-4	7.2	16
30	Small open reading frames in 5' untranslated regions of mRNAs. <i>Comptes Rendus - Biologies</i> , 2003 , 326, 987-91	1.4	17

29	PSORT-B: Improving protein subcellular localization prediction for Gram-negative bacteria. <i>Nucleic Acids Research</i> , 2003 , 31, 3613-7	20.1	318
28	Sequence-based approach for identification of cell wall proteins in <i>Saccharomyces cerevisiae</i> . <i>Current Genetics</i> , 2002 , 40, 311-6	2.9	19
27	DBTSS: DataBase of human Transcriptional Start Sites and full-length cDNAs. <i>Nucleic Acids Research</i> , 2002 , 30, 328-31	20.1	164
26	Extensive feature detection of N-terminal protein sorting signals. <i>Bioinformatics</i> , 2002 , 18, 298-305	7.2	691
25	Oligo-capped cDNAs for promoter identification and annotation. <i>International Congress Series</i> , 2002 , 1246, 233-239		1
24	The Origin and Evolution of Eukaryotic Protein Kinases. <i>Journal of Genome Science and Technology</i> , 2002 , 1, 83-104		2
23	Assessment of prediction accuracy of protein function from protein-protein interaction data. <i>Yeast</i> , 2001 , 18, 523-31	3.4	276
22	A novel bacterial gene-finding system with improved accuracy in locating start codons. <i>DNA Research</i> , 2001 , 8, 97-106	4.5	32
21	DBTBS: a database of <i>Bacillus subtilis</i> promoters and transcription factors. <i>Nucleic Acids Research</i> , 2001 , 29, 278-80	20.1	65
20	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	18.3	15
19	Review: prediction of in vivo fates of proteins in the era of genomics and proteomics. <i>Journal of Structural Biology</i> , 2001 , 134, 103-16	3.4	45
18	Differential display analysis of mutants for the transcription factor Pdr1p regulating multidrug resistance in the budding yeast. <i>FEBS Letters</i> , 2001 , 505, 103-8	3.8	8
17	Assessment of prediction accuracy of protein function from protein-protein interaction data 2001 , 18, 523		9
16	An alternative-exon database and its statistical analysis. <i>DNA and Cell Biology</i> , 2000 , 19, 739-56	3.6	138
15	Protein sorting signals and prediction of subcellular localization. <i>Advances in Protein Chemistry</i> , 2000 , 54, 277-344		225
14	PSORT: a program for detecting sorting signals in proteins and predicting their subcellular localization. <i>Trends in Biochemical Sciences</i> , 1999 , 24, 34-6	10.3	1844
13	Detection and isolation of a novel human gene located on Xp11.2-p11.4 that escapes X-inactivation using a two-dimensional DNA mapping method. <i>Genomics</i> , 1998 , 49, 237-46	4.3	19
12	Determination of the nucleotide sequence of <i>Bombyx mori</i> cytoplasmic polyhedrosis virus segment 9 and its expression in BmN4 cells. <i>Journal of Virology</i> , 1998 , 72, 5762-8	6.6	28

11	Identification of open reading frames in Schizosaccharomyces pombe cDNAs. <i>DNA Research</i> , 1997 , 4, 363-9	4.5	15
10	Construction of a novel database containing aberrant splicing mutations of mammalian genes. <i>Gene</i> , 1994 , 141, 171-7	3.8	269
9	How many yeast genes code for membrane-spanning proteins?. <i>Yeast</i> , 1993 , 9, 691-702	3.4	41
8	The membrane proteins encoded by yeast chromosome III genes. <i>FEBS Letters</i> , 1993 , 325, 112-7	3.8	36
7	A knowledge base for predicting protein localization sites in eukaryotic cells. <i>Genomics</i> , 1992 , 14, 897-914	3.3	1375
6	Expert system for predicting protein localization sites in gram-negative bacteria. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991 , 11, 95-110	4.2	578
5	Secondary structure of sphingomyelinase from Bacillus cereus. <i>Journal of Biochemistry</i> , 1990 , 108, 811-5	3.1	15
4	Cluster analysis of amino acid indices for prediction of protein structure and function. <i>Protein Engineering, Design and Selection</i> , 1988 , 2, 93-100	1.9	145
3	Prediction of in-vivo modification sites of proteins from their primary structures. <i>Journal of Biochemistry</i> , 1988 , 104, 693-9	3.1	23
2	Computational Inference of Gene Regulation from Whole-Transcriptome Analysis of Early Embryos. <i>Advances in Medical Technologies and Clinical Practice Book Series</i> , 241-279	0.3	
1	Waves of chromatin modifications in mouse dendritic cells in response to LPS stimulation		2