

Kenta Nakai

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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	WoLF PSORT: protein localization predictor. <i>Nucleic Acids Research</i> , 2007 , 35, W585-7	20.1	2146
171	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
170	A knowledge base for predicting protein localization sites in eukaryotic cells. <i>Genomics</i> , 1992 , 14, 897-914	14.3	1375
169	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
168	Complete sequencing and characterization of 21,243 full-length human cDNAs. <i>Nature Genetics</i> , 2004 , 36, 40-5	36.3	695
167	Extensive feature detection of N-terminal protein sorting signals. <i>Bioinformatics</i> , 2002 , 18, 298-305	7.2	691
166	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
165	PrognoScan: a new database for meta-analysis of the prognostic value of genes. <i>BMC Medical Genomics</i> , 2009 , 2, 18	3.7	507
164	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
163	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
162	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
161	PSORT-B: Improving protein subcellular localization prediction for Gram-negative bacteria. <i>Nucleic Acids Research</i> , 2003 , 31, 3613-7	20.1	318
160	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
159	Assessment of prediction accuracy of protein function from protein-protein interaction data. <i>Yeast</i> , 2001 , 18, 523-31	3.4	276
158	Construction of a novel database containing aberrant splicing mutations of mammalian genes. <i>Gene</i> , 1994 , 141, 171-7	3.8	269
157	Integrative annotation of 21,037 human genes validated by full-length cDNA clones. <i>PLoS Biology</i> , 2004 , 2, e162	9.7	255
156	Protein sorting signals and prediction of subcellular localization. <i>Advances in Protein Chemistry</i> , 2000 , 54, 277-344		225

155	DBTSS: DataBase of human Transcriptional Start Sites and full-length cDNAs. <i>Nucleic Acids Research</i> , 2002 , 30, 328-31	20.1	164
154	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
153	Prediction of transcriptional terminators in <i>Bacillus subtilis</i> and related species. <i>PLoS Computational Biology</i> , 2005 , 1, e25	5	140
152	An alternative-exon database and its statistical analysis. <i>DNA and Cell Biology</i> , 2000 , 19, 739-56	3.6	138
151	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
150	DBTSS, DataBase of Transcriptional Start Sites: progress report 2004. <i>Nucleic Acids Research</i> , 2004 , 32, D78-81	20.1	112
149	DBTSS: database of transcription start sites, progress report 2008. <i>Nucleic Acids Research</i> , 2008 , 36, D97-101	20.1	105
148	Genome-wide characterization of transcriptional start sites in humans by integrative transcriptome analysis. <i>Genome Research</i> , 2011 , 21, 775-89	9.7	100
147	Massive transcriptional start site analysis of human genes in hypoxia cells. <i>Nucleic Acids Research</i> , 2009 , 37, 2249-63	20.1	87
146	DBTSS: DataBase of Human Transcription Start Sites, progress report 2006. <i>Nucleic Acids Research</i> , 2006 , 34, D86-9	20.1	84
145	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
144	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
143	HitPredict: a database of quality assessed protein-protein interactions in nine species. <i>Nucleic Acids Research</i> , 2011 , 39, D744-9	20.1	74
142	Prediction of subcellular locations of proteins: where to proceed?. <i>Proteomics</i> , 2010 , 10, 3970-83	4.8	66
141	DBTBS: a database of <i>Bacillus subtilis</i> promoters and transcription factors. <i>Nucleic Acids Research</i> , 2001 , 29, 278-80	20.1	65
140	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
139	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
138	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

137	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
136	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
135	Genomic cis-regulatory networks in the early <i>Ciona intestinalis</i> embryo. <i>Development (Cambridge)</i> , 2010 , 137, 1613-23	6.6	54
134	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
133	Organism-Level Analysis of Vaccination Reveals Networks of Protection across Tissues. <i>Cell</i> , 2017 , 171, 398-413.e21	56.2	50
132	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
131	DBTSS provides a tissue specific dynamic view of Transcription Start Sites. <i>Nucleic Acids Research</i> , 2010 , 38, D98-104	20.1	46
130	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
129	DBTMEE: a database of transcriptome in mouse early embryos. <i>Nucleic Acids Research</i> , 2015 , 43, D771-6	20.1	44
128	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
127	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
126	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
125	DBTSS: DataBase of Transcriptional Start Sites progress report in 2012. <i>Nucleic Acids Research</i> , 2012 , 40, D150-4	20.1	42
124	How many yeast genes code for membrane-spanning proteins?. <i>Yeast</i> , 1993 , 9, 691-702	3.4	41
123	Sequence- and species-dependence of proteasomal processivity. <i>ACS Chemical Biology</i> , 2012 , 7, 1444-53	4.9	40
122	PROTEIN SUBCELLULAR LOCALIZATION PREDICTION WITH WOLF PSORT 2005,		40
121	Modeling tissue-specific structural patterns in human and mouse promoters. <i>Nucleic Acids Research</i> , 2010 , 38, 17-25	20.1	39
120	Effects of Alu elements on global nucleosome positioning in the human genome. <i>BMC Genomics</i> , 2010 , 11, 309	4.5	39

119	DBTSS/DBKERO for integrated analysis of transcriptional regulation. <i>Nucleic Acids Research</i> , 2018 , 46, D229-D238	20.1	37
118	Pseudocounts for transcription factor binding sites. <i>Nucleic Acids Research</i> , 2009 , 37, 939-44	20.1	36
117	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
116	The membrane proteins encoded by yeast chromosome III genes. <i>FEBS Letters</i> , 1993 , 325, 112-7	3.8	36
115	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
114	Retrotransposition as a source of new promoters. <i>Molecular Biology and Evolution</i> , 2008 , 25, 1231-8	8.3	35
113	Computational prediction of subcellular localization. <i>Methods in Molecular Biology</i> , 2007 , 390, 429-66	1.4	35
112	PAX6 Isoforms, along with Reprogramming Factors, Differentially Regulate the Induction of Cornea-specific Genes. <i>Scientific Reports</i> , 2016 , 6, 20807	4.9	34
111	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
110	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
109	A novel bacterial gene-finding system with improved accuracy in locating start codons. <i>DNA Research</i> , 2001 , 8, 97-106	4.5	32
108	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
107	Determination of the nucleotide sequence of Bombyx mori cytoplasmic polyhedrosis virus segment 9 and its expression in BmN4 cells. <i>Journal of Virology</i> , 1998 , 72, 5762-8	6.6	28
106	DBTGR: a database of tunicate promoters and their regulatory elements. <i>Nucleic Acids Research</i> , 2006 , 34, D552-5	20.1	27
105	Diverse DNA methylation statuses at alternative promoters of human genes in various tissues. <i>DNA Research</i> , 2006 , 13, 155-67	4.5	23
104	Prediction of in-vivo modification sites of proteins from their primary structures. <i>Journal of Biochemistry</i> , 1988 , 104, 693-9	3.1	23
103	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
102	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

101	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
100	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
99	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
98	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
97	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
96	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
95	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
94	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
93	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
92	Small open reading frames in 5' untranslated regions of mRNAs. <i>Comptes Rendus - Biologies</i> , 2003 , 326, 987-91	1.4	17
91	Evaluation of sequence features from intrinsically disordered regions for the estimation of protein function. <i>PLoS ONE</i> , 2014 , 9, e89890	3.7	17
90	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
89	Gradual transition from mosaic to global DNA methylation patterns during deuterostome evolution. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 7, S2	3.6	16
88	Melina: motif extraction from promoter regions of potentially co-regulated genes. <i>Bioinformatics</i> , 2003 , 19, 423-4	7.2	16
87	Biomarker discovery by integrated joint non-negative matrix factorization and pathway signature analyses. <i>Scientific Reports</i> , 2018 , 8, 9743	4.9	15
86	Identification of open reading frames in <i>Schizosaccharomyces pombe</i> cDNAs. <i>DNA Research</i> , 1997 , 4, 363-9	4.5	15
85	Genome-wide demethylation during neural differentiation of P19 embryonal carcinoma cells. <i>Journal of Human Genetics</i> , 2008 , 53, 185-191	4.3	15
84	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

83	Secondary structure of sphingomyelinase from <i>Bacillus cereus</i> . <i>Journal of Biochemistry</i> , 1990 , 108, 811-53.1	15
82	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
81	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
80	Large-scale collection and characterization of promoters of human and mouse genes. <i>In Silico Biology</i> , 2004 , 4, 429-44	2 13
79	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
78	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
77	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
76	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
75	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
74	Analysis of changes in transcription start site distribution by a classification approach. <i>Gene</i> , 2014 , 537, 29-40	3.8 10
73	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
72	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
71	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
70	Waves of chromatin modifications in mouse dendritic cells in response to LPS stimulation. <i>Genome Biology</i> , 2018 , 19, 138	18.3 9
69	Assessment of prediction accuracy of protein function from protein-protein interaction data 2001 , 18, 523	9
68	A systematic sequencing-based approach for microbial contaminant detection and functional inference. <i>BMC Biology</i> , 2019 , 17, 72	7.3 8
67	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
66	Predicting promoter activities of primary human DNA sequences. <i>Nucleic Acids Research</i> , 2011 , 39, e75	20.1 8

65	Finding Optimal Pairs of Patterns. <i>Lecture Notes in Computer Science</i> , 2004 , 450-462	0.9	8
64	Finding Optimal Pairs of Cooperative and Competing Patterns with Bounded Distance. <i>Lecture Notes in Computer Science</i> , 2004 , 32-46	0.9	8
63	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
62	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
61	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
60	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
59	Computational promoter modeling identifies the modes of transcriptional regulation in hematopoietic stem cells. <i>PLoS ONE</i> , 2014 , 9, e93853	3.7	7
58	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
57	Markov chain-based promoter structure modeling for tissue-specific expression pattern prediction. <i>DNA Research</i> , 2008 , 15, 3-11	4.5	7
56	Advances, practice, and clinical perspectives in high-throughput sequencing. <i>Oral Diseases</i> , 2016 , 22, 353-64	3.5	7
55	An assessment of prediction algorithms for nucleosome positioning. <i>Genome Informatics</i> , 2009 , 23, 169-78		7
54	HHEX promotes myeloid transformation in cooperation with mutant ASXL1. <i>Blood</i> , 2020 , 136, 1670-1684.2		6
53	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
52	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
51	Design and utility of CCN2 anchor peptide aptamers. <i>Biochimie</i> , 2010 , 92, 1010-5	4.6	6
50	Positional variations among heterogeneous nucleosome maps give dynamical information on chromatin. <i>Chromosoma</i> , 2010 , 119, 391-404	2.8	6
49	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
48	Whole genome sequencing analysis identifies recurrent structural alterations in esophageal squamous cell carcinoma. <i>PeerJ</i> , 2020 , 8, e9294	3.1	6

47	A Genetic Algorithm for Motif Finding Based on Statistical Significance. <i>Lecture Notes in Computer Science</i> , 2015 , 438-449	0.9	5
46	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
45	Intrinsic promoter activities of primary DNA sequences in the human genome. <i>DNA Research</i> , 2007 , 14, 71-7	4.5	5
44	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
43	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
42	Profiling ascidian promoters as the primordial type of vertebrate promoter. <i>BMC Genomics</i> , 2011 , 12 Suppl 3, S7	4.5	4
41	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
40	A bit-parallel dynamic programming algorithm suitable for DNA sequence alignment. <i>Journal of Bioinformatics and Computational Biology</i> , 2012 , 10, 1250002	1	4
39	AN ASSESSMENT OF PREDICTION ALGORITHMS FOR NUCLEOSOME POSITIONING 2009 ,		4
38	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
37	Existence and possible roles of independent non-CpG methylation in the mammalian brain. <i>DNA Research</i> , 2020 , 27,	4.5	4
36	A study on the application of topic models to motif finding algorithms. <i>BMC Bioinformatics</i> , 2016 , 17, 502	3.6	4
35	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
34	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
33	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
32	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
31	Alterations in rRNA-mRNA interaction during plastid evolution. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1728-40	8.3	2
30	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

29	Parameter Landscape Analysis for Common Motif Discovery Programs. <i>Lecture Notes in Computer Science</i> , 2005 , 79-87	0.9	2
28	The Origin and Evolution of Eukaryotic Protein Kinases. <i>Journal of Genome Science and Technology</i> , 2002 , 1, 83-104		2
27	Genome Structure, Functional Genomics, and Proteomics in Ascidians 2012 , 87-132		2
26	Waves of chromatin modifications in mouse dendritic cells in response to LPS stimulation		2
25	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
24	Information Science Should Take a Lead in Future Biomedical Research. <i>Engineering</i> , 2019 , 5, 1155-1158	9.7	1
23	Innate immunity interactome dynamics. <i>Gene Regulation and Systems Biology</i> , 2014 , 8, 1-15	2	1
22	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
21	USING SIMPLE RULES ON PRESENCE AND POSITIONING OF MOTIFS FOR PROMOTER STRUCTURE MODELING AND TISSUE-SPECIFIC EXPRESSION PREDICTION 2008 ,		1
20	Oligo-capped cDNAs for promoter identification and annotation. <i>International Congress Series</i> , 2002 , 1246, 233-239		1
19	Discovery of Intermediary Genes between Pathways Using Sparse Regression. <i>PLoS ONE</i> , 2015 , 10, e0133222	3.7	1
18	Modeling the -regulatory modules of genes expressed in developmental stages of. <i>PeerJ</i> , 2017 , 5, e33893	3.1	1
17	Prediction of Transcriptional Terminators in Bacillus subtilis and Related Species. <i>PLoS Computational Biology</i> , 2005 , preprint, e25	5	1
16	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
15	A hypothetical trivalent epigenetic code that affects the nature of human ESCs. <i>PLoS ONE</i> , 2020 , 15, e0238742	3.7	1
14	Prediction of Protein Localization 2019 , 53-59		0
13	Characterizing Promoter and Enhancer Sequences by a Deep Learning Method. <i>Frontiers in Genetics</i> , 2021 , 12, 681259	4.5	0
12	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

- 11 Extreme value theory as a framework for understanding mutation frequency distribution in cancer genomes. *PLoS ONE*, **2021**, 16, e0243595 3.7 ○
- 10 Prediction of Protein-Binding Sites in DNA Sequences **2019**, 447-451
- 9 3P303 Computational prediction of mitochondrial inner membrane proteins(Bioinformatics: Functional genomics,The 48th Annual Meeting of the Biophysical Society of Japan). *Seibutsu Butsuri* , **2010**, 50, S199 ○
- 8 THE JAPANESE SOCIETY OF BIOINFORMATICS (JSBi). *Asia Pacific Biotech News*, **2007**, 11, 1056-1057 ○
- 7 S2d2-2 Comparative analysis of firmicute promoters(S2-d2: "Bioinformatics of Transcriptional Regulation",Symposia,Abstract,Meeting Program of EABS & BSJ 2006). *Seibutsu Butsuri*, **2006**, 46, S129 ○
- 6 S2d2-3 Comparative analysis of mamalian transcriptomes(S2-d2: "Bioinformatics of Transcriptional Regulation",Symposia,Abstract,Meeting Program of EABS & BSJ 2006). *Seibutsu Butsuri*, **2006**, 46, S129 ○
- 5 Computational Inference of Gene Regulation from Whole-Transcriptome Analysis of Early Embryos. *Advances in Medical Technologies and Clinical Practice Book Series*,241-279 ○.3
- 4 Homeobox Transcription Factor Hhex Promotes Myeloid Leukemia in Cooperation with Mutant ASXL1. *Blood*, **2019**, 134, 2525-2525 2.2
- 3 Impacts of the ENCODE Project. *Seibutsu Butsuri*, **2013**, 53, 272-273 ○
- 2 Introduction to Selected Papers from GIW2018. *Journal of Bioinformatics and Computational Biology* , **2018**, 16, 1802005 1
- 1 TimeXNet Web: identifying cellular response networks from diverse omics time-course data. *Bioinformatics*, **2018**, 34, 3764-3765 7.2