

Minoru Kanehisa

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.

189
papers

66,103
citations

67
h-index

197
g-index

197
ext. papers

85,411
ext. citations

9.3
avg, IF

8.47
L-index

#	Paper	IF	Citations
189	KEGG: integrating viruses and cellular organisms. <i>Nucleic Acids Research</i> , 2021 , 49, D545-D551	20.1	702
188	KEGG mapping tools for uncovering hidden features in biological data. <i>Protein Science</i> , 2021 ,	6.3	54
187	KofamKOALA: KEGG Ortholog assignment based on profile HMM and adaptive score threshold. <i>Bioinformatics</i> , 2020 , 36, 2251-2252	7.2	263
186	KEGG Mapper for inferring cellular functions from protein sequences. <i>Protein Science</i> , 2020 , 29, 28-35	6.3	362
185	Toward understanding the origin and evolution of cellular organisms. <i>Protein Science</i> , 2019 , 28, 1947-1953	5.1	728
184	New approach for understanding genome variations in KEGG. <i>Nucleic Acids Research</i> , 2019 , 47, D590-D595	20.1	1001
183	Inferring Antimicrobial Resistance from Pathogen Genomes in KEGG. <i>Methods in Molecular Biology</i> , 2018 , 1807, 225-239	1.4	7
182	Enzyme Annotation and Metabolic Reconstruction Using KEGG. <i>Methods in Molecular Biology</i> , 2017 , 1611, 135-145	1.4	59
181	KEGG: new perspectives on genomes, pathways, diseases and drugs. <i>Nucleic Acids Research</i> , 2017 , 45, D353-D361	20.1	3970
180	KEGG GLYCAN 2017 , 177-193		5
179	Revealing phenotype-associated functional differences by genome-wide scan of ancient haplotype blocks. <i>PLoS ONE</i> , 2017 , 12, e0176530	3.7	
178	Identification of Enzyme Genes Using Chemical Structure Alignments of Substrate-Product Pairs. <i>Journal of Chemical Information and Modeling</i> , 2016 , 56, 510-6	6.1	8
177	KEGG as a reference resource for gene and protein annotation. <i>Nucleic Acids Research</i> , 2016 , 44, D457-62	20.1	3357
176	BlastKOALA and GhostKOALA: KEGG Tools for Functional Characterization of Genome and Metagenome Sequences. <i>Journal of Molecular Biology</i> , 2016 , 428, 726-731	6.5	1382
175	KEGG Bioinformatics Resource for Plant Genomics and Metabolomics. <i>Methods in Molecular Biology</i> , 2016 , 1374, 55-70	1.4	51
174	Symbol Nomenclature for Graphical Representations of Glycans. <i>Glycobiology</i> , 2015 , 25, 1323-4	5.8	585
173	Glycomic analysis using KEGG GLYCAN. <i>Methods in Molecular Biology</i> , 2015 , 1273, 97-107	1.4	13

172	Data, information, knowledge and principle: back to metabolism in KEGG. <i>Nucleic Acids Research</i> , 2014 , 42, D199-205	20.1	2277
171	PIERO ontology for analysis of biochemical transformations: effective implementation of reaction information in the IUBMB enzyme list. <i>Journal of Bioinformatics and Computational Biology</i> , 2014 , 12, 1442001	1	6
170	DINIES: drug-target interaction network inference engine based on supervised analysis. <i>Nucleic Acids Research</i> , 2014 , 42, W39-45	20.1	82
169	Predictive genomic and metabolomic analysis for the standardization of enzyme data. <i>Perspectives in Science</i> , 2014 , 1, 24-32	0.8	5
168	Pathways of Toxicity. <i>ALTEX: Alternatives To Animal Experimentation</i> , 2014 , 31, 53-61	4.3	59
167	Automated interpretation of metabolic capacity from genome and metagenome sequences. <i>Quantitative Biology</i> , 2013 , 1, 192-200	3.9	1
166	Chemical and genomic evolution of enzyme-catalyzed reaction networks. <i>FEBS Letters</i> , 2013 , 587, 2731-7.8	3.8	25
165	KCF-S: KEGG Chemical Function and Substructure for improved interpretability and prediction in chemical bioinformatics. <i>BMC Systems Biology</i> , 2013 , 7 Suppl 6, S2	3.5	20
164	Molecular network analysis of diseases and drugs in KEGG. <i>Methods in Molecular Biology</i> , 2013 , 939, 263-7.4	7.4	63
163	Modular architecture of metabolic pathways revealed by conserved sequences of reactions. <i>Journal of Chemical Information and Modeling</i> , 2013 , 53, 613-22	6.1	59
162	KEGG OC: a large-scale automatic construction of taxonomy-based ortholog clusters. <i>Nucleic Acids Research</i> , 2013 , 41, D353-7	20.1	81
161	KEGG for integration and interpretation of large-scale molecular data sets. <i>Nucleic Acids Research</i> , 2012 , 40, D109-14	20.1	3314
160	Evaluation method for the potential functionome harbored in the genome and metagenome. <i>BMC Genomics</i> , 2012 , 13, 699	4.5	40
159	Using the KEGG database resource. <i>Current Protocols in Bioinformatics</i> , 2012 , Chapter 1, Unit1.12	24.2	148
158	The KEGG databases and tools facilitating omics analysis: latest developments involving human diseases and pharmaceuticals. <i>Methods in Molecular Biology</i> , 2012 , 802, 19-39	1.4	73
157	Population model-based inter-diploidy similarity measure for accurate diploidy clustering. <i>Journal of Computational Biology</i> , 2012 , 19, 55-67	1.7	1
156	GENIES: gene network inference engine based on supervised analysis. <i>Nucleic Acids Research</i> , 2012 , 40, W162-7	20.1	33
155	2PT107 A classification of enzymatic reactions and its application to metabolic pathway search(The 50th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2012 , 52, S122	0	

154	Comparative genome analysis of three eukaryotic parasites with differing abilities to transform leukocytes reveals key mediators of Theileria-induced leukocyte transformation. <i>MBio</i> , 2012 , 3, e00204-12	7.8	48
153	Network-based analysis and characterization of adverse drug-drug interactions. <i>Journal of Chemical Information and Modeling</i> , 2011 , 51, 2977-85	6.1	44
152	KEGG and GenomeNet Resources for Predicting Protein Function from Omics Data Including KEGG PLANT Resource 2011 , 271-288		4
151	MUCHA: multiple chemical alignment algorithm to identify building block substructures of orphan secondary metabolites. <i>BMC Bioinformatics</i> , 2011 , 12 Suppl 14, S1	3.6	1
150	iPath2.0: interactive pathway explorer. <i>Nucleic Acids Research</i> , 2011 , 39, W412-5	20.1	244
149	SIMCOMP/SUBCOMP: chemical structure search servers for network analyses. <i>Nucleic Acids Research</i> , 2010 , 38, W652-6	20.1	88
148	PathPred: an enzyme-catalyzed metabolic pathway prediction server. <i>Nucleic Acids Research</i> , 2010 , 38, W138-43	20.1	191
147	KEGG for representation and analysis of molecular networks involving diseases and drugs. <i>Nucleic Acids Research</i> , 2010 , 38, D355-60	20.1	1710
146	Drug-target interaction prediction from chemical, genomic and pharmacological data in an integrated framework. <i>Bioinformatics</i> , 2010 , 26, i246-54	7.2	319
145	GENOME-WIDE ANALYSIS OF PLANT UGT FAMILY BASED ON SEQUENCE AND SUBSTRATE INFORMATION 2010 ,		1
144	Characterization of alpha-phosphoglucomutase isozymes from <i>Toxoplasma gondii</i> . <i>Parasitology International</i> , 2010 , 59, 206-10	2.1	7
143	varDB: a database of antigenic variant sequences--current status and future prospects. <i>Acta Tropica</i> , 2010 , 114, 144-51	3.2	3
142	NEW KERNEL METHODS FOR PHENOTYPE PREDICTION FROM GENOTYPE DATA 2010 ,		2
141	KEGG GLYCAN for Integrated Analysis of Pathways, Genes, and Glycan Structures 2010 , 197-210		
140	E-zyme: predicting potential EC numbers from the chemical transformation pattern of substrate-product pairs. <i>Bioinformatics</i> , 2009 , 25, i179-86	7.2	57
139	Domain shuffling and the evolution of vertebrates. <i>Genome Research</i> , 2009 , 19, 1393-403	9.7	72
138	Comprehensive analysis of glycosyltransferases in eukaryotic genomes for structural and functional characterization of glycans. <i>Carbohydrate Research</i> , 2009 , 344, 881-7	2.9	32
137	Extraction and analysis of chemical modification patterns in drug development. <i>Journal of Chemical Information and Modeling</i> , 2009 , 49, 1122-9	6.1	11

136	Systems biology approaches and pathway tools for investigating cardiovascular disease. <i>Molecular BioSystems</i> , 2009 , 5, 588-602		82
135	Characterization and evolutionary landscape of AmnSINE1 in Amniota genomes. <i>Gene</i> , 2009 , 441, 100-103,8		19
134	REPRESENTATION AND ANALYSIS OF MOLECULAR NETWORKS INVOLVING DISEASES AND DRUGS 2009 ,		2
133	Using KEGG in the Transition from Genomics to Chemical Genomics 2009 , 437-452		2
132	Knowledge-Based Analysis of Protein Interaction Networks in Neurodegenerative Diseases. <i>Frontiers in Neuroscience</i> , 2009 , 147-162		
131	Representation and analysis of molecular networks involving diseases and drugs. <i>Genome Informatics</i> , 2009 , 23, 212-3		10
130	iPath: interactive exploration of biochemical pathways and networks. <i>Trends in Biochemical Sciences</i> , 2008 , 33, 101-3	10.3	156
129	Prediction of drug-target interaction networks from the integration of chemical and genomic spaces. <i>Bioinformatics</i> , 2008 , 24, i232-40	7.2	641
128	Mining significant tree patterns in carbohydrate sugar chains. <i>Bioinformatics</i> , 2008 , 24, i167-73	7.2	27
127	KEGG Atlas mapping for global analysis of metabolic pathways. <i>Nucleic Acids Research</i> , 2008 , 36, W423-620.1		343
126	A new efficient probabilistic model for mining labeled ordered trees applied to glycobiology. <i>ACM Transactions on Knowledge Discovery From Data</i> , 2008 , 2, 1-30	4	6
125	The repertoire of desaturases and elongases reveals fatty acid variations in 56 eukaryotic genomes. <i>Journal of Lipid Research</i> , 2008 , 49, 183-91	6.3	125
124	Systematic survey for novel types of prokaryotic retroelements based on gene neighborhood and protein architecture. <i>Molecular Biology and Evolution</i> , 2008 , 25, 1395-404	8.3	37
123	NETWORK ANALYSIS OF ADVERSE DRUG INTERACTIONS 2008 ,		2
122	KEGG for linking genomes to life and the environment. <i>Nucleic Acids Research</i> , 2008 , 36, D480-4	20.1	3943
121	AAindex: amino acid index database, progress report 2008. <i>Nucleic Acids Research</i> , 2008 , 36, D202-5	20.1	623
120	KEGG GLYCAN for Integrated Analysis of Pathways, Genes, and Structures 2008 , 441-444		3
119	Network analysis of adverse drug interactions. <i>Genome Informatics</i> , 2008 , 20, 252-9		6

118	KAAS: an automatic genome annotation and pathway reconstruction server. <i>Nucleic Acids Research</i> , 2007 , 35, W182-5	20.1	2531
117	Identification of endocrine disruptor biodegradation by integration of structure-activity relationship with pathway analysis. <i>Environmental Science & Technology</i> , 2007 , 41, 7997-8003	10.3	11
116	The commonality of protein interaction networks determined in neurodegenerative disorders (NDDs). <i>Bioinformatics</i> , 2007 , 23, 2129-38	7.2	47
115	Systematic analysis of enzyme-catalyzed reaction patterns and prediction of microbial biodegradation pathways. <i>Journal of Chemical Information and Modeling</i> , 2007 , 47, 1702-12	6.1	64
114	Prediction of nitrogen metabolism-related genes in Anabaena by kernel-based network analysis. <i>Proteomics</i> , 2007 , 7, 900-9	4.8	7
113	Towards zoomable multidimensional maps of the cell. <i>Nature Biotechnology</i> , 2007 , 25, 547-54	44.5	73
112	Prediction of missing enzyme genes in a bacterial metabolic network. Reconstruction of the lysine-degradation pathway of <i>Pseudomonas aeruginosa</i> . <i>FEBS Journal</i> , 2007 , 274, 2262-73	5.7	24
111	Mining prokaryotic genomes for unknown amino acids: a stop-codon-based approach. <i>BMC Bioinformatics</i> , 2007 , 8, 225	3.6	16
110	Regulation of metabolic networks by small molecule metabolites. <i>BMC Bioinformatics</i> , 2007 , 8, 88	3.6	16
109	Characterization of relationships between transcriptional units and operon structures in <i>Bacillus subtilis</i> and <i>Escherichia coli</i> . <i>BMC Genomics</i> , 2007 , 8, 48	4.5	37
108	KEGG bioinformatics resource for plant genomics research. <i>Methods in Molecular Biology</i> , 2007 , 406, 437-58	1.4	22
107	Gene annotation and pathway mapping in KEGG. <i>Methods in Molecular Biology</i> , 2007 , 396, 71-91	1.4	196
106	Complete nucleotide sequence of the freshwater unicellular cyanobacterium <i>Synechococcus elongatus</i> PCC 6301 chromosome: gene content and organization. <i>Photosynthesis Research</i> , 2007 , 93, 55-67	3.7	67
105	EGENES: transcriptome-based plant database of genes with metabolic pathway information and expressed sequence tag indices in KEGG. <i>Plant Physiology</i> , 2007 , 144, 857-66	6.6	30
104	VisANT 3.0: new modules for pathway visualization, editing, prediction and construction. <i>Nucleic Acids Research</i> , 2007 , 35, W625-32	20.1	58
103	Comprehensive analysis of distinctive polyketide and nonribosomal peptide structural motifs encoded in microbial genomes. <i>Journal of Molecular Biology</i> , 2007 , 368, 1500-17	6.5	116
102	Evolutionary history and functional implications of protein domains and their combinations in eukaryotes. <i>Genome Biology</i> , 2007 , 8, R121	18.3	41
101	Observing metabolic functions at the genome scale. <i>Genome Biology</i> , 2007 , 8, R123	18.3	36

100	PREDICTING B CELL EPITOPE RESIDUES WITH NETWORK TOPOLOGY BASED AMINO ACID INDICES 2007 ,		4
99	NEW AMINO ACID INDICES BASED ON RESIDUE NETWORK TOPOLOGY 2007 ,		7
98	Inference of Protein-Protein Interactions by Using Co-evolutionary Information. <i>Lecture Notes in Computer Science</i> , 2007 , 322-333	0.9	
97	An improved scoring scheme for predicting glycan structures from gene expression data. <i>Genome Informatics</i> , 2007 , 18, 237-46		13
96	Analysis of common substructures of metabolic compounds within the different organism groups. <i>Genome Informatics</i> , 2007 , 18, 299-307		2
95	Extraction of phylogenetic network modules from the metabolic network. <i>BMC Bioinformatics</i> , 2006 , 7, 130	3.6	36
94	ProfilePSTMM: capturing tree-structure motifs in carbohydrate sugar chains. <i>Bioinformatics</i> , 2006 , 22, e25-34	7.2	25
93	ODB: a database of operons accumulating known operons across multiple genomes. <i>Nucleic Acids Research</i> , 2006 , 34, D358-62	20.1	41
92	Identification of metabolic units induced by environmental signals. <i>Bioinformatics</i> , 2006 , 22, e375-83	7.2	4
91	Partial correlation coefficient between distance matrices as a new indicator of protein-protein interactions. <i>Bioinformatics</i> , 2006 , 22, 2488-92	7.2	33
90	A new efficient probabilistic model for mining labeled ordered trees 2006 ,		6
89	KEGG as a glycome informatics resource. <i>Glycobiology</i> , 2006 , 16, 63R-70R	5.8	231
88	EGassembler: online bioinformatics service for large-scale processing, clustering and assembling ESTs and genomic DNA fragments. <i>Nucleic Acids Research</i> , 2006 , 34, W459-62	20.1	126
87	From genomics to chemical genomics: new developments in KEGG. <i>Nucleic Acids Research</i> , 2006 , 34, D354-71	20.1	2267
86	Quantitative elementary mode analysis of metabolic pathways: the example of yeast glycolysis. <i>BMC Bioinformatics</i> , 2006 , 7, 186	3.6	56
85	Extracting sequence motifs and the phylogenetic features of SNARE-dependent membrane traffic. <i>Traffic</i> , 2006 , 7, 1104-18	5.7	41
84	Structure-activity relationships and pathway analysis of biological degradation processes. <i>Journal of Pesticide Sciences</i> , 2006 , 31, 273-281	2.7	
83	A 6-Approximation Algorithm for Computing Smallest Common AoN-Supertree with Application to the Reconstruction of Glycan Trees. <i>Lecture Notes in Computer Science</i> , 2006 , 100-110	0.9	1

82	Bioinformatics approaches in glycomics and drug discovery. <i>Current Opinion in Molecular Therapeutics</i> , 2006 , 8, 514-20		12
81	The repertoire of desaturases for unsaturated fatty acid synthesis in 397 genomes. <i>Genome Informatics</i> , 2006 , 17, 173-83		9
80	Analysis of the differences in metabolic network expansion between prokaryotes and eukaryotes. <i>Genome Informatics</i> , 2006 , 17, 230-9		2
79	Prediction of glycan structures from gene expression data based on glycosyltransferase reactions. <i>Bioinformatics</i> , 2005 , 21, 3976-82	7.2	75
78	Using the KEGG database resource. <i>Current Protocols in Bioinformatics</i> , 2005 , Chapter 1, Unit 1.12	24.2	80
77	MRP1 mutated in the L0 region transports SN-38 but not leukotriene C4 or estradiol-17 (beta-D-glucuronate). <i>Biochemical Pharmacology</i> , 2005 , 70, 1056-65	6	9
76	Extraction of leukemia specific glycan motifs in humans by computational glycomics. <i>Carbohydrate Research</i> , 2005 , 340, 2270-8	2.9	35
75	A score matrix to reveal the hidden links in glycans. <i>Bioinformatics</i> , 2005 , 21, 1457-63	7.2	32
74	Global analysis of circadian expression in the cyanobacterium <i>Synechocystis</i> sp. strain PCC 6803. <i>Journal of Bacteriology</i> , 2005 , 187, 2190-9	3.5	131
73	Fast and accurate database homology search using upper bounds of local alignment scores. <i>Bioinformatics</i> , 2005 , 21, 912-21	7.2	18
72	The inference of protein-protein interactions by co-evolutionary analysis is improved by excluding the information about the phylogenetic relationships. <i>Bioinformatics</i> , 2005 , 21, 3482-9	7.2	126
71	Utilizing evolutionary information and gene expression data for estimating gene networks with bayesian network models. <i>Journal of Bioinformatics and Computational Biology</i> , 2005 , 3, 1295-313	1	42
70	Positive regulation of sugar catabolic pathways in the cyanobacterium <i>Synechocystis</i> sp. PCC 6803 by the group 2 sigma factor sigE. <i>Journal of Biological Chemistry</i> , 2005 , 280, 30653-9	5.4	128
69	Alteration of gene expression in human hepatocellular carcinoma with integrated hepatitis B virus DNA. <i>Clinical Cancer Research</i> , 2005 , 11, 5821-6	12.9	63
68	Conservation of gene co-regulation between two prokaryotes: <i>Bacillus subtilis</i> and <i>Escherichia coli</i> . <i>Genome Informatics</i> , 2005 , 16, 116-24		3
67	Comprehensive analysis and prediction of synthetic lethality using subcellular locations. <i>Genome Informatics</i> , 2005 , 16, 150-8		
66	A global representation of the carbohydrate structures: a tool for the analysis of glycan. <i>Genome Informatics</i> , 2005 , 16, 214-22		7
65	Autoimmune diseases and peptide variations. <i>Genome Informatics</i> , 2005 , 16, 272-80		

64	Managing and analyzing carbohydrate data. <i>SIGMOD Record</i> , 2004 , 33, 33-38	1.1	4
63	The evolutionary repertoires of the eukaryotic-type ABC transporters in terms of the phylogeny of ATP-binding domains in eukaryotes and prokaryotes. <i>Molecular Biology and Evolution</i> , 2004 , 21, 2149-60	8.3	27
62	Application of a new probabilistic model for recognizing complex patterns in glycans. <i>Bioinformatics</i> , 2004 , 20 Suppl 1, i6-14	7.2	10
61	The KEGG resource for deciphering the genome. <i>Nucleic Acids Research</i> , 2004 , 32, D277-80	20.1	3072
60	Response to oxidative stress involves a novel peroxiredoxin gene in the unicellular cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>Plant and Cell Physiology</i> , 2004 , 45, 290-9	4.9	99
59	Integrative annotation of 21,037 human genes validated by full-length cDNA clones. <i>PLoS Biology</i> , 2004 , 2, e162	9.7	255
58	Clustering under the line graph transformation: application to reaction network. <i>BMC Bioinformatics</i> , 2004 , 5, 207	3.6	10
57	Computational assignment of the EC numbers for genomic-scale analysis of enzymatic reactions. <i>Journal of the American Chemical Society</i> , 2004 , 126, 16487-98	16.4	108
56	KCaM (KEGG Carbohydrate Matcher): a software tool for analyzing the structures of carbohydrate sugar chains. <i>Nucleic Acids Research</i> , 2004 , 32, W267-72	20.1	89
55	Using protein motif combinations to update KEGG pathway maps and orthologue tables. <i>Genome Informatics</i> , 2004 , 15, 266-75		6
54	Extraction of species-specific glycan substructures. <i>Genome Informatics</i> , 2004 , 15, 69-81		5
53	Clustering of database sequences for fast homology search using upper bounds on alignment score. <i>Genome Informatics</i> , 2004 , 15, 93-104		7
52	Extraction of phylogenetic network modules from prokaryote metabolic pathways. <i>Genome Informatics</i> , 2004 , 15, 249-58		10
51	Prediction of protein subcellular locations by support vector machines using compositions of amino acids and amino acid pairs. <i>Bioinformatics</i> , 2003 , 19, 1656-63	7.2	297
50	Development of a chemical structure comparison method for integrated analysis of chemical and genomic information in the metabolic pathways. <i>Journal of the American Chemical Society</i> , 2003 , 125, 11853-65	16.4	348
49	Bioinformatics in the post-sequence era. <i>Nature Genetics</i> , 2003 , 33 Suppl, 305-10	36.3	128
48	Identification of a new cryptochrome class. Structure, function, and evolution. <i>Molecular Cell</i> , 2003 , 11, 59-67	17.6	269
47	DNA microarray analysis of redox-responsive genes in the genome of the cyanobacterium <i>Synechocystis</i> sp. strain PCC 6803. <i>Journal of Bacteriology</i> , 2003 , 185, 1719-25	3.5	140

46	Efficient tree-matching methods for accurate carbohydrate database queries. <i>Genome Informatics</i> , 2003 , 14, 134-43		16
45	Heuristics for chemical compound matching. <i>Genome Informatics</i> , 2003 , 14, 144-53		16
44	Screening for the target gene of cyanobacterial cAMP receptor protein SYCRP1. <i>Molecular Microbiology</i> , 2002 , 43, 843-53	4.1	50
43	The KEGG databases at GenomeNet. <i>Nucleic Acids Research</i> , 2002 , 30, 42-6	20.1	954
42	LIGAND: database of chemical compounds and reactions in biological pathways. <i>Nucleic Acids Research</i> , 2002 , 30, 402-4	20.1	215
41	A two-component Mn ²⁺ -sensing system negatively regulates expression of the mntCAB operon in <i>Synechocystis</i> . <i>Plant Cell</i> , 2002 , 14, 2901-13	11.6	67
40	Update of MAGEST: Maboaya Gene Expression patterns and Sequence Tags. <i>Nucleic Acids Research</i> , 2002 , 30, 119-20	20.1	12
39	KEGG: From Genes to Biochemical Pathways 2002 , 63-76		1
38	Extraction of organism groups from phylogenetic profiles using independent component analysis. <i>Genome Informatics</i> , 2002 , 13, 61-70		3
37	Cold-regulated genes under control of the cold sensor Hik33 in <i>Synechocystis</i> . <i>Molecular Microbiology</i> , 2001 , 40, 235-44	4.1	215
36	DNA microarray analysis of cyanobacterial gene expression during acclimation to high light. <i>Plant Cell</i> , 2001 , 13, 793-806	11.6	399
35	Prediction of higher order functional networks from genomic data. <i>Pharmacogenomics</i> , 2001 , 2, 373-85	2.6	10
34	Whole genome sequencing of meticillin-resistant <i>Staphylococcus aureus</i> . <i>Lancet, The</i> , 2001 , 357, 1225-40	4.0	1586
33	Pathway databases and higher order function. <i>Advances in Protein Chemistry</i> , 2000 , 54, 381-408		11
32	AAindex: amino acid index database. <i>Nucleic Acids Research</i> , 2000 , 28, 374	20.1	488
31	Tandem clusters of membrane proteins in complete genome sequences. <i>Genome Research</i> , 2000 , 10, 731-43	9.7	36
30	MAGEST: MAboya gene expression patterns and sequence tags. <i>Nucleic Acids Research</i> , 2000 , 28, 133-5	20.1	34
29	KEGG: kyoto encyclopedia of genes and genomes. <i>Nucleic Acids Research</i> , 2000 , 28, 27-30	20.1	15737

28	Contributory presentations/posters. <i>Journal of Biosciences</i> , 1999 , 24, 33-198	2.3	
27	KEGG: Kyoto Encyclopedia of Genes and Genomes. <i>Nucleic Acids Research</i> , 1999 , 27, 29-34	20.1	3093
26	Computation with the KEGG pathway database. <i>BioSystems</i> , 1998 , 47, 119-28	1.9	186
25	Reconstruction of amino acid biosynthesis pathways from the complete genome sequence. <i>Genome Research</i> , 1998 , 8, 203-10	9.7	136
24	A comparative analysis of ABC transporters in complete microbial genomes. <i>Genome Research</i> , 1998 , 8, 1048-59	9.7	111
23	Linking databases and organisms: GenomeNet resources in Japan. <i>Trends in Biochemical Sciences</i> , 1997 , 22, 442-4	10.3	51
22	A database for post-genome analysis. <i>Trends in Genetics</i> , 1997 , 13, 375-6	8.5	302
21	The size differences among mammalian introns are due to the accumulation of small deletions. <i>FEBS Letters</i> , 1996 , 390, 99-103	3.8	31
20	Construction and analysis of a profile library characterizing groups of structurally known proteins. <i>Protein Science</i> , 1996 , 5, 1991-9	6.3	27
19	Analysis of amino acid indices and mutation matrices for sequence comparison and structure prediction of proteins. <i>Protein Engineering, Design and Selection</i> , 1996 , 9, 27-36	1.9	249
18	A genetic algorithm based molecular modeling technique for RNA stem-loop structures. <i>Nucleic Acids Research</i> , 1995 , 23, 419-26	20.1	22
17	Distribution profiles of GC content around the translation initiation site in different species. <i>FEBS Letters</i> , 1994 , 352, 7-10	3.8	9
16	An assessment of neural network and statistical approaches for prediction of E. coli promoter sites. <i>Nucleic Acids Research</i> , 1992 , 20, 4331-8	20.1	62
15	Construction of a dictionary of sequence motifs that characterize groups of related proteins. <i>Protein Engineering, Design and Selection</i> , 1992 , 5, 479-88	1.9	32
14	A knowledge base for predicting protein localization sites in eukaryotic cells. <i>Genomics</i> , 1992 , 14, 897-914	14.3	1375
13	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
12	Fragment peptide library for classification and functional prediction of proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990 , 8, 341-51	4.2	13
11	A multivariate analysis method for discriminating protein secondary structural segments. <i>Protein Engineering, Design and Selection</i> , 1988 , 2, 87-92	1.9	20

10	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
9	Prediction of in-vivo modification sites of proteins from their primary structures. <i>Journal of Biochemistry</i> , 1988 , 104, 693-9	3.1	23
8	Nonrandom recurrence of consecutive repeats in noncoding mammalian sequences. <i>Mathematical Biosciences</i> , 1986 , 81, 43-52	3.9	1
7	L-aspartate ammonia-lyase and fumarate hydratase share extensive sequence homology. <i>Biochemical and Biophysical Research Communications</i> , 1986 , 138, 568-72	3.4	26
6	Prediction of splice junctions in mRNA sequences. <i>Nucleic Acids Research</i> , 1985 , 13, 5327-40	20.1	55
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