Minoru Kanehisa

List of Publications by Year
in descending order

192 papers	106,801 citations	10984 71 h-index	5120 166 g-index
197 all docs	197 docs citations	197 times ranked	103088 citing authors

#	Article	IF	Citations
1	<scp>KEGG</scp> mapping tools for uncovering hidden features in biological data. Protein Science, 2022, 31, 47-53.	7.6	365
2	KEGG: integrating viruses and cellular organisms. Nucleic Acids Research, 2021, 49, D545-D551.	14.5	2,276
3	KEGG Mapper for inferring cellular functions from protein sequences. Protein Science, 2020, 29, 28-35.	7.6	791
4	KofamKOALA: KEGG Ortholog assignment based on profile HMM and adaptive score threshold. Bioinformatics, 2020, 36, 2251-2252.	4.1	820
5	Toward understanding the origin and evolution of cellular organisms. Protein Science, 2019, 28, 1947-1951.	7.6	2,262
6	New approach for understanding genome variations in KEGG. Nucleic Acids Research, 2019, 47, D590-D595.	14.5	1,503
7	Inferring Antimicrobial Resistance from Pathogen Genomes in KEGG. Methods in Molecular Biology, 2018, 1807, 225-239.	0.9	10
8	Enzyme Annotation and Metabolic Reconstruction Using KEGG. Methods in Molecular Biology, 2017, 1611, 135-145.	0.9	111
9	KEGG: new perspectives on genomes, pathways, diseases and drugs. Nucleic Acids Research, 2017, 45, D353-D361.	14.5	6,666
10	KEGG GLYCAN. , 2017, , 177-193.		8
11	Revealing phenotype-associated functional differences by genome-wide scan of ancient haplotype blocks. PLoS ONE, 2017, 12, e0176530.	2.5	0
12	Identification of Enzyme Genes Using Chemical Structure Alignments of Substrate–Product Pairs. Journal of Chemical Information and Modeling, 2016, 56, 510-516.	5.4	17
13	KEGG as a reference resource for gene and protein annotation. Nucleic Acids Research, 2016, 44, D457-D462.	14.5	5,435
14	BlastKOALA and GhostKOALA: KEGG Tools for Functional Characterization of Genome and Metagenome Sequences. Journal of Molecular Biology, 2016, 428, 726-731.	4.2	2,872
15	KEGG Bioinformatics Resource for Plant Genomics and Metabolomics. Methods in Molecular Biology, 2016, 1374, 55-70.	0.9	86
16	Symbol Nomenclature for Graphical Representations of Glycans. Glycobiology, 2015, 25, 1323-1324.	2.5	818
17	Glycomic Analysis Using KEGG GLYCAN. Methods in Molecular Biology, 2015, 1273, 97-107.	0.9	15
18	PIERO ontology for analysis of biochemical transformations: Effective implementation of reaction information in the IUBMB enzyme list. Journal of Bioinformatics and Computational Biology, 2014, 12, 1442001.	0.8	7

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19	DINIES: drug–target interaction network inference engine based on supervised analysis. Nucleic Acids Research, 2014, 42, W39-W45.	14.5	97
20	Predictive genomic and metabolomic analysis for the standardization of enzyme data. Perspectives in Science, 2014, 1, 24-32.	0.6	8
21	Data, information, knowledge and principle: back to metabolism in KEGG. Nucleic Acids Research, 2014, 42, D199-D205.	14.5	2,846
22	Pathways of Toxicity. ALTEX: Alternatives To Animal Experimentation, 2014, 31, 53-61.	1.5	75
23	Automated interpretation of metabolic capacity from genome and metagenome sequences. Quantitative Biology, 2013, 1, 192-200.	0.5	1
24	Chemical and genomic evolution of enzyme–catalyzed reaction networks. FEBS Letters, 2013, 587, 2731-2737.	2.8	33
25	KCF-S: KEGG Chemical Function and Substructure for improved interpretability and prediction in chemical bioinformatics. BMC Systems Biology, 2013, 7, S2.	3.0	25
26	Molecular Network Analysis of Diseases and Drugs in KEGG. Methods in Molecular Biology, 2013, 939, 263-275.	0.9	79
27	Modular Architecture of Metabolic Pathways Revealed by Conserved Sequences of Reactions. Journal of Chemical Information and Modeling, 2013, 53, 613-622.	5.4	73
28	KEGG and GenomeNet, New Developments, Metagenomic Analysis. , 2013, , 1-11.		0
29	KEGG OC: a large-scale automatic construction of taxonomy-based ortholog clusters. Nucleic Acids Research, 2012, 41, D353-D357.	14.5	96
30	Population Model–Based Inter-Diplotype Similarity Measure for Accurate Diplotype Clustering. Journal of Computational Biology, 2012, 19, 55-67.	1.6	1
31	GENIES: gene network inference engine based on supervised analysis. Nucleic Acids Research, 2012, 40, W162-W167.	14.5	39
32	2PT107 A classification of enzymatic reactions and its application to metabolic pathway search(The) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.1	0
33	Comparative Genome Analysis of Three Eukaryotic Parasites with Differing Abilities To Transform Leukocytes Reveals Key Mediators of <i>Theileria</i> -Induced Leukocyte Transformation. MBio, 2012, 3, e00204-12.	4.1	64
34	KEGG for integration and interpretation of large-scale molecular data sets. Nucleic Acids Research, 2012, 40, D109-D114.	14.5	4,174
35	Evaluation method for the potential functionome harbored in the genome and metagenome. BMC Genomics, 2012, 13, 699.	2.8	65
36	Using the KEGG Database Resource. Current Protocols in Bioinformatics, 2012, 38, Unit1.12.	25.8	232

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37	The KEGG Databases and Tools Facilitating Omics Analysis: Latest Developments Involving Human Diseases and Pharmaceuticals. Methods in Molecular Biology, 2012, 802, 19-39.	0.9	104
38	Network-Based Analysis and Characterization of Adverse Drug–Drug Interactions. Journal of Chemical Information and Modeling, 2011, 51, 2977-2985.	5.4	54
39	KEGG and GenomeNet Resources for Predicting Protein Function from Omics Data Including KEGG PLANT Resource. , 2011, , 271-288.		5
40	MUCHA: multiple chemical alignment algorithm to identify building block substructures of orphan secondary metabolites. BMC Bioinformatics, 2011, 12, S1.	2.6	1
41	iPath2.0: interactive pathway explorer. Nucleic Acids Research, 2011, 39, W412-W415.	14.5	322
42	CHARACTERIZING COMMON SUBSTRUCTURES OF LIGANDS FOR GPCR PROTEIN SUBFAMILIES. , 2010, , .		0
43	NEW KERNEL METHODS FOR PHENOTYPE PREDICTION FROM GENOTYPE DATA. , 2010, , .		2
44	SIMCOMP/SUBCOMP: chemical structure search servers for network analyses. Nucleic Acids Research, 2010, 38, W652-W656.	14.5	125
45	PathPred: an enzyme-catalyzed metabolic pathway prediction server. Nucleic Acids Research, 2010, 38, W138-W143.	14.5	227
46	KEGG for representation and analysis of molecular networks involving diseases and drugs. Nucleic Acids Research, 2010, 38, D355-D360.	14.5	1,999
47	Drug-target interaction prediction from chemical, genomic and pharmacological data in an integrated framework. Bioinformatics, 2010, 26, i246-i254.	4.1	396
48	GENOME-WIDE ANALYSIS OF PLANT UGT FAMILY BASED ON SEQUENCE AND SUBSTRATE INFORMATION. , 2010, , .		2
49	Characterization of α-phosphoglucomutase isozymes from Toxoplasma gondii. Parasitology International, 2010, 59, 206-210.	1.3	11
50	varDB: A database of antigenic variant sequences–Current status and future prospects. Acta Tropica, 2010, 114, 144-151.	2.0	5
51	ANALYSIS OF A LIPID BIOSYNTHESIS PROTEIN FAMILY AND PHOSPHOLIPID STRUCTURAL VARIATIONS. , 2010, , .		1
52	KEGG GLYCAN for Integrated Analysis of Pathways, Genes, and Glycan Structures. , 2010, , 197-210.		0
53	E-zyme: predicting potential EC numbers from the chemical transformation pattern of substrate-product pairs. Bioinformatics, 2009, 25, i179-i186.	4.1	64
54	Domain shuffling and the evolution of vertebrates. Genome Research, 2009, 19, 1393-1403.	5.5	86

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55	Comprehensive analysis of glycosyltransferases in eukaryotic genomes for structural and functional characterization of glycans. Carbohydrate Research, 2009, 344, 881-887.	2.3	37
56	Extraction and Analysis of Chemical Modification Patterns in Drug Development. Journal of Chemical Information and Modeling, 2009, 49, 1122-1129.	5.4	12
57	Systems biology approaches and pathway tools for investigating cardiovascular disease. Molecular BioSystems, 2009, 5, 588.	2.9	96
58	Characterization and evolutionary landscape of AmnSINE1 in Amniota genomes. Gene, 2009, 441, 100-110.	2.2	24
59	REPRESENTATION AND ANALYSIS OF MOLECULAR NETWORKS INVOLVING DISEASES AND DRUGS. , 2009, , .		2
60	Using KEGG in the Transition from Genomics to Chemical Genomics. , 2009, , 437-452.		2
61	Knowledge-Based Analysis of Protein Interaction Networks in Neurodegenerative Diseases. Frontiers in Neuroscience, 2009, , 147-162.	0.0	0
62	Representation and analysis of molecular networks involving diseases and drugs. Genome Informatics, 2009, 23, 212-3.	0.4	10
63	iPath: interactive exploration of biochemical pathways and networks. Trends in Biochemical Sciences, 2008, 33, 101-103.	7.5	216
64	Prediction of drug–target interaction networks from the integration of chemical and genomic spaces. Bioinformatics, 2008, 24, i232-i240.	4.1	864
65	Mining significant tree patterns in carbohydrate sugar chains. Bioinformatics, 2008, 24, i167-i173.	4.1	33
66	KEGG Atlas mapping for global analysis of metabolic pathways. Nucleic Acids Research, 2008, 36, W423-W426.	14.5	445
67	A new efficient probabilistic model for mining labeled ordered trees applied to glycobiology. ACM Transactions on Knowledge Discovery From Data, 2008, 2, 1-30.	3.5	10
68	The repertoire of desaturases and elongases reveals fatty acid variations in 56 eukaryotic genomes. Journal of Lipid Research, 2008, 49, 183-191.	4.2	150
69	Systematic Survey for Novel Types of Prokaryotic Retroelements Based on Gene Neighborhood and Protein Architecture. Molecular Biology and Evolution, 2008, 25, 1395-1404.	8.9	48
70	NETWORK ANALYSIS OF ADVERSE DRUG INTERACTIONS. , 2008, , .		2
71	KEGG GLYCAN for Integrated Analysis of Pathways, Genes, and Structures. , 2008, , 441-444.		3
72	Network analysis of adverse drug interactions. Genome Informatics, 2008, 20, 252-9.	0.4	6

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73	KEGG for linking genomes to life and the environment. Nucleic Acids Research, 2007, 36, D480-D484.	14.5	5,451
74	EGENES: Transcriptome-Based Plant Database of Genes with Metabolic Pathway Information and Expressed Sequence Tag Indices in KEGG. Plant Physiology, 2007, 144, 857-866.	4.8	35
75	VisANT 3.0: new modules for pathway visualization, editing, prediction and construction. Nucleic Acids Research, 2007, 35, W625-W632.	14.5	66
76	Comprehensive Analysis of Distinctive Polyketide and Nonribosomal Peptide Structural Motifs Encoded in Microbial Genomes. Journal of Molecular Biology, 2007, 368, 1500-1517.	4.2	145
77	Evolutionary history and functional implications of protein domains and their combinations in eukaryotes. Genome Biology, 2007, 8, R121.	9.6	71
78	Observing metabolic functions at the genome scale. Genome Biology, 2007, 8, R123.	9.6	54
79	AAindex: amino acid index database, progress report 2008. Nucleic Acids Research, 2007, 36, D202-D205.	14.5	871
80	KAAS: an automatic genome annotation and pathway reconstruction server. Nucleic Acids Research, 2007, 35, W182-W185.	14.5	3,517
81	Identification of Endocrine Disruptor Biodegradation by Integration of Structure–activity Relationship with Pathway Analysis. Environmental Science & Technology, 2007, 41, 7997-8003.	10.0	12
82	The commonality of protein interaction networks determined in neurodegenerative disorders (NDDs). Bioinformatics, 2007, 23, 2129-2138.	4.1	52
83	Systematic Analysis of Enzyme-Catalyzed Reaction Patterns and Prediction of Microbial Biodegradation Pathways. Journal of Chemical Information and Modeling, 2007, 47, 1702-1712.	5.4	73
84	Prediction of nitrogen metabolism-related genes inAnabaena by kernel-based network analysis. Proteomics, 2007, 7, 900-909.	2.2	8
85	Towards zoomable multidimensional maps of the cell. Nature Biotechnology, 2007, 25, 547-554.	17.5	84
86	Prediction of missing enzyme genes in a bacterial metabolic network. FEBS Journal, 2007, 274, 2262-2273.	4.7	30
87	Mining prokaryotic genomes for unknown amino acids: a stop-codon-based approach. BMC Bioinformatics, 2007, 8, 225.	2.6	17
88	Regulation of metabolic networks by small molecule metabolites. BMC Bioinformatics, 2007, 8, 88.	2.6	23
89	Characterization of relationships between transcriptional units and operon structures in Bacillus subtilis and Escherichia coli. BMC Genomics, 2007, 8, 48.	2.8	51
90	KEGG Bioinformatics Resource for Plant Genomics Research. , 2007, 406, 437-458.		27

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91	Gene Annotation and Pathway Mapping in KEGG. Methods in Molecular Biology, 2007, 396, 71-91.	0.9	238
92	Complete nucleotide sequence of the freshwater unicellular cyanobacterium Synechococcus elongatus PCC 6301 chromosome: gene content and organization. Photosynthesis Research, 2007, 93, 55-67.	2.9	72
93	PREDICTING B CELL EPITOPE RESIDUES WITH NETWORK TOPOLOGY BASED AMINO ACID INDICES. , 2007, , .		5
94	NEW AMINO ACID INDICES BASED ON RESIDUE NETWORK TOPOLOGY. , 2007, , .		10
95	COMPARATIVE PAIR-WISE DOMAIN-COMBINATIONS FOR SCREENING THE CLADE SPECIFIC DOMAIN-ARCHITECTURES IN METAZOAN GENOMES. , 2007, , .		0
96	Inference of Protein-Protein Interactions by Using Co-evolutionary Information. Lecture Notes in Computer Science, 2007, , 322-333.	1.3	0
97	An improved scoring scheme for predicting glycan structures from gene expression data. Genome Informatics, 2007, 18, 237-46.	0.4	14
98	Analysis of common substructures of metabolic compounds within the different organism groups. Genome Informatics, 2007, 18, 299-307.	0.4	2
99	EGassembler: online bioinformatics service for large-scale processing, clustering and assembling ESTs and genomic DNA fragments. Nucleic Acids Research, 2006, 34, W459-W462.	14.5	139
100	From genomics to chemical genomics: new developments in KEGG. Nucleic Acids Research, 2006, 34, D354-D357.	14.5	2,662
101	Quantitative elementary mode analysis of metabolic pathways: the example of yeast glycolysis. BMC Bioinformatics, 2006, 7, 186.	2.6	66
102	Extracting Sequence Motifs and the Phylogenetic Features of SNARE-Dependent Membrane Traffic. Traffic, 2006, 7, 1104-1118.	2.7	44
103	Extraction of phylogenetic network modules from the metabolic network. BMC Bioinformatics, 2006, 7, 130.	2.6	44
104	ProfilePSTMM: capturing tree-structure motifs in carbohydrate sugar chains. Bioinformatics, 2006, 22, e25-e34.	4.1	28
105	ODB: a database of operons accumulating known operons across multiple genomes. Nucleic Acids Research, 2006, 34, D358-D362.	14.5	46
106	Identification of metabolic units induced by environmental signals. Bioinformatics, 2006, 22, e375-e383.	4.1	4
107	Partial correlation coefficient between distance matrices as a new indicator of protein-protein interactions. Bioinformatics, 2006, 22, 2488-2492.	4.1	35
108	A new efficient probabilistic model for mining labeled ordered trees. , 2006, , .		9

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109	KEGG as a glycome informatics resource. Glycobiology, 2006, 16, 63R-70R.	2.5	279
110	Structure-activity relationships and pathway analysis of biological degradation processes. Journal of Pesticide Sciences, 2006, 31, 273-281.	1.4	0
111	A 6-Approximation Algorithm for Computing Smallest Common AoN-Supertree with Application to the Reconstruction of Glycan Trees. Lecture Notes in Computer Science, 2006, , 100-110.	1.3	1
112	Bioinformatics approaches in glycomics and drug discovery. Current Opinion in Molecular Therapeutics, 2006, 8, 514-20.	2.8	12
113	The repertoire of desaturases for unsaturated fatty acid synthesis in 397 genomes. Genome Informatics, 2006, 17, 173-83.	0.4	9
114	Analysis of the differences in metabolic network expansion between prokaryotes and eukaryotes. Genome Informatics, 2006, 17, 230-9.	0.4	2
115	Design of KEGG and GO. , 2005, , .		0
116	MRP1 mutated in the L0 region transports SN-38 but not leukotriene C4 or estradiol-17 (Î²-d-glucuronate). Biochemical Pharmacology, 2005, 70, 1056-1065.	4.4	9
117	Extraction of leukemia specific glycan motifs in humans by computational glycomics. Carbohydrate Research, 2005, 340, 2270-2278.	2.3	44
118	A score matrix to reveal the hidden links in glycans. Bioinformatics, 2005, 21, 1457-1463.	4.1	34
119	Global Analysis of Circadian Expression in the Cyanobacterium Synechocystis sp. Strain PCC 6803. Journal of Bacteriology, 2005, 187, 2190-2199.	2.2	148
120	Fast and accurate database homology search using upper bounds of local alignment scores. Bioinformatics, 2005, 21, 912-921.	4.1	19
121	The inference of protein-protein interactions by co-evolutionary analysis is improved by excluding the information about the phylogenetic relationships. Bioinformatics, 2005, 21, 3482-3489.	4.1	143
122	UTILIZING EVOLUTIONARY INFORMATION AND GENE EXPRESSION DATA FOR ESTIMATING GENE NETWORKS WITH BAYESIAN NETWORK MODELS. Journal of Bioinformatics and Computational Biology, 2005, 03, 1295-1313.	0.8	51
123	Positive Regulation of Sugar Catabolic Pathways in the Cyanobacterium Synechocystis sp. PCC 6803 by the Group 2 Ïƒ Factor SigE. Journal of Biological Chemistry, 2005, 280, 30653-30659.	3.4	159
124	Alteration of Gene Expression in Human Hepatocellular Carcinoma with Integrated Hepatitis B Virus DNA. Clinical Cancer Research, 2005, 11, 5821-5826.	7.0	72
125	Prediction of glycan structures from gene expression data based on glycosyltransferase reactions. Bioinformatics, 2005, 21, 3976-3982.	4.1	78
126	Using the KEGG Database Resource. Current Protocols in Bioinformatics, 2005, 11, Unit 1.12.	25.8	115

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127	Conservation of gene co-regulation between two prokaryotes: Bacillus subtilis and Escherichia coli. Genome Informatics, 2005, 16, 116-24.	0.4	3
128	Comprehensive analysis and prediction of synthetic lethality using subcellular locations. Genome Informatics, 2005, 16, 150-8.	0.4	0
129	A global representation of the carbohydrate structures: a tool for the analysis of glycan. Genome Informatics, 2005, 16, 214-22.	0.4	7
130	Autoimmune diseases and peptide variations. Genome Informatics, 2005, 16, 272-80.	0.4	0
131	Managing and analyzing carbohydrate data. SIGMOD Record, 2004, 33, 33-38.	1.2	4
132	The Evolutionary Repertoires of the Eukaryotic-Type ABC Transporters in Terms of the Phylogeny of ATP-binding Domains in Eukaryotes and Prokaryotes. Molecular Biology and Evolution, 2004, 21, 2149-2160.	8.9	29
133	Application of a new probabilistic model for recognizing complex patterns in glycans. Bioinformatics, 2004, 20, i6-i14.	4.1	13
134	The KEGG resource for deciphering the genome. Nucleic Acids Research, 2004, 32, 277D-280.	14.5	4,093
135	Response to Oxidative Stress Involves a Novel Peroxiredoxin Gene in the Unicellular Cyanobacterium Synechocystis sp. PCC 6803. Plant and Cell Physiology, 2004, 45, 290-299.	3.1	110
136	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. PLoS Biology, 2004, 2, e162.	5.6	290
137	Clustering under the line graph transformation: application to reaction network. BMC Bioinformatics, 2004, 5, 207.	2.6	14
138	Computational Assignment of the EC Numbers for Genomic-Scale Analysis of Enzymatic Reactions. Journal of the American Chemical Society, 2004, 126, 16487-16498.	13.7	120
139	KCaM (KEGG Carbohydrate Matcher): a software tool for analyzing the structures of carbohydrate sugar chains. Nucleic Acids Research, 2004, 32, W267-W272.	14.5	95
140	Using protein motif combinations to update KEGG pathway maps and orthologue tables. Genome Informatics, 2004, 15, 266-75.	0.4	6
141	Extraction of species-specific glycan substructures. Genome Informatics, 2004, 15, 69-81.	0.4	5
142	Clustering of database sequences for fast homology search using upper bounds on alignment score. Genome Informatics, 2004, 15, 93-104.	0.4	7
143	Extraction of phylogenetic network modules from prokayrote metabolic pathways. Genome Informatics, 2004, 15, 249-58.	0.4	12
144	Development of a Chemical Structure Comparison Method for Integrated Analysis of Chemical and Genomic Information in the Metabolic Pathways. Journal of the American Chemical Society, 2003, 125, 11853-11865.	13.7	423

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145	Bioinformatics in the post-sequence era. Nature Genetics, 2003, 33, 305-310.	21.4	174
146	Identification of a New Cryptochrome Class. Molecular Cell, 2003, 11, 59-67.	9.7	301
147	DNA Microarray Analysis of Redox-Responsive Genes in the Genome of the Cyanobacterium *Synechocystis* sp. Strain PCC 6803. Journal of Bacteriology, 2003, 185, 1719-1725.	2.2	153
148	Prediction of protein subcellular locations by support vector machines using compositions of amino acids and amino acid pairs. Bioinformatics, 2003, 19, 1656-1663.	4.1	354
149	Efficient tree-matching methods for accurate carbohydrate database queries. Genome Informatics, 2003, 14, 134-43.	0.4	20
150	Heuristics for chemical compound matching. Genome Informatics, 2003, 14, 144-53.	0.4	16
151	The KEGG databases at GenomeNet. Nucleic Acids Research, 2002, 30, 42-46.	14.5	1,202
152	LIGAND: database of chemical compounds and reactions in biological pathways. Nucleic Acids Research, 2002, 30, 402-404.	14.5	255
153	A Two-Component Mn2+-Sensing System Negatively Regulates Expression of the mntCAB Operon in Synechocystis. Plant Cell, 2002, 14, 2901-2913.	6.6	76
154	Update of MAGEST: Maboya Gene Expression patterns and Sequence Tags. Nucleic Acids Research, 2002, 30, 119-120.	14.5	12
155	KEGG: From Genes to Biochemical Pathways. , 2002, , 63-76.		12
156	Screening for the target gene of cyanobacterial cAMP receptor protein SYCRP1. Molecular Microbiology, 2002, 43, 843-853.	2.5	63
157	Extraction of organism groups from phylogenetic profiles using independent component analysis. Genome Informatics, 2002, 13, 61-70.	0.4	3
158	Whole genome sequencing of meticillin-resistant Staphylococcus aureus. Lancet, The, 2001, 357, 1225-1240.	13.7	1,835
159	Cold-regulated genes under control of the cold sensor Hik33 in Synechocystis. Molecular Microbiology, 2001, 40, 235-244.	2.5	238
160	DNA Microarray Analysis of Cyanobacterial Gene Expression during Acclimation to High Light. Plant Cell, 2001, 13, 793-806.	6.6	444
161	Prediction of higher order functional networks from genomic data. Pharmacogenomics, 2001, 2, 373-385.	1.3	11
162	Pathway databases and higher order function. Advances in Protein Chemistry, 2000, 54, 381-408.	4.4	14

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163	AAindex: Amino Acid index database. Nucleic Acids Research, 2000, 28, 374-374.	14.5	641
164	Tandem Clusters of Membrane Proteins in Complete Genome Sequences. Genome Research, 2000, 10, 731-743.	5.5	42
165	MAGEST: MAboya Gene Expression patterns and Sequence Tags. Nucleic Acids Research, 2000, 28, 133-135.	14.5	36
166	KEGG: Kyoto Encyclopedia of Genes and Genomes. Nucleic Acids Research, 2000, 28, 27-30.	14.5	25,375
167	Contributory presentations/posters. Journal of Biosciences, 1999, 24, 33-198.	1.1	0
168	KEGG: Kyoto Encyclopedia of Genes and Genomes. Nucleic Acids Research, 1999, 27, 29-34.	14.5	13,711
169	Computation with the KEGG pathway database. BioSystems, 1998, 47, 119-128.	2.0	240
170	Reconstruction of Amino Acid Biosynthesis Pathways from the Complete Genomeâ€‰Sequence. Genome Research, 1998, 8, 203-210.	5.5	145
171	A Comparative Analysis of ABC Transporters in Complete Microbial Genomes. Genome Research, 1998, 8, 1048-1059.	5.5	126
172	Linking databases and organisms: GenomeNet resources in Japan. Trends in Biochemical Sciences, 1997, 22, 442-444.	7.5	58
173	A database for post-genome analysis. Trends in Genetics, 1997, 13, 375-376.	6.7	372
174	The size differences among mammalian introns are due to the accumulation of small deletions. FEBS Letters, 1996, 390, 99-103.	2.8	41
175	Construction and analysis of a profile library characterizing groups of structurally known proteins. Protein Science, 1996, 5, 1991-1999.	7.6	31
176	Analysis of amino acid indices and mutation matrices for sequence comparison and structure prediction of proteins. Protein Engineering, Design and Selection, 1996, 9, 27-36.	2.1	317
177	A genetic algorithm based molecular modeling technique for RNA stem-loop structures. Nucleic Acids Research, 1995, 23, 419-426.	14.5	29
178	Distribution profiles of GC content around the translation initiation site in different species. FEBS Letters, 1994, 352, 7-10.	2.8	10
179	An assessment of neural network and statistical approaches for prediction of E.coli Promoter sites. Nucleic Acids Research, 1992, 20, 4331-4338.	14.5	74
180	Construction of a dictionary of sequence motifs that characterize groups of related proteins. Protein Engineering, Design and Selection, 1992, 5, 479-488.	2.1	39

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181	A knowledge base for predicting protein localization sites in eukaryotic cells. Genomics, 1992, 14, 897-911.	2.9	1,465
182	Expert system for predicting protein localization sites in gram-negative bacteria. Proteins: Structure, Function and Bioinformatics, 1991, 11, 95-110.	2.6	677
183	Fragment peptide library for classification and functional prediction of proteins. Proteins: Structure, Function and Bioinformatics, 1990, 8, 341-351.	2.6	15
184	A multivariate analysis method for discriminating protein secondary structural segments. Protein Engineering, Design and Selection, 1988, 2, 87-92.	2.1	24
185	Cluster analysis of amino acid indices for prediction of protein structure and function. Protein Engineering, Design and Selection, 1988, 2, 93-100.	2.1	171
186	Prediction of In-Vivo Modification Sites of Proteins from Their Primary Structures. Journal of Biochemistry, 1988, 104, 693-699.	1.7	27
187	Nonrandom recurrence of consecutive repeats in noncoding mammalian sequences. Mathematical Biosciences, 1986, 81, 43-52.	1.9	1
188	L-aspartate ammonia-lyase and fumarate hydratase share extensive sequence homology. Biochemical and Biophysical Research Communications, 1986, 138, 568-572.	2.1	29
189	Predictlon of splice junctions in mRNA sequences. Nucleic Acids Research, 1985, 13, 5327-5340.	14.5	69
190	Assessing the significance of local sequence homologies. Mathematical Biosciences, 1984, 69, 77-85.	1.9	4
191	Fluctuation of an Î±-helix structure. Difference between the central and terminal portions. Journal of Molecular Biology, 1972, 64, 363-378.	4.2	39
192	Bioinformatics Analysis of Glycan Structures from a Genomic Perspective. , 0, , 125-141.		0