

Minoru Kanehisa

List of Publications by Year in descending order

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all docs

197
docs citations

197
times ranked

113314
citing authors

#	ARTICLE	IF	CITATIONS
1	<scp>KEGG</scp> mapping tools for uncovering hidden features in biological data. Protein Science, 2022, 31, 47-53.	3.1	365
2	KEGG: integrating viruses and cellular organisms. Nucleic Acids Research, 2021, 49, D545-D551.	6.5	2,276
3	KEGG Mapper for inferring cellular functions from protein sequences. Protein Science, 2020, 29, 28-35.	3.1	791
4	KofamKOALA: KEGG Ortholog assignment based on profile HMM and adaptive score threshold. Bioinformatics, 2020, 36, 2251-2252.	1.8	820
5	Toward understanding the origin and evolution of cellular organisms. Protein Science, 2019, 28, 1947-1951.	3.1	2,262
6	New approach for understanding genome variations in KEGG. Nucleic Acids Research, 2019, 47, D590-D595.	6.5	1,503
7	Inferring Antimicrobial Resistance from Pathogen Genomes in KEGG. Methods in Molecular Biology, 2018, 1807, 225-239.	0.4	10
8	Enzyme Annotation and Metabolic Reconstruction Using KEGG. Methods in Molecular Biology, 2017, 1611, 135-145.	0.4	111
9	KEGG: new perspectives on genomes, pathways, diseases and drugs. Nucleic Acids Research, 2017, 45, D353-D361.	6.5	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.	1.1	0
12	Identification of Enzyme Genes Using Chemical Structure Alignments of Substrateâ€“Product Pairs. Journal of Chemical Information and Modeling, 2016, 56, 510-516.	2.5	17
13	KEGG as a reference resource for gene and protein annotation. Nucleic Acids Research, 2016, 44, D457-D462.	6.5	5,435
14	BlastKOALA and GhostKOALA: KEGG Tools for Functional Characterization of Genome and Metagenome Sequences. Journal of Molecular Biology, 2016, 428, 726-731.	2.0	2,872
15	KEGG Bioinformatics Resource for Plant Genomics and Metabolomics. Methods in Molecular Biology, 2016, 1374, 55-70.	0.4	86
16	Symbol Nomenclature for Graphical Representations of Glycans. Glycobiology, 2015, 25, 1323-1324.	1.3	818
17	Glycomic Analysis Using KEGG GLYCAN. Methods in Molecular Biology, 2015, 1273, 97-107.	0.4	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.	0.3	7

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19	DINIES: drug-target interaction network inference engine based on supervised analysis. <i>Nucleic Acids Research</i> , 2014, 42, W39-W45.	6.5	97
20	Predictive genomic and metabolomic analysis for the standardization of enzyme data. <i>Perspectives in Science</i> , 2014, 1, 24-32.	0.6	8
21	Data, information, knowledge and principle: back to metabolism in KEGG. <i>Nucleic Acids Research</i> , 2014, 42, D199-D205.	6.5	2,846
22	Pathways of Toxicity. <i>ALTEX: Alternatives To Animal Experimentation</i> , 2014, 31, 53-61.	0.9	75
23	Automated interpretation of metabolic capacity from genome and metagenome sequences. <i>Quantitative Biology</i> , 2013, 1, 192-200.	0.3	1
24	Chemical and genomic evolution of enzyme-catalyzed reaction networks. <i>FEBS Letters</i> , 2013, 587, 2731-2737.	1.3	33
25	KCF-S: KEGG Chemical Function and Substructure for improved interpretability and prediction in chemical bioinformatics. <i>BMC Systems Biology</i> , 2013, 7, S2.	3.0	25
26	Molecular Network Analysis of Diseases and Drugs in KEGG. <i>Methods in Molecular Biology</i> , 2013, 939, 263-275.	0.4	79
27	Modular Architecture of Metabolic Pathways Revealed by Conserved Sequences of Reactions. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 613-622.	2.5	73
28	KEGG and GenomeNet, New Developments, <i>Metagenomic Analysis.</i> , 2013,, 1-11.		0
29	KEGG OC: a large-scale automatic construction of taxonomy-based ortholog clusters. <i>Nucleic Acids Research</i> , 2012, 41, D353-D357.	6.5	96
30	Population Model-Based Inter-Diplotype Similarity Measure for Accurate Diplotype Clustering. <i>Journal of Computational Biology</i> , 2012, 19, 55-67.	0.8	1
31	GENIES: gene network inference engine based on supervised analysis. <i>Nucleic Acids Research</i> , 2012, 40, W162-W167.	6.5	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	6.0	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. <i>MBio</i> , 2012, 3, e00204-12.	1.8	64
34	KEGG for integration and interpretation of large-scale molecular data sets. <i>Nucleic Acids Research</i> , 2012, 40, D109-D114.	6.5	4,174
35	Evaluation method for the potential functionome harbored in the genome and metagenome. <i>BMC Genomics</i> , 2012, 13, 699.	1.2	65
36	Using the KEGG Database Resource. <i>Current Protocols in Bioinformatics</i> , 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. <i>Methods in Molecular Biology</i> , 2012, 802, 19-39.	0.4	104
38	Network-Based Analysis and Characterization of Adverse Drug-Drug Interactions. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 2977-2985.	2.5	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. <i>BMC Bioinformatics</i> , 2011, 12, S1.	1.2	1
41	iPath2.0: interactive pathway explorer. <i>Nucleic Acids Research</i> , 2011, 39, W412-W415.	6.5	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. <i>Nucleic Acids Research</i> , 2010, 38, W652-W656.	6.5	125
45	PathPred: an enzyme-catalyzed metabolic pathway prediction server. <i>Nucleic Acids Research</i> , 2010, 38, W138-W143.	6.5	227
46	KEGG for representation and analysis of molecular networks involving diseases and drugs. <i>Nucleic Acids Research</i> , 2010, 38, D355-D360.	6.5	1,999
47	Drug-target interaction prediction from chemical, genomic and pharmacological data in an integrated framework. <i>Bioinformatics</i> , 2010, 26, i246-i254.	1.8	396
48	GENOME-WIDE ANALYSIS OF PLANT UGT FAMILY BASED ON SEQUENCE AND SUBSTRATE INFORMATION. , 2010, , .		2
49	Characterization of Δ -phosphoglucosyltransferase isozymes from <i>Toxoplasma gondii</i> . <i>Parasitology International</i> , 2010, 59, 206-210.	0.6	11
50	varDB: A database of antigenic variant sequencesâ€”Current status and future prospects. <i>Acta Tropica</i> , 2010, 114, 144-151.	0.9	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. <i>Bioinformatics</i> , 2009, 25, i179-i186.	1.8	64
54	Domain shuffling and the evolution of vertebrates. <i>Genome Research</i> , 2009, 19, 1393-1403.	2.4	86

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55	Comprehensive analysis of glycosyltransferases in eukaryotic genomes for structural and functional characterization of glycans. <i>Carbohydrate Research</i> , 2009, 344, 881-887.	1.1	37
56	Extraction and Analysis of Chemical Modification Patterns in Drug Development. <i>Journal of Chemical Information and Modeling</i> , 2009, 49, 1122-1129.	2.5	12
57	Systems biology approaches and pathway tools for investigating cardiovascular disease. <i>Molecular BioSystems</i> , 2009, 5, 588.	2.9	96
58	Characterization and evolutionary landscape of AmnSINE1 in Amniota genomes. <i>Gene</i> , 2009, 441, 100-110.	1.0	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. <i>Frontiers in Neuroscience</i> , 2009, , 147-162.	0.0	0
62	Representation and analysis of molecular networks involving diseases and drugs. <i>Genome Informatics</i> , 2009, 23, 212-3.	0.4	10
63	iPath: interactive exploration of biochemical pathways and networks. <i>Trends in Biochemical Sciences</i> , 2008, 33, 101-103.	3.7	216
64	Prediction of drug-target interaction networks from the integration of chemical and genomic spaces. <i>Bioinformatics</i> , 2008, 24, i232-i240.	1.8	864
65	Mining significant tree patterns in carbohydrate sugar chains. <i>Bioinformatics</i> , 2008, 24, i167-i173.	1.8	33
66	KEGG Atlas mapping for global analysis of metabolic pathways. <i>Nucleic Acids Research</i> , 2008, 36, W423-W426.	6.5	445
67	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.	2.5	10
68	The repertoire of desaturases and elongases reveals fatty acid variations in 56 eukaryotic genomes. <i>Journal of Lipid Research</i> , 2008, 49, 183-191.	2.0	150
69	Systematic Survey for Novel Types of Prokaryotic Retroelements Based on Gene Neighborhood and Protein Architecture. <i>Molecular Biology and Evolution</i> , 2008, 25, 1395-1404.	3.5	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. <i>Genome Informatics</i> , 2008, 20, 252-9.	0.4	6

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73	KEGG for linking genomes to life and the environment. <i>Nucleic Acids Research</i> , 2007, 36, D480-D484.	6.5	5,451
74	EGENES: Transcriptome-Based Plant Database of Genes with Metabolic Pathway Information and Expressed Sequence Tag Indices in KEGG. <i>Plant Physiology</i> , 2007, 144, 857-866.	2.3	35
75	VisANT 3.0: new modules for pathway visualization, editing, prediction and construction. <i>Nucleic Acids Research</i> , 2007, 35, W625-W632.	6.5	66
76	Comprehensive Analysis of Distinctive Polyketide and Nonribosomal Peptide Structural Motifs Encoded in Microbial Genomes. <i>Journal of Molecular Biology</i> , 2007, 368, 1500-1517.	2.0	145
77	Evolutionary history and functional implications of protein domains and their combinations in eukaryotes. <i>Genome Biology</i> , 2007, 8, R121.	13.9	71
78	Observing metabolic functions at the genome scale. <i>Genome Biology</i> , 2007, 8, R123.	13.9	54
79	AAindex: amino acid index database, progress report 2008. <i>Nucleic Acids Research</i> , 2007, 36, D202-D205.	6.5	871
80	KAAS: an automatic genome annotation and pathway reconstruction server. <i>Nucleic Acids Research</i> , 2007, 35, W182-W185.	6.5	3,517
81	Identification of Endocrine Disruptor Biodegradation by Integration of Structure-activity Relationship with Pathway Analysis. <i>Environmental Science & Technology</i> , 2007, 41, 7997-8003.	4.6	12
82	The commonality of protein interaction networks determined in neurodegenerative disorders (NDDs). <i>Bioinformatics</i> , 2007, 23, 2129-2138.	1.8	52
83	Systematic Analysis of Enzyme-Catalyzed Reaction Patterns and Prediction of Microbial Biodegradation Pathways. <i>Journal of Chemical Information and Modeling</i> , 2007, 47, 1702-1712.	2.5	73
84	Prediction of nitrogen metabolism-related genes in <i>Anabaena</i> by kernel-based network analysis. <i>Proteomics</i> , 2007, 7, 900-909.	1.3	8
85	Towards zoomable multidimensional maps of the cell. <i>Nature Biotechnology</i> , 2007, 25, 547-554.	9.4	84
86	Prediction of missing enzyme genes in a bacterial metabolic network. <i>FEBS Journal</i> , 2007, 274, 2262-2273.	2.2	30
87	Mining prokaryotic genomes for unknown amino acids: a stop-codon-based approach. <i>BMC Bioinformatics</i> , 2007, 8, 225.	1.2	17
88	Regulation of metabolic networks by small molecule metabolites. <i>BMC Bioinformatics</i> , 2007, 8, 88.	1.2	23
89	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.	1.2	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. <i>Methods in Molecular Biology</i> , 2007, 396, 71-91.	0.4	238
92	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.	1.6	72
93	PREDICTING B CELL EPIOTOPE 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. <i>Lecture Notes in Computer Science</i> , 2007, , 322-333.	1.0	0
97	An improved scoring scheme for predicting glycan structures from gene expression data. <i>Genome Informatics</i> , 2007, 18, 237-46.	0.4	14
98	Analysis of common substructures of metabolic compounds within the different organism groups. <i>Genome Informatics</i> , 2007, 18, 299-307.	0.4	2
99	EGassembler: online bioinformatics service for large-scale processing, clustering and assembling ESTs and genomic DNA fragments. <i>Nucleic Acids Research</i> , 2006, 34, W459-W462.	6.5	139
100	From genomics to chemical genomics: new developments in KEGG. <i>Nucleic Acids Research</i> , 2006, 34, D354-D357.	6.5	2,662
101	Quantitative elementary mode analysis of metabolic pathways: the example of yeast glycolysis. <i>BMC Bioinformatics</i> , 2006, 7, 186.	1.2	66
102	Extracting Sequence Motifs and the Phylogenetic Features of SNARE-Dependent Membrane Traffic. <i>Traffic</i> , 2006, 7, 1104-1118.	1.3	44
103	Extraction of phylogenetic network modules from the metabolic network. <i>BMC Bioinformatics</i> , 2006, 7, 130.	1.2	44
104	ProfilePSTMM: capturing tree-structure motifs in carbohydrate sugar chains. <i>Bioinformatics</i> , 2006, 22, e25-e34.	1.8	28
105	ODB: a database of operons accumulating known operons across multiple genomes. <i>Nucleic Acids Research</i> , 2006, 34, D358-D362.	6.5	46
106	Identification of metabolic units induced by environmental signals. <i>Bioinformatics</i> , 2006, 22, e375-e383.	1.8	4
107	Partial correlation coefficient between distance matrices as a new indicator of protein-protein interactions. <i>Bioinformatics</i> , 2006, 22, 2488-2492.	1.8	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. <i>Glycobiology</i> , 2006, 16, 63R-70R.	1.3	279
110	Structure-activity relationships and pathway analysis of biological degradation processes. <i>Journal of Pesticide Sciences</i> , 2006, 31, 273-281.	0.8	0
111	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.	1.0	1
112	Bioinformatics approaches in glycomics and drug discovery. <i>Current Opinion in Molecular Therapeutics</i> , 2006, 8, 514-20.	2.8	12
113	The repertoire of desaturases for unsaturated fatty acid synthesis in 397 genomes. <i>Genome Informatics</i> , 2006, 17, 173-83.	0.4	9
114	Analysis of the differences in metabolic network expansion between prokaryotes and eukaryotes. <i>Genome Informatics</i> , 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 (β -d-glucuronate). <i>Biochemical Pharmacology</i> , 2005, 70, 1056-1065.	2.0	9
117	Extraction of leukemia specific glycan motifs in humans by computational glycomics. <i>Carbohydrate Research</i> , 2005, 340, 2270-2278.	1.1	44
118	A score matrix to reveal the hidden links in glycans. <i>Bioinformatics</i> , 2005, 21, 1457-1463.	1.8	34
119	Global Analysis of Circadian Expression in the Cyanobacterium <i>Synechocystis</i> sp. Strain PCC 6803. <i>Journal of Bacteriology</i> , 2005, 187, 2190-2199.	1.0	148
120	Fast and accurate database homology search using upper bounds of local alignment scores. <i>Bioinformatics</i> , 2005, 21, 912-921.	1.8	19
121	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, 3482-3489.	1.8	143
122	UTILIZING EVOLUTIONARY INFORMATION AND GENE EXPRESSION DATA FOR ESTIMATING GENE NETWORKS WITH BAYESIAN NETWORK MODELS. <i>Journal of Bioinformatics and Computational Biology</i> , 2005, 03, 1295-1313.	0.3	51
123	Positive Regulation of Sugar Catabolic Pathways in the Cyanobacterium <i>Synechocystis</i> sp. PCC 6803 by the Group 2 σ Factor SigE. <i>Journal of Biological Chemistry</i> , 2005, 280, 30653-30659.	1.6	159
124	Alteration of Gene Expression in Human Hepatocellular Carcinoma with Integrated Hepatitis B Virus DNA. <i>Clinical Cancer Research</i> , 2005, 11, 5821-5826.	3.2	72
125	Prediction of glycan structures from gene expression data based on glycosyltransferase reactions. <i>Bioinformatics</i> , 2005, 21, 3976-3982.	1.8	78
126	Using the KEGG Database Resource. <i>Current Protocols in Bioinformatics</i> , 2005, 11, Unit 1.12.	25.8	115

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127	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.	0.4	3
128	Comprehensive analysis and prediction of synthetic lethality using subcellular locations. <i>Genome Informatics</i> , 2005, 16, 150-8.	0.4	0
129	A global representation of the carbohydrate structures: a tool for the analysis of glycan. <i>Genome Informatics</i> , 2005, 16, 214-22.	0.4	7
130	Autoimmune diseases and peptide variations. <i>Genome Informatics</i> , 2005, 16, 272-80.	0.4	0
131	Managing and analyzing carbohydrate data. <i>SIGMOD Record</i> , 2004, 33, 33-38.	0.7	4
132	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, 2149-2160.	3.5	29
133	Application of a new probabilistic model for recognizing complex patterns in glycans. <i>Bioinformatics</i> , 2004, 20, i6-i14.	1.8	13
134	The KEGG resource for deciphering the genome. <i>Nucleic Acids Research</i> , 2004, 32, 277D-280.	6.5	4,093
135	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, 290-299.	1.5	110
136	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	2.6	290
137	Clustering under the line graph transformation: application to reaction network. <i>BMC Bioinformatics</i> , 2004, 5, 207.	1.2	14
138	Computational Assignment of the EC Numbers for Genomic-Scale Analysis of Enzymatic Reactions. <i>Journal of the American Chemical Society</i> , 2004, 126, 16487-16498.	6.6	120
139	KCaM (KEGG Carbohydrate Matcher): a software tool for analyzing the structures of carbohydrate sugar chains. <i>Nucleic Acids Research</i> , 2004, 32, W267-W272.	6.5	95
140	Using protein motif combinations to update KEGG pathway maps and orthologue tables. <i>Genome Informatics</i> , 2004, 15, 266-75.	0.4	6
141	Extraction of species-specific glycan substructures. <i>Genome Informatics</i> , 2004, 15, 69-81.	0.4	5
142	Clustering of database sequences for fast homology search using upper bounds on alignment score. <i>Genome Informatics</i> , 2004, 15, 93-104.	0.4	7
143	Extraction of phylogenetic network modules from prokaryote metabolic pathways. <i>Genome Informatics</i> , 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. <i>Journal of the American Chemical Society</i> , 2003, 125, 11853-11865.	6.6	423

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145	Bioinformatics in the post-sequence era. <i>Nature Genetics</i> , 2003, 33, 305-310.	9.4	174
146	Identification of a New Cryptochrome Class. <i>Molecular Cell</i> , 2003, 11, 59-67.	4.5	301
147	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, 1719-1725.	1.0	153
148	Prediction of protein subcellular locations by support vector machines using compositions of amino acids and amino acid pairs. <i>Bioinformatics</i> , 2003, 19, 1656-1663.	1.8	354
149	Efficient tree-matching methods for accurate carbohydrate database queries. <i>Genome Informatics</i> , 2003, 14, 134-43.	0.4	20
150	Heuristics for chemical compound matching. <i>Genome Informatics</i> , 2003, 14, 144-53.	0.4	16
151	The KEGG databases at GenomeNet. <i>Nucleic Acids Research</i> , 2002, 30, 42-46.	6.5	1,202
152	LIGAND: database of chemical compounds and reactions in biological pathways. <i>Nucleic Acids Research</i> , 2002, 30, 402-404.	6.5	255
153	A Two-Component Mn ²⁺ -Sensing System Negatively Regulates Expression of the <i>mntCAB</i> Operon in <i>Synechocystis</i> . <i>Plant Cell</i> , 2002, 14, 2901-2913.	3.1	76
154	Update of MAGEST: Maboaya Gene Expression patterns and Sequence Tags. <i>Nucleic Acids Research</i> , 2002, 30, 119-120.	6.5	12
155	KEGG: From Genes to Biochemical Pathways. , 2002, , 63-76.		12
156	Screening for the target gene of cyanobacterial cAMP receptor protein SYCRP1. <i>Molecular Microbiology</i> , 2002, 43, 843-853.	1.2	63
157	Extraction of organism groups from phylogenetic profiles using independent component analysis. <i>Genome Informatics</i> , 2002, 13, 61-70.	0.4	3
158	Whole genome sequencing of meticillin-resistant <i>Staphylococcus aureus</i> . <i>Lancet</i> , The, 2001, 357, 1225-1240.	6.3	1,835
159	Cold-regulated genes under control of the cold sensor Hik33 in <i>Synechocystis</i> . <i>Molecular Microbiology</i> , 2001, 40, 235-244.	1.2	238
160	DNA Microarray Analysis of Cyanobacterial Gene Expression during Acclimation to High Light. <i>Plant Cell</i> , 2001, 13, 793-806.	3.1	444
161	Prediction of higher order functional networks from genomic data. <i>Pharmacogenomics</i> , 2001, 2, 373-385.	0.6	11
162	Pathway databases and higher order function. <i>Advances in Protein Chemistry</i> , 2000, 54, 381-408.	4.4	14

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163	AAindex: Amino Acid index database. Nucleic Acids Research, 2000, 28, 374-374.	6.5	641
164	Tandem Clusters of Membrane Proteins in Complete Genome Sequences. Genome Research, 2000, 10, 731-743.	2.4	42
165	MAGEST: MAboya Gene Expression patterns and Sequence Tags. Nucleic Acids Research, 2000, 28, 133-135.	6.5	36
166	KEGG: Kyoto Encyclopedia of Genes and Genomes. Nucleic Acids Research, 2000, 28, 27-30.	6.5	25,375
167	Contributory presentations/posters. Journal of Biosciences, 1999, 24, 33-198.	0.5	0
168	KEGG: Kyoto Encyclopedia of Genes and Genomes. Nucleic Acids Research, 1999, 27, 29-34.	6.5	13,711
169	Computation with the KEGG pathway database. BioSystems, 1998, 47, 119-128.	0.9	240
170	Reconstruction of Amino Acid Biosynthesis Pathways from the Complete Genomeâ€™s Sequence. Genome Research, 1998, 8, 203-210.	2.4	145
171	A Comparative Analysis of ABC Transporters in Complete Microbial Genomes. Genome Research, 1998, 8, 1048-1059.	2.4	126
172	Linking databases and organisms: GenomeNet resources in Japan. Trends in Biochemical Sciences, 1997, 22, 442-444.	3.7	58
173	A database for post-genome analysis. Trends in Genetics, 1997, 13, 375-376.	2.9	372
174	The size differences among mammalian introns are due to the accumulation of small deletions. FEBS Letters, 1996, 390, 99-103.	1.3	41
175	Construction and analysis of a profile library characterizing groups of structurally known proteins. Protein Science, 1996, 5, 1991-1999.	3.1	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.	1.0	317
177	A genetic algorithm based molecular modeling technique for RNA stem-loop structures. Nucleic Acids Research, 1995, 23, 419-426.	6.5	29
178	Distribution profiles of GC content around the translation initiation site in different species. FEBS Letters, 1994, 352, 7-10.	1.3	10
179	An assessment of neural network and statistical approaches for prediction of E.coli Promoter sites. Nucleic Acids Research, 1992, 20, 4331-4338.	6.5	74
180	Construction of a dictionary of sequence motifs that characterize groups of related proteins. Protein Engineering, Design and Selection, 1992, 5, 479-488.	1.0	39

#	ARTICLE	IF	CITATIONS
181	A knowledge base for predicting protein localization sites in eukaryotic cells. <i>Genomics</i> , 1992, 14, 897-911.	1.3	1,465
182	Expert system for predicting protein localization sites in gram-negative bacteria. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991, 11, 95-110.	1.5	677
183	Fragment peptide library for classification and functional prediction of proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990, 8, 341-351.	1.5	15
184	A multivariate analysis method for discriminating protein secondary structural segments. <i>Protein Engineering, Design and Selection</i> , 1988, 2, 87-92.	1.0	24
185	Cluster analysis of amino acid indices for prediction of protein structure and function. <i>Protein Engineering, Design and Selection</i> , 1988, 2, 93-100.	1.0	171
186	Prediction of In-Vivo Modification Sites of Proteins from Their Primary Structures. <i>Journal of Biochemistry</i> , 1988, 104, 693-699.	0.9	27
187	Nonrandom recurrence of consecutive repeats in noncoding mammalian sequences. <i>Mathematical Biosciences</i> , 1986, 81, 43-52.	0.9	1
188	L-aspartate ammonia-lyase and fumarate hydratase share extensive sequence homology. <i>Biochemical and Biophysical Research Communications</i> , 1986, 138, 568-572.	1.0	29
189	Prediction of splice junctions in mRNA sequences. <i>Nucleic Acids Research</i> , 1985, 13, 5327-5340.	6.5	69
190	Assessing the significance of local sequence homologies. <i>Mathematical Biosciences</i> , 1984, 69, 77-85.	0.9	4
191	Fluctuation of an $\hat{\alpha}$ -helix structure. Difference between the central and terminal portions. <i>Journal of Molecular Biology</i> , 1972, 64, 363-378.	2.0	39
192	Bioinformatics Analysis of Glycan Structures from a Genomic Perspective. , 0, , 125-141.		0