

# CITATION REPORT

List of articles citing

The identification of functional modules from the genomic association of genes

DOI: 10.1073/pnas.092632599

Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 5890-5.

**Source:** <https://exaly.com/paper-pdf/33801593/citation-report.pdf>

**Version:** 2024-04-10

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

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

#	Paper	IF	Citations
229	Roles for the two-hybrid system in exploration of the yeast protein interactome. <b>2002</b> , 1, 561-6		87
228	Intraproteomic networks: new forays into predicting interaction partners. <b>2002</b> , 12, 1156-8		
227	The society of genes: networks of functional links between genes from comparative genomics. <b>2002</b> , 3, research0064		24
226	Conservation of gene co-regulation in prokaryotes and eukaryotes. <b>2002</b> , 20, 407-10; discussion 410		79
225	Conservation of gene co-regulation in prokaryotes and eukaryotes. <b>2002</b> , 20, 410		2
224	Cell-selfish modes of evolution and mutations directed after transcriptional bypass. <b>2002</b> , 510, 141-52		21
223	Current Awareness on Comparative and Functional Genomics. <b>2002</b> , 3, 551-562		78
222	Mutants in flal and flaJ of the archaeon Methanococcus voltae are deficient in flagellum assembly. <b>2002</b> , 46, 879-87		46
221	Computational approaches to protein-protein interaction. <b>2003</b> , 4, 245-55		8
220	Function prediction and protein networks. <b>2003</b> , 15, 191-8		118
219	Computational methods of analysis of protein-protein interactions. <b>2003</b> , 13, 377-82		125
218	Metabolites: a helping hand for pathway evolution?. <b>2003</b> , 28, 336-41		117
217	Curation is forever: comparative genomics approaches to functional annotation. <b>2003</b> , 2, 138-146		7
216	Genome wide identification of regulatory motifs in Bacillus subtilis. <b>2003</b> , 4, 18		27
215	A method for classifying metabolites in topological pathway analyses based on minimization of pathway number. <b>2003</b> , 70, 255-70		39
214	Gene teams: a new formalization of gene clusters for comparative genomics. <b>2003</b> , 27, 59-67		47
213	Missing genes in metabolic pathways: a comparative genomics approach. <b>2003</b> , 7, 238-51		295

212	Evolutionary conservation of motif constituents in the yeast protein interaction network. <b>2003</b> , 35, 176-9	356
211	Gene organization: selection, selfishness, and serendipity. <b>2003</b> , 57, 419-40	67
210	Motifs, modules and games in bacteria. <b>2003</b> , 6, 125-34	227
209	Duplication models for biological networks. <b>2003</b> , 10, 677-87	208
208	Defining interacting partners for drug discovery. <b>2003</b> , 7, 287-97	4
207	Visualization and interpretation of protein networks in Mycobacterium tuberculosis based on hierarchical clustering of genome-wide functional linkage maps. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 7099-109	46
206	Genome evolution reveals biochemical networks and functional modules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 15428-33	11.5 123
205	Physical and functional modularity of the protein network in yeast. <b>2003</b> , 2, 292-8	23
204	Assessing experimentally derived interactions in a small world. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 4372-6	11.5 318
203	Hypergeometric Model of Evolution of Conserved Protein Coding Sequences in the Proteomes. <b>2003</b> , 03, L295-L324	4
202	Modular organization of cellular networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 1128-33	11.5 572
201	Unravelling Nature's networks. <b>2003</b> , 31, 1457-61	16
200	Gene order in Prokaryotes: conservation and implications. <b>2004</b> , 209-237	2
199	Molecules in Time and Space. <b>2004</b> ,	
198	Comparative analysis of protein domain organization. <b>2004</b> , 14, 343-53	65
197	Control of yeast filamentous-form growth by modules in an integrated molecular network. <b>2004</b> , 14, 380-90	72
196	The complete genomes of <i>Lactobacillus plantarum</i> and <i>Lactobacillus johnsonii</i> reveal extensive differences in chromosome organization and gene content. <b>2004</b> , 150, 3601-3611	87
195	Expression of two <i>Escherichia coli</i> acetyl-CoA carboxylase subunits is autoregulated. <b>2004</b> , 279, 2520-7	47

194	Discovering protein-protein interactions. <b>2004</b> , 1, 711-41	10
193	Quantifying modularity in the evolution of biomolecular systems. <b>2004</b> , 14, 391-7	81
192	Molecular networks in model systems. <b>2004</b> , 5, 177-87	18
191	A probabilistic view of gene function. <b>2004</b> , 36, 559-64	99
190	Network biology: understanding the cell's functional organization. <b>2004</b> , 5, 101-13	5439
189	The yeast coexpression network has a small-world, scale-free architecture and can be explained by a simple model. <b>2004</b> , 5, 280-4	186
188	Evidence for dynamically organized modularity in the yeast protein-protein interaction network. <b>2004</b> , 430, 88-93	1381
187	PTK7/CCK-4 is a novel regulator of planar cell polarity in vertebrates. <b>2004</b> , 430, 93-8	383
186	Protein interaction networks from yeast to human. <b>2004</b> , 14, 292-9	278
185	Early prediction of drug metabolism and toxicity: systems biology approach and modeling. <b>2004</b> , 9, 127-35	156
184	Systematic identification of immunoreceptor tyrosine-based inhibitory motifs in the human proteome. <b>2004</b> , 16, 435-56	40
183	Structural and functional characterization of gene products encoded in the human genome by homology detection. <b>2004</b> , 56, 317-31	4
182	Prediction of protein function and pathways in the genome era. <b>2004</b> , 61, 930-44	79
181	Gene duplication and hierarchical modularity in intracellular interaction networks. <b>2004</b> , 74, 51-62	28
180	Selection for gene clustering by tandem duplication. <b>2004</b> , 58, 119-42	75
179	How biologically relevant are interaction-based modules in protein networks?. <b>2004</b> , 5, R93	34
178	Modular decomposition of protein-protein interaction networks. <b>2004</b> , 5, R57	77
177	Protein interaction networks from yeast to human. <b>2004</b> ,	2

176	Bioinformatics and Systems Biology, rapidly evolving tools for interpreting plant response to global change. <b>2004</b> , 90, 117-131		10
175	Systems Biology: Applications in Drug Discovery. <b>2005</b> , 123-183		14
174	Chemical biology on PINs and NeeDLes. <b>2005</b> , 9, 31-7		3
173	Global properties of biological networks. <b>2005</b> , 10, 365-72		41
172	Phylogenetic detection of conserved gene clusters in microbial genomes. <b>2005</b> , 6, 243		31
171	A study of archaeal enzymes involved in polar lipid synthesis linking amino acid sequence information, genomic contexts and lipid composition. <b>2005</b> , 1, 399-410		42
170	Accessible Protein Interaction Data for Network Modeling. Structure of the Information and Available Repositories. <i>Lecture Notes in Computer Science</i> , <b>2005</b> , 1-13	0.9	2
169	Structural Proteomics and Computational Analysis of a Deadly Pathogen: Combating Mycobacterium tuberculosis from Multiple Fronts. <b>2005</b> , 245-269		
168	. <b>2005</b> ,		13
167	Inferring gene function and biochemical networks from protein interactions. <b>2005</b> ,		
166	Syntons, metabolons and interactons: an exact graph-theoretical approach for exploring neighbourhood between genomic and functional data. <b>2005</b> , 21, 4209-15		40
165	Global analysis of IL-2 target genes: identification of chromosomal clusters of expressed genes. <b>2005</b> , 17, 1009-21		42
164	A network of transcriptionally coordinated functional modules in <i>Saccharomyces cerevisiae</i> . <b>2005</b> , 15, 1298-306		27
163	Post-Genomic Design of Bioactive Molecules. <b>2005</b> , 1, 147-162		
162	Cell Engineering. <b>2005</b> ,		3
161	PRODOC: a resource for the comparison of tethered protein domain architectures with in-built information on remotely related domain families. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, W126-9	20.1	9
160	Nebulon: a system for the inference of functional relationships of gene products from the rearrangement of predicted operons. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, 2521-30	20.1	40
159	The <i>C. elegans</i> Interactome: Its Generation and Visualization. <b>2005</b> , 113-133		

158	The Proteomics Protocols Handbook. <b>2005</b> ,	204
157	Topological-based classification using artificial gene networks. <b>2005</b> ,	
156	A copper(I) protein possibly involved in the assembly of CuA center of bacterial cytochrome c oxidase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 3994-95	80
155	Variation and evolution of biomolecular systems: searching for functional relevance. <b>2005</b> , 579, 1839-45	12
154	Structure-based systems biology: a zoom lens for the cell. <b>2005</b> , 579, 1854-8	23
153	A general framework for weighted gene co-expression network analysis. <b>2005</b> , 4, Article17	2976
152	Ortholog search of proteins involved in copper delivery to cytochrome C oxidase and functional analysis of paralogs and gene neighbors by genomic context. <b>2005</b> , 4, 63-70	37
151	Computational Prediction of Protein-Protein Interactions. <b>2005</b> , 629-652	1
150	The rarity of gene shuffling in conserved genes. <b>2005</b> , 6, R50	13
149	An inventory of yeast proteins associated with nucleolar and ribosomal components. <b>2006</b> , 7, R98	6
148	Protein bipartivity and essentiality in the yeast protein-protein interaction network. <b>2006</b> , 5, 2177-84	61
147	Cytochrome c: occurrence and functions. <b>2006</b> , 106, 90-115	208
146	Model of interactions in biology and application to heterogeneous network in yeast. <b>2006</b> , 329, 945-52	6
145	Identification of SmtB/ArsR cis elements and proteins in archaea using the Prokaryotic InterGenic Exploration Database (PIGED). <b>2006</b> , 2, 39-49	8
144	Positional Homology in Bacterial Genomes. <i>Evolutionary Bioinformatics</i> , <b>2006</b> , 2, 117693430600200	1.9 1
143	Completing the uric acid degradation pathway through phylogenetic comparison of whole genomes. <b>2006</b> , 2, 144-8	167
142	Horizontal gene transfer in aminoacyl-tRNA synthetases including leucine-specific subtypes. <b>2006</b> , 63, 437-47	18
141	Stable evolutionary signal in a yeast protein interaction network. <b>2006</b> , 6, 8	43

140	Exploring the cell's network with molecular imaging. <b>2006</b> , 24, 257-66		3
139	Detecting Functional Modules from Protein Interaction Networks. <b>2006</b> ,		
138	A metabolic network in the evolutionary context: multiscale structure and modularity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 8774-9	11.5	69
137	Resources and tools for investigating biomolecular networks in mammals. <b>2006</b> , 12, 3723-34		2
136	Describing ancient horizontal gene transfers at the nucleotide and gene levels by comparative pathogenicity island genomics. <b>2006</b> , 22, 1072-9		16
135	The origins and evolution of functional modules: lessons from protein complexes. <b>2006</b> , 361, 507-17		113
134	Identification and analysis of evolutionarily cohesive functional modules in protein networks. <b>2006</b> , 16, 374-82		54
133	Modular organization of protein interaction networks. <b>2007</b> , 23, 207-14		133
132	Simple stochastic model for the evolution of protein lengths. <b>2007</b> , 76, 011924		
131	A large-scale protein protein interaction analysis in <i>Synechocystis</i> sp. PCC6803. <b>2007</b> , 14, 207-16		149
130	24 Bioinformatic Prediction of Yeast Gene Function. <b>2007</b> , 597-628		3
129	Gene Networks and Evolutionary Computation. 67-96		1
128	Formal Models of Gene Clusters. <b>2007</b> , 175-202		10
127	Protein annotation at genomic scale: the current status. <b>2007</b> , 107, 3448-66		58
126	Deduction of intracellular sub-systems from a topological description of the network. <b>2007</b> , 3, 523-9		7
125	DNA Array Decoding from Nonlinear Measurements by Belief Propagation. <b>2007</b> ,		17
124	Consistent dissection of the protein interaction network by combining global and local metrics. <b>2007</b> , 8, R271		20
123	Analysis of integrated biomolecular networks using a generic network analysis suite. <b>2007</b> , 4, 147-157		

122	Spectral clustering and its use in bioinformatics. <b>2007</b> , 204, 25-37		79
121	Universal strategies in research and drug discovery based on protein-fragment complementation assays. <b>2007</b> , 6, 569-82		258
120	Characterization of relationships between transcriptional units and operon structures in <i>Bacillus subtilis</i> and <i>Escherichia coli</i> . <b>2007</b> , 8, 48		37
119	Comparing the biological coherence of network clusters identified by different detection algorithms. <b>2007</b> , 52, 2938-2944		5
118	Computational prediction of protein-protein interactions. <b>2008</b> , 38, 1-17		152
117	Characterization of local geometry of protein surfaces with the visibility criterion. <b>2008</b> , 71, 670-83		72
116	PSAT: a web tool to compare genomic neighborhoods of multiple prokaryotic genomes. <b>2008</b> , 9, 170		25
115	CASCADE: a novel quasi all paths-based network analysis algorithm for clustering biological interactions. <b>2008</b> , 9, 64		18
114	Practical and theoretical advances in predicting the function of a protein by its phylogenetic distribution. <b>2008</b> , 5, 151-70		80
113	CREB binding and activity in brain: regional specificity and induction by electroconvulsive seizure. <b>2008</b> , 63, 710-20		51
112	Comparative Genomics. <i>Lecture Notes in Computer Science</i> , <b>2008</b> ,	0.9	2
111	Modularity of stress response evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 7500-5	11.5	48
110	A large scale analysis of protein-protein interactions in the nitrogen-fixing bacterium <i>Mesorhizobium loti</i> . <b>2008</b> , 15, 13-23		63
109	A genomewide functional network for the laboratory mouse. <b>2008</b> , 4, e1000165		94
108	GeConT 2: gene context analysis for orthologous proteins, conserved domains and metabolic pathways. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, W176-80	20.1	32
107	Complete genome sequence of <i>Nitrosospira multiformis</i> , an ammonia-oxidizing bacterium from the soil environment. <b>2008</b> , 74, 3559-72		158
106	Modular cell biology: retroactivity and insulation. <b>2008</b> , 4, 161		359
105	Identification and analysis of co-occurrence networks with NetCutter. <i>PLoS ONE</i> , <b>2008</b> , 3, e3178	3.7	14



104	. <b>2009</b> ,	7
103	Gene team tree: a hierarchical representation of gene teams for all gap lengths. <b>2009</b> , 16, 1383-98	9
102	Comparing Pearson, Spearman and Hoeffding's D measure for gene expression association analysis. <b>2009</b> , 7, 663-84	29
101	Identification of genes involved in the same pathways using a Hidden Markov Model-based approach. <b>2009</b> , 25, 2945-54	5
100	Global functional atlas of Escherichia coli encompassing previously uncharacterized proteins. <b>2009</b> , 7, e96	280
99	Detecting gene clusters under evolutionary constraint in a large number of genomes. <b>2009</b> , 25, 571-7	42
98	The human protein coevolution network. <b>2009</b> , 19, 1861-71	39
97	GIBA: a clustering tool for detecting protein complexes. <b>2009</b> , 10 Suppl 6, S11	18
96	Mathematical Modeling of Genetic Regulatory Networks: Stress Responses in Escherichia coli. 235-271	3
95	Plant Metabolic Networks. <b>2009</b> ,	3
94	Network-assisted protein identification and data interpretation in shotgun proteomics. <b>2009</b> , 5, 303	45
93	Bioinformatics and Computational Biology. <i>Lecture Notes in Computer Science</i> , <b>2009</b> ,	0.9
92	Engineering Principles in Bio-molecular Systems: From Retroactivity to Modularity. <b>2009</b> , 15, 389-397	15
91	Comparative Genomics: Algorithms and Applications. <b>2010</b> , 723-747	
90	Pyrosequencing-based comparative genome analysis of the nosocomial pathogen Enterococcus faecium and identification of a large transferable pathogenicity island. <b>2010</b> , 11, 239	151
89	Bidirectional best hit r-window gene clusters. <b>2010</b> , 11 Suppl 1, S63	14
88	LAB-Secretome: a genome-scale comparative analysis of the predicted extracellular and surface-associated proteins of Lactic Acid Bacteria. <b>2010</b> , 11, 651	67
87	Modularity and anti-modularity in networks with arbitrary degree distribution. <b>2010</b> , 5, 32	13

86	A Heuristic Algorithm for Finding the Longest Pathways in a Biochemical Network. <b>2010</b> ,	1
85	Metatranscriptome analysis of the human fecal microbiota reveals subject-specific expression profiles, with genes encoding proteins involved in carbohydrate metabolism being dominantly expressed. <b>2010</b> , 76, 5533-40	66
84	Systems Biology: Applications in Drug Discovery. <b>2010</b> , 1	1
83	Bioinformatics in bioinorganic chemistry. <b>2010</b> , 2, 39-51	16
82	Beyond the bounds of orthology: functional inference from metagenomic context. <b>2010</b> , 6, 1247-54	6
81	SIPPER: A flexible method to integrate heterogeneous data into a metabolic network. <b>2011</b> ,	2
80	Retroactivity Attenuation in Bio-Molecular Systems Based on Timescale Separation. <b>2011</b> , 56, 748-761	53
79	A simple protocol for the comparative analysis of the structure and occurrence of biochemical pathways across superkingdoms. <b>2011</b> , 51, 730-8	21
78	Comparative genomics analysis of completely sequenced microbial genomes reveals the ubiquity of N-linked glycosylation in prokaryotes. <b>2011</b> , 7, 1629-45	8
77	Atrial fibrillation: current knowledge and future directions in epidemiology and genomics. <b>2011</b> , 124, 1982-93	197
76	The Impact of Retroactivity on the Behavior of Biomolecular Systems. <b>2011</b> , 161-181	
75	Integrated analysis of the gene neighbouring impact on bacterial metabolic networks. <b>2011</b> , 5, 261-8	4
74	Carbohydrate catabolic flexibility in the mammalian intestinal commensal <i>Lactobacillus ruminis</i> revealed by fermentation studies aligned to genome annotations. <b>2011</b> , 10 Suppl 1, S12	35
73	Identification of conserved gene clusters in multiple genomes based on synteny and homology. <b>2011</b> , 12 Suppl 9, S18	6
72	Network-based function prediction and interactomics: the case for metabolic enzymes. <b>2011</b> , 13, 1-10	37
71	Improved algorithms for finding gene teams and constructing gene team trees. <b>2011</b> , 8, 1258-72	6
70	Network clustering revealed the systemic alterations of mitochondrial protein expression. <b>2011</b> , 7, e1002093	11
69	On the Spectral Characterization and Scalable Mining of Network Communities. <b>2012</b> , 24, 326-337	30

68	On the gene team mining problem. <b>2012</b> ,		0
67	Retroactivity to the input in complex gene transcription networks. <b>2012</b> ,		6
66	Using pathway modules as targets for assay development in xenobiotic screening. <b>2012</b> , 8, 531-42		8
65	A new efficient algorithm for the gene-team problem on general sequences. <b>2012</b> , 9, 330-44		5
64	Output-sensitive algorithms for finding the nested common intervals of two general sequences. <b>2012</b> , 9, 548-59		1
63	Multifactorial diversity sustains microbial community stability. <b>2013</b> , 7, 2126-36		113
62	A novel function prediction approach using protein overlap networks. <b>2013</b> , 7, 61		8
61	Random walk distances in data clustering and applications. <b>2013</b> , 7, 83-108		5
60	Topology of molecular interaction networks. <b>2013</b> , 7, 90		65
59	Two Pfam protein families characterized by a crystal structure of protein lpg2210 from <i>Legionella pneumophila</i> . <b>2013</b> , 14, 265		3
58	A global analysis of adaptive evolution of operons in cyanobacteria. <b>2013</b> , 103, 331-46		19
57	Use of the operon structure of the <i>C. elegans</i> genome as a tool to identify functionally related proteins. <b>2013</b> , 32, 41-56		3
56	Recent recombination events in the core genome are associated with adaptive evolution in <i>Enterococcus faecium</i> . <i>Genome Biology and Evolution</i> , <b>2013</b> , 5, 1524-35	3.9	64
55	How slaves affect a master module in gene transcription networks. <b>2013</b> ,		3
54	Proteome-wide protein interaction measurements of bacterial proteins of unknown function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 477-82	11.5	35
53	Modularization and Evolvability in Antibiotic Resistance. <b>2014</b> , 231-247		2
52	Atrial fibrillation: a progressive atrial myopathy or a distinct disease?. <b>2014</b> , 171, 126-33		18
51	Identifying protein complexes and functional modules--from static PPI networks to dynamic PPI networks. <b>2014</b> , 15, 177-94		104

50	Constructing a Gene Team Tree in Almost $O(n \lg n)$ Time. <b>2014</b> , 11, 142-53	3
49	A fast and high performance multiple data integration algorithm for identifying human disease genes. <b>2015</b> , 8 Suppl 3, S2	36
48	Exploring the genomic traits of fungus-feeding bacterial genus <i>Collimonas</i> . <b>2015</b> , 16, 1103	39
47	Predicting Functional Interactions Among Genes in Prokaryotes by Genomic Context. <b>2015</b> , 883, 97-106	3
46	Prokaryotic Systems Biology. <b>2015</b> ,	1
45	An efficient algorithm for pairwise local alignment of protein interaction networks. <b>2015</b> , 13, 1550003	
44	The power of operon rearrangements for predicting functional associations. <b>2015</b> , 13, 402-6	12
43	Molecular principles of human virus protein-protein interactions. <b>2015</b> , 31, 1025-33	28
42	Gene-Family Extension Measures and Correlations. <b>2016</b> , 6,	0
41	Integrative Systems Biology. <b>2016</b> , 245-251	
40	Trimeric autotransporter adhesins contribute to <i>Actinobacillus pleuropneumoniae</i> pathogenicity in mice and regulate bacterial gene expression during interactions between bacteria and porcine primary alveolar macrophages. <b>2016</b> , 109, 51-70	4
39	A protein network descriptor server and its use in studying protein, disease, metabolic and drug targeted networks. <b>2017</b> , 18, 1057-1070	26
38	Exploring bacterial interspecific interactions for discovery of novel antimicrobial compounds. <b>2017</b> , 10, 910-925	37
37	The STRING database in 2017: quality-controlled protein-protein association networks, made broadly accessible. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D362-D368	20.1 4068
36	IAS: Interaction Specific GO Term Associations for Predicting Protein-Protein Interaction Networks. <b>2018</b> , 15, 1247-1258	11
35	A New Efficient Algorithm for the Frequent Gene Team Problem. <b>2018</b> , 15, 588-598	1
34	Merging in-silico and in vitro salivary protein complex partners using the STRING database: A tutorial. <b>2018</b> , 171, 87-94	31
33	Involvement of Burkholderiaceae and sulfurous volatiles in disease-suppressive soils. <b>2018</b> , 12, 2307-2321	76

32	A survey of computational methods in protein-protein interaction networks. <b>2019</b> , 276, 35-87		6
31	Toward Sustainable Environmental Quality: Priority Research Questions for North America. <b>2019</b> , 38, 1606-1624		29
30	Operon Concatenation Is an Ancient Feature That Restricts the Potential to Rearrange Bacterial Chromosomes. <b>2019</b> , 36, 1990-2000		7
29	A Two-Enzyme Adaptive Unit within Bacterial Folate Metabolism. <i>Cell Reports</i> , <b>2019</b> , 27, 3359-3370.e7	10.6	18
28	Cyanobacterial phylogenetic analysis based on phylogenomics approaches render evolutionary diversification and adaptation: an overview of representative orders. <i>3 Biotech</i> , <b>2019</b> , 9, 87	2.8	3
27	Network-Based Combinatorial CRISPR-Cas9 Screens Identify Synergistic Modules in Human Cells. <i>ACS Synthetic Biology</i> , <b>2019</b> , 8, 482-490	5.7	23
26	InteGene: An Integer Linear Programming Tool for Discovering Approximate Gene Clusters. <b>2019</b> ,		
25	STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D607-D613	20.1	5966
24	The cell cycle regulator GpsB functions as cytosolic adaptor for multiple cell wall enzymes. <i>Nature Communications</i> , <b>2019</b> , 10, 261	17.4	25
23	A network approach to analyze neuronal lineage and layer innervation in the Drosophila optic lobes. <i>PLoS ONE</i> , <b>2020</b> , 15, e0227897	3.7	3
22	Evolutionarily conserved plant genes responsive to root-knot nematodes identified by comparative genomics. <i>Molecular Genetics and Genomics</i> , <b>2020</b> , 295, 1063-1078	3.1	4
21	Reconstructing the Evolutionary History of a Highly Conserved Operon Cluster in Gammaproteobacteria and Bacilli. <i>Genome Biology and Evolution</i> , <b>2021</b> , 13,	3.9	2
20	Accelerating biological insight for understudied genes. <i>Integrative and Comparative Biology</i> , <b>2021</b> ,	2.8	1
19	Integer Linear Programs for Discovering Approximate Gene Clusters. <i>Lecture Notes in Computer Science</i> , <b>2006</b> , 298-309	0.9	13
18	Gene Team Tree: A Compact Representation of All Gene Teams. <i>Lecture Notes in Computer Science</i> , <b>2008</b> , 100-112	0.9	3
17	Vertebrate 5-Hydroxyisourate Hydrolase Identification, Function, Structure, and Evolutionary Relationship with Transthyretin. <b>2009</b> , 95-108		2
16	Cross-species multiple environmental stress responses: An integrated approach to identify candidate genes for multiple stress tolerance in sorghum ( <i>Sorghum bicolor</i> (L.) Moench) and related model species. <i>PLoS ONE</i> , <b>2018</b> , 13, e0192678	3.7	8
15	Topology of Plant Metabolic Networks. <b>2009</b> , 173-209		

14 Sequence and Genome Bioinformatics. 1812-1844

13 Improved Algorithms for the Gene Team Problem. *Lecture Notes in Computer Science*, **2009**, 61-72 0.9

12 Mutual Information Based Extrinsic Similarity for Microarray Analysis. *Lecture Notes in Computer Science*, **2009**, 424-436 0.9 0

11 Encyclopedia of Complexity and Systems Science. **2009**, 570-589

10 Detecting Genetic Association and Gene-Gene Interaction using Network Analysis in Case-Control Study. *Ungyong Ttonggye Yontgu = the Korean Journal of Applied Statistics*, **2012**, 25, 563-573

9 Encyclopedia of Complexity and Systems Science. **2015**, 1-25

8 A two-enzyme adaptive unit within bacterial folate metabolism.

7 The cell cycle regulator GpsB functions as cytosolic adaptor for multiple cell wall enzymes.

6 A Systems View of Cell Death. **2004**, 153-179

5 Positional homology in bacterial genomes. *Evolutionary Bioinformatics*, **2007**, 2, 77-90 1.9 7

4 Phylogenetic organization in the assimilation of chemically distinct substrates by soil bacteria. *Environmental Microbiology*, **2021**, 5.2 1

3 The STRING database in 2023: protein-protein association networks and functional enrichment analyses for any sequenced genome of interest. 9

2 Integrative Systems Biology. **2016**, 484-491 0

1 Network-medicine approach for the identification of genetic association of parathyroid adenoma with cardiovascular disease and type-2 diabetes. 0