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Cytoscape: a software environment for integrated models of biomolecular interaction networks

DOI: 10.1101/gr.1239303 Genome Research, 2003, 13, 2498-504.

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#	Paper	IF	Citations
2242	Building with a scaffold: emerging strategies for high- to low-level cellular modeling. 2003 , 21, 255-62		158
2241	Systems biology is taking off. <i>Genome Research</i> , 2003 , 13, 2377-80	9.7	30
2240	The Logic of Life. Genome Research, 2003, 13, 2375-2376	9.7	78
2239	Challenges in the Overall Analysis of Microbial Proteomes. 2004 , 2, 79-86		
2238	T1DBase, a community web-based resource for type 1 diabetes research. 2005 , 33, D544-9		41
2237	Systems level insights into the stress response to UV radiation in the halophilic archaeon Halobacterium NRC-1. <i>Genome Research</i> , 2004 , 14, 1025-35	9.7	115
2236	The Biomolecular Interaction Network Database and related tools 2005 update. 2005 , 33, D418-24		437
2235	Control of yeast filamentous-form growth by modules in an integrated molecular network. <i>Genome Research</i> , 2004 , 14, 380-90	9.7	72
2234	ArrayXPath: mapping and visualizing microarray gene-expression data with integrated biological pathway resources using Scalable Vector Graphics. 2004 , 32, W460-4		51
2233	Multi-layered representation for cell signaling pathways. 2004 , 3, 1009-22		6
2232	WebInterViewer: visualizing and analyzing molecular interaction networks. 2004 , 32, W89-95		19
2231	Global network analysis of phenotypic effects: protein networks and toxicity modulation in Saccharomyces cerevisiae. 2004 , 101, 18006-11		105
2230	Genome sequence of Haloarcula marismortui: a halophilic archaeon from the Dead Sea. <i>Genome Research</i> , 2004 , 14, 2221-34	9.7	246
2229	Understanding the yeast proteome: a bioinformatics perspective. 2004 , 1, 193-205		3
2228	Molecular networks in model systems. 2004 , 5, 177-87		18
2227	PathBLAST: a tool for alignment of protein interaction networks. 2004 , 32, W83-8		293
2226	Exploiting biological complexity for strain improvement through systems biology. 2004 , 22, 1261-7		150

(2005-2004)

2225	A common open representation of mass spectrometry data and its application to proteomics research. 2004 , 22, 1459-66	632
2224	DNA-microarray analysis of brain cancer: molecular classification for therapy. 2004 , 5, 782-92	166
2223	Proteomics. 2004 , 5, 267-93	159
2222	Towards a systems biology understanding of human health: interplay between genotype, environment and nutrition. 2004 , 10, 51-84	37
2221	Integrating phenotypic and expression profiles to map arsenic-response networks. 2004, 5, R95	143
2220	Comprehensive de novo structure prediction in a systems-biology context for the archaea Halobacterium sp. NRC-1. 2004 , 5, R52	36
2219	System-based proteomic analysis of the interferon response in human liver cells. 2004 , 5, R54	55
2218	Systems biology and new technologies enable predictive and preventative medicine. 2004, 306, 640-3	821
2217	Bioinformatics and Systems Biology, rapidly evolving tools for interpreting plant response to global change. 2004 , 90, 117-131	10
2216	Hot spots for modulating toxicity identified by genomic phenotyping and localization mapping. 2004 , 16, 117-25	82
2215	Toward an integrative systems toxicology. 2004 , 5, 1163-6	4
2214	Charting gene regulatory networks: strategies, challenges and perspectives. 2004 , 381, 1-12	61
2213	Pathway analysis of coronary atherosclerosis. 2005 , 23, 103-18	136
2212	High-throughput metabolic state analysis: the missing link in integrated functional genomics of yeasts. 2005 , 388, 669-77	134
2211	Systematic interpretation of genetic interactions using protein networks. 2005 , 23, 561-6	341
2210	Probabilistic model of the human protein-protein interaction network. 2005 , 23, 951-9	338
2209	Bioinformatic methods for integrating whole-genome expression results into cellular networks. 2005 , 10, 727-34	37
2208	Tools enabling the elucidation of molecular pathways active in human disease: application to Hepatitis C virus infection. 2005 , 6, 154	13

2207	Component-based software architecture for biosystem reverse engineering. 2005 , 10, 400-407	2
2206	Phenotype analysis using network motifs derived from changes in regulatory network dynamics. 2005 , 60, 525-46	3
2205	Further steps towards data standardisation: the Proteomic Standards Initiative HUPO 3(rd) annual congress, Beijing 25-27(th) October, 2004. 2005 , 5, 337-9	31
2204	Protein interaction databases. 2005,	
2203	Refining protein subcellular localization. 2005 , 1, e66	68
2202	Balancing protein similarity and gene co-expression reveals new links between genetic conservation and developmental diversity in invertebrates. 2005 , 21, 1550-8	13
2201	Study of coordinative gene expression at the biological process level. 2005 , 21, 3651-7	10
2200	Dynamic properties of network motifs contribute to biological network organization. 2005 , 3, e343	259
2199	A grid layout algorithm for automatic drawing of biochemical networks. 2005 , 21, 2036-42	50
2198	Retroviruses and yeast retrotransposons use overlapping sets of host genes. <i>Genome Research</i> , 2005 , 15, 641-54	74
2197	Genetical genomics analysis of a yeast segregant population for transcription network inference. 2005 , 170, 533-42	76
2196	Visualizing Biological Pathways: Requirements Analysis, Systems Evaluation and Research Agenda. 2005 , 4, 191-205	68
2195	ProViz: protein interaction visualization and exploration. 2005 , 21, 272-4	90
2194	Creating, Modeling, and Visualizing Metabolic Networks. 2005 , 491-518	4
2193	Medusa: a simple tool for interaction graph analysis. 2005 , 21, 4432-3	146
2192	Divergent mechanisms of cis9, trans11-and trans10, cis12-conjugated linoleic acid affecting insulin resistance and inflammation in apolipoprotein E knockout mice: a proteomics approach. 2005 , 19, 1746-8	69
2191	Response of apolipoprotein E*3-Leiden transgenic mice to dietary fatty acids: combining liver proteomics with physiological data. 2005 , 19, 813-5	52
2190	Drosophila melanogaster: a case study of a model genomic sequence and its consequences. <i>Genome Research</i> , 2005 , 15, 1661-7 9-7	59

(2005-2005)

2189	Identifying regulatory subnetworks for a set of genes. 2005 , 4, 683-92	53
2188	Dizzy: stochastic simulation of large-scale genetic regulatory networks (supplementary material). 2005 , 3, 437-54	21
2187	Gene function prediction from congruent synthetic lethal interactions in yeast. 2005 , 1, 2005.0026	101
2186	Conserved patterns of protein interaction in multiple species. 2005 , 102, 1974-9	586
2185	BiNGO: a Cytoscape plugin to assess overrepresentation of gene ontology categories in biological networks. 2005 , 21, 3448-9	3065
2184	Discovering functional transcription factor binding from superimposed gene networks.	
2183	Systems biology for the virtual plant. 2005 , 138, 550-4	72
2182	Proteomic resources: integrating biomedical information in humans. 2005 , 364, 13-8	10
2181	Genetic network interactions among replication, repair and nuclear pore deficiencies in yeast. 2005 , 4, 459-68	97
2180	From protein networks to biological systems. 2005 , 579, 1821-7	65
2179	An integrated approach for inference and mechanistic modeling for advancing drug development. 2005 , 579, 1878-83	24
2178	Computational representation of developmental genetic regulatory networks. 2005 , 283, 1-16	181
2177	Managing genomic and proteomic knowledge. 2005 , 2, 197-204	2
2176	Chapter 12 Bioinformatics standards and tools in proteomics. 2005 , 46, 501-521	
2175	Ontological analysis of gene expression data: current tools, limitations, and open problems. 2005 , 21, 3587-95	669
2174	PIMWalker: visualising protein interaction networks using the HUPO PSI molecular interaction format. 2005 , 4, 137-9	5
2173	BioLayout(Java): versatile network visualisation of structural and functional relationships. 2005, 4, 71-4	46
2172	Dizzy: stochastic simulation of large-scale genetic regulatory networks. 2005 , 3, 415-36	174

2171	A compendium of Caenorhabditis elegans regulatory transcription factors: a resource for mapping transcription regulatory networks. 2005 , 6, R110	142
2170	iVici: Interrelational Visualization and Correlation Interface. 2005 , 6, R115	9
2169	Ulysses - an application for the projection of molecular interactions across species. 2005 , 6, R106	20
2168	Validation and refinement of gene-regulatory pathways on a network of physical interactions. 2005 , 6, R62	63
2167	Derivation of genetic interaction networks from quantitative phenotype data. 2005 , 6, R38	100
2166	Recurrent insertion and duplication generate networks of transposable element sequences in the Drosophila melanogaster genome. 2006 , 7, R112	134
2165	Systematic screening of polyphosphate (poly P) levels in yeast mutant cells reveals strong interdependence with primary metabolism. 2006 , 7, R109	54
2164	Inferring transcriptional modules from ChIP-chip, motif and microarray data. 2006, 7, R37	78
2163	Comparative analysis of Saccharomyces cerevisiae WW domains and their interacting proteins. 2006 , 7, R30	48
2162	. 2006 , 53, 2438-2443	O
2161	Have Green - A Visual Analytics Framework for Large Semantic Graphs. 2006 ,	11
2160	exploRase: Exploratory Data Analysis of Systems Biology Data.	3
2159	Integrative Data Mining for Assessing International Conflict Events. 2006,	
2158	PathBank: Web-Based Querying and Visualziation of an Integrated Biological Pathway Database.	
2157	Systems biology approaches identify ATF3 as a negative regulator of Toll-like receptor 4. 2006 , 441, 173-8	608
2156	PathSys: integrating molecular interaction graphs for systems biology. 2006 , 7, 55	36
2155	Effects of prostratin on Cyclin T1/P-TEFb function and the gene expression profile in primary resting CD4+ T cells. 2006 , 3, 66	61
2154	Visualizing networks. 2006 , 411, 408-21	14

(2006-2006)

2153	A network-based analysis of the late-phase reaction of the skin. 2006 , 118, 220-5	25
2152	Modulation of the TLR-mediated inflammatory response by the endogenous human host defense peptide LL-37. 2006 , 176, 2455-64	430
2151	Motif search in graphs: application to metabolic networks. 2006 , 3, 360-8	117
2150	Act globally, think locally: systems biology addresses the PDZ domain. 2006 , 1, 207-10	20
2149	Pathway analysis using random forests classification and regression. 2006 , 22, 2028-36	182
2148	A DNA integrity network in the yeast Saccharomyces cerevisiae. 2006 , 124, 1069-81	456
2147	A gene-centered C. elegans protein-DNA interaction network. 2006 , 125, 1193-205	194
2146	Integrated analysis of multiple data sources reveals modular structure of biological networks. 2006 , 345, 302-9	25
2145	Coevolution, modularity and human disease. 2006 , 16, 637-44	19
2144	Engineering yeast transcription machinery for improved ethanol tolerance and production. 2006 , 314, 1565-8	638
2143	Modularity of the transcriptional response of protein complexes in yeast. 2006 , 363, 589-610	21
2142	A wiring of the human nucleolus. 2006 , 22, 285-95	52
2141	CFinder: locating cliques and overlapping modules in biological networks. 2006 , 22, 1021-3	673
2140	Working together to respond to the challenges of EU policy to replace animal testing. 2006 , 34, 11-8	3
2139	BioPAX (biological pathway data exchange format. 2006,	6
2138	Virology in the 21st century: finding function with functional genomics. 2006 , 1, 47-53	10
2137	Microarray analysis of gene expression: considerations in data mining and statistical treatment. 2006 , 25, 355-63	56
2136	Transcriptional activators in yeast. 2006 , 34, 955-67	77

2135	Comprehensive curation and analysis of global interaction networks in Saccharomyces cerevisiae. 2006 , 5, 11	246
2134	Reconstructing protein complexes: from proteomics to systems biology. 2006 , 6, 4724-31	16
2133	Functional annotation of proteins identified in human brain during the HUPO Brain Proteome Project pilot study. 2006 , 6, 5059-75	23
2132	The pitfalls of proteomics experiments without the correct use of bioinformatics tools. 2006 , 6, 5577-96	77
2131	Proteome informatics II: bioinformatics for comparative proteomics. 2006 , 6, 5445-66	30
2130	A first global analysis of plasmid encoded proteins in the ACLAME database. 2006 , 30, 980-94	34
2129	Toward the systems biology of vesicle transport. 2006 , 7, 761-8	7
2128	Global mapping of pharmacological space. 2006 , 24, 805-15	686
2127	Reverse engineering cellular networks. 2006 , 1, 662-71	273
2126	The model organism as a system: integrating 'omics' data sets. 2006 , 7, 198-210	572
2125	Global landscape of protein complexes in the yeast Saccharomyces cerevisiae. 2006 , 440, 637-43	2327
2124	Systems biology as a foundation for genome-scale synthetic biology. 2006 , 17, 488-92	100
2123	Aggregation of bioinformatics data using Semantic Web technology. 2006 , 4, 216-221	23
2122	A semantic web approach to biological pathway data reasoning and integration. 2006 , 4, 207-215	6
2121	Algorithms for network analysis in systems-ADME/Tox using the MetaCore and MetaDrug platforms. 2006 , 36, 877-901	110
2120	Designing highly flexible and usable cyberinfrastructures for convergence. 2006 , 1093, 161-79	12
2119	Modeling network growth with assortative mixing. 2006 , 50, 617-630	12
2118	Analysis of microarray experiments of gene expression profiling. 2006 , 195, 373-88	177

(2006-2006)

2117	One hundred years of high-throughput Drosophila research. 2006 , 14, 349-62	17
2116	Advances in the analysis of dynamic protein complexes by proteomics and data processing. 2006 , 386, 482-93	9
2115	Functional gene analysis of individual response to challenge of SIVmac239 in M. mulatta PBMC culture. 2006 , 348, 242-52	8
2114	Information integration of protein-protein interactions as essential tools for immunomics. 2006 , 244, 84-6	3
2113	Systems biology of innate immunity. 2006 , 244, 105-9	34
2112	Genomics of TGF-beta1 signaling in stem cell commitment and dendritic cell development. 2006 , 244, 116-20	6
2111	Biological microarray interpretation: the rules of engagement. 2006 , 1759, 319-27	35
2110	simBio: a Java package for the development of detailed cell models. 2006 , 90, 360-77	34
2109	VANTED: a system for advanced data analysis and visualization in the context of biological networks. 2006 , 7, 109	350
2108	The Gaggle: an open-source software system for integrating bioinformatics software and data sources. 2006 , 7, 176	120
2107	A database and tool, IM Browser, for exploring and integrating emerging gene and protein interaction data for Drosophila. 2006 , 7, 195	24
2106	Exploration of biological network centralities with CentiBiN. 2006 , 7, 219	134
2105	Integrated biclustering of heterogeneous genome-wide datasets for the inference of global regulatory networks. 2006 , 7, 280	178
2104	SBEAMS-Microarray: database software supporting genomic expression analyses for systems biology. 2006 , 7, 286	45
2103	WholePathwayScope: a comprehensive pathway-based analysis tool for high-throughput data. 2006 , 7, 30	177
2102	Evaluation of clustering algorithms for protein-protein interaction networks. 2006 , 7, 488	577
2101	cPath: open source software for collecting, storing, and querying biological pathways. 2006 , 7, 497	83
2100	IntNetDB v1.0: an integrated protein-protein interaction network database generated by a probabilistic model. 2006 , 7, 508	54

2099	An evaluation of human protein-protein interaction data in the public domain. 2006, 7 Suppl 5, S19	168
2098	Global similarity and local divergence in human and mouse gene co-expression networks. 2006 , 6, 70	58
2097	A high-throughput screen identifying sequence and promiscuity characteristics of the loxP spacer region in Cre-mediated recombination. 2006 , 7, 73	45
2096	Transforming omics data into context: bioinformatics on genomics and proteomics raw data. 2006 , 27, 2659-75	31
2095	Integrative Array Analyzer: a software package for analysis of cross-platform and cross-species microarray data. 2006 , 22, 1665-7	13
2094	Computational modeling of the Plasmodium falciparum interactome reveals protein function on a genome-wide scale. <i>Genome Research</i> , 2006 , 16, 542-9	79
2093	Using Web Agents for Data Mining of Fungal Genomes. 2006 , 6, 297-309	
2092	Hierarchical visualization of metabolic networks using virtual reality. 2006,	6
2091	BioCAD. 2006 ,	
2090	Identification of the proliferation/differentiation switch in the cellular network of multicellular organisms. 2006 , 2, e145	78
2089	Heterotachy in mammalian promoter evolution. 2006 , 2, e30	90
2088	NetAlign: a web-based tool for comparison of protein interaction networks. 2006 , 22, 2175-7	53
2087	Graph-based analysis and visualization of experimental results with ONDEX. 2006, 22, 1383-90	159
2086	PIANA: protein interactions and network analysis. 2006 , 22, 1015-7	43
2085	Network analysis of human in-stent restenosis. 2006 , 114, 2644-54	56
2084	A systematic RNA interference screen reveals a cell migration gene network in C. elegans. 2006 , 119, 4811-8	67
2083	Proteome analysis of Halobacterium sp. NRC-1 facilitated by the biomodule analysis tool BMSorter. 2006 , 5, 987-97	13
2082	Disentangling information flow in the Ras-cAMP signaling network. <i>Genome Research</i> , 2006 , 16, 520-6 9.7	13

2081	SEBINI: Software Environment for Biological Network Inference. 2006 , 22, 2706-8	18
2080	Local similarity analysis reveals unique associations among marine bacterioplankton species and environmental factors. 2006 , 22, 2532-8	183
2079	PRODISTIN Web Site: a tool for the functional classification of proteins from interaction networks. 2006 , 22, 248-50	18
2078	Expression and functional profiling reveal distinct gene classes involved in fatty acid metabolism. 2006 , 2, 2006.0009	39
2077	Bioinformatics Approaches to Integrate Metabolomics and Other Systems Biology Data. 2006 , 105-115	9
2076	Dry work in a wet world: computation in systems biology. 2006 , 2, 40	14
2075	A network-based analysis of polyanion-binding proteins utilizing yeast protein arrays. 2006 , 5, 2263-78	12
2074	Unraveling transcription regulatory networks by protein-DNA and protein-protein interaction mapping. <i>Genome Research</i> , 2006 , 16, 1445-54	121
2073	Transcriptional coordination of the metabolic network in Arabidopsis. 2006 , 142, 762-74	163
2072	Development and Implementation of the PSI MI Standard for Molecular Interaction. 2006,	1
2071	Multiplexed protein array platforms for analysis of autoimmune diseases. 2006 , 24, 391-418	94
2070	BiologicalNetworks: visualization and analysis tool for systems biology. 2006 , 34, W466-71	70
2069	The tYNA platform for comparative interactomics: a web tool for managing, comparing and mining multiple networks. 2006 , 22, 2968-70	61
2068	GenePro: a Cytoscape plug-in for advanced visualization and analysis of interaction networks. 2006 , 22, 2178-9	40
2067	BioNetBuilder: automatic integration of biological networks. 2007 , 23, 392-3	73
2066	Integration of expression profiles and genetic mapping data to identify candidate genes in intracranial aneurysm. 2007 , 32, 45-57	27
2065	Bacteriome.organ integrated protein interaction database for E. coli. 2008 , 36, D632-6	43
2064	IntActopen source resource for molecular interaction data. 2007 , 35, D561-5	626

2063	Making database systems usable. 2007 ,	130
2062	Network genomics. 2007 , 89-115	9
2061	Systems analysis of chaperone networks in the malarial parasite Plasmodium falciparum. 2007, 3, 1701-15	88
2060	Identification of putative androgen receptor interaction protein modules: cytoskeleton and endosomes modulate androgen receptor signaling in prostate cancer cells. 2007 , 6, 252-71	46
2059	Sungear: interactive visualization and functional analysis of genomic datasets. 2007 , 23, 259-61	32
2058	Inferring genome-wide functional linkages in E. coli by combining improved genome context methods: comparison with high-throughput experimental data. <i>Genome Research</i> , 2007 , 17, 527-35	50
2057	A predicted interactome for Arabidopsis. 2007 , 145, 317-29	233
2056	Michigan Molecular Interactions (MiMI): putting the jigsaw puzzle together. 2007 , 35, D566-71	88
2055	Systematic discovery of functional modules and context-specific functional annotation of human genome. 2007 , 23, i222-9	62
2054	Expression of a tumor-related gene network increases in the mammalian hypothalamus at the time of female puberty. 2007 , 148, 5147-61	73
2053	The rice kinase database. A phylogenomic database for the rice kinome. 2007 , 143, 579-86	116
2052	T1DBase: integration and presentation of complex data for type 1 diabetes research. 2007 , 35, D742-6	56
2051	Regulation of yeast oscillatory dynamics. 2007 , 104, 2241-6	120
2050	. 2007,	
2049	A network of genes regulated by light in cyanobacteria. 2007 , 11, 166-85	12
2048	SEBINI-CABIN: An Analysis Pipeline for Biological Network Inference, with a Case Study in Protein-Protein Interaction Network Reconstruction. 2007 ,	1
2047	Kinetic Modeling using BioPAX ontology. 2007 , 2007, 339-348	10
2046	A Graph-Theoretic Analysis of the Human Protein-Interaction Network Using Multicore Parallel Algorithms. 2007 ,	4

(2007-2007)

2045	Differential binding of calmodulin-related proteins to their targets revealed through high-density Arabidopsis protein microarrays. 2007 , 104, 4730-5	299
2044	A large-scale protein protein interaction analysis in Synechocystis sp. PCC6803. 2007 , 14, 207-16	149
2043	Onto-Tools: new additions and improvements in 2006. 2007 , 35, W206-11	84
2042	In-depth analysis of the adipocyte proteome by mass spectrometry and bioinformatics. 2007 , 6, 1257-73	91
2041	Literature-based compound profiling: application to toxicogenomics. 2007, 8, 1521-34	20
2040	The BioGRID Interaction Database: 2008 update. 2008 , 36, D637-40	548
2039	Transcriptional responses to fatty acid are coordinated by combinatorial control. 2007, 3, 115	53
2038	VisANT 3.0: new modules for pathway visualization, editing, prediction and construction. 2007 , 35, W625-32	58
2037	NetMatch: a Cytoscape plugin for searching biological networks. 2007, 23, 910-2	62
2036	GOlorize: a Cytoscape plug-in for network visualization with Gene Ontology-based layout and coloring. 2007 , 23, 394-6	84
2035	Cerebral: a Cytoscape plugin for layout of and interaction with biological networks using subcellular localization annotation. 2007 , 23, 1040-2	145
2034	structureViz: linking Cytoscape and UCSF Chimera. 2007 , 23, 2345-7	60
2033	The MiSink Plugin: Cytoscape as a graphical interface to the Database of Interacting Proteins. 2007 , 23, 2193-5	16
2032	Quantitative phosphoproteome profiling of Wnt3a-mediated signaling network: indicating the involvement of ribonucleoside-diphosphate reductase M2 subunit phosphorylation at residue serine 20 in canonical Wnt signal transduction. 2007 , 6, 1952-67	54
2031	Reliable prediction of regulator targets using 12 Drosophila genomes. <i>Genome Research</i> , 2007 , 17, 1919-3.†	123
2030	Cyclone: java-based querying and computing with Pathway/Genome databases. 2007 , 23, 1299-300	10
2029	A tandem affinity purification-based technology platform to study the cell cycle interactome in Arabidopsis thaliana. 2007 , 6, 1226-38	175
2028	Assessing significance of connectivity and conservation in protein interaction networks. 2007 , 14, 747-64	45

2027	Identification of tightly regulated groups of genes during Drosophila melanogaster embryogenesis. 2007 , 3, 72	62
2026	CellCircuits: a database of protein network models. 2007 , 35, D538-45	18
2025	Analyzing Gene Relationships for Down Syndrome with Labeled Transition Graphs. 2007,	0
2024	Getting connected: analysis and principles of biological networks. 2007 , 21, 1010-24	380
2023	Broad network-based predictability of Saccharomyces cerevisiae gene loss-of-function phenotypes. 2007 , 8, R258	71
2022	Integrative analysis for finding genes and networks involved in diabetes and other complex diseases. 2007 , 8, R253	45
2021	PAZAR: a framework for collection and dissemination of cis-regulatory sequence annotation. 2007 , 8, R207	77
2020	Cross-species cluster co-conservation: a new method for generating protein interaction networks. 2007 , 8, R185	10
2019	Metabolic peculiarities of Aspergillus niger disclosed by comparative metabolic genomics. 2007 , 8, R182	42
2018	Network motif analysis of a multi-mode genetic-interaction network. 2007 , 8, R160	10
2017	A functional map of NFkappaB signaling identifies novel modulators and multiple system controls. 2007 , 8, R104	16
2016	Toxicogenomic analysis of Caenorhabditis elegans reveals novel genes and pathways involved in the resistance to cadmium toxicity. 2007 , 8, R122	124
2015	Reactome: a knowledge base of biologic pathways and processes. 2007 , 8, R39	454
2014	Genome mapping and expression analyses of human intronic noncoding RNAs reveal tissue-specific patterns and enrichment in genes related to regulation of transcription. 2007 , 8, R43	159
2013	Qualitative network models and genome-wide expression data define carbon/nitrogen-responsive molecular machines in Arabidopsis. 2007 , 8, R7	240
2012	Clustering of genes into regulons using integrated modeling-COGRIM. 2007 , 8, R4	48
2011	Network visualization and network analysis. 2007 , 97, 245-75	19
2010	Analysis of expression data: an overview. 2007 , Chapter 11, Unit11.4	1

2009 How to infer gene networks from expression profiles. 2007 , 3, 78	437
2008 Selective Raf inhibition in cancer therapy. 2007 , 11, 1587-609	50
2007 Proteomics in 2005/2006: developments, applications and challenges. 2007 , 79, 4325-43	53
Pathway analysis software as a tool for drug target selection, prioritization and validation of drug mechanism. 2007 , 11, 411-21	23
2005 GraphScape: integrated multivariate network visualization. 2007,	5
2004 Comparing protein interaction networks via a graph match-and-split algorithm. 2007 , 14, 892-907	49
Enabling high-throughput data management for systems biology: the Bioinformatics Resource Manager. 2007 , 23, 906-9	42
2002 MotifNetwork: Genome-Wide Domain Analysis using Grid-enabled Workflows. 2007 ,	2
2001 Regulation of gene expression by small non-coding RNAs: a quantitative view. 2007 , 3, 138	231
2000 Tools for visually exploring biological networks. 2007 , 23, 2651-9	180
1999 A systems biology approach for pathway level analysis. <i>Genome Research</i> , 2007 , 17, 1537-45 9.7	796
1999 A systems biology approach for pathway level analysis. <i>Genome Research</i> , 2007 , 17, 1537-45 9.7 1998 Comparative proteome analysis of human epithelial ovarian cancer. 2007 , 5, 16	796 46
1998 Comparative proteome analysis of human epithelial ovarian cancer. 2007 , 5, 16	46
Comparative proteome analysis of human epithelial ovarian cancer. 2007 , 5, 16 1997 The intracellular region of Notch ligands: does the tail make the difference?. 2007 , 2, 19	46 39
1998 Comparative proteome analysis of human epithelial ovarian cancer. 2007 , 5, 16 1997 The intracellular region of Notch ligands: does the tail make the difference?. 2007 , 2, 19 1996 Network-based prediction of protein function. 2007 , 3, 88	46 39 743
1998 Comparative proteome analysis of human epithelial ovarian cancer. 2007, 5, 16 1997 The intracellular region of Notch ligands: does the tail make the difference?. 2007, 2, 19 1996 Network-based prediction of protein function. 2007, 3, 88 1995 E. coli metabolomics: capturing the complexity of a BimpleImodel. 2007, 189-234	46 39 743 3

1991	Transcriptional networks in S. cerevisiae linked to an accumulation of base excision repair intermediates. 2007 , 2, e1252	14
1990	Public Databases and Software for the Pathway Analysis of Cancer Genomes. 2007 , 3, 117693510700300	9
1989	Integrative database management for mouse development: systems and concepts. 2007, 81, 1-19	5
1988	Systems level analysis of osteoclastogenesis reveals intrinsic and extrinsic regulatory interactions. 2007 , 236, 2181-97	24
1987	CABIN: collective analysis of biological interaction networks. 2007 , 31, 222-5	16
1986	An integrative in silico approach for discovering candidates for drug-targetable protein-protein interactions in interactome data. 2007 , 7, 10	16
1985	The urologic epithelial stem cell database (UESC) - a web tool for cell type-specific gene expression and immunohistochemistry images of the prostate and bladder. 2007 , 7, 19	22
1984	Broadening the horizonlevel 2.5 of the HUPO-PSI format for molecular interactions. 2007 , 5, 44	204
1983	A global analysis of genetic interactions in Caenorhabditis elegans. 2007 , 6, 8	120
1982	A 1.55 A resolution X-ray crystal structure of HEF2/ERH and insights into its transcriptional and cell-cycle interaction networks. 2007 , 68, 427-37	16
1981	Systematic investigation of lycopene effects in LNCaP cells by use of novel large-scale proteomic analysis software. 2007 , 1, 513-523	27
1980	Nine steps to proteomic wisdom: A practical guide to using protein-protein interaction networks and molecular pathways as a framework for interpreting disease proteomic profiles. 2007 , 1, 1156-68	5
1979	The extant core bacterial proteome is an archive of the origin of life. 2007 , 7, 875-89	44
1978	WI-PHI: a weighted yeast interactome enriched for direct physical interactions. 2007 , 7, 932-43	72
1977	Identifying functional modules in the physical interactome of Saccharomyces cerevisiae. 2007 , 7, 944-60	112
1976	Computational analysis of human protein interaction networks. 2007 , 7, 2541-52	57
1975	Discovering functions and revealing mechanisms at molecular level from biological networks. 2007 , 7, 2856-69	90
1974	Quantitative proteomics using uniform (15)N-labeling, MASCOT, and the trans-proteomic pipeline. 2007 , 7, 3462-9	40

(2007-2007)

1973	Relating protein pharmacology by ligand chemistry. 2007 , 25, 197-206	1278
1972	An integrated mass spectrometric and computational framework for the analysis of protein interaction networks. 2007 , 25, 345-52	147
1971	Towards zoomable multidimensional maps of the cell. 2007 , 25, 547-54	73
1970	The minimum information required for reporting a molecular interaction experiment (MIMIx). 2007 , 25, 894-8	229
1969	Functional atlas of the integrin adhesome. 2007 , 9, 858-67	899
1968	Prediction and assignment of function for a divergent N-succinyl amino acid racemase. 2007 , 3, 486-91	87
1967	Scaffold composition and biological relevance of screening libraries. 2007 , 3, 442-6	148
1966	Integration of biological networks and gene expression data using Cytoscape. 2007 , 2, 2366-82	1798
1965	MetaNetwork: a computational protocol for the genetic study of metabolic networks. 2007, 2, 685-94	25
1964	Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox. 2007 , 2, 727-38	661
1963	Beyond standardization: dynamic software infrastructures for systems biology. 2007 , 8, 235-43	39
1962	Disrupted in Schizophrenia 1 Interactome: evidence for the close connectivity of risk genes and a potential synaptic basis for schizophrenia. 2007 , 12, 74-86	349
1961	Model-based clustering for social networks. 2007 , 170, 301-354	359
1960	Metabolic network visualization eliminating node redundance and preserving metabolic pathways. 2007 , 1, 29	32
1959	A systems biology approach to modelling tea (Camellia sinensis). 2007 , 1,	2
1958	BioPP: a tool for web-publication of biological networks. 2007 , 8, 168	12
1957	Discovering functional linkages and uncharacterized cellular pathways using phylogenetic profile comparisons: a comprehensive assessment. 2007 , 8, 173	66
1956	Genome Expression Pathway Analysis Toolanalysis and visualization of microarray gene expression data under genomic, proteomic and metabolic context. 2007 , 8, 179	16

1955	GenMAPP 2: new features and resources for pathway analysis. 2007 , 8, 217	207
1954	Characterization of protein-interaction networks in tumors. 2007 , 8, 224	81
1953	A high-accuracy consensus map of yeast protein complexes reveals modular nature of gene essentiality. 2007 , 8, 236	194
1952	An exploration of alternative visualisations of the basic helix-loop-helix protein interaction network. 2007 , 8, 289	5
1951	Classification of microarray data using gene networks. 2007 , 8, 35	149
1950	BNDB - the Biochemical Network Database. 2007 , 8, 367	33
1949	Genes2Networks: connecting lists of gene symbols using mammalian protein interactions databases. 2007 , 8, 372	114
1948	The Firegoose: two-way integration of diverse data from different bioinformatics web resources with desktop applications. 2007 , 8, 456	27
1947	An efficient grid layout algorithm for biological networks utilizing various biological attributes. 2007 , 8, 76	22
1946	Inferring biological networks with output kernel trees. 2007 , 8 Suppl 2, S4	18
1946 1945	Inferring biological networks with output kernel trees. 2007, 8 Suppl 2, S4 Shared transcriptional correlations in seed formation and in plants response to drought. 2007, 8,	18
•		
•	Shared transcriptional correlations in seed formation and in plants response to drought. 2007 , 8,	
1945 1944	Shared transcriptional correlations in seed formation and in plants response to drought. 2007 , 8, BioCAD: an information fusion platform for bio-network inference and analysis. 2007 , 8 Suppl 9, S2	1
1945 1944 1943	Shared transcriptional correlations in seed formation and in plants response to drought. 2007 , 8, BioCAD: an information fusion platform for bio-network inference and analysis. 2007 , 8 Suppl 9, S2 CAG-encoded polyglutamine length polymorphism in the human genome. 2007 , 8, 126 Evidence for systems-level molecular mechanisms of tumorigenesis. 2007 , 8, 185	1 6 60
1945 1944 1943	Shared transcriptional correlations in seed formation and in plants response to drought. 2007 , 8, BioCAD: an information fusion platform for bio-network inference and analysis. 2007 , 8 Suppl 9, S2 CAG-encoded polyglutamine length polymorphism in the human genome. 2007 , 8, 126 Evidence for systems-level molecular mechanisms of tumorigenesis. 2007 , 8, 185	1 6 60 28
1945 1944 1943 1942	Shared transcriptional correlations in seed formation and in plants response to drought. 2007, 8, BioCAD: an information fusion platform for bio-network inference and analysis. 2007, 8 Suppl 9, S2 CAG-encoded polyglutamine length polymorphism in the human genome. 2007, 8, 126 Evidence for systems-level molecular mechanisms of tumorigenesis. 2007, 8, 185 EGFR associated expression profiles vary with breast tumor subtype. 2007, 8, 258 Genes involved in TGF beta1-driven epithelial-mesenchymal transition of renal epithelial cells are	1 6 60 28 208

(2008-2007)

1937	Global mapping of gene/protein interactions in PubMed abstracts: a framework and an experiment with P53 interactions. 2007 , 40, 453-64	12
1936	A new framework for identifying combinatorial regulation of transcription factors: a case study of the yeast cell cycle. 2007 , 40, 707-25	25
1935	Expanding the metabolic engineering toolbox: more options to engineer cells. 2007 , 25, 132-7	183
1934	A framework for elucidating regulatory networks based on prior information and expression data. 2007 , 1115, 240-8	15
1933	Dialogue on reverse-engineering assessment and methods: the DREAM of high-throughput pathway inference. 2007 , 1115, 1-22	267
1932	PhosphoPepa phosphoproteome resource for systems biology research in Drosophila Kc167 cells. 2007 , 3, 139	160
1931	Inferring the skeleton cell cycle regulatory network of malaria parasite using comparative genomic and variational Bayesian approaches. 2008 , 132, 131-42	7
1930	Genomics and functional genomics with haloarchaea. 2008 , 190, 197-215	31
1929	Uncovering the gene knockout landscape for improved lycopene production in E. coli. 2008 , 78, 801-10	51
1928	Differential Plasma Glycoproteome of p19 Skin Cancer Mouse Model Using the Corra Label-Free LC-MS Proteomics Platform. 2008 , 4, 105	10
1927	Computational prediction of protein-protein interactions. 2008 , 38, 1-17	152
1926	Functional genomics in radiation biology: a gateway to cellular systems-level studies. 2008 , 47, 25-31	39
1925	Monitoring of multiple sclerosis immunotherapy: from single candidates to biomarker networks. 2008 , 255 Suppl 6, 48-57	73
1924	A global view of drug-therapy interactions. 2008 , 8, 5	66
1923	Efficiency of the immunome protein interaction network increases during evolution. 2008, 4, 4	12
1922	Biological processes, properties and molecular wiring diagrams of candidate low-penetrance breast cancer susceptibility genes. 2008 , 1, 62	13
1921	A survey of visualization tools for biological network analysis. 2008 , 1, 12	134
1920	Mining tissue specificity, gene connectivity and disease association to reveal a set of genes that modify the action of disease causing genes. 2008 , 1, 8	28

1919	PTPepsilon has a critical role in signaling transduction pathways and phosphoprotein network topology in red cells. 2008 , 8, 4695-708	26
1918	Proteomic approaches to the analysis of multiprotein signaling complexes. 2008 , 8, 832-51	42
1917	Protein networking: insights into global functional organization of proteomes. 2008 , 8, 799-816	62
1916	PATIKAmad: putting microarray data into pathway context. 2008 , 8, 2196-8	7
1915	Phosphoproteomics: A possible route to novel biomarkers of breast cancer. 2008 , 2, 181-94	7
1914	Transcriptional profiling of the megabladder mouse: a unique model of bladder dysmorphogenesis. 2008 , 237, 170-86	11
1913	Proteomic analysis to characterize differential mouse strain sensitivity to cadmium-induced forelimb teratogenesis. 2008 , 82, 187-99	13
1912	Applications of domain-domain interactions in pathway study. 2008 , 32, 81-7	3
1911	Gene module level analysis: identification to networks and dynamics. 2008 , 19, 482-91	76
1910	A graph-theoretic analysis of the human protein-interaction network using multicore parallel algorithms. 2008 , 34, 627-639	14
1909	Selected reaction monitoring for quantitative proteomics: a tutorial. 2008 , 4, 222	1081
1908	Evolution of mammals and their gut microbes. 2008 , 320, 1647-51	2355
1907	A systems biology approach to prediction of oncogenes and molecular perturbation targets in B-cell lymphomas. 2008 , 4, 169	161
1906	Comprehensive microRNA profiling reveals a unique human embryonic stem cell signature dominated by a single seed sequence. 2008 , 26, 1506-16	184
1905	Phylogenetic profiling. 2008 , 453, 201-16	4
1904	Walking the interactome for prioritization of candidate disease genes. 2008 , 82, 949-58	875
1903	The Human Phenotype Ontology: a tool for annotating and analyzing human hereditary disease. 2008 , 83, 610-5	585
1902	Understanding biological functions through molecular networks. 2008 , 18, 224-37	117

(2008-2008)

1901	stem cells. 2008 , 18, 1177-89	85
1900	Mapping the human protein interactome. 2008 , 18, 716-24	40
1899	The fibromatosis signature defines a robust stromal response in breast carcinoma. 2008 , 88, 591-601	86
1898	Regulatory potential for concerted modulation of Nrf2- and Nfkb1-mediated gene expression in inflammation and carcinogenesis. 2008 , 99, 2070-82	125
1897	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. 2008 , 26, 1155-60	471
1896	Network pharmacology: the next paradigm in drug discovery. 2008 , 4, 682-90	2255
1895	Towards a cyberinfrastructure for the biological sciences: progress, visions and challenges. 2008 , 9, 678-88	123
1894	Global monitoring of autumn gene expression within and among phenotypically divergent populations of Sitka spruce (Picea sitchensis). 2008 , 178, 103-122	103
1893	Comprehensive gene expression atlas for the Arabidopsis MAP kinase signalling pathways. 2008 , 179, 643-662	81
1892	Visualizing Genome Expression and Regulatory Network Dynamics in Genomic and Metabolic Context. 2008 , 27, 887-894	17
1891	Molecular and cellular approaches for the detection of protein-protein interactions: latest techniques and current limitations. 2008 , 53, 610-35	142
1890	SPIKEa database, visualization and analysis tool of cellular signaling pathways. 2008 , 9, 110	48
1889	Inferring the role of transcription factors in regulatory networks. 2008 , 9, 228	10
1888	A visual analytics approach for understanding biclustering results from microarray data. 2008 , 9, 247	32
1887	GenCLiP: a software program for clustering gene lists by literature profiling and constructing gene co-occurrence networks related to custom keywords. 2008 , 9, 308	34
1886	FERN - a Java framework for stochastic simulation and evaluation of reaction networks. 2008 , 9, 356	23
1885	Methodology capture: discriminating between the "best" and the rest of community practice. 2008 , 9, 359	12
1884	Predicting protein linkages in bacteria: which method is best depends on task. 2008 , 9, 397	14

1883	Presenting and exploring biological pathways with PathVisio. 2008 , 9, 399	272
1882	iRefIndex: a consolidated protein interaction database with provenance. 2008 , 9, 405	404
1881	GeneTrailExpress: a web-based pipeline for the statistical evaluation of microarray experiments. 2008 , 9, 552	63
1880	RPPAML/RIMS: a metadata format and an information management system for reverse phase protein arrays. 2008 , 9, 555	13
1879	Building pathway clusters from Random Forests classification using class votes. 2008 , 9, 87	24
1878	SynechoNET: integrated protein-protein interaction database of a model cyanobacterium Synechocystis sp. PCC 6803. 2008 , 9 Suppl 1, S20	22
1877	A protein interaction based model for schizophrenia study. 2008 , 9 Suppl 12, S23	9
1876	RDFScape: Semantic Web meets systems biology. 2008 , 9 Suppl 4, S6	20
1875	ProteoLens: a visual analytic tool for multi-scale database-driven biological network data mining. 2008 , 9 Suppl 9, S5	18
1874	Linking Cytoscape and the corynebacterial reference database CoryneRegNet. 2008, 9, 184	28
1873	Arabidopsis mRNA polyadenylation machinery: comprehensive analysis of protein-protein interactions and gene expression profiling. 2008 , 9, 220	72
1872	The topology of the bacterial co-conserved protein network and its implications for predicting protein function. 2008 , 9, 313	13
1871	T2D-Db: an integrated platform to study the molecular basis of Type 2 diabetes. 2008 , 9, 320	31
1870	Transcription factor control of growth rate dependent genes in Saccharomyces cerevisiae: a three factor design. 2008 , 9, 341	43
1869	Sequence conservation and combinatorial complexity of Drosophila neural precursor cell enhancers. 2008 , 9, 371	8
1868	Comparative analysis of function and interaction of transcription factors in nematodes: extensive conservation of orthology coupled to rapid sequence evolution. 2008 , 9, 399	41
1867	DroID: the Drosophila Interactions Database, a comprehensive resource for annotated gene and protein interactions. 2008 , 9, 461	88
1866	The prediction of protein-protein interaction networks in rice blast fungus. 2008 , 9, 519	39

1865	A cross-species transcriptomics approach to identify genes involved in leaf development. 2008 , 9, 589	32
1864	Meta-analysis of expression signatures of muscle atrophy: gene interaction networks in early and late stages. 2008 , 9, 630	46
1863	Inferring gene regulatory networks by thermodynamic modeling. 2008 , 9 Suppl 2, S19	13
1862	In silico comparison of transcript abundances during Arabidopsis thaliana and Glycine max resistance to Fusarium virguliforme. 2008 , 9 Suppl 2, S6	14
1861	Mycobacterium tuberculosis interactome analysis unravels potential pathways to drug resistance. 2008 , 8, 234	77
1860	Identification of a set of genes showing regionally enriched expression in the mouse brain. 2008, 9, 66	23
1859	Genetic and systems level analysis of Drosophila sticky/citron kinase and dFmr1 mutants reveals common regulation of genetic networks. 2008 , 2, 101	7
1858	Arena3D: visualization of biological networks in 3D. 2008 , 2, 104	73
1857	Interactive analysis of systems biology molecular expression data. 2008 , 2, 23	7
1856	An integrated genetic, genomic and systems approach defines gene networks regulated by the interaction of light and carbon signaling pathways in Arabidopsis. 2008 , 2, 31	50
1855	The Systems Biology Research Tool: evolvable open-source software. 2008 , 2, 55	39
1854	Seeded Bayesian Networks: constructing genetic networks from microarray data. 2008 , 2, 57	71
1853	The genome-scale metabolic model iIN800 of Saccharomyces cerevisiae and its validation: a scaffold to query lipid metabolism. 2008 , 2, 71	129
1852	Rapidly exploring structural and dynamic properties of signaling networks using PathwayOracle. 2008 , 2, 76	12
1851	Large-scale prediction of drug-target relationships. 2008 , 582, 1283-90	75
1850	ROS-deficient monocytes have aberrant gene expression that correlates with inflammatory disorders of chronic granulomatous disease. 2008 , 129, 90-102	62
1849	Advanced microarray analysis highlights modified neuro-immune signaling in nucleated blood cells from Parkinson's disease patients. 2008 , 201-202, 227-36	32
1848	Integrating metabolomics and phenomics with systems models of cardiac hypoxia. 2008 , 96, 209-25	14

1847	Scale relativity theory and integrative systems biology: 1. Founding principles and scale laws. 2008 , 97, 79-114	55
1846	Low duplicability and network fragility of cancer genes. 2008 , 24, 427-30	56
1845	Relationships among carbohydrate intermediate metabolites and DNA damage and repair in yeast from a systems biology perspective. 2008 , 642, 43-56	10
1844	Candida albicans-macrophage interactions: genomic and proteomic insights. 2008 , 3, 661-81	11
1843	Protein interaction data set highlighted with human Ras-MAPK/PI3K signaling pathways. 2008 , 7, 3879-89	34
1842	Software Infrastructure and Data Model for Pathway Analysis. 2008, 27-45	
1841	Mammalian Proteome and Toxicant Network Analysis. 2008, 165-193	
1840	Cardioinductive network guiding stem cell differentiation revealed by proteomic cartography of tumor necrosis factor alpha-primed endodermal secretome. 2008 , 26, 387-400	62
1839	WGCNA: an R package for weighted correlation network analysis. 2008 , 9, 559	8760
1838	Characterization of the mouse pancreatic islet proteome and comparative analysis with other mouse tissues. 2008 , 7, 3114-26	41
1837	Proteomics of cancer of hormone-dependent tissues. 2008 , 630, 133-47	8
1836	Data analysis and bioinformatics tools for tandem mass spectrometry in proteomics. 2008 , 33, 18-25	122
1835	In vivo identification of the outer membrane protein OmcA-MtrC interaction network in Shewanella oneidensis MR-1 cells using novel hydrophobic chemical cross-linkers. 2008 , 7, 1712-20	61
1834	KEGG spider: interpretation of genomics data in the context of the global gene metabolic network. 2008 , 9, R179	56
1833	ArrayPlex: distributed, interactive and programmatic access to genome sequence, annotation, ontology, and analytical toolsets. 2008 , 9, R159	1
1832	Functional architecture of Escherichia coli: new insights provided by a natural decomposition approach. 2008 , 9, R154	32
1831	NetGrep: fast network schema searches in interactomes. 2008 , 9, R138	29
1830	The hidden universal distribution of amino acid biosynthetic networks: a genomic perspective on their origins and evolution. 2008 , 9, R95	27

(2008-2008)

1829	gene expression profiling. 2008 , 9, R72	17
1828	Text-mining assisted regulatory annotation. 2008 , 9, R31	29
1827	MetaReg: a platform for modeling, analysis and visualization of biological systems using large-scale experimental data. 2008 , 9, R1	15
1826	Adipose tissue transcriptomic signature highlights the pathological relevance of extracellular matrix in human obesity. 2008 , 9, R14	300
1825	Handling Diverse Protein Interaction Data: Integration, Storage and Retrieval. 2008, 33-51	
1824	Exploring biological networks with Cytoscape software. 2008 , Chapter 8, Unit 8.13	41
1823	A personal journey of discovery: developing technology and changing biology. 2008 , 1, 1-43	53
1822	A systems biology analysis of protein-protein interactions in the APOBEC family. 2008 , 83, 521-30	О
1821	Functional organisation of Escherichia coli transcriptional regulatory network. 2008, 381, 238-47	94
1820	The expression level of the chromatin-associated HMGB1 protein influences growth, stress tolerance, and transcriptome in Arabidopsis. 2008 , 384, 9-21	37
1819	Challenges in plant cellular pathway reconstruction based on gene expression profiling. 2008, 13, 44-50	20
1818	Canonical WNT/beta-catenin signaling is required for ureteric branching. 2008, 317, 83-94	122
1817	Identification of dilated cardiomyopathy signature genes through gene expression and network data integration. 2008 , 92, 404-13	35
1816	Global Bayesian models for the prioritization of antitubercular agents. 2008 , 48, 2362-70	79
1815	Transcriptional regulatory networks in haematopoiesis. 2008 , 18, 530-5	25
1814	An extended transcriptional network for pluripotency of embryonic stem cells. 2008 , 132, 1049-61	1095
1813	Global sequencing of proteolytic cleavage sites in apoptosis by specific labeling of protein N termini. 2008 , 134, 866-76	363
1812	Taming data. 2008 , 4, 312-3	1

1811	Atlas of gene expression in the developing kidney at microanatomic resolution. 2008, 15, 781-91	184
1810	Network Analysis Tools: from biological networks to clusters and pathways. 2008 , 3, 1616-29	91
1809	Cerebral: visualizing multiple experimental conditions on a graph with biological context. 2008 , 14, 1253-60	68
1808	Dynamic visualization of coexpression in systems genetics data. 2008 , 14, 1081-94	4
1807	Differential use of protease families for invasion by schistosome cercariae. 2008 , 90, 345-58	87
1806	TiO(2)-based phosphoproteomic analysis of the plasma membrane and the effects of phosphatase inhibitor treatment. 2008 , 7, 3304-13	90
1805	Network integration and graph analysis in mammalian molecular systems biology. 2008, 2, 206-21	31
1804	Complexity and modularity of intracellular networks: a systematic approach for modelling and simulation. 2008 , 2, 363-8	20
1803	Interactive three-dimensional visualization and contextual analysis of protein interaction networks. 2008 , 7, 104-12	32
1802	SIRENE: supervised inference of regulatory networks. 2008 , 24, i76-82	124
1801	A comparative study of electrostatic repulsion-hydrophilic interaction chromatography (ERLIC) versus SCX-IMAC-based methods for phosphopeptide isolation/enrichment. 2008 , 7, 4869-77	86
1800	Model-based prediction of cis-acting RNA elements regulating tissue-specific alternative splicing. 2008 ,	1
1799	An outlook into ultra-scale visualization of large-scale biological data. 2008,	2
1798	Stable isotope labeling by amino acids in cell culture (SILAC) and proteome quantitation of mouse embryonic stem cells to a depth of 5,111 proteins. 2008 , 7, 672-83	242
1797	Natural selection on gene function drives the evolution of LTR retrotransposon families in the rice genome. <i>Genome Research</i> , 2009 , 19, 243-54	68
1796	Arabidopsis mitogen-activated protein kinase kinases MKK1 and MKK2 have overlapping functions in defense signaling mediated by MEKK1, MPK4, and MKS1. 2008 , 148, 212-22	221
1795	60S ribosomal subunit assembly dynamics defined by semi-quantitative mass spectrometry of purified complexes. 2008 , 36, 4988-99	44
1794	Phosphoproteome analysis of E. coli reveals evolutionary conservation of bacterial Ser/Thr/Tyr phosphorylation. 2008 , 7, 299-307	334

1793	MetaNetter: inference and visualization of high-resolution metabolomic networks. 2008, 24, 143-5	46
1792	Identifying functional modules in protein-protein interaction networks: an integrated exact approach. 2008 , 24, i223-31	367
1791	OmicsViz: Cytoscape plug-in for visualizing omics data across species. 2008 , 24, 2557-8	6
1790	Fast grid layout algorithm for biological networks with sweep calculation. 2008 , 24, 1433-41	17
1789	The fusidic acid stimulon of Staphylococcus aureus. 2008 , 62, 1207-14	18
1788	QGene 4.0, an extensible Java QTL-analysis platform. 2008 , 24, 2788-9	263
1787	The protein information and property explorer: an easy-to-use, rich-client web application for the management and functional analysis of proteomic data. 2008 , 24, 2110-1	30
1786	ProCopeprotein complex prediction and evaluation. 2008 , 24, 2115-6	25
1785	Probabilistic assembly of human protein interaction networks from label-free quantitative proteomics. 2008 , 105, 1454-9	201
1784	FunNet: an integrative tool for exploring transcriptional interactions. 2008 , 24, 2636-8	72
1783	New regulators of Wnt/beta-catenin signaling revealed by integrative molecular screening. 2008, 1, ra12	121
1782	KEGG Atlas mapping for global analysis of metabolic pathways. 2008 , 36, W423-6	343
1781	Genomic analysis of estrogen cascade reveals histone variant H2A.Z associated with breast cancer progression. 2008 , 4, 188	146
1780	A comprehensive modular map of molecular interactions in RB/E2F pathway. 2008 , 4, 173	99
 0	The biological function of some human transcription factor binding motifs varies with position	19
1779	relative to the transcription start site. 2008 , 36, 2777-86	
1778	A C. elegans genome-scale microRNA network contains composite feedback motifs with high flux capacity. 2008 , 22, 2535-49	178
	A C. elegans genome-scale microRNA network contains composite feedback motifs with high flux	

1775	The glomerular transcriptome and a predicted protein-protein interaction network. 2008, 19, 260-8	29
1774	Computing topological parameters of biological networks. 2008 , 24, 282-4	1117
1773	Design and application of genome-scale reconstructed metabolic models. 2008 , 416, 409-31	40
1772	Genome-wide analysis of signaling networks regulating fatty acid-induced gene expression and organelle biogenesis. 2008 , 181, 281-92	48
1771	Global transcriptomic analysis of Cyanothece 51142 reveals robust diurnal oscillation of central metabolic processes. 2008 , 105, 6156-61	143
1770	Perceptual dependencies in information visualization assessed by complex visual search. 2008, 4, 1-21	5
1769	Unraveling transcriptional regulatory programs by integrative analysis of microarray and transcription factor binding data. 2008 , 24, 1874-80	25
1768	Network inference algorithms elucidate Nrf2 regulation of mouse lung oxidative stress. 2008 , 4, e1000166	72
1767	Uncovering a macrophage transcriptional program by integrating evidence from motif scanning and expression dynamics. 2008 , 4, e1000021	139
1766	Global transcriptome and deletome profiles of yeast exposed to transition metals. 2008, 4, e1000053	120
1765	NeAT: a toolbox for the analysis of biological networks, clusters, classes and pathways. 2008 , 36, W444-51	73
1764	Functional maps of protein complexes from quantitative genetic interaction data. 2008, 4, e1000065	116
1763	A specificity map for the PDZ domain family. 2008 , 6, e239	348
1762	Unraveling protein networks with power graph analysis. 2008, 4, e1000108	90
1761	Dynamic changes in protein functional linkage networks revealed by integration with gene expression data. 2008 , 4, e1000237	28
1760	The extensive and condition-dependent nature of epistasis among whole-genome duplicates in yeast. <i>Genome Research</i> , 2008 , 18, 1092-9	84
1759	NetworkBLAST: comparative analysis of protein networks. 2008 , 24, 594-6	86
1758	Identification and functional analysis of light-responsive unique genes and gene family members in rice. 2008 , 4, e1000164	59

(2008-2008)

1757	The landscape of human proteins interacting with viruses and other pathogens. 2008 , 4, e32	245
1756	Cytoscape ESP: simple search of complex biological networks. 2008 , 24, 1465-6	9
1755	The protein interaction network of the epithelial junctional complex: a system-level analysis. 2008 , 19, 5409-21	22
1754	A global pathway crosstalk network. 2008 , 24, 1442-7	105
1753	VisANT: an integrative framework for networks in systems biology. 2008 , 9, 317-25	89
1752	Proteome-wide identification of poly(ADP-ribose) binding proteins and poly(ADP-ribose)-associated protein complexes. 2008 , 36, 6959-76	298
1751	jSquid: a Java applet for graphical on-line network exploration. 2008 , 24, 1467-8	16
1750	Genome-wide hepatitis C virus amino acid covariance networks can predict response to antiviral therapy in humans. 2009 , 119, 225-36	63
1749	Reconstruction of genetic association networks from microarray data: a partial least squares approach. 2008 , 24, 561-8	43
1748	DrugViz: a Cytoscape plugin for visualizing and analyzing small molecule drugs in biological networks. 2008 , 24, 2117-8	13
1747	Integrating global gene expression and radiation survival parameters across the 60 cell lines of the National Cancer Institute Anticancer Drug Screen. 2008 , 68, 415-24	197
1746	Arabidopsis reactome: a foundation knowledgebase for plant systems biology. 2008 , 20, 1426-36	44
1745	A Dynamic Multiscale Magnifying Tool for Exploring Large Sparse Graphs. 2008 , 7, 105-117	9
1744	Fish and chips: functional genomics of social plasticity in an African cichlid fish. 2008 , 211, 3041-56	150
1743	VistaClara: an expression browser plug-in for Cytoscape. 2008 , 24, 2112-4	20
1742	BiNoM: a Cytoscape plugin for manipulating and analyzing biological networks. 2008 , 24, 876-7	87
1741	Systems biology at the Institute for Systems Biology. 2008 , 7, 239-48	52
1740	Global analysis of yeast endosomal transport identifies the vps55/68 sorting complex. 2008 , 19, 1282-94	26

1739	Mass media influence spreading in social networks with community structure. 2008, 2008, P07007	19
1738	CompariMotif: quick and easy comparisons of sequence motifs. 2008 , 24, 1307-9	38
1737	Graph summarization with bounded error. 2008,	178
1736	CressExpress: a tool for large-scale mining of expression data from Arabidopsis. 2008, 147, 1004-16	98
1735	Information systems for cancer research. 2008 , 26, 1060-7	11
1734	An Extensible, Scalable Architecture for Managing Bioinformatics Data and Analyses. 2008,	4
1733	Network-Constrained Support Vector Machine for Classification. 2008,	
1732	Novel proteins, putative membrane transporters, and an integrated metabolic network are revealed by quantitative proteomic analysis of Arabidopsis cell culture peroxisomes. 2008 , 148, 1809-29	156
1731	InnateDB: facilitating systems-level analyses of the mammalian innate immune response. 2008 , 4, 218	282
1730	Deep cap analysis gene expression (CAGE): genome-wide identification of promoters, quantification of their expression, and network inference. 2008 , 44, 627-8, 630, 632	74
1729	From E-MAPs to module maps: dissecting quantitative genetic interactions using physical interactions. 2008 , 4, 209	59
1728	The MAPK signaling cascade is a central hub in the regulation of cell cycle, apoptosis and cytoskeleton remodeling by tripeptidyl-peptidase II. 2008 , 2, 253-65	8
1727	Assuring consumer safety without animal testing: a feasibility case study for skin sensitisation. 2008 , 36, 557-68	18
1726	Organization of physical interactomes as uncovered by network schemas. 2008 , 4, e1000203	14
1725	The binary protein interactome of Treponema pallidumthe syphilis spirochete. 2008 , 3, e2292	80
1724	Inferring condition-specific modulation of transcription factor activity in yeast through regulon-based analysis of genomewide expression. 2008 , 3, e3112	32
1723	Discovery and expansion of gene modules by seeking isolated groups in a random graph process. 2008 , 3, e3358	1
1722	Non-animal approaches for consumer safety risk assessments: Unilever's scientific research programme. 2009 , 37, 595-610	12

1721	Network Properties for Ranking Predicted miRNA Targets in Breast Cancer. 2009 , 182689	2
1720	Modulated modularity clustering as an exploratory tool for functional genomic inference. 2009 , 5, e1000479	97
1719	A genome-wide characterization of microRNA genes in maize. 2009 , 5, e1000716	265
1718	Sequencing, mapping, and analysis of 27,455 maize full-length cDNAs. 2009 , 5, e1000740	124
1717	Correlated mutation analysis on the catalytic domains of serine/threonine protein kinases. 2009, 4, e5913	8
1716	Maximum entropy reconstructions of dynamic signaling networks from quantitative proteomics data. 2009 , 4, e6522	22
1715	Something old, something new, something borrowed; how the thermoacidophilic archaeon Sulfolobus solfataricus responds to oxidative stress. 2009 , 4, e6964	61
1714	Systems integration of biodefense omics data for analysis of pathogen-host interactions and identification of potential targets. 2009 , 4, e7162	16
1713	Determining protein complex connectivity using a probabilistic deletion network derived from quantitative proteomics. 2009 , 4, e7310	28
1712	Proteomic and phospho-proteomic profile of human platelets in basal, resting state: insights into integrin signaling. 2009 , 4, e7627	106
1711	Stability of metabolic correlations under changing environmental conditions in Escherichia colia systems approach. 2009 , 4, e7441	29
1710	Meta-analysis of kindling-induced gene expression changes in the rat hippocampus. 2009 , 3, 53	8
1709	Practical network approaches and biologic interpretations of co-expression analyses in plants. 2009 , 26, 3-7	3
1708	STRING 8a global view on proteins and their functional interactions in 630 organisms. 2009 , 37, D412-6	1799
1707	Metabolic flux correlations, genetic interactions, and disease. 2009 , 16, 291-302	6
1706	Revealing Social Networks of Spammers Through Spectral Clustering. 2009,	8
1705	Collection of Disease Networks by Hybrid Curation Method and the Application for Pathway Analysis. 2009 ,	3
1704	. 2009,	5

1703	ClueGO: a Cytoscape plug-in to decipher functionally grouped gene ontology and pathway annotation networks. 2009 , 25, 1091-3	3395
1702	CTFMining: A Method to Predict Candidate Disease Genes Based on the Combined Network Topological Features Mining. 2009 ,	1
1701	PMAP: databases for analyzing proteolytic events and pathways. 2009 , 37, D611-8	50
1700	Data integration for plant genomicsexemplars from the integration of Arabidopsis thaliana databases. 2009 , 10, 676-93	19
1699	Dysregulated gene expression networks in human acute myelogenous leukemia stem cells. 2009 , 106, 3396-401	219
1698	Analyzing biological network parameters with CentiScaPe. 2009 , 25, 2857-9	349
1697	The thioredoxin-like protein rod-derived cone viability factor (RdCVFL) interacts with TAU and inhibits its phosphorylation in the retina. 2009 , 8, 1206-18	45
1696	Derivation of Transcriptional Regulatory Relationships by Partial Least Squares Regression. 2009,	1
1695	Assessing the Most Effective Depth for PPI Analysis. 2009,	
1694	SimplevisGrid: grid services for visualization of diverse biomedical knowledge and molecular systems data. 2009 , 2009, 4178-81	
1693	Prediction of therapeutic mechanisms of tripterygium wilfordii in rheumatoid arthritis using text mining and network-based analysis. 2009 ,	1
1692	Gene Network Study Revealed Molecular Links Among Genes for Alcohol Metabolism and Breast Cancer Susceptibility. 2009 ,	1
1691	The receptor tyrosine kinase EPHB4 has tumor suppressor activities in intestinal tumorigenesis. 2009 , 69, 7430-8	52
1690	KEGGgraph: a graph approach to KEGG PATHWAY in R and bioconductor. 2009 , 25, 1470-1	221
1689	An integrated network approach identifies the isobutanol response network of Escherichia coli. 2009 , 5, 277	155
1688	Coexpression network based on natural variation in human gene expression reveals gene interactions and functions. <i>Genome Research</i> , 2009 , 19, 1953-62	84
1687	Clustering of gene expression data based on shape similarity. 2009 , 195712	14
1686	Using a state-space model and location analysis to infer time-delayed regulatory networks. 2009 , 484601	7

(2009-2009)

1685	The Prion Disease Database: a comprehensive transcriptome resource for systems biology research in prion diseases. 2009 , 2009, bap011	16
1684	Blocking the metabolism of starch breakdown products in Arabidopsis leaves triggers chloroplast degradation. 2009 , 2, 1233-46	106
1683	Discrete logic modelling as a means to link protein signalling networks with functional analysis of mammalian signal transduction. 2009 , 5, 331	252
1682	TORQUE: topology-free querying of protein interaction networks. 2009 , 37, W106-8	23
1681	DASMI: exchanging, annotating and assessing molecular interaction data. 2009 , 25, 1321-8	14
1680	The first draft of the endostatin interaction network. 2009 , 284, 22041-22047	64
1679	Reconstruction of the yeast Snf1 kinase regulatory network reveals its role as a global energy regulator. 2009 , 5, 319	78
1678	Application of an integrated physical and functional screening approach to identify inhibitors of the Wnt pathway. 2009 , 5, 315	38
1677	Comparison of substrate specificity of the ubiquitin ligases Nedd4 and Nedd4-2 using proteome arrays. 2009 , 5, 333	100
1676	Integrating and annotating the interactome using the MiMI plugin for cytoscape. 2009 , 25, 137-8	133
1675	Genoscape: a Cytoscape plug-in to automate the retrieval and integration of gene expression data and molecular networks. 2009 , 25, 2617-8	12
1674	Mechanisms of tumor resistance to EGFR-targeted therapies. 2009 , 13, 339-62	66
1673	NAViGaTOR: Network Analysis, Visualization and Graphing Toronto. 2009 , 25, 3327-9	188
1672	A pathway-based view of human diseases and disease relationships. 2009 , 4, e4346	133
1671	The proteome of seed development in the model legume Lotus japonicus. 2009 , 149, 1325-40	68
1670	Global gene expression analysis of reactive stroma in prostate cancer. 2009 , 15, 3979-89	123
1669	Regulators of yeast endocytosis identified by systematic quantitative analysis. 2009, 185, 1097-110	86
1668	EcID. A database for the inference of functional interactions in E. coli. 2009 , 37, D629-35	26

1667	SNOW, a web-based tool for the statistical analysis of protein-protein interaction networks. 2009 , 37, W109-14	41
1666	Cell biologists expand their networks. 2009 , 186, 305-11	6
1665	Sys-BodyFluid: a systematical database for human body fluid proteome research. 2009 , 37, D907-12	71
1664	Identification of an inter-transcription factor regulatory network in human hepatoma cells by Matrix RNAi. 2009 , 37, 1049-60	28
1663	Microarray and bioinformatics analysis of gene expression in experimental membranous nephropathy. 2009 , 112, e43-58	30
1662	An integrated systems analysis implicates EGR1 downregulation in simian immunodeficiency virus encephalitis-induced neural dysfunction. 2009 , 29, 12467-76	28
1661	Systems-wide analysis of a phosphatase knock-down by quantitative proteomics and phosphoproteomics. 2009 , 8, 1908-20	88
1660	Defining elastic fiber interactions by molecular fishing: an affinity purification and mass spectrometry approach. 2009 , 8, 2715-32	24
1659	MatrixDB, a database focused on extracellular protein-protein and protein-carbohydrate interactions. 2009 , 25, 690-1	85
1658	Rapid evolution of functional complexity in a domain family. 2009 , 2, ra50	47
1657	Integrative analysis of genome-wide RNA interference screens. 2009, 2, pt4	8
1656	Graph Partitioning Method for Functional Module Detections of Protein Interaction Network. 2009,	6
1655	Change in gene expression of mouse embryonic stem cells derived from parthenogenetic activation. 2009 , 24, 805-14	19
1654	L'āriture augmentē. 2009 ,	1
1653	Longitudinal system-based analysis of transcriptional responses to type I interferons. 2009 , 38, 362-71	25
1652	Physiological and toxicological transcriptome changes in HepG2 cells exposed to copper. 2009 , 38, 386-401	52
1651	Global analysis of protein damage by the lipid electrophile 4-hydroxy-2-nonenal. 2009, 8, 670-80	120
1650	Global networks of functional coupling in eukaryotes from comprehensive data integration. <i>Genome Research</i> , 2009 , 19, 1107-16	123

	Novel regulators of Fgf23 expression and mineralization in Hyp bone. 2009 , 23, 1505-18	97
1648	VisANT 3.5: multi-scale network visualization, analysis and inference based on the gene ontology. 2009 , 37, W115-21	154
1647	Bruton's tyrosine kinase revealed as a negative regulator of Wnt-beta-catenin signaling. 2009 , 2, ra25	47
1646	Cohesive versus flexible evolution of functional modules in eukaryotes. 2009 , 5, e1000276	15
1645	Evolutionarily conserved herpesviral protein interaction networks. 2009 , 5, e1000570	133
1644	Biomedical discovery acceleration, with applications to craniofacial development. 2009 , 5, e1000215	52
1643	Annotation error in public databases: misannotation of molecular function in enzyme superfamilies. 2009 , 5, e1000605	464
1642	Bayesian modeling of the yeast SH3 domain interactome predicts spatiotemporal dynamics of endocytosis proteins. 2009 , 7, e1000218	151
1641	Webb Miller and Trey Ideker to receive top international bioinformatics awards for 2009 from the International Society for Computational Biology. 2009 , 5, e1000375	
1640	Biomedical text mining and its applications. 2009 , 5, e1000597	63
1640 1639	Biomedical text mining and its applications. 2009 , 5, e1000597 Integrating computational biology and forward genetics in Drosophila. 2009 , 5, e1000351	63
	Integrating computational biology and forward genetics in Drosophila. 2009 , 5, e1000351	
1639	Integrating computational biology and forward genetics in Drosophila. 2009 , 5, e1000351 Genome-wide association data reveal a global map of genetic interactions among protein	24
1639 1638	Integrating computational biology and forward genetics in Drosophila. 2009, 5, e1000351 Genome-wide association data reveal a global map of genetic interactions among protein complexes. 2009, 5, e1000782 A CitationRank algorithm inheriting Google technology designed to highlight genes responsible for	24 51
1639 1638 1637	Integrating computational biology and forward genetics in Drosophila. 2009, 5, e1000351 Genome-wide association data reveal a global map of genetic interactions among protein complexes. 2009, 5, e1000782 A CitationRank algorithm inheriting Google technology designed to highlight genes responsible for serious adverse drug reaction. 2009, 25, 2244-50 A differential wiring analysis of expression data correctly identifies the gene containing the causal	24 51 22
1639 1638 1637	Integrating computational biology and forward genetics in Drosophila. 2009, 5, e1000351 Genome-wide association data reveal a global map of genetic interactions among protein complexes. 2009, 5, e1000782 A CitationRank algorithm inheriting Google technology designed to highlight genes responsible for serious adverse drug reaction. 2009, 25, 2244-50 A differential wiring analysis of expression data correctly identifies the gene containing the causal mutation. 2009, 5, e1000382 Interactome analyses identify ties of PrP and its mammalian paralogs to oligomannosidic N-glycans	24 51 22 150
1639 1638 1637 1636	Integrating computational biology and forward genetics in Drosophila. 2009, 5, e1000351 Genome-wide association data reveal a global map of genetic interactions among protein complexes. 2009, 5, e1000782 A CitationRank algorithm inheriting Google technology designed to highlight genes responsible for serious adverse drug reaction. 2009, 25, 2244-50 A differential wiring analysis of expression data correctly identifies the gene containing the causal mutation. 2009, 5, e1000382 Interactome analyses identify ties of PrP and its mammalian paralogs to oligomannosidic N-glycans and endoplasmic reticulum-derived chaperones. 2009, 5, e1000608 Coordinated regulation of virulence during systemic infection of Salmonella enterica serovar	24 51 22 150

1631	Challenges and rewards of interaction proteomics. 2009 , 8, 3-18	72
1630	SciMiner: web-based literature mining tool for target identification and functional enrichment analysis. 2009 , 25, 838-40	69
1629	Michigan molecular interactions r2: from interacting proteins to pathways. 2009 , 37, D642-6	78
1628	Human cancer protein-protein interaction network: a structural perspective. 2009 , 5, e1000601	150
1627	Using network component analysis to dissect regulatory networks mediated by transcription factors in yeast. 2009 , 5, e1000311	26
1626	Capturing the spectrum of interaction effects in genetic association studies by simulated evaporative cooling network analysis. 2009 , 5, e1000432	66
1625	A mapping of drug space from the viewpoint of small molecule metabolism. 2009 , 5, e1000474	30
1624	Identifying drug effects via pathway alterations using an integer linear programming optimization formulation on phosphoproteomic data. 2009 , 5, e1000591	96
1623	Functional states of the genome-scale Escherichia coli transcriptional regulatory system. 2009 , 5, e1000403	31
1622	Shwachman-Bodian Diamond syndrome is a multi-functional protein implicated in cellular stress responses. 2009 , 18, 3684-95	58
1621	Construction and application of a protein and genetic interaction network (yeast interactome). 2009 , 37, e54	7
1620	A comparative genomics, network-based approach to understanding virulence in Vibrio cholerae. 2009 , 191, 6262-72	9
1619	Computational identification of potential molecular interactions in Arabidopsis. 2009, 151, 34-46	23
1618	PathBuilderopen source software for annotating and developing pathway resources. 2009 , 25, 2860-2	35
1617	Systems-level comparison of host-responses elicited by avian H5N1 and seasonal H1N1 influenza viruses in primary human macrophages. 2009 , 4, e8072	92
1616	The macrophage colony-stimulating factor 1 response signature in breast carcinoma. 2009 , 15, 778-87	138
1615	RiceGeneThresher: a web-based application for mining genes underlying QTL in rice genome. 2009 , 37, D996-1000	10
1614	Dynamic and complex transcription factor binding during an inducible response in yeast. 2009 , 23, 1351-63	77

1613	Comparative analysis and unification of domain-domain interaction networks. 2009 , 25, 3020-5		22
1612	POLAR MAPPER: a computational tool for integrated visualization of protein interaction networks and mRNA expression data. 2009 , 6, 881-96		9
1611	Large-scale proteomics analysis of the human kinome. 2009 , 8, 1751-64		236
1610	The human protein coevolution network. <i>Genome Research</i> , 2009 , 19, 1861-71	9.7	39
1609	Model-based redesign of global transcription regulation. 2009 , 37, e38		27
1608	Dynamic reprogramming of transcription factors to and from the subtelomere. <i>Genome Research</i> , 2009 , 19, 1014-25	9.7	15
1607	Combinatorial network of primary and secondary microRNA-driven regulatory mechanisms. 2009 , 37, 5969-80		62
1606	Human microRNAs co-silence in well-separated groups and have different predicted essentialities. 2009 , 25, 1063-9		31
1605	Detection of treatment-induced changes in signaling pathways in gastrointestinal stromal tumors using transcriptomic data. 2009 , 69, 9125-32		50
1604	Mapping and characterization of two relevance networks from SNP and gene levels. 2009 , 19, 653-657		1
1603	The global cysteine peptidase landscape in parasites. 2009 , 25, 573-81		68
1602	Early gene expression changes during embryonic stem cell differentiation into cardiomyocytes and their modulation by monobutyl phthalate. 2009 , 27, 93-102		65
1601	Aging defined by a chronologic-replicative protein network in Saccharomyces cerevisiae: an interactome analysis. 2009 , 130, 444-60		13
1600	POINeT: protein interactome with sub-network analysis and hub prioritization. 2009 , 10, 114		40
1599	Seeking unique and common biological themes in multiple gene lists or datasets: pathway pattern extraction pipeline for pathway-level comparative analysis. 2009 , 10, 200		14
1598	mSpecs: a software tool for the administration and editing of mass spectral libraries in the field of metabolomics. 2009 , 10, 229		4
1597	The B6 database: a tool for the description and classification of vitamin B6-dependent enzymatic activities and of the corresponding protein families. 2009 , 10, 273		179
1596	VANLOinteractive visual exploration of aligned biological networks. 2009 , 10, 327		9

1595	Arabidopsis gene co-expression network and its functional modules. 2009 , 10, 346	141
1594	Phylogeny-guided interaction mapping in seven eukaryotes. 2009 , 10, 393	13
1593	Bioclipse 2: a scriptable integration platform for the life sciences. 2009 , 10, 397	46
1592	Exploring complex miRNA-mRNA interactions with Bayesian networks by splitting-averaging strategy. 2009 , 10, 408	58
1591	In silico evaluation of predicted regulatory interactions in Arabidopsis thaliana. 2009 , 10, 435	3
1590	Gene set-based module discovery in the breast cancer transcriptome. 2009 , 10, 71	23
1589	Disease candidate gene identification and prioritization using protein interaction networks. 2009 , 10, 73	247
1588	JNets: exploring networks by integrating annotation. 2009 , 10, 95	10
1587	Markov clustering versus affinity propagation for the partitioning of protein interaction graphs. 2009 , 10, 99	148
1586	A new graph-based method for pairwise global network alignment. 2009 , 10 Suppl 1, S59	130
1585	NATbox: a network analysis toolbox in R. 2009 , 10 Suppl 11, S14	4
1584		
	Structural and functional-annotation of an equine whole genome oligoarray. 2009 , 10 Suppl 11, S8	18
1583	Structural and functional-annotation of an equine whole genome oligoarray. 2009 , 10 Suppl 11, S8 Protopia: a protein-protein interaction tool. 2009 , 10 Suppl 12, S17	18
1583 1582		
	Protopia: a protein-protein interaction tool. 2009 , 10 Suppl 12, S17 Identification of functionally related genes using data mining and data integration: a breast cancer	9
1582	Protopia: a protein-protein interaction tool. 2009 , 10 Suppl 12, S17 Identification of functionally related genes using data mining and data integration: a breast cancer case study. 2009 , 10 Suppl 12, S8 Leveraging existing biological knowledge in the identification of candidate genes for facial dysmorphology. 2009 , 10 Suppl 2, S12	9
1582 1581	Protopia: a protein-protein interaction tool. 2009 , 10 Suppl 12, S17 Identification of functionally related genes using data mining and data integration: a breast cancer case study. 2009 , 10 Suppl 12, S8 Leveraging existing biological knowledge in the identification of candidate genes for facial dysmorphology. 2009 , 10 Suppl 2, S12	9 16 14

(2009-2009)

1577	Uncovering new signaling proteins and potential drug targets through the interactome analysis of Mycobacterium tuberculosis. 2009 , 10, 118	66
1576	Transcription and splicing regulation in human umbilical vein endothelial cells under hypoxic stress conditions by exon array. 2009 , 10, 126	43
1575	Reconstruction and functional analysis of altered molecular pathways in human atherosclerotic arteries. 2009 , 10, 13	67
1574	A network-based integrative approach to prioritize reliable hits from multiple genome-wide RNAi screens in Drosophila. 2009 , 10, 220	33
1573	BioQuali Cytoscape plugin: analysing the global consistency of regulatory networks. 2009 , 10, 244	20
1572	A genome-wide deletion mutant screen identifies pathways affected by nickel sulfate in Saccharomyces cerevisiae. 2009 , 10, 524	32
1571	Colorectal cancer cell-derived microvesicles are enriched in cell cycle-related mRNAs that promote proliferation of endothelial cells. 2009 , 10, 556	312
1570	Transcriptomic response of the mycoparasitic fungus Trichoderma atroviride to the presence of a fungal prey. 2009 , 10, 567	118
1569	Deciphering the transcriptional circuitry of microRNA genes expressed during human monocytic differentiation. 2009 , 10, 595	57
1568	Filling gaps in PPAR-alpha signaling through comparative nutrigenomics analysis. 2009 , 10, 596	8
1567	Genome-wide prediction of cis-acting RNA elements regulating tissue-specific pre-mRNA alternative splicing. 2009 , 10 Suppl 1, S4	20
1566	BioNetBuilder2.0: bringing systems biology to chicken and other model organisms. 2009 , 10 Suppl 2, S6	13
1565	Alternative paths in HIV-1 targeted human signal transduction pathways. 2009 , 10 Suppl 3, S30	16
1564	Five QTL hotspots for yield in short rotation coppice bioenergy poplar: the Poplar Biomass Loci. 2009 , 9, 23	60
1563	Identification of tyrosine-phosphorylated proteins associated with metastasis and functional analysis of FER in human hepatocellular carcinoma cells. 2009 , 9, 366	53
1562	SNAVI: Desktop application for analysis and visualization of large-scale signaling networks. 2009 , 3, 10	23
1561	Human synthetic lethal inference as potential anti-cancer target gene detection. 2009, 3, 116	33
1560	FORG3D: force-directed 3D graph editor for visualization of integrated genome scale data. 2009 , 3, 26	9

1559	Identifying disease-specific genes based on their topological significance in protein networks. 2009 , 3, 36	95
1558	Connecting extracellular metabolomic measurements to intracellular flux states in yeast. 2009 , 3, 37	330
1557	Genetic and environmental pathways to complex diseases. 2009 , 3, 46	62
1556	A system biology approach highlights a hormonal enhancer effect on regulation of genes in a nitrate responsive "biomodule". 2009 , 3, 59	43
1555	The Symbiosis Interactome: a computational approach reveals novel components, functional interactions and modules in Sinorhizobium meliloti. 2009 , 3, 63	8
1554	BowTieBuilder: modeling signal transduction pathways. 2009 , 3, 67	33
1553	Adapted Boolean network models for extracellular matrix formation. 2009, 3, 77	14
1552	Visualizing post genomics data-sets on customized pathway maps by ProMeTra-aeration-dependent gene expression and metabolism of Corynebacterium glutamicum as an example. 2009 , 3, 82	56
1551	The crosstalk between EGF, IGF, and Insulin cell signaling pathwayscomputational and experimental analysis. 2009 , 3, 88	41
1550	Network module detection: Affinity search technique with the multi-node topological overlap measure. 2009 , 2, 142	35
1549	Computing consistency between microarray data and known gene regulation relationships. 2009 , 13, 1075-82	2
1548	Differential HIV-1 integration targets more actively transcribed host genes in neonatal than adult blood mononuclear cells. 2009 , 385, 28-38	12
1547	Screening a genome-wide S. pombe deletion library identifies novel genes and pathways involved in genome stability maintenance. 2009 , 8, 672-9	47
1546	Bioinformatics analysis of mass spectrometry-based proteomics data sets. 2009 , 583, 1703-12	123
1545	Filling and mining the reactive metabolite target protein database. 2009, 179, 38-44	30
1544	Identification of novel hub genes associated with liver metastasis of gastric cancer. 2009 , 125, 2844-53	54
1543	Developmental shifts in gene expression in the auditory forebrain during the sensitive period for song learning. 2009 , 69, 437-50	46
1542	Dynamical approaches to modeling developmental gene regulatory networks. 2009 , 87, 131-42	11

(2009-2009)

1541	neoplasms. 2009 , 388, 5057-5069	15
1540	Computational challenges in systems biology. 2009 , 3, 1-17	29
1539	Target selection and annotation for the structural genomics of the amidohydrolase and enolase superfamilies. 2009 , 10, 107-25	24
1538	A survey of integral alpha-helical membrane proteins. 2009 , 10, 269-80	12
1537	In silico construction of a protein interaction landscape for nucleotide excision repair. 2009 , 53, 101-14	O
1536	Intercalated discs: multiple proteins perform multiple functions in non-failing and failing human hearts. 2009 , 1, 43	36
1535	PIAS proteins: pleiotropic interactors associated with SUMO. 2009 , 66, 3029-41	201
1534	Desmosomal interactome in keratinocytes: a systems biology approach leading to an understanding of the pathogenesis of skin disease. 2009 , 66, 3517-33	24
1533	Analyse und Visualisierung biologischer Netzwerke. 2009 , 32, 301-309	
1532	Dissecting the human plasma proteome and inflammatory response biomarkers. 2009 , 9, 470-84	15
1531	Recent developments in public proteomic MS repositories and pipelines. 2009, 9, 861-81	40
1530	PPI spider: a tool for the interpretation of proteomics data in the context of protein-protein interaction networks. 2009 , 9, 2740-9	56
1529	The properties of hub proteins in a yeast-aggregated cell cycle network and its phase sub-networks. 2009 , 9, 4812-24	9
1528	High-accuracy identification and bioinformatic analysis of in vivo protein phosphorylation sites in yeast. 2009 , 9, 4642-52	103
1527	Systematic prediction of human membrane receptor interactions. 2009 , 9, 5243-55	16
1526	The Interactorium: visualising proteins, complexes and interaction networks in a virtual 3-D cell. 2009 , 9, 5309-15	7
1525	Identification of group specific motifs in beta-lactamase family of proteins. 2009, 16, 109	15
1524	myGRN: a database and visualisation system for the storage and analysis of developmental genetic regulatory networks. 2009 , 9, 33	3

1523	Bioinformatic analysis of xenobiotic reactive metabolite target proteins and their interacting partners. 2009 , 9, 5	19
1522	Construction of a polycystic ovarian syndrome (PCOS) pathway based on the interactions of PCOS-related proteins retrieved from bibliomic data. 2009 , 6, 18	21
1521	The apoptotic machinery as a biological complex system: analysis of its omics and evolution, identification of candidate genes for fourteen major types of cancer, and experimental validation in CML and neuroblastoma. 2009 , 2, 20	18
1520	Network analysis of human glaucomatous optic nerve head astrocytes. 2009 , 2, 24	40
1519	Identification of the Arabidopsis dry2/sqe1-5 mutant reveals a central role for sterols in drought tolerance and regulation of reactive oxygen species. 2009 , 59, 63-76	87
1518	Theoretical framework for the histone modification network: modifications in the unstructured histone tails form a robust scale-free network. 2009 , 14, 789-806	12
1517	More synergetic cooperation of Yamanaka factors in induced pluripotent stem cells than in embryonic stem cells. 2009 , 19, 1127-38	44
1516	Temporal and spatial profiling of nuclei-associated proteins upon TNF-alpha/NF-kappaB signaling. 2009 , 19, 651-64	16
1515	Genome-wide analysis of Notch signalling in Drosophila by transgenic RNAi. 2009 , 458, 987-92	245
1514	Predicting new molecular targets for known drugs. 2009 , 462, 175-81	1212
1514 1513	Predicting new molecular targets for known drugs. 2009, 462, 175-81 Dynamic modularity in protein interaction networks predicts breast cancer outcome. 2009, 27, 199-204	1212 568
1513	Dynamic modularity in protein interaction networks predicts breast cancer outcome. 2009 , 27, 199-204 Mass-spectrometric identification and relative quantification of N-linked cell surface glycoproteins.	568
1513 1512	Dynamic modularity in protein interaction networks predicts breast cancer outcome. 2009 , 27, 199-204 Mass-spectrometric identification and relative quantification of N-linked cell surface glycoproteins. 2009 , 27, 378-86	568 422
1513 1512 1511	Dynamic modularity in protein interaction networks predicts breast cancer outcome. 2009 , 27, 199-204 Mass-spectrometric identification and relative quantification of N-linked cell surface glycoproteins. 2009 , 27, 378-86 Proteomics strategy for quantitative protein interaction profiling in cell extracts. 2009 , 6, 741-4 Tn-seq: high-throughput parallel sequencing for fitness and genetic interaction studies in	568 422 121
1513 1512 1511 1510	Dynamic modularity in protein interaction networks predicts breast cancer outcome. 2009 , 27, 199-204 Mass-spectrometric identification and relative quantification of N-linked cell surface glycoproteins. 2009 , 27, 378-86 Proteomics strategy for quantitative protein interaction profiling in cell extracts. 2009 , 6, 741-4 Tn-seq: high-throughput parallel sequencing for fitness and genetic interaction studies in microorganisms. 2009 , 6, 767-72	568 422 121 595
1513 1512 1511 1510 1509	Dynamic modularity in protein interaction networks predicts breast cancer outcome. 2009, 27, 199-204 Mass-spectrometric identification and relative quantification of N-linked cell surface glycoproteins. 2009, 27, 378-86 Proteomics strategy for quantitative protein interaction profiling in cell extracts. 2009, 6, 741-4 Tn-seq: high-throughput parallel sequencing for fitness and genetic interaction studies in microorganisms. 2009, 6, 767-72 My5C: web tools for chromosome conformation capture studies. 2009, 6, 690-1 A general pipeline for quality and statistical assessment of protein interaction data using R and	568 422 121 595 74

1505	Identifying coevolutionary patterns in human leukocyte antigen (HLA) molecules. 2010 , 64, 1429-45	3
1504	A network inference workflow applied to virulence-related processes in Salmonella typhimurium. 2009 , 1158, 143-58	4
1503	TRANSCRIPTIONAL ANALYSIS OF THE UNICELLULAR, DIAZOTROPHIC CYANOBACTERIUM CYANOTHECE SP. ATCC 51142 GROWN UNDER SHORT DAY/NIGHT CYCLES(1). 2009 , 45, 610-20	27
1502	Proteome analysis of a human liver carcinoma cell line stably expressing hepatitis delta virus ribonucleoproteins. 2009 , 72, 616-27	20
1501	Nuclear factor-kappaB bioluminescence imaging-guided transcriptomic analysis for the assessment of host-biomaterial interaction in vivo. 2009 , 30, 3042-9	33
1500	The phagosomal proteome in interferon-gamma-activated macrophages. 2009 , 30, 143-54	177
1499	Gene regulatory network inference: data integration in dynamic models-a review. 2009 , 96, 86-103	537
1498	Identification of microRNA expression patterns and definition of a microRNA/mRNA regulatory network in distinct molecular groups of multiple myeloma. 2009 , 114, e20-6	213
1497	Functional analysis of OMICs data and small molecule compounds in an integrated "knowledge-based" platform. 2009 , 563, 177-96	63
1496	Systems Approach for Understanding Metastasis. 2009 , 383-394	
1495	Integrating proteomic, transcriptional, and interactome data reveals hidden components of signaling and regulatory networks. 2009 , 2, ra40	137
1494	Systems biology approaches and pathway tools for investigating cardiovascular disease. 2009 , 5, 588-602	82
1493	MAPK target networks in Arabidopsis thaliana revealed using functional protein microarrays. 2009 , 23, 80-92	370
1492	Top-down identification of protein biomarkers in bacteria with unsequenced genomes. 2009 , 81, 9633-42	66
1491	Proteomic analysis of chemonaive pediatric osteosarcomas and corresponding normal bone reveals multiple altered molecular targets. 2009 , 8, 3882-8	33
1490	Annotating enzymes of uncertain function: the deacylation of D-amino acids by members of the amidohydrolase superfamily. 2009 , 48, 6469-81	13
1489	FPPI: Fusarium graminearum protein-protein interaction database. 2009 , 8, 4714-21	52
1488	ATP-sensitive K+ channel knockout induces cardiac proteome remodeling predictive of heart disease susceptibility. 2009 , 8, 4823-34	32

1487	Knowledge-based characterization of similarity relationships in the human protein-tyrosine phosphatase family for rational inhibitor design. 2009 , 52, 6649-59	9
1486	Fishing the target of antitubercular compounds: in silico target deconvolution model development and validation. 2009 , 8, 2788-98	26
1485	Linking high-resolution metabolic flux phenotypes and transcriptional regulation in yeast modulated by the global regulator Gcn4p. 2009 , 106, 6477-82	134
1484	PubChem as a source of polypharmacology. 2009 , 49, 2044-55	118
1483	Assessing the impact of network depth on the analysis of PPI networks: A case study. 2009,	О
1482	Caenorhabditis elegans has a phosphoproteome atypical for metazoans that is enriched in developmental and sex determination proteins. 2009 , 8, 4039-49	59
1481	Visualization, documentation, analysis, and communication of large-scale gene regulatory networks. 2009 , 1789, 363-74	83
1480	Shotgun proteomics in neuroscience. 2009 , 63, 12-26	44
1479	Systems based mapping demonstrates that recovery from alkylation damage requires DNA repair, RNA processing, and translation associated networks. 2009 , 93, 42-51	15
1478	Construction of a functional network for common DNA damage responses in Escherichia coli. 2009 , 93, 514-24	8
1477	14-3-3 Proteins: insights from genome-wide studies in yeast. 2009 , 94, 287-93	46
1476	Investigating transcriptional regulation: from analysis of complex networks to discovery of cis-regulatory elements. 2009 , 48, 277-86	2
1475	Enabling a systems biology approach to immunology: focus on innate immunity. 2009 , 30, 249-62	96
1474	Transcript elongation factor TFIIS is involved in arabidopsis seed dormancy. 2009 , 386, 598-611	59
1473	Transcriptional response to mitochondrial NADH kinase deficiency in Saccharomyces cerevisiae. 2009 , 9, 211-21	4
1472	Cytoscape: a community-based framework for network modeling. 2009 , 563, 219-39	150
1471	Biological Network Inference and analysis using SEBINI and CABIN. 2009, 541, 551-76	8
1470	Solution and crystal molecular dynamics simulation study of m4-cyanovirin-N mutants complexed with di-mannose. 2009 , 97, 2532-40	32

1469	Predicting drug side-effects by chemical systems biology. 2009 , 10, 238	51
1468	Glutathione transferases are structural and functional outliers in the thioredoxin fold. 2009 , 48, 11108-16	107
1467	An atlas of the thioredoxin fold class reveals the complexity of function-enabling adaptations. 2009 , 5, e1000541	101
1466	Mapping adverse drug reactions in chemical space. 2009 , 52, 3103-7	136
1465	Systems biology evaluation of immune responses induced by human host defence peptide LL-37 in mononuclear cells. 2009 , 5, 483-96	75
1464	Deciphering peculiar protein-protein interacting modules in Deinococcus radiodurans. 2009 , 4, 12	3
1463	Evolution of enzymatic activities in the enolase superfamily: stereochemically distinct mechanisms in two families of cis,cis-muconate lactonizing enzymes. 2009 , 48, 1445-53	34
1462	The EVER proteins as a natural barrier against papillomaviruses: a new insight into the pathogenesis of human papillomavirus infections. 2009 , 73, 348-70	97
1461	A global view of protein expression in human cells, tissues, and organs. 2009 , 5, 337	142
1460	Structural interactomics: informatics approaches to aid the interpretation of genetic variation and the development of novel therapeutics. 2009 , 5, 1456-72	8
1459	Network-assisted protein identification and data interpretation in shotgun proteomics. 2009 , 5, 303	45
1458	Identification of cis-regulatory elements in gene co-expression networks using A-GLAM. 2009 , 541, 1-22	10
1457	Breaking the hierarchya new cluster selection mechanism for hierarchical clustering methods. 2009 , 4, 12	13
1456	Regulatory interdependence of myeloid transcription factors revealed by Matrix RNAi analysis. 2009 , 10, R121	14
1455	Reverse-engineering the Arabidopsis thaliana transcriptional network under changing environmental conditions. 2009 , 10, R96	59
1454	Gene networks in Drosophila melanogaster: integrating experimental data to predict gene function. 2009 , 10, R97	38
1453	The conservation and evolutionary modularity of metabolism. 2009 , 10, R63	99
1452	Insights into female sperm storage from the spermathecal fluid proteome of the honeybee Apis mellifera. 2009 , 10, R67	84

1451	Global expression analysis of the brown alga Ectocarpus siliculosus (Phaeophyceae) reveals large-scale reprogramming of the transcriptome in response to abiotic stress. 2009 , 10, R66	113
1450	The Cell Cycle Ontology: an application ontology for the representation and integrated analysis of the cell cycle process. 2009 , 10, R58	26
1449	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. 2009 , 10, R39	56
1448	Reconstructing the ubiquitin network: cross-talk with other systems and identification of novel functions. 2009 , 10, R33	29
1447	Using prior knowledge and genome-wide association to identify pathways involved in multiple sclerosis. 2009 , 1, 65	21
1446	Systems medicine: the future of medical genomics and healthcare. 2009 , 1, 2	279
1445	Strategies for efficient disruption of metabolism in Mycobacterium tuberculosis from network analysis. 2009 , 5, 1740-51	28
1444	Pattern discovery in expression profiling data. 2009 , Chapter 22, Unit 22.5	8
1443	Enzyme kinetics and computational modeling for systems biology. 2009 , 467, 583-599	19
1442	. 2009,	
1442 1441	. 2009, High-confidence mapping of chemical compounds and protein complexes reveals novel aspects of chemical stress response in yeast. 2010, 6, 175-81	12
	High-confidence mapping of chemical compounds and protein complexes reveals novel aspects of	12
1441	High-confidence mapping of chemical compounds and protein complexes reveals novel aspects of chemical stress response in yeast. 2010 , 6, 175-81 Mining gene functional networks to improve mass-spectrometry-based protein identification. 2009 ,	
1441 1440	High-confidence mapping of chemical compounds and protein complexes reveals novel aspects of chemical stress response in yeast. 2010 , 6, 175-81 Mining gene functional networks to improve mass-spectrometry-based protein identification. 2009 , 25, 2955-61 A Semiautomatic Method to Achieve Independent and Intact Gene Ontology Slim (InitGO) and its	
1441 1440 1439	High-confidence mapping of chemical compounds and protein complexes reveals novel aspects of chemical stress response in yeast. 2010, 6, 175-81 Mining gene functional networks to improve mass-spectrometry-based protein identification. 2009, 25, 2955-61 A Semiautomatic Method to Achieve Independent and Intact Gene Ontology Slim (InitGO) and its Cytoscape Plugin Implementation. 2009, Possible Occurrence of Scale-Free Topology in Highly Statistically Associated Polymorphic Positions	31
1441 1440 1439 1438	High-confidence mapping of chemical compounds and protein complexes reveals novel aspects of chemical stress response in yeast. 2010, 6, 175-81 Mining gene functional networks to improve mass-spectrometry-based protein identification. 2009, 25, 2955-61 A Semiautomatic Method to Achieve Independent and Intact Gene Ontology Slim (InitGO) and its Cytoscape Plugin Implementation. 2009, Possible Occurrence of Scale-Free Topology in Highly Statistically Associated Polymorphic Positions in Two Potyviral Proteins. 2009, Applying Graph Theory on Protein - Protein Interaction Data. 2009,	31
1441 1440 1439 1438	High-confidence mapping of chemical compounds and protein complexes reveals novel aspects of chemical stress response in yeast. 2010, 6, 175-81 Mining gene functional networks to improve mass-spectrometry-based protein identification. 2009, 25, 2955-61 A Semiautomatic Method to Achieve Independent and Intact Gene Ontology Slim (InitGO) and its Cytoscape Plugin Implementation. 2009, Possible Occurrence of Scale-Free Topology in Highly Statistically Associated Polymorphic Positions in Two Potyviral Proteins. 2009, Applying Graph Theory on Protein - Protein Interaction Data. 2009,	31 O

1433 Visualizing a Correlative Multi-level Graph of Biology Entity Interactions. 2009,

1432 Revealing biological modules via graph summarization. 2009 , 16, 253-64	40
Comprehensive evaluation of a novel nuclear factor-kappaB inhibitor, quinoclamine, by transcriptomic analysis. 2009 , 157, 746-56	10
GeneShelf: a web-based visual interface for large gene expression time-series data repositories. 2009 , 15, 905-12	9
1429 Prioritizing genes for pathway impact using network analysis. 2009 , 563, 141-56	5
Pathway enrichment based on text mining and its validation on carotenoid and vitamin A metabolism. 2009 , 13, 367-79	9
Mapping human metabolic pathways in the small molecule chemical space. 2009 , 49, 2272-89	10
Pathway databases and tools for their exploitation: benefits, current limitations and challenges. 2009 , 5, 290	144
1425 Biological Resource Centers and Systems Biology. 2009 , 59, 113-125	3
Histogenomics: association of gene expression patterns with histological parameters in kidney biopsies. 2009 , 87, 290-5	35
Network graph analysis of category fluency testing. 2009 , 22, 45-52	29
Computational Methods to Identify Transcription Factor Binding Sites Using CAGE Information. 2009 , 137-151	
Tomato transcriptional responses to a foliar and a vascular fungal pathogen are distinct. 2009 , 22, 245-58	44
An Efficient Method to Identify Conditionally Activated Transcription Factors and their Corresponding Signal Transduction Pathway Segments. 2009 , 3, 179-87	
Muscle genome-wide expression profiling during disease evolution in mdx mice. 2009 , 37, 119-32	41
1418 Genomics software: The view from 10,000 feet. 2009 , 4, 56-8	
Isolation stress for 30 days alters hepatic gene expression profiles, especially with reference to lipid metabolism in mice. 2009 , 37, 79-87	18
1416 AtPIN: Arabidopsis thaliana protein interaction network. 2009 , 10, 454	76

1415	Graph methods for the investigation of metabolic networks in parasitology. 2010 , 137, 1393-407	17
1414	Functional modularity of nuclear hormone receptors in a Caenorhabditis elegans metabolic gene regulatory network. 2010 , 6, 367	65
1413	Strategies for online inference of model-based clustering in large and growing networks. 2010 , 4,	18
1412	Computational Models for Condition-Specific Gene and Pathway Inference. 2010 , 665-689	
1411	Novel systems biology insights using antifibrotic approaches for diabetic kidney disease. 2010 , 5, 127-135	1
1410	An integrated model for visualizing biclusters from gene expression data and PPI networks. 2010 ,	
1409	Systems Biology and TOR. 2010 , 28, 317-348	1
1408	Early Career Research Award Lecture. Structure, evolution and dynamics of transcriptional regulatory networks. 2010 , 38, 1155-78	18
1407	Exploring target-selectivity patterns of molecular scaffolds. 2010 , 1, 54-8	14
1406	Protein-Protein Interaction Network and Gene Ontology. 2010 , 159-169	1
1405	The use of network analyses for elucidating mechanisms in cardiovascular disease. 2010 , 6, 289-304	76
1404	From experimental setup to bioinformatics: an RNAi screening platform to identify host factors involved in HIV-1 replication. 2010 , 5, 39-49	36
1403	Protein-to-protein interactions. 2010 , 43, 1-36	65
1402	Current Progress in Static and Dynamic Modeling of Biological Networks. 2010 , 13-73	3
1401	Visuelle Analytik biologischer Daten. 2010 , 33, 559-568	
1400	Reconstruction of gene association network reveals a transmembrane protein required for adipogenesis and targeted by PPARII 2010 , 67, 4049-64	32
1399	Proteomics for quality-control processes in transfusion medicine. 2010 , 398, 111-24	11
1398	Temporal patterns in glycolate-utilizing bacterial community composition correlate with phytoplankton population dynamics in humic lakes. 2010 , 60, 406-18	32

1397	Integrated protein network and microarray analysis to identify potential biomarkers after myocardial infarction. 2010 , 10, 329-37	27
1396	The NetAge database: a compendium of networks for longevity, age-related diseases and associated processes. 2010 , 11, 513-22	66
1395	Interaction networks as a tool to investigate the mechanisms of aging. 2010 , 11, 463-73	14
1394	A mouse protein interactome through combined literature mining with multiple sources of interaction evidence. 2010 , 38, 1237-52	21
1393	Enriching the viral-host interactomes with interactions mediated by SH3 domains. 2010 , 38, 1541-7	7
1392	Cytochrome P450 networks in chemical space. 2010 , 33, 1361-74	3
1391	Quantitative proteomic analysis of S-nitrosated proteins in diabetic mouse liver with ICAT switch method. 2010 , 1, 675-87	21
1390	Revealing system-level correlations between aging and calorie restriction using a mouse transcriptome. 2010 , 32, 15-30	17
1389	Metagenomics: Facts and Artifacts, and Computational Challenges*. 2009, 25, 71-81	98
1388	A linear programming model based on network flow for pathway inference. 2010 , 23, 971-977	
1387	Protein-protein interaction networks suggest different targets have different propensities for triggering drug resistance. 2010 , 4, 311-22	18
1386	A preliminary approach to creating an overview of lactoferrin multi-functionality utilizing a text mining method. 2010 , 23, 453-63	2
1385	Use of reconstituted metabolic networks to assist in metabolomic data visualization and mining. 2010 , 6, 312-321	27
1384	A gene family encoding RING finger proteins in rice: their expansion, expression diversity, and co-expressed genes. 2010 , 72, 369-80	62
1383	Belief Propagation Estimation of Protein and Domain Interactions Using the Sum B roduct Algorithm. 2010 , 56, 742-755	3
1382	Information technology solutions for integration of biomolecular and clinical data in the identification of new cancer biomarkers and targets for therapy. 2010 , 128, 488-98	10
1382	identification of new cancer biomarkers and targets for therapy. 2010 , 128, 488-98 AutoSOME: a clustering method for identifying gene expression modules without prior knowledge	10 77

1379	Response network analysis of differential gene expression in human epithelial lung cells during avian influenza infections. 2010 , 11, 170	15
1378	Consolidating metabolite identifiers to enable contextual and multi-platform metabolomics data analysis. 2010 , 11, 214	34
1377	GOAL: a software tool for assessing biological significance of genes groups. 2010 , 11, 229	22
1376	Towards the systematic discovery of signal transduction networks using phosphorylation dynamics data. 2010 , 11, 232	13
1375	Detecting disease associated modules and prioritizing active genes based on high throughput data. 2010 , 11, 26	62
1374	Functional enrichment analyses and construction of functional similarity networks with high confidence function prediction by PFP. 2010 , 11, 265	16
1373	LucidDraw: efficiently visualizing complex biochemical networks within MATLAB. 2010 , 11, 31	7
1372	Introducing W.A.T.E.R.S.: a workflow for the alignment, taxonomy, and ecology of ribosomal sequences. 2010 , 11, 317	26
1371	An efficient biological pathway layout algorithm combining grid-layout and spring embedder for complicated cellular location information. 2010 , 11, 335	5
1370	Identifying differentially regulated subnetworks from phosphoproteomic data. 2010 , 11, 351	26
1369	Flexible network reconstruction from relational databases with Cytoscape and CytoSQL. 2010, 11, 360	
1368	Integration and visualization of systems biology data in context of the genome. 2010 , 11, 382	24
1367	Consistency, comprehensiveness, and compatibility of pathway databases. 2010 , 11, 449	55
1366	MetNetGE: interactive views of biological networks and ontologies. 2010 , 11, 469	6
1365	Protein network prediction and topological analysis in Leishmania major as a tool for drug target selection. 2010 , 11, 484	60
1364	The BridgeDb framework: standardized access to gene, protein and metabolite identifier mapping services. 2010 , 11, 5	125
1363	MCL-CAw: a refinement of MCL for detecting yeast complexes from weighted PPI networks by incorporating core-attachment structure. 2010 , 11, 504	44
1362	Inferring gene regression networks with model trees. 2010 , 11, 517	20

1361	Biana: a software framework for compiling biological interactions and analyzing networks. 2010 , 11, 56	58
1360	BiologicalNetworks 2.0an integrative view of genome biology data. 2010 , 11, 610	21
1359	A temporal precedence based clustering method for gene expression microarray data. 2010 , 11, 68	9
1358	Lists2Networks: integrated analysis of gene/protein lists. 2010 , 11, 87	34
1357	BisoGenet: a new tool for gene network building, visualization and analysis. 2010, 11, 91	222
1356	A statistical framework for differential network analysis from microarray data. 2010 , 11, 95	107
1355	An ontology-based search engine for protein-protein interactions. 2010 , 11 Suppl 1, S23	3
1354	NeMo: Network Module identification in Cytoscape. 2010 , 11 Suppl 1, S61	93
1353	Modularity of Escherichia coli sRNA regulation revealed by sRNA-target and protein network analysis. 2010 , 11 Suppl 7, S11	7
1352	Positive selection of HIV host factors and the evolution of lentivirus genes. 2010 , 10, 186	12
1351	Assembling networks of microbial genomes using linear programming. 2010 , 10, 360	4
1350	Transcriptomic changes arising during light-induced sporulation in Physarum polycephalum. 2010 , 11, 115	23
1349	Transcriptional profiling of an Fd-GOGAT1/GLU1 mutant in Arabidopsis thaliana reveals a multiple stress response and extensive reprogramming of the transcriptome. 2010 , 11, 190	25
1348	The ancient mammalian KRAB zinc finger gene cluster on human chromosome 8q24.3 illustrates principles of C2H2 zinc finger evolution associated with unique expression profiles in human tissues. 2010 , 11, 206	24
1347	Computational prediction of the osmoregulation network in Synechococcus sp. WH8102. 2010 , 11, 291	12
1346	Prednisolone-induced differential gene expression in mouse liver carrying wild type or a dimerization-defective glucocorticoid receptor. 2010 , 11, 359	91
1345	Proteome-wide survey of phosphorylation patterns affected by nuclear DNA polymorphisms in Arabidopsis thaliana. 2010 , 11, 411	19
1344	A potential role for intragenic miRNAs on their hosts' interactome. 2010 , 11, 533	120

1343	Genome-wide inference of regulatory networks in Streptomyces coelicolor. 2010 , 11, 578	32
1342	Gene duplications in prokaryotes can be associated with environmental adaptation. 2010 , 11, 588	57
1341	Bovine proteins containing poly-glutamine repeats are often polymorphic and enriched for components of transcriptional regulatory complexes. 2010 , 11, 654	13
1340	Perturbation of the yeast N-acetyltransferase NatB induces elevation of protein phosphorylation levels. 2010 , 11, 685	61
1339	Relationship between operon preference and functional properties of persistent genes in bacterial genomes. 2010 , 11, 71	20
1338	Data integration and exploration for the identification of molecular mechanisms in tumor-immune cells interaction. 2010 , 11 Suppl 1, S7	15
1337	Expression profile and specific network features of the apoptotic machinery explain relapse of acute myeloid leukemia after chemotherapy. 2010 , 10, 377	23
1336	Investigation of PARP-1, PARP-2, and PARG interactomes by affinity-purification mass spectrometry. 2010 , 8, 22	114
1335	ReCGiP, a database of reproduction candidate genes in pigs based on bibliomics. 2010 , 8, 96	6
1334	Snazer: the simulations and networks analyzer. 2010 , 4, 1	98
1334	Snazer: the simulations and networks analyzer. 2010 , 4, 1 Minimally perturbing a gene regulatory network to avoid a disease phenotype: the glioma network as a test case. 2010 , 4, 15	98
	Minimally perturbing a gene regulatory network to avoid a disease phenotype: the glioma network	
1333	Minimally perturbing a gene regulatory network to avoid a disease phenotype: the glioma network as a test case. 2010 , 4, 15 Inference of hierarchical regulatory network of estrogen-dependent breast cancer through	14
1333 1332	Minimally perturbing a gene regulatory network to avoid a disease phenotype: the glioma network as a test case. 2010 , 4, 15 Inference of hierarchical regulatory network of estrogen-dependent breast cancer through ChIP-based data. 2010 , 4, 170	14
1333 1332 1331	Minimally perturbing a gene regulatory network to avoid a disease phenotype: the glioma network as a test case. 2010, 4, 15 Inference of hierarchical regulatory network of estrogen-dependent breast cancer through ChIP-based data. 2010, 4, 170 Integrated cellular network of transcription regulations and protein-protein interactions. 2010, 4, 20	14 37 47
1333 1332 1331 1330	Minimally perturbing a gene regulatory network to avoid a disease phenotype: the glioma network as a test case. 2010, 4, 15 Inference of hierarchical regulatory network of estrogen-dependent breast cancer through ChIP-based data. 2010, 4, 170 Integrated cellular network of transcription regulations and protein-protein interactions. 2010, 4, 20 Building and analyzing protein interactome networks by cross-species comparisons. 2010, 4, 36	14 37 47 48
1333 1332 1331 1330 1329	Minimally perturbing a gene regulatory network to avoid a disease phenotype: the glioma network as a test case. 2010, 4, 15 Inference of hierarchical regulatory network of estrogen-dependent breast cancer through ChIP-based data. 2010, 4, 170 Integrated cellular network of transcription regulations and protein-protein interactions. 2010, 4, 20 Building and analyzing protein interactome networks by cross-species comparisons. 2010, 4, 36 OptFlux: an open-source software platform for in silico metabolic engineering. 2010, 4, 45 Construction of a large scale integrated map of macrophage pathogen recognition and effector	14374748258

1325	Construction and analysis of protein-protein interaction networks. 2010 , 2, 2	104
1324	Loss of Caenorhabditis elegans UNG-1 uracil-DNA glycosylase affects apoptosis in response to DNA damaging agents. 2010 , 9, 861-70	13
1323	Protein interaction network underpins concordant prognosis among heterogeneous breast cancer signatures. 2010 , 43, 385-96	45
1322	Gene pathways and subnetworks distinguish between major glioma subtypes and elucidate potential underlying biology. 2010 , 43, 945-52	11
1321	Low malignant potential tumors with micropapillary features are molecularly similar to low-grade serous carcinoma of the ovary. 2010 , 117, 9-17	52
1320	Analysis of chemotherapy response programs in ovarian cancers by the next-generation sequencing technologies. 2010 , 117, 159-69	48
1319	A systems biology approach to understanding atherosclerosis. 2010 , 2, 79-89	57
1318	Sensing the mechanical state of the axoneme and integration of Ca2+ signaling by outer arm dynein. 2010 , 67, 207-13	16
1317	Scaffold distributions in bioactive molecules, clinical trials compounds, and drugs. 2010 , 5, 187-90	22
1316	Modulators of cancer cell invasiveness. 2010 , 111, 791-6	7
1316 1315	Modulators of cancer cell invasiveness. 2010 , 111, 791-6 Architectural repertoire of ligand-binding pockets on protein surfaces. 2010 , 11, 556-63	7
1315		
1315	Architectural repertoire of ligand-binding pockets on protein surfaces. 2010 , 11, 556-63	19
1315	Architectural repertoire of ligand-binding pockets on protein surfaces. 2010 , 11, 556-63 Network-based modeling of the human gut microbiome. 2010 , 7, 1040-50	19
1315 1314 1313	Architectural repertoire of ligand-binding pockets on protein surfaces. 2010 , 11, 556-63 Network-based modeling of the human gut microbiome. 2010 , 7, 1040-50 Subcellular phosphoproteomics. 2010 , 29, 962-90	19 34 35
1315 1314 1313 1312	Architectural repertoire of ligand-binding pockets on protein surfaces. 2010, 11, 556-63 Network-based modeling of the human gut microbiome. 2010, 7, 1040-50 Subcellular phosphoproteomics. 2010, 29, 962-90 Drug-Target Networks. 2010, 29, 10-4 Iterative Shannon Entropy - a Methodology to Quantify the Information Content of Value Range Dependent Data Distributions. Application to Descriptor and Compound Selectivity Profiling. 2010,	19 34 35 62
1315 1314 1313 1312 1311	Architectural repertoire of ligand-binding pockets on protein surfaces. 2010, 11, 556-63 Network-based modeling of the human gut microbiome. 2010, 7, 1040-50 Subcellular phosphoproteomics. 2010, 29, 962-90 Drug-Target Networks. 2010, 29, 10-4 Iterative Shannon Entropy - a Methodology to Quantify the Information Content of Value Range Dependent Data Distributions. Application to Descriptor and Compound Selectivity Profiling. 2010, 29, 432-40	19 34 35 62 1

1307	Proteomics data repositories: providing a safe haven for your data and acting as a springboard for further research. 2010 , 73, 2136-46	49
1306	The Drosophila melanogaster sperm proteome-II (DmSP-II). 2010 , 73, 2171-85	106
1305	Regulatory dynamics of standard two-component systems in bacteria. 2010 , 264, 560-9	7
1304	eNelator: A simulation system for large-scale vulnerability analysis of species-, disease- and process-specific protein networks. 2010 , 1, 197-205	3
1303	A new analysis of debris mitigation and removal using networks. 2010 , 66, 257-268	4
1302	Ground testing of Arabidopsis preservation protocol for the microarray analysis to be used in the ISS EMCS Multigen-2 experiment. 2010 , 46, 1249-1256	5
1301	Incorporating multiple genomic features with the utilization of interacting domain patterns to improve the prediction of protein protein interactions. 2010 , 180, 3955-3973	3
1300	Modifiers of notch transcriptional activity identified by genome-wide RNAi. 2010 , 10, 107	18
1299	Hydrocarbon phenotyping of algal species using pyrolysis-gas chromatography mass spectrometry. 2010 , 10, 40	24
1298	Concept and application of a computational vaccinology workflow. 2010 , 6 Suppl 2, S7	27
1297	GTC: A web server for integrating systems biology data with web tools and desktop applications. 2010 , 5, 7	0
1296	Open source tool for prediction of genome wide protein-protein interaction network based on ortholog information. 2010 , 5, 8	21
1295	A novel microRNA and transcription factor mediated regulatory network in schizophrenia. 2010 , 4, 10	129
1294	Integration of metabolic databases for the reconstruction of genome-scale metabolic networks. 2010 , 4, 114	67
1293	Curating the innate immunity interactome. 2010 , 4, 117	59
1292	The mEPN scheme: an intuitive and flexible graphical system for rendering biological pathways. 2010 , 4, 65	17
1291	Co-expression module analysis reveals biological processes, genomic gain, and regulatory mechanisms associated with breast cancer progression. 2010 , 4, 74	94
1290	The biological context of HIV-1 host interactions reveals subtle insights into a system hijack. 2010 , 4, 80	26

1289	Identification of transcription factor's targets using tissue-specific transcriptomic data in Arabidopsis thaliana. 2010 , 4 Suppl 2, S2	9
1288	Shrunken methodology to genome-wide SNPs selection and construction of SNPs networks. 2010 , 4 Suppl 2, S5	6
1287	Gene regulatory network reveals oxidative stress as the underlying molecular mechanism of type 2 diabetes and hypertension. 2010 , 3, 45	37
1286	mspecLINE: bridging knowledge of human disease with the proteome. 2010 , 3, 7	5
1285	Predicting cytotoxicity from heterogeneous data sources with Bayesian learning. 2010 , 2, 11	31
1284	Comparison of human solute carriers. 2010 , 19, 412-28	83
1283	Domain distribution and intrinsic disorder in hubs in the human protein-protein interaction network. 2010 , 19, 1461-8	54
1282	From proteome lists to biological impacttools and strategies for the analysis of large MS data sets. 2010 , 10, 1270-83	49
1281	Pathway analysis of dilated cardiomyopathy using global proteomic profiling and enrichment maps. 2010 , 10, 1316-27	53
1280	The impact of miR-34a on protein output in hepatocellular carcinoma HepG2 cells. 2010 , 10, 1557-72	56
1279	MASPECTRAS 2: An integration and analysis platform for proteomic data. 2010 , 10, 2719-22	20
1278	N-terminal strands of filamin Ig domains act as a conformational switch under biological forces. 2010 , 78, 12-24	14
1277	Regional covariation and its application for predicting protein contact patches. 2010 , 78, 548-58	6
1276	The evolutionary landscape of the chromatin modification machinery reveals lineage specific gains, expansions, and losses. 2010 , 78, 2075-89	15
1275	Undifferentiated embryonic cell transcription factor 1 regulates ESC chromatin organization and gene expression. 2010 , 28, 1703-14	28
1274	In silico models of cancer. 2010 , 2, 438-459	81
1273	Genome-wide analysis of caesium and strontium accumulation in Saccharomyces cerevisiae. 2010 , 27, 817-35	12
1272	Genome wide expression analysis of the effect of Pinelliae Rhizoma extract on psychological stress. 2010 , 24, 384-92	5

1271 Reciprocal regulation of gene expression by Ephedra herba in mouse brain. 2010 , 24, 531-7	1
A comprehensive and non-prefractionation on the protein level approach for the human urinary proteome: touching phosphorylation in urine. 2010 , 24, 823-32	65
1269 Hubs and bottlenecks in plant molecular signalling networks. 2010 , 188, 919-38	56
1268 An update on clinical proteomics in Alzheimer's research. 2010 , 112, 1386-414	70
Global gene profiling and comprehensive bioinformatics analysis of a 46,XY female with pericentric inversion of the Y chromosome. 2010 , 50, 40-51	3
1266 Immunoinformatics: an integrated scenario. 2010 , 131, 153-68	92
The proximal signaling network of the BCR-ABL1 oncogene shows a modular organization. 2010 , 29, 5895-910	34
Phylogenetic diversity and community structure of anaerobic gut fungi (phylum Neocallimastigomycota) in ruminant and non-ruminant herbivores. 2010 , 4, 1225-35	167
1263 A human gut microbial gene catalogue established by metagenomic sequencing. 2010 , 464, 59-65	7044
Transcriptional profiling of growth perturbations of the human malaria parasite Plasmodium falciparum. 2010 , 28, 91-8	155
1261 The BioPAX community standard for pathway data sharing. 2010 , 28, 935-42	499
Rice structural variation: a comparative analysis of structural variation between rice and three of its closest relatives in the genus Oryza. 2010 , 63, 990-1003	38
New perspectives on the biology of acute GVHD. 2010 , 45, 1-11	132
1258 ProHits: integrated software for mass spectrometry-based interaction proteomics. 2010 , 28, 1015-7	156
1257 A basic helix-loop-helix transcription factor controls cell growth and size in root hairs. 2010 , 42, 264	-7 210
A global network of transcription factors, involving E2A, EBF1 and Foxo1, that orchestrates B cell fate. 2010 , 11, 635-43	376
1255 Visualization of omics data for systems biology. 2010 , 7, S56-68	459
1254 Visualizing biological data-now and in the future. 2010 , 7, S2-4	85

1253	Detecting interactions with membrane proteins using a membrane two-hybrid assay in yeast. 2010 , 5, 1281-93	105
1252	Statistical analysis strategies for association studies involving rare variants. 2010 , 11, 773-85	378
1251	Analysing biological pathways in genome-wide association studies. 2010 , 11, 843-54	629
1250	Differential bacterial dynamics promote emergent community robustness to lake mixing: an epilimnion to hypolimnion transplant experiment. 2010 , 12, 455-66	40
1249	SmallWorlds: Visualizing Social Recommendations. 2010 , 29, 833-842	65
1248	Pathline: A Tool For Comparative Functional Genomics. 2010 , 29, 1043-1052	44
1247	A network analysis of the single nucleotide polymorphisms in acute allergic diseases. 2010 , 65, 40-7	10
1246	Protein Interaction Data Resources. 2010 , 1375-1385	1
1245	On the Logic of Natural Product Binding in Protein Protein Interactivity. 2010 , 53-73	
1244	A membrane protein/signaling protein interaction network for Arabidopsis version AMPv2. 2010 , 1, 24	104
1243	Current trends and new challenges of databases and web applications for systems driven biological research. 2010 , 1, 147	10
1242	Systems biology: the next frontier for bioinformatics. 2010 , 268925	37
1241	Protein Bioinformatics Infrastructure for the Integration and Analysis of Multiple High-Throughput "omics" Data. 2010 , 423589	15
1240	Automated network analysis identifies core pathways in glioblastoma. 2010 , 5, e8918	268
1239	A Boolean model of the Pseudomonas syringae hrp regulon predicts a tightly regulated system. 2010 , 5, e9101	15
1238	Xenopus meiotic microtubule-associated interactome. 2010 , 5, e9248	32
1237	A comprehensive resource of interacting protein regions for refining human transcription factor	
	networks. 2010 , 5, e9289	51
1236	networks. 2010 , 5, e9289	13

1235	A comprehensive molecular interaction map for rheumatoid arthritis. 2010 , 5, e10137	43
1234	Identifying molecular effects of diet through systems biology: influence of herring diet on sterol metabolism and protein turnover in mice. 2010 , 5, e12361	16
1233	Network analysis identifies ELF3 as a QTL for the shade avoidance response in Arabidopsis. 2010 , 6, e1001100) 88
1232	Structural and functional roles of coevolved sites in proteins. 2010 , 5, e8591	40
1231	Inference of cancer-specific gene regulatory networks using soft computing rules. 2010, 4, 19-34	10
1230	A two-tiered compensatory response to loss of DNA repair modulates aging and stress response pathways. 2010 , 2, 133-59	21
1229	Investigating the correlations among the chemical structures, bioactivity profiles and molecular targets of small molecules. 2010 , 26, 2881-8	22
1228	Interactome mapping of the phosphatidylinositol 3-kinase-mammalian target of rapamycin pathway identifies deformed epidermal autoregulatory factor-1 as a new glycogen synthase kinase-3 interactor. 2010 , 9, 1578-93	43
1227	Functional modules in the Arabidopsis core cell cycle binary protein-protein interaction network. 2010 , 22, 1264-80	127
1226	Molecular and physiological analysis of drought stress in Arabidopsis reveals early responses leading to acclimation in plant growth. 2010 , 154, 1254-71	467
1225	Recent progress in automatically extracting information from the pharmacogenomic literature. 2010 , 11, 1467-89	52
1224	Coexpression analysis identifies Rice Starch Regulator1, a rice AP2/EREBP family transcription factor, as a novel rice starch biosynthesis regulator. 2010 , 154, 927-38	238
1223	DRYGIN: a database of quantitative genetic interaction networks in yeast. 2010 , 38, D502-7	67
1222	Comorbidity: a network perspective. 2010 , 33, 137-50; discussion 150-93	711
1221	EGAN: exploratory gene association networks. 2010 , 26, 285-6	50
1220	geWorkbench: an open source platform for integrative genomics. 2010 , 26, 1779-80	75
1219	Genomic cis-regulatory networks in the early Ciona intestinalis embryo. 2010 , 137, 1613-23	54
1218	A Novel Grid-Based Visualization Approach for Metabolic Networks with Advanced Focus&Context View. 2010 , 268-279	10

1217	ToppCluster: a multiple gene list feature analyzer for comparative enrichment clustering and network-based dissection of biological systems. 2010 , 38, W96-102	234
1216	PROFESS: a PROtein function, evolution, structure and sequence database. 2010 , 2010, baq011	5
1215	GeneMANIA Cytoscape plugin: fast gene function predictions on the desktop. 2010 , 26, 2927-8	413
1214	Trivalent arsenic inhibits the functions of chaperonin complex. 2010 , 186, 725-34	41
1213	SpotXplore: a Cytoscape plugin for visual exploration of hotspot expression in gene regulatory networks. 2010 , 26, 2922-3	6
1212	Measuring the physical cohesiveness of proteins using physical interaction enrichment. 2010 , 26, 2737-43	15
1211	SimBoolNeta Cytoscape plugin for dynamic simulation of signaling networks. 2010 , 26, 141-2	43
121 0	CORNET: a user-friendly tool for data mining and integration. 2010 , 152, 1167-79	56
1209	Building promoter aware transcriptional regulatory networks using siRNA perturbation and deepCAGE. 2010 , 38, 8141-8	11
1208	Upstream transcription factor 1 influences plasma lipid and metabolic traits in mice. 2010 , 19, 597-608	28
1207	Regulators of cyclin-dependent kinases are crucial for maintaining genome integrity in S phase. 2010 , 188, 629-38	130
1206	MicroRNA miR-183 functions as an oncogene by targeting the transcription factor EGR1 and promoting tumor cell migration. 2010 , 70, 9570-80	238
1205	Defining the budding yeast chromatin-associated interactome. 2010 , 6, 448	51
1204	Mapping plant interactomes using literature curated and predicted protein-protein interaction data sets. 2010 , 22, 997-1005	25
1203	Adaptation to herbivory by the Tammar wallaby includes bacterial and glycoside hydrolase profiles different from other herbivores. 2010 , 107, 14793-8	163
1202	Quantitative site-specific phosphorylation dynamics of human protein kinases during mitotic progression. 2010 , 9, 1167-81	41
1201	Computational tools for the interactive exploration of proteomic and structural data. 2010 , 9, 1703-15	7
1200	R spider: a network-based analysis of gene lists by combining signaling and metabolic pathways from Reactome and KEGG databases. 2010 , 38, W78-83	56

1199	RNA G-Quadruplexes in the model plant species Arabidopsis thaliana: prevalence and possible functional roles. 2010 , 38, 8149-63	69
1198	GSearcher: agile attribute querying for biological networks. 2010 , 26, 3138-9	1
1197	Parallel genetic and proteomic screens identify Msps as a CLASP-Abl pathway interactor in Drosophila. 2010 , 185, 1311-25	26
1196	Network-based Identification of novel cancer genes. 2010 , 9, 648-55	46
1195	Preferential use of protein domain pairs as interaction mediators: order and transitivity. 2010 , 26, 2564-70	10
1194	Engineered human skin substitutes undergo large-scale genomic reprogramming and normal skin-like maturation after transplantation to athymic mice. 2010 , 130, 587-601	32
1193	Chemotherapy and signaling: How can targeted therapies supercharge cytotoxic agents?. 2010 , 10, 839-53	55
1192	Extended Constraint-Based Boolean Analysis: A Computational Method in Genetic Network Inference. 2010 , 71-82	
1191	Massively parallel signature sequencing and bioinformatics analysis identifies up-regulation of TGFBI and SOX4 in human glioblastoma. 2010 , 5, e10210	68
1190	MetExplore: a web server to link metabolomic experiments and genome-scale metabolic networks. 2010 , 38, W132-7	127
1189	DisGeNET: a Cytoscape plugin to visualize, integrate, search and analyze gene-disease networks. 2010 , 26, 2924-6	143
1188	Metscape: a Cytoscape plug-in for visualizing and interpreting metabolomic data in the context of human metabolic networks. 2010 , 26, 971-3	148
1187	Evidence mining and novelty assessment of protein-protein interactions with the ConsensusPathDB plugin for Cytoscape. 2010 , 26, 2796-7	24
1186	OmicsAnalyzer: a Cytoscape plug-in suite for modeling omics data. 2010 , 26, 2995-6	19
1185	Unfolding of metastable linker region is at the core of Hsp33 activation as a redox-regulated chaperone. 2010 , 285, 11243-51	40
1184	MODEVO: exploring modularity and evolution of protein interaction networks. 2010 , 26, 1790-1	15
1183	Synthetic lethal screen of an EGFR-centered network to improve targeted therapies. 2010 , 3, ra67	118
1182	GATE: software for the analysis and visualization of high-dimensional time series expression data. 2010 , 26, 143-4	25

1181	Genetic associations of variants in genes encoding HIV-dependency factors required for HIV-1 infection. 2010 , 202, 1836-45	22
1180	Molecular Association between Diabetes-Specific Local Gene Network and Nutrient Metabolism Modules. 2010 ,	1
1179	seGOsa: Software environment for gene ontology-driven similarity assessment. 2010 ,	2
1178	Classification of genome-wide copy number variations and their associated SNP and gene networks analysis. 2010 ,	
1177	Toward automatically drawn metabolic pathway atlas with peripheral node abstraction algorithm. 2010 ,	
1176	An Integrative Scoring Approach to Identify Transcriptional Regulations Controlling Lung Surfactant Homeostasis. 2010 ,	
1175	AtMetExpress development: a phytochemical atlas of Arabidopsis development. 2010 , 152, 566-78	149
1174	Functional genomics and networks: new approaches in the extraction of complex gene modules. 2010 , 7, 55-63	10
1173	Simulation and Analysis of the Network Model of the Quorum Sensing Process during Biofilm Creation. 2010 ,	
1172	Detection of locally over-represented GO terms in protein-protein interaction networks. 2010 , 17, 443-57	10
1171	Comparative transcriptomic and proteomic profiling of industrial wine yeast strains. 2010, 76, 3911-23	35
1170	Flipping DNA to generate and regulate microbial consortia. 2010 , 184, 285-93	4
1169	Site-specific phosphorylation dynamics of the nuclear proteome during the DNA damage response. 2010 , 9, 1314-23	195
1168	Systematic interpretation of comutated genes in large-scale cancer mutation profiles. 2010 , 9, 2186-95	11
1167	Mass spectrometry-based proteomics in biomedical research: emerging technologies and future strategies. 2010 , 12, e30	24
1166		26
1100	Global approaches to study protein-protein interactions among viruses and hosts. 2010 , 5, 289-301	
1165	Glioblastoma-specific protein interaction network identifies PP1A and CSK21 as connecting molecules between cell cycle-associated genes. 2010 , 70, 6437-47	19

1163	Software Tools for Systems Biology. 2010 , 289-314	3
1162	Synthetic biology: tools to design, build, and optimize cellular processes. 2010 , 2010, 130781	51
1161	IQGAP1 and vimentin are key regulator genes in naturally occurring hepatotumorigenesis induced by oxidative stress. 2010 , 31, 504-11	23
1160	PhenoHM: human-mouse comparative phenome-genome server. 2010 , 38, W165-74	18
1159	Network-based comparison of temporal gene expression patterns. 2010 , 26, 2944-51	7
1158	PhosphoGRID: a database of experimentally verified in vivo protein phosphorylation sites from the budding yeast Saccharomyces cerevisiae. 2010 , 2010, bap026	78
1157	How to understand the cell by breaking it: network analysis of gene perturbation screens. 2010 , 6, e1000655	45
1156	Network-based elucidation of human disease similarities reveals common functional modules enriched for pluripotent drug targets. 2010 , 6, e1000662	234
1155	Learning "graph-mer" motifs that predict gene expression trajectories in development. 2010, 6, e1000761	5
1154	Graph-based analysis of the metabolic exchanges between two co-resident intracellular symbionts, Baumannia cicadellinicola and Sulcia muelleri, with their insect host, Homalodisca coagulata. 2010 , 6, e1000904	27
1153	Modeling conformational ensembles of slow functional motions in Pin1-WW. 2010 , 6, e1001015	60
1152	FuncBase: a resource for quantitative gene function annotation. 2010 , 26, 1806-7	11
1151	Pivotal Advance: Avian colony-stimulating factor 1 (CSF-1), interleukin-34 (IL-34), and CSF-1 receptor genes and gene products. 2010 , 87, 753-64	136
1150	A computational approach to analyze the mechanism of action of the kinase inhibitor bafetinib. 2010 , 6, e1001001	18
1149	Prediction of human functional genetic networks from heterogeneous data using RVM-based ensemble learning. 2010 , 26, 807-13	21
1148	Polymorphic cis- and trans-regulation of human gene expression. 2010 , 8, e1000480	120
1147	Network modeling identifies molecular functions targeted by miR-204 to suppress head and neck tumor metastasis. 2010 , 6, e1000730	128
1146	Practical application of toxicogenomics for profiling toxicant-induced biological perturbations. 2010 , 11, 3397-412	21

1145	Functional toxicogenomics: mechanism-centered toxicology. 2010 , 11, 4796-813	44
1144	Ontology- and graph-based similarity assessment in biological networks. 2010 , 26, 2643-4	14
1143	A scalable approach for discovering conserved active subnetworks across species. 2010 , 6, e1001028	15
1142	Large-scale analysis of network bistability for human cancers. 2010 , 6, e1000851	53
1141	Feedback between p21 and reactive oxygen production is necessary for cell senescence. 2010 , 6, 347	578
1140	A cytoscape based framework for efficient sub-graph isomorphic protein-protein interaction motif lookup. 2010 ,	1
1139	A global census of fission yeast deubiquitinating enzyme localization and interaction networks reveals distinct compartmentalization profiles and overlapping functions in endocytosis and polarity. 2010 , 8, e1000471	62
1138	Patterns of HIV-1 protein interaction identify perturbed host-cellular subsystems. 2010 , 6, e1000863	50
1137	Comparative pathogenesis and systems biology for biodefense virus vaccine development. 2010 , 2010, 236528	8
1136	Protein-protein interactions essentials: key concepts to building and analyzing interactome networks. 2010 , 6, e1000807	357
1135	SBRML: a markup language for associating systems biology data with models. 2010 , 26, 932-8	50
1134	Constructing metabolic networks based on bipartite model within MATLAB. 2010 ,	
1133	Screening chromosomal aberrations by array comparative genomic hybridization in 80 patients with congenital hypothyroidism and thyroid dysgenesis. 2010 , 95, 3446-52	23
1132	Construction of a large extracellular protein interaction network and its resolution by spatiotemporal expression profiling. 2010 , 9, 2654-65	35
1131	The IntAct molecular interaction database in 2010. 2010 , 38, D525-31	522
1130	Inference of RhoGAP/GTPase regulation using single-cell morphological data from a combinatorial RNAi screen. <i>Genome Research</i> , 2010 , 20, 372-80	23
1129	VirtualPlant: a software platform to support systems biology research. 2010 , 152, 500-15	205
1128	Robin: an intuitive wizard application for R-based expression microarray quality assessment and analysis. 2010 , 153, 642-51	90

1127	The association of multiple interacting genes with specific phenotypes in rice using gene coexpression networks. 2010 , 154, 13-24		83
1126	Emergence and evolution of modern molecular functions inferred from phylogenomic analysis of ontological data. 2010 , 27, 1710-33		38
1125	PerturbationAnalyzer: a tool for investigating the effects of concentration perturbation on protein interaction networks. 2010 , 26, 275-7		14
1124	A novel cancer classifier based on differentially expressed gene network. 2010 ,		
1123	Networks inferred from biochemical data reveal profound differences in toll-like receptor and inflammatory signaling between normal and transformed hepatocytes. 2010 , 9, 1849-65		92
1122	Genes and pathways contributing to obesity: a systems biology view. 2010 , 94, 9-38		2
1121	Computational modeling of the effects of oxidative stress on the IGF-1 signaling pathway in human articular chondrocytes. 2010 ,		
1120	Pervasive gene content variation and copy number variation in maize and its undomesticated progenitor. <i>Genome Research</i> , 2010 , 20, 1689-99	-7	236
1119	Advanced querying interface for biochemical network databases. 2010,		
1118	Simple sequence-based kernels do not predict protein-protein interactions. 2010 , 26, 2610-4		78
1117	Conservation and canalization of gene expression during angiosperm diversification accompany the origin and evolution of the flower. 2010 , 107, 22570-5		54
1116	Microarray analysis reveals the inhibition of nuclear factor-kappa B signaling by aristolochic acid in normal human kidney (HK-2) cells. 2010 , 31, 227-36		27
1115	BioMet Toolbox: genome-wide analysis of metabolism. 2010 , 38, W144-9		82
1114	PINT: Pathways INtegration Tool. 2010 , 38, W124-31		8
1113	Direct transfer of alpha-synuclein from neuron to astroglia causes inflammatory responses in synucleinopathies. 2010 , 285, 9262-72		555
1112	Joint genome-wide profiling of miRNA and mRNA expression in Alzheimer's disease cortex reveals altered miRNA regulation. 2010 , 5, e8898		251
1111	Brain phosphoproteome obtained by a FASP-based method reveals plasma membrane protein topology. 2010 , 9, 3280-9		221
1110	Systems biology of embryogenesis. 2010 , 22, 98-105		9

1109	Computational Challenges in Systems Biology. 2010 , 175-223	2
1108	An in silico analysis of microRNAs: mining the miRNAome. 2010 , 6, 1853-62	37
1107	Quantitative phosphoproteomics reveals widespread full phosphorylation site occupancy during mitosis. 2010 , 3, ra3	1106
1106	Long-term genome-wide blood RNA expression profiles yield novel molecular response candidates for IFN-beta-1b treatment in relapsing remitting MS. 2010 , 11, 147-61	38
1105	Synthetic genetic array (SGA) analysis in Saccharomyces cerevisiae and Schizosaccharomyces pombe. 2010 , 470, 145-79	136
1104	Microvesicles derived from adult human bone marrow and tissue specific mesenchymal stem cells shuttle selected pattern of miRNAs. 2010 , 5, e11803	489
1103	Evolution of the 12-spanner drug:H+ antiporter DHA1 family in hemiascomycetous yeasts. 2010 , 14, 701-10	15
1102	Knowledge-Driven Approaches to Genome-Scale Analysis. 2010 , 33-65	1
1101	Biological Pathway Analysis: An Overview of Reactome and Other Integrative Pathway Knowledge Bases. 2010 , 289-314	
1100	Molecular Network Analysis and Applications. 2010 , 251-287	9
1099	Analysis of the bacterial luciferase mobile loop by replica-exchange molecular dynamics. 2010 , 99, 4012-9	18
1098	Systems biology visualization tools for drug target discovery. 2010 , 5, 425-39	5
1097	Comparative functional genomics of stress responses in yeasts. 2010 , 14, 501-15	9
1096	MicroRNA-regulated protein-protein interaction networks: how could they help in searching for pro-longevity targets?. 2010 , 13, 373-7	26
1095	Robust TLR4-induced gene expression patterns are not an accurate indicator of human immunity. 2010 , 8, 6	3
1094	Structural similarity-based predictions of protein interactions between HIV-1 and Homo sapiens. 2010 , 7, 82	55
1093	Chaperone expression profiles correlate with distinct physiological states of Plasmodium falciparum in malaria patients. 2010 , 9, 236	35
1092	High-Throughput Biological Data Analysis. 2010 , 30, 81-100	2

1091 Hub Gene Selection Methods for the Reconstruction of Transcription Networks. 2010 , 506-521	2
1090 Quantitative analysis of HGF and EGF-dependent phosphotyrosine signaling networks. 2010 , 9, 2734-4	2 46
Quantitative proteomics reveals a "poised quiescence" cellular state after triggering the DNA replication origin activation checkpoint. 2010 , 9, 5445-60	6
Immunomodulatory effect of 5-azacytidine (5-azaC): potential role in the transplantation setting. 2010 , 115, 107-21	175
Gene network visualization and quantitative synteny analysis of more than 300 marine T4-like phage scaffolds from the GOS metagenome. 2010 , 27, 1935-44	21
1086 Molecular scaffolds with high propensity to form multi-target activity cliffs. 2010 , 50, 500-10	42
1085 Network-based modeling for analyzing the human skin microbiome. 2010 ,	1
Gene association networks from microarray data using a regularized estimation of partial correlation based on PLS regression. 2010 , 7, 251-62	26
1083 Topology-free querying of protein interaction networks. 2010 , 17, 237-52	80
Polypharmacology directed compound data mining: identification of promiscuous chemotypes with different activity profiles and comparison to approved drugs. 2010 , 50, 2112-8	50
Changes in protein expression profiles between a low phytic acid rice (Oryza sativa L. Ssp. japonica) line and its parental line: a proteomic and bioinformatic approach. 2010 , 58, 6912-22	15
$_{1080}$ Association weight matrix for the genetic dissection of puberty in beef cattle. 2010 , 107, 13642-7	104
Proteomics and transcriptomics investigation on longissimus muscles in Large White and Casertana pig breeds. 2010 , 9, 6450-66	49
1078 Molecular networks for the study of TCM pharmacology. 2010 , 11, 417-30	164
Phospholipid transfer protein in human plasma associates with proteins linked to immunity and inflammation. 2010 , 49, 7314-22	45
Disrupted-in-schizophrenia 1 (DISC1) plays essential roles in mitochondria in collaboration with Mitofilin. 2010 , 107, 17785-90	115
1075 BioRuby: bioinformatics software for the Ruby programming language. 2010 , 26, 2617-9	122
1074 Cytoscape Web: an interactive web-based network browser. 2010 , 26, 2347-8	547

1073 PathwayAccess: CellDesigner plugins for pathway databases. 2010 , 26, 2345-6	11
1072 Databases of protein-protein interactions and complexes. 2010 , 609, 145-59	17
Geometric similarities of protein-protein interfaces at atomic resolution are only observed within homologous families: an exhaustive structural classification study. 2010 , 399, 526-40	16
Global network analysis of lipid-raft-related proteins reveals their centrality in the network and their roles in multiple biological processes. 2010 , 402, 761-73	5
1069 Disease progression and solid tumor survival: a transcriptome decoherence model. 2010 , 24, 53-60	5
1068 Prediction of regulatory networks in mouse abdominal wall. 2010 , 469, 1-8	4
Expression of cytokine genes in the aorta is altered by the deficiency in MCP-1: effect of a high-fat, high-cholesterol diet. 2010 , 50, 121-8	18
1066 Transcriptional control of a plant stem cell niche. 2010 , 18, 849-61	190
A combined ex vivo and in vivo RNAi screen for notch regulators in Drosophila reveals an extensive notch interaction network. 2010 , 18, 862-76	115
1064 Identification of modules in Aspergillus niger by gene co-expression network analysis. 2010 , 47, 539-50	14
Precision mapping of an in vivo N-glycoproteome reveals rigid topological and sequence constraints. 2010 , 141, 897-907	700
1062 An alternative splicing network links cell-cycle control to apoptosis. 2010 , 142, 625-36	238
Extensive in vivo metabolite-protein interactions revealed by large-scale systematic analyses. 2010 , 143, 639-50	162
Functional overlap and regulatory links shape genetic interactions between signaling pathways. 2010 , 143, 991-1004	105
1059 A tissue-specific atlas of mouse protein phosphorylation and expression. 2010 , 143, 1174-89	1218
Carbon dioxide sequestration by carbon nanotubes: Application of graph theoretical approach. 2010 , 48, 402-408	2
Lab-specific gene expression signatures in pluripotent stem cells. 2010 , 7, 258-62	171
Investigation of low-dose ritonavir on human peripheral blood mononuclear cells using gene expression whole genome microarrays. 2010 , 96, 57-65	8

1055	Gene set-level network analysis using a toxicogenomics database. 2010 , 96, 39-49	11
1054	Systematic analysis of public domain compound potency data identifies selective molecular scaffolds across druggable target families. 2010 , 53, 752-8	41
1053	Analysis of protein complexes through model-based biclustering of label-free quantitative AP-MS data. 2010 , 6, 385	30
1052	ATM-dependent and -independent dynamics of the nuclear phosphoproteome after DNA damage. 2010 , 3, rs3	212
1051	Dynamic cross-talk analysis among TNF-R, TLR-4 and IL-1R signalings in TNFalpha-induced inflammatory responses. 2010 , 3, 19	28
1050	A decade of systems biology. 2010 , 26, 721-44	230
1049	Functional Modules in Protein Protein Interaction Networks. 2010, 353-369	
1048	Interaction with diurnal and circadian regulation results in dynamic metabolic and transcriptional changes during cold acclimation in Arabidopsis. 2010 , 5, e14101	125
1047	The profile of mitochondrial proteins and their phosphorylation signaling network in INS-1 beta cells. 2010 , 9, 2898-908	19
1046	Visual integration of quantitative proteomic data, pathways, and protein interactions. 2010 , 16, 609-20	10
1045	Pathway Tools version 13.0: integrated software for pathway/genome informatics and systems biology. 2010 , 11, 40-79	378
1044	Global protein-protein interaction network in the human pathogen Mycobacterium tuberculosis H37Rv. 2010 , 9, 6665-77	82
1043	Targeted interactomics reveals a complex core cell cycle machinery in Arabidopsis thaliana. 2010 , 6, 397	254
1042	Multilocus haplotypes reveal variable levels of diversity and population structure of Plasmodium falciparum in Papua New Guinea, a region of intense perennial transmission. 2010 , 9, 336	69
1041	Novel genes exhibit distinct patterns of function acquisition and network integration. 2010 , 11, R127	60
1040	Constructing a fish metabolic network model. 2010 , 11, R115	39
1039	A human functional protein interaction network and its application to cancer data analysis. 2010 , 11, R53	453
1038	Characterizing regulatory path motifs in integrated networks using perturbational data. 2010 , 11, R32	10

1037 NetPath: a public resource of curated signal transduction pathways. 2010 , 11, R3	331
Proteomic profile regulated by the anticancer peptide CIGB-300 in non-small cell lung cancer (NSCLC) cells. 2010 , 9, 5473-83	19
SARANEA: a freely available program to mine structure-activity and structure-selectivity relationship information in compound data sets. 2010 , 50, 68-78	70
1034 . 2010,	6
1033 BioNet: an R-Package for the functional analysis of biological networks. 2010 , 26, 1129-30	171
1032 Global assessment of scaffold hopping potential for current pharmaceutical targets. 2010 , 1, 339-344	20
Robustness and evolvability in natural chemical resistance: identification of novel systems properties, biochemical mechanisms and regulatory interactions. 2010 , 6, 1475-91	10
1030 Gene-centered regulatory networks. 2010 , 9, 4-12	35
1029 Proteomic profiling of early life stages of European grayling (Thymallus thymallus). 2010 , 9, 4790-800	9
1028 PBSK browser: Navigate biological pathways of PSI-MI, BioPAX, SBML and KGML formats. 2010 ,	
Self-organizing fuzzy graphs for structure-based comparison of protein pockets. 2010 , 9, 6498-510	25
1026 Investigating microRNA-transcription factor mediated regulatory network in glioblastoma. 2010 ,	1
HepatoNet1: a comprehensive metabolic reconstruction of the human hepatocyte for the analysis of liver physiology. 2010 , 6, 411	219
Comparison of Co-Temporal Modeling Algorithms on Sparse Experimental Time Series Data Sets. 2010 , 2010, 79-85	O
1023 Interferon-inducible factor 16 is a novel modulator of glucocorticoid action. 2010 , 24, 1700-13	10
Isobaric labeling and tandem mass spectrometry: a novel approach for profiling and quantifying proteins differentially expressed in amniotic fluid in preterm labor with and without intra-amniotic infection/inflammation. 2010 , 23, 261-80	69
Prediction of Protein-Protein Interaction Using Distance Frequency of Amino Acids Grouped with their Physicochemical Properties. 2011 ,	2
Secretory pathway genes assessed by high-throughput microscopy and synthetic genetic array analysis. 2011 , 7, 2589-98	30

Obvious: A meta-toolkit to encapsulate information visualization toolkits ©ne toolkit to bind them all. 2011 ,	6
The STRING database in 2011: functional interaction networks of proteins, globally integrated and scored. 2011 , 39, D561-8	2514
1017 NAViGaTOR: Large Scalable and Interactive Navigation and Analysis of Large Graphs. 2011 , 7, 314-347	9
1016 Dupuytren's: a systems biology disease. 2011 , 13, 238	31
A novel integrative network approach to understand the interplay between cardiovascular disease and other complex disorders. 2011 , 7, 2205-19	11
1014 G-PARE: A visual analytic tool for comparative analysis of uncertain graphs. 2011 ,	10
A predicted protein-protein interaction network of the filamentous fungus Neurospora crassa. 2011 , 7, 2278-85	18
1012 Rule-based modelling of iron homeostasis in tuberculosis. 2011 , 7, 2750-68	13
Automated model-driven generation of software components for the simulation of epithelial tissues. 2011 ,	
Identification and modeling of genes with diurnal oscillations from microarray time series data. 2011, 8, 108-21	7
1009 . 2011 ,	3
1008 Visual exploration of microbial populations. 2011 ,	5
Large scale identification of protein-protein interaction of Aspergillus terreus NIH2624 using computational approaches. 2011 ,	
The protein folding network indicates that the ultrafast folding mutant of villin headpiece subdomain has a deeper folding funnel. 2011 , 134, 205104	12
1005 EVEVis: A multi-scale visualization system for dense evolutionary data. 2011 ,	4
Characterizing the diversity and biological relevance of the MLPCN assay manifold and screening set. 2011 , 51, 1205-15	11
1003 Mapping the subcellular protein distribution in three human cell lines. 2011 , 10, 3766-77	34
FLOWERING LOCUS C (FLC) regulates development pathways throughout the life cycle of Arabidopsis. 2011 , 108, 6680-5	219

1001	Using the Human Plasma PeptideAtlas to study human plasma proteins. 2011 , 728, 349-74	21
1000	Community structures of fecal bacteria in cattle from different animal feeding operations. 2011 , 77, 2992-3001	230
999	NMR analysis of a stress response metabolic signaling network. 2011 , 10, 3743-54	39
998	Network modeling of the transcriptional effects of copy number aberrations in glioblastoma. 2011 , 7, 486	67
997	Combining horizontal and vertical substructure relationships in scaffold hierarchies for activity prediction. 2011 , 51, 248-57	12
996	A data set of human endogenous protein ubiquitination sites. 2011 , 10, M110.002089	75
995	Proteomic analysis of membrane proteins from Streptococcus pneumoniae with multiple separation methods plus high accuracy mass spectrometry. 2011 , 15, 683-94	14
994	Enzymatic deamination of the epigenetic base N-6-methyladenine. 2011 , 133, 2080-3	22
993	A face in the crowd: recognizing peptides through database search. 2011 , 10, R111.009522	106
992	G-DOC: a systems medicine platform for personalized oncology. 2011 , 13, 771-83	42
991	Genome-Wide Analysis of MuDR-Related Transposable Elements Insertion Population in Maize. 2011 , 37, 772-777	2
990	Molecular simulation uncovers the conformational space of the Cro dimer in solution. 2011, 101, 2516-24	11
989	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. 2011 , 8, 528-9	227
988	The footprints of gut microbial-mammalian co-metabolism. 2011 , 10, 5512-22	229
987	Enhanced Y1H assays for Arabidopsis. 2011 , 8, 1053-5	92
986	Structural and functional protein network analyses predict novel signaling functions for rhodopsin. 2011 , 7, 551	33
985	Topographical continuity of bacterial populations in the healthy human respiratory tract. 2011 , 184, 957-63	693
984	From Visual Biological Models toward Mathematical Models of the Biology of Complex Traits. 2011 , 137-159	1

983	Whole-genome sequencing and social-network analysis of a tuberculosis outbreak. 2011 , 364, 730-9	561
982	Phosphoproteome profile of human lung cancer cell line A549. 2011 , 7, 472-9	12
981	Computational tools for polypharmacology and repurposing. 2011 , 3, 961-8	56
980	Network models of TEM flactamase mutations coevolving under antibiotic selection show modular structure and anticipate evolutionary trajectories. 2011 , 7, e1002184	28
979	MatrixDB, the extracellular matrix interaction database. 2011 , 39, D235-40	99
978	A refinement and coarsening indicator algorithm for finding sparse solutions of inverse problems. 2011 , 5, 391-406	3
977	Comparative analysis of nuclear estrogen receptor alpha and beta interactomes in breast cancer cells. 2011 , 7, 667-76	29
976	Diet drives convergence in gut microbiome functions across mammalian phylogeny and within humans. 2011 , 332, 970-4	1215
975	Integrating Omics data for signaling pathways, interactome reconstruction, and functional analysis. 2011 , 719, 415-33	20
974	Cancer computational biology. 2011 , 12, 120	11
973	Constructing gene regulatory networks for long term photosynthetic light acclimation in Arabidopsis thaliana. 2011 , 12, 335	15
972	gViz, a novel tool for the visualization of co-expression networks. 2011 , 4, 452	5
971	Displaying chemical information on a biological network using Cytoscape. 2011 , 781, 363-76	5
970	Yeast protein-protein interaction assays and screens. 2011 , 754, 145-65	28
969	MiRNA-miRNA synergistic network: construction via co-regulating functional modules and disease miRNA topological features. 2011 , 39, 825-36	218
968	Discovery of a cytokinin deaminase. 2011 , 6, 1036-40	15
967	Mass spectrometry-driven proteomics: an introduction. 2011 , 753, 1-27	4
	Large-scale analysis of chromosomal aberrations in cancer karyotypes reveals two distinct paths to	

965	A quantitative literature-curated gold standard for kinase-substrate pairs. 2011 , 12, R39	44
964	Bringing order to protein disorder through comparative genomics and genetic interactions. 2011 , 12, R14	105
963	ScaffViz: visualizing metagenome assemblies. 2011 , 12, P8	78
962	Network analysis of skin tumor progression identifies a rewired genetic architecture affecting inflammation and tumor susceptibility. 2011 , 12, R5	34
961	Gene-centered regulatory network mapping. 2011 , 106, 271-88	15
960	Data Integration: Towards Understanding Biological Complexity. 2011 , 66-82	
959	Relating protein adduction to gene expression changes: a systems approach. 2011 , 7, 2118-27	25
958	Gene expression profiling of the androgen receptor antagonists flutamide and vinclozolin in zebrafish (Danio rerio) gonads. 2011 , 101, 447-58	45
957	Shift in chicken intestinal gene association networks after infection with Salmonella. 2011, 6, 339-47	8
956	Responses of threespine stickleback (Gasterosteus aculeatus, L) transcriptome to hypoxia. 2011 , 6, 370-81	24
955	Phenotypic landscape of a bacterial cell. 2011 , 144, 143-56	484
954	Mapping the NPHP-JBTS-MKS protein network reveals ciliopathy disease genes and pathways. 2011 , 145, 513-28	435
953	Genome-wide RNAi screens identify genes required for Ricin and PE intoxications. 2011, 21, 231-44	52
952	Networks in Caenorhabditis elegans. 2011 , 21, 787-98	10
951	Synthetic biosensing systems. 2011 , 43, 310-9	18
950	Expression of HOXB genes is significantly different in acute myeloid leukemia with a partial tandem duplication of MLL vs. a MLL translocation: a cross-laboratory study. 2011 , 204, 252-9	10
949	Sex-biased protein expression in threespine stickleback, Gasterosteus aculeatus. 2011 , 10, 4033-40	12
948	Target family-directed exploration of scaffolds with different SAR profiles. 2011 , 51, 3138-48	7

947	Atrial fibrillation: current knowledge and future directions in epidemiology and genomics. 2011 , 124, 1982-93	197
946	Molecular evolution and network-level analysis of the N-glycosylation metabolic pathway across primates. 2011 , 28, 813-23	25
945	Assembling global maps of cellular function through integrative analysis of physical and genetic networks. 2011 , 6, 1308-23	21
944	Spliceosomal RNA infrastructure: the network of splicing components and their regulation by miRNAs. 2011 , 722, 86-102	3
943	A comprehensive genomic binding map of gene and chromatin regulatory proteins in Saccharomyces. 2011 , 41, 480-92	220
942	The specificity and topology of chromatin interaction pathways in yeast. 2011 , 42, 536-49	175
941	Functional analysis of beef tenderness. 2011 , 75, 352-65	87
940	TCM grammar systems: an approach to aid the interpretation of the molecular interactions in Chinese herbal medicine. 2011 , 137, 77-84	14
939	Traditional phytotherapy remedies used in Southern Rwanda for the treatment of liver diseases. 2011 , 138, 415-31	45
938	iWRAP: An interface threading approach with application to prediction of cancer-related protein-protein interactions. 2011 , 405, 1295-310	44
937	Comprehensive gene expression analysis of human embryonic stem cells during differentiation into neural cells. 2011 , 6, e22856	51
936	Cross-species Functionome analysis identifies proteins associated with DNA repair, translation and aerobic respiration as conserved modulators of UV-toxicity. 2011 , 97, 133-47	6
935	Identification of candidate genes in Arabidopsis and Populus cell wall biosynthesis using text-mining, co-expression network analysis and comparative genomics. 2011 , 181, 675-87	25
934	Computational analysis of drought stress-associated miRNAs and miRNA co-regulation network in Physcomitrella patens. 2011 , 9, 37-44	20
933	Cytoscape: software for visualization and analysis of biological networks. 2011 , 696, 291-303	673
932	Application of systems biology approach identifies and validates GRB2 as a risk gene for schizophrenia in the Irish Case Control Study of Schizophrenia (ICCSS) sample. 2011 , 125, 201-8	23
931	Identification of 14-3-3[In human gastric cancer cells and its potency as a diagnostic and prognostic biomarker. 2011 , 11, 2423-39	34
930	Toxins and stress in fish: proteomic analyses and response network. 2011 , 57, 959-69	31

929	Spermidine and resveratrol induce autophagy by distinct pathways converging on the acetylproteome. 2011 , 192, 615-29	362
928	Large scale microarray profiling and coexpression network analysis of CHO cells identifies transcriptional modules associated with growth and productivity. 2011 , 155, 350-9	57
927	Proteomics and HostPathogen Interactions. 2011, 263-303	3
926	Study of the Gene Expressions in Rheumatoid Arthritis Synovial Macrophages Using Network Analysis. 2011 , 18, 101	
925	Grand Challenge: Accelerating Discovery through Technology Development. 2011 , 2, 41	2
924	Functional genomic and proteomic analysis reveals disruption of myelin-related genes and translation in a mouse model of early life neglect. 2011 , 2, 18	40
923	Systems-biology approaches to discover anti-viral effectors of the human innate immune response. 2011 , 3, 1112-30	8
922	Defining the role of essential genes in human disease. 2011 , 6, e27368	70
921	Diurnal rhythms result in significant changes in the cellular protein complement in the cyanobacterium Cyanothece 51142. 2011 , 6, e16680	47
920	The light responsive transcriptome of the zebrafish: function and regulation. 2011 , 6, e17080	76
919	MicroRNA genes derived from repetitive elements and expanded by segmental duplication events in mammalian genomes. 2011 , 6, e17666	69
918	A protein domain co-occurrence network approach for predicting protein function and inferring species phylogeny. 2011 , 6, e17906	27
917	GOBO: gene expression-based outcome for breast cancer online. 2011 , 6, e17911	295
916	Computational integration of homolog and pathway gene module expression reveals general stemness signatures. 2011 , 6, e18968	6
915	A bioinformatics classifier and database for heme-copper oxygen reductases. 2011 , 6, e19117	40
914	Mapping the conformational dynamics and pathways of spontaneous steric zipper Peptide oligomerization. 2011 , 6, e19129	38
913	Quantitative proteomic and interaction network analysis of cisplatin resistance in HeLa cells. 2011 , 6, e19892	30
912	Unraveling molecular signatures of immunostimulatory adjuvants in the female genital tract through systems biology. 2011 , 6, e20448	14

911	Design, synthesis and characterization of a highly effective inhibitor for analog-sensitive (as) kinases. 2011 , 6, e20789	6
910	Intuitive visualization and analysis of multi-omics data and application to Escherichia coli carbon metabolism. 2011 , 6, e21318	15
909	Induction of immune mediators in glioma and prostate cancer cells by non-lethal photodynamic therapy. 2011 , 6, e21834	38
908	Proteomic analysis shows synthetic oleanane triterpenoid binds to mTOR. 2011 , 6, e22862	74
907	Global analysis of proline-rich tandem repeat proteins reveals broad phylogenetic diversity in plant secretomes. 2011 , 6, e23167	14
906	Genome-wide functional profiling reveals genes required for tolerance to benzene metabolites in yeast. 2011 , 6, e24205	42
905	MicroRNA regulation and tissue-specific protein interaction network. 2011 , 6, e25394	15
904	An integrated transcriptomic and meta-analysis of hepatoma cells reveals factors that influence susceptibility to HCV infection. 2011 , 6, e25584	15
903	Gene expression analysis reveals the cell cycle and kinetochore genes participating in ischemia reperfusion injury and early development in kidney. 2011 , 6, e25679	8
902	A new methodology to associate SNPs with human diseases according to their pathway related context. 2011 , 6, e26277	41
901	Modeling the mechanism of action of a DGAT1 inhibitor using a causal reasoning platform. 2011 , 6, e27009	19
900	Gene expression profile change and associated physiological and pathological effects in mouse liver induced by fasting and refeeding. 2011 , 6, e27553	42
899	BinTree seeking: a novel approach to mine both bi-sparse and cohesive modules in protein interaction networks. 2011 , 6, e27646	6
898	Transcriptional regulation of ribosome components are determined by stress according to cellular compartments in Arabidopsis thaliana. 2011 , 6, e28070	64
897	Heterozygous yeast deletion collection screens reveal essential targets of Hsp90. 2011 , 6, e28211	20
896	A brain region-specific predictive gene map for autism derived by profiling a reference gene set. 2011 , 6, e28431	15
895	Prediction of the Mechanisms of Salvia Miltiorrhiza against Atherosclerosis Using Text Mining and Network-Based Analysis. 2011 , 5, 139-144	3
894	Abnormal expression of FLI1 protein is an adverse prognostic factor in acute myeloid leukemia. 2011 , 118, 5604-12	38

893	Introduction to Systems Biology for Animal Scientists. 2011 , 1-30	5
892	Dissecting the retinoid-induced differentiation of F9 embryonal stem cells by integrative genomics. 2011 , 7, 538	68
891	Proteome-wide systems analysis of a cellulosic biofuel-producing microbe. 2011 , 7, 461	74
890	Exploring and challenging the network of angiogenesis. 2011 , 1, 61	7
889	Pathway Preserving Representation of Metabolic Networks. 2011 , 30, 1021-1030	7
888	Genomic expression profiles of blood and placenta reveal significant immune-related pathways and categories in Chinese women with gestational diabetes mellitus. 2011 , 28, 237-46	34
887	Strong male/male competition allows for nonchoosy females: high levels of polygynandry in a territorial frog with paternal care. 2011 , 20, 1759-71	64
886	Using a genetic network to parameterize a landscape resistance surface for fishers, Martes pennanti. 2011 , 20, 3978-88	50
885	The effects of mitochondrial genotype on hypoxic survival and gene expression in a hybrid population of the killifish, Fundulus heteroclitus. 2011 , 20, 4503-20	22
884	Interactions between flowering and senescence regulation and the influence of low temperature in Arabidopsis and crop plants. 2011 , 159, 320-338	21
883	A review of ecological models for brown trout: towards a new demogenetic model. 2011 , 20, 167-198	30
882	Isoform-specific localization of the deubiquitinase USP33 to the Golgi apparatus. 2011 , 12, 1563-74	23
881	Antagonistic interaction networks among bacteria from a cold soil environment. 2011 , 78, 376-85	20
880	Activation of nuclear factor-kappa B signalling promotes cellular senescence. 2011 , 30, 2356-66	117
879	Gene-ontology enrichment analysis in two independent family-based samples highlights biologically plausible processes for autism spectrum disorders. 2011 , 19, 1082-9	30
878	Peripheral blood gene expression profiles in metabolic syndrome, coronary artery disease and type 2 diabetes. 2011 , 12, 341-51	45
877	Analysis of human and animal fecal microbiota for microbial source tracking. 2011 , 5, 362-5	73
876	Coral-mucus-associated Vibrio integrons in the Great Barrier Reef: genomic hotspots for environmental adaptation. 2011 , 5, 962-72	32

875	Marine bacterial, archaeal and protistan association networks reveal ecological linkages. 2011 , 5, 1414-25	413
874	Dosage suppression genetic interaction networks enhance functional wiring diagrams of the cell. 2011 , 29, 505-11	72
873	Reconstruction of the regulatory network of Lactobacillus plantarum WCFS1 on basis of correlated gene expression and conserved regulatory motifs. 2011 , 4, 333-44	18
872	Drawing networks of rejection - a systems biological approach to the identification of candidate genes in heart transplantation. 2011 , 15, 949-56	8
871	The effects of deoxynivalenol on gene expression in the murine thymus. 2011 , 250, 299-311	22
870	Exposure of Jurkat cells to bis (tri-n-butyltin) oxide (TBTO) induces transcriptomics changes indicative for ER- and oxidative stress, T cell activation and apoptosis. 2011 , 254, 311-22	35
869	Analyzing and visualizing residue networks of protein structures. 2011 , 36, 179-82	182
868	Plasmodium falciparum enolase complements yeast enolase functions and associates with the parasite food vacuole. 2011 , 179, 8-17	11
867	Predicting interactions between T cell receptors and MHC-peptide complexes. 2011 , 48, 553-62	12
866	Proteomic profiling of the human T-cell nucleolus. 2011 , 49, 441-52	35
865	Chemical class-specific gene expression changes in the zebrafish embryo after exposure to glycol ether alkoxy acids and 1,2,4-triazole antifungals. 2011 , 32, 245-52	40
864	Preconceptional paternal glycidamide exposure affects embryonic gene expression: single embryo gene expression study following in vitro fertilization. 2011 , 32, 463-71	10
863	A Network Representation of Households by Health Exclusion, Poverty, and Unemployment. 2011 , 22, 69-79	
862	Metabolomics IA robust bioanalytical approach for the discovery of the modes-of-action of pesticides: A review. 2011 , 100, 105-117	72
861	Interactive, graph-based visual analysis of high-dimensional, multi-parameter fluorescence microscopy data in toponomics. 2011 , 17, 1882-91	7
860	CIGB-300, a proapoptotic peptide, inhibits angiogenesis in vitro and in vivo. 2011 , 317, 1677-88	16
859	Medusa: A tool for exploring and clustering biological networks. 2011 , 4, 384	44
858	Functional Genomics Assistant (FUGA): a toolbox for the analysis of complex biological networks. 2011 , 4, 462	16

857	The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications. 2011 , 2, 4	15
856	Stringent response of Escherichia coli: revisiting the bibliome using literature mining. 2011 , 1, 14	9
855	Dynamic gene network reconstruction from gene expression data in mice after influenza A (H1N1) infection. 2011 , 1, 27	11
854	Population genetic structure and history of a generalist parasite infecting multiple sympatric host species. 2011 , 41, 89-98	59
853	Graphical simulation environments for modelling and simulation of integrative physiology. 2011 , 102, 295-304	8
852	TC-VGC: a tumor classification system using variations in genes' correlation. 2011 , 104, e87-101	6
851	The physiological, transcriptional and genetic responses of an ozone-sensitive and an ozone tolerant poplar and selected extremes of their F2 progeny. 2011 , 159, 45-54	25
850	Directing human embryonic stem cell differentiation by non-viral delivery of siRNA in 3D culture. 2011 , 32, 7793-800	39
849	The influence of scaffold elasticity on germ layer specification of human embryonic stem cells. 2011 , 32, 9612-21	122
848	A methodology based on molecular interactions and pathways to find candidate genes associated to diseases: its application to schizophrenia and Alzheimer's disease. 2011 , 9, 541-57	4
848		73
	to diseases: its application to schizophrenia and Alzheimer's disease. 2011 , 9, 541-57 Lessons learned from molecular scaffold analysis. 2011 , 51, 1742-53	
847	to diseases: its application to schizophrenia and Alzheimer's disease. 2011 , 9, 541-57 Lessons learned from molecular scaffold analysis. 2011 , 51, 1742-53	73
8 ₄₇ 8 ₄ 6	to diseases: its application to schizophrenia and Alzheimer's disease. 2011 , 9, 541-57 Lessons learned from molecular scaffold analysis. 2011 , 51, 1742-53 Mapping the protein interaction network in methicillin-resistant Staphylococcus aureus. 2011 , 10, 1139-50	73 49
847 846 845	Lessons learned from molecular scaffold analysis. 2011, 51, 1742-53 Mapping the protein interaction network in methicillin-resistant Staphylococcus aureus. 2011, 10, 1139-50 Software for systems biology: from tools to integrated platforms. 2011, 12, 821-32 NetDS: a Cytoscape plugin to analyze the robustness of dynamics and feedforward/feedback loop	73 49 191
847 846 845	Lessons learned from molecular scaffold analysis. 2011, 51, 1742-53 Mapping the protein interaction network in methicillin-resistant Staphylococcus aureus. 2011, 10, 1139-50 Software for systems biology: from tools to integrated platforms. 2011, 12, 821-32 NetDS: a Cytoscape plugin to analyze the robustness of dynamics and feedforward/feedback loop structures of biological networks. 2011, 27, 2767-8 Proteomic analysis of virus-host interactions in an infectious context using recombinant viruses.	73 49 191 22
847 846 845 844	Lessons learned from molecular scaffold analysis. 2011, 51, 1742-53 Mapping the protein interaction network in methicillin-resistant Staphylococcus aureus. 2011, 10, 1139-50 Software for systems biology: from tools to integrated platforms. 2011, 12, 821-32 NetDS: a Cytoscape plugin to analyze the robustness of dynamics and feedforward/feedback loop structures of biological networks. 2011, 27, 2767-8 Proteomic analysis of virus-host interactions in an infectious context using recombinant viruses. 2011, 10, M110.007443 Community ecology of hot spring cyanobacterial mats: predominant populations and their	73 49 191 22 42
847 846 845 844 843	Lessons learned from molecular scaffold analysis. 2011, 51, 1742-53 Mapping the protein interaction network in methicillin-resistant Staphylococcus aureus. 2011, 10, 1139-50 Software for systems biology: from tools to integrated platforms. 2011, 12, 821-32 NetDS: a Cytoscape plugin to analyze the robustness of dynamics and feedforward/feedback loop structures of biological networks. 2011, 27, 2767-8 Proteomic analysis of virus-host interactions in an infectious context using recombinant viruses. 2011, 10, M110.007443 Community ecology of hot spring cyanobacterial mats: predominant populations and their functional potential. 2011, 5, 1262-78 Biochemical investigation and gene expression analysis of the immunostimulatory functions of an	73 49 191 22 42

839	Visualizing gene-set enrichment results using the Cytoscape plug-in enrichment map. 2011 , 781, 257-77	51
838	Protein-protein interaction and pathway databases, a graphical review. 2011 , 12, 702-13	49
837	Comparing bioassay response and similarity ensemble approaches to probing protein pharmacology. 2011 , 27, 3044-9	12
836	Cytoscape 2.8: new features for data integration and network visualization. 2011 , 27, 431-2	3291
835	A Heuristic Algorithm for Detecting Intercellular Interactions. 2011,	
834	Embryonic stem cells: protein interaction networks. 2011 , 2, 13-25	10
833	Networks in plant epidemiology: from genes to landscapes, countries, and continents. 2011 , 101, 392-403	69
832	The Structural Biology Knowledgebase: a portal to protein structures, sequences, functions, and methods. 2011 , 12, 45-54	60
831	Metabolomics in pesticide research and development: review and future perspectives. 2011 , 7, 35-53	89
830	Genome-wide gene expression profiles in response to plastid division perturbations. 2011 , 234, 1055-63	4
829	Integrative computational biology for cancer research. 2011 , 130, 465-81	21
828	Proteome analysis of microtubule-associated proteins and their interacting partners from mammalian brain. 2011 , 41, 363-85	14
827	The semantic organization of the animal category: evidence from semantic verbal fluency and network theory. 2011 , 12, 183-96	68
826	The developmental aging and origins of health and disease hypotheses explained by different protein networks. 2011 , 12, 293-308	20
825	Increasing phosphoproteome coverage and identification of phosphorylation motifs through combination of different HPLC fractionation methods. 2011 , 879, 25-34	32
824	Using views of Systems Biology Cloud: application for model building. 2011 , 130, 45-54	1
823	Interactomic study on interaction between lipid droplets and mitochondria. 2011 , 2, 487-96	102
822	Cross experimental analysis of microarray gene expression data from volatile organic compounds treated targets. 2011 , 7, 233-241	10

821	Potential synergistic and multitarget effect of herbal pair Chuanxiong Rhizome-Paeonia Albifora Pall on osteoarthritis disease: a computational pharmacology approach. 2011 , 17, 698-703	14
820	Correlation between cold and hot pattern in traditional Chinese medicine and gene expression profiles in rheumatoid arthritis. 2011 , 5, 219-28	29
819	Ai2NU: A Cytoscape plugin for uniformization of biomolecular accession identifiers. 2011 , 15, 456-462	
818	Effects of abiotic stress on plants: a systems biology perspective. 2011 , 11, 163	771
817	Dengue-2 structural proteins associate with human proteins to produce a coagulation and innate immune response biased interactome. 2011 , 11, 34	17
816	Construction of gene regulatory networks using biclustering and Bayesian networks. 2011 , 8, 39	15
815	Nonsynonymous substitution rate (Ka) is a relatively consistent parameter for defining fast-evolving and slow-evolving protein-coding genes. 2011 , 6, 13	27
814	Multi-membership gene regulation in pathway based microarray analysis. 2011 , 6, 22	3
813	Decreased expression of B cell related genes in leukocytes of women with Parkinson's disease. 2011 , 6, 66	16
812	WordCloud: a Cytoscape plugin to create a visual semantic summary of networks. 2011 , 6, 7	66
811	A metabolic model of the mitochondrion and its use in modelling diseases of the tricarboxylic acid cycle. 2011 , 5, 102	51
810	Simulating quantitative cellular responses using asynchronous threshold Boolean network ensembles. 2011 , 5, 109	25
809	Exploring pathway interactions in insulin resistant mouse liver. 2011 , 5, 127	14
808	Genomic phenotyping of the essential and non-essential yeast genome detects novel pathways for alkylation resistance. 2011 , 5, 157	17
807	Prioritizing cancer-related genes with aberrant methylation based on a weighted protein-protein interaction network. 2011 , 5, 158	16
806	Identifying cancer biomarkers by network-constrained support vector machines. 2011 , 5, 161	61
805	Initial characterization of the human central proteome. 2011 , 5, 17	56
804	Genome-scale reconstruction and system level investigation of the metabolic network of Methylobacterium extorquens AM1. 2011 , 5, 189	91

803	Dynamic proteomic profiling of a unicellular cyanobacterium Cyanothece ATCC51142 across light-dark diurnal cycles. 2011 , 5, 194	34
802	Model-based clustering reveals vitamin D dependent multi-centrality hubs in a network of vitamin-related proteins. 2011 , 5, 195	11
801	Regulatory coordination of clustered microRNAs based on microRNA-transcription factor regulatory network. 2011 , 5, 199	43
800	Codon usage variability determines the correlation between proteome and transcriptome fold changes. 2011 , 5, 33	30
799	Knowledge management for systems biology a general and visually driven framework applied to translational medicine. 2011 , 5, 38	36
798	Predictive integration of gene functional similarity and co-expression defines treatment response of endothelial progenitor cells. 2011 , 5, 46	7
797	Global network analysis of drug tolerance, mode of action and virulence in methicillin-resistant S. aureus. 2011 , 5, 68	31
796	BiologicalNetworkstools enabling the integration of multi-scale data for the host-pathogen studies. 2011 , 5, 7	17
795	Using next generation transcriptome sequencing to predict an ectomycorrhizal metabolome. 2011 , 5, 70	52
794	Understanding and predicting synthetic lethal genetic interactions in Saccharomyces cerevisiae using domain genetic interactions. 2011 , 5, 73	9
793	Large-scale analysis of expression signatures reveals hidden links among diverse cellular processes. 2011 , 5, 87	6
79 ²	Characterization the regulation of herpesvirus miRNAs from the view of human protein interaction network. 2011 , 5, 93	4
791	Proteomic patterns of cervical cancer cell lines, a network perspective. 2011 , 5, 96	46
790	State Space Model with hidden variables for reconstruction of gene regulatory networks. 2011 , 5 Suppl 3, S3	9
789	A network-based biomarker approach for molecular investigation and diagnosis of lung cancer. 2011 , 4, 2	64
788	CDCOCA: a statistical method to define complexity dependence of co-occuring chromosomal aberrations. 2011 , 4, 21	6
787	Cell cycle and aging, morphogenesis, and response to stimuli genes are individualized biomarkers of glioblastoma progression and survival. 2011 , 4, 49	65
786	Transforming growth factor [receptor 1 is a new candidate prognostic biomarker after acute myocardial infarction. 2011 , 4, 83	26

785	Using graph theory to analyze biological networks. 2011 , 4, 10	357
784	The Regulatory Network of Pseudomonas aeruginosa. 2011 , 1, 3	45
783	Predicted Relative Metabolomic Turnover (PRMT): determining metabolic turnover from a coastal marine metagenomic dataset. 2011 , 1, 4	73
782	The PathOlogist: an automated tool for pathway-centric analysis. 2011 , 12, 133	28
781	CASCADE_SCAN: mining signal transduction network from high-throughput data based on steepest descent method. 2011 , 12, 164	11
780	Web-based metabolic network visualization with a zooming user interface. 2011 , 12, 176	26
779	Context-dependent transcriptional regulations between signal transduction pathways. 2011 , 12, 19	4
778	Mapping the distribution of packing topologies within protein interiors shows predominant preference for specific packing motifs. 2011 , 12, 195	15
777	GraphCrunch 2: Software tool for network modeling, alignment and clustering. 2011 , 12, 24	52
776	Bio::Homology::InterologWalka Perl module to build putative protein-protein interaction networks through interolog mapping. 2011 , 12, 289	11
775	GPS-Prot: a web-based visualization platform for integrating host-pathogen interaction data. 2011 , 12, 298	43
774	NETGEM: Network Embedded Temporal GEnerative Model for gene expression data. 2011 , 12, 327	6
773	Quantitative utilization of prior biological knowledge in the Bayesian network modeling of gene expression data. 2011 , 12, 359	16
772	iCTNet: a Cytoscape plugin to produce and analyze integrative complex traits networks. 2011 , 12, 380	30
771	iRefScape. A Cytoscape plug-in for visualization and data mining of protein interaction data from iRefIndex. 2011 , 12, 388	13
770	clusterMaker: a multi-algorithm clustering plugin for Cytoscape. 2011 , 12, 436	337
769	Network based transcription factor analysis of regenerating axolotl limbs. 2011 , 12, 80	20
768	Network-based functional enrichment. 2011 , 12 Suppl 13, S14	10

767	SNP and gene networks construction and analysis from classification of copy number variations data. 2011 , 12 Suppl 5, S4	10
766	Proceedings of the Tenth Annual UT-ORNL-KBRIN Bioinformatics Summit 2011. 2011 , 12 Suppl 7, A1	
765	Functional specialization in nucleotide sugar transporters occurred through differentiation of the gene cluster EamA (DUF6) before the radiation of Viridiplantae. 2011 , 11, 123	28
764	Molecular evolution of the vertebrate TLR1 gene familya complex history of gene duplication, gene conversion, positive selection and co-evolution. 2011 , 11, 149	50
763	Genetic adaptation of the antibacterial human innate immunity network. 2011 , 11, 202	20
762	Visualization and exploration of conserved regulatory modules using ReXSpecies 2. 2011 , 11, 267	3
761	Comparative tissue transcriptomics reveal prompt inter-organ communication in response to local bacterial kidney infection. 2011 , 12, 123	13
760	Common and unique elements of the ABA-regulated transcriptome of Arabidopsis guard cells. 2011 , 12, 216	134
759	MicroRNA genes preferentially expressed in dendritic cells contain sites for conserved transcription factor binding motifs in their promoters. 2011 , 12, 330	20
758	Drosophila selenophosphate synthetase 1 regulates vitamin B6 metabolism: prediction and confirmation. 2011 , 12, 426	14
757	Functional annotation of the transcriptome of Sorghum bicolor in response to osmotic stress and abscisic acid. 2011 , 12, 514	153
756	Comparative analysis and assessment of M. tuberculosis H37Rv protein-protein interaction datasets. 2011 , 12 Suppl 3, S20	24
755	Predicting sequence and structural specificities of RNA binding regions recognized by splicing factor SRSF1. 2011 , 12 Suppl 5, S8	20
754	Ontology-based Brucella vaccine literature indexing and systematic analysis of gene-vaccine association network. 2011 , 12, 49	29
753	Caries induced cytokine network in the odontoblast layer of human teeth. 2011 , 12, 9	70
75 ²	Identification of functional motions in the adenylate kinase (ADK) protein family by computational hybrid approaches. 2011 , 79, 1662-71	12
751	The evolution of function in strictosidine synthase-like proteins. 2011 , 79, 3082-98	39
750	Combining peptide recognition specificity and context information for the prediction of the 14-3-3-mediated interactome in S. cerevisiae and H. sapiens. 2011 , 11, 128-43	32

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749	The Protein Information and Property Explorer 2: gaggle-like exploration of biological proteomic data within one webpage. 2011 , 11, 154-8	9
748	Four-dimensional visualisation and analysis of protein-protein interaction networks. 2011 , 11, 2672-82	14
747	An expanded protein-protein interaction network in Bacillus subtilis reveals a group of hubs: Exploration by an integrative approach. 2011 , 11, 2981-91	43
746	Reactome pathway analysis to enrich biological discovery in proteomics data sets. 2011 , 11, 3598-613	71
745	Quantitative proteomics of microbes: Principles and applications to virulence. 2011 , 11, 2947-56	22
744	Advances in analysis of transcriptional regulatory networks. 2011 , 3, 21-35	27
743	Adaptation of cells to new environments. 2011 , 3, 544-61	112
742	Occurrence and distribution of pineapple mealybug wilt-associated viruses (PMWaVs) in MD2 pineapple fields in the Valle del Cauca Department, Colombia. 2023 , 48, 217-225	О
741	Expression of EMT-related genes in lymph node metastasis in endometrial cancer: a TCGA-based study. 2023 , 21,	O
740	Identifying immune cell infiltration and constructing a ceRNA network to explore novel diagnostic biomarkers and therapeutic targets in atopic dermatitis.	O
739	Exploring Core Genes by Comparative Transcriptomics Analysis for Early Diagnosis, Prognosis, and Therapies of Colorectal Cancer. 2023 , 15, 1369	О
738	New Phenylspirodrimanes from the Sponge-Associated Fungus Stachybotrys chartarum MUT 3308. 2023 , 21, 135	O
737	Identification of Parkinson⊠ disease-associated chromatin regulators. 2023 , 13,	O
736	Fecal Microbiota, Forage Nutrients, and Metabolic Responses of Horses Grazing Warm- and Cool-Season Grass Pastures. 2023 , 13, 790	O
735	ARPC1A correlates with poor prognosis in prostate cancer and is up-regulated by glutamine metabolism to promote tumor cell migration, invasion and cytoskeletal changes. 2023 , 13,	O
734	Dynamics of bacterial community in the foregut and hindgut of earthworms with the nutrition supplied by kitchen waste during vermicomposting. 2023 , 374, 128777	O
733	Proteomic Variability and Nutrient-Related Proteins across Pigmented and Non-Pigmented Rice Grains. 2023 , 3, 63-77	О
732	USP15 Represses Hepatocellular Carcinoma Progression by Regulation of Pathways of Cell Proliferation and Cell Migration: A System Biology Analysis. 2023 , 15, 1371	О

731	Exploiting moderate hypoxia to benefit patients with brain disease: Molecular mechanisms and translational research in progress.	O
730	Androgen Receptor driven gene score identifies tumors with Epithelial to Mesenchymal Transition features in triple negative breast cancer.	O
729	Pharmacology-Based Prediction of the Targets and Mechanisms for Icariin against Myocardial Infarction. 2023 , 59, 420	O
728	Epigenetic association study uncovered H3K27 acetylation enhancers and dysregulated genes in high-fat-diet-induced nonalcoholic fatty liver disease in rats. 2022 , 14, 1523-1540	O
727	The gut microbiota in experimental abdominal aortic aneurysm. 10,	0
726	Comparative transcriptome analysis of adult worker bees under short-term heat stress. 11,	O
725	Coupling Environmental Whole Mixture Toxicity Screening with Unbiased RNA-Seq Reveals Site-Specific Biological Responses in Zebrafish. 2023 , 11, 201	O
724	Identification of the regulatory network and potential markers for type 2 diabetes mellitus related to internal exposure to metals in Chinese adults.	O
723	Feasibility of detecting snake envenomation biomarkers from dried blood spots. 2023 , 4, 26-36	O
722	Beyond bacteria: Reconstructing microorganism connections and deciphering the predicted mutualisms in mammalian gut metagenomes. 2023 , 13,	O
721	RNA m6A methylation regulator-mediated modification patterns and tumor microenvironment characterization in hepatocellular carcinoma.	O
720	A conserved gene regulatory network controls root epidermal cell patterning in superrosid species.	O
719	Skeletal dysplasia-causing TRPV4 mutations suppress the hypertrophic differentiation of human iPSC-derived chondrocytes. 12,	O
718	Effects of Long-Term Physical Activity and BCAA Availability on the Subcellular Associations between Intramyocellular Lipids, Perilipins and PGC-1⊕2023, 24, 4282	O
717	Probing the Mechanisms of Inhibitors Binding to Presenilin Homologue Using Molecular Dynamics Simulations. 2023 , 28, 2076	O
716	Single-cell transcriptomic dissection of the cellular and molecular events underlying the triclosan-induced liver fibrosis in mice. 2023 , 10,	O
715	Liquid Crystal Monomer: A Potential PPAR Antagonist. 2023, 57, 3758-3771	0
714	Exploring Myocardial Ischemia-Reperfusion Injury Mechanism of Cinnamon by Network Pharmacology, Molecular Docking, and Experiment Validation. 2023 , 2023, 1-14	O

713	Whole transcriptome analysis to explore the impaired immunological features in critically ill elderly patients with sepsis. 2023 , 21,	O
712	Anastrozole-mediated modulation of mitochondrial activity by inhibition of mitochondrial permeability transition pore opening: an initial perspective. 1-17	O
711	Proteomic Fingerprint of Lung Fibrosis Progression and Response to Therapy in Bleomycin-Induced Mouse Model. 2023 , 24, 4410	О
710	IMPPAT 2.0: An Enhanced and Expanded Phytochemical Atlas of Indian Medicinal Plants. 2023 , 8, 8827-8845	O
709	Identification of hub genes associated with osteoporosis development by comprehensive bioinformatics analysis. 14,	О
708	A comprehensive pan-cancer analysis reveals cancer-associated robust isomiR expression landscapes in miRNA arm switching.	O
707	Comparative and Temporal Characterization of LPS and Blue-Light-Induced TLR4 Signal Transduction and Gene Expression in Optogenetically Manipulated Endothelial Cells. 2023 , 12, 697	О
706	Comprehensive analysis reveals hub genes associated with immune cell infiltration in allergic rhinitis.	O
705	Co-expression network of mRNA and DNA methylation in first-episode and drug-naive adolescents with major depressive disorder. 14,	О
704	Dimensionality reduction methods for extracting functional networks from large-scale CRISPR screens.	O
703	Discovery-Based Proteomics Identify Skeletal Muscle Mitochondrial Alterations as an Early Metabolic Defect in a Mouse Model of EThalassemia. 2023 , 24, 4402	О
702	Potential diagnostic markers and therapeutic targets for rheumatoid arthritis with comorbid depression based on bioinformatics analysis. 14,	O
701	Comparative gene regulatory network analysis in Alzheimer disease and major depressive disorder.	О
700	Network analysis of 16S rRNA sequences suggests microbial keystone taxa contribute to marine N2O cycling. 2023 , 6,	Ο
699	Identification of novel prognostic targets in coronary artery disease and related complications using bioinformatics and next generation sequencing data analysis.	О
698	PI3K/AKT/SERBP-1 pathway regulates Alisma orientalis beverage treatment of atherosclerosis in APOE/Ihigh-fat diet mice. 2023 , 61, 473-487	Ο
697	Comprehensive study of rice YABBY gene family: evolution, expression and interacting proteins analysis. 11, e14783	О
696	FTSH3 facilitates complex I degradation through a direct interaction with the complex I subunit PSST.	O

695	Sour Orange Microbiome Is Affected by Infections of Plenodomus tracheiphilus Causal Agent of Citrus Mal Secco Disease. 2023 , 13, 654	O
694	Network pharmacology and bioinformatics study on the treatment of renal fibrosis with persicae semen-carthami flos drug pair. 2023 , 102, e32946	O
693	Single-cell transcriptomic analysis in two patients with rare systemic autoinflammatory diseases treated with anti-TNF therapy. 14,	О
692	DNA damage, nucleolar stress and dysregulated energy metabolism as mechanisms of multimorbidity.	O
691	Complete Workflow for High Throughput Human Single Skeletal Muscle Fiber Proteomics.	0
690	A novel method for multiple phenotype association studies based on genotype and phenotype network.	O
689	Identifying Eukaryotes and Factors Influencing Their Biogeography in Drinking Water Metagenomes. 2023 , 57, 3645-3660	0
688	Visualizing Semantic Web Data using Various Tools Focusing RDF, OWL and SPARQL. 2022,	Ο
687	Ecogenomics reveals distinctive viral-bacterial communities in the surface microlayer of a natural surface slick.	0
686	Dietary intake of table olives exerts antihypertensive effects in association with changes in gut microbiota in spontaneously hypertensive rats. 2023 , 14, 2793-2806	O
685	Phenolic acids-rich fraction from Ficus drupacea leaves for the prevention and treatment of ethanol-induced gastric mucosal injury in rats.	0
684	A novel circRNA, hsa_circ_0069382, regulates gastric cancer progression. 2023 , 23,	O
683	Duo-role Platelet-rich Plasma: temperature-induced fibrin gel and growth factorslieservoir for microneedles to promote hair regrowth. 2023 ,	0
682	Association of Circular RNAs levels in blood and Essential Hypertension with Carotid Plaque. 2023 , 45,	O
681	Elucidation of the Late Steps during Hexacosalactone A Biosynthesis in Streptomyces samsunensis OUCT16-12. 2023 , 89,	O
680	Identification and validation of metabolism-related hub genes in idiopathic pulmonary fibrosis. 14,	O
679	Network pharmacology and bioinformatics analysis on the underlying mechanisms of baicalein against oral squamous cell carcinoma.	O
678	Studying the mechanism underlying lipid metabolism in osteosarcoma based on transcriptomic RNA sequencing and single-cell data.	O

677	Twenty Novel MicroRNAs in the Aqueous Humor of Pseudoexfoliation Glaucoma Patients. 2023, 12, 737	O
676	Comparative transcriptomic and metabolomic analyses reveal differences in flavonoid biosynthesis between PCNA and PCA persimmon fruit. 14,	1
675	Genome-Wide Investigation of the NAC Transcription Factor Family in Apocynum venetum Revealed Their Synergistic Roles in Abiotic Stress Response and Trehalose Metabolism. 2023 , 24, 4578	0
674	Investigation on Metabolites in Structure and Biosynthesis from the Deep-Sea Sediment-Derived Actinomycete Janibacter sp. SCSIO 52865. 2023 , 28, 2133	O
673	Analysis of proteomes I 2023, 111-138	O
672	CD40LG and GZMB were correlated with adipose tissue macrophage infiltration and involved in obstructive sleep apnea related metabolic dysregulation: Evidence from bioinformatics analysis. 14,	O
671	Machine Learning Model Based on Insulin Resistance Metagenes Underpins Genetic Basis of Type 2 Diabetes. 2023 , 13, 432	0
670	From the Sunlit to the Aphotic Zone: Assembly Mechanisms and Co-Occurrence Patterns of Protistan-Bacterial Microbiotas in the Western Pacific Ocean.	O
669	Integrated mRNA and miRNA expression analyses for Cryptocaryon irritans resistance in large yellow croaker (Larimichthys crocea). 2023 , 135, 108650	O
668	Homocysteine impedes neurite outgrowth recovery after intracerebral haemorrhage by downregulating pCAMK2A. svn-2022-002165	O
667	Life-Threatening Cardiogenic Shock Related to Venlafaxine Poisoning Case Report with Metabolomic Approach. 2023 , 13, 353	0
666	The eukaryotic translation initiation factor eIF4E reprograms alternative splicing. 2023, 42,	O
665	Decitabine priming increases anti P D-1 antitumor efficacy by promoting CD8+ progenitor exhausted T cell expansion in tumor models. 2023 , 133,	0
664	Genome-Wide Identification and Expression Analysis of RCC1 Gene Family under Abiotic Stresses in Rice (Oryza sativa L.). 2023 , 13, 703	O
663	Requirements for establishment and epigenetic stability of mammalian heterochromatin.	O
662	Differential Expression Analysis of Blood MicroRNA in Identifying Potential Genes Relevant to Alzheimer Disease Pathogenesis, Using an Integrated Bioinformatics and Machine Learning Approach. 2023 , 13, 3071	O
661	Meta-Analysis of Exploring the Effect of Curcumin Supplementation with or without Other Advice on Biochemical and Anthropometric Parameters in Patients with Metabolic-Associated Fatty Liver Disease (MAFLD). 2023 , 20, 4266	О
660	Imbalanced IL-1B and IL-18 Expression in SZary Syndrome. 2023 , 24, 4674	Ο

659	Integrated proteome and acetylome analyses provide novel insights into early somatic embryogenesis of Dimocarpus longan. 2023 , 196, 903-916	O
658	Combined Multiomics and In Silico Approach Uncovers PRKAR1A as a Putative Therapeutic Target in Multi-Organ Dysfunction Syndrome. 2023 , 8, 9555-9568	O
657	Therapeutic Target Identification in Pancreatic Ductal Adenocarcinoma: A Comprehensive In-Silico Study employing WGCNA and Trader.	0
656	Use of an Integrated Multi-Omics Approach To Identify Molecular Mechanisms and Critical Factors Involved in the Pathogenesis of Leptospira. 2023 , 11,	O
655	Tcf21 marks visceral adipose mesenchymal progenitors and functions as a rate-limiting factor during visceral adipose tissue development. 2023 , 42, 112166	0
654	Bifidobacterium-derived short-chain fatty acids and indole compounds attenuate nonalcoholic fatty liver disease by modulating gut-liver axis. 14,	O
653	The Transcription Factor Twist1 Has a Significant Role in Mycosis Fungoides (MF) Cell Biology: An RNA Sequencing Study of 40 MF Cases. 2023 , 15, 1527	0
652	AUF1 Recognizes 8-Oxo-Guanosine Embedded in DNA and Stimulates APE1 Endoribonuclease Activity.	O
651	Quantitative Proteomics Reveal the Inherent Antibiotic Resistance Mechanism against Norfloxacin Resistance in Aeromonas hydrophila. 2023 , 22, 1193-1200	0
650	Microbial profiles and immune responses in seahorse gut and brood pouch under chronic exposure to environmental antibiotics. 2023 , 253, 114711	O
649	Analysis for drug metabolism-related prognostic subtypes and gene signature in liver cancer. 2022 , 97, 271-284	O
648	Identification and verification of feature biomarkers associated in heart failure by bioinformatics analysis. 2023 , 13,	O
647	Identification of autophagy-related genes in neuropathic pain through bioinformatic analysis. 2023 , 160,	O
646	Proteomic analysis identifies dysregulated proteins and associated molecular pathways in a cohort of gallbladder cancer patients of African ancestry. 2023 , 20,	O
645	Integrated analysis of Dendrobium nobile extract Dendrobin A against pancreatic ductal adenocarcinoma based on network pharmacology, bioinformatics, and validation experiments. 14,	O
644	A New Technique for Use in Culturing Prokaryotes Comprising the Mouse Intestinal Microbiome. 2023 , 13, 119-147	O
643	Molecular characterization of circadian gene expression and its correlation with survival percentage in colorectal cancer patients. 2023 ,	O
642	Circular RNA Expression Signatures Provide Promising Diagnostic and Therapeutic Biomarkers for Chronic Lymphocytic Leukemia. 2023 , 15, 1554	O

641	Elucidation of Phytochemicals Affecting Platelet Responsiveness in Dangguisu-san: Active Ingredient Prediction and Experimental Research Using Network Pharmacology. 2023 , 12, 1120	О
640	Involvement of 2?-5? oligoadenylate synthetase-like protein in the survival of Mycobacterium tuberculosis avirulent strain in macrophages. 2023 , 3,	O
639	Associating brain imaging phenotypes and genetic risk factors via a hypergraph based netNMF method. 15,	О
638	Identification of miR-671-5p and Its Related Pathways as General Mechanisms of Both Form-Deprivation and Lens-Induced Myopia in Mice. 2023 , 45, 2060-2072	O
637	The IL-10 receptor inhibits cell extrinsic signals necessary for STAT1-dependent macrophage accumulation during colitis. 2023 ,	0
636	An updated C. elegans nuclear body muscle transcriptome for studies in muscle formation and function. 2023 , 13,	O
635	Whole-transcriptome analyses identify key differentially expressed mRNAs, lncRNAs, and miRNAs associated with male sterility in watermelon. 14,	О
634	Diversity and potential function of pig gut DNA viruses. 2023 , 9, e14020	О
633	Network-informed discovery of multidrug combinations for ER⊞/HER2-/PI3K⊞mutant breast cancer. 2023 , 80,	О
632	CYP27A1 deficiency promoted osteoclast differentiation. 11, e15041	O
631	ARF-family global interactome mapping uncovers spatial organization of cellular signaling pathways.	0
630	Unique metabolism and protein expression signature in human decidual NK cells. 14,	О
629	Integrated Bioinformatics Analysis of Shared Genes, miRNA, Biological Pathways and Their Potential Role as Therapeutic Targets in Huntington Disease Stages. 2023 , 24, 4873	О
628	A gene regulatory network for neural induction. 12,	О
627	Short-term transcriptomic analysis at organ scale reveals candidate genes involved in low N responses in NUE-contrasting tomato genotypes. 14,	0
626	A direct examination of microbial specialized metabolites associated with ocean sediments from Baffin Bay and the Gulf of Maine.	O
625	Transcriptome profile of skeletal muscle using different sources of dietary fatty acids in male pigs. 2023 , 23,	О
624	MyeloidZfhx3Deficiency Protects Against Hypercapnia-induced Suppression of Host Defense Against Influenza A Virus.	O

623	Single-cell sequencing reveals the evolution of immune molecules across multiple vertebrate species. 2023 ,	О
622	RNA sequencing analysis of the longissimus dorsi to identify candidate genes underlying the intramuscular fat content in Anqing Six-end-white pigs.	O
621	Omics and imaging combinatorial approach reveals butyrate-induced inflammatory effects in the zebrafish gut. 2023 , 5,	О
620	Experimental community coalescence sheds light on microbial interactions in soil and restores impaired functions. 2023 , 11,	O
619	Maternal obesity and gestational diabetes reprogram the methylome of offspring beyond birth by inducing epigenetic signatures in metabolic and developmental pathways. 2023 , 22,	О
618	MAW: the reproducible Metabolome Annotation Workflow for untargeted tandem mass spectrometry. 2023 , 15,	O
617	Type I interferon signaling induces a delayed antiproliferative response in Calu-3 cells during SARS-CoV-2 infection.	О
616	BRD9-SMAD2/3 orchestrates stemness and tumorigenesis in pancreatic ductal adenocarcinoma.	O
615	The mechanism of Croci stigma in the treatment of melasma based on network pharmacology and molecular docking.	O
614	Bioinformatics and cheminformatics approaches to identify pathways, molecular mechanisms and drug substances related to genetic basis of cervical cancer. 1-16	O
613	NDEx IQuery: a multi-method network gene set analysis leveraging the Network Data Exchange. 2023 , 39,	О
612	A mechanistic analysis of spontaneous cancer remission phenomenon: identification of genomic basis and effector biomolecules for therapeutic applicability. 2023 , 13,	O
611	Mycobiome structure does not affect field litter decomposition in Eucalyptus and Acacia plantations. 14,	О
610	miRNome and Proteome Profiling of Human Keratinocytes and Adipose Derived Stem Cells Proposed miRNA-Mediated Regulations of Epidermal Growth Factor and Interleukin 1-Alpha. 2023 , 24, 4956	O
609	Identification and Analysis of Necroptosis-Related Genes in COPD by Bioinformatics and Experimental Verification. 2023 , 13, 482	О
608	StkP- and PhpP-Mediated Posttranslational Modifications Modulate the S. pneumoniae Metabolism, Polysaccharide Capsule, and Virulence. 2023 , 91,	O
607	Transcriptome Analysis Reveals Differentially Expressed Genes Involved in Cadmium and Arsenic Accumulation in Tea Plant (Camellia sinensis). 2023 , 12, 1182	О
606	Phylogeny, Expression Profiling, and Coexpression Networks Reveals the Critical Roles of Nucleotide-BindingLeucine-Rich Repeats on Valsa Canker Resistance. 2023 , 9, 345	O

605	Data-Driven Radiogenomic Approach for Deciphering Molecular Mechanisms Underlying Imaging Phenotypes in Lung Adenocarcinoma: A Pilot Study. 2023 , 24, 4947	O
604	Development and Experimental Validation of a Novel Prognostic Signature for Gastric Cancer. 2023 , 15, 1610	O
603	Identification of Distinct Vaginal Microbiota Signatures Contributing Toward Preterm Birth Using an Integrative Computational Approach. 2023 , 51, 109-123	O
602	Computational analysis of crosstalk between transcriptional regulators and RNA-binding proteins suggests mutual regulation of polycomb proteins and SRSF1 influencing adult hippocampal neurogenesis. 2023 , 3,	O
601	Genome-Wide Identification and Expression Analysis of the HSF Gene Family in Poplar. 2023, 14, 510	O
600	Transcriptomic analysis of the cerebral hippocampal tissue in spontaneously hypertensive rats exposed to acute hypobaric hypoxia: associations with inflammation and energy metabolism. 2023 , 13,	O
599	Transcriptome sequencing and microRNAthRNA regulatory network construction in the lens from a Na 2 Se0 3 -induced Sprague Dawley rat cataract model.	0
598	Identification of a novel circRNAthiRNAthRNA regulatory axis in hepatocellular carcinoma based on bioinformatics analysis. 2023 , 13,	O
597	Proteome Dynamics Analysis Reveals the Potential Mechanisms of Salinity and Drought Response during Seed Germination and Seedling Growth in Tamarix hispida. 2023 , 14, 656	0
596	Detection and targeting of splicing deregulation in pediatric acute myeloid leukemia stem cells. 2023 , 4, 100962	O
595	The proteome and transcriptome of stress granules and P bodies during human T lymphocyte activation. 2023 , 42, 112211	O
594	Small Moleculein situResin Capture - an Organism Independent Strategy for Natural Product Discovery.	O
593	The shared genetic architecture of suicidal behaviour and psychiatric disorders: A genomic structural equation modelling study. 14,	О
592	Insights into the mechanisms of triptolide nephrotoxicity through network pharmacology-based analysis and RNA-seq. 14,	O
591	Integrative single-cell transcriptome analysis reveals new insights into post-COVID-19 pulmonary fibrosis and potential therapeutic targets.	O
590	Parental Preconception and Pre-Hatch Exposure to A Developmental Insult Alters Offspring Gene Expression and Epigenetic Regulations: An Avian Model. 2023 , 24, 5047	O
589	Terpene synthases and pathways in animals: enzymology and structural evolution in the biosynthesis of volatile infochemicals.	0
588	Identification of ferroptosis-related diagnostic biomarkers in ischemic cardiomyopathy Abstract.	O

587	A knowledge empowered explainable gene ontology fingerprint approach to improve gene functional explication and prediction. 2023 , 26, 106356	0
586	Quantitative Proteomics of Nervous System Regeneration: From Sample Preparation to Functional Data Analyses. 2023 , 343-366	O
585	Simultaneous Analysis of Single-nucleus Transcriptome and Chromatin Accessibility Unveils the Mechanisms of Leaf Cell Development in Arachis hypogaea L	0
584	The rotation of Phallus impudicus benefits the soil microenvironment via improving the soil microbiome structure and soil properties.	0
583	Development of an immune-related gene prognostic risk model and identification of an immune infiltration signature in the tumor microenvironment of colon cancer. 2023 , 23,	0
582	Integrated bioinformatics analysis identifies shared immune changes between ischemic stroke and COVID 19. 14,	0
581	Exploring the components and mechanism of Solanum nigrum L. for colon cancer treatment based on network pharmacology and molecular docking. 13,	0
580	Brain injury accelerates the onset of a reversible age-related microglial phenotype associated with inflammatory neurodegeneration. 2023 , 9,	O
579	Data-Independent Acquisition Proteomics Reveals the Effects of Red and Blue Light on the Growth and Development of Moso Bamboo (Phyllostachys edulis) Seedlings. 2023 , 24, 5103	0
578	Unique gene duplications and conserved microsynteny potentially associated with resistance to wood decay in the Lauraceae. 14,	O
577	Gene Expression Profiling Unveils the Temporal Dynamics of CIGB-300-Regulated Transcriptome in AML Cells.	0
576	A meta-analysis of genome-wide association studies of childhood wheezing phenotypes identifiesANXA1as a susceptibility locus for persistent wheezing.	O
575	Urban living can rescue Darwin⊠ finches from the lethal effects of invasive vampire flies.	0
574	Evidence of polygenic regulation of the physiological presence of neurofilament light chain in human serum. 14,	O
573	Overexpression of Parkin in the Neuronal Progenitor Cells from a Patient with Parkinson Disease Shifts the Transcriptome Towards the Normal State.	0
572	Tissue-embedded stretchable nanoelectronics reveal endothelial cellfhediated electrical maturation of human 3D cardiac microtissues. 2023 , 9,	0
571	Genomic Analysis, Evolution and Characterization of E3 Ubiquitin Protein Ligase (TRIM) Gene Family in Common Carp (Cyprinus carpio). 2023 , 14, 667	0
570	The use of data independent acquisition based proteomic analysis and machine learning to reveal potential biomarkers for autism spectrum disorder. 2023 , 278, 104872	O

569	Integrated analysis of cell-specific gene expression in peripheral blood using ISG15 as a marker of rejection in kidney transplantation. 14,	O
568	An EBV-associated atypical B cell signature in clinically isolated syndrome is implicated in progression of multiple sclerosis.	O
567	An Integrated Analysis of Network Pharmacology, Molecular Docking, and Experiment Validation to Explore the Mechanism of Danbai Granules in Treating Sequelae of Pelvic Inflammatory Disease.	0
566	Discovery of therapeutic targets of quercetin for endometrial carcinoma patients infected with COVID-19 through network pharmacology. 13,	O
565	Genome-wide association studies for additive and dominance effects for body composition traits in commercial crossbred PiErain pigs.	0
564	Comparative Analyses of Human Exosome Proteomes.	1
563	Phototrophic Biofilms Transform Soil-Dissolved Organic Matter Similarly Despite Compositional and Environmental Differences. 2023 , 57, 4679-4689	0
562	Prioritization of Microorganisms Isolated from the Indian Ocean Sponge Scopalina hapalia Based on Metabolomic Diversity and Biological Activity for the Discovery of Natural Products. 2023 , 11, 697	o
561	Variation in synonymous evolutionary rates in the SARS-CoV-2 genome. 14,	0
560	Novel Data Science Methodologies for Essential Genes Identification Based on Network Analysis. 2023 , 117-145	o
559	Molecular mechanism and diagnostic marker investigation of endoplasmic reticulum stress on periodontitis. 2023 , 23,	0
558	Bulk and single-cell transcriptome analyses of islet tissue unravel gene signatures associated with pyroptosis and immune infiltration in type 2 diabetes. 14,	o
557	Comparative transcriptome analysis identifies candidate genes related to seed coat color in rapeseed. 14,	0
556	Platelet-Derived MicroRNAs Regulate Cardiac Remodeling After Myocardial Ischemia. 2023 , 132,	0
555	Identification of immune-related genes in diagnosing atherosclerosis with rheumatoid arthritis through bioinformatics analysis and machine learning. 14,	0
554	Bioherbicidal Activity and Metabolic Profiling of Allelopathic Metabolites of Three Cassia species using UPLC-qTOF-MS/MS and Molecular Networking. 2023 , 19,	0
553	Analysis of Corynebacterium silvaticum genomes from Portugal reveals a single cluster and a clade suggested to produce diphtheria toxin. 11, e14895	О
552	GWAS and genetic and phenotypic correlations of plasma metabolites with complete blood count traits in healthy young pigs reveal implications for pig immune response. 10,	O

551	Operant training for highly palatable food alters translating mRNA in nucleus accumbens D2 neurons and reveals a modulatory role ofNeurochondrin.	0
550	Proteomic and Bioinformatic Tools to Identify Potential Hub Proteins in the Audiogenic Seizure-Prone Hamster GASH/Sal. 2023 , 13, 1048	O
549	The human sperm proteomelloward a panel for male fertility testing.	0
548	Integrated analyses of single-cell RNA-seq public data reveal the gene regulatory network landscape of respiratory epithelial and peripheral immune cells in COVID-19 patients.	O
547	Dissecting the effect of ethylene in the transcriptional regulation of chilling treatment in grapevine leaves. 2023 , 196, 1084-1097	O
546	Network pharmacology and experimental validation to reveal the target of matrine against PRRSV. 2023 , 26, 106371	O
545	Debottlenecking and reformulating feed media for improved CHO cell growth and titer by data-driven and model-guided analyses.	О
544	Bioinformatics analysis and verification of m6A related genes based on the construction of keloid diagnostic model.	O
543	Development and validation of a genomic nomogram based on a ceRNA network for comprehensive analysis of obstructive sleep apnea. 14,	О
542	Dissection of the role of a SH3 domain in the evolution of binding preference of paralogous proteins.	O
541	Transcriptome and Co-Expression Network Analysis Reveals the Molecular Mechanism of Rice Root Systems in Response to Low-Nitrogen Conditions. 2023 , 24, 5290	О
540	Assessment of lipid metabolism-disrupting effects of non-phthalate plasticizer diisobutyl adipate through in silico and in vitro approaches.	O
539	Characteristics of plant trait network and its influencing factors in impounded lakes and channel rivers of South-to-North Water Transfer Project, China. 14,	O
538	An integrated approach of high-performance liquid chromatographythass spectrometry-based chemical profiling, network pharmacology, and molecular docking to reveal the potential mechanisms of Qishen Gubiao granules for treating coronavirus disease 2019. 2200953	О
537	Network Pharmacology Prediction and Experimental Verification for Anti-Ferroptosis of Edaravone After Experimental Intracerebral Hemorrhage.	О
536	Global expression and functional analysis of human piRNAs during HSV-1 infection. 2023 , 328, 199087	O
535	The genetic overlap between Alzheimer disease, amyotrophic lateral sclerosis, Lewy body dementia, and Parkinson disease. 2023 ,	0
534	Systematic review of molecular pathways in burn wound healing. 2023,	O

533	A multi-omics integrative analysis based on CRISPR screens re-defines the pluripotency regulatory network in ESCs.	O
532	Airway transcriptome networks identify susceptibility to frequent asthma exacerbations in children. 2023 ,	O
531	Genomic clines across the species boundary between a hybrid pine and its progenitor in the eastern Tibetan Plateau. 2023 , 100574	О
530	Genome-wide identification and characterization of tomato 14-3-3 (SlTFT) genes and functional analysis of SlTFT6 under heat stress. 2023 , 175,	O
529	Ontology for Cellular Senescence Mechanisms.	О
528	A learning experience elicits sex-dependent neurogenomic responses in Bicyclus anynana butterflies.	O
527	Bioinformatics-Based Analysis of Key Genes in Steroid-Induced Osteonecrosis of the Femoral Head That Are Associated with Copper Metabolism. 2023 , 11, 873	О
526	Design and Computational Analysis of an MMP9 Inhibitor in Hypoxia-Induced Glioblastoma Multiforme. 2023 , 8, 10565-10590	O
525	Identification of CNGCs in Glycine max and Screening of Related Resistance Genes after Fusarium solani Infection. 2023 , 12, 439	О
524	Triap1 upregulation promotes escape from mitotic-slippage-induced G1 arrest. 2023 , 42, 112215	O
523	Single-cell analysis of lymphatic endothelial cell fate specification and differentiation during zebrafish development.	О
522	Quantitative proteomic landscape of unstable atherosclerosis identifies molecular signatures and therapeutic targets for plaque stabilization. 2023 , 6,	O
521	Characteristic Analysis of Featured Genes Associated with Cholangiocarcinoma Progression. 2023 , 11, 847	0
520	Cholinesterase Inhibitors from an Endophytic Fungus Aspergillus niveus Fv-er401: Metabolomics, Isolation and Molecular Docking. 2023 , 28, 2559	O
519	Systematic identification of potential key microRNAs and circRNAs in the dorsal root ganglia of mice with sciatic nerve injury. 16,	О
518	Plasma proteomics of SARS-CoV-2 infection and severity reveals impact on Alzheimer and coronary disease pathways. 2023 , 26, 106408	O
517	Abl depletion via autophagy mediates the beneficial effects of quercetin against Alzheimer pathology across species.	О
516	Increased intracellular persulfide levels attenuate HlyU-mediated hemolysin transcriptional activation inVibrio cholerae.	O

515	Network pharmacology and molecular modelling study of Enhydra fluctuans for the prediction of the molecular mechanisms involved in the amelioration of nephrolithiasis. 1-11	O
514	Genetic architecture of spatial electrical biomarkers for cardiac arrhythmia and relationship with cardiovascular disease. 2023 , 14,	o
513	Genome-wide analysis of genetic pleiotropy and causal genes across three age-related ocular disorders. 2023 , 142, 507-522	0
512	UV -induced mutagenesis of Beauveria bassiana (Hypocreales: Clavicipitaceae) yields two hypervirulent isolates with different transcriptomic profiles.	О
511	Identification of long noncoding RNAs involved in plumule-vernalization of Chinese cabbage. 14,	О
510	The potential value of cuprotosis in myocardial immune infiltration that occurs in pediatric congenital heart disease in response to surgery with cardiopulmonary bypass. 2023 , 11,	О
509	Engineered Mesenchymal Stem Cells Over-Expressing BDNF Protect the Brain from Traumatic Brain Injury-Induced Neuronal Death, Neurological Deficits, and Cognitive Impairments. 2023 , 16, 436	O
508	RPflex: A Coarse-Grained Network Model for RNA Pocket Flexibility Study. 2023 , 24, 5497	О
507	Arabidopsis cell suspension culture and RNA sequencing reveal regulatory networks underlying plant programmed cell death.	О
506	Bacterial hemophilin homologs and their specific type eleven secretor proteins have conserved roles in heme capture and are diversifying as a family.	О
505	Identification of potential selective autophagy receptors from protein-content profiling of autophagosomes.	0
504	MFGE8 links absorption of dietary fatty acids with catabolism of enterocyte lipid stores through HNF4Edependent transcription of CES enzymes. 2023 , 42, 112249	О
503	Interactomics in plant defence: progress and opportunities.	0
502	PDE3A and GSK3B as Atrial Fibrillation Susceptibility Genes in the Chinese Population via Bioinformatics and Genome-Wide Association Analysis. 2023 , 11, 908	О
501	Exploration of the Production of Three Thiodiketopiperazines by an Endophytic Fungal Strain of Cophinforma mamane.	0
500	Unraveling the Gene Regulatory Networks of the Global Regulators VeA and LaeA in Aspergillus nidulans. 2023 , 11,	o
499	Estrogen receptor alpha deficiency in cardiomyocytes reprograms the heart-derived extracellular vesicle proteome and induces obesity in female mice. 2023 , 2, 268-289	0
498	Mycorrhizal-based inoculants in the root microbiome enhanced phytocannabinoid production in medical Cannabis cultivars.	О

497	Revealing evolution of tropane alkaloid biosynthesis by analyzing two genomes in the Solanaceae family. 2023 , 14,	O
496	Human Polo-like Kinase Inhibitors as Antiplasmodials. 2023 , 9, 1004-1021	0
495	Increasing lysergic acid levels for ergot alkaloid biosynthesis: Directing catalysis via the F-G loop of Clavine oxidases. 14,	0
494	Molecular mechanisms of Huanglian Jiedu decoction in treating Alzheimer disease by regulating microbiome via network pharmacology and molecular docking analysis. 13,	O
493	Microbial network and composition changes according to tobacco varieties and interferes differently in black shank disease defense. 2023 , 134,	0
492	Potential Toxic Mechanisms of Neonicotinoid Insecticides in Rice: Inhibiting Auxin-Mediated Signal Transduction. 2023 , 57, 4852-4862	O
491	Diseased-induced multifaceted variations in community assembly and functions of plant-associated microbiomes. 14,	0
490	The clusterin connectome: Emerging players in chondrocyte biology and putative exploratory biomarkers of osteoarthritis. 14,	O
489	Exploring Tabular Data Through Networks. 2023 , 195-200	0
488	The reciprocal changes in dominant species with complete metabolic functions explain the decoupling phenomenon of microbial taxonomic and functional composition in a grassland. 14,	O
487	Moderate maternal nutrient reduction in pregnancy alters fatty acid oxidation and RNA splicing in the nonhuman primate fetal liver. 1-8	0
486	Proteomic and phosphoproteomic characteristics of the cortex, hippocampus, thalamus, lung, and kidney in COVID-19-infected female K18-hACE2 mice. 2023 , 90, 104518	O
485	Integration of Human and Viral miRNAs in Epstein-Barr Virus-Associated Tumors and Implications for Drug Repurposing. 2023 , 27, 93-108	0
484	An in silico approach to the identification of diagnostic and prognostic markers in low-grade gliomas. 11, e15096	O
483	Identification of potential LncRNAs as papillary thyroid carcinoma biomarkers based on integrated bioinformatics analysis using TCGA and RNA sequencing data. 2023 , 13,	0
482	MOPA: An integrative multi-omics pathway analysis method for measuring omics activity. 2023 , 18, e0278272	0
481	Cervicovaginal Human Papillomavirus Genomes, Microbiota Composition and Cytokine Concentrations in South African Adolescents. 2023 , 15, 758	0
480	Transcriptome analysis reveals defense-related genes and pathways during dodder (Cuscuta australis) parasitism on white clover (Trifolium repens). 14,	O

479	Matured compost amendment improves compost nutrient content by changing the bacterial community during the composting of Chinese herb residues. 14,	0
478	Genome-Wide Identification and Characterization of Bovine Fibroblast Growth Factor (FGF) Gene and Its Expression during Adipocyte Differentiation. 2023 , 24, 5663	O
477	Network pharmacology predicts combinational effect of novel herbal pair consist of Ephedrae herba and Coicis semen on adipogenesis in 3T3-L1 cells. 2023 , 18, e0282875	О
476	In silico analysis to identify miR-1271-5p/PLCB4 (phospholipase C Beta 4) axis mediated oxaliplatin resistance in metastatic colorectal cancer. 2023 , 13,	O
475	Intratumoral Bacteria Dysbiosis Is Associated with Human Papillary Thyroid Cancer and Correlated with Oncogenic Signaling Pathways. 2023 ,	О
474	Insights into the genomic evolution and the alkali tolerance mechanisms of Agaricus sinodeliciosus by comparative genomic and transcriptomic analyses. 2023 , 9,	O
473	Mining the potential therapeutic targets for COVID -19 infection in patients with severe burn injuries via bioinformatics analysis.	О
472	A central chaperone-like role for 14-3-3 proteins in human cells. 2023 , 83, 974-993.e15	O
471	In the light of evolution:Ikeratins as exceptional tumor biomarkers. 11, e15099	О
470	Comparison of gene expression between human and mouse iPSC-derived cardiomyocytes for stem cell therapies of cardiovascular defects via bioinformatic analysis. 2023 , 8,	O
469	Antiviral and anti-inflammatory activity of natural compounds against Japanese encephalitis virus via inhibition of NS5 protein and regulation of key immune and inflammatory signaling pathways. 2023 , 95,	О
468	Demystifying the Role of Prognostic Biomarkers in Breast Cancer through Integrated Transcriptome and Pathway Enrichment Analyses. 2023 , 13, 1142	O
467	dupA+H. pylori reduces diversity of gastric microbiome and increases risk of erosive gastritis. 13,	О
466	BZINB Model-Based Pathway Analysis and Module Identification Facilitates Integration of Microbiome and Metabolome Data. 2023 , 11, 766	O
465	State of the Art of the Molecular Biology of the Interaction between Cocoa and Witches Broom Disease: A Systematic Review. 2023 , 24, 5684	О
464	Rhizosphere Fungal Dynamics in Sugarcane during Different Growth Stages. 2023 , 24, 5701	O
463	Susceptibility and Permissivity of Zebrafish (Danio rerio) Larvae to Cypriniviruses. 2023, 15, 768	О
462	Identification of predictors for neurological outcome after cardiac arrest in peripheral blood mononuclear cells through integrated bioinformatics analysis and machine learning. 2023 , 23,	O

461	A Comparative Study on Growth Performance, Body Composition, and Liver Tissue Metabolism Rearing on Soybean Lecithin-Enriched Artemia Nauplii and Microdiet in Rock Bream (Oplegnathus fasciatus) Larvae. 2023 , 2023, 1-18	0
460	Identification of immune cells infiltrating in hippocampus and key genes associated with Alzheimer disease. 2023 , 16,	O
459	An integrated approach of network pharmacology, molecular docking, and experimental verification uncovers kaempferol as the effective modulator of HSD17B1 for treatment of endometrial cancer. 2023 , 21,	0
458	COL3A1, CXCL8, VCAN, THBS2, and COL1A2 are correlated with the onset of biliary atresia. 2023 , 102, e33299	O
457	Identification of a pediatric acute hypoxemic respiratory failure signature in peripheral blood leukocytes at 24 hours post-ICU admission with machine learning. 11,	O
456	FERMT1 Is a Prognostic Marker Involved in Immune Infiltration of Pancreatic Adenocarcinoma Correlating with m6A Modification and Necroptosis. 2023 , 14, 734	0
455	Identification of new potential downstream transcriptional targets of the strigolactone pathway including glucosinolate biosynthesis. 2023 , 7,	O
454	Vacuolar protein sorting 35 (VPS35) acts as a tumor promoter via facilitating cell cycle progression in pancreatic ductal adenocarcinoma. 2023 , 23,	O
453	HBV rewires liver cancer signaling by altering PP2A complexes.	0
452	CRISPR/Cas9-mediated knockout of the ubiquitin variant UbKEKSreveals a role in regulating nucleolar structures and composition.	O
451	Xanthohumol improves cognitive impairment by regulating miRNA-532-3p/Mpped1 in ovariectomized mice. 2023 , 240, 1169-1178	O
450	SCL14 Inhibits the Functions of the NAC043MYB61 Signaling Cascade to Reduce the Lignin Content in Autotetraploid Populus hopeiensis. 2023 , 24, 5809	O
449	A multi-omic approach identifies an autism spectrum disorder (ASD) regulatory complex of functional epimutations in placentas from children born preterm.	0
448	Mechanistic convergence of depression and suicidality on astrocyte fatty acid metabolism.	O
447	Differences in Whole-Blood Transcriptional Profiles in Inflammatory Bowel Disease Patients Responding to Vedolizumab Compared with Non-Responders. 2023 , 24, 5820	O
446	MicroRNAs in tear fluids predict underlying molecular changes associated with Alzheimer∃ disease. 2023 , 6, e202201757	O
445	Fire and Rhizosphere Effects on Bacterial Co-Occurrence Patterns. 2023, 11, 790	O
444	Transcriptomic Modulation Reveals the Specific Cellular Response in Chinese Sea Bass (Lateolabrax maculatus) Gills under Salinity Change and Alkalinity Stress. 2023 , 24, 5877	O

443	Exploration of the common genetic landscape of COVID-19 and male infertility. 14,	O
442	Genome-wide characterization of ubiquitin-conjugating enzyme gene family explores its genetic effects on the oil content and yield of Brassica napus. 14,	O
441	The Molecular Mechanism of the TEAD1 Gene and miR-410-5p Affect Embryonic Skeletal Muscle Development: A miRNA-Mediated ceRNA Network Analysis. 2023 , 12, 943	О
440	Cyclin B1 is a novel prognostic biomarker and promotes proliferation, migration and invasion in Wilms Tumour.	O
439	Cancer-derived mutation in the OGA stalk domain promotes cell malignancy through dysregulating PDLIM7 and p53.	O
438	A Large-Scale Proteomics Resource of Circulating Extracellular Vesicles for Biomarker Discovery in Pancreatic Cancer.	O
437	SARS-CoV-2 NSP12 associates with the TRiC complex and the P323L substitution is a host adaption.	O
436	Trends of therapy in the treatment of asthma. 2023 , 17, 175346662311557	O
435	Comparative transcriptome analysis of molecular mechanisms underlying adventitious root developments in Huangshan Bitter tea (Camellia gymnogyna Chang) under red light quality. 14,	O
434	Sexual behavior shapes male genitourinary microbiome composition. 2023 , 4, 100981	O
433	Lower respiratory tract microbiome composition and community interactions in smokers. 2023 , 5,	O
432	The characteristics of soil microbial co-occurrence networks across a high-latitude forested wetland ecotone in China. 14,	O
431	Biosynthesis of 3,6-Dideoxy-heptoses for the Capsular Polysaccharides of Campylobacter jejuni. 2023 , 62, 1287-1297	O
430	Epigenetic dosage identifies two major and functionally distinct (Lell subtypes. 2023,	O
429	Integrating network pharmacology approaches for the investigation of multi-target pharmacological mechanism of 6-shogaol against cervical cancer. 1-17	О
428	Identification of common molecular signatures of SARS-CoV-2 infection and its influence on acute kidney injury and chronic kidney disease. 14,	O
427	The gut microbiota of tropical marine fish is largely uncultured and distinct from surrounding water microbiota.	О
426	Ras-dependent activation of BMAL2 regulates hypoxic metabolism in pancreatic cancer.	O

425	Network-level analysis of ageing and its relationship with diseases and tissue regeneration in the mouse liver. 2023 , 13,	О
424	The eTMthiR858IMYB62 - like module regulates anthocyanin biosynthesis under low-nitrogen conditions in Malus spectabilis.	O
423	Neutrophil Activation and Immune Thrombosis Profiles Persist in Convalescent COVID-19.	О
422	Longevity-Associated Transcription Factor ATF7 Promotes Healthspan by Suppressing Cellular Senescence and Systematic Inflammation. 2022 , 0	O
421	Toward novel treatment against filariasis: Insight into genome-wide co-evolutionary analysis of filarial nematodes and Wolbachia. 14,	О
420	Characteristics of the rumen virome in Japanese cattle.	O
419	Bioinformatics-based investigation on the genetic influence between SARS-CoV-2 infections and idiopathic pulmonary fibrosis (IPF) diseases, and drug repurposing. 2023 , 13,	О
418	Accelerating network layouts using graph neural networks. 2023, 14,	O
417	Downregulation of lncRNA SNHG1 in hypoxia and stem cells is associated with poor disease prognosis in gliomas. 2023 , 22, 1135-1153	О
416	The RBPome of influenza A virus mRNA reveals a role for TDP-43 in viral replication.	0
415	Genome-centric metagenomics reveals the host-driven dynamics and ecological role of CPR bacteria in an activated sludge system. 2023 , 11,	О
414	Cellular proteomic profiling of esophageal epithelial cells cultured under physioxia or normoxia reveals high correlation of radiation response. 2023 ,	0
413	A novel miR-99b-5p-Zbp1pathway in microglia contributes to the pathogenesis of schizophrenia.	О
412	Network Analysis Reveals the Molecular Bases of Statin Pleiotropy That Vary with Genetic Background. 2023 , 11,	O
411	Antileishmanial Activity of Cinnamic Acid Derivatives against Leishmania infantum. 2023, 28, 2844	О
410	Construction and analysis of proteinprotein interaction networks based on nuclear proteomics data of the desiccation-tolerant Xerophyta schlechteri leaves subjected to dehydration stress. 2023 , 16,	O
409	Full-length RNA sequencing reveals the mechanisms by which an TSWV卧CRV complex suppresses plant basal resistance. 14,	Ο
408	Floral Development Stage-Specific Transcriptomic Analysis Reveals the Formation Mechanism of Different Shapes of Ray Florets in Chrysanthemum. 2023 , 14, 766	O

407	Pneumolysin as a target for new therapies against pneumococcal infections: A systematic review. 2023 , 18, e0282970	O
406	Identification and analysis of lignin biosynthesis genes related to fruit ripening and stress response in banana (Musa acuminata L. AAA group, cv. Cavendish). 14,	O
405	DDX58 expression promotes inflammation and growth arrest in Sertoli cells by stabilizing p65 mRNA in patients with Sertoli cell-only syndrome. 14,	0
404	Integrative omics-analysis of lipid metabolism regulation by peroxisome proliferator-activated receptor a and b agonists in male Atlantic cod. 14,	O
403	Capture RIC-seq reveals positional rules of PTBP1-associated RNA loops in splicing regulation. 2023 , 83, 1311-1327.e7	0
402	Temporal genome-wide fitness analysis of Mycobacterium marinumduring infection reveals genetic requirement for virulence and survival in amoebae and microglial cells.	O
401	Systemic Anti-Inflammatory Therapy Aided by Curcumin-Laden Double-Headed Nanoparticles Combined with Injectable Long-Acting Insulin in a Rodent Model of Diabetes Eye Disease. 2023 , 17, 6857-6874	0
400	Centipeda minima active components and mechanisms in lung cancer. 2023 , 23,	O
399	Exploring the mechanism of action of herbal compounding in the treatment of myasthenia gravis based on network pharmacology. 1-16	О
398	Comparison of hepatic responses to glucose perturbation between healthy and obese mice based on the edge type of network structures. 2023 , 13,	O
397	The m6A methylation landscape, molecular characterization and clinical relevance in prostate adenocarcinoma. 14,	0
396	An Interaction Network Driven Approach for Identifying Cervical, Endometrial, Vulvar Carcinomic Biomarkers and Their Multi-targeted Inhibitory Agents from Few Widely Available Medicinal Plants.	O
395	Notch activation promotes bone metastasis via SPARC inhibition in adenoid cystic carcinoma.	0
394	Enterohemorrhagic Escherichia coli responds to gut microbiota metabolites by altering metabolism and activating stress responses. 2023 , 15,	Ο
393	fRNC: Uncovering the dynamic and condition-specific RBP-ncRNA circuits from multi-omics data. 2023 , 21, 2276-2285	0
392	Identification of a stable major sucrose-related QTL and diagnostic marker for flavor improvement in peanut. 2023 , 136,	0
391	Mena regulates nesprin-2 to control actinfluclear lamina associations, trans-nuclear membrane signalling and gene expression. 2023 , 14,	0
390	Individualized Lipid Metabolism-Associated Six-Gene Signature for Prediction of Overall Survival, Immune Infiltration, Immunotherapy Response, and Potential Candidate Drugs in Lung Squamous Cell Carcinoma Patients: Development and Validation.	О

389	NetDriller-V3: A Powerful Social Network Analysis Tool. 2022 ,	O
388	Bioinformatics and systematic biology methods to determine the pathogenic link between COVID-19 and atrial fibrillation.	Ο
387	Upregulation of CXCL1 and FCGR1A is Associated With the ischemic stroke and Crohn⊞ Disease.	0
386	Urinary-derived extracellular vesicles reveal a distinct microRNA signature associated with the development and progression of Fabry nephropathy. 10,	O
385	Immune and ionic mechanisms mediating the effect of dexamethasone in severe COVID-19. 14,	O
384	DiaPASEF proteotype analysis indicates changes in cell growth and metabolic switch induced by caspase-9 inhibition in chondrogenic cells.	O
383	Mind of a dauer: Comparative connectomics reveals developmental plasticity.	O
382	Integrated metabolomic and transcriptomic analysis reveals the mechanism underlying the accumulation of anthocyanins and other flavonoids in the flesh and skin of teinturier grapes. 2023 , 197, 107667	0
381	Upregulation of Biomarker Limd1 Was Correlated with Immune Infiltration in Doxorubicin-Related Cardiotoxicity. 2023 , 2023, 1-23	0
380	Stem cell-based modeling and single-cell multiomics reveal gene-regulatory mechanisms underlying human skeletal development. 2023 , 112276	O
379	Photobiomodulation Reduces the Cytokine Storm Syndrome Associated with COVID-19 in the Zebrafish Model. 2023 , 24, 6104	О
378	Metabarcoding and Metabolomics Reveal the Effect of the Invasive Alien Tree Miconia calvescens DC. on Soil Diversity on the Tropical Island of MoBrea (French Polynesia). 2023 , 11, 832	O
377	Ginsenoside Rk3 is a novel PI3K/AKT-targeting therapeutics agent that regulates autophagy and apoptosis in hepatocellular carcinoma. 2023 ,	O
376	Reductive Enzyme Cascades for Valorization of Polyethylene Terephthalate Deconstruction Products. 2023 , 13, 4778-4789	O
375	FZD7, Regulated by Non-CpG Methylation, Plays an Important Role in Immature Porcine Sertoli Cell Proliferation. 2023 , 24, 6179	O
374	Risk stratification based on DNA damage-repair-related signature reflects the microenvironmental feature, metabolic status and therapeutic response of breast cancer. 14,	O
373	Predictive investigation of idiopathic pulmonary fibrosis subtypes based on cellular senescence-related genes for disease treatment and management. 14,	О
372	Proteomic Profiling of Colorectal Adenomas Identifies a Predictive Risk Signature for Development of Metachronous Advanced Colorectal Neoplasia. 2023 ,	0

371	Exploring the common pathogenesis of calcific aortic valve disease and atherosclerotic cardiovascular disease through bioinformatics analysis.	0
370	Identification of Genomic Signatures in Bullmastiff Dogs Using Composite Selection Signals Analysis of 23 Purebred Clades. 2023 , 13, 1149	O
369	The Related Mechanisms Predicted through Network-Based Pharmacological Analysis and the Anti-Inflammatory Effects of Fraxinus rhynchophylla Hance Bark on Contact Dermatitis in Mice. 2023 , 24, 6091	О
368	Proteome-wide lysine acetylation profiling to investigate the involvement of histone deacetylase HDA5 in the salt stress response of Arabidopsis leaves.	O
367	Comparative Study of Transcriptome Profile and Immune-related Genes Network Associated with Intestinal Epithelial Tissue based on Microarray Data in Poultry with Coccidiosis. 2022 , 13, 154-162	O
366	Comparative transcriptome analysis reveals the phosphate starvation alleviation mechanism of phosphate accumulating Pseudomonas putida in Arabidopsis thaliana. 2023 , 13,	O
365	A novel feedback regulated loop of circRRM2-IGF2BP1-MYC promotes breast cancer metastasis. 2023 , 23,	O
364	Weighted gene co-expression network analysis revealed T cell differentiation associated with the age-related phenotypes in COVID-19 patients. 2023 , 16,	O
363	The genomic landscape of reference genomes of cultivated human gut bacteria. 2023, 14,	0
362	Apigenin exerts anti-cancer effects in colon cancer possibly by regulating Heat shock protein 90 alpha family class A member 1 (HSP90AA1).	O
361	Microbial composition of tumorous and adjacent gastric tissue is associated with prognosis of gastric cancer. 2023 , 13,	O
360	Physiological, transcriptome and co-expression network analysis of chlorophyll-deficient mutants in flue-cured tobacco. 2023 , 23,	O
359	Investigation of targets and anticancer mechanisms of covalently acting natural products by functional proteomics.	O
358	Tweedle gene family of Drosophila suzukii (Matsumura) larva enhances the basal tolerance to cold and hypoxia.	O
357	Proteome integral solubility alteration high-throughput proteomics assay identifies Collectin-12 as a non-apoptotic microglial caspase-3 substrate. 2023 , 14,	O
356	Lipid metabolism-related miRNAs with potential diagnostic roles in prostate cancer. 2023 , 22,	O
355	Deciphering molecular mechanisms of SARS-CoV-2 pathogenesis and drug repurposing through GRN motifs: a comprehensive systems biology study. 2023 , 13,	O
354	Identification of FCN1 as a novel macrophage infiltration-associated biomarker for diagnosis of pediatric inflammatory bowel diseases. 2023 , 21,	O

353	Identification of Diagnostic Markers in Synovial Tissue of Osteoarthritis by Weighted Gene Coexpression Network.	0
352	Proteomic analysis of sialoliths from calcified, lipid and mixed groups as a source of potential biomarkers of deposit formation in the salivary glands. 2023 , 20,	O
351	Identification of potential ferroptosis hub genes in acute-on-chronic liver failure based on bioinformatics analysis and experimental verification. 2023 , 16,	0
350	Genome-wide identification of the TIFY family reveals JAZ subfamily function in response to hormone treatment in Betula platyphylla. 2023 , 23,	0
349	SLAPSHOT reveals rapid dynamics of extracellularly exposed proteome in response to calcium-activated plasma membrane phospholipid scrambling.	0
348	A multi-omics strategy for the study of microbial metabolism: application to the human skins microbiome.	O
347	Identification and validation of ferroptosis-related genes in patients infected with dengue virus: implication in the pathogenesis of DENV.	0
346	Anti-CHAC1 exosomes for nose-to-brain delivery of miR-760-3p in cerebral ischemia/reperfusion injury mice inhibiting neuron ferroptosis. 2023 , 21,	O
345	Meta-analyses of host metagenomes from colorectal cancer patients reveal strong relationship between colorectal cancer-associated species.	0
344	Circulating Metabolomic and Lipidomic Signatures Identify a Type 2 Diabetes Risk Profile in Low-Birth-Weight Men with Non-Alcoholic Fatty Liver Disease. 2023 , 15, 1590	Ο
343	Interferon-inducible phospholipids govern IFITM3 -dependent endosomal antiviral immunity.	0
342	Uncovering biomarkers for potential therapeutic targeting for COVID-19-related acute kidney injury: A bioinformatic approach. 2023 , 5,	O
341	Bone Marrow Mesenchymal Stem Cells Expanded Inside the Nichoid Micro-Scaffold: a Focus on Anti-Inflammatory Response.	Ο
340	Clinical features and shared mechanisms of chronic gastritis and osteoporosis. 2023, 13,	Ο
339	Identification of Immune Microenvironment Changes, Immune-Related Pathways and Genes in Male Androgenetic Alopecia.	0
338	Integrated analysis of transcriptomics and metabolomics of peach under cold stress. 14,	O
337	Integrated Analysis of lncRNAThRNA Regulatory Networks Related to Lipid Metabolism in High-Oleic-Acid Rapeseed. 2023 , 24, 6277	0
336	Systemic Alterations of Cancer Cells and Their Boost by Polyploidization: Unicellular Attractor (UCA) Model. 2023 , 24, 6196	O

335	Highlighting In Vitro the Role of Brain-like Endothelial Cells on the Maturation and Metabolism of Brain Pericytes by SWATH Proteomics. 2023 , 12, 1010	0
334	Microporous membrane and culture medium affect in vitro seedling development of Dalbergia nigra (Vell.) Ex Benth. (Fabaceae) by modulation of the protein profile and accumulation of ethylene and CO2.	O
333	Exploration of the Shared Gene Signatures and Molecular Mechanisms Between Breast Cancer and Endometriosis.	O
332	Genome-Scale Analysis of Cellular Restriction Factors That Inhibit Transgene Expression from Adeno-Associated Virus Vectors.	o
331	Phylogenetic Analyses and Transcriptional Survey Reveal the Characteristics, Evolution, and Expression Profile of NBS-Type Resistance Genes in Papaya. 2023 , 13, 970	0
330	Anticancer Effect of Active Component of Astragalus Membranaceus Combined with Olaparib on Ovarian Cancer Predicted by Network-Based Pharmacology.	o
329	Identifying potential biomarkers for the diagnosis and treatment of IgA nephropathy based on bioinformatics analysis. 2023 , 16,	0
328	The 2020 derecho revealed limited overlap between maize genes associated with root lodging and root system architecture.	o
327	Loss of the Maternal Effect Gene Nlrp2 Alters the Transcriptome of Ovulated Mouse Oocytes and Impacts Expression of Histone Demethylase KDM1B.	0
326	Potential Targets and Mechanisms of Jiedu Quyu Ziyin Decoction for Treating SLE-GIOP: Based on Network Pharmacology and Molecular Docking. 2023 , 2023, 1-15	О
325	Pharmacological Mechanism of Aucklandiae Radix against Gastric Ulcer Based on Network Pharmacology and In Vivo Experiment. 2023 , 59, 666	O
324	Bioactive Compounds and Signaling Pathways of Wolfiporia extensa in Suppressing Inflammatory Response by Network Pharmacology. 2023 , 13, 893	О
323	PDGF-D-induced immunoproteasome activation and cell-cell interactions. 2023 , 21, 2405-2418	O
322	Combining bioinformatics and machine learning to identify common mechanisms and biomarkers of chronic obstructive pulmonary disease and atrial fibrillation. 10,	О
321	Identification of Novel Necroptosis and Immune Infiltration in the Progression of Idiopathic Pulmonary Fibrosis.	0
320	Distinct gene dysregulation patterns herald precision medicine potentiality in systemic lupus erythematosus. 2023 , 136, 103025	O
319	Collagen Hydrogel Containing Polyethylenimine-Gold Nanoparticles for Drug Release and Enhanced Beating Properties of Engineered Cardiac Tissues.	0
318	Urinary Metabolomics Identified Metabolic Perturbations Associated with Gutka, a Smokeless Form of Tobacco. 2023 , 36, 669-684	О

317	IDSL.GOA: Gene Ontology Analysis for Metabolomics.	O
316	时间 dentification of potential drug for dengue hemorrhagic fever : Network-based drug reprofiling approach [Preprint].	0
315	The rotation of Phallus impudicus benefits the microenvironment via improving the soil microbial structure and soil properties.	0
314	Molecular mechanism study and tumor heterogeneity of Chinese angelica and Fructus aurantii in the treatment of colorectal cancer through computational and molecular dynamics. 2023 , 23,	O
313	Downregulated annexin A1 expression correlates with poor prognosis, metastasis, and immunosuppressive microenvironment in Ewing sarcoma. 2023 , 15, 2321-2346	0
312	Soil conditions and the plant microbiome boost the accumulation of monoterpenes in the fruit of Citrus reticulata [Ihachi 2023, 11,	o
311	Identification of transcription factors related to diabetic tubulointerstitial injury. 2023, 21,	0
310	The genome of Lactuca saligna , a wild relative of lettuce, provides insight into non-host resistance to the downy mildew Bremia lactucae.	O
309	The inhibitory role of microRNA-141-3p in human cutaneous melanoma growth and metastasis through the fibroblast growth factor 13-mediated mitogen-activated protein kinase axis. Publish Ahead of Print,	0
308	Transcriptomic analysis reveals shared gene signatures and molecular mechanisms between obesity and periodontitis. 14,	o
307	Comprehensive analysis of the expression and prognosis for RAI2: A promising biomarker in breast cancer. 13,	0
306	Use of pain-related gene features to predict depression by support vector machine model in patients with fibromyalgia. 14,	О
305	Molecular targets of metformin against ovarian cancer based on network pharmacology.	0
304	Bioinformatics screening of colorectal-cancer causing molecular signatures through gene expression profiles to discover therapeutic targets and candidate agents. 2023 , 16,	0
303	Two haplotype-resolved genomes of highly heterozygous AAB allotriploid bananas provide insights into subgenome asymmetric evolution and banana wilt control.	O
302	Phylobone: A comprehensive database of bone extracellular matrix proteins in human and model organisms.	0
301	Generating Functional and Highly Proliferative Melanocytes Derived from Human Pluripotent Stem Cells: A Promising Tool for Biotherapeutic Approaches to Treat Skin Pigmentation Disorders. 2023 , 24, 6398	0
300	Gene enrichment and co-expression analysis shed light on transcriptional responses to Ralstonia solanacearum in tomato. 2023 , 24,	O

299	Global multi-omics profiling reveals evolutionary drivers of phylogeographic diversity of fungal specialized metabolism.	О
298	Learning transcriptional and regulatory dynamics driving cancer cell plasticity using neural ODE-based optimal transport.	O
297	Transcriptome Analysis Reveals the Profile of Long Non-Coding RNAs during Myogenic Differentiation in Goats. 2023 , 24, 6370	0
296	Tobacco Alkaloid Assessment in a DSS-Induced Colitis Mouse Model with a Fully Humanized Immune System. 2023 , 24, 6419	O
295	Infection strategies of different chytrids in a diatom spring bloom.	0
294	Identifying diseases associated with Post-COVID syndrome through an integrated network biology approach. 1-20	O
293	NGS-based profiling identifies miRNAs and pathways dysregulated in cisplatin-resistant esophageal cancer cells. 2023 , 23,	0
292	Regulatory Networks of lncRNAs, miRNAs, and mRNAs in Response to Heat Stress in Wheat (Triticum Aestivum L.): An Integrated Analysis. 2023 , 2023, 1-17	Ο
291	p21 facilitates chronic lung inflammation via epithelial and endothelial cells. 2023 , 15, 2395-2417	0
2 90	Potential molecular mechanisms of Erlongjiaonang action in idiopathic sudden hearing loss: A network pharmacology and molecular docking analyses. 14,	Ο
289	Spermiogenesis alterations in the absence of CTCF revealed by single cell RNA sequencing. 11,	0
288	The Secretome of Parental and Bone Metastatic Breast Cancer Elicits Distinct Effects in Human Osteoclast Activity after Activation of 2 Adrenergic Signaling. 2023 , 13, 622	O
287	Human thymopoiesis produces polyspecific CD8+ 和 cells responding to multiple viral antigens. 12,	O
286	Inferring Gene Regulatory Networks from RNA-seq Data Using Kernel Classification. 2023 , 12, 518	O
285	Comprehensive chemical profiling and quantitative analysis of ethnicYi medicine Miao-Fu-Zhi-Tong granules using UHPLC-MS/MS. 2023 , 21, 214-225	0
284	Novel Transcriptomic Interactomes of Noncoding RNAs in the Heart under Altered Thyroid Hormonal States. 2023 , 24, 6560	O
283	The Bacterial Microbiome of the Coral Skeleton Algal Symbiont Ostreobium Shows Preferential Associations and Signatures of Phylosymbiosis.	0
282	Prognostic biomarkers and molecular pathways mediating Helicobacter pylori I hduced gastric cancer: a network-biology approach. 2023 , 21, e8	O

281	Global Transcriptomic Analyses Provide New Insight into the Molecular Mechanisms of Endocarp Formation and Development in Iron Walnut (Juglans sigillata Dode). 2023 , 24, 6543	О
280	Identification of the NAC Transcription Factor Family during Early Seed Development in Akebia trifoliata (Thunb.) Koidz. 2023 , 12, 1518	O
279	Network Pharmacological Analysis and Experimental Validation of the Effect of Smilacis Glabrae Rhixoma on Gastrointestinal Motility Disorder. 2023 , 12, 1509	О
278	AutophagyNet: High-resolution data source for the analysis of autophagy and its regulation.	О
277	Mechanism of skin whitening through San-Bai decoction-induced tyrosinase inhibition and discovery of natural products targeting tyrosinase. 2023 , 102, e33420	0
276	A network pharmacology and molecular docking approach in the exploratory investigation of the biological mechanisms of lagundi (Vitex negundo L.) compounds against COVID-19. 2023 , 21, e4	О
275	Transcriptome profiling reveals transcriptional regulation of VISTA in T cell activation. 2023, 157, 101-111	O
274	Runs of homozygosity and signatures of selection for number of oocytes and embryos in the Gir Indicine cattle.	Ο
273	Insight into the mechanism of DNA methylation and miRNA-mRNA regulatory network in ischemic stroke. 2023 , 20, 10264-10283	О
272	Executable Network Models of Integrated Multiomics Data.	Ο
272 271	Executable Network Models of Integrated Multiomics Data. Exploration of 'the mechanisms of Cyperi Rhizoma in the treatment of endometriosis through GEO datasets, network pharmacology, and molecular docking studies.	0
	Exploration of 'the mechanisms of Cyperi Rhizoma in the treatment of endometriosis through GEO	
271	Exploration of 'the mechanisms of Cyperi Rhizoma in the treatment of endometriosis through GEO datasets, network pharmacology, and molecular docking studies. Knowledge Graph Construction based on Granulosa Cells Transcriptome from polycystic ovary	0
271	Exploration of 'the mechanisms of Cyperi Rhizoma in the treatment of endometriosis through GEO datasets, network pharmacology, and molecular docking studies. Knowledge Graph 'Construction based on 'Granulosa Cells Transcriptome from polycystic ovary syndrome with Normoandrogen and Hyperandrogen. Divergent contributions of coding and noncoding sequences to initial high-altitude adaptation in	0
271 270 269	Exploration of 'the mechanisms of Cyperi Rhizoma in the treatment of endometriosis through GEO datasets, network pharmacology, and molecular docking studies. Knowledge Graph 'Construction based on 'Granulosa Cells Transcriptome from polycystic ovary syndrome with Normoandrogen and Hyperandrogen. Divergent contributions of coding and noncoding sequences to initial high-altitude adaptation in passerine birds endemic to the Qinghaillibet Plateau.	0 0
271 270 269 268	Exploration of 'the mechanisms of Cyperi Rhizoma in the treatment of endometriosis through GEO datasets, network pharmacology, and molecular docking studies. Knowledge Graph 'Construction based on 'Granulosa Cells Transcriptome from polycystic ovary syndrome with Normoandrogen and Hyperandrogen. Divergent contributions of coding and noncoding sequences to initial high-altitude adaptation in passerine birds endemic to the Qinghai libet Plateau. Analysis of biofilm and bacterial communities in the towel environment with daily use.	0 0
271 270 269 268 267	Exploration of 'the mechanisms of Cyperi Rhizoma in the treatment of endometriosis through GEO datasets, network pharmacology, and molecular docking studies. Knowledge Graph 'Construction based on 'Granulosa Cells Transcriptome from polycystic ovary syndrome with Normoandrogen and Hyperandrogen. Divergent contributions of coding and noncoding sequences to initial high-altitude adaptation in passerine birds endemic to the Qinghaillibet Plateau. Analysis of biofilm and bacterial communities in the towel environment with daily use. V-Mapper: topological data analysis for high-dimensional data with velocity. 2023, 14, 92-105 The m6A-regulation and single cell effect pattern in sunitinib resistance on clear cell renal cell	00000

263	Extracellular Matrix and Protein Phosphorylation Dysregulation Related to Diabetes-Induced Erectile Dysfunction. 2023 , 2023, 1-13	О
262	Glycosylation increases active site rigidity leading to improved enzyme stability and turnover.	О
261	Establishment of killer whale (Orcinus orca) primary fibroblast cell cultures and their transcriptomic responses to pollutant exposure. 2023 , 174, 107915	0
2 60	T9GPred: A Comprehensive Computational Tool for the Prediction of Type 9 Secretion System, Gliding Motility and the Associated Secreted Proteins.	О
259	Dynamics of inflammatory cytokine expression in bovine endometrial cells exposed to cow blood plasma small extracellular vesicles (sEV) may reflect high fertility. 2023 , 13,	О
258	Genome-wide DNA methylation profiling after Ayurveda intervention to bronchial asthmatics identifies differential methylation in several transcription factors with immune process related function. 2023 , 14, 100692	О
257	GWAS across multiple environments and WGCNA suggest the involvement of ZmARF23 in embryonic callus induction from immature maize embryos. 2023 , 136,	О
256	The Unusual Dominance of the Yeast Genus Glaciozyma in the Deeper Layer in an Antarctic Permafrost Core (Adlie Cove, Northern Victoria Land) Is Driven by Elemental Composition. 2023 , 9, 435	O
255	Transcriptomic data meta-analysis reveals common and injury model specific gene expression changes in the regenerating zebrafish heart. 2023 , 13,	0
254	Altered Expression of CYSLTR1 is Associated With Adverse Clinical Outcome in Triple Negative Breast Tumors: An <i>In Silico</i> Approach. 2023 , 19, 148-158	o
253	Identification of Bone Metastatic and Prognostic Alternative Splicing Signatures in Prostate Adenocarcinoma.	О
252	Skeletal muscle gene expression dysregulation in long-term spaceflights and aging is clock-dependent. 2023 , 9,	O
251	Serum soluble mediators as prognostic biomarkers for morbidity, disease outcome, and late-relapsing hepatitis in yellow fever patients. 2023 , 109321	O
250	Inter- and intraspecific phytochemical variation correlate with epiphytic flower and leaf bacterial communities.	o
249	Network Pharmacologic Study of Radix Pae-oniae Rubra in the Treatment of Diabetes Retinopathy. 2023 , 13, 5002-5016	О
248	mIR-99a-5p and mIR-148a-3p as Candidate Molecular Biomarkers for the Survival of Lung Cancer Patients. 2023 , 52, 87-100	O
247	CORE CONSERVED TRANSCRIPTIONAL REGULATORY NETWORKS DEFINE THE INVASIVE TROPHOBLAST CELL LINEAGE.	0
246	Smoking-related epigenetic modifications are associated with the prognosis and chemotherapeutics of patients with bladder cancer. 2023 , 37, 039463202311667	О

245	CircPVT1 promotes ER-positive breast tumorigenesis and drug resistance by targeting ESR1 and MAVS.	0
244	Allelic phenotype prediction of phenylketonuria based on the machine learning method. 2023, 17,	O
243	Quantitative proteomic analysis reveals apoE4-dependent phosphorylation of the actin-regulating protein VASP. 2023 , 100541	O
242	Shared molecular signatures between coronavirus infection and neurodegenerative diseases provide targets for broad-spectrum drug development. 2023 , 13,	O
241	Anti-inflammatory potential of selective small compounds by targeting TNF-Bamp; NF-kB signaling: a comprehensive molecular docking and simulation study. 1-14	O
240	Extensive, transient, and long-lasting gene regulation in a song-controlling brain area during testosterone-induced song development in adult female canaries.	O
239	Identifying determinants of synaptic specificity by integrating connectomes and transcriptomes.	O
238	Significance of oxidative stress in the diagnosis and subtype classification of intervertebral disc degeneration.	O
237	Multi-omics analysis reveals a crucial role for Retinoic Acid in promoting epigenetic and transcriptional competence of anin vitromodel of human Pharyngeal Endoderm.	0
236	A Systematic Review of Molecular Pathway Analysis of Drugs for Potential Use in Liver Cancer Treatment. 2023 , 2, 210-231	O
235	Systemic Metabolic and Mitochondrial Defects in Rett Syndrome Models.	O
234	Investigation of shared genes and regulatory mechanisms associated with coronavirus disease 2019 and ischemic stroke. 14,	O
233	Hypoxia-inducible factor stabilisation-related lncRNAs in retinopathy of prematurity. 2023, 43,	O
232	Small RNA sequencing of circulating small extracellular vesicles microRNAs in patients with amyotrophic lateral sclerosis. 2023 , 13,	O
231	Vertically stratified methane, nitrogen and sulphur cycling and coupling mechanisms in mangrove sediment microbiomes. 2023 , 11,	O
230	clusterMaker2: a major update to clusterMaker, a multi-algorithm clustering app for Cytoscape. 2023 , 24,	O
229	Exploring the Pharmacological Mechanisms of Ginkgo biloba Extract in the Treatment of Sensorineural Hearing Loss.	О
228	An oxidative stress-related lncRNA prognostic risk model for thyroid cancer.	O

227	Identification and validation of new MADS-box homologous genes in 3010 rice pan-genome.	O
226	Rewiring of miRNA-mRNA bipartite co-expression network as a novel way to understand the prostate cancer related players. 1-12	O
225	TnpB structure reveals minimal functional core of Cas12 nuclease family. 2023, 616, 384-389	О
224	Identification of Potential Drug Targets in Erythrocyte Invasion Pathway of Plasmodium falciparum. 2023 , 80,	O
223	Graph Visualization: Alternative Models Inspired by Bioinformatics. 2023, 23, 3747	O
222	Advanced Electronic and Optoelectronic Sensors, Applications, Modelling and Industry 5.0 Perspectives. 2023 , 13, 4582	O
221	Viruses interact with hosts that span distantly related microbial domains in dense hydrothermal mats.	О
220	Network Pharmacology Prediction and Experimental Verification of Rhubarb-Peach Kernel Promoting Apoptosis in Endometriosis.	O
219	A fluorescent reporter model for the visualization and characterization of TDC.	О
218	Nervous system-related gene regulatory networks and functional evolution of ETS proteins across species. 2023 , 104891	O
217	Novel mutations reduce expression of meiotic regulators SYCE1 and BOLL in testis of azoospermic men from West Bengal, India.	О
216	Genomics to Notebook (g2nb): extending the electronic notebook to address the challenges of bioinformatics analysis.	0
215	Metabolite Analysis of Alternaria Mycotoxins by LC-MS/MS and Multiple Tools. 2023, 28, 3258	О
214	Genome-wide association and transcriptome analysis provide the SNPs and molecular insights into the hypoxia tolerance in large yellow croaker (Larimichthys crocea). 2023 , 573, 739547	O
213	Soil organic carbon fraction accumulation and bacterial characteristics in curtilage soil: Effects of land conversion and land use. 2023 , 18, e0283802	О
212	Nuclear translocation of cGAS orchestrates VEGF-A-mediated angiogenesis. 2023 , 42, 112328	О
211	Esearch3D: propagating gene expression in chromatin networks to illuminate active enhancers.	0
2 10	Application of TraDIS to define the core essential genome of Campylobacter jejuni and Campylobacter coli. 2023 , 23,	O

209	THAPBI PICT - a fast, cautious, and accurate metabarcoding analysis pipeline.	O
208	Ferroptosis Signature Shapes the Immune Profiles to Enhance the Response to Immune Checkpoint Inhibitors in Head and Neck Cancer.	o
207	Investigation on the mechanism of Ginkgo Folium in the treatment of Non-alcoholic Fatty Liver Disease by strategy of network pharmacology and molecular docking. 2023 , 1-13	O
206	Study on mechanism of hepatoprotective effect of Chrysanthemum morifolium Ramat. based on metabolomics with network analysis and network pharmacology. 2023 , 1222, 123711	O
205	Distinct maternal metabolites are associated with obesity and glucose-insulin axis in the first trimester of pregnancy.	0
204	Widespread RNA hypoediting in schizophrenia and its relevance to mitochondrial function. 2023 , 9,	O
203	Identification of key genes and immune infiltration based on weighted gene co-expression network analysis in vestibular schwannoma. 2023 , 102, e33470	0
202	Transcriptome and Anatomical Comparisons Reveal the Effects of Methyl Jasmonate on the Seed Development of Camellia oleifera.	O
201	Amplification of protease-activated receptors signaling in sporadic cerebral cavernous malformation endothelial cells. 2023 , 1870, 119474	0
200	Standardization and Interpretation of RNA-sequencing for Transplantation. Publish Ahead of Print,	O
199	Structure-based molecular networking, molecular docking, dynamics simulation and pharmacokinetic studies of Olax subscorpioidea for identification of potential inhibitors against selected cancer targets. 1-16	O
198	Pan-cancer analysis of the ion permeome reveals functional regulators of glioblastoma aggression.	O
197	Extensive variation of leaf specialized metabolite production in sessile oak (Quercus petraea) populations is to a large extent genetically determined but not locally adaptive.	0
196	Archaeal self-activating GPN-loop GTPases involve a lock-switch-rock mechanism for GTP hydrolysis.	O
195	Identification and tracking of HTLV-1[hfected T cell clones in virus-associated neurologic disease. 2023 , 8,	O
194	Genome-Wide Meta-Analysis Identifies Multiple Novel Rare Variants to Predict Common Human Infectious Diseases Risk. 2023 , 24, 7006	O
193	Identification of RPD3/HDA1 Family Genes in Sugar Beet and Response to Abiotic Stresses.	0
192	Identification of Long Intergenic Noncoding RNAs in Rhizoctonia cerealis following Inoculation of Wheat.	O

191	Integrated analysis of hub genes and miRNA- transcription factor-hub gene interaction network in necrotizing enterocolitis.	О
190	Bioinformatics and network pharmacology-based study to elucidate the multi-target pharmacological mechanism of the indigenous plants of Medina valley in treating HCV-related hepatocellular carcinoma. 2023 ,	O
189	Mori fructus aqueous extracts attenuates liver injury by inhibiting ferroptosis via the Nrf2 pathway. 2023 , 14,	О
188	Insights into microRNA regulation of flower coloration in a lily cultivar Vivian petal. 2023, 0-0	O
187	The effect of temperature and invasive alien predator on genetic and phenotypic variation in the damselfly Ischnura elegans: cross-latitude comparison. 2023 , 20,	О
186	Multi-omic characterization of the maize GPI synthesis mutant gwt1 with defects in kernel development. 2023 , 23,	O
185	Unrevealing of dysregulated hub genes linked with immune system and inflammatory signaling pathways in the pathogenesis of irritable bowel syndrome by system biology approaches. 2023 , 39, 101241	О
184	Identification and Validation of m7G-Related Prognostic Signatures and Associated Regulatory Axis in Head and Neck Squamous Cell Carcinoma.	O
183	The mature phyllosphere microbiome of grapevine is associated with resistance against Plasmopara viticola. 14,	О
182	Exploring the mechanism of action of Glycyrrhiza glabraee for diabetic encephalopathy based on network pharmacology and in vitro experiments.	O
181	A prognostic and immunological analysis of 7B-containing Kelch structural domain (KLHDC7B) in pan-cancer: a potential target for immunotherapy and survival.	O
180	MicroRNAs-mediated regulation of the differentiation of dental pulp-derived mesenchymal stem cells: a systematic review and bioinformatic analysis. 2023 , 14,	O
179	Targeting Essential Hypothetical Proteins of Pseudomonas aeruginosa PAO1 for Mining of Novel Therapeutics: An In Silico Approach. 2023 , 2023, 1-28	О
178	VisWaterNet: A Python package for visualization of water distribution networks. 2023 , 8, 5139	O
177	SIR telomere silencing depends on nuclear envelope lipids and modulates sensitivity to a lysolipid. 2023 , 222,	0
176	Activation of AMPK promotes cardiac differentiation by stimulating the autophagy pathway.	O
175	Monkeypox virus: phylogenomics, hostpathogen interactome and mutational cascade. 2023 , 9,	0
174	An automated proximity proteomics pipeline for subcellular proteome and protein interaction mapping.	O

173	Identification of common factors among Fibrosarcoma, Rhabdomyosarcoma, and Osteosarcoma by network analysis.	O
172	Transcriptomics reveals the effects of NTRK1 on endoplasmic reticulum stress response-associated genes in human neuronal cell lines. 11, e15219	O
171	Large-scale phage cultivation for commensal human gut bacteria. 2023, 31, 665-677.e7	O
170	De novo full length transcriptome analysis of a naturally caffeine-free tea plant reveals specificity in secondary metabolic regulation. 2023 , 13,	O
169	Integrative analysis of HASMCs gene expression profile revealed the role of thrombin in the pathogenesis of atherosclerosis. 2023 , 23,	O
168	Plasma Exosomal Non-Coding RNA Profile Associated with Renal Damage Reveals Potential Therapeutic Targets in Lupus Nephritis. 2023 , 24, 7088	O
167	Evolutionary analysis of TCP gene family and its response to hormonal and abiotic stress in rye (Secale cereale L.).	О
166	Integrated LC-MS/MS and network pharmacology approach for predictingactive ingredients and pharmacological mechanisms of Tribulus terrestris L. against cardiac diseases. 1-16	O
165	Multiomics and spatial mapping characterizes human CD8 + T cell states in cancer. 2023, 15,	O
164	Identifying a dynamic transcriptomic landscape of the cynomolgus macaque placenta during pregnancy at single-cell resolution. 2023 ,	O
163	Long-Term Transcriptomic Changes and Cardiomyocyte Hyperpolyploidy after Lactose Intolerance in Neonatal Rats. 2023 , 24, 7063	O
162	Coliphages of the human urinary microbiota. 2023 , 18, e0283930	O
161	Identification of diagnostic biomarks and immune cell infiltration in ulcerative colitis. 2023, 13,	0
160	Exercise training remodels inguinal white adipose tissue through adaptations in innervation, vascularization, and the extracellular matrix. 2023 , 42, 112392	O
159	Transcriptomic analysis identified SLC40A1 as a key iron metabolism-related gene in airway macrophages in childhood allergic asthma. 11,	O
158	Connecting islet-specific hub genes and pathways in type 2 diabetes mellitus through the bioinformatics lens. 2023 , 36, 201177	0
157	Serum metabolic alterations in peritoneal dialysis patients with excessive daytime sleepiness. 2023 , 45,	О
156	Computational Screen for Sex-Specific Drug Effects in a Cardiac Fibroblast Network Model.	O

155	Graphene oxide exposure alters gut microbial community composition and metabolism in an in vitro human model. 2023 , 100463	0
154	Mapping CircRNAthiRNAthRNA regulatory axis identifies hsa_circ_0080942 and hsa_circ_0080135 as a potential theranostic agents for SARS-CoV-2 infection. 2023 , 18, e0283589	О
153	Genomic and transcriptomic analyses support a silk gland origin of spider venom glands. 2023, 21,	O
152	Identification of common candidate genes and pathways for Spina Bifida and Wilm⊠Tumor using an integrative bioinformatics analysis. 1-16	O
151	Single-step genome-wide association studies and post-GWAS analyses for the number of oocytes and embryos in Gir cattle.	0
150	Mosaic results after preimplantation genetic testing for aneuploidy may be accompanied by changes in global gene expression. 10,	О
149	Genomic and metabolic analyses reveal antagonistic lanthipeptides in archaea. 2023, 11,	O
148	Sequence-Based Platforms for Discovering Biomarkers in Liquid Biopsy of Non-Small-Cell Lung Cancer. 2023 , 15, 2275	О
147	Molecular Docking and Network Pharmacology Interaction Analysis of Gingko Biloba (EGB761) Extract with Dual Target Inhibitory Mechanism in Alzheimer Disease. 2023 , 1-22	0
146	Macrophage-Induced Exacerbation of Nasopharyngeal Inflammatory Lymphocytes in COVID-19 Disease. 2023 , 3, 567-591	О
145	Construction of an m6A-related lncRNA model for predicting prognosis and immunotherapy in patients with lung adenocarcinoma. 2023 , 102, e33530	0
144	Specific pupylation as IDEntity reporter (SPIDER) for the identification of protein-biomolecule interactions.	o
143	Antidepressants amitriptyline, fluoxetine, and traditional Chinese medicine Xiaoyaosan caused alterations in gut DNA virome composition and function in rats exposed chronic unpredictable mild stress. 14,	0
142	Identification and validation of chemokine system-related genes in idiopathic pulmonary fibrosis. 14,	O
141	Investigation of changes in DNA methylation associated with alterations in gene expression resulting in differences between lean and obese adipogenesis. 2023 , 115, 110623	0
140	Analysis of Nipah Virus Replication and Host Proteome Response Patterns in Differentiated Porcine Airway Epithelial Cells Cultured at the Airliquid Interface. 2023 , 15, 961	O
139	Identification of Differentially Expressed Genes and Molecular Pathways Involved in Osteoclastogenesis Using RNA-seq. 2023 , 14, 916	0
138	From observational to actionable: rethinking omics in biologics production. 2023,	O

137	Multi-omics analysis reveals a macrophage-related marker gene signature for prognostic prediction, immune landscape, genomic heterogeneity, and drug choices in prostate cancer. 14,	0
136	Identification of Critical Modules and Biomarkers of Ulcerative Colitis by Using WGCNA. Volume 16, 1617	-16280
135	Identification of Common Dysregulated Genes in COVID-19 and Hypersensitivity Pneumonitis: A Systems Biology and Machine Learning Approach.	O
134	Clinical features and molecular genetics associated with brain metastasis in suspected early-stage non-small cell lung cancer. 13,	O
133	Genomic Identification and Expression Analysis of Acid Invertase (AINV) Gene Family in Dendrobium officinale Kimura et Migo.	O
132	Drug Discovery in Canine Pyometra Disease Identified by Text Mining and Microarray Data Analysis. 2023 , 2023, 1-11	O
131	Origin and early divergence of tandem duplicated sorbitol transporter genes in Rosaceae: insights from evolutionary analysis of the SOT gene family in Angiosperms.	О
130	Network Biology Analyses and Dynamic Modeling of Gene Regulatory Networks under Drought Stress Reveal Major Transcriptional Regulators in Arabidopsis. 2023 , 24, 7349	O
129	SMARCAD1 and TOPBP1 contribute to heterochromatin maintenance at the transition from the 2C-like to the pluripotent state.	O
128	Secretome Screening of BRAFV600E-Mutated Colon Cancer Cells Resistant to Vemurafenib. 2023 , 12, 608	O
127	Phosphorylation and stabilization of EZH2 by DCAF1/VprBP trigger aberrant gene silencing in colon cancer. 2023 , 14,	О
126	The diagnostic combination of serum circulating miR-488 and lncRNA AC018761 as biomarkers for hypopharyngeal squamous cell carcinoma (HPSCC). 2023 , 104909	O
125	Proteomics and machine learning identify a distinct biomarker panel to detect prodromal and early Parkinson disease.	О
124	Unexplored diversity and ecological functions of transposable phages.	O
123	A new window into fish welfare: A proteomic discovery study of stress biomarkers in the skin mucus of gilthead seabream (Sparus aurata). 2023 , 104904	О
122	Evolutionary analysis of the OSCA gene family in sunflower (Helianthus annuus L) and expression analysis under NaCl stress. 11, e15089	O
121	MicroRNA Signatures in Cartilage Ageing and Osteoarthritis. 2023 , 11, 1189	О
120	m7G-related genesINCBP2 and EIF4E3 determine immune contexture in head and neck squamous cell carcinoma by regulating CCL4 / CCL5 expression.	O

119	Early-life stress and ovarian hormones alter transcriptional regulation in the nucleus accumbens resulting in sex-specific responses to cocaine.	O
118	Integrated analysis of endoplasmic reticulum stress regulators Lexpression identifies distinct subtypes of autism spectrum disorder. 14,	O
117	Elucidating the Corneal Endothelial Cell Proliferation Capacity through an Interspecies Transcriptome Comparison.	O
116	The Bynuclein Monomer May Have Different Misfolding Mechanisms in the Induction of Bynuclein Fibrils with Different Polymorphs. 2023 , 13, 682	O
115	Proanthocyanidins Inhibit Osteoblast Apoptosis via the PI3K/AKT/Bcl-xL Pathway in the Treatment of Steroid-Induced Osteonecrosis of the Femoral Head in Rats. 2023 , 15, 1936	O
114	A systematic antidiarrhoeal evaluation of a vegetable root Begonia roxburghii and its marker flavonoids against nonpathogenic and pathogenic diarrhoea. 2023 , 102672	O
113	Integrative analysis of TP53 mutations in lung adenocarcinoma for immunotherapies and prognosis. 2023 , 24,	0
112	Preserved correlation matrices pinpoint extracellular matrix organization as a critical factor in pancreatic ductal adenocarcinoma. 12, 418	O
111	Dysregulation of hypoxia-inducible factor 1\(\text{H}\)n the sympathetic nervous system accelerates diabetic cardiomyopathy. 2023 , 22,	0
110	FARSB serves as a novel hypomethylated and immune cell infiltration related prognostic biomarker in hepatocellular carcinoma.	O
109	microRNA-96 targets the INS/AKT/GLUT4 signaling axis: Association with and effect on diabetic retinopathy. 2023 , e15539	O
108	Screening and identification of key biomarkers in diabetic kidney disease and its complications: Evidence from bioinformatics and next generation sequencing data analysis.	O
107	Serum proteome and metabolome uncover novel biomarkers for the assessment of disease activity and diagnosing of systemic lupus erythematosus. 2023 , 251, 109330	O
106	Dosage sensitivity to Pumilio1 variants in the mouse brain reflects distinct molecular mechanisms.	O
105	Biotic interactions explain seasonal dynamics of the alpine soil microbiome.	0
104	Prognostic value of immunogenic cell death genes in bladder cancer.	O
103	Comprehensive Interactome Mapping of the DNA Repair Scaffold SLX4 Using Proximity Labeling and Affinity Purification.	O
102	Genome-wide differential expression profiling of long non-coding RNAs in FOXA2 knockout iPSC-derived pancreatic cells.	O

101	Mining for a New Class of Fungal Natural Products: The Evolution, Diversity, and Distribution of Isocyanide Synthase Biosynthetic Gene Clusters.	0
100	Metabolic alterations of the gutliver axis induced by cholic acid contribute to hepatic steatosis in rats. 2023 , 1868, 159319	O
99	Metabolic switch in the aging astrocyte supported via integrative approach comprising network and transcriptome analyses.	0
98	Bioinformatics analysis of the pathogenic link between Epstein-Barr virus infection, systemic lupus erythematosus and diffuse large B cell lymphoma. 2023 , 13,	O
97	The comprehensive bioinformatic analysis of the hsa-miR-3613-5p in kidney renal clear cell carcinoma.	0
96	Bexmarilimab-induced macrophage activation leads to treatment benefit in solid tumors: the phase I/II first-in-human MATINS trial.	O
95	Nucleosome reorganisation in breast cancer tissues.	0
94	Integrated glycoproteomic characterization of clear cell renal cell carcinoma. 2023, 42, 112409	O
93	Network pharmacology-based identification for the therapeutic mechanism of Zhizi in the depression.	0
92	Meta-analysis of expression and the targeting of cell adhesion associated genes in nine cancer types had one research lab re-evaluation. 2023 ,	O
91	Attractor dynamics drives self-reproduction in protobiological catalytic networks. 2023, 101384	0
90	Meta-analysis of commonly mutated genes in leptomeningeal carcinomatosis. 11, e15250	O
89	Whole transcriptome analysis of trifoliate orange (Poncirus trifoliata (L.) Raf.) under osmotic stress. 2023 , 317, 112045	0
88	Metagenomic and metatranscriptomic exploration of the Egyptian Red Sea sponge Theonella sp. associated microbial community. 2023 , 70, 101032	O
87	Transcriptome-Wide Association Study Reveals New Molecular Interactions Associated with Melanoma.	0
86	The impact of metabolic endotoxaemia on the browning process in human adipocytes. 2023, 21,	0
85	RWP-RK Domain 3 (OsRKD3) induces somatic embryogenesis in black rice. 2023 , 23,	0
84	De novo transcriptome sequencing and gene co-expression reveal a genomic basis for drought sensitivity and evidence of a rapid local adaptation on Atlas cedar (Cedrus atlantica). 14,	O

83	Key Genes and Biological Regulatory Mechanisms in Focal and Segmental Glomerulosclerosis: A Meta-Analysis and Validation of Expression Profiles.	O
82	Mitochondrial DNA Supplementation of Oocytes Has Downstream Effects on the Transcriptional Profiles of Sus scrofa Adult Tissues with High mtDNA Copy Number. 2023 , 24, 7545	O
81	A statistical learning method for simultaneous copy number estimation and subclone clustering with single cell sequencing data.	0
80	Effects of Atherogenic Factors on Endothelial Cells: Bioinformatics Analysis of Differentially Expressed Genes and Signaling Pathways. 2023 , 11, 1216	O
79	The Role of transcription factor FOXA1/C2/M1/O3/P1/Q1 in breast cancer.	O
78	Combination of single-nucleus and bulk RNA-seq reveals the molecular mechanism of thalamus haemorrhage-induced central poststroke pain. 14,	O
77	Mechanisms of action of Fu Fang Gang Liu liquid in treating condyloma acuminatum by network pharmacology and experimental validation. 2023 , 23,	O
76	A comparison of anatomic and cellular transcriptome structures across 40 human brain diseases. 2023 , 21, e3002058	O
75	Genome-wide analyses of LATERAL ORGAN BOUNDARIES in cassava reveal the role of LBD47 in defence against bacterial blight. 2023 , 18, e0282100	O
74	Discovery of New Siderophores from a Marine Streptomycetes sp. via Combined Metabolomics and Analysis of Iron-Chelating Activity.	O
73	An Operational Burden Issue: Deciding on a Corneal Recipient From the Corneal Transplant Wait List for Elective Corneal Transplant.	O
72	Distribution and molecular evolution of the anti-CRISPR family AcrIF7. 2023 , 21, e3002072	O
71	Common factors among three types of cells aged in mice.	O
70	Bioinformatics analysis combined with molecular dynamics simulation validation to elucidate the potential molecular mechanisms of Jianshen Decoction for treatment of osteoporotic fracture. 2023 , 102, e33610	O
69	Screening of feature genes related to immune and inflammatory responses in periodontitis. 2023 , 23,	O
68	Prognostic and Immunological Significance of the Molecular Subtypes and Risk Signatures Based on Cuproptosis in Hepatocellular Carcinoma. 2023 , 2023, 1-23	O
67	Serum amyloid A proteins reduce bone mass during mycobacterial infections. 14,	0
66	Systems biology tools for the identification of potential drug targets and biological markers effective for cancer therapeutics. 2023 , 259-292	O

65	MyBrain-Seq: A Pipeline for MiRNA-Seq Data Analysis in Neuropsychiatric Disorders. 2023 , 11, 1230	О
64	Identification and validation of autophagy-related genes in Kawasaki disease. 2023, 160,	О
63	Comprehensive Analysis of NABP2 as a Prognostic Biomarker and Its Correlation with Immune Infiltration in Hepatocellular Carcinoma. Volume 16, 1783-1804	0
62	Comparative Physiological and Transcriptomic Mechanisms of Defoliation in Cotton in Response to Thidiazuron versus Ethephon. 2023 , 24, 7590	o
61	A Pseudomonas Lysogenic Bacteriophage Crossing the Antarctic and Arctic, Representing a New Genus of Autographiviridae. 2023 , 24, 7662	0
60	Comprehensive analysis of circular RNAs in porcine small intestine epithelial cells associated with susceptibility to Escherichia coli F4ac diarrhea. 2023 , 24,	0
59	Screening and introduction of key cell cycle microRNAs deregulated in colorectal cancer by integrated bioinformatics analysis.	0
58	Diversity, distribution, and functional potentials of magroviruses from marine and brackish waters. 14,	o
57	Rhinovirus-induced epithelial RIG-I inflammasome suppresses antiviral immunity and promotes inflammation in asthma and COVID-19. 2023 , 14,	0
56	Identification and Potential Value of Candidate Genes in Patients with Sinonasal inverted papilloma.	o
55	Single-cell RNA sequencing of Sox17-expressing lineages reveals distinct gene regulatory networks and dynamic developmental trajectories.	O
54	The hindgut microbiome contributes to host oxidative stress in postpartum dairy cows by affecting glutathione synthesis process. 2023 , 11,	O
53	Elucidation of a Dearomatization Route in the Biosynthesis of Oxysporidinone Involving a TenA-like Cytochrome P450 Enzyme.	0
52	RRM2 as a novel prognostic and therapeutic target of NF1-associated MPNST.	o
51	In Silico Interactions of Natural and Synthetic Compounds with Key Proteins Involved in Alzheimer Disease: Prospects for Designing New Therapeutics Compound.	0
50	Transcriptional dissection of symptomatic profiles across the brain of men and women with depression.	o
49	Cardiac performance and heart gene network provide dynamic responses of bay scallop Argopecten irradians irradians exposure to marine heatwaves. 2023 , 163594	0
48	Bioinformatics analysis of key candidate genes and pathways in Chinese patients with keratoconus. 2023 , 231, 109488	O

47	Oxylipin biosynthetic gene families of Cannabis sativa. 2023 , 18, e0272893	O
46	Alterations in the intestinal microbiome and metabolic profile of patients with cirrhosis supplemented with lactulose, Clostridium butyricum, and Bifidobacterium longum infantis: a randomized placebo-controlled trial. 14,	O
45	The evolutionary patterns, expression profiles, and genetic diversity of expanded genes in barley. 14,	O
44	Large-scale phage-based screening reveals extensive pan-viral mimicry of host short linear motifs. 2023 , 14,	O
43	Elucidation of bezlotoxumab binding specificity to toxin B in Clostridioides difficile. 1-12	0
42	Profiling Plant Proteome and Transcriptome Changes during Grapevine Fanleaf Virus Infection.	O
41	Computer-aided analysis of quercetin mechanism of overcoming docetaxel resistance in docetaxel-resistant prostate cancer. 2023 , 21,	O
40	Bacterial inoculation of Quercus pyrenaica trees alters co-occurrence patterns but not the composition of the rhizosphere bacteriome in wild conditions.	O
39	Phosphorylation of SiRAV1 at Ser31 regulates the SiCAT expression to enhance salt tolerance in Setaria italica. 2023 ,	O
38	Genome-wide identification and molecular characterization of CRK gene family in cucumber (Cucumis sativus L.) under cold stress and sclerotium rolfsii infection. 2023 , 24,	O
37	Phylogenomics of Globally Spread Clonal Groups 14 and 15 of Klebsiella pneumoniae.	0
36	Gene expression and expression quantitative trait loci analyses uncover natural variations underlying the improvement of important agronomic traits during modern maize breeding.	O
35	Gegen Qinlian standard decoction alleviated irinotecan-induced diarrhea via PI3K/AKT/NF-B axis by network pharmacology prediction and experimental validation combination. 2023, 18,	0
34	WGCNA and molecular docking identify hub genes for cardiac aging. 10,	O
33	Extending inherited metabolic disorder diagnostics with biomarker interaction visualizations. 2023 , 18,	0
32	Therapeutic effects of Crataegus monogyna inhibitors against breast cancer. 14,	O
31	A systematically biosynthetic investigation of lactic acid bacteria reveals diverse antagonistic bacteriocins that potentially shape the human microbiome. 2023 , 11,	О
30	Chemical Diversity and In Vitro/In Silico Antiviral Activity of Extracts from Different Parts of Phyllanthus brasiliensis (Aubl.) Poir.	0

29	Horizontal Transposon Transfer and Their Ecological Drivers: The Case of Flower-breeding Drosophila. 2023 , 15,	Ο
28	Key Pathways and Genes of Arabidopsis thaliana and Arabidopsis halleri Roots under Cadmium Stress Responses: Differences and Similarities. 2023 , 12, 1793	Ο
27	Application of Lipidomics in Psychiatry: Plasma-Based Potential Biomarkers in Schizophrenia and Bipolar Disorder. 2023 , 13, 600	0
26	The key mediators involved in myocardial endoplasmic reticulum stress induced by ischaemia reperfusion injury in rats. 2023 , 21, 1721727X2311731	Ο
25	The R2R3-MYB transcription factor GaPC controls petal coloration in cotton. 2023,	0
24	Identifying Key Genes and Related Molecules as Potential Biomarkers in Human Dilated Cardiomyopathy by Comprehensive Bioinformatics Analysis. 2023 , 8,	O
23	DDX5 (p68) orchestrates Etatenin, RelA and SP1 mediated MGMT gene expression: Implication in TMZ chemoresistance.	0
22	Identification of key upregulated genes involved in foam cell formation and the modulatory role of statin therapy. 2023 , 119, 110209	Ο
21	A comparative study of dietary lipid sources on growth performance, body composition, fillet quality, and nutrient retention in juvenile yellow drum (Nibea albiflora). 2023 , 574, 739630	Ο
20	A Novel Assessment of Metabolic Pathways in Peritoneal Metastases from Low-Grade Appendiceal Mucinous Neoplasms.	Ο
19	Intestinal microbiota analyses of five economic fishery resources in the South China Sea. 2023 , 46, 101085	Ο
18	Methadone alters transcriptional programs associated with synapse formation in human cortical organoids. 2023 , 13,	O
17	Abnormal homeostasis of P53 gene knockout mice can be reflected in urinary proteome.	Ο
16	Paired associated SARS-CoV-2 spike variable positions: a network analysis approach to emerging variants.	Ο
15	A single-cell view on host immune transcriptional response to in vivo BCG-induced trained immunity. 2023 , 42, 112487	Ο
14	Prenatal DEHP exposure predicts neurological disorders via transgenerational epigenetics. 2023 , 13,	Ο
13	Comparative transcriptome profiling reveals the multiple levels of crosstalk in phytohormone networks in Brassica napus.	0
12	Physiology and transcriptomic analysis of endogenous hormones regulating in vitro adventitious root formation in tree peony. 2023 , 318, 112122	O

11	Genome-Wide Expression Analysis of Long Noncoding RNAs and Their Target Genes in Metafemale Drosophila. 2023 , 24, 8381	0
10	Transcriptional Signatures in Contrasting Cultivars of Barley During Early Reproductive Development of Meristem.	O
9	Using Advanced Bioinformatics Tools to Identify Novel Therapeutic Candidates for Proliferative Vitreoretinopathy. 2023 , 12, 19	O
8	Bioinformatics analyses suggest that mutations in COL12A1 and its miRNAs promote stomach adenocarcinoma via loss of COL12A1 suppression. 2023 ,	o
7	Transcriptome profiling of barley in response to mineral and organic fertilizers. 2023, 23,	0
6	Screening and identification of key chromatin regulator biomarkers for ankylosing spondylitis and drug prediction: evidence from bioinformatics analysis. 2023 , 24,	O
5	Identification of mRNA and lncRNA profiles and potential targeted agents for fibrolamellar carcinoma based on RNA-sequencing data.	0
4	Identification of immune-related genes in acute myocardial infarction based on integrated bioinformatical methods and experimental verification. 11, e15058	o
3	N/S element transformation modulating lithospheric microbial communities by single-species manipulation. 2023 , 11,	О
2	Chromosome-scale genome sequence assemblies of the Autumn Blissland Malling Jewelltultivars of the highly heterozygous red raspberry (Rubus idaeus L.) derived from long-read Oxford Nanopore sequence data. 2023 , 18, e0285756	o
1	Basal forebrain cholinergic neurons are vulnerable in a mouse model of Down syndrome and their molecular fingerprint is rescued by maternal choline supplementation. 2023 , 37,	0