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KEGG for linking genomes to life and the environment

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2233	Peptide-mediated interactions in biological systems: new discoveries and applications. **2008**, 19, 344-50		185
2232	The Comparative Toxicogenomics Database facilitates identification and understanding of chemical-gene-disease associations: arsenic as a case study. **2008**, 1, 48		53
2231	Filling the gap between biology and computer science. **2008**, 1, 1		11
2230	Crystallization and preliminary X-ray diffraction studies of the prototypal homologue of mitoNEET (Tth-NEET0026) from the extreme thermophile Thermus thermophilus HB8. **2008**, 64, 1146-8		9
2229	FiD: a software for ab initio structural identification of product ions from tandem mass spectrometric data. **2008**, 22, 3043-52		104
2228	Web resources for the glycoscientist. **2008**, 9, 2155-60		22
2227	Iron homeostasis strategies in acidophilic iron oxidizers: Studies in Acidithiobacillus and Leptospirillum. **2008**, 94, 175-179		11
2226	Comparative genome analysis of Acidithiobacillus ferrooxidans, A. thiooxidans and A. caldus: Insights into their metabolism and ecophysiology. **2008**, 94, 180-184		70
2225	Comparative metabolite profiling of carboxylic acids in rat urine by CE-ESI MS/MS through positively pre-charged and (2)H-coded derivatization. **2008**, 29, 4549-60		43
2224	Liquid chromatography-mass spectrometry in metabolite profiling. **2008**, 34, 159-69		6
2223	Targeting and tinkering with interaction networks. **2008**, 4, 666-73		80
2222	The Pristionchus pacificus genome provides a unique perspective on nematode lifestyle and parasitism. **2008**, 40, 1193-8		280
2221	Towards a cyberinfrastructure for the biological sciences: progress, visions and challenges. **2008**, 9, 678-88		123
2220	Information-based methods for predicting gene function from systematic gene knock-downs. **2008**, 9, 463		4
2219	Gene set analyses for interpreting microarray experiments on prokaryotic organisms. **2008**, 9, 469		12
2218	Comprehensive analysis of circadian periodic pattern in plant transcriptome. **2008**, 9 Suppl 9, S18		10
2217	Prosecutor: parameter-free inference of gene function for prokaryotes using DNA microarray data, genomic context and multiple gene annotation sources. **2008**, 9, 495		5

2216	Multiple genome alignment for identifying the core structure among moderately related microbial genomes. **2008**, 9, 515	23
2215	Comparative genomic analysis of carbon and nitrogen assimilation mechanisms in three indigenous bioleaching bacteria: predictions and validations. **2008**, 9, 581	86
2214	Human and mouse switch-like genes share common transcriptional regulatory mechanisms for bimodality. **2008**, 9, 628	12
2213	The RAST Server: rapid annotations using subsystems technology. **2008**, 9, 75	7153
2212	Machine learning based analyses on metabolic networks supports high-throughput knockout screens. **2008**, 2, 67	33
2211	The use of Gene Ontology terms for predicting highly-connected 'hub' nodes in protein-protein interaction networks. **2008**, 2, 80	44
2210	Origin of structural difference in metabolic networks with respect to temperature. **2008**, 2, 82	11
2209	The public road to high-quality curated biological pathways. **2008**, 13, 856-62	37
2208	iPath: interactive exploration of biochemical pathways and networks. **2008**, 33, 101-3	156
2207	Protein interactions: integration leads to belief. **2008**, 33, 241-2; author reply 242-3	29
2206	Lipidomics: a new window to biomedical frontiers. **2008**, 26, 647-52	133
2205	Complete genome sequence of the extremely acidophilic methanotroph isolate V4, Methylacidiphilum infernorum, a representative of the bacterial phylum Verrucomicrobia. **2008**, 3, 26	168
2204	Changes in the gene expression profile of Arabidopsis thaliana after infection with Tobacco etch virus. **2008**, 5, 92	50
2203	Computational identification of obligatorily autocatalytic replicators embedded in metabolic networks. **2008**, 9, R51	45
2202	Identification of mitochondrial disease genes through integrative analysis of multiple datasets. **2008**, 46, 248-55	9
2201	Reconstruction of genome scale metabolic model for naturally xylose fermenting yeast Pichia stipitis. **2008**, 136, S49	1
2200	Using glycome databases for drug discovery. **2008**, 3, 877-90	4
2199	Web‐Enabled Classification of SNPs for Genome‐Wide Association Studies. **2008**,	

2198	PIPA: A High-Throughput Pipeline for Protein Function Annotation. **2008**,		
2197	A candidate gene survey of quantitative trait loci affecting chemical composition in tomato fruit. **2008**, 59, 2875-90		39
2196	Modularity of cellular networks shows general center-periphery polarization. **2008**, 24, 2814-7		11
2195	Solutions for data integration in functional genomics: a critical assessment and case study. **2008**, 9, 532-44		21
2194	KEGG Atlas mapping for global analysis of metabolic pathways. *Nucleic Acids Research*, **2008**, 36, W423-6	20.1	343
2193	Paradoxical effect of mitochondrial respiratory chain impairment on insulin signaling and glucose transport in adipose cells. **2008**, 283, 30658-67		49
2192	ProdoNet: identification and visualization of prokaryotic gene regulatory and metabolic networks. *Nucleic Acids Research*, **2008**, 36, W460-4	20.1	15
2191	Tricarboxylic acid cycle-dependent regulation of Staphylococcus epidermidis polysaccharide intercellular adhesin synthesis. **2008**, 190, 7621-32		60
2190	Regulation of glycan structures in animal tissues: transcript profiling of glycan-related genes. **2008**, 283, 17298-313		156
2189	Genetic and computational identification of a conserved bacterial metabolic module. **2008**, 4, e1000310		24
2188	Physical protein-protein interactions predicted from microarrays. **2008**, 24, 2608-14		34
2187	GraphWeb: mining heterogeneous biological networks for gene modules with functional significance. *Nucleic Acids Research*, **2008**, 36, W452-9	20.1	74
2186	Evolutionary design principles of modules that control cellular differentiation: consequences for hysteresis and multistationarity. **2008**, 24, 1516-22		12
2185	A genetic screen for increased loss of heterozygosity in Saccharomyces cerevisiae. **2008**, 179, 1179-95		62
2184	VisANT: an integrative framework for networks in systems biology. **2008**, 9, 317-25		89
2183	Comparative Pathway Analyzer--a web server for comparative analysis, clustering and visualization of metabolic networks in multiple organisms. *Nucleic Acids Research*, **2008**, 36, W433-7	20.1	9
2182	jSquid: a Java applet for graphical on-line network exploration. **2008**, 24, 1467-8		16
2181	GeConT 2: gene context analysis for orthologous proteins, conserved domains and metabolic pathways. *Nucleic Acids Research*, **2008**, 36, W176-80	20.1	32

2180	Regulation of fructose transport and its effect on fructose toxicity in Anabaena spp. **2008**, 190, 8115-25		35
2179	Predicting pathway membership via domain signatures. **2008**, 24, 2137-42		13
2178	SWARM. **2008**,		2
2177	ENDEAVOUR update: a web resource for gene prioritization in multiple species. *Nucleic Acids Research*, **2008**, 36, W377-84	20.1	182
2176	Chapter 1. Target selection in structural genomics projects to increase knowledge of protein structure and function space. **2008**, 75, 1-52		1
2175	Network-Constrained Support Vector Machine for Classification. **2008**,		
2174	Towards dynamic database infrastructures for mouse genetics. **2008**,		
2173	Computational Models of Metabolism: Stability and Regulation in Metabolic Networks. **2008**, 105-251		21
2172	InnateDB: facilitating systems-level analyses of the mammalian innate immune response. **2008**, 4, 218		282
2171	Metabolomic and flux-balance analysis of age-related decline of hypoxia tolerance in Drosophila muscle tissue. **2008**, 4, 233		42
2170	Exploring the evolutionary history of the differentially expressed genes between human populations: action of recent positive selection. **2008**, 4, 171-9		1
2169	Association of interacting genes in the toll-like receptor signaling pathway and the antibody response to pertussis vaccination. **2008**, 3, e3665		41
2168	Genome-wide co-expression analysis in multiple tissues. **2008**, 3, e4033		19
2167	Metabolomics provide new insight on the metabolism of dietary phytochemicals in rats. **2008**, 138, 1282-7		52
2166	Coenzyme and Prosthetic Group Biosynthesis. **2009**, 79-88		1
2165	Genome-wide profile of pleural mesothelioma versus parietal and visceral pleura: the emerging gene portrait of the mesothelioma phenotype. **2009**, 4, e6554		55
2164	Detection of molecular paths associated with insulitis and type 1 diabetes in non-obese diabetic mouse. **2009**, 4, e7323		13
2163	Assessment of metabolome annotation quality: a method for evaluating the false discovery rate of elemental composition searches. **2009**, 4, e7490		56

2162	Pathway projector: web-based zoomable pathway browser using KEGG atlas and Google Maps API. **2009**, 4, e7710		68
2161	Sialic acid utilisation and synthesis in the neonatal rat revisited. **2009**, 4, e8241		32
2160	Pathway analysis of GWAS provides new insights into genetic susceptibility to 3 inflammatory diseases. **2009**, 4, e8068		110
2159	A New Recursive Approach for Reconstructing Metabolic Networks from KEGG. **2009**,		
2158	STRING 8--a global view on proteins and their functional interactions in 630 organisms. *Nucleic Acids Research*, **2009**, 37, D412-6	20.1	1799
2157	Large-scale proteome profile of the zebrafish (Danio rerio) gill for physiological and biomarker discovery studies. **2009**, 6, 229-38		41
2156	Meta-analysis of cancer microarray data reveals signaling pathway hotspots. **2009**,		
2155	Mining large heterogeneous data sets in drug discovery. **2009**, 4, 995-1004		13
2154	Collection of Disease Networks by Hybrid Curation Method and the Application for Pathway Analysis. **2009**,		3
2153	Bayesian network approach to understand regulation of biological processes in cyanobacteria. **2009**,		
2152	Measuring Structural Robustness of Metabolic Networks under a Boolean Model Using Integer Programming and Feedback Vertex Sets. **2009**,		6
2151	Comprehensive analysis of the impact of SNPs and CNVs on human microRNAs and their regulatory genes. **2009**, 6, 412-25		55
2150	Considerations to improve functional annotations in biological databases. **2009**, 13, 527-35		8
2149	Focal adhesion kinase signaling regulates the expression of caveolin 3 and beta1 integrin, genes essential for normal myoblast fusion. **2009**, 20, 3422-35		92
2148	IMG ER: a system for microbial genome annotation expert review and curation. **2009**, 25, 2271-8		742
2147	Complete genome sequence of the ethanol producer Zymomonas mobilis NCIMB 11163. **2009**, 191, 7140-1		36
2146	A novel regulatory protein involved in motility of Vibrio cholerae. **2009**, 191, 7027-38		28
2145	Quantitative proteomics characterization of a mouse embryonic stem cell model of Down syndrome. **2009**, 8, 585-95		18

2144	TrichOME: a comparative omics database for plant trichomes. **2010**, 152, 44-54		87
2143	The microRNA signature in response to insulin reveals its implication in the transcriptional action of insulin in human skeletal muscle and the role of a sterol regulatory element-binding protein-1c/myocyte enhancer factor 2C pathway. **2009**, 58, 2555-64		116
2142	Disease gene-fishing in molecular interaction networks: a case study in colorectal cancer. **2009**, 2009, 6416-9		2
2141	Small RNA identification in Enterobacteriaceae using synteny and genomic backbone retention II. **2009**, 13, 261-84		5
2140	Pathway Activity Inferences with Negatively Correlated Features for Pancreatic Cancer Classification. **2009**,		1
2139	KEGGgraph: a graph approach to KEGG PATHWAY in R and bioconductor. **2009**, 25, 1470-1		221
2138	ARDB--Antibiotic Resistance Genes Database. *Nucleic Acids Research*, **2009**, 37, D443-7	20.1	796
2137	SNPLogic: an interactive single nucleotide polymorphism selection, annotation, and prioritization system. *Nucleic Acids Research*, **2009**, 37, D803-9	20.1	23
2136	Combining tissue transcriptomics and urine metabolomics for breast cancer biomarker identification. **2009**, 25, 3151-7		94
2135	SchistoDB: a Schistosoma mansoni genome resource. *Nucleic Acids Research*, **2009**, 37, D579-82	20.1	67
2134	UniHI 4: new tools for query, analysis and visualization of the human protein-protein interactome. *Nucleic Acids Research*, **2009**, 37, D657-60	20.1	56
2133	AS-ALPS: a database for analyzing the effects of alternative splicing on protein structure, interaction and network in human and mouse. *Nucleic Acids Research*, **2009**, 37, D305-9	20.1	27
2132	WhichGenes: a web-based tool for gathering, building, storing and exporting gene sets with application in gene set enrichment analysis. *Nucleic Acids Research*, **2009**, 37, W329-34	20.1	25
2131	Path: a tool to facilitate pathway-based genetic association analysis. **2009**, 25, 2444-6		15
2130	Efficiently finding genome-wide three-way gene interactions from transcript- and genotype-data. **2009**, 25, 2735-43		17
2129	Combining multiple positive training sets to generate confidence scores for protein-protein interactions. **2009**, 25, 105-11		40
2128	Variable locus length in the human genome leads to ascertainment bias in functional inference for non-coding elements. **2009**, 25, 578-84		21
2127	E-zyme: predicting potential EC numbers from the chemical transformation pattern of substrate-product pairs. **2009**, 25, i179-86		57

2126	Complete genome sequence of Burkholderia glumae BGR1. **2009**, 191, 3758-9		48
2125	PID: the Pathway Interaction Database. *Nucleic Acids Research*, **2009**, 37, D674-9	20.1	1068
2124	Strepto-DB, a database for comparative genomics of group A (GAS) and B (GBS) streptococci, implemented with the novel database platform 'Open Genome Resource' (OGeR). *Nucleic Acids Research*, **2009**, 37, D494-8	20.1	4
2123	The National Center for Biotechnology Information's Protein Clusters Database. *Nucleic Acids Research*, **2009**, 37, D216-23	20.1	208
2122	The impact of incomplete knowledge on evaluation: an experimental benchmark for protein function prediction. **2009**, 25, 2404-10		29
2121	Comparative Toxicogenomics Database: a knowledgebase and discovery tool for chemical-gene-disease networks. *Nucleic Acids Research*, **2009**, 37, D786-92	20.1	210
2120	Complete genome sequence of Rhodobacter sphaeroides KD131. **2009**, 191, 1118-9		27
2119	OKCAM: an ontology-based, human-centered knowledgebase for cell adhesion molecules. *Nucleic Acids Research*, **2009**, 37, D251-60	20.1	17
2118	Enrichment constrained time-dependent clustering analysis for finding meaningful temporal transcription modules. **2009**, 25, 1521-7		17
2117	NAD biosynthesis evolution in bacteria: lateral gene transfer of kynurenine pathway in Xanthomonadales and Flavobacteriales. **2009**, 26, 399-406		36
2116	Response to comment on 'Can sugars be produced from fatty acids? A test case for pathway analysis tools'. **2009**, 25, 3330-1		7
2115	EcID. A database for the inference of functional interactions in E. coli. *Nucleic Acids Research*, **2009**, 37, D629-35	20.1	26
2114	ATTED-II provides coexpressed gene networks for Arabidopsis. *Nucleic Acids Research*, **2009**, 37, D987-91	20.1	306
2113	Sys-BodyFluid: a systematical database for human body fluid proteome research. *Nucleic Acids Research*, **2009**, 37, D907-12	20.1	71
2112	A community-curated consensual annotation that is continuously updated: the Bacillus subtilis centred wiki SubtiWiki. **2009**, 2009, bap012		28
2111	KAGIANA: an excel-based tool for retrieving summary information on Arabidopsis genes. **2009**, 50, 173-7		10
2110	Integrated analyses of the rice secretome. **2009**, 4, 345-7		2
2109	Efficient computation of impact degrees for multiple reactions in metabolic networks with cycles. **2009**,		2

2108	CNVVdb: a database of copy number variations across vertebrate genomes. **2009**, 25, 1419-21		7
2107	LitInspector: literature and signal transduction pathway mining in PubMed abstracts. *Nucleic Acids Research*, **2009**, 37, W135-40	20.1	42
2106	Simultaneous inference of biological networks of multiple species from genome-wide data and evolutionary information: a semi-supervised approach. **2009**, 25, 2962-8		37
2105	Plant MetGenMAP: an integrative analysis system for plant systems biology. **2009**, 151, 1758-68		120
2104	Influence of fatty acid diets on gene expression in rat mammary epithelial cells. **2009**, 38, 80-8		15
2103	Modulation of the allergic asthma transcriptome following resiquimod treatment. **2009**, 38, 303-18		16
2102	The noncanonical WNT pathway is operative in idiopathic pulmonary arterial hypertension. **2009**, 40, 683-91		80
2101	Androgen-responsive gene database: integrated knowledge on androgen-responsive genes. **2009**, 23, 1927-33		54
2100	Caleydo: connecting pathways and gene expression. **2009**, 25, 2760-1		23
2099	Sequence-based prediction of type III secreted proteins. **2009**, 5, e1000376		194
2098	Geometric de-noising of protein-protein interaction networks. **2009**, 5, e1000454		134
2097	Rapid pathway evolution facilitated by horizontal gene transfers across prokaryotic lineages. **2009**, 5, e1000402		34
2096	Annotation error in public databases: misannotation of molecular function in enzyme superfamilies. **2009**, 5, e1000605		464
2095	Use of GenMAPP and MAPPFinder to analyse pathways involved in chickens infected with the protozoan parasite Eimeria. **2009**, 3 Suppl 4, S7		5
2094	Incorporating biological knowledge in the search for gene x gene interaction in genome-wide association studies. **2009**, 3 Suppl 7, S81		2
2093	A genome-scale metabolic reconstruction of Mycoplasma genitalium, iPS189. **2009**, 5, e1000285		105
2092	1+1 = 3: a fusion of 2 enzymes in the methionine salvage pathway of Tetrahymena thermophila creates a trifunctional enzyme that catalyzes 3 steps in the pathway. **2009**, 5, e1000701		8
2091	Comparative genomic characterization of Francisella tularensis strains belonging to low and high virulence subspecies. **2009**, 5, e1000459		100

2090	A CitationRank algorithm inheriting Google technology designed to highlight genes responsible for serious adverse drug reaction. **2009**, 25, 2244-50		22
2089	Forging links between human mental retardation-associated CNVs and mouse gene knockout models. **2009**, 5, e1000531		39
2088	In response to 'Can sugars be produced from fatty acids? A test case for pathway analysis tools'. **2009**, 25, 3202-5		9
2087	MicroScope: a platform for microbial genome annotation and comparative genomics. **2009**, 2009, bap021		203
2086	Modelling in systems biology, neurology and pharmacy. **2009**, 15, 479-491		2
2085	KiPar, a tool for systematic information retrieval regarding parameters for kinetic modelling of yeast metabolic pathways. **2009**, 25, 1404-11		12
2084	Prediction of candidate primary immunodeficiency disease genes using a support vector machine learning approach. **2009**, 16, 345-51		23
2083	Michigan molecular interactions r2: from interacting proteins to pathways. *Nucleic Acids Research*, **2009**, 37, D642-6	20.1	78
2082	Transcriptional profiling of the dose response: a more powerful approach for characterizing drug activities. **2009**, 5, e1000512		21
2081	Linking human diseases to animal models using ontology-based phenotype annotation. **2009**, 7, e1000247		209
2080	GrowMatch: an automated method for reconciling in silico/in vivo growth predictions. **2009**, 5, e1000308		169
2079	Gene conversion maintains nonfunctional transposable elements in an obligate mutualistic endosymbiont. **2009**, 26, 1679-82		17
2078	GeneCodis: interpreting gene lists through enrichment analysis and integration of diverse biological information. *Nucleic Acids Research*, **2009**, 37, W317-22	20.1	354
2077	SMART 6: recent updates and new developments. *Nucleic Acids Research*, **2009**, 37, D229-32	20.1	779
2076	Genome scale reconstruction of a Salmonella metabolic model: comparison of similarity and differences with a commensal Escherichia coli strain. **2009**, 284, 29480-8		75
2075	Massive transcriptional start site analysis of human genes in hypoxia cells. *Nucleic Acids Research*, **2009**, 37, 2249-63	20.1	87
2074	Exploring the pathogenesis of renal cell carcinoma: pathway and bioinformatics analysis of dysregulated genes and proteins. **2009**, 390, 125-35		13
2073	FIGfams: yet another set of protein families. *Nucleic Acids Research*, **2009**, 37, 6643-54	20.1	101

2072	Reconciling ecological and genomic divergence among lineages of listeria under an "extended mosaic genome concept". **2009**, 26, 2605-15		22
2071	OryGenesDB 2008 update: database interoperability for functional genomics of rice. *Nucleic Acids Research*, **2009**, 37, D992-5	20.1	32
2070	Seeing is believing: on the use of image databases for visually exploring plant organelle dynamics. **2009**, 50, 2000-14		20
2069	Multi-dimensional correlations for gene coexpression and application to the large-scale data of Arabidopsis. **2009**, 25, 2677-84		19
2068	Exploring the human genome with functional maps. **2009**, 19, 1093-106		159
2067	Designing and encoding models for synthetic biology. **2009**, 6 Suppl 4, S405-17		41
2066	VisHiC--hierarchical functional enrichment analysis of microarray data. *Nucleic Acids Research*, **2009**, 37, W587-92	20.1	7
2065	Metabolic capacity of Sinorhizobium (Ensifer) meliloti strains as determined by phenotype MicroArray analysis. **2009**, 75, 5396-404		48
2064	ncRNAppi--a tool for identifying disease-related miRNA and siRNA targeting pathways. **2009**, 25, 3199-201		1
2063	CycSim--an online tool for exploring and experimenting with genome-scale metabolic models. **2009** , 25, 1987-8		22
2062	Predicting homologous signaling pathways using machine learning. **2009**, 25, 2913-20		8
2061	FINDSITE: a combined evolution/structure-based approach to protein function prediction. **2009**, 10, 378-91		79
2060	ESG: extended similarity group method for automated protein function prediction. **2009**, 25, 1739-45		71
2059	FMM: a web server for metabolic pathway reconstruction and comparative analysis. *Nucleic Acids Research*, **2009**, 37, W129-34	20.1	80
2058	The High Throughput Sequence Annotation Service (HT-SAS) - the shortcut from sequence to true Medline words. **2009**, 10, 148		4
2057	CLEAN: CLustering Enrichment ANalysis. **2009**, 10, 234		53
2056	Detecting purely epistatic multi-locus interactions by an omnibus permutation test on ensembles of two-locus analyses. **2009**, 10, 294		27
2055	Genome Projector: zoomable genome map with multiple views. **2009**, 10, 31		32

2054	Sparse canonical correlation analysis for identifying, connecting and completing gene-expression networks. **2009**, 10, 315	23
2053	Deterministic Effects Propagation Networks for reconstructing protein signaling networks from multiple interventions. **2009**, 10, 322	22
2052	Text mining and manual curation of chemical-gene-disease networks for the comparative toxicogenomics database (CTD). **2009**, 10, 326	97
2051	Graphle: Interactive exploration of large, dense graphs. **2009**, 10, 417	14
2050	KA-SB: from data integration to large scale reasoning. **2009**, 10 Suppl 10, S5	1
2049	XML-based approaches for the integration of heterogeneous bio-molecular data. **2009**, 10 Suppl 12, S7	16
2048	Systematic analysis of insertions and deletions specific to nematode proteins and their proposed functional and evolutionary relevance. **2009**, 9, 23	23
2047	Phylogenomics of the oxidative phosphorylation in fungi reveals extensive gene duplication followed by functional divergence. **2009**, 9, 295	58
2046	Chromosome Y variants from different inbred mouse strains are linked to differences in the morphologic and molecular responses of cardiac cells to postpubertal testosterone. **2009**, 10, 150	14
2045	ChlamyCyc: an integrative systems biology database and web-portal for Chlamydomonas reinhardtii. **2009**, 10, 209	72
2044	A network-based integrative approach to prioritize reliable hits from multiple genome-wide RNAi screens in Drosophila. **2009**, 10, 220	33
2043	Transcriptional profiling in response to terminal drought stress reveals differential responses along the wheat genome. **2009**, 10, 279	120
2042	Hmrbase: a database of hormones and their receptors. **2009**, 10, 307	22
2041	Gene expression profiles in mouse embryo fibroblasts lacking stathmin, a microtubule regulatory protein, reveal changes in the expression of genes contributing to cell motility. **2009**, 10, 343	13
2040	Comparative 454 pyrosequencing of transcripts from two olive genotypes during fruit development. **2009**, 10, 399	191
2039	Deciphering the transcriptional circuitry of microRNA genes expressed during human monocytic differentiation. **2009**, 10, 595	57
2038	Molecular evolution of the hyperthermophilic archaea of the Pyrococcus genus: analysis of adaptation to different environmental conditions. **2009**, 10, 639	22
2037	Somatic, germline and sex hierarchy regulated gene expression during Drosophila metamorphosis. **2009**, 10, 80	44

2036	Systematic identification of genes involved in divergent skeletal muscle growth rates of broiler and layer chickens. **2009**, 10, 87	56
2035	BioNetBuilder2.0: bringing systems biology to chicken and other model organisms. **2009**, 10 Suppl 2, S6	13
2034	PDbase: a database of Parkinson's disease-related genes and genetic variation using substantia nigra ESTs. **2009**, 10 Suppl 3, S32	13
2033	Regulation of phenylacetic acid degradation genes of Burkholderia cenocepacia K56-2. **2009**, 9, 222	22
2032	Computational annotation of genes differentially expressed along olive fruit development. **2009**, 9, 128	65
2031	Inferring branching pathways in genome-scale metabolic networks. **2009**, 3, 103	51
2030	13C-metabolic flux ratio and novel carbon path analyses confirmed that Trichoderma reesei uses primarily the respirative pathway also on the preferred carbon source glucose. **2009**, 3, 104	18
2029	Proteomic and network analysis characterize stage-specific metabolism in Trypanosoma cruzi. **2009** , 3, 52	37
2028	LeishCyc: a biochemical pathways database for Leishmania major. **2009**, 3, 57	58
2027	A systems biology framework for modeling metabolic enzyme inhibition of Mycobacterium tuberculosis. **2009**, 3, 92	31
2026	Wnt pathway regulation in chronic renal allograft damage. **2009**, 9, 2223-39	74
2025	Effect of fluid flow-induced shear stress on human mesenchymal stem cells: differential gene expression of IL1B and MAP3K8 in MAPK signaling. **2009**, 9, 381-8	79
2024	Whole genome survey of coding SNPs reveals a reproducible pathway determinant of Parkinson disease. **2009**, 30, 228-38	33
2023	Bioinformatics and computational approaches applicable to lipidomics. **2009**, 111, 99-106	19
2022	Domain-ligand mapping for enzymes. **2010**, 23, 194-208	4
2021	Computational identification of altered metabolism using gene expression and metabolic pathways. **2009**, 103, 835-43	10
2020	Making the right connections: biological networks in the light of evolution. **2009**, 31, 1080-90	19
2019	Nested effects models for learning signaling networks from perturbation data. **2009**, 51, 304-23	22

2018	A model for the spatiotemporal organization of DNA replication in Saccharomyces cerevisiae. **2009**, 282, 25-35	18
2017	Insights into the molecular basis of the microaerophily of three Campylobacterales: a comparative study. **2009**, 96, 545-57	8
2016	Computational challenges in systems biology. **2009**, 3, 1-17	29
2015	Selenoprotein W modulates control of cell cycle entry. **2009**, 131, 229-44	34
2014	Differential Gene Expression of Integrins Alpha 2 and Beta 8 in Human Mesenchymal Stem Cells Exposed to Fluid Flow. **2009**, 2, 544-553	3
2013	Cellular senescence: unravelling complexity. **2009**, 31, 353-63	36
2012	CsrA interacting small RNAs in Haemophilus spp genomes: a theoretical analysis. **2009**, 191, 451-9	2
2011	Oxygen and guanine-cytosine profiles in marine environments. **2009**, 69, 203-6	16
2010	Elementary mode analysis: a useful metabolic pathway analysis tool for characterizing cellular metabolism. **2009**, 81, 813-26	217
2009	Perspectives and limits of engineering the isoprenoid metabolism in heterologous hosts. **2009**, 84, 1003-19	50
2008	Proteopathogen, a protein database for studying Candida albicans--host interaction. **2009**, 9, 4664-8	21
2007	Proteomic analysis of mitochondria from Caenorhabditis elegans. **2009**, 9, 4539-53	50
2006	Integrative analysis of cancer pathway progression and coherence. **2009**, 3, 473-85	
2005	Charting online OMICS resources: A navigational chart for clinical researchers. **2009**, 3, 18-29	11
2004	Structure and function of Pseudomonas aeruginosa protein PA1324 (21-170). **2009**, 18, 606-18	11
2003	Crystallization and preliminary crystallographic analysis of cgHle, a homoserine acetyltransferase homologue, from Corynebacterium glutamicum. **2009**, 65, 34-8	5
2002	Biosynthesis of the proteasome inhibitor syringolin A: the ureido group joining two amino acids originates from bicarbonate. **2009**, 10, 26	32
2001	Local and global modes of drug action in biochemical networks. **2009**, 9, 4	5

2000	Quantitative assessment of the expanding complementarity between public and commercial databases of bioactive compounds. **2009**, 1, 10	49
1999	Small Molecule Subgraph Detector (SMSD) toolkit. **2009**, 1, 12	92
1998	Linking genotypes to phenotypes and fitness: how mechanistic biology can inform molecular ecology. **2009**, 18, 4997-5017	144
1997	The transcriptionally active regions in the genome of Bacillus subtilis. **2009**, 73, 1043-57	139
1996	Data-driven methods to discover molecular determinants of serious adverse drug events. **2009**, 85, 259-68	39
1995	The Schistosoma japonicum genome reveals features of host-parasite interplay. **2009**, 460, 345-51	562
1994	The proteomic analysis of human neonatal umbilical cord serum by mass spectrometry. **2009**, 30, 1550-8	15
1993	Evolution of efficient pathways for degradation of anthropogenic chemicals. **2009**, 5, 559-66	140
1992	A practical guide to the MaxQuant computational platform for SILAC-based quantitative proteomics. **2009**, 4, 698-705	637
1991	Evolution of biomolecular networks: lessons from metabolic and protein interactions. **2009**, 10, 791-803	210
1990	Regulation by transcription factors in bacteria: beyond description. **2009**, 33, 133-51	119
1989	Genome-scale models of bacterial metabolism: reconstruction and applications. **2009**, 33, 164-90	233
1988	Genome dynamics in major bacterial pathogens. **2009**, 33, 453-70	77
1987	Mutation of epidermal growth factor receptor is associated with MIG6 expression. **2009**, 276, 5239-51	21
1986	Dynamic interactions of proteins in complex networks: a more structured view. **2009**, 276, 5390-405	81
1985	CREDO: a protein-ligand interaction database for drug discovery. **2009**, 73, 157-67	64
1984	Dynamics of global gene expression changes during brain metastasis formation. **2009**, 29, 389-97	4
1983	The Populus Genome Integrative Explorer (PopGenIE): a new resource for exploring the Populus genome. **2009**, 182, 1013-1025	171

1982	From systems biology to fuel--Chlamydomonas reinhardtii as a model for a systems biology approach to improve biohydrogen production. **2009**, 142, 10-20		92
1981	Bioinformatics and computational methods for lipidomics. **2009**, 877, 2855-62		78
1980	Comparative proteomics and transcriptomics analyses of livers from two different Bos taurus breeds: "Chianina and Holstein Friesian". **2009**, 73, 309-22		35
1979	Comprehensive analysis of glycosyltransferases in eukaryotic genomes for structural and functional characterization of glycans. **2009**, 344, 881-7		32
1978	Genome-based expression profiles as a single standardized microarray platform for the diagnosis of bladder pain syndrome/interstitial cystitis: an array of 139 genes model. **2009**, 20, 515-22		5
1977	Aminoacetone as the penultimate precursor to the antitumor agent azinomycin A. **2009**, 11, 4006-9		14
1976	Tools and ingredients for the biocatalytic synthesis of metabolites. **2009**, 4, 1253-65		19
1975	Integrating proteomic, transcriptional, and interactome data reveals hidden components of signaling and regulatory networks. **2009**, 2, ra40		137
1974	Functional genomics for plant natural product biosynthesis. **2009**, 26, 1466-87		104
1973	Reactome knowledgebase of human biological pathways and processes. *Nucleic Acids Research*, **2009**, 37, D619-22	20.1	675
1972	Plant developmental genetics: Integrating data from different experiments in databases. **2009**, 45, 1302-1316		
1971	Systems biology approaches and pathway tools for investigating cardiovascular disease. **2009**, 5, 588-602		82
1970	Soybean proteome database: a data resource for plant differential omics. **2009**, 8, 3539-48		57
1969	PubChem as a source of polypharmacology. **2009**, 49, 2044-55		118
1968	The origin and evolution of modern metabolism. **2009**, 41, 285-97		84
1967	The disease relevance of human hepatocellular xenograft models: molecular characterization and review of the literature. **2009**, 286, 121-8		6
1966	Characteristics of genes up-regulated and down-regulated after 24 h starvation in the head of Drosophila. **2009**, 446, 11-7		41
1965	Metabolomics, a novel tool for studies of nutrition, metabolism and lipid dysfunction. **2009**, 19, 816-24		107

1964	Loss of protein interactions and regulatory divergence in yeast whole-genome duplicates. **2009**, 93, 534-42	6
1963	Domain-based and family-specific sequence identity thresholds increase the levels of reliable protein function transfer. **2009**, 387, 416-30	65
1962	Metabolic pathfinding using RPAIR annotation. **2009**, 388, 390-414	52
1961	Questioning our perceptions about evolution of biodegradative enzymes. **2009**, 12, 244-51	32
1960	Mass spectrometry based metabolomics and enzymatic assays for functional genomics. **2009**, 12, 547-52	57
1959	Acinetobacter baylyi ADP1 as a model for metabolic system biology. **2009**, 12, 568-76	40
1958	System-level analysis of Salmonella metabolism during infection. **2009**, 12, 559-67	39
1957	Chemical databases for environmental health and clinical research. **2009**, 186, 62-5	14
1956	Complete genome sequence of citrus huanglongbing bacterium, 'Candidatus Liberibacter asiaticus' obtained through metagenomics. **2009**, 22, 1011-20	368
1955	Genomic analyses of the microsporidian Nosema ceranae, an emergent pathogen of honey bees. **2009**, 5, e1000466	167
1954	Parallel methods for expression and purification. **2009**, 463, 767-85	11
1953	Mass spectrometry tools and metabolite-specific databases for molecular identification in metabolomics. **2009**, 134, 1322-32	215
1952	Unraveling the signal-transduction networks in cancer metastasis [Life Sciences]. **2009**, 26, 129-132	2
1951	Game theory in signal processing and communications [From the Guest Editors]. **2009**, 26, 17-132	23
1950	Mitochondrial proteomics on human fibroblasts for identification of metabolic imbalance and cellular stress. **2009**, 7, 20	33
1949	Phylogenetic diversity and metabolic potential revealed in a glacier ice metagenome. **2009**, 75, 7519-26	169
1948	Genome and proteome annotation: organization, interpretation and integration. **2009**, 6, 129-47	36
1947	Global protein-level responses of Halobacterium salinarum NRC-1 to prolonged changes in external sodium chloride concentrations. **2009**, 8, 2218-25	37

1946	Molecular network of the comprehensive multiple sclerosis brain-lesion proteome. **2009**, 15, 531-41	42
1945	Better Decomposition Heuristics for the Maximum-Weight Connected Graph Problem Using Betweenness Centrality. **2009**, 465-472	1
1944	BioGPS: an extensible and customizable portal for querying and organizing gene annotation resources. **2009**, 10, R130	1059
1943	Transcriptome analysis of functional differentiation between haploid and diploid cells of Emiliania huxleyi, a globally significant photosynthetic calcifying cell. **2009**, 10, R114	85
1942	MouseCyc: a curated biochemical pathways database for the laboratory mouse. **2009**, 10, R84	47
1941	Insights into female sperm storage from the spermathecal fluid proteome of the honeybee Apis mellifera. **2009**, 10, R67	84
1940	Linking genes to diseases: it's all in the data. **2009**, 1, 77	40
1939	Antirheumatic drug response signatures in human chondrocytes: potential molecular targets to stimulate cartilage regeneration. **2009**, 11, R15	37
1938	An integrative approach towards completing genome-scale metabolic networks. **2009**, 5, 1889-903	56
1937	Systems biology meets synthetic biology: a case study of the metabolic effects of synthetic rewiring. **2009**, 5, 1214-23	12
1936	Signals of recent positive selection in a worldwide sample of human populations. **2009**, 19, 826-37	557
1935	Differential retention of metabolic genes following whole-genome duplication. **2009**, 26, 1067-72	32
1934	Connecting Genes with Diseases. **2009**,	4
1933	The Storage, Retrieval, and Visualization of Biological Pathway Data. **2009**,	
1932	A dictionary to identify small molecules and drugs in free text. **2009**, 25, 2983-91	95
1931	Proteome organization in a genome-reduced bacterium. **2009**, 326, 1235-40	383
1930	A minimal model for hepatic fatty acid balance during fasting: application to PPAR alpha-deficient mice. **2009**, 261, 266-78	6
1929	An atlas of chaperone-protein interactions in Saccharomyces cerevisiae: implications to protein folding pathways in the cell. **2009**, 5, 275	176

1928	Pathway databases and tools for their exploitation: benefits, current limitations and challenges. **2009**, 5, 290	144
1927	Comprehensive analytical strategy for biomarker identification based on liquid chromatography coupled to mass spectrometry and new candidate confirmation tools. **2009**, 81, 7677-94	27
1926	Histogenomics: association of gene expression patterns with histological parameters in kidney biopsies. **2009**, 87, 290-5	35
1925	MODA: an efficient algorithm for network motif discovery in biological networks. **2009**, 84, 385-95	92
1924	Reaction Similarities Focusing Substructure Changes of Chemical Compounds and Metabolic Pathway Alignments. **2009**, 2, 15-24	1
1923	Logical network of genotoxic stress-induced NF-κB signal transduction predicts putative target structures for therapeutic intervention strategies. **2009**, 2, 125-38	2
1922	The evolution of protein functions and networks: a family-centric approach. **2009**, 37, 745-50	2
1921	Complete genome sequence of Methanoculleus marisnigri Romesser et al. 1981 type strain JR1. **2009**, 1, 189-96	28
1920	The DOE-JGI Standard Operating Procedure for the Annotations of Microbial Genomes. **2009**, 1, 63-7	177
1919	Metabolomic systems biology of trypanosomes. **2010**, 137, 1285-90	17
1918	A combined ^{1}H nuclear magnetic resonance and electrospray ionization-mass spectrometry analysis to understand the basal metabolism of plant-pathogenic Fusarium spp. **2010**, 23, 1605-18	23
1917	Reconstruction and flux-balance analysis of the Plasmodium falciparum metabolic network. **2010**, 6, 408	101
1916	Gene expression profiling in multiple sclerosis: a disease of the central nervous system, but with relapses triggered in the periphery?. **2010**, 37, 613-21	45
1915	The use of network analyses for elucidating mechanisms in cardiovascular disease. **2010**, 6, 289-304	76
1914	Microbial 1-butanol production: Identification of non-native production routes and in silico engineering interventions. **2010**, 5, 716-25	39
1913	Metabolomic analysis via reversed-phase ion-pairing liquid chromatography coupled to a stand alone orbitrap mass spectrometer. **2010**, 82, 3212-21	380
1912	Generation of functional hepatocytes from mouse germ line cell-derived pluripotent stem cells in vitro. **2010**, 19, 1183-94	19
1911	Large-scale integration of MicroRNA and gene expression data for identification of enriched microRNA-mRNA associations in biological systems. **2010**, 667, 297-315	28

1910	Activation of the mitogen-activated protein kinase (MAPK) signalling pathway in the liver of mice is related to plasma glucose levels after acute exercise. **2010**, 53, 1131-41	25
1909	Proteomic biomarkers in plasma that differentiate rapid and slow decline in lung function in adult cigarette smokers with chronic obstructive pulmonary disease (COPD). **2010**, 397, 1809-19	17
1908	Evolution of dopamine-related systems: biosynthesis, degradation and receptors. **2010**, 71, 374-84	10
1907	Somatic polyploidy promotes cell function under stress and energy depletion: evidence from tissue-specific mammal transcriptome. **2010**, 10, 433-46	44
1906	Coexpression landscape in ATTED-II: usage of gene list and gene network for various types of pathways. **2010**, 123, 311-9	55
1905	Extra-cellular matrix suppresses expression of the apoptosis mediator Fas by epigenetic DNA methylation. **2010**, 15, 728-37	19
1904	Comparison of HCV-associated gene expression and cell signaling pathways in cells with or without HCV replicon and in replicon-cured cells. **2010**, 45, 523-36	28
1903	Advances in structure elucidation of small molecules using mass spectrometry. **2010**, 2, 23-60	343
1902	Expression profile of rat hippocampal neurons treated with the neuroprotective compound 2,4-dinitrophenol: up-regulation of cAMP signaling genes. **2010**, 18, 112-23	15
1901	Potential physiological effects of pharmaceutical compounds in Atlantic salmon (Salmo salar) implied by transcriptomic analysis. **2010**, 17, 917-33	18
1900	Bioinformatics study indicates possible microRNA-regulated pathways in the differentiation of breast cancer. **2010**, 55, 927-936	3
1899	Construction of a gene regulatory network for Arabidopsis based on metabolic pathway data. **2010**, 55, 158-162	3
1898	Ranking effects of candidate drugs on biological process by integrating network analysis and Gene Ontology. **2010**, 55, 2974-2980	9
1897	Database resources in metabolomics: an overview. **2010**, 5, 18-30	73
1896	Role of OsNPR1 in rice defense program as revealed by genome-wide expression analysis. **2010**, 74, 549-62	82
1895	Proteomic Analysis of Interactions Between the Generalist Herbivore Spodoptera exigua (Lepidoptera: Noctuidae) and Arabidopsis thaliana. **2010**, 28, 324-333	19
1894	Detailed analysis of function divergence in a large and diverse domain superfamily: toward a refined protocol of function classification. **2010**, 18, 1522-35	21
1893	Potential of Arabidopsis systems biology to advance the biofuel field. **2010**, 28, 543-7	39

1892	Mayday--integrative analytics for expression data. **2010**, 11, 121	90
1891	Gene set enrichment meta-learning analysis: next- generation sequencing versus microarrays. **2010**, 11, 176	12
1890	Consolidating metabolite identifiers to enable contextual and multi-platform metabolomics data analysis. **2010**, 11, 214	34
1889	Predicting the network of substrate-enzyme-product triads by combining compound similarity and functional domain composition. **2010**, 11, 293	50
1888	FACT: functional annotation transfer between proteins with similar feature architectures. **2010**, 11, 417	19
1887	MetNetGE: interactive views of biological networks and ontologies. **2010**, 11, 469	6
1886	Detecting variants with Metabolic Design, a new software tool to design probes for explorative functional DNA microarray development. **2010**, 11, 478	10
1885	Systematic integration of experimental data and models in systems biology. **2010**, 11, 582	20
1884	Knowledge-based matrix factorization temporally resolves the cellular responses to IL-6 stimulation. **2010**, 11, 585	10
1883	Extracting consistent knowledge from highly inconsistent cancer gene data sources. **2010**, 11, 76	41
1882	Simulation of a Petri net-based model of the terpenoid biosynthesis pathway. **2010**, 11, 83	6
1881	HDAPD: a web tool for searching the disease-associated protein structures. **2010**, 11, 88	
1880	BisoGenet: a new tool for gene network building, visualization and analysis. **2010**, 11, 91	222
1879	Time lagged information theoretic approaches to the reverse engineering of gene regulatory networks. **2010**, 11 Suppl 6, S19	16
1878	Transcriptomic changes arising during light-induced sporulation in Physarum polycephalum. **2010**, 11, 115	23
1877	Global transcriptome analysis of spore formation in Myxococcus xanthus reveals a locus necessary for cell differentiation. **2010**, 11, 264	44
1876	Genomics Portals: integrative web-platform for mining genomics data. **2010**, 11, 27	9
1875	Computational prediction of the osmoregulation network in Synechococcus sp. WH8102. **2010**, 11, 291	12

1874	Characterizing Ancylostoma caninum transcriptome and exploring nematode parasitic adaptation. **2010**, 11, 307	48
1873	Understanding the evolutionary relationships and major traits of Bacillus through comparative genomics. **2010**, 11, 332	114
1872	MLTreeMap--accurate Maximum Likelihood placement of environmental DNA sequences into taxonomic and functional reference phylogenies. **2010**, 11, 461	93
1871	Deep sequencing-based transcriptome profiling analysis of bacteria-challenged Lateolabrax japonicus reveals insight into the immune-relevant genes in marine fish. **2010**, 11, 472	153
1870	Discovery of pathway biomarkers from coupled proteomics and systems biology methods. **2010**, 11 Suppl 2, S12	22
1869	A comparative study of cancer proteins in the human protein-protein interaction network. **2010**, 11 Suppl 3, S5	68
1868	SoyDB: a knowledge database of soybean transcription factors. **2010**, 10, 14	89
1867	ReCGiP, a database of reproduction candidate genes in pigs based on bibliomics. **2010**, 8, 96	6
1866	Reconstruction and analysis of genome-scale metabolic model of a photosynthetic bacterium. **2010** , 4, 156	94
1865	Improving the iMM904 S. cerevisiae metabolic model using essentiality and synthetic lethality data. **2010**, 4, 178	81
1864	Genome-scale metabolic analysis of Clostridium thermocellum for bioethanol production. **2010**, 4, 31	90
1863	Construction of a large scale integrated map of macrophage pathogen recognition and effector systems. **2010**, 4, 63	32
1862	Maternal gene expression in Atlantic halibut (Hippoglossus hippoglossus L.) and its relation to egg quality. **2010**, 3, 138	40
1861	The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows. The DBCLS BioHackathon Consortium*. **2010**, 1, 8	24
1860	The alternative complex III: a different architecture using known building modules. **2010**, 1797, 1869-76	37
1859	On the reproducibility of results of pathway analysis in genome-wide expression studies of colorectal cancers. **2010**, 43, 397-406	10
1858	An ontological modeling approach to cerebrovascular disease studies: the NEUROWEB case. **2010**, 43, 469-84	14
1857	Machine learning approach identifies new pathways associated with demyelination in a viral model of multiple sclerosis. **2010**, 14, 434-48	48

1856	The Roche Cancer Genome Database (RCGDB). **2010**, 31, 407-13	11
1855	Genetic pathway-based hierarchical clustering analysis of older adults with cognitive complaints and amnestic mild cognitive impairment using clinical and neuroimaging phenotypes. **2010**, 153B, 1060-9	21
1854	When metabolism meets topology: Reconciling metabolite and reaction networks. **2010**, 32, 246-256	36
1853	Pathogen proteomes during infection: A basis for infection research and novel control strategies. **2010**, 73, 2267-76	32
1852	Organising metabolic networks: Cycles in flux distributions. **2010**, 265, 250-60	7
1851	Comparative genomics begins to unravel the ecophysiology of bioleaching. **2010**, 104, 471-476	31
1850	MI-Pack: Increased confidence of metabolite identification in mass spectra by integrating accurate masses and metabolic pathways. **2010**, 104, 75-82	72
1849	Characterisation of odour active volatile compounds of New Zealand sea urchin (Evechinus chloroticus) roe using gas chromatography–olfactometry–finger span cross modality (GC–O–FSCM) method. **2010**, 121, 601-607	12
1848	MLDB: macromolecule ligand database. **2010**, 43, 200-202	1
1847	Detection of gene orthology from gene co-expression and protein interaction networks. **2010**, 11 Suppl 3, S7	14
1846	BIAdb: a curated database of benzylisoquinoline alkaloids. **2010**, 10, 4	34
1845	The role of T cell PPAR gamma in mice with experimental inflammatory bowel disease. **2010**, 10, 60	60
1844	Modulation of hepatic PPAR expression during Ft LVS LPS-induced protection from Francisella tularensis LVS infection. **2010**, 10, 10	13
1843	Tracking the transcriptional host response from the acute to the regenerative phase of experimental pneumococcal meningitis. **2010**, 10, 176	15
1842	A metabolic signature of long life in Caenorhabditis elegans. **2010**, 8, 14	115
1841	Nutrient control of eukaryote cell growth: a systems biology study in yeast. **2010**, 8, 68	58
1840	Non-homologous isofunctional enzymes: a systematic analysis of alternative solutions in enzyme evolution. **2010**, 5, 31	97
1839	GTC: A web server for integrating systems biology data with web tools and desktop applications. **2010**, 5, 7	0

1838	Integration of metabolic databases for the reconstruction of genome-scale metabolic networks. **2010**, 4, 114	67
1837	Curating the innate immunity interactome. **2010**, 4, 117	59
1836	The mEPN scheme: an intuitive and flexible graphical system for rendering biological pathways. **2010**, 4, 65	17
1835	A novel gene network inference algorithm using predictive minimum description length approach. **2010**, 4 Suppl 1, S7	22
1834	Identifying dysfunctional crosstalk of pathways in various regions of Alzheimer's disease brains. **2010**, 4 Suppl 2, S11	66
1833	Comparing biological networks via graph compression. **2010**, 4 Suppl 2, S13	11
1832	Analyzing the regulation of metabolic pathways in human breast cancer. **2010**, 3, 39	34
1831	LNCaP Atlas: gene expression associated with in vivo progression to castration-recurrent prostate cancer. **2010**, 3, 43	57
1830	Gene regulatory network reveals oxidative stress as the underlying molecular mechanism of type 2 diabetes and hypertension. **2010**, 3, 45	37
1829	From proteome lists to biological impact--tools and strategies for the analysis of large MS data sets. **2010**, 10, 1270-83	49
1828	Protein Information and Knowledge Extractor: Discovering biological information from proteomics data. **2010**, 10, 3262-71	7
1827	Real-time ligand binding pocket database search using local surface descriptors. **2010**, 78, 2007-28	49
1826	The secretome of Campylobacter concisus. **2010**, 277, 1606-17	54
1825	Bowman-Birk inhibitor affects pathways associated with energy metabolism in Drosophila melanogaster. **2010**, 19, 303-13	12
1824	Mutated genes, pathways and processes in tumours. **2010**, 11, 805-10	27
1823	SZGR: a comprehensive schizophrenia gene resource. **2010**, 15, 453-62	76
1822	Genomic and functional adaptation in surface ocean planktonic prokaryotes. **2010**, 468, 60-6	215
1821	[Attenuation regulation of amino acid and amino acyl-tRNA biosynthetic operons in bacteria: comparative genomics analysis]. **2010**, 44, 140-51	10

1820	Visualization of omics data for systems biology. **2010**, 7, S56-68	459
1819	A protocol for generating a high-quality genome-scale metabolic reconstruction. **2010**, 5, 93-121	1156
1818	Gene--environment-wide association studies: emerging approaches. **2010**, 11, 259-72	488
1817	Protein Interaction Data Resources. **2010**, 1375-1385	1
1816	Introduction to Systems Biology. **2010**, 81-95	
1815	The Marriage of Phenomics and Genetical Genomics: A Systems Approach to Complex Trait Analysis. **2010**, 207-227	
1814	Glycotranscriptomics. **2010**, 95-135	3
1813	Genomics, Bioinformatics, and Computational Biology. **2010**, 641-661	0
1812	Analysis of protein pathway networks using hybrid properties. **2010**, 15, 8177-92	25
1811	Multidimensional gene set analysis of genomic data. **2010**, 5, e10348	53
1810	Metagenomic profiling of a microbial assemblage associated with the California mussel: a node in networks of carbon and nitrogen cycling. **2010**, 5, e10518	37
1809	Tissue-specific target analysis of disease-associated microRNAs in human signaling pathways. **2010**, 5, e11154	14
1808	The gene expression profile in the synovium as a predictor of the clinical response to infliximab treatment in rheumatoid arthritis. **2010**, 5, e11310	70
1807	Combining next-generation sequencing strategies for rapid molecular resource development from an invasive aphid species, Aphis glycines. **2010**, 5, e11370	67
1806	Gene expression analysis of forskolin treated basilar papillae identifies microRNA181a as a mediator of proliferation. **2010**, 5, e11502	17
1805	Systematic analysis of a novel human renal glomerulus-enriched gene expression dataset. **2010**, 5, e11545	58
1804	Analysis of human and mouse reprogramming of somatic cells to induced pluripotent stem cells. What is in the plate?. **2010**, 5, e12664	42
1803	Tissue-specific transcriptomics of the exotic invasive insect pest emerald ash borer (Agrilus planipennis). **2010**, 5, e13708	81

1802	Longissimus muscle transcriptome profiles related to carcass and meat quality traits in fresh meat Pietrain carcasses. **2010**, 88, 4044-55		26
1801	Finding Minimum Reaction Cuts of Metabolic Networks Under a Boolean Model Using Integer Programming and Feedback Vertex Sets. **2010**, 1, 14-31		35
1800	Toxicogenomic and pathway analysis. 284-301		
1799	Creation of a genome-wide metabolic pathway database for Populus trichocarpa using a new approach for reconstruction and curation of metabolic pathways for plants. **2010**, 153, 1479-91		102
1798	Finding metabolic pathways using atom tracking. **2010**, 26, 1548-55		47
1797	SIMCOMP/SUBCOMP: chemical structure search servers for network analyses. *Nucleic Acids Research*, **2010**, 38, W652-6	20.1	88
1796	SmashCommunity: a metagenomic annotation and analysis tool. **2010**, 26, 2977-8		77
1795	Conserved elements associated with ribosomal genes and their trans-splice acceptor sites in Caenorhabditis elegans. *Nucleic Acids Research*, **2010**, 38, 2990-3004	20.1	3
1794	Comprehensive reanalysis of transcription factor knockout expression data in Saccharomyces cerevisiae reveals many new targets. *Nucleic Acids Research*, **2010**, 38, 4768-77	20.1	75
1793	Genome sequence of Kitasatospora setae NBRC 14216T: an evolutionary snapshot of the family Streptomycetaceae. **2010**, 17, 393-406		55
1792	Genomic arrangement of bacterial operons is constrained by biological pathways encoded in the genome. **2010**, 107, 6310-5		31
1791	A critical role for ceramide synthase 2 in liver homeostasis: II. insights into molecular changes leading to hepatopathy. **2010**, 285, 10911-23		164
1790	DRYGIN: a database of quantitative genetic interaction networks in yeast. *Nucleic Acids Research*, **2010**, 38, D502-7	20.1	67
1789	Airway PI3K pathway activation is an early and reversible event in lung cancer development. **2010**, 2, 26ra25		175
1788	EMAGE mouse embryo spatial gene expression database: 2010 update. *Nucleic Acids Research*, **2010**, 38, D703-9	20.1	78
1787	Characterization of macaque pulmonary fluid proteome during monkeypox infection: dynamics of host response. **2010**, 9, 2760-71		9
1786	Proteome bioprofiles distinguish between M1 priming and activation states in human macrophages. **2010**, 87, 655-62		25
1785	Connecting parts with processes: SubtiWiki and SubtiPathways integrate gene and pathway annotation for Bacillus subtilis. **2010**, 156, 849-859		36

1784	PROFESS: a PROtein function, evolution, structure and sequence database. **2010**, 2010, baq011		5
1783	Gene3D: merging structure and function for a Thousand genomes. *Nucleic Acids Research*, **2010**, 38, D296-300	20.1	45
1782	Cross-species common regulatory network inference without requirement for prior gene affiliation. **2010**, 26, 1082-90		15
1781	The comprehensive microbial resource. *Nucleic Acids Research*, **2010**, 38, D340-5	20.1	82
1780	MIRAGAA--a methodology for finding coordinated effects of microRNA expression changes and genome aberrations in cancer. **2010**, 26, 161-7		14
1779	Coupled amino acid deamidase-transport systems essential for Helicobacter pylori colonization. **2010**, 78, 2782-92		38
1778	Selective modification of rice (Oryza sativa) gene expression by rice stripe virus infection. **2010**, 91, 294-305		74
1777	AraGEM, a genome-scale reconstruction of the primary metabolic network in Arabidopsis. **2010**, 152, 579-89		260
1776	Autophagy-dependent rhodopsin degradation prevents retinal degeneration in Drosophila. **2010**, 30, 10703-19		47
1775	Exploring metabolomic approaches to analyse phospholipid biosynthetic pathways in Plasmodium. **2010**, 137, 1343-56		20
1774	A genome-wide map of human genetic interactions inferred from radiation hybrid genotypes. **2010**, 20, 1122-32		56
1773	Coexistence of two different photosynthetic operons in Citromicrobium bathyomarinum JL354 as revealed by whole-genome sequencing. **2010**, 192, 1169-70		22
1772	Impact of probe annotation on the integration of miRNA-mRNA expression profiles for miRNA target detection. *Nucleic Acids Research*, **2010**, 38, e97	20.1	7
1771	The integrated microbial genomes system: an expanding comparative analysis resource. *Nucleic Acids Research*, **2010**, 38, D382-90	20.1	210
1770	VISIBIOweb: visualization and layout services for BioPAX pathway models. *Nucleic Acids Research*, **2010**, 38, W150-4	20.1	11
1769	MetPA: a web-based metabolomics tool for pathway analysis and visualization. **2010**, 26, 2342-4		447
1768	Checks and balances: the ocular response to infection. **2010**, 1, 222		20
1767	Development of an integrated genomic classifier for a novel agent in colorectal cancer: approach to individualized therapy in early development. **2010**, 16, 3193-204		65

1766	Genomics and bioinformatics resources for crop improvement. **2010**, 51, 497-523		150
1765	eggNOG v2.0: extending the evolutionary genealogy of genes with enhanced non-supervised orthologous groups, species and functional annotations. *Nucleic Acids Research*, **2010**, 38, D190-5	20.1	179
1764	CLIC: clustering analysis of large microarray datasets with individual dimension-based clustering. *Nucleic Acids Research*, **2010**, 38, W246-53	20.1	11
1763	Genome analysis of Moraxella catarrhalis strain BBH18, [corrected] a human respiratory tract pathogen. **2010**, 192, 3574-83		73
1762	Analysis of next-generation genomic data in cancer: accomplishments and challenges. **2010**, 19, R188-96		102
1761	IsoKEGG: A logic based system for querying biological pathways in KEGG. **2010**,		2
1760	MicroRNA, mRNA, and protein expression link development and aging in human and macaque brain. **2010**, 20, 1207-18		225
1759	KEGG for representation and analysis of molecular networks involving diseases and drugs. *Nucleic Acids Research*, **2010**, 38, D355-60	20.1	1710
1758	Functional genomics and networks: new approaches in the extraction of complex gene modules. **2010**, 7, 55-63		10
1757	Is LGI2 the candidate gene for partial epilepsy with pericentral spikes?. **2010**, 8, 117-27		7
1756	Discriminating between different acute chemical toxicities via changes in the daphnid metabolome. **2010**, 118, 307-17		57
1755	Agmatine-conjugated cytidine in a tRNA anticodon is essential for AUA decoding in archaea. **2010**, 6, 277-82		107
1754	ChEA: transcription factor regulation inferred from integrating genome-wide ChIP-X experiments. **2010**, 26, 2438-44		533
1753	Detection of locally over-represented GO terms in protein-protein interaction networks. **2010**, 17, 443-57		10
1752	Comparative transcriptomic and proteomic profiling of industrial wine yeast strains. **2010**, 76, 3911-23		35
1751	PathWave: discovering patterns of differentially regulated enzymes in metabolic pathways. **2010**, 26, 1225-31		19
1750	Prognostic and predictive gene signature for adjuvant chemotherapy in resected non-small-cell lung cancer. **2010**, 28, 4417-24		350
1749	Advances in translational bioinformatics: computational approaches for the hunting of disease genes. **2010**, 11, 96-110		66

1748	Drug-target interaction prediction from chemical, genomic and pharmacological data in an integrated framework. **2010**, 26, i246-54		319
1747	The Virtual Cell Project. **2010**, 273-288		
1746	Molecular signatures-based prediction of enzyme promiscuity. **2010**, 26, 2012-9		61
1745	Using NMR metabolomics to investigate tricarboxylic acid cycle-dependent signal transduction in Staphylococcus epidermidis. **2010**, 285, 36616-24		40
1744	Crystal structure of aminomethyltransferase in complex with dihydrolipoyl-H-protein of the glycine cleavage system: implications for recognition of lipoyl protein substrate, disease-related mutations, and reaction mechanism. **2010**, 285, 18684-92		22
1743	Induction of Salmonella pathogenicity island 1 under different growth conditions can affect Salmonella-host cell interactions in vitro. **2010**, 156, 1120-1133		100
1742	Contributions of Francisella tularensis subsp. novicida chitinases and Sec secretion system to biofilm formation on chitin. **2010**, 76, 596-608		50
1741	Global modeling of transcriptional responses in interaction networks. **2010**, 26, 2713-20		8
1740	The early whole-blood transcriptional signature of dengue virus and features associated with progression to dengue shock syndrome in Vietnamese children and young adults. **2010**, 84, 12982-94		84
1739	HHMD: the human histone modification database. *Nucleic Acids Research*, **2010**, 38, D149-54	20.1	65
1738	Pathema: a clade-specific bioinformatics resource center for pathogen research. *Nucleic Acids Research*, **2010**, 38, D408-14	20.1	17
1737	The NCBI BioSystems database. *Nucleic Acids Research*, **2010**, 38, D492-6	20.1	526
1736	Accurate distinction of pathogenic from benign CNVs in mental retardation. **2010**, 6, e1000752		42
1735	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
1734	An integrative multi-network and multi-classifier approach to predict genetic interactions. **2010**, 6, e1000928		51
1733	Babelomics: an integrative platform for the analysis of transcriptomics, proteomics and genomic data with advanced functional profiling. *Nucleic Acids Research*, **2010**, 38, W210-3	20.1	267
1732	Detecting subtle functional differences in ketopantoate reductase and related enzymes using a rule-based approach with sequence-structure homology recognition scores. **2010**, 23, 859-69		1
1731	ChiBE: interactive visualization and manipulation of BioPAX pathway models. **2010**, 26, 429-31		37

1730	CyanoBase: the cyanobacteria genome database update 2010. *Nucleic Acids Research*, **2010**, 38, D379-81	20.1	128
1729	A Bayesian approach to the evolution of metabolic networks on a phylogeny. **2010**, 6, e1000868		15
1728	Finding the "dark matter" in human and yeast protein network prediction and modelling. **2010**, 6, e1000945		19
1727	Computational Toxicology. **2010**, 307-337		
1726	The Universal Protein Resource (UniProt) in 2010. *Nucleic Acids Research*, **2010**, 38, D142-8	20.1	1035
1725	Meeting report: a workshop on Best Practices in Genome Annotation. **2010**, 2010, baq001		15
1724	Regulatory network nodes ofcheck point factorsin DNA repair pathways. **2010**,		
1723	Effects of cDNA microarray time-series data size on gene regulatory network inference accuracy. **2010**,		0
1722	Patterns of HIV-1 protein interaction identify perturbed host-cellular subsystems. **2010**, 6, e1000863		50
1721	NBRP databases: databases of biological resources in Japan. *Nucleic Acids Research*, **2010**, 38, D26-32	20.1	37
1720	The association of multiple interacting genes with specific phenotypes in rice using gene coexpression networks. **2010**, 154, 13-24		83
1719	C4GEM, a genome-scale metabolic model to study C4 plant metabolism. **2010**, 154, 1871-85		155
1718	Apomictic and sexual ovules of Boechera display heterochronic global gene expression patterns. **2010**, 22, 655-71		124
1717	Control of ATP homeostasis during the respiro-fermentative transition in yeast. **2010**, 6, 344		55
1716	The genome of the amoeba symbiont "Candidatus Amoebophilus asiaticus" reveals common mechanisms for host cell interaction among amoeba-associated bacteria. **2010**, 192, 1045-57		113
1715	Noncoding sequences near duplicated genes evolve rapidly. **2010**, 2, 518-33		16
1714	Checks and balances: The ocular response to infection. **2010**, 1, 222-222		
1713	Transcript analysis of stem cells. **2010**, 479, 73-91		22

1712	Demosponge EST sequencing reveals a complex genetic toolkit of the simplest metazoans. **2010**, 27, 2747-56	41
1711	Gene expression in hypothalamus, liver, and adipose tissues and food intake response to melanocortin-4 receptor agonist in pigs expressing melanocortin-4 receptor mutations. **2010**, 41, 254-68	12
1710	Analysis of the human intestinal epithelial cell transcriptional response to Lactobacillus acidophilus, Lactobacillus salivarius, Bifidobacterium lactis and Escherichia coli. **2010**, 1, 283-95	15
1709	Systemic delivery of synthetic microRNA-16 inhibits the growth of metastatic prostate tumors via downregulation of multiple cell-cycle genes. **2010**, 18, 181-7	359
1708	Metabolic pathways in the apicoplast of apicomplexa. **2010**, 281, 161-228	109
1707	Integration of metabolomics and transcriptomics data to aid biomarker discovery in type 2 diabetes. **2010**, 6, 909-21	143
1706	Computational approaches to metabolomics. **2010**, 593, 283-313	57
1705	Identification of cellular genes induced in human cells after activation of the OAS/RNaseL pathway by vaccinia virus recombinants expressing these antiviral enzymes. **2010**, 30, 171-88	13
1704	An in silico analysis of microRNAs: mining the miRNAome. **2010**, 6, 1853-62	37
1703	The bait compatibility index: computational bait selection for interaction proteomics experiments. **2010**, 9, 4972-81	7
1702	Fundamentals of Gene Ontology Functional Annotation. **2010**, 169-208	2
1701	Biological Pathway Analysis: An Overview of Reactome and Other Integrative Pathway Knowledge Bases. **2010**, 289-314	
1700	Gene expression analysis in predicting the effectiveness of insect venom immunotherapy. **2010**, 125, 1092-7	14
1699	IGERS: inferring Gibbs energy changes of biochemical reactions from reaction similarities. **2010**, 98, 2478-86	11
1698	Malignant pleural mesothelioma: genome-wide expression patterns reflecting general resistance mechanisms and a proposal of novel targets. **2010**, 67, 57-68	56
1697	Supervised Inference of Metabolic Networks from the Integration of Genomic Data and Chemical Information. **2010**, 189-211	5
1696	A novel paradigm for cell and molecule interaction ontology: from the CMM model to IMGT-ONTOLOGY. **2010**, 6, 1	15
1695	Constructing Method of the Functional Network of Activating Blood and Dissolving Stasis. **2010**, 12, 764-767	

1694	Monitoring the Effect of Docetaxel Treatment in MCF7 Xenografts Using Multimodal In Vivo and Ex Vivo Magnetic Resonance Methods, Histopathology, and Gene Expression. **2010**, 3, 252-63	9
1693	Novel candidate cancer genes identified by a large-scale cross-species comparative oncogenomics approach. **2010**, 70, 883-95	36
1692	Functional Genomics: Uncovering Cellular and Subcellular Mechanisms of Action. **2010**, 717-729	
1691	Phosphoproteome analysis of rat L6 myotubes using reversed-phase C18 prefractionation and titanium dioxide enrichment. **2010**, 9, 777-88	31
1690	microRNA-122 as a regulator of mitochondrial metabolic gene network in hepatocellular carcinoma. **2010**, 6, 402	147
1689	A global network of coexisting microbes from environmental and whole-genome sequence data. **2010**, 20, 947-59	305
1688	Microbial community transcriptomes reveal microbes and metabolic pathways associated with dissolved organic matter turnover in the sea. **2010**, 107, 16420-7	297
1687	BioRuby: bioinformatics software for the Ruby programming language. **2010**, 26, 2617-9	122
1686	The biomass objective function. **2010**, 13, 344-9	419
1685	Effects of Salmonella on spatial-temporal processes of jejunal development in chickens. **2010**, 34, 1090-100	18
1684	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
1683	Systems biology strategy to study lipotoxicity and the metabolic syndrome. **2010**, 1801, 235-9	9
1682	Identification of immune-relevant genes by expressed sequence tag analysis of head kidney from grass carp (Ctenopharyngodon idella). **2010**, 5, 116-23	8
1681	The transcriptome of the early life history stages of the California Sea Hare Aplysia californica. **2010**, 5, 165-70	24
1680	Extensive in vivo metabolite-protein interactions revealed by large-scale systematic analyses. **2010**, 143, 639-50	162
1679	Plant molecular stress responses face climate change. **2010**, 15, 664-74	655
1678	Gene expression profiling and pathway analysis of superficial bladder cancer in rats. **2010**, 75, 742-9	10
1677	Human transcriptome nexuses: basic-eukaryotic and metazoan. **2010**, 95, 345-54	10

1676	Association analysis of the general environmental conditions and prokaryotes' gene distributions in various functional groups. **2010**, 96, 27-38		9
1675	Influence of ovarian stage on transcript profiles in fathead minnow (Pimephales promelas) ovary tissue. **2010**, 98, 354-66		36
1674	A systematic screen for protein-lipid interactions in Saccharomyces cerevisiae. **2010**, 6, 430		132
1673	Metabolomic analysis and visualization engine for LC-MS data. **2010**, 82, 9818-26		381
1672	Complete genome sequence of the photosynthetic purple nonsulfur bacterium Rhodobacter capsulatus SB 1003. **2010**, 192, 3545-6		77
1671	Functional and evolutionary insights from the genomes of three parasitoid Nasonia species. **2010**, 327, 343-8		682
1670	Database resources of the National Center for Biotechnology Information. *Nucleic Acids Research*, **2010**, 38, D5-16	20.1	374
1669	Circadian control of global gene expression patterns. **2010**, 44, 419-44		218
1668	Constructing the HBV-human protein interaction network to understand the relationship between HBV and hepatocellular carcinoma. **2010**, 29, 146		18
1667	Multi-species integrative biclustering. **2010**, 11, R96		29
1666	Inferring the functions of longevity genes with modular subnetwork biomarkers of Caenorhabditis elegans aging. **2010**, 11, R13		35
1665	Identification of functional modules that correlate with phenotypic difference: the influence of network topology. **2010**, 11, R23		60
1664	Large-scale data integration framework provides a comprehensive view on glioblastoma multiforme. **2010**, 2, 65		133
1663	High-resolution mass spectrometry proteomics for the identification of candidate plasma protein biomarkers for chronic obstructive pulmonary disease. **2010**, 15, 367-77		8
1662	Enzyme databases. **2010**, 609, 113-28		12
1661	Identification of novel L2HGDH gene mutations and update of the pathological spectrum. **2010**, 55, 55-8		5
1660	Stable isotope labeling by amino acids in cell culture (SILAC) applied to quantitative proteomics of Bacillus subtilis. **2010**, 9, 3638-46		91
1659	Trace of evolutionary evidence by analyzing clustering information of metabolic pathways in eukaryotes. **2010**,		

1658	Translation efficiency in humans: tissue specificity, global optimization and differences between developmental stages. *Nucleic Acids Research*, **2010**, 38, 2964-74	20.1	54
1657	HepatoNet1: a comprehensive metabolic reconstruction of the human hepatocyte for the analysis of liver physiology. **2010**, 6, 411		219
1656	Application of metabolomics to investigate the process of human orthotopic liver transplantation: a proof-of-principle study. **2010**, 14, 143-50		36
1655	Predicting metabolic pathways from metabolic networks with limited biological knowledge. **2010**,		1
1654	Comparison of Co-Temporal Modeling Algorithms on Sparse Experimental Time Series Data Sets. **2010**, 2010, 79-85		0
1653	Modeling and analysis of retinoic acid induced differentiation of uncommitted precursor cells. **2011** , 3, 578-91		17
1652	An experiential analysis of microarray time series data of cancer metastasis using XMAS. **2011**,		
1651	MicroRNA expression analysis reveals significant biological pathways in human prostate cancer. **2011**,		1
1650	TCLUST: a fast method for clustering genome-scale expression data. **2011**, 8, 808-18		12
1649	A mathematical model for the validation of gene selection methods. **2011**, 8, 1385-92		4
1648	Complete genome sequence of the haloaromatic acid-degrading bacterium Achromobacter xylosoxidans A8. **2011**, 193, 791-2		30
1647	Origins of specificity and promiscuity in metabolic networks. **2011**, 286, 43994-44004		53
1646	Pathway analysis of high-throughput biological data within a Bayesian network framework. **2011**, 27, 1667-74		30
1645	Database resources of the National Center for Biotechnology Information. *Nucleic Acids Research*, **2011**, 39, D38-51	20.1	510
1644	The Comparative Toxicogenomics Database: update 2011. *Nucleic Acids Research*, **2011**, 39, D1067-72	20.1	192
1643	Reductive evolution of bacterial genome in insect gut environment. **2011**, 3, 702-14		108
1642	NMR analysis of a stress response metabolic signaling network. **2011**, 10, 3743-54		39
1641	REPAIRtoire--a database of DNA repair pathways. *Nucleic Acids Research*, **2011**, 39, D788-92	20.1	44

1640	A simple protocol for the comparative analysis of the structure and occurrence of biochemical pathways across superkingdoms. **2011**, 51, 730-8	21
1639	Differential lipid partitioning between adipocytes and tissue macrophages modulates macrophage lipotoxicity and M2/M1 polarization in obese mice. **2011**, 60, 797-809	248
1638	Analysis of transcriptome differences between resistant and susceptible strains of the citrus red mite Panonychus citri (Acari: Tetranychidae). **2011**, 6, e28516	62
1637	Genomic profiling in Down syndrome acute lymphoblastic leukemia identifies histone gene deletions associated with altered methylation profiles. **2011**, 25, 1555-63	36
1636	Identifying consensus disease pathways in Parkinson's disease using an integrative systems biology approach. **2011**, 6, e16917	58
1635	Systematic computational prediction of protein interaction networks. **2011**, 8, 035008	30
1634	From Visual Biological Models toward Mathematical Models of the Biology of Complex Traits. **2011**, 137-159	1
1633	Transcriptomics of the bed bug (Cimex lectularius). **2011**, 6, e16336	116
1632	Metabolomic data processing, analysis, and interpretation using MetaboAnalyst. **2011**, Chapter 14, Unit 14.10	124
1631	Metagenomic Contrasts of Viruses in Soil and Aquatic Environments. **2011**, 25-36	2
1630	Metagenomic Approach Studying the Taxonomic and Functional Diversity of the Bacterial Community in a Lacustrine Ecosystem. **2011**, 287-293	2
1629	Improved biological network reconstruction using graph Laplacian regularization. **2011**, 18, 987-96	3
1628	Bioinformatic approach to identify chaperone pathway relationship from large-scale interaction networks. **2011**, 787, 189-203	2
1627	In silico protein interaction analysis using the global proteome machine database. **2011**, 10, 656-68	14
1626	Seaweeds: The Wealth of Oceans. **2011**, 36-44	1
1625	Omics-based molecular target and biomarker identification. **2011**, 719, 547-71	31
1624	Ln-norm Multiple Kernel Learning and Least Squares Support Vector Machines. **2011**, 39-88	
1623	Protein Functional Motions: Basic Concepts and Computational Methodologies. **2011**, 35-82	7

1622	Metagenomic analyses: past and future trends. **2011**, 77, 1153-61	490
1621	Functional enrichment analysis with structural variants: pitfalls and strategies. **2011**, 135, 277-85	21
1620	BioGraph: unsupervised biomedical knowledge discovery via automated hypothesis generation. **2011**, 12, R57	89
1619	Modeling antibiotic and cytotoxic effects of the dimeric isoquinoline IQ-143 on metabolism and its regulation in Staphylococcus aureus, Staphylococcus epidermidis and human cells. **2011**, 12, R24	19
1618	The gene expression profile of preclinical autoimmune arthritis and its modulation by a tolerogenic disease-protective antigenic challenge. **2011**, 13, R143	5
1617	The moderately efficient enzyme: evolutionary and physicochemical trends shaping enzyme parameters. **2011**, 50, 4402-10	574
1616	Current production by bacterial communities in microbial fuel cells enriched from wastewater sludge with different electron donors. **2011**, 45, 1139-46	59
1615	Standards, tools, and databases for the analysis of yeast 'omics data. **2011**, 759, 345-65	2
1614	Interactome networks and human disease. **2011**, 144, 986-98	1187
1613	Composition of dissolved organic matter in groundwater. **2011**, 75, 2752-2761	61
1612	Connecting genotype to phenotype in the era of high-throughput sequencing. **2011**, 1810, 967-77	24
1611	Informatics and computational strategies for the study of lipids. **2011**, 1811, 991-9	29
1610	Isolation of Succinivibrionaceae implicated in low methane emissions from Tammar wallabies. **2011**, 333, 646-8	119
1609	Systems biology of infectious diseases: a focus on fungal infections. **2011**, 216, 1212-27	27
1608	Phenylalanine induces Burkholderia cenocepacia phenylacetic acid catabolism through degradation to phenylacetyl-CoA in synthetic cystic fibrosis sputum medium. **2011**, 51, 186-93	11
1607	Proteomic analysis of 1,25-dihydroxyvitamin D3 action on human colon cancer cells reveals a link to splicing regulation. **2011**, 75, 384-97	31
1606	Gene set analysis of genome-wide association studies: methodological issues and perspectives. **2011**, 98, 1-8	162
1605	Metabolic flux analysis and visualization. **2011**, 10, 3313-23	26

1604	Chemical inhibition of RNA viruses reveals REDD1 as a host defense factor. **2011**, 7, 712-9	60
1603	Darwinian demons, evolutionary complexity, and information maximization. **2011**, 21, 037110	30
1602	Discriminative graph embedding for label propagation. **2011**, 22, 1395-405	12
1601	FDR-FET: an optimizing gene set enrichment analysis method. **2011**, 4, 37-42	2
1600	Databases and bioinformatics tools for the study of DNA repair. **2011**, 2011, 475718	3
1599	GenSensor Suite: A Web-Based Tool for the Analysis of Gene and Protein Interactions, Pathways, and Regulation. **2011**, 2011, 271563	6
1598	Mass spectra-based framework for automated structural elucidation of metabolome data to explore phytochemical diversity. **2011**, 2, 40	25
1597	Ultra performance liquid chromatography and high resolution mass spectrometry for the analysis of plant lipids. **2011**, 2, 54	134
1596	Transcriptomic signatures of ash (Fraxinus spp.) phloem. **2011**, 6, e16368	48
1595	Data integration workflow for search of disease driving genes and genetic variants. **2011**, 6, e18636	3
1594	Common peptides study of aminoacyl-tRNA synthetases. **2011**, 6, e20361	4
1593	The response of Lactococcus lactis to membrane protein production. **2011**, 6, e24060	29
1592	Genome-wide functional profiling reveals genes required for tolerance to benzene metabolites in yeast. **2011**, 6, e24205	42
1591	Network based consensus gene signatures for biomarker discovery in breast cancer. **2011**, 6, e25364	20
1590	Metabolic network modularity in archaea depends on growth conditions. **2011**, 6, e25874	17
1589	Transcriptomics of a giant freshwater prawn (Macrobrachium rosenbergii): de novo assembly, annotation and marker discovery. **2011**, 6, e27938	90
1588	Data Warehouses in Bioinformatics: Integration of Molecular Biological Data. **2011**, 53, 241-249	
1587	An Efficient Method of Computing Impact Degrees for Multiple Reactions in Metabolic Networks with Cycles. **2011**, E94-D, 2393-2399	3

1586	The curation paradigm and application tool used for manual curation of the scientific literature at the Comparative Toxicogenomics Database. **2011**, 2011, bar034	31
1585	Myocardial depressant effects of interleukin 6 in meningococcal sepsis are regulated by p38 mitogen-activated protein kinase. **2011**, 39, 1692-711	51
1584	Introduction to Systems Biology for Animal Scientists. **2011**, 1-30	5
1583	Toward molecular trait-based ecology through integration of biogeochemical, geographical and metagenomic data. **2011**, 7, 473	129
1582	Gene expression profile, pathways, and transcriptional system regulation in indolent systemic mastocytosis. **2011**, 66, 229-37	17
1581	Gene expression analysis predicts insect venom anaphylaxis in indolent systemic mastocytosis. **2011**, 66, 648-57	17
1580	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
1579	Genome-wide phylogenetic analysis of Gluconobacter, Acetobacter, and Gluconacetobacter. **2011**, 315, 122-8	30
1578	The draft genome of the parasitic nematode Trichinella spiralis. **2011**, 43, 228-35	230
1577	Increased mitochondrial oxidative phosphorylation in the liver is associated with obesity and insulin resistance. **2011**, 19, 917-24	28
1576	Comparative metagenomics of microbial traits within oceanic viral communities. **2011**, 5, 1178-90	119
1575	Symbiont of the stink bug Plautia stali synthesizes rough-type lipopolysaccharide. **2011**, 167, 48-54	13
1574	Phenome-transcriptome correlation unravels anxiety and depression related pathways. **2011**, 45, 973-9	51
1573	Modelling and analysis of an ensemble of eukaryotic translation initiation models. **2011**, 5, 2	18
1572	Integrated analysis of the gene neighbouring impact on bacterial metabolic networks. **2011**, 5, 261-8	4
1571	Partition decoupling for multi-gene analysis of gene expression profiling data. **2011**, 12, 497	9
1570	Comparative analysis of expressed sequence tags (ESTs) between drought-tolerant and -susceptible genotypes of chickpea under terminal drought stress. **2011**, 11, 70	74
1569	Comparisons of seven algorithms for pathway analysis using the WTCCC Crohn's Disease dataset. **2011**, 4, 386	45

1568	The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications. **2011**, 2, 4	15
1567	The Trichomonas vaginalis hydrogenosome proteome is highly reduced relative to mitochondria, yet complex compared with mitosomes. **2011**, 41, 1421-34	82
1566	Species-Metabolite Relation Database KNApSAcK and Its Multifaceted Retrieval System, KNApSAcK Family. **2011**,	1
1565	The complexity hypothesis revisited: connectivity rather than function constitutes a barrier to horizontal gene transfer. **2011**, 28, 1481-9	135
1564	Catalytic residues in hydrolases: analysis of methods designed for ligand-binding site prediction. **2011**, 25, 117-33	26
1563	Heavy metal resistance in Cupriavidus metallidurans CH34 is governed by an intricate transcriptional network. **2011**, 24, 1133-51	90
1562	Learning to predict cancer-associated skeletal muscle wasting from 1H-NMR profiles of urinary metabolites. **2011**, 7, 25-34	38
1561	The effect of temperature and pH gradients on Lactobacillus rhamnosus gene expression of stress-related genes. **2011**, 34, 1169-76	5
1560	Integrative computational biology for cancer research. **2011**, 130, 465-81	21
1559	Uncovering the transcriptional circuitry in skeletal muscle regeneration. **2011**, 22, 272-81	1
1558	Taxonomic and functional metagenomic profiling of the microbial community in the anoxic sediment of a sub-saline shallow lake (Laguna de Carrizo, Central Spain). **2011**, 62, 824-37	43
1557	TSdb: a database of transporter substrates linking metabolic pathways and transporter systems on a genome scale via their shared substrates. **2011**, 54, 60-4	23
1556	Assessing quality and completeness of human transcriptional regulatory pathways on a genome-wide scale. **2011**, 6, 15	44
1555	A retrosynthetic biology approach to metabolic pathway design for therapeutic production. **2011**, 5, 122	85
1554	Initial characterization of the human central proteome. **2011**, 5, 17	56
1553	Metabolic reconstruction of the archaeon methanogen Methanosarcina Acetivorans. **2011**, 5, 28	38
1552	Analog regulation of metabolic demand. **2011**, 5, 40	47
1551	A community effort towards a knowledge-base and mathematical model of the human pathogen Salmonella Typhimurium LT2. **2011**, 5, 8	105

1550	Kinetic modeling and exploratory numerical simulation of chloroplastic starch degradation. **2011**, 5, 94	13
1549	Difference in the distribution pattern of substrate enzymes in the metabolic network of Escherichia coli, according to chaperonin requirement. **2011**, 5, 98	11
1548	Network target for screening synergistic drug combinations with application to traditional Chinese medicine. **2011**, 5 Suppl 1, S10	236
1547	Functional pathway mapping analysis for hypoxia-inducible factors. **2011**, 5 Suppl 1, S3	4
1546	An integrated proteomics analysis of bone tissues in response to mechanical stimulation. **2011**, 5 Suppl 3, S7	16
1545	MetaPath: identifying differentially abundant metabolic pathways in metagenomic datasets. **2011**, 5 Suppl 2, S9	35
1544	Quantification of intracellular nucleotide sugars and formulation of a mathematical model for prediction of their metabolism. **2011**, 5 Suppl 8, P10	1
1543	A synthetic system links FeFe-hydrogenases to essential E. coli sulfur metabolism. **2011**, 5, 7	13
1542	An integrative approach to identifying cancer chemoresistance-associated pathways. **2011**, 4, 23	16
1541	The functional cancer map: a systems-level synopsis of genetic deregulation in cancer. **2011**, 4, 53	29
1540	Comparative analyses of Campylobacter concisus strains reveal the genome of the reference strain BAA-1457 is not representative of the species. **2011**, 3, 15	19
1539	Structural diversity of biologically interesting datasets: a scaffold analysis approach. **2011**, 3, 30	28
1538	Context-dependent transcriptional regulations between signal transduction pathways. **2011**, 12, 19	4
1537	A scan statistic to extract causal gene clusters from case-control genome-wide rare CNV data. **2011**, 12, 205	4
1536	Inferring signalling networks from longitudinal data using sampling based approaches in the R-package 'ddepn'. **2011**, 12, 291	10
1535	HOMER: a human organ-specific molecular electronic repository. **2011**, 12 Suppl 10, S4	13
1534	Molecular evolution of cyclin proteins in animals and fungi. **2011**, 11, 224	23
1533	Back to the sea twice: identifying candidate plant genes for molecular evolution to marine life. **2011**, 11, 8	61

1532	Stochastic variation of transcript abundance in C57BL/6J mice. **2011**, 12, 167	18
1531	Shotgun sequencing of Yersinia enterocolitica strain W22703 (biotype 2, serotype O:9): genomic evidence for oscillation between invertebrates and mammals. **2011**, 12, 168	16
1530	Sequencing of a QTL-rich region of the Theobroma cacao genome using pooled BACs and the identification of trait specific candidate genes. **2011**, 12, 379	12
1529	Tissue-specific gene expression templates for accurate molecular characterization of the normal physiological states of multiple human tissues with implication in development and cancer studies. **2011**, 12, 439	11
1528	Differential gene expression profiling of human bone marrow-derived mesenchymal stem cells during adipogenic development. **2011**, 12, 461	76
1527	Identification of genes associated with nitrogen-use efficiency by genome-wide transcriptional analysis of two soybean genotypes. **2011**, 12, 525	85
1526	The genome sequence of E. coli W (ATCC 9637): comparative genome analysis and an improved genome-scale reconstruction of E. coli. **2011**, 12, 9	121
1525	Differential gene expression in liver and small intestine from lactating rats compared to age-matched virgin controls detects increased mRNA of cholesterol biosynthetic genes. **2011**, 12, 95	18
1524	DetoxiProt: an integrated database for detoxification proteins. **2011**, 12 Suppl 3, S2	8
1523	AlgaGEM--a genome-scale metabolic reconstruction of algae based on the Chlamydomonas reinhardtii genome. **2011**, 12 Suppl 4, S5	93
1522	The Protein Information and Property Explorer 2: gaggle-like exploration of biological proteomic data within one webpage. **2011**, 11, 154-8	9
1521	Less label, more free: approaches in label-free quantitative mass spectrometry. **2011**, 11, 535-53	528
1520	Proteome reference map of Lactobacillus acidophilus NCFM and quantitative proteomics towards understanding the prebiotic action of lactitol. **2011**, 11, 3470-81	40
1519	Metabolomics in Plant Biotechnology. **2011**, 373-388	
1518	Data Processing, Metabolomic Databases and Pathway Analysis. **2011**, 367-406	11
1517	Meta-analysis of heterogeneous data sources for genome-scale identification of risk genes in complex phenotypes. **2011**, 35, 318-32	28
1516	High-resolution array CGH identifies common mechanisms that drive embryonal rhabdomyosarcoma pathogenesis. **2011**, 50, 397-408	86
1515	An overview of techniques for linking high-dimensional molecular data to time-to-event endpoints by risk prediction models. **2011**, 53, 170-89	13

1514	Applications of liquid chromatography coupled to mass spectrometry-based metabolomics in clinical chemistry and toxicology: A review. **2011**, 44, 119-35		168
1513	Prediction of metabolic pathways from genome-scale metabolic networks. **2011**, 105, 109-21		23
1512	A spectral approach to clustering numerical vectors as nodes in a network. **2011**, 44, 236-251		4
1511	Redundancy in putrescine catabolism in solvent tolerant Pseudomonas putida S12. **2011**, 154, 1-10		10
1510	Modeling metabolic networks for mammalian cell systems: general considerations, modeling strategies, and available tools. **2012**, 127, 71-108		6
1509	A scalable approach for inferring transcriptional regulation in the yeast cell cycle. **2011**,		
1508	A metabolomic and systems biology perspective on the brain of the fragile X syndrome mouse model. **2011**, 21, 2190-202		84
1507	Feature selection of pathway markers for microarray-based disease classification using negatively correlated feature sets. **2011**,		5
1506	Reconstruction of genome-scale metabolic pathway in Aspergillus terreus NIH2624. **2011**,		
1505	Transcriptional and proteomic responses of Pseudomonas aeruginosa PAO1 to spaceflight conditions involve Hfq regulation and reveal a role for oxygen. **2011**, 77, 1221-30		114
1504	Social pathway annotation: extensions of the systems biology metabolic modelling assistant. **2011**, 12, 576-87		2
1503	Prediction of human protein-protein interaction by a mixed Bayesian model and its application to exploring underlying cancer-related pathway crosstalk. **2011**, 8, 555-67		14
1502	Genome sequence of the 17□-estradiol-utilizing bacterium Sphingomonas strain KC8. **2011**, 193, 4266-7		14
1501	Flagellin redundancy in Caulobacter crescentus and its implications for flagellar filament assembly. **2011**, 193, 2695-707		35
1500	Maternal undernourished fetal kidneys exhibit differential regulation of nephrogenic genes including downregulation of the Notch signaling pathway. **2011**, 18, 563-76		9
1499	Genome sequence of Citromicrobium strain JLT1363, isolated from the South China Sea. **2011**, 193, 2074-5		8
1498	18F-fluorodeoxy-glucose positron emission tomography marks MYC-overexpressing human basal-like breast cancers. **2011**, 71, 5164-74		101
1497	HIT: linking herbal active ingredients to targets. *Nucleic Acids Research*, **2011**, 39, D1055-9	20.1	205

1496	GreenPhylDB v2.0: comparative and functional genomics in plants. *Nucleic Acids Research*, **2011**, 39, D1095-102	20.1	95
1495	An experimentally validated genome-scale metabolic reconstruction of Klebsiella pneumoniae MGH 78578, iYL1228. **2011**, 193, 1710-7		85
1494	Resveratrol improves insulin resistance hyperglycemia and hepatosteatosis but not hypertriglyceridemia, inflammation, and life span in a mouse model for Werner syndrome. **2011**, 66, 264-78		56
1493	Common and divergent features in transcriptional control of the homologous small RNAs GlmY and GlmZ in Enterobacteriaceae. *Nucleic Acids Research*, **2011**, 39, 1294-309	20.1	48
1492	Complete genome sequence of Bacillus amyloliquefaciens XH7, which exhibits production of purine nucleosides. **2011**, 193, 5593-4		15
1491	ADGO 2.0: interpreting microarray data and list of genes using composite annotations. *Nucleic Acids Research*, **2011**, 39, W302-6	20.1	6
1490	Complete genome sequence of multidrug-resistant Acinetobacter baumannii strain 1656-2, which forms sturdy biofilm. **2011**, 193, 6393-4		42
1489	Complete genome sequence of Bifidobacterium bifidum S17. **2011**, 193, 301-2		32
1488	Comparative analysis of metabolic networks provides insight into the evolution of plant pathogenic and nonpathogenic lifestyles in Pseudomonas. **2011**, 28, 483-99		37
1487	Specific and nonhomologous isofunctional enzymes of the genetic information processing pathways as potential therapeutical targets for tritryps. **2011**, 2011, 543912		3
1486	miTALOS: analyzing the tissue-specific regulation of signaling pathways by human and mouse microRNAs. **2011**, 17, 809-19		44
1485	MGV: a generic graph viewer for comparative omics data. **2011**, 27, 2248-55		13
1484	Genome sequence of Escherichia coli XH140A, which produces L-threonine. **2011**, 193, 6090-1		1
1483	Functional diversification of the twin-arginine translocation pathway mediates the emergence of novel ecological adaptations. **2011**, 28, 3183-93		4
1482	Core and panmetabolism in Escherichia coli. **2011**, 193, 1461-72		42
1481	Using the Acropora digitifera genome to understand coral responses to environmental change. **2011**, 476, 320-3		608
1480	RxnFinder: biochemical reaction search engines using molecular structures, molecular fragments and reaction similarity. **2011**, 27, 2465-7		29
1479	Pseudomonas Genome Database: improved comparative analysis and population genomics capability for Pseudomonas genomes. *Nucleic Acids Research*, **2011**, 39, D596-600	20.1	481

1478	Massive changes in genome architecture accompany the transition to self-fertility in the filamentous fungus Neurospora tetrasperma. **2011**, 189, 55-69		61
1477	Genome sequence of the ethanol-producing Zymomonas mobilis subsp. mobilis lectotype strain ATCC 10988. **2011**, 193, 5051-2		28
1476	Genome sequence of the ethanol-producing Zymomonas mobilis subsp. pomaceae lectotype strain ATCC 29192. **2011**, 193, 5049-50		20
1475	Comparative and functional analysis of intron-mediated enhancement signals reveals conserved features among plants. *Nucleic Acids Research*, **2011**, 39, 5328-37	20.1	115
1474	Extending biochemical databases by metabolomic surveys. **2011**, 286, 23637-43		61
1473	Genome-scale transcriptome analysis of the desert poplar, Populus euphratica. **2011**, 31, 452-61		116
1472	Genome sequence of Corynebacterium glutamicum S9114, a strain for industrial production of glutamate. **2011**, 193, 6096-7		24
1471	Involvement of the TGF-beta and beta-catenin pathways in pelvic lymph node metastasis in early-stage cervical cancer. **2011**, 17, 1317-30		101
1470	Homocysteine suppresses the expression of the collagen cross-linker lysyl oxidase involving IL-6, Fli1, and epigenetic DNA methylation. **2011**, 286, 5578-88		88
1469	Integrated quantitative analysis of the phosphoproteome and transcriptome in tamoxifen-resistant breast cancer. **2011**, 286, 818-29		37
1468	Prostate Cancer Related Gene Analysis Based on Literature Mining. **2011**,		
1467	An algorithm for efficient identification of branched metabolic pathways. **2011**, 18, 1575-97		11
1466	Gene Coexpression Networks for the Analysis of DNA Microarray Data. **2011**, 215-250		31
1465	The plant cell wall-decomposing machinery underlies the functional diversity of forest fungi. **2011**, 333, 762-5		417
1464	BRISK--research-oriented storage kit for biology-related data. **2011**, 27, 2422-5		15
1463	Genes and biological processes commonly disrupted in rare and heterogeneous developmental delay syndromes. **2011**, 20, 880-93		21
1462	MicroRNA-driven developmental remodeling in the brain distinguishes humans from other primates. **2011**, 9, e1001214		159
1461	Metabolic regulation in progression to autoimmune diabetes. **2011**, 7, e1002257		65

1460	Patient-specific data fusion defines prognostic cancer subtypes. **2011**, 7, e1002227		66
1459	Loss of genetic redundancy in reductive genome evolution. **2011**, 7, e1001082		47
1458	The Reactome BioMart. **2011**, 2011, bar031		29
1457	Evolution of protein phosphorylation for distinct functional modules in vertebrate genomes. **2011**, 28, 1131-40		20
1456	Pathways of distinction analysis: a new technique for multi-SNP analysis of GWAS data. **2011**, 7, e1002101		49
1455	Tripal: a construction toolkit for online genome databases. **2011**, 2011, bar044		51
1454	Communication: limitations of the stochastic quasi-steady-state approximation in open biochemical reaction networks. **2011**, 135, 181103		43
1453	MyBioNet: interactively visualize, edit and merge biological networks on the web. **2011**, 27, 3321-2		1
1452	Phylogeny-wide analysis of social amoeba genomes highlights ancient origins for complex intercellular communication. **2011**, 21, 1882-91		112
1451	Gene coexpression network alignment and conservation of gene modules between two grass species: maize and rice. **2011**, 156, 1244-56		106
1450	RuleGO: a logical rules-based tool for description of gene groups by means of Gene Ontology. *Nucleic Acids Research*, **2011**, 39, W293-301	20.1	12
1449	OptCom: a multi-level optimization framework for the metabolic modeling and analysis of microbial communities. **2012**, 8, e1002363		245
1448	Reconstruction of genome-scale active metabolic networks for 69 human cell types and 16 cancer types using INIT. **2012**, 8, e1002518		289
1447	Identification of novel type 2 diabetes candidate genes involved in the crosstalk between the mitochondrial and the insulin signaling systems. **2012**, 8, e1003046		17
1446	The Biofuel Feedstock Genomics Resource: a web-based portal and database to enable functional genomics of plant biofuel feedstock species. **2012**, 2012, bar061		13
1445	Deciphering the genome of polyphosphate accumulating actinobacterium Microlunatus phosphovorus. **2012**, 19, 383-94		33
1444	Using functional signatures to identify repositioned drugs for breast, myelogenous leukemia and prostate cancer. **2012**, 8, e1002347		50
1443	Genome-scale modeling of light-driven reductant partitioning and carbon fluxes in diazotrophic unicellular cyanobacterium Cyanothece sp. ATCC 51142. **2012**, 8, e1002460		69

1442	Comparative genomics suggests an independent origin of cytoplasmic incompatibility in Cardinium hertigii. **2012**, 8, e1003012		100
1441	Chapter 12: Human microbiome analysis. **2012**, 8, e1002808		310
1440	Transcriptome analysis of the oriental river prawn, Macrobrachium nipponense using 454 pyrosequencing for discovery of genes and markers. **2012**, 7, e39727		83
1439	LegumeIP: an integrative database for comparative genomics and transcriptomics of model legumes. *Nucleic Acids Research*, **2012**, 40, D1221-9	20.1	83
1438	Comparative genomics of enterococci: variation in Enterococcus faecalis, clade structure in E. faecium, and defining characteristics of E. gallinarum and E. casseliflavus. **2012**, 3, e00318-11		198
1437	An integrated open framework for thermodynamics of reactions that combines accuracy and coverage. **2012**, 28, 2037-44		85
1436	Draft genome sequence of the novel agarolytic bacterium Aquimarina agarilytica ZC1. **2012**, 194, 2769		10
1435	Draft genome sequence of Rhodococcus sp. strain P14, a biodegrader of high-molecular-weight polycyclic aromatic hydrocarbons. **2012**, 194, 3546		20
1434	Sample preparation of Mycobacterium tuberculosis extracts for nuclear magnetic resonance metabolomic studies. **2012**, e3673		4
1433	Draft genome sequence of butanol-acetone-producing Clostridium beijerinckii strain G117. **2012**, 194, 5470-1		18
1432	Database resources of the National Center for Biotechnology Information. *Nucleic Acids Research*, **2012**, 40, D13-25	20.1	458
1431	Breaking free from the chains of pathway annotation: de novo pathway discovery for the analysis of disease processes. **2012**, 13, 1967-78		6
1430	Database resources of the National Center for Biotechnology Information. *Nucleic Acids Research*, **2013**, 41, D8-D20	20.1	375
1429	MoNetFamily: a web server to infer homologous modules and module-module interaction networks in vertebrates. *Nucleic Acids Research*, **2012**, 40, W263-70	20.1	10
1428	Research resource: whole transcriptome RNA sequencing detects multiple 1,25-dihydroxyvitamin D(3)-sensitive metabolic pathways in developing zebrafish. **2012**, 26, 1630-42		33
1427	A Visual Cross-Database Comparison of Metabolic Networks. **2012**, 678-687		
1426	NetwoRx: connecting drugs to networks and phenotypes in Saccharomyces cerevisiae. *Nucleic Acids Research*, **2013**, 41, D720-7	20.1	8
1425	Complete genome sequence of Bacillus anthracis H9401, an isolate from a Korean patient with anthrax. **2012**, 194, 4116-7		15

1424	Bacterial responses to a simulated colon tumor microenvironment. **2012**, 11, 851-62		31
1423	Genome sequence of Pseudomonas putida strain SJTE-1, a bacterium capable of degrading estrogens and persistent organic pollutants. **2012**, 194, 4781-2		25
1422	Does the F508-CFTR mutation induce a proinflammatory response in human airway epithelial cells?. **2012**, 303, L509-18		19
1421	Improved T-Cluster based scheme for combination gene scale expression data. **2012**,		0
1420	Genome sequence of Pseudomonas aeruginosa strain SJTD-1, a bacterium capable of degrading long-chain alkanes and crude oil. **2012**, 194, 4783-4		19
1419	Draft genome sequence of the flocculating Zymomonas mobilis strain ZM401 (ATCC 31822). **2012**, 194, 7008-9		15
1418	Genome sequence of Corynebacterium glutamicum ATCC 14067, which provides insight into amino acid biosynthesis in coryneform bacteria. **2012**, 194, 742-3		24
1417	KOMODO: a web tool for detecting and visualizing biased distribution of groups of homologous genes in monophyletic taxa. *Nucleic Acids Research*, **2012**, 40, W491-7	20.1	2
1416	Genome sequence of Pedobacter arcticus sp. nov., a sea ice bacterium isolated from tundra soil. **2012**, 194, 6688		3
1415	De novo sequencing and characterization of the floral transcriptome of Dendrocalamus latiflorus (Poaceae: Bambusoideae). **2012**, 7, e42082		104
1414	PathVar: analysis of gene and protein expression variance in cellular pathways using microarray data. **2012**, 28, 446-7		11
1413	Analyzing Thiol-Dependent Redox Networks in the Presence of Methylene Blue and Other Antimalarial Agents with RT-PCR-Supported in silico Modeling. **2012**, 6, 287-302		5
1412	BioNetwork Bench: Database and Software for Storage, Query, and Analysis of Gene and Protein Networks. **2012**, 6, BBI.S9728		78
1411	Genomic analysis of the hydrocarbon-producing, cellulolytic, endophytic fungus Ascocoryne sarcoides. **2012**, 8, e1002558		64
1410	Novel search method for the discovery of functional relationships. **2012**, 28, 269-76		9
1409	MUC1 mucin stabilizes and activates hypoxia-inducible factor 1 alpha to regulate metabolism in pancreatic cancer. **2012**, 109, 13787-92		156
1408	Genome sequences of Pseudomonas fragi strains A22 and B25. **2012**, 194, 3276-7		3
1407	Mutual exclusivity analysis identifies oncogenic network modules. **2012**, 22, 398-406		452

1406	AutismKB: an evidence-based knowledgebase of autism genetics. *Nucleic Acids Research*, **2012**, 40, D1016-22	20.1	129
1405	Common PIK3CA mutants and a novel 3' UTR mutation are associated with increased sensitivity to saracatinib. **2012**, 18, 2704-14		38
1404	The genome portal of the Department of Energy Joint Genome Institute. *Nucleic Acids Research*, **2012**, 40, D26-32	20.1	359
1403	CytoSaddleSum: a functional enrichment analysis plugin for Cytoscape based on sum-of-weights scores. **2012**, 28, 893-4		2
1402	Drug target prediction using adverse event report systems: a pharmacogenomic approach. **2012**, 28, i611-i618		85
1401	VIROME: a standard operating procedure for analysis of viral metagenome sequences. **2012**, 6, 427-39		132
1400	Application of Top-Down and Bottom-up Systems Approaches in Ruminant Physiology and Metabolism. **2012**, 13, 379-94		34
1399	Architecture and conservation of the bacterial DNA replication machinery, an underexploited drug target. **2012**, 13, 352-72		82
1398	Complete genome sequence of Oscillibacter valericigenes Sjm18-20(T) (=NBRC 101213(T)). **2012**, 6, 406-14		29
1397	Analysis of the Cholesterol Biosynthesis Feedback Control and its Consequences for the Hypercholesteremia Treatment Strategies. **2012**, 45, 624-628		
1396	Adenosine A2A receptor upregulation in human PMNs is controlled by miRNA-214, miRNA-15, and miRNA-16. **2012**, 37, 156-63		29
1395	Methodological Requirements for Lipidomics Research. 30-53		
1394	The first Illumina-based de novo transcriptome sequencing and analysis of safflower flowers. **2012**, 7, e38653		111
1393	Prediction and identification of sequences coding for orphan enzymes using genomic and metagenomic neighbours. **2012**, 8, 581		25
1392	A Preliminary microRNA Analysis of Non Syndromic Thoracic Aortic Aneurysms. **2012**, 15, 51-5		22
1391	Virtual metagenome reconstruction from 16S rRNA gene sequences. **2012**, 3, 1203		18
1390	The human small intestinal microbiota is driven by rapid uptake and conversion of simple carbohydrates. **2012**, 6, 1415-26		416
1389	Predicting drug targets and biomarkers of cancer via genome-scale metabolic modeling. **2012**, 18, 5572-84		77

1388	Metabolic and evolutionary costs of herbivory defense: systems biology of glucosinolate synthesis. **2012**, 196, 596-605		117
1387	Mathematical optimization applications in metabolic networks. **2012**, 14, 672-86		100
1386	Sex peptide of Drosophila melanogaster males is a global regulator of reproductive processes in females. **2012**, 279, 4423-32		57
1385	Cross species integration of functional genomics experiments. **2012**, 104, 1-24		5
1384	A molecular analysis of desiccation tolerance mechanisms in the anhydrobiotic nematode Panagrolaimus superbus using expressed sequenced tags. **2012**, 5, 68		32
1383	A network-based gene-weighting approach for pathway analysis. **2012**, 22, 565-80		38
1382	Advances in the methods for studying gut microbiota and their relevance to the research of dietary fiber functions. **2012**, 48, 916-929		38
1381	Tumor suppressive microRNAs (miR-222 and miR-31) regulate molecular pathways based on microRNA expression signature in prostate cancer. **2012**, 57, 691-9		86
1380	Using pathway modules as targets for assay development in xenobiotic screening. **2012**, 8, 531-42		8
1379	A Gaussian graphical model for identifying significantly responsive regulatory networks from time series gene expression data. **2012**,		
1378	Extension of cortical synaptic development distinguishes humans from chimpanzees and macaques. **2012**, 22, 611-22		157
1377	Automation on the generation of genome-scale metabolic models. **2012**, 19, 1295-306		12
1376	KEGG for integration and interpretation of large-scale molecular data sets. *Nucleic Acids Research*, **2012**, 40, D109-14	20.1	3314
1375	Systematic analysis of human lysine acetylation proteins and accurate prediction of human lysine acetylation through bi-relative adapted binomial score Bayes feature representation. **2012**, 8, 2964-73		57
1374	An integrative framework for identifying consistent microRNA expression signatures associated with clear cell renal cell carcinoma. **2012**,		
1373	enRoute: Dynamic path extraction from biological pathway maps for in-depth experimental data analysis. **2012**,		11
1372	Pathway-directed weighted testing procedures for the integrative analysis of gene expression and metabolomic data. **2012**, 99, 265-74		8
1371	Comparison of pathways associated with hepatitis B- and C-infected hepatocellular carcinoma using pathway-based class discrimination method. **2012**, 99, 347-54		19

1370	Predicting metabolic pathways by sub-network extraction. **2012**, 804, 107-30	7
1369	Oxygen and hydrogen peroxide in the early evolution of life on earth: in silico comparative analysis of biochemical pathways. **2012**, 12, 775-84	33
1368	Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. **2012**, 194, 1001-1013	168
1367	A fine scale phenotype-genotype virulence map of a bacterial pathogen. **2012**, 22, 2541-51	155
1366	Global probabilistic annotation of metabolic networks enables enzyme discovery. **2012**, 8, 848-54	47
1365	Deep sequencing-based transcriptome profiling analysis of Oryzias melastigma exposed to PFOS. **2012**, 120-121, 54-8	53
1364	Oligomeric amyloid-□peptide affects the expression of genes involved in steroid and lipid metabolism in primary neurons. **2012**, 61, 321-33	15
1363	The genome of the xerotolerant mold Wallemia sebi reveals adaptations to osmotic stress and suggests cryptic sexual reproduction. **2012**, 49, 217-26	83
1362	MHC class I target recognition, immunophenotypes and proteomic profiles of natural killer cells within the spleens of day-14 chick embryos. **2012**, 37, 446-56	11
1361	Comparative transcriptomics and gene expression in larval tiger salamander (Ambystoma tigrinum) gill and lung tissues as revealed by pyrosequencing. **2012**, 492, 329-38	21
1360	Identifying disease related sub-pathways for analysis of genome-wide association studies. **2012**, 503, 101-9	14
1359	Orchestrating hi-fi annotations. **2012**, 8, 810-1	
1358	Identifying dysregulated pathways in cancers from pathway interaction networks. **2012**, 13, 126	93
1357	The M5nr: a novel non-redundant database containing protein sequences and annotations from multiple sources and associated tools. **2012**, 13, 141	215
1356	Propagating semantic information in biochemical network models. **2012**, 13, 18	9
1355	MetRxn: a knowledgebase of metabolites and reactions spanning metabolic models and databases. **2012**, 13, 6	96
1354	Prognostic gene signatures for patient stratification in breast cancer: accuracy, stability and interpretability of gene selection approaches using prior knowledge on protein-protein interactions. **2012**, 13, 69	34
1353	An in silico platform for the design of heterologous pathways in nonnative metabolite production. **2012**, 13, 93	19

1352	MetaMapp: mapping and visualizing metabolomic data by integrating information from biochemical pathways and chemical and mass spectral similarity. **2012**, 13, 99	161
1351	Protein interactions of the transcription factor Hoxa1. **2012**, 12, 29	33
1350	Identification of differentially expressed genes and pathways for intramuscular fat deposition in pectoralis major tissues of fast-and slow-growing chickens. **2012**, 13, 213	86
1349	Comparative genomics of the white-rot fungi, Phanerochaete carnosa and P. chrysosporium, to elucidate the genetic basis of the distinct wood types they colonize. **2012**, 13, 444	97
1348	Evaluation method for the potential functionome harbored in the genome and metagenome. **2012**, 13, 699	40
1347	De novo assembly and characterisation of the transcriptome during seed development, and generation of genic-SSR markers in peanut (Arachis hypogaea L.). **2012**, 13, 90	183
1346	Olive phenolic compounds: metabolic and transcriptional profiling during fruit development. **2012**, 12, 162	108
1345	Host-pathogen interactome mapping for HTLV-1 and -2 retroviruses. **2012**, 9, 26	62
1344	Sets2Networks: network inference from repeated observations of sets. **2012**, 6, 89	14
1343	Bioenergy grass feedstock: current options and prospects for trait improvement using emerging genetic, genomic, and systems biology toolkits. **2012**, 5, 80	42
1342	Interaction among apoptosis-associated sequence variants and joint effects on aggressive prostate cancer. **2012**, 5, 11	24
1341	LDGIdb: a database of gene interactions inferred from long-range strong linkage disequilibrium between pairs of SNPs. **2012**, 5, 212	3
1340	Topological features of cancer proteins in the human NR-RTK interaction network. **2012**, 32, 257-62	5
1339	Using the KEGG database resource. **2012**, Chapter 1, Unit1.12	148
1338	A compendium of inborn errors of metabolism mapped onto the human metabolic network. **2012**, 8, 2545-58	55
1337	Analysis of bacterial biofilms using NMR-based metabolomics. **2012**, 4, 1273-306	73
1336	Comparative metagenomics of two microbial mats at Cuatro Ciénegas Basin I: ancient lessons on how to cope with an environment under severe nutrient stress. **2012**, 12, 648-58	50
1335	B-cell ligand processing pathways detected by large-scale comparative analysis. **2012**, 10, 142-52	1

1334	ALDH+ tumor-initiating cells exhibiting gain in NOTCH1 gene copy number have enhanced regrowth sensitivity to a secretase inhibitor and irinotecan in colorectal cancer. **2012**, 6, 370-81	28
1333	Pathway analysis of cancer-associated microRNA targets. **2012**, 41, 2213-26	9
1332	Translational Biology Approaches to Improve Abiotic Stress Tolerance in Crops. **2012**, 207-239	2
1331	Role of proteomics in understanding prion infection. **2012**, 9, 649-66	6
1330	Heptalactone is an endogenously produced quorum-sensing molecule regulating growth and secondary metabolite production by Aspergillus nidulans. **2012**, 96, 773-81	22
1329	The effects of pH oscillation on Lactobacillus rhamnosus batch cultivation. **2012**, 95, 1265-73	3
1328	The role and clinical implications of microRNAs in hepatocellular carcinoma. **2012**, 55, 906-19	34
1327	Cassava Genetic Improvement: Omics Approaches for Facing Global Challenges. **2012**, 1049-1065	
1326	DNA Methylation and Toxicogenomics. **2012**, 25-50	2
1325	Comparative Analysis of Biological Networks: Hidden Markov model and Markov chain-based approach. **2012**, 29, 22-34	16
1324	Linking genome content to biofuel production yields: a meta-analysis of major catabolic pathways among select H2 and ethanol-producing bacteria. **2012**, 12, 295	53
1323	PathNet: a tool for pathway analysis using topological information. **2012**, 7, 10	46
1322	Interplay of gene expression noise and ultrasensitive dynamics affects bacterial operon organization. **2012**, 8, e1002672	16
1321	Identification of fluorescent compounds with non-specific binding property via high throughput live cell microscopy. **2012**, 7, e28802	6
1320	Post-GWAS functional characterization of susceptibility variants for chronic lymphocytic leukemia. **2012**, 7, e29632	30
1319	Coordinating environmental genomics and geochemistry reveals metabolic transitions in a hot spring ecosystem. **2012**, 7, e38108	50
1318	Prediction and analysis of the protein interactome in Pseudomonas aeruginosa to enable network-based drug target selection. **2012**, 7, e41202	29
1317	Genome-scale reconstruction and analysis of the metabolic network in the hyperthermophilic archaeon Sulfolobus solfataricus. **2012**, 7, e43401	32

1316	Systematic analysis of small RNAs associated with human mitochondria by deep sequencing: detailed analysis of mitochondrial associated miRNA. **2012**, 7, e44873	125
1315	De novo foliar transcriptome of Chenopodium amaranticolor and analysis of its gene expression during virus-induced hypersensitive response. **2012**, 7, e45953	19
1314	Multiscale modeling of metabolism and macromolecular synthesis in E. coli and its application to the evolution of codon usage. **2012**, 7, e45635	87
1313	Reconstruction and in silico analysis of metabolic network for an oleaginous yeast, Yarrowia lipolytica. **2012**, 7, e51535	65
1312	Inferring microRNA regulation of mRNA with partially ordered samples of paired expression data and exogenous prediction algorithms. **2012**, 7, e51480	2
1311	Different transcriptional profiles of RAW264.7 infected with Mycobacterium tuberculosis H37Rv and BCG identified via deep sequencing. **2012**, 7, e51988	8
1310	Biomarker gene signature discovery integrating network knowledge. **2012**, 1, 5-17	22
1309	Using bioinformatic approaches to identify pathways targeted by human leukemogens. **2012**, 9, 2479-503	6
1308	Metabolic Consequences of TGFb Stimulation in CulturedPrimary Mouse Hepatocytes Screened from Transcript Data with ModeScore´. **2012**, 2, 983-1003	2
1307	Applications for next-generation sequencing in fish ecotoxicogenomics. **2012**, 3, 62	47
1306	Tracing lifestyle adaptation in prokaryotic genomes. **2012**, 3, 48	24
1305	Mutational Analyses of the Enzymes Involved in the Metabolism of Hydrogen by the Hyperthermophilic Archaeon Pyrococcus furiosus. **2012**, 3, 163	34
1304	Comparison of sepsis-induced transcriptomic changes in a murine model to clinical blood samples identifies common response patterns. **2012**, 3, 284	11
1303	In silicoanalysis strategies and resources for psychiatric genetics research. 34-48	
1302	Expression profiling based on coexpressed modules in obese prepubertal children. **2012**, 11, 3077-85	4
1301	Tutorial on biological networks. **2012**, 2, 298-325	10
1300	Systems biology analysis of protein-drug interactions. **2012**, 6, 102-16	19
1299	A database of annotated promoters of genes associated with common respiratory and related diseases. **2012**, 47, 112-9	5

1298	Development of petri net-based dynamic model for improved production of farnesyl pyrophosphate by integrating mevalonate and methylerythritol phosphate pathways in yeast. **2012** , 167, 1172-82	3
1297	COVAIN: a toolbox for uni- and multivariate statistics, time-series and correlation network analysis and inverse estimation of the differential Jacobian from metabolomics covariance data. **2012**, 8, 81-93	98
1296	Short- and long-term dynamic responses of the metabolic network and gene expression in yeast to a transient change in the nutrient environment. **2012**, 8, 1760-74	6
1295	Large-scale objective association of mouse phenotypes with human symptoms through structural variation identified in patients with developmental disorders. **2012**, 33, 874-83	16
1294	Amyloid-□oligomers induce differential gene expression in adult human brain slices. **2012**, 287, 7436-45	60
1293	Network- and attribute-based classifiers can prioritize genes and pathways for autism spectrum disorders and intellectual disability. **2012**, 160C, 130-42	25
1292	Metagenomic and metaproteomic insights into bacterial communities in leaf-cutter ant fungus gardens. **2012**, 6, 1688-701	100
1291	RNA-sequencing tag profiling of the placenta and pericarp of pungent pepper provides robust candidates contributing to capsaicinoid biosynthesis. **2012**, 110, 111-121	24
1290	Missing values in mass spectrometry based metabolomics: an undervalued step in the data processing pipeline. **2012**, 8, 161-174	137
1289	Aligning extracted LC-MS peak lists via density maximization. **2012**, 8, 175-185	44
1288	De novo characterization of the root transcriptome of a traditional Chinese medicinal plant Polygonum cuspidatum. **2012**, 55, 452-66	63
1287	The Cold Awakening of Doritaenopsis □Tinny Tender□Orchid Flowers: The Role of Leaves in Cold-induced Bud Dormancy Release. **2012**, 31, 139-155	20
1286	Pathway-based microarray analysis for robust disease classification. **2012**, 21, 649-660	10
1285	Mitochondrial proteomics--a tool for the study of metabolic disorders. **2012**, 35, 715-26	39
1284	Predictive mathematical models of cancer signalling pathways. **2012**, 271, 155-65	45
1283	Computational approaches to disease-gene prediction: rationale, classification and successes. **2012**, 279, 678-96	106
1282	The genome of wine yeast Dekkera bruxellensis provides a tool to explore its food-related properties. **2012**, 157, 202-9	85
1281	Parental phase status affects the cold hardiness of progeny eggs in locusts. **2012**, 26, 379-389	13

1280	Modulation of Wnt and Hedgehog signaling pathways is linked to retinoic acid-induced amelioration of chronic allograft dysfunction. **2012**, 12, 55-68	8
1279	Targeted and shotgun metagenomic approaches provide different descriptions of dryland soil microbial communities in a manipulated field study. **2012**, 4, 248-56	45
1278	Ethanol modulation of gene networks: implications for alcoholism. **2012**, 45, 115-21	21
1277	Runx1 is a tumor suppressor gene in the mouse gastrointestinal tract. **2012**, 103, 593-9	33
1276	Alteration of gene expression profile in maize infected with a double-stranded RNA fijivirus associated with symptom development. **2012**, 13, 251-62	37
1275	Recent advances in Schistosoma genomics. **2012**, 34, 151-62	12
1274	StratomeX: Visual Analysis of Large-Scale Heterogeneous Genomics Data for Cancer Subtype Characterization. **2012**, 31, 1175-1184	59
1273	A systematic comparison of genome-scale clustering algorithms. **2012**, 13 Suppl 10, S7	34
1272	Compound toxicity screening and structure-activity relationship modeling in Escherichia coli. **2012**, 109, 846-50	47
1271	Recent advances of metabolomics in plant biotechnology. **2012**, 6, 1-15	102
1270	Comparative transcriptome analysis of AP2/EREBP gene family under normal and hormone treatments, and under two drought stresses in NILs setup by Aday Selection and IR64. **2012**, 287, 1-19	27
1269	SignatureClust: a tool for landmark gene-guided clustering. **2012**, 16, 411-418	
1268	The application of quantification techniques in proteomics for biomedical research. **2013**, 32, 1-26	51
1267	Identification of new biomarker candidates for glucocorticoid induced insulin resistance using literature mining. **2013**, 6, 2	5
1266	Differential gene expression analysis between anagen and telogen of Capra hircus skin based on the de novo assembled transcriptome sequence. **2013**, 520, 30-8	26
1265	Genome-wide expression profiles of seasonal bud dormancy at four critical stages in Japanese apricot. **2013**, 83, 247-64	51
1264	RNA-seq Analysis Reveals Ethylene-Mediated Reproductive Organ Development and Abscission in Soybean (Glycine max L. Merr.). **2013**, 31, 607-619	15
1263	Structural composition of alternative complex III: variations on the same theme. **2013**, 1827, 1378-82	19

1262	Recent advances in cardiovascular proteomics. **2013**, 81, 3-14	25
1261	Review: toxicometabolomics. **2013**, 33, 1365-83	129
1260	Transcriptomic profiling of Aspergillus flavus in response to 5-azacytidine. **2013**, 56, 78-86	58
1259	Systems biology characterization of engineered tissues. **2013**, 15, 55-70	9
1258	Seq2Ref: a web server to facilitate functional interpretation. **2013**, 14, 30	5
1257	Detecting recurrent gene mutation in interaction network context using multi-scale graph diffusion. **2013**, 14, 29	28
1256	De novo sequencing and transcriptome analysis of the desert shrub, Ammopiptanthus mongolicus, during cold acclimation using Illumina/Solexa. **2013**, 14, 488	69
1255	Transcriptome analysis of porcine M. semimembranosus divergent in intramuscular fat as a consequence of dietary protein restriction. **2013**, 14, 453	36
1254	Comparative transcriptome analysis of microsclerotia development in Nomuraea rileyi. **2013**, 14, 411	33
1253	Transcriptome analysis of Cymbidium sinense and its application to the identification of genes associated with floral development. **2013**, 14, 279	93
1252	Comparative genomic analysis of four representative plant growth-promoting rhizobacteria in Pseudomonas. **2013**, 14, 271	98
1251	Genome sequencing of bacteria: sequencing, de novo assembly and rapid analysis using open source tools. **2013**, 14, 211	36
1250	Biclustering for the comprehensive search of correlated gene expression patterns using clustered seed expansion. **2013**, 14, 144	19
1249	Transcriptomic profiling of the salt-stress response in the wild recretohalophyte Reaumuria trigyna. **2013**, 14, 29	122
1248	Members of the Sinorhizobium meliloti ChvI regulon identified by a DNA binding screen. **2013**, 13, 132	11
1247	Microarray gene expression profiling of neural tissues in bovine spastic paresis. **2013**, 9, 122	4
1246	Maximizing capture of gene co-expression relationships through pre-clustering of input expression samples: an Arabidopsis case study. **2013**, 7, 44	17
1245	Proximity Measures and Results Validation in Biclustering ▯A Survey. **2013**, 206-217	7

1244	Extracellular matrix of adipogenically differentiated mesenchymal stem cells reveals a network of collagen filaments, mostly interwoven by hexagonal structural units. **2013**, 32, 452-65	16
1243	Quantitative proteomic studies on TNBC in premenopausal patients. **2013**, 29, 500-505	1
1242	Rank-based genome-wide analysis reveals the association of ryanodine receptor-2 gene variants with childhood asthma among human populations. **2013**, 7, 16	38
1241	Analysis of the steady-state relations and control-algorithm characterisation in a mathematical model of cholesterol biosynthesis. **2013**, 33, 18-27	9
1240	Qualitative Modelling of Metabolic Networks. **2013**, 67, 557-591	
1239	Getting to the guts of the matter: the status and potential of 'omics' research of parasitic protists of the human gastrointestinal system. **2013**, 43, 971-82	8
1238	Reconstructing Gapless Ancestral Metabolic Networks. **2013**, 126-140	1
1237	The Contribution of New Technologies Toward Understanding Plant–Fungus Symbioses. **2013**, 201-214	2
1236	Computational Models of Algae Metabolism for Industrial Applications. **2013**, 9, 185-195	7
1235	Transcriptome responses in the rectal gland of fed and fasted spiny dogfish shark (Squalus acanthias) determined by suppression subtractive hybridization. **2013**, 8, 334-43	7
1234	Effects of bisphosphonate treatment on DNA methylation in osteonecrosis of the jaw. **2013**, 757, 104-13	9
1233	Succinct interval-splitting tree for scalable similarity search of compound-protein pairs with property constraints. **2013**,	1
1232	microRNA regulation of skin pigmentation in fish. **2013**, 126, 3401-8	51
1231	MyCompoundID: using an evidence-based metabolome library for metabolite identification. **2013**, 85, 3401-8	143
1230	Analysis of the NCI-60 dataset for cancer-related microRNA and mRNA using expression profiles. **2013**, 44, 15-21	4
1229	Gigabase-scale transcriptome analysis on four species of pearl oysters. **2013**, 15, 253-64	47
1228	Elevated specific peripheral cytokines found in major depressive disorder patients with childhood trauma exposure: a cytokine antibody array analysis. **2013**, 54, 953-61	69
1227	Flux balance analysis of Chlorella sp. FC2 IITG under photoautotrophic and heterotrophic growth conditions. **2013**, 118, 167-79	57

1226	Trascriptome analysis of the Pacific white shrimp Litopenaeus vannamei exposed to nitrite by RNA-seq. **2013**, 35, 2008-16	70
1225	Identification of novel microRNA regulatory pathways associated with heterogeneous prostate cancer. **2013**, 7 Suppl 3, S6	34
1224	Steiner tree methods for optimal sub-network identification: an empirical study. **2013**, 14, 144	18
1223	Bolbase: a comprehensive genomics database for Brassica oleracea. **2013**, 14, 664	85
1222	Experimental characterization of the human non-sequence-specific nucleic acid interactome. **2013**, 14, R81	3
1221	The predicted secretome and transmembranome of the poultry red mite Dermanyssus gallinae. **2013**, 6, 259	30
1220	Identification of reproducible gene expression signatures in lung adenocarcinoma. **2013**, 14, 371	12
1219	Analysis of porcine adipose tissue transcriptome reveals differences in de novo fatty acid synthesis in pigs with divergent muscle fatty acid composition. **2013**, 14, 843	58
1218	Soil bacterial communities shaped by geochemical factors and land use in a less-explored area, Tibetan Plateau. **2013**, 14, 820	35
1217	Genome-wide transcriptional analysis of two soybean genotypes under dehydration and rehydration conditions. **2013**, 14, 687	29
1216	Comparative antigen-induced gene expression profiles unveil novel aspects of susceptibility/resistance to adjuvant arthritis in rats. **2013**, 56, 531-9	6
1215	Early transcriptomic adaptation to Na$_2$CO$_3$ stress altered the expression of a quarter of the total genes in the maize genome and exhibited shared and distinctive profiles with NaCl and high pH stresses. **2013**, 55, 1147-65	19
1214	Catabolite control protein E (CcpE) is a LysR-type transcriptional regulator of tricarboxylic acid cycle activity in Staphylococcus aureus. **2013**, 288, 36116-28	27
1213	Basic and applied uses of genome-scale metabolic network reconstructions of Escherichia coli. **2013**, 9, 661	244
1212	Integrative variable selection via Bayesian model uncertainty. **2013**, 32, 4938-53	27
1211	Reconciling differential gene expression data with molecular interaction networks. **2013**, 29, 622-9	6
1210	A missing link between complex I and group 4 membrane-bound [NiFe] hydrogenases. **2013**, 1827, 198-209	82
1209	Setting up an intronic miRNA database. **2013**, 936, 69-76	6

1208	Deciphering gene expression program of MAP3K1 in mouse eyelid morphogenesis. **2013**, 374, 96-107	13
1207	A large-scale protein phosphorylation analysis reveals novel phosphorylation motifs and phosphoregulatory networks in Arabidopsis. **2013**, 78, 486-98	79
1206	Computational and experimental analysis identified 6-diazo-5-oxonorleucine as a potential agent for treating infection by Plasmodium falciparum. **2013**, 20, 389-95	10
1205	Comparative genomics reveals 'novel' Fur regulated sRNAs and coding genes in diverse proteobacteria. **2013**, 516, 335-44	1
1204	Transcriptome profile analysis of young floral buds of fertile and sterile plants from the self-pollinated offspring of the hybrid between novel restorer line NR1 and Nsa CMS line in Brassica napus. **2013**, 14, 26	69
1203	Biochemical Networks, Bioinformatics and Systems Biology. **2013**, 366-373	1
1202	Chemogenomic approaches to infer drug-target interaction networks. **2013**, 939, 97-113	28
1201	Finding the targets of a drug by integration of gene expression data with a protein interaction network. **2013**, 9, 1676-85	47
1200	Web resources for microRNA research. **2013**, 774, 225-50	15
1199	An essential requirement for the SCAP/SREBP signaling axis to protect cancer cells from lipotoxicity. **2013**, 73, 2850-62	116
1198	Universally increased mRNA stability downstream of the translation initiation site in eukaryotes and prokaryotes. **2013**, 517, 230-5	6
1197	Systems biology approaches for discovering biomarkers for traumatic brain injury. **2013**, 30, 1101-16	46
1196	Global transcriptome analysis and identification of a CONSTANS-like gene family in the orchid Erycina pusilla. **2013**, 237, 1425-41	26
1195	Linking genome-scale metabolic modeling and genome annotation. **2013**, 985, 61-83	6
1194	Genome-scale reconstruction and in silico analysis of Aspergillus terreus metabolism. **2013**, 9, 1939-48	24
1193	An algorithm for rapid computational construction of metabolic networks: a cholesterol biosynthesis example. **2013**, 43, 471-80	9
1192	Recognition of nontrivial remote homology relationships involving proteins of Helicobacter pylori: implications for function recognition. **2013**, 993, 155-75	
1191	Bioinformatic progress and applications in metaproteogenomics for bridging the gap between genomic sequences and metabolic functions in microbial communities. **2013**, 13, 2786-804	39

1190	De novo characterization of Lentinula edodes C(91-3) transcriptome by deep Solexa sequencing. **2013**, 431, 111-5	23
1189	Comparison of transcriptome under red and blue light culture of Saccharina japonica (Phaeophyceae). **2013**, 237, 1123-33	47
1188	Comparative proteomic and phosphoproteomic profiling of pancreatic adenocarcinoma cells treated with CB1 or CB2 agonists. **2013**, 34, 1359-68	11
1187	Global metabolite profiling of human colorectal cancer xenografts in mice using HPLC-MS/MS. **2013** , 12, 2980-6	10
1186	Screening and expression of genes from metagenomes. **2013**, 83, 1-68	39
1185	Proteome analysis of silkworm, Bombyx mori, larval gonads: characterization of proteins involved in sexual dimorphism and gametogenesis. **2013**, 12, 2422-38	17
1184	Bioinformatics Approach for Finding Target Protein in Infectious Disease. **2013**, 235-255	
1183	A new metabolomic workflow for early detection of Alzheimer's disease. **2013**, 1302, 65-71	67
1182	Rhizosphere Metatranscriptomics: Challenges and Opportunities. **2013**, 1137-1144	9
1181	Integrated LC-MS/MS system for plant metabolomics. **2013**, 4, e201301011	21
1180	Stereo signature molecular descriptor. **2013**, 53, 887-97	42
1179	Computational reconstruction of metabolic networks from KEGG. **2013**, 930, 235-49	13
1178	Expression analysis of the genes involved in osmotic adjustment in bread wheat (Triticum aestivum L.) cultivars under terminal drought stress conditions. **2013**, 16, 173-181	12
1177	Characterizing developmental and inducible differentiation between juvenile and adult plants of Aechmea fasciata treated with ethylene by transcriptomic analysis. **2013**, 69, 247-257	13
1176	Fuzi-Lizhong pill compensates hypothyroid-hypothermia via ghrelin release. **2013**, 149, 707-12	7
1175	Transcriptome analysis of Japanese pear (Pyrus pyrifolia Nakai) flower buds transitioning through endodormancy. **2013**, 54, 1132-51	129
1174	Integrative transcriptome and proteome study to identify the signaling network regulated by POPX2 phosphatase. **2013**, 12, 2525-36	17
1173	In-depth bioinformatic analysis of lung cancer-associated microRNA targets. **2013**, 30, 2945-56	3

1172	Whole-Genome Shotgun Assembly and Analysis of the Genome of Streptomyces mobaraensis DSM 40847, a Strain for Industrial Production of Microbial Transglutaminase. **2013**, 1, e0014313		13
1171	Genome Sequence of Mycoplasma columbinum Strain SF7. **2013**, 1, e0015713		2
1170	Epigenome-wide profiling identifies significant differences in DNA methylation between matched-pairs of T- and B-lymphocytes from healthy individuals. **2013**, 8, 1188-97		34
1169	Identification of gene sets and pathways associated with lactation performance in mice. **2013**, 45, 171-81		11
1168	Inactivation of the phosphoglucomutase gene pgm in Corynebacterium glutamicum affects cell shape and glycogen metabolism. **2013**, 33,		9
1167	Identification of recurrence related microRNAs in hepatocellular carcinoma after surgical resection. **2013**, 14, 1105-18		21
1166	Silicon era of carbon-based life: application of genomics and bioinformatics in crop stress research. **2013**, 14, 11444-83		7
1165	Building the repertoire of dispensable chromosome regions in Bacillus subtilis entails major refinement of cognate large-scale metabolic model. *Nucleic Acids Research*, **2013**, 41, 687-99	20.1	62
1164	Comparison of 26 sphingomonad genomes reveals diverse environmental adaptations and biodegradative capabilities. **2013**, 79, 3724-33		115
1163	Identification of a cyclosporine-specific P450 hydroxylase gene through targeted cytochrome P450 complement (CYPome) disruption in Sebekia benihana. **2013**, 79, 2253-62		12
1162	Transcriptome and proteome data reveal candidate genes for pollinator attraction in sexually deceptive orchids. **2013**, 8, e64621		37
1161	Identification of well-differentiated gene expressions between Han Chinese and Japanese using genome-wide microarray data analysis. **2013**, 50, 534-42		4
1160	A scan for human-specific relaxation of negative selection reveals unexpected polymorphism in proteasome genes. **2013**, 30, 1808-15		16
1159	Genome-wide analysis of miRNA signature differentially expressed in doxorubicin-resistant and parental human hepatocellular carcinoma cell lines. **2013**, 8, e54111		26
1158	IQdb: an intelligence quotient score-associated gene resource for human intelligence. **2013**, 2013, bat063		13
1157	Simple topological properties predict functional misannotations in a metabolic network. **2013**, 29, i154-61		13
1156	Complete genome sequence of Bacillus thuringiensis subsp. kurstaki strain HD73. **2013**, 1, e0008013		39
1155	Inactivation of the Pta-AckA pathway causes cell death in Staphylococcus aureus. **2013**, 195, 3035-44		49

1154	Maltose uptake by the novel ABC transport system MusEFGK2I causes increased expression of ptsG in Corynebacterium glutamicum. **2013**, 195, 2573-84	13
1153	A Complex Network of MicroRNAs Expressed in Brain and Genes Associated with Amyotrophic Lateral Sclerosis. **2013**, 2013, 383024	10
1152	Bioinformatics and Gene Network Analyses of the Swine Mammary Gland Transcriptome during Late Gestation. **2013**, 7, 193-216	12
1151	Mountain pine beetles colonizing historical and naive host trees are associated with a bacterial community highly enriched in genes contributing to terpene metabolism. **2013**, 79, 3468-75	166
1150	De Novo Transcriptome Assembly and Differential Gene Expression Profiling of Three Capra hircus Skin Types during Anagen of the Hair Growth Cycle. **2013**, 2013, 269191	10
1149	Tripal v1.1: a standards-based toolkit for construction of online genetic and genomic databases. **2013**, 2013, bat075	41
1148	Global gene expression response of a population exposed to benzene: a pilot study exploring the use of RNA-sequencing technology. **2013**, 54, 566-73	9
1147	In silico cloning and annotation of genes involved in the digestion, detoxification and RNA interference mechanism in the midgut of Bactrocera dorsalis [Hendel (Diptera: Tephritidae)]. **2013**, 22, 354-65	43
1146	Identification of differentially expressed genes in the oviduct of two rabbit lines divergently selected for uterine capacity using suppression subtractive hybridization. **2013**, 44, 296-304	1
1145	Analysis of the genomic response of human prostate cancer cells to histone deacetylase inhibitors. **2013**, 8, 907-20	28
1144	Number variation of high stability regions is correlated with gene functions. **2013**, 5, 484-93	6
1143	WEB-based GEne SeT AnaLysis Toolkit (WebGestalt): update 2013. *Nucleic Acids Research*, **2013**, 41, W77-83 2031	1179
1142	Tumours with elevated levels of the Notch and Wnt pathways exhibit efficacy to PF-03084014, a -secretase inhibitor, in a preclinical colorectal explant model. **2013**, 109, 667-75	30
1141	Metagenomic sequencing reveals microbiota and its functional potential associated with periodontal disease. **2013**, 3, 1843	158
1140	Genome Sequencing of Bacillus subtilis Strain XF-1 with High Efficiency in the Suppression of Plasmodiophora brassicae. **2013**, 1, e0006613	8
1139	Clear cell renal cell carcinoma associated microRNA expression signatures identified by an integrated bioinformatics analysis. **2013**, 11, 169	44
1138	Breeding and Genetics Symposium: networks and pathways to guide genomic selection. **2013**, 91, 537-52	46
1137	Complete genome sequence of Ilumatobacter coccineum YM16-304(T.). **2013**, 8, 430-40	5

1136	Draft Genome Sequence of Amphibacillus jilinensis Y1(T), a Facultatively Anaerobic, Alkaliphilic and Halotolerant Bacterium. **2013**, 8, 491-9	0
1135	The genome sequence of the most widely cultivated cacao type and its use to identify candidate genes regulating pod color. **2013**, 14, r53	157
1134	Complete Genome Sequence of Antarctic Bacterium Psychrobacter sp. Strain G. **2013**, 1,	5
1133	Transcriptomic and proteomic analysis of human hepatic stellate cells treated with natural taurine. **2013**, 7, 1442-52	8
1132	InterMOD: integrated data and tools for the unification of model organism research. **2013**, 3, 1802	23
1131	Gaussian graphical model for identifying significantly responsive regulatory networks from time course high-throughput data. **2013**, 7, 143-52	14
1130	Sequencing and de novo assembly of the western tarnished plant bug (Lygus hesperus) transcriptome. **2013**, 8, e55105	44
1129	Post-embryonic transcriptomes of the prawn Macrobrachium rosenbergii: multigenic succession through metamorphosis. **2013**, 8, e55322	35
1128	Transcriptome analysis of artificial hybrid pufferfish Jiyan-1 and its parental species: implications for pufferfish heterosis. **2013**, 8, e58453	19
1127	Digital gene expression tag profiling analysis of the gene expression patterns regulating the early stage of mouse spermatogenesis. **2013**, 8, e58680	18
1126	Genomic evaluation of Thermoanaerobacter spp. for the construction of designer co-cultures to improve lignocellulosic biofuel production. **2013**, 8, e59362	34
1125	Genome-wide identification of bone metastasis-related microRNAs in lung adenocarcinoma by high-throughput sequencing. **2013**, 8, e61212	23
1124	Biological networks for predicting chemical hepatocarcinogenicity using gene expression data from treated mice and relevance across human and rat species. **2013**, 8, e63308	15
1123	Rapidly evolving genes and stress adaptation of two desert poplars, Populus euphratica and P. pruinosa. **2013**, 8, e66370	29
1122	Boosting probabilistic graphical model inference by incorporating prior knowledge from multiple sources. **2013**, 8, e67410	9
1121	A systems-genetics approach and data mining tool to assist in the discovery of genes underlying complex traits in Oryza sativa. **2013**, 8, e68551	15
1120	Reverse differentiation as a gene filtering tool in genome expression profiling of adipogenesis for fat marker gene selection and their analysis. **2013**, 8, e69754	17
1119	Identification and characterization of long non-coding RNAs related to mouse embryonic brain development from available transcriptomic data. **2013**, 8, e71152	38

1118	Network and data integration for biomarker signature discovery via network smoothed T-statistics. **2013**, 8, e73074	45
1117	Genome-wide analysis of selective constraints on high stability regions of mRNA reveals multiple compensatory mutations in Escherichia coli. **2013**, 8, e73299	2
1116	A metagenomic framework for the study of airborne microbial communities. **2013**, 8, e81862	87
1115	Ecological adaption analysis of the cotton aphid (Aphis gossypii) in different phenotypes by transcriptome comparison. **2013**, 8, e83180	26
1114	Deep sequencing-based analysis of the Cymbidium ensifolium floral transcriptome. **2013**, 8, e85480	54
1113	The Metabolic Interplay between Plants and Phytopathogens. **2013**, 3, 1-23	30
1112	Revisiting Protocols for the NMR Analysis of Bacterial Metabolomes. **2013**, 3, 120-137	35
1111	Transcriptome characterization analysis of Bactrocera minax and new insights into its pupal diapause development with gene expression analysis. **2014**, 10, 1051-63	30
1110	Genome-wide analysis of miRNA signature in the APPswe/PS1E9 mouse model of alzheimer's disease. **2014**, 9, e101725	22
1109	Computational Identification and Systematic Classification of Novel Cytochrome P450 Genes in Salvia miltiorrhiza. **2014**, 9, e115149	41
1108	Comprehensive analysis of alternative splicing in Digitalis purpurea by strand-specific RNA-Seq. **2014**, 9, e106001	12
1107	Functional annotation of rheumatoid arthritis and osteoarthritis associated genes by integrative genome-wide gene expression profiling analysis. **2014**, 9, e85784	17
1106	Characterization of changes in gene expression and biochemical pathways at low levels of benzene exposure. **2014**, 9, e91828	29
1105	Transcriptomic analysis of fiber strength in upland cotton chromosome introgression lines carrying different Gossypium barbadense chromosomal segments. **2014**, 9, e94642	13
1104	Exosomes from drug-resistant breast cancer cells transmit chemoresistance by a horizontal transfer of microRNAs. **2014**, 9, e95240	270
1103	Genome-wide transcriptome profiling revealed cotton fuzz fiber development having a similar molecular model as Arabidopsis trichome. **2014**, 9, e97313	44
1102	Fatty acids from membrane lipids become incorporated into lipid bodies during Myxococcus xanthus differentiation. **2014**, 9, e99622	9
1101	Characterization of transcriptional complexity during adipose tissue development in bovines of different ages and sexes. **2014**, 9, e101261	23

1100	De novo transcriptome of the Hemimetabolous German cockroach (Blattella germanica). **2014**, 9, e106932	18
1099	Identification of differentially expressed genes in breast muscle and skin fat of postnatal Pekin duck. **2014**, 9, e107574	16
1098	De novo transcriptome sequencing analysis and comparison of differentially expressed genes (DEGs) in Macrobrachium rosenbergii in China. **2014**, 9, e109656	12
1097	Genome-scale transcriptome analysis of the alpine "glasshouse" plant Rheum nobile (Polygonaceae) with special translucent bracts. **2014**, 9, e110712	5
1096	Transcriptome-wide profiling and expression analysis of diploid and autotetraploid Paulownia tomentosa □Paulownia fortunei under drought stress. **2014**, 9, e113313	17
1095	Differential expression of granulopoiesis related genes in neutrophil subsets distinguished by membrane expression of CD177. **2014**, 9, e99671	25
1094	Comparison of transcriptional profiles of Clostridium thermocellum grown on cellobiose and pretreated yellow poplar using RNA-Seq. **2014**, 5, 142	35
1093	Bayesian joint selection of genes and pathways: applications in multiple myeloma genomics. **2014**, 13, 113-23	6
1092	Towards the fecal metabolome derived from moderate red wine intake. **2014**, 4, 1101-18	16
1091	Gene expression profiling in winged and wingless cotton aphids, Aphis gossypii (Hemiptera: Aphididae). **2014**, 10, 257-67	27
1090	The Family Succinivibrionaceae. **2014**, 639-648	9
1089	Predicting Phenotype from Genotype Through Reconstruction and Integrative Modeling of Metabolic and Regulatory Networks. **2014**, 307-325	1
1088	Genome sequence of Brevibacillus agri strain 5-2, isolated from the formation water of petroleum reservoir. **2014**, 18 Pt B, 123-5	3
1087	Permanent draft genome sequence of Geobacillus thermocatenulatus strain GS-1. **2014**, 18PB, 129-131	7
1086	NMDB: NETWORK MOTIF DATABASE ENVISAGED AND EXPLICATED FROM HUMAN DISEASE SPECIFIC PATHWAYS. **2014**, 22, 89-100	3
1085	Permanent draft genome sequence of Bacillus flexus strain T6186-2, a multidrug-resistant bacterium isolated from a deep-subsurface oil reservoir. **2014**, 18 Pt B, 135-7	10
1084	Development of bio-based fine chemical production through synthetic bioengineering. **2014**, 13, 173	33
1083	Integrated analysis of miRNA and mRNA expression profiles in response to Cd exposure in rice seedlings. **2014**, 15, 835	62

1082	Endocrine regulation of predator-induced phenotypic plasticity. **2014**, 176, 625-35		14
1081	A transcriptomic analysis of Chrysanthemum nankingense provides insights into the basis of low temperature tolerance. **2014**, 15, 844		53
1080	Profiling and comparison of color body wall transcriptome of normal juvenile sea cucumber (Apostichopus japonicus) and those produced by crossing albino. **2014**, 13, 1033-1042		7
1079	De novo characterization of the Rehmannia glutinosa leaf transcriptome and analysis of gene expression associated with replanting disease. **2014**, 34, 905-915		14
1078	FOAM (Functional Ontology Assignments for Metagenomes): a Hidden Markov Model (HMM) database with environmental focus. *Nucleic Acids Research*, **2014**, 42, e145	20.1	66
1077	Cotton fiber elongation network revealed by expression profiling of longer fiber lines introgressed with different Gossypium barbadense chromosome segments. **2014**, 15, 838		24
1076	Transcriptomic analysis of developmental features of Bombyx mori wing disc during metamorphosis. **2014**, 15, 820		45
1075	Impact of fire on active layer and permafrost microbial communities and metagenomes in an upland Alaskan boreal forest. **2014**, 8, 1904-19		106
1074	Two residues predominantly dictate functional difference in motility between Shewanella oneidensis flagellins FlaA and FlaB. **2014**, 289, 14547-59		18
1073	Potential of fecal microbiota for early-stage detection of colorectal cancer. **2014**, 10, 766		575
1072	Disease-Gene Association Using a Genetic Algorithm. **2014**,		2
1071	Comparative genome-scale reconstruction of gapless metabolic networks for present and ancestral species. **2014**, 10, e1003465		59
1070	MicroRNA regulation of bovine monocyte inflammatory and metabolic networks in an in vivo infection model. **2014**, 4, 957-71		32
1069	Gene expression profiling in adipose tissue from growing broiler chickens. **2014**, 3, 297-303		3
1068	Draft Genome Sequences of Two Clinical Isolates of Streptococcus mutans. **2014**, 2,		1
1067	Gene expression profiling of biological pathway alterations by radiation exposure. **2014**, 2014, 834087		12
1066	Characterizing protein interactions employing a genome-wide siRNA cellular phenotyping screen. **2014**, 10, e1003814		7
1065	Pathway thermodynamics highlights kinetic obstacles in central metabolism. **2014**, 10, e1003483		165

1064	Revealing molecular mechanisms by integrating high-dimensional functional screens with protein interaction data. **2014**, 10, e1003801	2
1063	Molecular evidence for the inverse comorbidity between central nervous system disorders and cancers detected by transcriptomic meta-analyses. **2014**, 10, e1004173	116
1062	The evolution of fungal metabolic pathways. **2014**, 10, e1004816	121
1061	Prenatal exposure to arsenic and cadmium impacts infectious disease-related genes within the glucocorticoid receptor signal transduction pathway. **2014**, 15, 22374-91	25
1060	Draft Genome Sequence of Streptomyces sp. Strain PRh5, a Novel Endophytic Actinomycete Isolated from Dongxiang Wild Rice Root. **2014**, 2,	4
1059	Draft Genome Sequence of Nafulsella turpanensis ZLM-10T, a Novel Member of the Family Flammeovirgaceae. **2014**, 2,	1
1058	Draft Genome Sequence of Bacillus thuringiensis Strain LM1212, Isolated from the Cadaver of an Oryctes gigas Larva in Madagascar. **2014**, 2,	3
1057	Draft Genome Sequence of ´Polaromonas glacialis Strain R3-9, a Psychrotolerant Bacterium Isolated from Arctic Glacial Foreland. **2014**, 2,	4
1056	Draft Genome Sequence of the Novel Exopolysaccharide-Producing Bacterium Altibacter lentus Strain JLT2010T, Isolated from Deep Seawater of the South China Sea. **2014**, 2,	2
1055	Draft Genome Sequence of Pseudomonas nitroreducens Strain TX1, Which Degrades Nonionic Surfactants and Estrogen-Like Alkylphenols. **2014**, 2,	10
1054	Draft Genome Sequence of a Xylanase-Producing Bacterial Strain, Cellvibrio mixtus J3-8. **2014**, 2,	2
1053	BeMADS1 is a key to delivery MADSs into nucleus in reproductive tissues-De novo characterization of Bambusa edulis transcriptome and study of MADS genes in bamboo floral development. **2014**, 14, 179	27
1052	Genome sequencing of four Aureobasidium pullulans varieties: biotechnological potential, stress tolerance, and description of new species. **2014**, 15, 549	193
1051	Basics of mass spectrometry based metabolomics. **2014**, 14, 2369-88	63
1050	Draft Genome Sequence of Bacillus thuringiensis NBIN-866 with High Nematocidal Activity. **2014**, 2,	3
1049	Genome-wide identification and expression analyses of cytochrome P450 genes in mulberry (Morus notabilis). **2014**, 56, 887-901	25
1048	Biosynthetic origin of the antibiotic cyclocarbamate brabantamide A (SB-253514) in plant-associated Pseudomonas. **2014**, 15, 259-66	39
1047	An alternative, arginase-independent pathway for arginine metabolism in Kluyveromyces lactis involves guanidinobutyrase as a key enzyme. **2014**, 93, 369-89	14

1046	Engineering microorganisms based on molecular evolutionary analysis: a succinate production case study. **2014**, 7, 913-20		4
1045	Encyclopedia of Metagenomics. **2014**, 1-7		2
1044	Transcription of angiogenin and ribonuclease 4 is regulated by RNA polymerase III elements and a CCCTC binding factor (CTCF)-dependent intragenic chromatin loop. **2014**, 289, 12520-34		20
1043	Identification of Wolbachia-responsive microRNAs in the two-spotted spider mite, Tetranychus urticae. **2014**, 15, 1122		15
1042	Deciphering the genetic basis of microcystin tolerance. **2014**, 15, 776		34
1041	Differential expression of endogenous plant cell wall degrading enzyme genes in the stick insect (Phasmatodea) midgut. **2014**, 15, 917		27
1040	Specific-detection of clinical samples, systematic functional investigations, and transcriptome analysis reveals that splice variant MUC4/Y contributes to the malignant progression of pancreatic cancer by triggering malignancy-related positive feedback loops signaling. **2014**, 12, 309		7
1039	Gene expression in the skin of dogs sensitized to the house dust mite Dermatophagoides farinae. **2014**, 4, 1787-95		16
1038	UniHI 7: an enhanced database for retrieval and interactive analysis of human molecular interaction networks. *Nucleic Acids Research*, **2014**, 42, D408-14	20.1	65
1037	Yarrowia lipolytica as an Oleaginous Cell Factory Platform for Production of Fatty Acid-Based Biofuel and Bioproducts. **2014**, 2,		79
1036	Systems analysis of high-throughput data. **2014**, 844, 153-87		16
1035	Transcript profiling reveals auxin and cytokinin signaling pathways and transcription regulation during in vitro organogenesis of Ramie (Boehmeria nivea L. Gaud). **2014**, 9, e113768		23
1034	De Novo characterization of a Cephalotaxus hainanensis transcriptome and genes related to paclitaxel biosynthesis. **2014**, 9, e106900		15
1033	Genome Sequencing of a Mung Bean Plant Growth Promoting Strain of P. aeruginosa with Biocontrol Ability. **2014**, 2014, 123058		11
1032	Metabolic network prediction through pairwise rational kernels. **2014**, 15, 318		4
1031	Novel cardiovascular gene functions revealed via systematic phenotype prediction in zebrafish. **2014**, 141, 224-35		19
1030	Gene network inference by probabilistic scoring of relationships from a factorized model of interactions. **2014**, 30, i246-i254		3
1029	In silico predicted structural and functional robustness of piscine steroidogenesis. **2014**, 345, 99-108		1

1028	Identification of differentially expressed genes in hepatopancreas of oriental river prawn, Macrobrachium nipponense exposed to environmental hypoxia. **2014**, 534, 298-306	53
1027	Molecular deconstruction, detection, and computational prediction of microenvironment-modulated cellular responses to cancer therapeutics. **2014**, 69-70, 123-31	10
1026	Metabolic model reconstruction and analysis of an artificial microbial ecosystem for vitamin C production. **2014**, 182-183, 61-7	25
1025	The transcriptomic response to copper exposure by the gill tissue of Japanese scallops (Mizuhopecten yessoensis) using deep-sequencing technology. **2014**, 38, 287-93	26
1024	Predictive genomic and metabolomic analysis for the standardization of enzyme data. **2014**, 1, 24-32	5
1023	Complete genome of a new Firmicutes species belonging to the dominant human colonic microbiota ('Ruminococcus bicirculans') reveals two chromosomes and a selective capacity to utilize plant glucans. **2014**, 16, 2879-90	40
1022	Engineering of Corynebacterium glutamicum for growth and L-lysine and lycopene production from N-acetyl-glucosamine. **2014**, 98, 5633-43	50
1021	Comparative transcriptome profiles of the WRKY gene family under control, hormone-treated, and drought conditions in near-isogenic rice lines reveal differential, tissue specific gene activation. **2014**, 171, 2-13	15
1020	Evolution of tryptophan biosynthetic pathway in microbial genomes: a comparative genetic study. **2014**, 8, 59-72	12
1019	Anatomy and transcript profiling of gynoecium development in female sterile Brassica napus mediated by one alien chromosome from Orychophragmus violaceus. **2014**, 15, 61	12
1018	Transcription profiling using RNA-Seq demonstrates expression differences in the body walls of juvenile albino and normal sea cucumbers Apostichopus japonicus. **2014**, 32, 34-46	11
1017	Characterization of mango (Mangifera indica L.) transcriptome and chloroplast genome. **2014**, 85, 193-208	38
1016	The BRANCHING ENZYME1 gene, encoding a glycoside hydrolase family 13 protein, is required for in vitro plant regeneration in Arabidopsis. **2014**, 117, 279-291	7
1015	Histone methylation mediates plasticity of human FOXP3(+) regulatory T cells by modulating signature gene expressions. **2014**, 141, 362-76	12
1014	Impact of gestational chronodisruption on fetal cardiac genomics. **2014**, 66, 1-11	19
1013	Transcriptional data mining of Salvia miltiorrhiza in response to methyl jasmonate to examine the mechanism of bioactive compound biosynthesis and regulation. **2014**, 152, 241-55	67
1012	Genomic features of a bumble bee symbiont reflect its host environment. **2014**, 80, 3793-803	22
1011	Microarray analysis of differentially expressed genes engaged in fruit development between table and wine grape. **2014**, 41, 4397-412	1

1010	A systematic analysis of predicted MiR-31-targets identifies a diagnostic and prognostic signature for lung cancer. **2014**, 68, 419-27		17
1009	Bioinformatics analysis of time-series genes profiling to explore key genes affected by age in fracture healing. **2014**, 41, 3881-9		5
1008	Nitrite-induced hepatotoxicity in Bluntsnout bream (Megalobrama amblycephala): the mechanistic insight from transcriptome to physiology analysis. **2014**, 37, 55-65		31
1007	Genomic adaptations of the halophilic Dead Sea filamentous fungus Eurotium rubrum. **2014**, 5, 3745		45
1006	Database resources of the National Center for Biotechnology Information. *Nucleic Acids Research*, **2014**, 42, D7-17	20.1	313
1005	Thermoanaerobacter thermohydrosulfuricus WC1 shows protein complement stability during fermentation of key lignocellulose-derived substrates. **2014**, 80, 1602-15		22
1004	De novo transcriptome analysis of Liriodendron chinense petals and leaves by Illumina sequencing. **2014**, 534, 155-62		50
1003	Introduction to opportunities and pitfalls in functional mass spectrometry based proteomics. **2014**, 1844, 12-20		24
1002	Retropath: automated pipeline for embedded metabolic circuits. **2014**, 3, 565-77		62
1001	Pathway analysis for drug repositioning based on public database mining. **2014**, 54, 407-18		34
1000	Rhizosphere microbiome assemblage is affected by plant development. **2014**, 8, 790-803		707
999	Transcriptome analysis of the Ophiocordyceps sinensis fruiting body reveals putative genes involved in fruiting body development and cordycepin biosynthesis. **2014**, 103, 154-9		56
998	Growth and preparation of Staphylococcus epidermidis for NMR metabolomic analysis. **2014**, 1106, 71-91		5
997	Encyclopedia of Metagenomics. **2014**, 1-15		4
996	Identification of Cdca7 as a novel Notch transcriptional target involved in hematopoietic stem cell emergence. **2014**, 211, 2411-23		38
995	The gene expression profile of Monochamus alternatus in response to deltamethrin exposure. **2014**, 17, 893-899		2
994	Identification of genes related to the phenotypic variations of a synthesized Paulownia (Paulownia tomentosaPaulownia fortunei) autotetraploid. **2014**, 553, 75-83		5
993	Hypothalamic miR-103 protects from hyperphagic obesity in mice. **2014**, 34, 10659-74		50

992	An in silico toxicogenomics approach for inferring potential diseases associated with maleic acid. **2014**, 223, 38-44	11
991	Ensemble learning prediction of protein-protein interactions using proteins functional annotations. **2014**, 10, 820-30	36
990	Detection of 1,□25-dihydroxyvitamin D-regulated miRNAs in zebrafish by whole transcriptome sequencing. **2014**, 11, 207-18	12
989	Niche and host-associated functional signatures of the root surface microbiome. **2014**, 5, 4950	219
988	Transcriptome profiling of biliary atresia from new born infants by deep sequencing. **2014**, 41, 8063-9	4
987	Global gene expression changes in human peripheral blood after H7N9 infection. **2014**, 551, 255-60	15
986	Characterization of the global transcriptome for cotton (Gossypium hirsutum L.) anther and development of SSR marker. **2014**, 551, 206-13	15
985	Exosomes from docetaxel-resistant breast cancer cells alter chemosensitivity by delivering microRNAs. **2014**, 35, 9649-59	112
984	Large-scale development of EST-SSR markers in sponge gourd via transcriptome sequencing. **2014**, 34, 1903-1915	27
983	Toxicological effect of single contaminants and contaminant mixtures associated with plant ingredients in novel salmon feeds. **2014**, 73, 157-74	39
982	Dissecting the global variation of gene expression for the functional interpretation of transcriptome data. **2014**, 104, 279-86	1
981	Exploring differentially expressed genes in the ovaries of uniparous and multiparous goats using the RNA-Seq (Quantification) method. **2014**, 550, 148-53	22
980	FindPath: a Matlab solution for in silico design of synthetic metabolic pathways. **2014**, 30, 2986-8	16
979	Transcriptomic analysis of floral initiation in litchi (Litchi chinensis Sonn.) based on de novo RNA sequencing. **2014**, 33, 1723-35	34
978	Identification and characterization of microRNAs in the spleen of common carp immune organ. **2014**, 115, 1768-78	28
977	Including network knowledge into Cox regression models for biomarker signature discovery. **2014**, 56, 287-306	9
976	ChIPseek, a web-based analysis tool for ChIP data. **2014**, 15, 539	51
975	Identification of collaborative driver pathways in breast cancer. **2014**, 15, 605	10

974	Genome-wide transcriptome analysis of genes involved in flavonoid biosynthesis between red and white strains of Magnolia sprengeri pamp. **2014**, 15, 706	34
973	Biological pattern and transcriptomic exploration and phylogenetic analysis in the odd floral architecture tree: Helwingia willd. **2014**, 7, 402	1
972	Genetic analysis of lipolytic activities in Thermus thermophilus HB27. **2014**, 191, 150-7	11
971	Metabolic characteristics of a glycogen-accumulating organism in Defluviicoccus cluster II revealed by comparative genomics. **2014**, 68, 716-28	13
970	Comparative transcriptomic analysis of the heat stress response in the filamentous fungus Metarhizium anisopliae using RNA-Seq. **2014**, 98, 5589-97	37
969	A novel regio-specific cyclosporin hydroxylase gene revealed through the genome mining of Pseudonocardia autotrophica. **2014**, 41, 879-86	3
968	Metaproteomic characterization of dissolved organic matter in coastal seawater. **2014**, 70, 105-113	4
967	Deep-sequencing transcriptome analysis of low temperature perception in a desert tree, Populus euphratica. **2014**, 15, 326	44
966	Identification and characterization of microRNAs in the ovaries of multiple and uniparous goats (Capra hircus) during follicular phase. **2014**, 15, 339	43
965	Comparative transcriptome analysis of eggplant (Solanum melongena L.) and turkey berry (Solanum torvum Sw.): phylogenomics and disease resistance analysis. **2014**, 15, 412	42
964	Mining biomass-degrading genes through Illumina-based de novo sequencing and metagenomic analysis of free-living bacteria in the gut of the lower termite Coptotermes gestroi harvested in Vietnam. **2014**, 118, 665-71	47
963	Comprehensive foodomics study on the mechanisms operating at various molecular levels in cancer cells in response to individual rosemary polyphenols. **2014**, 86, 9807-15	48
962	Metabolomics analysis identifies d-Alanine-d-Alanine ligase as the primary lethal target of d-Cycloserine in mycobacteria. **2014**, 13, 1065-76	52
961	Metaproteogenomic analysis of a sulfate-reducing enrichment culture reveals genomic organization of key enzymes in the m-xylene degradation pathway and metabolic activity of proteobacteria. **2014**, 37, 488-501	26
960	BRIC-seq: a genome-wide approach for determining RNA stability in mammalian cells. **2014**, 67, 55-63	52
959	Building and exploring an integrated human kinase network: global organization and medical entry points. **2014**, 107, 113-27	14
958	De novo analysis of the Nilaparvata lugens (St□) antenna transcriptome and expression patterns of olfactory genes. **2014**, 9, 31-9	43
957	Rapidly expanding knowledge on the role of the gut microbiome in health and disease. **2014**, 1842, 1981-1992	110

956	Analysis of chemosensory gene families in the beetle Monochamus alternatus and its parasitoid Dastarcus helophoroides. **2014**, 11, 1-8	36
955	Comparative analysis of microRNAs from the lungs and trachea of dogs (Canis familiaris) infected with canine influenza virus. **2014**, 21, 367-74	14
954	Transcriptome and gene expression analysis during flower blooming in Rosa chinensis 'Pallida'. **2014**, 540, 96-103	26
953	Enhanced translocation and growth of Rhodococcus erythropolis PR4 in the alkane phase of aqueous-alkane two phase cultures were mediated by GroEL2 overexpression. **2014**, 29, 346-52	12
952	Genome-wide analysis of salt-responsive and novel microRNAs in Populus euphratica by deep sequencing. **2014**, 15 Suppl 1, S6	32
951	Draft genome sequence of Dyadobacter tibetensis type strain (Y620-1) isolated from glacial ice. **2014**, 9, 883-92	3
950	Deep sequencing of the microRNA expression in fall dormant and non-dormant alfalfa. **2014**, 2, 305-7	0
949	Draft Genome Sequence of Vibrio fortis Dalian14 Isolated from Diseased Sea Urchin (Strongylocentrotus intermedius). **2014**, 2,	5
948	Whole transcriptome analysis of the poultry red mite Dermanyssus gallinae (De Geer, 1778). **2014**, 141, 336-46	32
947	An ENA ATPase, MaENA1, of Metarhizium acridum influences the Na(+)-, thermo- and UV-tolerances of conidia and is involved in multiple mechanisms of stress tolerance. **2015**, 83, 68-77	8
946	A systems biology strategy to identify molecular mechanisms of action and protein indicators of traumatic brain injury. **2015**, 93, 199-214	10
945	Systems biology of host-microbe metabolomics. **2015**, 7, 195-219	64
944	Systematic functional genomics resource and annotation for poplar. **2015**, 9, 164-71	
943	dbEMT: an epithelial-mesenchymal transition associated gene resource. **2015**, 5, 11459	85
942	Microbial metabolic networks in a complex electrogenic biofilm recovered from a stimulus-induced metatranscriptomics approach. **2015**, 5, 14840	37
941	Module organization and variance in protein-protein interaction networks. **2015**, 5, 9386	25
940	Transcriptome analysis identifies genes involved in adventitious branches formation of Gracilaria lichenoides in vitro. **2015**, 5, 17099	17
939	An evidence-based knowledgebase of metastasis suppressors to identify key pathways relevant to cancer metastasis. **2015**, 5, 15478	15

938	Identification of differentially expressed genes related to aphid resistance in cucumber (Cucumis sativus L.). **2015**, 5, 9645	19
937	Characterization of the Transcriptional Complexity of the Receptive and Pre-receptive Endometria of Dairy Goats. **2015**, 5, 14244	24
936	Transcriptome analysis of genes involved in defence response in Polyporus umbellatus with Armillaria mellea infection. **2015**, 5, 16075	31
935	Identification, characterization and molecular analysis of the viable but nonculturable Rhodococcus biphenylivorans. **2015**, 5, 18590	55
934	Transcriptome analysis of human OXR1 depleted cells reveals its role in regulating the p53 signaling pathway. **2015**, 5, 17409	36
933	LegumeIP: An Integrative Platform for Comparative Genomics and Transcriptomics of Model Legumes. **2015**, 807-816	2
932	RNAi knockdown of acetyl-CoA carboxylase gene eliminates jinggangmycin-enhanced reproduction and population growth in the brown planthopper, Nilaparvata lugens. **2015**, 5, 15360	11
931	PathwayMatrix: visualizing binary relationships between proteins in biological pathways. **2015**, 9, S3	9
930	Complete genome sequence of the chromate-reducing bacterium Thermoanaerobacter thermohydrosulfuricus strain BSB-33. **2015**, 10, 74	11
929	Marine Microalgae: Exploring the Systems through an Omics Approach for Biofuel Production. **2015** , 168-181	1
928	Draft-genome sequence of Shewanella algae strain C6G3. **2015**, 10, 43	6
927	The pan-genome of Lactobacillus reuteri strains originating from the pig gastrointestinal tract. **2015**, 16, 1023	28
926	Nuclear-localized AtHSPR links abscisic acid-dependent salt tolerance and antioxidant defense in Arabidopsis. **2015**, 84, 1274-94	29
925	High quality genome sequence and description of Enterobacter mori strain 5-4, isolated from a mixture of formation water and crude-oil. **2015**, 10, 9	5
924	RNA-Seq in Mytilus galloprovincialis: comparative transcriptomics and expression profiles among different tissues. **2015**, 16, 728	70
923	Genome-wide expression profiling of microRNAs in poplar upon infection with the foliar rust fungus Melampsora larici-populina. **2015**, 16, 696	23
922	Large-scale identification of wheat genes resistant to cereal cyst nematode Heterodera avenae using comparative transcriptomic analysis. **2015**, 16, 801	29
921	RNA-seq reveals differentially expressed genes of rice (Oryza sativa) spikelet in response to temperature interacting with nitrogen at meiosis stage. **2015**, 16, 959	21

920	Comparative transcriptome analysis of lufenuron-resistant and susceptible strains of Spodoptera frugiperda (Lepidoptera: Noctuidae). **2015**, 16, 985	35
919	A transcriptomic analysis of bermudagrass (Cynodon dactylon) provides novel insights into the basis of low temperature tolerance. **2015**, 15, 216	33
918	Differential sialotranscriptomes of unfed and fed Rhipicephalus haemaphysaloides, with particular regard to differentially expressed genes of cysteine proteases. **2015**, 8, 597	25
917	Transcriptomic analysis of the host response to an iridovirus infection in Chinese giant salamander, Andrias davidianus. **2015**, 46, 136	24
916	Complete genome sequencing of Dehalococcoides sp. strain UCH007 using a differential reads picking method. **2015**, 10, 102	12
915	Draft genome sequence of Halopiger salifodinae KCY07-B2(T), an extremly halophilic archaeon isolated from a salt mine. **2015**, 10, 124	2
914	Colorectal cancer drug target prediction using ontology-based inference and network analysis. **2015**, 2015,	15
913	Global transcriptional profiling of longissimus thoracis muscle tissue in fetal and juvenile domestic goat using RNA sequencing. **2015**, 46, 655-65	10
912	Differential mRNA expression profiling of oral squamous cell carcinoma by high-throughput RNA sequencing. **2015**, 29,	9
911	Companion cropping with potato onion enhances the disease resistance of tomato against Verticillium dahliae. **2015**, 6, 726	20
910	Comparative Analysis of the Brassica napus Root and Leaf Transcript Profiling in Response to Drought Stress. **2015**, 16, 18752-77	31
909	Digital Gene Expression Analysis to Screen Disease Resistance-Relevant Genes from Leaves of Herbaceous Peony (Paeonia lactiflora Pall.) Infected by Botrytis cinerea. **2015**, 10, e0133305	10
908	Transcriptomic Response to Nitric Oxide Treatment in Larix olgensis Henry. **2015**, 16, 28582-97	20
907	Reconstructing genome-wide protein-protein interaction networks using multiple strategies with homologous mapping. **2015**, 10, e0116347	6
906	Comparison of the transcriptomes of mouse skin derived precursors (SKPs) and SKP-derived fibroblasts (SFBs) by RNA-Seq. **2015**, 10, e0117739	10
905	Differential gene expression in ovaries of Qira black sheep and Hetian sheep using RNA-Seq technique. **2015**, 10, e0120170	38
904	Comparative transcriptome profiling of the early infection of wheat roots by Gaeumannomyces graminis var. tritici. **2015**, 10, e0120691	17
903	Transcriptome Analysis Comparison of Lipid Biosynthesis in the Leaves and Developing Seeds of Brassica napus. **2015**, 10, e0126250	17

902	APOE Stabilization by Exercise Prevents Aging Neurovascular Dysfunction and Complement Induction. **2015**, 13, e1002279	66
901	HEPNet: A Knowledge Base Model of Human Energy Pool Network for Predicting the Energy Availability Status of an Individual. **2015**, 10, e0127918	1
900	High-Throughput Sequencing Identifies Novel and Conserved Cucumber (Cucumis sativus L.) microRNAs in Response to Cucumber Green Mottle Mosaic Virus Infection. **2015**, 10, e0129002	20
899	Exploring Differentially Expressed Genes and Natural Antisense Transcripts in Sheep (Ovis aries) Skin with Different Wool Fiber Diameters by Digital Gene Expression Profiling. **2015**, 10, e0129249	13
898	In-Depth Transcriptome Sequencing of Mexican Lime Trees Infected with Candidatus Phytoplasma aurantifolia. **2015**, 10, e0130425	31
897	Transcriptome Analysis of Beta macrocarpa and Identification of Differentially Expressed Transcripts in Response to Beet Necrotic Yellow Vein Virus Infection. **2015**, 10, e0132277	10
896	De Novo Assembly and Annotation of the Chinese Chive (Allium tuberosum Rottler ex Spr.) Transcriptome Using the Illumina Platform. **2015**, 10, e0133312	19
895	Characterization of the Transcriptome of the Xerophyte Ammopiptanthus mongolicus Leaves under Drought Stress by 454 Pyrosequencing. **2015**, 10, e0136495	4
894	Differential microRNA Analysis of Glandular Trichomes and Young Leaves in Xanthium strumarium L. Reveals Their Putative Roles in Regulating Terpenoid Biosynthesis. **2015**, 10, e0139002	40
893	Transcriptomic Analysis of Ovaries from Pigs with High And Low Litter Size. **2015**, 10, e0139514	36
892	Reproductive Hormone and Transcriptomic Responses of Pituitary Tissue in Anestrus Gilts Induced by Nutrient Restriction. **2015**, 10, e0143219	5
891	Transcriptome Analysis of Short Fiber Mutant Ligon lintless-1 (Li1) Reveals Critical Genes and Key Pathways in Cotton Fiber Elongation and Leaf Development. **2015**, 10, e0143503	18
890	Analysis of Pigeon (Columba) Ovary Transcriptomes to Identify Genes Involved in Blue Light Regulation. **2015**, 10, e0143568	6
889	Transcriptomic Analysis and the Expression of Disease-Resistant Genes in Oryza meyeriana under Native Condition. **2015**, 10, e0144518	9
888	Comparative Transcriptome Analysis of the Pacific Oyster Crassostrea gigas Characterized by Shell Colors: Identification of Genetic Bases Potentially Involved in Pigmentation. **2015**, 10, e0145257	60
887	Expression profiling and functional analysis reveals that TOR is a key player in regulating photosynthesis and phytohormone signaling pathways in Arabidopsis. **2015**, 6, 677	100
886	Identification and characterization of miRNAs in ripening fruit of Lycium barbarum L. using high-throughput sequencing. **2015**, 6, 778	22
885	Transcriptome profiling reveals differential gene expression in proanthocyanidin biosynthesis associated with red/green skin color mutant of pear (Pyrus communis L.). **2015**, 6, 795	42

884	De novo Transcriptome Assembly of a Chinese Locoweed (Oxytropis ochrocephala) Species Provides Insights into Genes Associated with Drought, Salinity, and Cold Tolerance. **2015**, 6, 1086		15
883	Comparative Proteomic Analysis of Gossypium thurberi in Response to Verticillium dahliae Inoculation. **2015**, 16, 25121-40		10
882	High-Throughput Sequencing Reveals Diverse Sets of Conserved, Nonconserved, and Species-Specific miRNAs in Jute. **2015**, 2015, 125048		10
881	Identification of Circulating miRNAs in a Mouse Model of Nerve Allograft Transplantation under FK506 Immunosuppression by Illumina Small RNA Deep Sequencing. **2015**, 2015, 863192		2
880	MicroRNAs-mRNAs Expression Profile and Their Potential Role in Malignant Transformation of Human Bronchial Epithelial Cells Induced by Cadmium. **2015**, 2015, 902025		21
879	Periodic Solutions of Some Polynomial Differential Systems in Dimension 3 via Averaging Theory. **2015**, 2015, 1-10		1
878	Predicting Drug-Target Interactions via Within-Score and Between-Score. **2015**, 2015, 350983		15
877	Identifying communities from multiplex biological networks. **2015**, 3, e1525		36
876	Database resources of the National Center for Biotechnology Information. *Nucleic Acids Research*, **2015**, 43, D6-17	20.1	235
875	Small RNA deep sequencing reveals the important role of microRNAs in the halophyte Halostachys caspica. **2015**, 13, 395-408		28
874	Phloem sap proteome studied by iTRAQ provides integrated insight into salinity response mechanisms in cucumber plants. **2015**, 125, 54-67		31
873	Ocean plankton. Structure and function of the global ocean microbiome. **2015**, 348, 1261359		1261
872	Ocean plankton. Environmental characteristics of Agulhas rings affect interocean plankton transport. **2015**, 348, 1261447		100
871	Dynamic transcriptome profiles of skeletal muscle tissue across 11 developmental stages for both Tongcheng and Yorkshire pigs. **2015**, 16, 377		38
870	Meta-omics uncover temporal regulation of pathways across oral microbiome genera during in vitro sugar metabolism. **2015**, 9, 2605-19		48
869	Metabolic dynamics analysis by massive data integration: application to tsunami-affected field soils in Japan. **2015**, 10, 1908-15		14
868	Temporal and technical variability of human gut metagenomes. **2015**, 16, 73		108
867	De novo assembly and characterization of the skeletal muscle transcriptome of sheep using Illumina paired-end sequencing. **2015**, 37, 1747-56		3

866	The transcriptomic response to copper exposure in the digestive gland of Japanese scallops (Mizuhopecten yessoensis). **2015**, 46, 161-7	18
865	Detoxification strategies and regulation of oxygen production and flowering of Platanus acerifolia under lead (Pb) stress by transcriptome analysis. **2015**, 22, 12747-58	9
864	In silico identification of potential transcriptional regulators associated with human MAPK signaling. **2015**,	
863	Potent antitumor activity of cabozantinib, a c-MET and VEGFR2 inhibitor, in a colorectal cancer patient-derived tumor explant model. **2015**, 136, 1967-75	35
862	Scrutinizing the immune defence inventory of Camponotus floridanus applying total transcriptome sequencing. **2015**, 16, 540	27
861	Large-Scale Prediction of Beneficial Drug Combinations Using Drug Efficacy and Target Profiles. **2015**, 55, 2705-16	22
860	Draft Genome Sequence of Staphylococcus gallinarum DSM 20610T, Originally Isolated from the Skin of a Chicken. **2015**, 3,	3
859	Differential expression profiling of the early response to Ustilaginoidea virens between false smut resistant and susceptible rice varieties. **2015**, 16, 955	31
858	High-Throughput Transcriptome Analysis of Plant Stress Responses. **2015**, 195-209	
857	High-throughput transcriptome analysis of barley (Hordeum vulgare) exposed to excessive boron. **2015**, 557, 71-81	48
856	Analysis of the transcriptomic profilings of Mandarin fish (Siniperca chuatsi) infected with Flavobacterium columnare with an emphasis on immune responses. **2015**, 43, 111-9	26
855	Construction of a genome-scale metabolic network of the plant pathogen Pectobacterium carotovorum provides new strategies for bactericide discovery. **2015**, 589, 285-94	15
854	Aggression is associated with aerobic glycolysis in the honey bee brain(1). **2015**, 14, 158-66	45
853	Transcription factors and anthocyanin genes related to low-temperature tolerance in rd29A:RdreB1BI transgenic strawberry. **2015**, 89, 31-43	19
852	Faecal metabolomic fingerprint after moderate consumption of red wine by healthy subjects. **2015**, 14, 897-905	48
851	News in livestock research - use of Omics-technologies to study the microbiota in the gastrointestinal tract of farm animals. **2015**, 13, 55-63	65
850	Analysis of differential gene expression under low-temperature stress in Nile tilapia (Oreochromis niloticus) using digital gene expression. **2015**, 564, 134-40	27
849	Systematic drug repositioning for a wide range of diseases with integrative analyses of phenotypic and molecular data. **2015**, 55, 446-59	51

848	Transcriptome sequencing and comparative analysis of diploid and autotetraploid Paulownia australis. **2015**, 11, 1	2
847	Transcriptome-wide identification of the genes responding to replanting disease in Rehmannia glutinosa L. roots. **2015**, 42, 881-92	17
846	Isofunctional enzymes PAD1 and UbiX catalyze formation of a novel cofactor required by ferulic acid decarboxylase and 4-hydroxy-3-polyprenylbenzoic acid decarboxylase. **2015**, 10, 1137-44	65
845	Genome-scale modeling for metabolic engineering. **2015**, 42, 327-38	71
844	Modelling antibiotic and cytotoxic isoquinoline effects in Staphylococcus aureus, Staphylococcus epidermidis and mammalian cells. **2015**, 305, 96-109	14
843	Transcriptome characterization and SSR discovery in large-scale loach Paramisgurnus dabryanus (Cobitidae, Cypriniformes). **2015**, 557, 201-8	22
842	Transcriptome analysis of eyestalk and hemocytes in the ridgetail white prawn Exopalaemon carinicauda: assembly, annotation and marker discovery. **2015**, 42, 135-47	21
841	Aquatic metagenomes implicate Thaumarchaeota in global cobalamin production. **2015**, 9, 461-71	95
840	Impacts of the Three Gorges Dam on microbial structure and potential function. **2015**, 5, 8605	106
839	ocsESTdb: a database of oil crop seed EST sequences for comparative analysis and investigation of a global metabolic network and oil accumulation metabolism. **2015**, 15, 19	7
838	Pathways associated with lignin biosynthesis in lignomaniac jute fibres. **2015**, 290, 1523-42	33
837	Genome sequence of aerobic anoxygenic phototrophic bacterium Erythrobacter sp. JL475, isolated from the South China Sea. **2015**, 21, 15-6	1
836	Transcriptome sequencing and analysis of the entomopathogenic fungus Hirsutella sinensis isolated from Ophiocordyceps sinensis. **2015**, 16, 106	23
835	Metabolomics of adherent mammalian cells by capillary electrophoresis-mass spectrometry: HT-29 cells as case study. **2015**, 110, 83-92	26
834	Analytical workflow profiling gene expression in murine macrophages. **2015**, 13, 1550010	7
833	Transcriptome analysis of sexually dimorphic Chinese white wax scale insects reveals key differences in developmental programs and transcription factor expression. **2015**, 5, 8141	25
832	Pedican: an online gene resource for pediatric cancers with literature evidence. **2015**, 5, 11435	7
831	Transcriptome-based gene profiling provides novel insights into the characteristics of radish root response to Cr stress with next-generation sequencing. **2015**, 6, 202	45

830	Effects of sorafenib on lung metastasis in rats with hepatocellular carcinoma: the role of microRNAs. **2015**, 36, 8455-63	12
829	Recent advances in elementary flux modes and yield space analysis as useful tools in metabolic network studies. **2015**, 31, 1315-28	2
828	De novo assembly and analysis of tissue-specific transcriptomes revealed the tissue-specific genes and profile of immunity from Strongylocentrotus intermedius. **2015**, 46, 723-36	16
827	Metabolic faecal fingerprinting of trans-resveratrol and quercetin following a high-fat sucrose dietary model using liquid chromatography coupled to high-resolution mass spectrometry. **2015**, 6, 2758-67	20
826	De novo transcriptome of the European brittle star Amphiura filiformis pluteus larvae. **2015**, 23, 109-21	18
825	Global genome and transcriptome analyses of Magnaporthe oryzae epidemic isolate 98-06 uncover novel effectors and pathogenicity-related genes, revealing gene gain and lose dynamics in genome evolution. **2015**, 11, e1004801	96
824	Analysis of antennal transcriptome and odorant binding protein expression profiles of the recently identified parasitoid wasp, Sclerodermus sp. **2015**, 16, 10-9	16
823	Transcriptomic and proteomic analysis of pre-diapause and non-diapause eggs of migratory locust, Locusta migratoria L. (Orthoptera: Acridoidea). **2015**, 5, 11402	48
822	Transcriptional profiling analysis of genic male sterilefertile Capsicum annuum reveal candidate genes for pollen development and maturation by RNA-Seq technology. **2015**, 122, 465-476	14
821	Publisher's Note:Abstraction for data integration:Fusing mammalian molecular, cellular and phenotype big datasets for better knowledge extraction. **2015**, 58, 104-19	2
820	Identification and expression pattern of candidate olfactory genes in Chrysoperla sinica by antennal transcriptome analysis. **2015**, 15, 28-38	14
819	A systematic simulation of the effect of salicylic acid on sphingolipid metabolism. **2015**, 6, 186	12
818	Complete genome sequence of Selenomonas ruminantium subsp. lactilytica will accelerate further understanding of the nature of the class Negativicutes. **2015**, 362,	3
817	Global analysis of transcriptional response of Chinese cabbage to methyl jasmonate reveals JA signaling on enhancement of secondary metabolism pathways. **2015**, 189, 159-167	11
816	Biochemical functional predictions for protein structures of unknown or uncertain function. **2015**, 13, 182-91	58
815	Expression profiling of cadmium response genes in ramie (Boehmeria nivea L.) root. **2015**, 94, 453-9	11
814	Comparative transcriptome analysis of the petal degeneration mutant pdm in Chinese cabbage (Brassica campestris ssp. pekinensis) using RNA-Seq. **2015**, 290, 1833-47	14
813	Whole-genome sequencing of Bacillus subtilis XF-1 reveals mechanisms for biological control and multiple beneficial properties in plants. **2015**, 42, 925-37	27

812	RNA-Seq analysis for transcriptome assembly, gene identification, and SSR mining in ginkgo (Ginkgo biloba L.). **2015**, 11, 1	20
811	Inhibition of Hedgehog signaling pathway impedes cancer cell proliferation by promotion of autophagy. **2015**, 94, 223-33	17
810	Accurate multiple network alignment through context-sensitive random walk. **2015**, 9 Suppl 1, S7	15
809	Transcriptome analysis between invasive Pomacea canaliculata and indigenous Cipangopaludina cahayensis reveals genomic divergence and diagnostic microsatellite/SSR markers. **2015**, 16, 12	11
808	Global gene expression patterns of grass carp following compensatory growth. **2015**, 16, 184	27
807	Transcriptomic analysis of Litchi chinensis pericarp during maturation with a focus on chlorophyll degradation and flavonoid biosynthesis. **2015**, 16, 225	58
806	Comparative analysis of testis transcriptomes from triploid and fertile diploid cyprinid fish. **2015**, 92, 95	24
805	Complete genome sequence of Corynebacterium glutamicum B253, a Chinese lysine-producing strain. **2015**, 207, 10-1	7
804	Boolean network model for GPR142 against Type 2 diabetes and relative dynamic change ratio analysis using systems and biological circuits approach. **2015**, 9, 45-54	18
803	Analysing human metabolic networks using metabolomics: understanding the impact of diet on health. **2015**, 85-114	1
802	Complementing DIGE proteomics and DNA subarray analyses to shed light on Oenococcus oeni adaptation to ethanol in wine-simulated conditions. **2015**, 123, 114-27	25
801	In-depth proteomic analysis of nacre, prism, and myostracum of Mytilus shell. **2015**, 122, 26-40	64
800	Draft Genome Sequence of Microbacterium profundi Shh49T, an Actinobacterium Isolated from Deep-Sea Sediment of a Polymetallic Nodule Environment. **2015**, 3,	14
799	Differential gene expression analysis of early-ripening mutants of grape (Vitis vinifera L.). **2015**, 194, 7-17	1
798	Systematic prediction of health-relevant human-microbial co-metabolism through a computational framework. **2015**, 6, 120-30	76
797	Complete genome sequence of the heavy metal resistant bacterium Altererythrobacter atlanticus 26DY36(T), isolated from deep-sea sediment of the North Atlantic Mid-ocean ridge. **2015**, 24 Pt 3, 289-92	9
796	Phenylpropanoid metabolism, hormone biosynthesis and signal transduction-related genes play crucial roles in the resistance of Paulownia fortunei to paulownia witches-broom phytoplasma infection. **2015**, 37, 913-929	22
795	A microRNAs-mRNAs network involved in the control of graphene oxide toxicity in Caenorhabditis elegans. **2015**, 5, 92394-92405	38

794	Analysis of image-based phenotypic parameters for high throughput gene perturbation assays. **2015**, 58, 192-8	4
793	Integrating Microarray Data and GRNs. **2016**, 1375, 137-53	4
792	Evolutionary computation for disease gene association. **2015**,	1
791	Complete genome sequence of Rufibacter tibetensis strain 1351, a radiation-resistant bacterium from Tibet plateau. **2015**, 216, 125-6	1
790	Transcriptome comparison of the sex pheromone glands from two sibling Helicoverpa species with opposite sex pheromone components. **2015**, 5, 9324	21
789	Transcriptome analysis for identification of indigo biosynthesis pathway genes in Polygonum tinctorium. **2015**, 70, 1026-1032	10
788	Transciptomic and histological analysis of hepatopancreas, muscle and gill tissues of oriental river prawn (Macrobrachium nipponense) in response to chronic hypoxia. **2015**, 16, 491	55
787	Recurrence-associated pathways in hepatitis B virus-positive hepatocellular carcinoma. **2015**, 16, 279	7
786	Generation and analysis of expressed sequence tags (ESTs) of Camelina sativa to mine drought stress-responsive genes. **2015**, 467, 83-93	10
785	Malignant pleural mesothelioma: history, controversy and future of a manmade epidemic. **2015**, 24, 115-31	100
784	Transcriptome sequencing and analysis of rubber tree (Hevea brasiliensis Muell.) to discover putative genes associated with tapping panel dryness (TPD). **2015**, 16, 398	30
783	Reprint of "Abstraction for data integration: Fusing mammalian molecular, cellular and phenotype big datasets for better knowledge extraction". **2015**, 59 Pt B, 123-38	9
782	Digital gene expression analysis of Helicoverpa armigera in the early stage of infection with Helicoverpa armigera nucleopolyhedrovirus. **2015**, 132, 66-76	7
781	Comparative transcriptome analysis of Chrysanthemum nankingense in response to nitrogen deficiency. **2015**, 195, 101-107	8
780	Phylogenomic analysis and predicted physiological role of the proton-translocating NADH:quinone oxidoreductase (complex I) across bacteria. **2015**, 6,	33
779	A systems biology approach for the identification of significantly perturbed genes. **2015**,	4
778	De novo transcriptome analysis of Osmanthus serrulatus Rehd. flowers and leaves by Illumina sequencing. **2015**, 61, 531-540	6
777	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. **2015**, 528, 262-266	1107

776	Target-Based Drug Repositioning Using Large-Scale Chemical-Protein Interactome Data. **2015**, 55, 2717-30	44
775	Bridging miRNAs and pathway analysis in clinical decision support: a case study in nephroblastoma. **2015**, 4, 1	
774	Bacterial Whole-Genome Determination and Applications. **2015**, 357-368	2
773	Identifying cancer-related microRNAs based on gene expression data. **2015**, 31, 1226-34	66
772	RNA-seq based on transcriptome reveals differ genetic expressing in Chlamys farreri exposed to carcinogen PAHs. **2015**, 39, 313-20	19
771	An RNA-Sequencing Study of the Genes and Metabolic Pathways Involved in Aspergillus niger Weathering of Potassium Feldspar. **2015**, 32, 689-700	15
770	Characterizing the proteome and oxi-proteome of apple in response to a host (Penicillium expansum) and a non-host (Penicillium digitatum) pathogen. **2015**, 114, 136-51	21
769	Sinbase: an integrated database to study genomics, genetics and comparative genomics in Sesamum indicum. **2015**, 56, e2	38
768	RNA-Seq-based transcriptome analysis of dormant flower buds of Chinese cherry (Prunus pseudocerasus). **2015**, 555, 362-76	71
767	De novo characterization of the Lycium chinense Mill. leaf transcriptome and analysis of candidate genes involved in carotenoid biosynthesis. **2015**, 555, 458-63	15
766	M-path: a compass for navigating potential metabolic pathways. **2015**, 31, 905-11	25
765	Affinity chromatography revealed insights into unique functionality of two 14-3-3 protein species in developing maize kernels. **2015**, 114, 274-86	14
764	Protein-protein interaction predictions using text mining methods. **2015**, 74, 47-53	53
763	Transcriptome profiling of the UV-B stress response in the desert shrub Lycium ruthenicum. **2015**, 42, 639-49	11
762	Phenotypic plasticity in heterotrophic marine microbial communities in continuous cultures. **2015**, 9, 1141-51	11
761	Differential profiling analysis of miRNAs reveals a regulatory role in low N stress response of Populus. **2015**, 15, 93-105	23
760	Metagenomics for Bacteriology. **2015**, 113-134	1
759	Genetic and metabolic engineering of microorganisms for the development of new flavor compounds from terpenic substrates. **2015**, 35, 313-25	12

758	Myostatin/activin blocking combined with exercise reconditions skeletal muscle expression profile of mdx mice. **2015**, 399, 131-42	18
757	The transcriptional response of prokaryotes to phytoplankton-derived dissolved organic matter in seawater. **2015**, 17, 3466-80	23
756	Identification and validation co-differentially expressed genes with NAFLD and insulin resistance. **2015**, 48, 143-51	8
755	How do hosts react to endosymbionts? A new insight into the molecular mechanisms underlying the Wolbachia-host association. **2015**, 24, 1-12	21
754	Organellar proteome analyses of ricin toxin-treated HeLa cells. **2016**, 32, 1166-78	2
753	Comparative genomics of an endophytic Pseudomonas putida isolated from mango orchard. **2016**, 39, 465-73	8
752	Fungi Contribute Critical but Spatially Varying Roles in Nitrogen and Carbon Cycling in Acid Mine Drainage. **2016**, 7, 238	40
751	A quantitative transcriptomic analysis of the physiological significance of mTOR signaling in goat fetal fibroblasts. **2016**, 17, 879	2
750	Complete Genome Sequence of Pontibacter akesuensis Strain AKS 1T, Which Exhibits Robust Nutrient Metabolism in Harsh Environments. **2016**, 4,	
749	Identification of the Key Genes and Pathways in Esophageal Carcinoma. **2016**, 2016, 2968106	17
748	De Novo Transcriptome Sequencing of Olea europaea L. to Identify Genes Involved in the Development of the Pollen Tube. **2016**, 2016, 4305252	10
747	Pathogenic Network Analysis Predicts Candidate Genes for Cervical Cancer. **2016**, 2016, 3186051	14
746	Differential Gene Expression during Larval Metamorphic Development in the Pearl Oyster, , Based on Transcriptome Analysis. **2016**, 2016, 2895303	7
745	A Systematic Framework for Drug Repositioning from Integrated Omics and Drug Phenotype Profiles Using Pathway-Drug Network. **2016**, 2016, 7147039	24
744	Anesthetic Propofol-Induced Gene Expression Changes in Patients Undergoing Coronary Artery Bypass Graft Surgery Based on Dynamical Differential Coexpression Network Analysis. **2016**, 2016, 7097612	1
743	Innovation for Sustainable Agriculture and Food Production. **2016**,	1
742	Identification of Heat Shock Transcription Factor Genes Involved in Thermotolerance of Octoploid Cultivated Strawberry. **2016**, 17,	13
741	Improved Environmental Genomes via Integration of Metagenomic and Single-Cell Assemblies. **2016**, 7, 143	17

740	Reconstructing the Genetic Potential of the Microbially-Mediated Nitrogen Cycle in a Salt Marsh Ecosystem. **2016**, 7, 902	22
739	Gut Microbiota Profiling: Metabolomics Based Approach to Unravel Compounds Affecting Human Health. **2016**, 7, 1144	195
738	Species Divergence vs. Functional Convergence Characterizes Crude Oil Microbial Community Assembly. **2016**, 7, 1254	18
737	Comparative Transcriptomic Analysis Reveals Novel Insights into the Adaptive Response of to Changing Ambient Phosphorus. **2016**, 7, 1476	22
736	De Novo Transcriptome Assembly in Shiraia bambusicola to Investigate Putative Genes Involved in the Biosynthesis of Hypocrellin A. **2016**, 17, 311	29
735	Genome-Wide Transcriptome Profiling of Mycobacterium smegmatis MC□155 Cultivated in Minimal Media Supplemented with Cholesterol, Androstenedione or Glycerol. **2016**, 17,	9
734	Identification and Functional Analysis of microRNAs Involved in the Anther Development in Cotton Genic Male Sterile Line Yu98-8A. **2016**, 17,	14
733	Table_6.XLSX. **2019**,	
732	Image_1.JPEG. **2020**,	
731	Table_1.DOCX. **2020**,	
730	Table_2.XLS. **2020**,	
729	Table_3.XLSX. **2020**,	
728	Table_4.DOCX. **2020**,	
727	Image_1.jpeg. **2019**,	
726	Image_2.jpeg. **2019**,	
725	Image_3.jpeg. **2019**,	
724	Table_1.xlsx. **2019**,	
723	Table_2.xlsx. **2019**,	

722 Data_Sheet_1.docx. **2019**,

721 Data_Sheet_2.xlsx. **2019**,

720 Table_1.XLSX. **2019**,

719 Table_2.XLSX. **2019**,

718 Data_Sheet_1.docx. **2020**,

717 Image_1.TIF. **2019**,

716 Image_2.TIF. **2019**,

715 Image_3.TIF. **2019**,

714 Image_4.TIF. **2019**,

713 Table_1.xlsx. **2019**,

712 data_sheet_1.xlsx. **2018**,

711 data_sheet_2.xlsx. **2018**,

710 presentation_1.PDF. **2018**,

709 Table_1.docx. **2018**,

708 Table_1.DOCX. **2018**,

707 Image_1.TIF. **2018**,

706 Image_2.TIF. **2018**,

705 Image_3.TIF. **2018**,

704 Image_4.TIF. **2018**,

703 Image_5.TIF. **2018**,

702 Table_1.xlsx. **2018**,

701 Table_2.xlsx. **2018**,

700 Table_3.xlsx. **2018**,

699 Table_4.xlsx. **2018**,

698 Table_1.DOCX. **2019**,

697 Table_2.XLSX. **2019**,

696 Data_Sheet_1.docx. **2019**,

695 Data_Sheet_2.xlsx. **2019**,

694 Image_1.TIF. **2019**,

693 Image_2.TIF. **2019**,

692 Image_3.TIF. **2019**,

691 Table_1.DOCX. **2019**,

690 Table_2.XLSX. **2019**,

689 Presentation_1.PDF. **2018**,

688 Image_1.TIF. **2020**,

687 Image_2.TIF. **2020**,

686 Table_1.XLSX. **2020**,

685 Table_2.XLSX. **2020**,

684 Table_3.xlsx. **2020**,

683 Table_4.xlsx. **2020**,

682 Data_Sheet_1.docx. **2019**,

681 Data_Sheet_1.XLS. **2018**,

680 Data_Sheet_2.XLS. **2018**,

679 Image_1.JPEG. **2018**,

678 Image_2.JPEG. **2018**,

677 Image_3.jpg. **2018**,

676 Table_1.DOCX. **2018**,

675 Table_2.DOCX. **2018**,

674 Data_Sheet_1.zip. **2020**,

673 Data_Sheet_1.docx. **2020**,

672 Image_1.tiff. **2020**,

671 Table_1.XLSX. **2020**,

670 Table_2.XLSX. **2020**,

669 Table_3.XLSX. **2020**,

668 Table_4.XLSX. **2020**,

667 Image_1.TIF. **2020**,

666 Image_2.TIF. **2020**,

665 Table_1.DOCX. **2020**,

664 Table_2.DOCX. **2020**,

663 Table_1.docx. **2019**,

662 Data_Sheet_1.docx. **2020**,

661 Image1.JPEG. **2018**,

660 Image2.JPEG. **2018**,

659 Image3.JPEG. **2018**,

658 Image4.JPEG. **2018**,

657 Image5.JPEG. **2018**,

656 Table1.XLSX. **2018**,

655 Table2.XLSX. **2018**,

654 Table3.XLS. **2018**,

653 Table4.XLSX. **2018**,

652 Table5.XLS. **2018**,

651 Table6.XLSX. **2018**,

650 Table7.XLSX. **2018**,

649 Table_1.docx. **2020**,

648 Table_2.xlsx. **2020**,

647 Table_3.xlsx. **2020**,

646 Table_4.xlsx. **2020**,

645 Data_Sheet_1.docx. **2020**,

644 Data_Sheet_2.doc. **2020**,

643 Image_1.TIF. **2020**,

642 Image_2.TIF. **2020**,

641 Image_3.TIF. **2020**,

640 Image_4.TIF. **2020**,

639 Image_5.TIF. **2020**,

638 Image_1.TIF. **2018**,

637 Table_1.xlsx. **2018**,

636 Table_1.XLSX. **2020**,

635 Image_1.tif. **2020**,

634 Image_2.tif. **2020**,

633 Table_1.docx. **2020**,

632 Table_2.xlsx. **2020**,

631 Table_1.XLSX. **2020**,

630 Image_1.JPEG. **2020**,

629 Image_2.PNG. **2020**,

628 Image_3.PNG. **2020**,

627 Image_4.PNG. **2020**,

626 Image_5.PNG. **2020**,

625 Image_6.PNG. **2020**,

624 Image_7.PNG. **2020**,

623 Table_1.docx. **2020**,

622 Table_2.docx. **2020**,

621 Table_3.docx. **2020**,

620 Table_4.docx. **2020**,

619 Table_5.docx. **2020**,

618 Image_1.tif. **2018**,

617 Image_2.TIF. **2018**,

616 Image_3.PDF. **2018**,

615 Image_4.TIF. **2018**,

614 Table_1.DOCX. **2018**,

613 Table_2.XLSX. **2018**,

612 Table_3.DOCX. **2018**,

611 Table_4.XLSX. **2018**,

610 Table_5.XLSX. **2018**,

609 Table_6.XLSX. **2018**,

608 Table_7.xlsx. **2018**,

607 Table_1.XLS. **2019**,

606 Data_Sheet_1.XLSX. **2018**,

605 Data_Sheet_2.XLSX. **2018**,

604 Image_1.JPEG. **2018**,

603 Table_1.DOCX. **2018**,

602 Table_2.DOCX. **2018**,

601 Table_3.DOCX. **2018**,

600 Table_4.DOCX. **2018**,

599 Table_5.DOCX. **2018**,

598 Table_6.DOCX. **2018**,

597 Presentation1.pdf. **2018**,

596 Table1.XLS. **2018**,

595 Table10.DOC. **2018**,

594 Table2.XLS. **2018**,

593 Table3.XLS. **2018**,

592 Table4.XLS. **2018**,

591 Table5.XLS. **2018**,

590 Table6.XLS. **2018**,

589 Table7.XLS. **2018**,

588 Table8.DOC. **2018**,

587 Table9.DOC. **2018**,

586 Image_1.PNG. **2018**,

585 Image_2.pdf. **2018**,

584 Image_3.pdf. **2018**,

583 Image_4.jpeg. **2018**,

582 Table_1.DOCX. **2018**,

581 Table_2.XLSX. **2018**,

580 Table_3.XLSX. **2018**,

579 Table_4.DOCX. **2018**,

578 DataSheet_1.pdf. **2020**,

577 DataSheet_2.xlsx. **2020**,

576 Table_1.XLSX. **2018**,

575 Table_2.XLSX. **2018**,

574 Table_3.XLSX. **2018**,

573 Table_4.XLSX. **2018**,

572 Table_5.XLSX. **2018**,

571 Table_1.docx. **2019**,

570 Table_2.docx. **2019**,

569 Table_3.docx. **2019**,

568 Data_Sheet_1.PDF. **2020**,

567 Table_1.XLSX. **2020**,

566 DataSheet_1.zip. **2019**,

565 DataSheet_1.zip. **2019**,

564 Data_Sheet_1.xls. **2018**,

563 Data_Sheet_2.xls. **2018**,

562 Data_Sheet_3.xls. **2018**,

561 Data_Sheet_4.xlsx. **2018**,

560 Presentation_1.pdf. **2018**,

559 Table_1.docx. **2019**,

558 Table_2.docx. **2019**,

557 Table_3.docx. **2019**,

556 Table_4.docx. **2019**,

555 DataSheet_1.zip. **2020**,

554 Image_1.JPEG. **2019**,

553 Image_2.JPEG. **2019**,

552 Table_1.docx. **2019**,

551 Table_2.docx. **2019**,

550 Table_3.docx. **2019**,

549 Table_4.docx. **2019**,

548 Table_5.XLS. **2019**,

547 Table_6.XLS. **2019**,

546 Image_1.JPEG. **2019**,

545 Image_2.JPEG. **2019**,

544 Table_1.docx. **2019**,

543 Table_2.xls. **2019**,

542	Table_1.DOCX. **2020**,	
541	Table_1.doc. **2019**,	
540	Data_Sheet_1.pdf. **2018**,	
539	Data_Sheet_1.docx. **2020**,	
538	Table_1.DOCX. **2020**,	
537	Table_1.XLS. **2020**,	
536	Table_2.docx. **2020**,	
535	Table_3.xls. **2020**,	
534	Table_4.xls. **2020**,	
533	Table_5.xls. **2020**,	
532	Table_6.xls. **2020**,	
531	Transcriptome analysis of fasudil treatment in the APPswe/PSEN1dE9 transgenic (APP/PS1) mice model of Alzheimer's disease.. **2022**, 12, 6625	0
530	SARS-COV-2 as potential microRNA sponge in COVID-19 patients.. **2022**, 15, 94	3
529	Potential Clinical Value of Biomarker-Guided Emergency Triage for Thoracic Aortic Dissection.. **2021**, 8, 777327	0
528	RNA methylation-mediated LINC01559 suppresses colorectal cancer progression by regulating the miR-106b-5p/PTEN axis.. **2022**, 18, 3048-3065	1
527	Screening and identification of key microRNAs and regulatory pathways associated with the renal fibrosis process.. **2022**,	
526	Identification and functional prediction of long non-coding RNAs related to skeletal muscle development in Duroc pigs.. **2022**,	
525	Transcriptomic and Metabolomic Analyses Reveal a Potential Mechanism to Improve Soybean Resistance to Anthracnose.. **2022**, 13, 850829	0

524	Comparative Transcriptome Analysis of Ts (Resistant genotype) and Ma (Susceptible genotype) Marigold (Tagetes erecta L.) Leaves in Response to Alternaria tagetica. **2022**,	
523	Construction of two regulatory networks related to salt stress and lignocellulosic synthesis under salt stress based on a Populus davidiana P. bolleana transcriptome analysis.. **2022**,	1
522	Alleviation of Tris(2-chloroethyl) Phosphate Toxicity on the Marine Rotifer by Polystyrene Microplastics: Features and Molecular Evidence.. **2022**, 23,	0
521	Cell type-specific response of colon cancer tumor cell lines to oncolytic HSV-1 virotherapy in hypoxia.. **2022**, 22, 164	0
520	Circulating cell-free mtDNA release is associated with the activation of cGAS-STING pathway and inflammation in mitochondrial diseases.. **2022**, 1	0
519	Integrative Analysis of lncRNA-miRNA-mRNA Regulatory Network Reveals the Key lncRNAs Implicated Potentially in the Differentiation of Adipocyte in Goats. **2022**, 13,	0
518	Whole-Transcriptome Analysis Reveals Long Noncoding RNAs Involved in Female Floral Development of Hickory (Carya cathayensis Sarg.). **2022**, 13,	0
517	CO-WT DTI: Chronological Order based Wrapper Technique for Drug-Target Interaction Prediction. **2022**, 17,	0
516	Genome-Wide Characterization of the Methyl CpG Binding Domain-Containing Proteins in Watermelon and Functional Analysis of Their Roles in Disease Resistance Through Ectopic Overexpression in Arabidopsis thaliana. **2022**, 13,	0
515	Temporal Expression Profiles Reveal Potential Targets during Postembryonic Development of Forensically Important Sarcophaga peregrina (Diptera: Sarcophagidae). **2022**, 13, 453	1
514	Exploring Key Genes and Mechanisms in Respiratory Syncytial Virus-Infected BALB/c Mice Multi-Organ Expression Profiles.. **2022**, 12, 858305	
513	Generalist endophyte Phomopsis liquidambaris colonization of Oryza sativa L. promotes plant growth under nitrogen starvation.. **2022**,	0
512	Multi-staged gene expression profiling reveals potential genes and the critical pathways in kidney cancer.. **2022**, 12, 7240	0
511	miR-375 Induced the Formation and Transgenerational Inheritance of Fatty Liver in Poultry by Targeting .. **2022**,	
510	Leaf and rhizome transcriptome assembly and expression analysis of genes involved in terpene biosynthesis in Dioscorea opposita. 1	
509	Full Issue PDF.. **2022**, 35, 368-438	
508	Longitudinal physiological and transcriptomic analyses reveal the short term and long term response of Synechocystis sp. PCC6803 to cadmium stress.. **2022**, 303, 134727	0
507	Comparative Transcriptome Analyses Characterize Expression Signatures Among Males, Females, Neo-Males, and Gynogenetic Females in the Yellow Drum (Nibea albiflora). **2022**, 13,	

506	Genetic regulation of male sexual development in the oriental river prawn Macrobrachium nipponense during reproductive vs. non-reproductive season.	0
505	Comprehensive transcriptomic analysis reveals insights into the gill response to hypoxia and Poly I:C in Qihe crucian carp Carassius auratus. **2022**, 24, 101154	0
504	Integrated insights into the mechanisms underlying sepsis-induced myocardial depression using a quantitative global proteomic analysis.. **2022**, 262, 104599	1
503	Transcriptome analysis of inbreeding depression in the Pacific oyster Crassostrea gigas. **2022**, 557, 738314	
502	The nutrient, hormone, and antioxidant status of scion affects the rootstock activity in apple. **2022**, 302, 111157	0
501	Metabolomics combined with physiological and transcriptomic analyses reveal regulatory features associated with blueberry growth in different soilless substrates. **2022**, 302, 111145	0
500	Identification of crucial circRNAs in skeletal muscle during chicken embryonic development.. **2022**, 23, 330	0
499	Micro-synteny conservation analysis revealed the evolutionary history of bacterial biphenyl degradation pathway.. **2022**,	1
498	Characterization of ampicillin-resistant genes in Vibrio parahaemolyticus.. **2022**, 105573	0
497	Transcriptome Profiling Analysis Identifies LCP1 as a Contributor for Chidamide Resistance in Gastric Cancer.. **2022**,	0
496	Enhanced reactive oxygen detoxification occurs in salt-stressed soybean roots expressing GmSALT3.. **2022**, e13709	2
495	Dihydroartemisinin Exerts Antifibrotic and Anti-Inflammatory Effects in Graves□Ophthalmopathy by Targeting Orbital Fibroblasts. **2022**, 13,	0
494	Low humidity altered the gene expression profile of keratinocytes in a three-dimensional skin model.. **2022**,	0
493	Characterization of m A modifications in the contemporary Zika virus genome and host cellular transcripts.. **2022**,	
492	gen. nov., sp. nov., isolated from marine sediment, and description of fam. nov. and fam. nov.. **2022**, 72,	0
491	Genetic mapping and physiological analysis of chlorophyll-deficient mutant in Brassica napus L.. **2022**, 22, 244	0
490	The vaginal microbiome is associated with endometrial cancer grade and histology.	0
489	Transcriptomic analysis identifies differentially expressed genes in´purple tender shoots and green mature leaves of Zijuan tea.	

488	Melatonin Alleviates Oxidative Stress Induced by H2O2 in Porcine Trophectodern Cells. **2022**, 11, 1047	1
487	Transcriptomic Analysis of Trigeminal Ganglion and Spinal Trigeminal Nucleus Caudalis in Mice with Inflammatory Temporomandibular Joint Pain. Volume 15, 1487-1502	0
486	Comparative transcriptome provides insights into differentially expressed genes between testis and ovary of Onychostoma macrolepis in reproduction period. **2022**, 114066	
485	The whole transcriptome analysis and the circRNA-lncRNA network construction in arsenic trioxide-treated mice myocardium. **2022**, 151, 113183	0
484	Analysis of morphological change mechanism of linear Arthrospira platensis based on transcriptome results. **2022**, 834, 146573	
483	Transcriptomics in Plant. **2022**, 99-127	
482	A time-course transcriptome analysis of gonads from yellow catfish (Pelteobagrus fulvidraco) reveals genes associated with gonad development. **2022**, 23,	0
481	1H-NMR-based metabolic profiling of rat urine to assess the toxicity-attenuating effect of the sweat-soaking method on Radix Wikstroemia indica. **2022**, 24,	
480	Transcriptomic Analysis Reveals That Exogenous Indole-3-Butyric Acid Affects the Rooting Process During Stem Segment Culturing of Cinnamomum camphora Linalool Type.	0
479	Identification and Regulatory Network Analysis of Genes Related to Reproductive Performance in the Hypothalamus and Pituitary of Angus Cattle. **2022**, 13, 965	
478	Plasmodium manipulates the expression of host long non-coding RNA during red blood cell intracellular infection. **2022**, 15,	1
477	Bacterial Infection Induces Ultrastructural and Transcriptional Changes in the King Oyster Mushroom (Pleurotus eryngii).	1
476	Comparative Transcriptomic Immune Responses of Mullet (Mugil cephalus) Infected by Planktonic and Biofilm Lactococcus Garvieae. **2022**, 12,	
475	Maternal urban particulate matter exposure and signaling pathways in fetal brains and neurobehavioral development in offspring. **2022**, 474, 153225	
474	Transcriptome analysis reveals distinct innate immunity and ribosomal response at early stage of AcMNPV infection in haemocyte of silkworm resistant and susceptible strains. **2022**, 101938	1
473	Exogenous melatonin improves the resistance to cucumber bacterial angular leaf spot caused by Pseudomonas syringae pv. Lachrymans. **2022**, 174,	2
472	Transcriptional cascades in the regulation of 2-AP biosynthesis under Zn supply in fragrant rice.	1
471	Comparative Transcriptomics and Metabolites Analysis of Two Closely Related Euphorbia Species Reveal Environmental Adaptation Mechanism and Active Ingredients Difference. **2022**, 13,	0

470	Genome of a novel Sediminibacterium discovered in association with two species of freshwater cyanobacteria from streams in Southern California.	0
469	Transcriptional Analysis of Listeria monocytogenes Invasion of Macrophages. **2022**, 58, 302-308	
468	ITRAQ-Based Proteomic Analysis of Wheat (Triticum aestivum) Spikes in Response to Tilletia controversa K�n and Tilletia foetida K�n Infection, Causal Organisms of Dwarf Bunt and Common Bunt of Wheat. **2022**, 11, 865	0
467	The Particular Expression Profiles of Circular RNA in Peripheral Blood of Myocardial Infarction Patients by RNA Sequencing. 9,	2
466	Assessing the influence of the Mediterranean diet on dental calculus microbiome composition: a pilot study.	
465	Synergistic antitumor effects of compound-composed optimal formula from Aidi injection on hepatocellular carcinoma and colorectal cancer. **2022**, 154231	0
464	Health impact assessment of pet cats caused by organohalogen contaminants by serum metabolomics and thyroid hormone analysis. **2022**, 156490	0
463	Temporal transcriptome analysis provides molecular insights into flower development in red-flesh pitaya. **2022**,	0
462	Effects of dietary 2-(2H-benzotriazol-2-yl)-4-methylphenol (UV-P) exposure on Japanese medaka (Oryzias latipes) in a short-term reproduction assay. **2022**, 248, 106206	0
461	Integrated transcriptomic and gibberellin analyses reveal genes related to branch development in Eucalyptus urophylla. **2022**, 185, 69-79	
460	Elevated Co2 Exacerbates Effects of Tio2 Nanoparticles on Rice (Oryza Sativa L. Cv. Yongyou) Leaf Transcriptome and Soil Bacteria.	
459	Exploring kinase family inhibitors and their moiety preferences using deep SHapley additive exPlanations. **2022**, 23,	1
458	Identification of Hub Genes and Key Pathways in TNF-�and IFN-�Induced Cytokine Storms via Bioinformatics. **2022**,	0
457	Dual Specific Phosphatase 7 Exacerbates Dilated Cardiomyopathy, Heart Failure, and Cardiac Death by Inactivating the ERK1/2 Signaling Pathway.	0
456	Combined transcriptome and metabolome analysis of a new species of microalgae from Tibetan plateau and its response to sewage treatment.	
455	miRNA-mRNA analysis of sheep adrenal glands reveals the network regulating reproduction. **2022**, 23,	
454	AuCoMe: inferring and comparing metabolisms across heterogeneous sets of annotated genomes.	0
453	Dysbiosis of the Gut Microbiome Is Associated With Histopathology of Lung Cancer. 13,	0

452	Deep Small RNA Sequencing Reveals Important miRNAs Related to Muscle Development and Intramuscular Fat Deposition in Longissimus dorsi Muscle From Different Goat Breeds. 9,	0
451	The Identification of Broomcorn Millet bZIP Transcription Factors, Which Regulate Growth and Development to Enhance Stress Tolerance and Seed Germination. **2022**, 23, 6448	
450	Metabolomic and Transcriptomic Profiling Uncover the Underlying Mechanism of Color Differentiation in Scutellaria baicalensis Georgi. Flowers. 13,	0
449	Transcriptome Integration Analysis at Different Embryonic Ages Reveals Key lncRNAs and mRNAs for Chicken Skeletal Muscle. 9,	1
448	Characterizing the Interplay of Rubisco and Nitrogenase Enzymes in Anaerobic-Photoheterotrophically Grown Rhodopseudomonas palustris CGA009 through a Genome-Scale Metabolic and Expression Model.	
447	Effects of Early Life Adversity on Tooth Enamel Formation. 3,	
446	Differential expression profiles of miRNA in granulomatous lobular mastitis and identification of possible biomarkers. **2022**, 24,	0
445	Transcriptome Analysis and Identification of a Female-Specific SSR Marker in Pistacia chinensis Based on Illumina Paired-End RNA Sequencing. **2022**, 13, 1024	1
444	The Female Gametophyte Characteristics and Gene Expression Analysis Involved in Apomixis of Wild Germplasm Materials of Kentucky Bluegrass in Gansu Province of China.	0
443	Metabolome and Transcriptome Analyses of Cucurbitacin Biosynthesis in Luffa (Luffa acutangula). 13,	0
442	Transcriptomic Analysis of Mature Transgenic Poplar Expressing the Transcription Factor JERF36 Gene in Two Different Environments. 10,	
441	Modulating Microglia/Macrophage Activation by CDNF Promotes Transplantation of Fetal Ventral Mesencephalic Graft Survival and Function in a Hemiparkinsonian Rat Model. **2022**, 10, 1446	2
440	MicroRNA-27a is essential for bone remodeling by modulating p62-mediated osteoclast signaling.	
439	The substitution at residue 218 of the NS5 protein methyltransferase domain of Tembusu virus impairs viral replication and translation and may triggers RIG-I-like receptor signaling. **2022**, 102017	
438	Translational Frameshifting in the chlD Gene Gives a Clue to the Coevolution of the Chlorophyll and Cobalamin Biosyntheses. **2022**, 10, 1200	
437	Regulation of the Cell Cycle, Apoptosis, and Proline Accumulation Plays an Important Role in the Stress Response of the Eastern Oyster Crassostrea Virginica. 9,	0
436	Distinct gut microbiota and health outcomes in asymptomatic infection, viral nucleic acid test re-positive, and convalescent COVID-19 cases.	0
435	Combined QTL mapping and RNA-Seq pro-filing reveal candidate genes related to low-temperature tolerance in maize. **2022**, 42,	1

434	Unravelling Stratified Microbial Assemblages in Australia□s Only Deep Anchialine System, The Bundera Sinkhole. 9,	2
433	MicroRNA expression signature in the striated and smooth adductor muscles of Yesso scallop Patinopecten yessoensis. **2022**, 114, 110409	1
432	Transcriptomics analysis provides new insights into the fish antiviral mechanism and identification of interferon-stimulated genes in grass carp (Ctenopharyngodon idella). **2022**, 148, 81-90	0
431	A novel root-specific Di19 transcription factor from Glycine max compromises drought tolerance in Arabidopsis thaliana through suppression of auxin-related pathway. **2022**, 201, 104951	
430	Effects of age on subcutaneous adipose tissue proteins in Chinese indigenous Ningxiang pig by TMT-labeled quantitative proteomics. **2022**, 265, 104650	1
429	RNA-seq analysis of the differential response to low-temperature stress in two morphs of mud crabs (Scylla paramamosain). **2022**, 43, 101010	0
428	Regulation of mi-RNAs Target Cancer Genes Between Exercise and Non-exercise in Rat Rheumatoid Arthritis Induction: Pilot Study. **2022**, 15, 251686572211104	0
427	BnKAT2 Positively Regulates the Main Inflorescence Length and Silique Number in Brassica napus by Regulating the Auxin and Cytokinin Signaling Pathways. **2022**, 11, 1679	0
426	The Necrotroph Botrytis cinerea BcSpd1 Plays a Key Role in Modulating Both Fungal Pathogenic Factors and Plant Disease Development. 13,	0
425	Reviving human □ cells from apoptosis induced by IL-12/18 via p-JNK inhibition.	0
424	Transcriptome Analysis Reveals the Response Mechanism of Frl-Mediated Resistance to Fusarium oxysporum f. sp. radicis-lycopersici (FORL) Infection in Tomato. **2022**, 23, 7078	0
423	Intermittent theta-burst stimulation improves motor function by inhibiting neuronal pyroptosis and regulating microglial polarization via TLR4/NF□B/NLRP3 signaling pathway in cerebral ischemic mice. **2022**, 19,	1
422	Combined Analysis of BSA-Seq Based Mapping, RNA-Seq, and Metabolomic Unraveled Candidate Genes Associated with Panicle Grain Number in Rice (Oryza sativa L.). **2022**, 12, 918	1
421	Molecular evolutionary trends and biosynthesis pathways in the Oribatida revealed by the genome of Archegozetes longisetosus. **2022**, 62, 532-573	
420	MicroRNA expression profile of chicken cecum in different stages during Histomonas meleagridis infection. **2022**, 18,	
419	Resistance to Powdery Mildew in Qingke Involves the Accumulation of Aromatic Phenolamides Through Jasmonate-Mediated Activation of Defense-Related Genes. 13,	0
418	Liver Transcriptome and Gut Microbiome Analysis Reveals the Effects of High Fructose Corn Syrup in Mice. 9,	1
417	Melatonin Alters the miRNA Transcriptome of Inflammasome Activation in Murine Microglial Cells.	0

416	Comparative physiology and transcriptome analysis reveals that chloroplast development influences silver-white leaf color formation in Hydrangea macrophylla var. maculata. **2022**, 22,	
415	Differential expression profile of plasma exosomal microRNAs in acute type A aortic dissection with acute lung injury. **2022**, 12,	
414	Multi-Cell-Type Openness-Weighted Association Studies for Trait-Associated Genomic Segments Prioritization. **2022**, 13, 1220	
413	Differential expression profile and in-silico functional analysis of long noncoding RNA and mRNA in duck embryo fibroblasts infected with duck plague virus. **2022**, 23,	0
412	How candidate genes respond to aluminum toxicity in Citrus x limonia Osbeck?.	0
411	Folate Carrier Deficiency Drives Differential Methylation and Enhanced Cellular Potency in the Neural Plate Border. 10,	0
410	Transcriptomic analysis reveals the key role of histone deacetylation via mediating different phytohormone signalings in fiber initiation of cotton. **2022**, 12,	
409	Transcriptomic Insight into Viviparous Growth in Water Lily. **2022**, 2022, 1-18	
408	Seco-Lupane Triterpene Derivatives Induce Ferroptosis through GPX4/ACSL4 Axis and Target Cyclin D1 to Block the Cell Cycle.	0
407	Revealing the difference of □-amylase and CYP6AE76 gene between polyphagous Conogethes punctiferalis and oligophagous C. pinicolalis by multiple-omics and molecular biological technique. **2022**, 23,	
406	Transcriptome comparison for identification of pigmentation-related genes in different color varieties of Siamese fighting fish Betta splendens. **2022**, 101014	
405	Swimming Impedes Intestinal Microbiota and Lipid Metabolites of Tumorigenesis in Colitis-Associated Cancer. 12,	1
404	Comparative Physiological and Transcriptome Analysis Reveal the Molecular Mechanism of Melatonin in Regulating Salt Tolerance in Alfalfa (Medicago sativa L.). 13,	0
403	GEARS: Predicting transcriptional outcomes of novel multi-gene perturbations.	0
402	Transcriptome Analysis Reveals Molecular Mechanisms under Salt Stress in Leaves of Foxtail Millet (Setaria italica L.). **2022**, 11, 1864	0
401	Effects of air exposure stress on crustaceans: Histopathological changes, antioxidant and immunity of the red swamp crayfish Procambarus clarkii. **2022**, 135, 104480	1
400	Innovation for Sustainable Agriculture and Food Production. **2023**,	
399	Transcriptome Analysis of Propylaea quatuordecimpunctata L. (Coleoptera: Coccinellidae) under High Temperature Stress. **2022**, 12, 1088	0

398	Integrative analysis uncovers response mechanism of Pirata subpiraticus to chronic cadmium stress.	0
397	Transcriptomic Analysis Reveals Potential Gene Regulatory Networks Under Cold Stress of Loquat (Eriobotrya japonica Lindl.). 13,	0
396	GWAS and RNA-seq analysis uncover candidate genes associated with alkaline stress tolerance in maize (Zea mays L.) seedlings. 13,	0
395	RNA profiling of human dorsal root ganglia reveals sex-differences in mechanisms promoting neuropathic pain.	1
394	Differential MicroRNA Expression in Porcine Endometrium Related to Spontaneous Embryo Loss during Early Pregnancy. **2022**, 23, 8157	0
393	miRNA-mRNA associations with inosine monophosphate specific deposition in the muscle of Jingyuan chicken.	
392	Discovery of Tropolone Stipitaldehyde as a Potential Agent for Controlling Phytophthora Blight and Its Action Mechanism Research. **2022**, 70, 8693-8703	4
391	Effects of nitrogen application after abrupt drought-flood alternation on rice root nitrogen uptake and rhizosphere soil microbial diversity. **2022**, 201, 105007	0
390	Hypoxia inducible factor-1 signaling pathway in macrophage involved angiogenesis in materials-instructed osteo-induction.	0
389	Ribonuclease H-like gene Small Grain2 regulates grain size in rice through brassinosteroids signal pathway.	0
388	Comparative Transcriptome Analyses between Resistant and Susceptible Varieties in Response to Soybean Mosaic Virus Infection. **2022**, 12, 1785	
387	ROS-activated CXCR2+ neutrophils recruited by CXCL1 delay denervated skeletal muscle atrophy and undergo P53-mediated apoptosis. **2022**, 54, 1011-1023	
386	Effect of the FA2H Gene on cashmere fineness of Jiangnan cashmere goats based on transcriptome sequencing. **2022**, 23,	1
385	Transcriptome and Metabolome Analyses Reveal Differences in Terpenoid and Flavonoid Biosynthesis in Cryptomeria fortunei Needles Across Different Seasons. 13,	0
384	Genome-wide identification of long non-coding (lncRNA) in Nilaparvata lugens□ adaptability to resistant rice. 10, e13587	
383	The molecular diversity of transcriptional factor TfoX is a determinant in natural transformation in Glaesserella parasuis. 13,	
382	Transcriptomic Insights Into Root Development and Overwintering Transcriptional Memory of Brassica rapa L. Grown in the Field. 13,	
381	Growing DAGs: Optimization Functions for Pathway Reconstruction Algorithms.	

380	Transcriptomic analysis of the effects of melatonin on genes potentially related to the browning of broccoli (Brassica oleracea L. var. italica Planch) hairy roots.	1
379	RNA-seq Provides Novel Insights into Response to Acute Salinity Stress in Oriental River Prawn Macrobrachium nipponense. **2022**, 24, 820-829	1
378	Comparative transcriptome analysis reveals the non-neuronal cholinergic system in the ovary of the oriental armyworm, Mythimna separata Walker (Lepidoptera: Noctuidae).	0
377	An integrative-omics analysis of an industrial clavulanic acid-overproducing Streptomyces clavuligerus.	
376	CHDbase: A comprehensive knowledgebase for congenital heart disease-related genes and clinical manifestations. **2022**,	0
375	Metabolic profiling and transcriptomic data providing critical flavonoid biosynthesis mechanisms disclose color differences of purple heading Chinese cabbages (Brassica rapa L.). **2022**, 113885	1
374	A SlCLV3-SlWUS module regulates auxin and ethylene homeostasis in low light-induced tomato flower abscission.	0
373	Mining of publicly available RNA-seq data to reveal phenotypic differences between Landsberg erecta-0 and Columbia-0 ecotypes in Arabidopsis thaliana.	
372	De novo RNA sequencing for identification of growth-related genes in Silurus lanzhouensis muscle tissues.	
371	Artificial Intelligence-Based Clustering and Characterization of Parkinson's Disease Trajectories.	
370	Transcriptome and Metabolome Analyses Revealed the Response Mechanism of Sugar Beet to Salt Stress of Different Durations. **2022**, 23, 9599	1
369	A new perspective on endocrine disrupting effects of triphenyltin on marine medaka: Frombrain transcriptome, gut content metabolome and behavior. **2022**, 136190	
368	Contrasting genome patterns of two pseudomonas strains isolated from the date palm rhizosphere to assess survival in a hot arid environment. **2022**, 38,	0
367	Preparation, characterization, and osteogenic activity mechanism of casein phosphopeptide-calcium chelate. 9,	0
366	Phosphoproteome profiling of mouse liver during normal aging. **2022**, 20,	0
365	Prkra Mutation Alters Long Noncoding RNA Expression During Embryonic External Ear Development. Publish Ahead of Print,	
364	Integrative analysis of transcriptome and metabolome reveals flavonoid biosynthesis regulation in Rhododendron pulchrum petals. **2022**, 22,	0
363	Utilization of diverse organophosphorus pollutants by marine bacteria. **2022**, 119,	1

362	Identification of biomarkers, pathways and potential therapeutic agents for salt-sensitive hypertension using RNA-seq. 9,	
361	Determining the Effects of Light on the Fruit Peel Quality of Photosensitive and Nonphotosensitive Eggplant. **2022**, 11, 2095	
360	Vitrification of bovine germinal vesicle oocytes significantly decreased the methylation level of their. **2022**, 34, 889-903	
359	Combined Transcriptomic and Metabolomic Analysis Reveals the Mechanism of Flavonoid Biosynthesis in Handroanthus chrysanthus (Jacq.) S.O.Grose. **2022**, 13, 1285	
358	Defect in BrMS1, a PHD-finger transcription factor, induces male sterility in ethyl methane sulfonate-mutagenized Chinese cabbage (Brassica rapa L. ssp. pekinensis). 13,	0
357	RNA sequencing reveals dynamic expression of spleen lncRNAs and mRNAs in Beagle dogs infected by Toxocara canis. **2022**, 15,	0
356	Comparative Transcriptome Analysis on the Regulatory Mechanism of Thoracic Ganglia in Eriocheir sinensis at Post-Molt and Inter-Molt Stages. **2022**, 12, 1181	
355	Integrated metabolomic and transcriptomic strategies to reveal adaptive mechanisms in castor plant during germination stage under alkali stress. **2022**, 105031	1
354	Microbial Interaction between Lactiplantibacillus plantarum and Saccharomyces cerevisiae: Transcriptome Level Mechanism of Cell-Cell Antagonism.	0
353	Gene expression and methylation profiles show the involvement of POMC in primary hyperparathyroidsm. **2022**, 20,	
352	Analysis of gene expression changes in wheat in response to Rhizoctonia cerealis infection using RNA-Seq.	
351	Differential analysis of ergosterol function in response to high salt and sugar stress in Zygosaccharomyces rouxii.	
350	Prmt7 Downregulation in Mouse Spermatogonia Functions through miR-877-3p/Col6a3. **2022**, 12, 1194	
349	Transcriptome analysis revealed the expression levels of genes related to abscisic acid and auxin biosynthesis in grapevine (Vitis vinifera L.) under root restriction. 13,	
348	A dysregulated sebum□microbial metabolite□IL-33 axis initiates skin inflammation in atopic dermatitis. **2022**, 219,	0
347	Aberrant peribiliary gland niche exacerbates fibrosis in primary sclerosing cholangitis and a potential therapeutic strategy. **2022**, 153, 113512	0
346	Lowfat functions downstream of Myo20 to regulate wing and leg morphogenesis in Tribolium castaneum. **2022**, 148, 103829	
345	DNA methylome of primary spermatocyte reveals epigenetic dysregulation associated with male sterility of cattleyak. **2022**, 191, 153-167	0

344	Transcriptomic analysis reveals crucial regulatory roles of immediate-early response genes and related signaling pathways in coronavirus infectious bronchitis virus infection. **2022**, 575, 1-9	0
343	Identification of candidate genes associated with sex differentiation and determination of gender diphasic plant Lilium apertum (Liliaceae). **2022**, 306, 111431	
342	Energy status regulated umami compound metabolism in harvested shiitake mushrooms (Lentinus edodes) with spores triggered to release. **2023**, 12, 303-311	1
341	Identification of potential key genes for immune infiltration in childhood asthma by data mining and biological validation. 13,	0
340	Transcriptome Profiling of Different State Callus Induced from Immature Embryo in Maize. **2022**, 2022, 1-12	0
339	ER whorls triggered by GhCNX6 were discovered involved in drought stress on cotton. **2022**, 203, 105062	0
338	The pattern of DNA methylation alteration, and its association with the expression changes of non-coding RNAs and mRNAs in Moso bamboo under abiotic stress. **2022**, 325, 111451	1
337	Multi-omics reveals response mechanism of liver metabolism of hybrid sturgeon under ship noise stress. **2022**, 851, 158348	0
336	Antifungal activity of vitamin D3 against Candida albicans in vitro and in vivo. **2022**, 265, 127200	0
335	Application of network composite module analysis and verification to explore the bidirectional immunomodulatory effect of Zukamu granules on Th1 / Th2 cytokines in lung injury. **2022**, 299, 115674	0
334	Examination of sex-related differences in intestinal and gonadal lipid metabolism in the sea cucumber Apostichopus japonicus. **2023**, 562, 738787	1
333	Methylome and transcriptome analysis of alters leaf phenotype with autotetraploid in grape. **2023**, 307, 111534	0
332	Comparative Transcriptome Analysis of Salt-Stress-Responsive Genes in Rice Roots. **2023**, 92, 237-250	0
331	Dufulin Upregulates Integral Membrane Protein Duf6 to Enhance Salt Resistance of Rice.	0
330	Single-cell analysis of gene expression in the substantia nigra pars compacta of a pesticide-induced mouse model of Parkinson’s disease. **2022**, 13, 255-269	0
329	Quantum machine learning for chemistry and physics. **2022**, 51, 6475-6573	5
328	Reduce Bioaccumulation of Cd Pollutants Through the Antagonism of Se:Bioaccumulation of Cd and Comparative Transcriptome Analysis in the Hepatopancreas of Estuary Mud Crab (Scylla Paramamosain).	0
327	Physiological and transcriptomic analysis reveals the postharvest ripening differences between “Nantianhuang” and “Brazilian” banana fruit. **2023**, 195, 112138	0

326	Bioaccumulation of Cd and comparative transcriptome analysis after the antagonism of Se in the hepatopancreas of estuary mud crab (Scylla paramamosain). **2023**, 263, 109474	0
325	Integrated physiologic and proteomic analysis of Stropharia rugosoannulata mycelia in response to Cd stress. **2023**, 441, 129877	0
324	Celda: a Bayesian model to perform co-clustering of genes into modules and cells into subpopulations using single-cell RNA-seq data. **2022**, 4,	0
323	Integrated RNA-seq and RNAi Analysis of the Roles of the Hsp70 and SP Genes in Red-Shell Meretrix meretrix Tolerance to the Pathogen Vibrio parahaemolyticus.	0
322	miRNA transcriptome and myofiber characteristics of lamb skeletal muscle during hypertrophic growth1. 13,	0
321	Integrated Analysis of Transcriptome and Metabolome Reveals New Insights into the Formation of Purple Leaf Veins and Leaf Edge Cracks in Brassica juncea. **2022**, 11, 2229	0
320	Transcriptome Analysis Provides Insights into Potentilla bifurca Adaptation to High Altitude. **2022**, 12, 1337	1
319	Pre- and Post-Harvest Conditions Affect Polyphenol Content in Strawberry (Fragaria □ananassa). **2022**, 11, 2220	0
318	Vasorin Deletion in C57BL/6J Mice Induces Hepatocyte Autophagy through Glycogen-Mediated mTOR Regulation. **2022**, 14, 3600	0
317	Dynamic transcriptome analysis suggests the key genes regulating seed development and filling in Tartary buckwheat (Fagopyrum tataricum Garetn.). 13,	0
316	Analysis of body color formation of leopard coral grouper Plectropomus leopardus. 9,	0
315	Integrated volatile metabolomic and transcriptomic analysis provides insights into the regulation of floral scents between two contrasting varieties of Lonicera japonica. 13,	0
314	Adaptive biomineralization in two morphotypes of Sternaspidae (Annelida) from the Northern China Seas. 9,	0
313	Transcriptomics provides insights into toxicological effects and molecular mechanisms associated with the exposure of Chinese mitten crab, Eriocheir sinensis, to dioxin. **2022**, 104540	0
312	The role of OsOFP8 gene in regulating rice leaf angle.	0
311	Mature biofloc harbor similar bacterial communities regardless of the vegetal floating substrates (oat, amaranth, or wheat) used as promoters.	0
310	Differential expression of circRNAs of testes with high and low sperm motility in Yili geese. 13,	0
309	HeberFERON distinctively targets Cell Cycle in the glioblastoma-derived cell line U-87MG.	0

308	The interaction of the pathogen Fusarium proliferatum with Trichoderma asperellum characterized by transcriptome changes in apple rootstock roots. **2022**, 121, 101894	1
307	Daphnia as a Sentinel Species for Environmental Health Protection: A Perspective on Biomonitoring and Bioremediation of Chemical Pollution.	2
306	Circadian dysregulation induces alterations of visceral sensitivity and the gut microbiota in Light/Dark phase shift mice. 13,	0
305	Identification of kaempferol as an OSX upregulator by network pharmacology-based analysis of qianggu Capsule for osteoporosis. 13,	0
304	An integrated metabolome and transcriptome analysis of the Hibiscus syriacus L. petals reveal the molecular mechanisms of anthocyanin accumulation. 13,	1
303	Integrative analyses of morphology, physiology, and transcriptional expression profiling reveal miRNAs involved in culm color in bamboo. 13,	0
302	The updated weeping forsythia genome reveals the genomic basis for the evolution and the forsythin and forsythoside A biosynthesis. **2022**,	0
301	Exploration of the regulatory mechanisms of regeneration, anti-oxidation, anti-aging and the immune response at the post-molt stage of Eriocheir sinensis. 13,	0
300	A review of biomedical datasets relating to drug discovery: a knowledge graph perspective.	2
299	Integrated Transcriptome and Proteome Analysis Reveals that the Antimicrobial Griseofulvin Targets Didymella segeticola beta-Tubulin to Control Tea Leaf Spot.	0
298	RNA sequencing and weighted gene co-expression network analysis uncover the hub genes controlling cold tolerance in Helictotrichon virescens seedlings. 13,	0
297	Integrated PPI- and WGCNA-retrieval of hub gene signatures for soft substrates inhibition of human fibroblasts proliferation and differentiation. **2022**, 14, 6957-6974	0
296	Transcriptome analysis provides insight into adaptive mechanisms of scallops under environmental stress. 9,	1
295	Comparative Transcriptome Analysis Reveals the Molecular Mechanism of UV-B Irradiation in Promoting the Accumulation of Phenolic Compounds in Wounded Carrot. **2022**, 8, 896	1
294	Fluorous-Tagged Peptide Nanoparticles Ameliorate Acute Lung Injury via Lysosomal Stabilization and Inflammation Inhibition in Pulmonary Macrophages. **2022**, 18, 2203432	0
293	Integrative metabolome and transcriptome analyses reveal the molecular mechanism underlying variation in floral scent during flower development of Chrysanthemum indicum var. aromaticum. 13,	0
292	Root and shoot biology of Arabidopsis halleri dissected by WGCNA: an insight into the organ pivotal pathways and genes of an hyperaccumulator.	0
291	Molecular signatures in diabetic foot ulcer by integrated gene expression profiling via bioinformatics analysis. **2022**, 42, 713-719	0

290	Exogenous Betaine Enhances the Protrusion Vigor of Rice Seeds under Heat Stress by Regulating Plant Hormone Signal Transduction and Its Interaction Network. **2022**, 11, 1792	1
289	Outcomes of Low-Temperature Stress on Biological Alterations within Pothos (Epipremnum aureum) Leaves. **2022**, 12, 1432	0
288	The Injections of Mitochondrial Fusion Promoter M1 during Proestrus Disrupt the Progesterone Secretion and the Estrous Cycle in the Mouse.	0
287	Interactions Among Non-Coding RNAs and mRNAs in the Trigeminal Ganglion Associated with Neuropathic Pain. Volume 15, 2967-2988	1
286	WGCNA Identifies a Comprehensive and Dynamic Gene Co-Expression Network That Associates with Smut Resistance in Sugarcane. **2022**, 23, 10770	1
285	Characterization of differentially expressed and lipid metabolism-related lncRNA-mRNA interaction networks during the growth of liver tissue through rabbit models. 9,	0
284	Identification and Functional Prediction of Circular RNAs Related to Growth Traits and Skeletal Muscle Development in Duroc pigs. 13,	0
283	Inhibition of XPO1 with KPT-330 induces autophagy-dependent apoptosis in gallbladder cancer by activating the p53/mTOR pathway. **2022**, 20,	0
282	Decoding the formation of diverse petal colors of Lagerstroemia indica by integrating the data from transcriptome and metabolome. 13,	0
281	Gut Microbiota Profiles in Dairy Cattle from Highland and Coastal Regions Using Shotgun Metagenomic Approach. **2022**, 2022, 1-8	0
280	Comprehensive transcriptome analysis of sika deer antler using PacBio and Illumina sequencing. **2022**, 12,	0
279	Bmp5 Mutation Alters mRNA Expression During External Ear Development. Publish Ahead of Print,	0
278	Integration of mRNA and miRNA analysis reveals the differentially regulatory network in two different Camellia oleifera cultivars under drought stress. 13,	1
277	Integrative Analysis of Motor Neuron and Microglial Transcriptomes from SOD1G93A Mice Models Uncover Potential Drug Treatments for ALS.	0
276	Comparative Transcriptomic Analysis of mRNAs, miRNAs and lncRNAs in the Longissimus dorsi Muscles between Fat-Type and Lean-Type Pigs. **2022**, 12, 1294	1
275	Integrated transcriptomics and metabolomics analysis of the hippocampus reveals altered neuroinflammation, downregulated metabolism and synapse in sepsis-associated encephalopathy. 13,	0
274	Comparative physiological, transcriptomic, and WGCNA analyses reveal the key genes and regulatory pathways associated with drought tolerance in Tartary buckwheat. 13,	0
273	Epigenetic and pharmacological control of pigmentation via Bromodomain Protein 9 (BRD9).	0

272	Shikonin Mediates Apoptosis through G Protein-Coupled Estrogen Receptor of Ovarian Cancer Cells. **2022**, 2022, 1-18	0
271	Loss of endothelial EMCN drives tumor lung metastasis through the premetastatic niche. **2022**, 20,	0
270	The Potential Regulation of A-to-I RNA editing on Genes in Parkinson□ Disease.	0
269	Transcriptomic insights into the molecular mechanism of wheat response to stripe rust fungus. **2022**, e10951	0
268	Uncovering the mechanism of anthocyanin accumulation in a purple-leaved variety of foxtail millet (Setaria italica) by transcriptome analysis. 10, e14099	0
267	Effects and mechanisms of decabromodiphenyl ethane on Chlorella sorokiniana: Transcriptomics, proteins and fatty acid production. **2022**, 181, 105764	0
266	Characterization of zearalenone-induced hepatotoxicity and its mechanisms by transcriptomics in zebrafish model. **2022**, 309, 136637	0
265	Integrative metabolomic and transcriptomic analyses reveal the mechanisms of Tibetan hulless barley grain coloration. 13,	1
264	Discovery of gene-gene co-perturbation through big data.	0
263	Dynamic Analysis of microRNAs from Different Life Stages of Rhipicephalus microplus (Acari: Ixodidae) by High-Throughput Sequencing. **2022**, 11, 1148	0
262	Comparative transcriptome profiling reveals the role of phytohormones and phenylpropanoid pathway in early-stage resistance against powdery mildew in watermelon (Citrullus lanatus L.). 13,	0
261	Expression profile of long non-coding RNAs in the intestine of black rockfish Sebastes schlegelii in response to Edwardsiella tarda infection.	0
260	Liver comparative transcriptome analysis reveals the mechanism of the Hainan medaka, Oryzias curvinotus , to adapt to salinity.	0
259	Transcriptome Analysis to Identify Responsive Genes under Sublethal Concentration of Bifenazate in the Diamondback Moth, Plutella xylostella (Linnaeus, 1758) (Lepidoptera: Plutellidae). **2022**, 23, 13173	1
258	Transcriptomic Analysis of the Differences in Leaf Color Formation during Stage Transitions in Populus □euramericana □Zhonghuahongye□**2022**, 12, 2396	0
257	Genome-Wide Identification of miRNAs and Its Downstream Transcriptional Regulatory Network during Seed Maturation in Tilia tuan. **2022**, 13, 1750	0
256	Genes associated with depression and coronary artery disease are enriched for inflammation and cardiomyopathy-associated pathways..	0
255	Combined transcriptomic and physiological metabolomic analyses elucidate key biological pathways in the response of two sorghum genotypes to salinity stress. 13,	0

254	Fine-Tuned Immune Antagonism and Nodule-Specific Cysteine-Rich Peptides Govern the Symbiotic Specificity Between Alfalfa Cultivars and Ensifer meliloti.	0
253	A novel promising diagnostic candidate selected by screening the transcriptome of Babesia gibsoni (Wuhan isolate) asexual stages in infected beagles. **2022**, 15,	0
252	Transcriptional and Metabolic Characterization of Feeding Ramie Growth Enhanced by a Combined Application of Gibberellin and Ethrel. **2022**, 23, 12025	0
251	ORF355 confers enhanced salinity stress adaptability to CMS-S maize by modulating the mitochondrial metabolic homeostasis.	0
250	Epigenomic and transcriptomic landscaping unraveled candidate repositioned therapeutics for non-functioning pituitary neuroendocrine tumors.	0
249	A Transcriptomic Analysis of Tobacco Leaf with the Functional Loss of the Plastid rpoB Operon Caused by TALEN-Mediated Double-Strand Breakage. **2022**, 11, 2860	0
248	Regulation of Tyrosinase Gene Expression by Retinoic Acid Pathway in the Pacific Oyster Crassostrea gigas. **2022**, 23, 12840	0
247	Network Pharmacological Analysis of the Red Sea Sponge Hyrtios erectus Extract to Reveal Anticancer Efficacy of Corresponding Loaded Niosomes. **2022**, 20, 628	0
246	The mechanism analysis of exogenous melatonin in limiting pear fruit aroma decrease under low temperature storage. 10, e14166	1
245	De Novo Transcriptome Dataset Generation of the Swamp Buffalo Brain and Non-Brain Tissues. **2022**, 2022, 1-15	0
244	Combined Transcriptome and Metabolome Analysis of a New Species of Microalgae from the Tibetan Plateau and Its Response to Sewage Treatment. **2022**, 14, 3391	0
243	Glycosylation Analysis of Feline Small Intestine Following Toxoplasma gondii Infection. **2022**, 12, 2858	0
242	Resistance to dinotefuran in Bemisia tabaci in China status and characteristics.	1
241	Transcriptome Analysis Reveals the Genes Related to Pollen Abortion in a Cytoplasmic Male-Sterile Soybean (Glycine max (L.) Merr.). **2022**, 23, 12227	0
240	Comparative Transcriptomic and Metabolomic Analyses Reveal the Regulatory Effect and Mechanism of Tea Extracts on the Biosynthesis of Monascus Pigments. **2022**, 11, 3159	1
239	Genetic and Transcriptome Analysis of Leaf Trichome Development in Chinese Cabbage (Brassica rapa L. subsp. pekinensis) and Molecular Marker Development. **2022**, 23, 12721	1
238	Identification of Key Genes during Ethylene-Induced Adventitious Root Development in Cucumber (Cucumis sativus L.). **2022**, 23, 12981	0
237	Targeted Metabolome and Transcriptome Analyses Reveal the Pigmentation Mechanism of Hippophae (Sea Buckthorn) Fruit. **2022**, 11, 3278	0

236	Transcriptome analysis reveals the proline metabolic pathway and its potential regulation TF-hub genes in salt-stressed potato. 13,	0
235	Tanshinone IIA Regulates Keap1/Nrf2 Signal Pathway by Activating Sestrin2 to Restrain Pulmonary Fibrosis. 1-27	0
234	Comparative transcriptome analysis reveals an insight into the candidate genes involved in anthocyanin and scent volatiles biosynthesis in color changing flowers of Combretum indicum (L.) DeFilipps.	0
233	RNA-Sequencing approach for exploring the therapeutic effect of umbilical cord mesenchymal stem/stromal cells on lipopolysaccharide-induced acute lung injury. 13,	1
232	Physiological and Transcriptional Analysis Reveals the Response Mechanism of Camellia vietnamensis Huang to Drought Stress. **2022**, 23, 11801	0
231	An integrated analysis of gut microbiota and the brain transcriptome reveals host-gut microbiota interactions following traumatic brain injury. **2022**, 148149	0
230	Combined transcriptome and metabolome analysis reveals the effects of light quality on maize hybrids.	0
229	Transcriptome and metabolome analyses of Shatian pomelo (Citrus grandis var. Shatinyu Hort) leaves provide insights into the overexpression of the gibberellin-induced gene CcGASA4. 13,	0
228	Genome sequence dataset of Bacillus altitudinis strain ST14 isolated from Tunggak River in Gebeng Industrial Park, Kuantan, Pahang. **2022**, 108718	0
227	Toxic effects of triphenyltin on the silkworm Bombyx mori as a lepidopterous insect model. **2022**, 247, 114245	0
226	Polystyrene microplastic ingestion induces the damage in digestive gland of Amphioctopus fangsiao at the physiological, inflammatory, metabolome and transcriptomic levels. **2022**, 315, 120480	0
225	Transcriptomic and physiological analyses unravel the effect and mechanism of halosulfuron-methyl on the symbiosis between rhizobium and soybean. **2022**, 247, 114248	0
224	Integrated transcriptomic and metabolic analysis response in gills, hepatopancreas, and muscle metabolism in oriental river prawn Macrobrachium nipponense in response to acute high salinity stress. **2022**, 27, 101358	0
223	Toxic effects and transcriptional responses in zebrafish liver cells following perfluorooctanoic acid exposure. **2022**, 253, 106328	1
222	Transcriptome and targeted metabolomics revealed that cholesterol nutrition promotes ovarian development by regulating steroid hormone metabolism in swimming crab. **2022**, 27, 101396	1
221	RNA-sequencing analysis of candidate genes involved in berry development in 'Summer Black' grapes and its early bud mutants varieties. **2023**, 308, 111568	0
220	Elevated CO2 exacerbates effects of TiO2 nanoparticles on rice (Oryza sativa L.) leaf transcriptome and soil bacteria. **2023**, 857, 159689	0
219	Comprehensive analysis of mRNA-lncRNA co-expression profiles in mouse brain during infection with Toxoplasma gondii. **2023**, 237, 106722	1

218	Transcriptome analysis of <i>Clematis lanuginosa</i>: Novel features of the molecular events occurring under heat-shock stress. **2022**, 1-9	0
217	Astrocytic dysfunction induced by ABCA1 deficiency causes optic neuropathy. **2022**, 8,	1
216	Revealing the Phenotypic and Genomic Background for PHA Production from Rapeseed-Biodiesel Crude Glycerol Using Photobacterium ganghwense C2.2. **2022**, 23, 13754	0
215	Transcriptome analysis of response strategy in Hemerocallis fulva under drought stress.	0
214	Antipsychotic drug trifluoperazine as a potential therapeutic agent against nasopharyngeal carcinoma.	0
213	Comprehensive transcriptome analysis discovers genes related to leaf color in Cymbidium □Sakura□ etiolated mutant. **2023**, 45,	0
212	Dysbiosis and reduced small intestinal function are required to induce intestinal insufficiency in mice.	0
211	Integrated eco-physiological, biochemical, and molecular biological analyses of selenium fortification mechanism in alfalfa. **2022**, 256,	0
210	PD-L1 negatively regulates antifungal immunity by inhibiting neutrophil release from bone marrow. **2022**, 13,	1
209	Physiological response and transcriptome profiling reveal phosphate-mediated amelioration of arsenic accumulation and toxicity in Panax notoginseng. **2022**, 105136	0
208	YMLA: A comparative platform to carry out functional enrichment analysis for multiple gene lists in yeast. **2022**, 106314	0
207	Drug Repositioning Identifies Six Drug Candidates for Systemic Autoimmune Diseases by Integrative Analyses of Transcriptomes from Scleroderma, Systemic Lupus Erythematosus, and Sjogren's Syndrome.	0
206	Integrative analysis on insect-resistant characteristics and widely targeted metabolic differences of Malus sieversii. **2022**, 87,	0
205	Transcription Factor VdCf2 Regulates Growth, Pathogenicity, and the Expression of a Putative Secondary Metabolism Gene Cluster in Verticillium dahliae.	1
204	Differentially expressed long noncoding RNAs and mRNAs in PC12 cells under lysophosphatidylcholine stimulation. **2022**, 12,	0
203	Systems Biology in ELIXIR: modelling in the spotlight. 11, 1265	0
202	Identification of a 17□-estradiol-degrading Microbacterium hominis SJTG1 With High Adaptability and Characterization of the Genes for Estrogen Degradation. **2022**, 130371	0
201	Isotope-Assisted Metabolic Flux Analysis: A Powerful Technique to Gain New Insights into the Human Metabolome in Health and Disease. **2022**, 12, 1066	0

200	Comparative transcriptomics reveals unique pine wood decay strategies in the Sparassis latifolia. **2022**, 12,	0
199	Targeting Type I IFN/STAT1 signaling inhibited and reversed corneal squamous metaplasia in Aire-deficient mouse. **2023**, 187, 106615	0
198	Transcriptome analysis provides insights into lignin synthesis and MAPK signaling pathway that strengthen the resistance of bitter gourd (Momordica charantia) to Fusarium wilt. **2023**, 115, 110538	0
197	Integration of the transcriptome and metabolome reveals the mechanism of resistance to low phosphorus in wild soybean seedling leaves. **2023**, 194, 406-417	0
196	Integrated biochemical, transcriptomic and metabolomic analyses provide insight into heat stress response in Yangtze sturgeon (Acipenser dabryanus). **2023**, 249, 114366	0
195	Multi-omics eco-surveillance of bacterial community function in legacy contaminated estuary sediments. **2023**, 318, 120857	0
194	Transcriptomic insights into the effects of abscisic acid on the germination of Magnolia sieboldii K. Koch seed. **2023**, 853, 147066	0
193	Avermectin induces cardiac toxicity in early embryonic stage of zebrafish. **2023**, 264, 109529	0
192	RNA-Seq analysis of ovary and testis reveals potential differentially expressed transcripts associated with gonadal unsynchronization development in Onychostoma macrolepis. **2023**, 47, 119303	0
191	Integration of metabolomics and transcriptomics to reveal ferroptosis is involved in Tripterygium wilfordii polyglycoside tablet-induced testicular injury. **2023**, 304, 116055	0
190	Shen-Qi-Jiang-Tang granule ameliorates diabetic nephropathy via modulating tumor necrosis factor signaling pathway. **2023**, 303, 116031	0
189	Scrophulariae Radix-Atractylodes sinensis pair and metformin inhibit inflammation by modulating gut microbiota of high-fat diet/streptozotocin-induced diabetes in rats. 13,	0
188	Pretreatment of NaCl enhances the drought resistance of cotton by regulating the biosynthesis of carotenoids and abscisic acid. 10,	0
187	Genomic analysis and in vivo efficacy of Pediococcus acidilactici as a potential probiotic to prevent hyperglycemia, hypercholesterolemia and gastrointestinal infections. **2022**, 12,	1
186	Lutein inhibits tumor progression through the ATR /Chk1/p53 signaling pathway in non-small cell lung cancer.	0
185	Multi-layer guilt-by-association-based drug repurposing by integrating clinical knowledge on biological heterogeneous networks.	0
184	An Intestinal Symbiotic Bacterial Strain of Oscheius chongmingensis Modulates Host Viability at Both Global and Post-Transcriptional Levels. **2022**, 23, 14692	0
183	Comparative proteomic analysis of mustard lung as a complicated disease using systems biology approach. **2022**, 22,	0

182	Genomic profiling and network-level understanding uncover the potential genes and the pathways in hepatocellular carcinoma. 13,	0
181	Laminarin ameliorates alcohol-induced liver damage and its molecular mechanism in mice.	0
180	Rapid induction and long-term self-renewal of neural crest-derived ectodermal chondrogenic cells from hPSCs. **2022**, 7,	0
179	Complete genome sequence analysis of a plant growth-promoting phylloplane Bacillus altitudinis FD48 offers mechanistic insights into priming drought stress tolerance in rice. **2022**, 110550	1
178	Leaf transcriptome analysis of Medicago ruthenica revealed its response and adaptive strategy to drought and drought recovery. **2022**, 22,	0
177	MicroRNA Profiling of Root Meristematic Zone in Contrasting Genotypes Reveals Novel Insight into in Rice Response to Water Deficiency.	0
176	Testing the chilling- before drought-tolerance hypothesis in Pooideae grasses.	0
175	Transcriptome-phenotype matching analysis of how nitrogen sources influence Lacticaseibacillus rhamnosus tolerance to heat stress and oxidative stress. **2022**, 21,	0
174	miR-615 facilitates porcine epidemic diarrhea virus replication by targeting IRAK1 to inhibit type III interferon expression. 13,	0
173	The effects of glyphosate exposure on gene transcription and immune function of the silkworm, Bombyx mori.	0
172	Comparative transcriptome profiling of resistant and susceptible foxtail millet responses to Sclerospora graminicola infection. **2022**, 22,	0
171	bHLH57 confers chilling tolerance and grain yield improvement in rice.	1
170	The methanogen core and pangenome: conservation and variability across biology� growth temperature extremes.	0
169	ATAC-seq exposes differences in chromatin accessibility leading to distinct leaf shapes in mulberry. **2022**, 6,	0
168	The immune-related circRNA-miRNA-mRNA ceRNA regulatory network in the liver of turbot (Scophthalmus maximus L.) induced by Vibrio anguillarum. **2022**, 108506	0
167	Comparative Analysis of mRNA and miRNA Expression between Dermal Papilla Cells and Hair Matrix Cells of Hair Follicles in Yak. **2022**, 11, 3985	0
166	Transcriptome sequencing analysis and WGCNA reveal the internal molecular mechanism that triggers programmed cell death in rice mutant zj-lm.	0
165	Transcriptome analysis and cytochrome P450 monooxygenase reveal the molecular mechanism of Bisphenol A degradation by Pseudomonas putida strain YC-AE1. **2022**, 22,	0

164	RNA-seq Gene Profiling Reveals Transcriptional Changes in the Late Phase during Compatible Interaction between a Korean Soybean Cultivar (Glycine max cv. Kwangan) and Pseudomonas syringae pv. syringae B728a. **2022**, 38, 603-615	0
163	TIPARP is involved in the regulation of intraocular pressure. **2022**, 5,	0
162	Integrated transcriptome and metabolome analysis reveals the anthocyanin biosynthesis mechanisms in blueberry (Vaccinium corymbosum L.) leaves under different light qualities. 13,	0
161	DNA Methylation Variation Is a Possible Mechanism in the Response of Haemaphysalis longicornis to Low-Temperature Stress. **2022**, 23, 15207	0
160	Metagenomic characterization of the maternal prenatal gastrointestinal microbiome by pregravid BMI.	0
159	Comprehensive investigation of pathway enrichment methods for functional interpretation of LC-MS global metabolomics data.	0
158	Transcriptome analysis of PK-15 cells expressing CSFV NS4A. **2022**, 18,	0
157	Transcriptome profiling of male and female Ascaris lumbricoides reproductive tissues. **2022**, 15,	0
156	RNA-seq analysis of a zebrafish caudal fin cell line in response to infection with spring viraemia of carp virus. **2022**,	0
155	Anti-cancer effects of ginsenoside CK on acute myeloid leukemia in vitro and in vivo. **2022**, 8, e12106	0
154	Comparative Meta-analysis of Adipose Tissue Transcriptomics Data in PCOS Patients and Healthy Control Women.	0
153	Transcriptome analysis of the muscle of fast- and slow-growing phoenix barb (Spinibarbus denticulatus denticulatus).	0
152	Metformin modulates the gut microbiome in a mice model of high-fat diet-induced glycolipid metabolism disorder. **2022**, 10, e003149	1
151	High throughput sequencing revealed enhanced cell cycle signaling in SLE patients. **2023**, 13,	0
150	LncRNA EN-90756 promotes CPB2-induced proliferation and inhibits apoptosis in IPEC-J2 cells by affecting the JAK-STAT signaling pathway activation. 13,	1
149	Transcriptome Analysis of the Immune Process of Golden Pompano (Trachinotus ovatus) Infected with Streptococcus agalactiae. **2023**, 8, 52	1
148	Molecular and physiological mechanisms of tea (Camellia sinensis (L.) O. Kuntze) leaf and root in response to nitrogen deficiency. **2023**, 24,	0
147	Liver transcriptome analysis reveals the energy regulation and functional impairment of Onychosoma sima during starvation.	0

146	Bioinformatic analysis and machine learning to identify the diagnostic biomarkers and immune infiltration in adenomyosis. 13,	0
145	Host Transcriptome Analysis of Spodoptera frugiperda Larvae Parasitized by Microplitis manilae. **2023**, 14, 100	0
144	Urate oxidase from tea microbe Colletotrichum camelliae is involved in the caffeine metabolism pathway and plays a role in fungal virulence. 9,	1
143	Interactions between the gut micro-community and transcriptome of Culex pipiens pallens under low-temperature stress. **2023**, 16,	0
142	Superior Antioxidant Capacity and Auxin Production Promote Seedling Formation of Rice Seeds under Submergence Stress. **2023**, 13, 171	0
141	Isolation and Characterization of SPOTTED LEAF42 Encoding a Porphobilinogen Deaminase in Rice. **2023**, 12, 403	0
140	Duplicated Flagellins in Pseudomonas Divergently Contribute to Motility and Plant Immune Elicitation.	0
139	Comprehensive analysis of transcriptomics and metabolomics to understand tail-suspension-induced myocardial injury in rat. 9,	0
138	A Review of Basic Bioinformatic Techniques for Microbial Community Analysis in an Anaerobic Digester. **2023**, 9, 62	0
137	Duplicate mutations of GhCYP450 lead to the production of ms5m6 male sterile line in cotton. **2023**, 136, 1-14	0
136	Protein aggregation in plant mitochondria inhibits translation and induces an NAC017-dependent ethylene-associated unfolded protein response.	0
135	Protective effects of blocking PD-1 pathway on retinal ganglion cells in a mouse model of chronic ocular hypertension. 13,	0
134	Celsr2 Knockout Alleviates Inhibitory Synaptic Stripping and Benefits Motoneuron Survival and Axon Regeneration After Branchial Plexus Avulsion.	0
133	Metabolism response mechanism in the gill of Oreochromis mossambicus under salinity, alkalinity and saline-alkalinity stresses. **2023**, 251, 114523	0
132	Elucidation of the mechanism underlying seedless blueberry formation after GA3 treatment based on the phenotype, physiology, metabolism and transcriptome. **2023**, 311, 111781	0
131	miR-34a Regulates Lipid Droplet Deposition in 3T3-L1 and C2C12 Cells by Targeting LEF1. **2023**, 12, 167	0
130	Different impacts of TP53 mutations on cell cycle-related gene expression among cancer types.	0
129	Identification of AP-1 as a Critical Regulator of Glutathione Peroxidase 4 (GPX4) Transcriptional Suppression and Acinar Cell Ferroptosis in Acute Pancreatitis. **2023**, 12, 100	0

128	A chromosome-scale genome assembly of Dasypyrum villosum, a genetic resource for wheat improvement, provides insights into its broad-spectrum disease resistance. **2022**,	0
127	Imaginal disc growth factor is involved in melanin synthesis and energy metabolism in Bombyx mori.	0
126	Integrating Prior Knowledge with Graph Encoder for Gene Regulatory Inference from Single-cell RNA-Seq Data. **2022**,	0
125	Transcriptional Analysis of Tea Plants (Camellia sinensis) in Response to Salicylic Acid Treatment. **2023**, 71, 2377-2389	0
124	Identification and expression analyses of the olfactory-related genes in different tissues' transcriptome of a predacious soldier beetle, Podabrus annulatus (Coleoptera, Cantharidae).	0
123	Global Gene Expression in Cotton Fed Upon by Aphis gossypii and Acyrthosiphon gossypii (Hemiptera: Aphididae). **2023**, 58, 47-68	0
122	Comparative Transcriptomic Analysis of Genes in the 20-Hydroxyecdysone Biosynthesis in the Fern Microsorum´scolopendria towards Challenges with Foliar Application of Chitosan. **2023**, 24, 2397	0
121	Genome-wide screen in human plasma identifies multifaceted complement evasion of Pseudomonas aeruginosa. **2023**, 19, e1011023	0
120	Identification and Functional Prediction of Long Non-Coding RNA in Longissimus Dorsi Muscle of Queshan Black and Large White Pigs. **2023**, 14, 197	0
119	Comprehensive profile and contrastive analysis of circular RNA expression in cervical squamous carcinoma and adenocarcinoma. 11, e14759	0
118	Genomic and physiological characterization of Novosphingobium terrae sp. nov., an alphaproteobacterium isolated from Cerrado soil containing a mega-sized chromid.	0
117	Network analyses of upper and lower airway transcriptomes identify shared mechanisms among children with recurrent wheezing and school-age asthma. 14,	0
116	A Comprehensive Landscape of Imaging Feature-Associated RNA Expression Profiles in Human Breast Tissue. **2023**, 23, 1432	0
115	Network pharmacology integrated with experimental validation to explore the therapeutic role and potential mechanism of Epimedium for spinal cord injury. 16,	0
114	Unlocking the magic in mycelium: Using synthetic biology to optimize filamentous fungi for biomanufacturing and sustainability. **2023**, 19, 100560	0
113	Creating PROV-DM Graphs from Model Databases. **2022**,	0
112	Behavioural effects and RNA-seq analysis of A□42 mediated toxicity in a Drosophila Alzheimer□ disease model.	0
111	Hepatic Transcriptome Analysis Reveals Genes, Polymorphisms, and Molecules Related to Lamb Tenderness. **2023**, 13, 674	0

110	PFOS Induces Lipometabolism Change, Immune Defense, and Endocrine Disorders in Black-Spotted Frogs: Application of Transcriptome Profiling. **2023**, 15, 196	0
109	Transcriptome analysis reveals association of carotenoid metabolism pathway with fruit color in melon. **2023**, 13,	0
108	Microbial Communities of Flor Velums and the Genetic Stability of Flor Yeasts Used for a Long Time for the Industrial Production of Sherry-like Wines. **2023**, 9, 367	0
107	Spectral light quality regulates the morphogenesis, architecture, and flowering in pepper (Capsicum annuum L.). **2023**, 241, 112673	0
106	Comparative transcriptome analysis revealed genes involved in the sexual size dimorphisms and expressed sequence tag-Simple Sequence Repeat loci validation in Odorrana graminea. 11,	0
105	The effects of short-term dietary exposure to SiO2 nanoparticle on the domesticated lepidopteran insect model silkworm (Bombyx mori): Evidence from the perspective of multi-omics. **2023**, 323, 138257	0
104	TMT-based quantitative proteomics analysis reveals the differential proteins between fresh and frozen-thawed sperm of yak (Bos grunniens). **2023**, 200, 60-69	0
103	Integrating physiological and transcriptome analyses clarified the molecular regulation mechanism of PyWRKY48 in poplar under cadmium stress. **2023**, 238, 124072	0
102	Jinfeng pills ameliorate premature ovarian insufficiency induced by cyclophosphamide in rats and correlate to modulating IL-17A/IL-6 axis and MEK/ERK signals. **2023**, 307, 116242	0
101	Lactate induces tumor-associated macrophage polarization independent of mitochondrial pyruvate carrier-mediated metabolism. **2023**, 237, 123810	0
100	Protective effects of MNQ against Lipopolysaccharide-induced inflammatory damage in bovine ovarian follicular granulosa cells in Vitro. **2023**, 230, 106274	0
99	Extracellular self-DNA induced a PTI-related local defence against Rhizopus rot in postharvest peach fruit. **2023**, 200, 112306	0
98	Enantioselectivity effects of energy metabolism in honeybees (Apis mellifera) by triticonazole. **2023**, 877, 162884	0
97	DiDang decoction improves mitochondrial function and lipid metabolism via the HIF-1 signaling pathway to treat atherosclerosis and hyperlipidemia. **2023**, 308, 116289	0
96	Single-cell transcriptomic dissection of the toxic impact of di(2-ethylhexyl) phthalate on immature testicular development at the neonatal stage. **2023**, 176, 113780	0
95	The use of physiological and transcriptional analyses to examine molting regulatory mechanisms in juvenile horseshoe crab Tachypleus tridentatus. **2023**, 572, 739518	0
94	Analyses of circRNAs profiles of the lactating and nonlactating crops in pigeon (Columba livia). **2023**, 102, 102464	0
93	QTL Mapping and a Transcriptome Integrative Analysis Uncover the Candidate Genes That Control the Cold Tolerance of Maize Introgression Lines at the Seedling Stage. **2023**, 24, 2629	0

92	CRISPR/Cas9-mediated gene editing of vacuolar ATPase subunit d mediates phytohormone biosynthesis and virus resistance in rice. 14,	O
91	Ginsenoside Rg1 as a promising adjuvant agent for enhancing the anti-cancer functions of granulocytes inhibited by noradrenaline. 14,	O
90	Uterine Flushing Fluid-Derived Let-7b Targets CXCL10 to Regulate Uterine Receptivity in Goats during Embryo Implantation. **2023**, 24, 2799	O
89	Proteomic analysis of fetal skin by iTRAQ reveals molecular signals underlying Inner Mongolia Cashmere goat hair follicle initiation. **2023**, 16,	O
88	Transcriptomic Analysis and Functional Gene Expression in Different Stages of Gonadal Development of Macrobrachium rosenbergii. **2023**, 8, 94	O
87	Transcriptome analysis of the Mizuhopecten yessoensis gills under high temperature fluctuations. **2023**, 142,	O
86	Combined Analysis of the Whole Transcriptome of Piglets Infected with SADS□CoV Virulent and Avirulent Strains. **2023**, 11, 409	O
85	Transcriptome analysis of the hepatopancreas in Penaeus vannamei under experimental infection with Enterocytozoon hepatopenaei (EHP). **2023**, 134, 108605	O
84	Susceptibility monitoring and comparative gene expression of susceptible and resistant strains of Spodoptera frugiperda to lambda-cyhalothrin and chlorpyrifos.	O
83	miRNA-27a is essential for bone remodeling by modulating p62-mediated osteoclast signaling. 12,	O
82	Comparison of Metabolomic Profile Between Colistin Susceptible and Colistin Resistant Strains of A. baumanni.	O
81	The injections of mitochondrial fusion promoter M1 during proestrus disrupt the progesterone secretion and the estrous cycle in the mouse. **2023**, 13,	O
80	The RNase III enzyme Dicer1 is essential for larval development in Bombyx mori.	O
79	Comparative Transcriptome Analysis Reveals Potential Genes Conferring Resistance or Susceptibility to Bacterial Canker in Tomato. **2023**, 9, 242	O
78	Transcriptome and Metabolome Analysis Reveals Salt-Tolerance Pathways in the Leaves and Roots of ZM-4 (Malus zumi) in the Early Stages of Salt Stress. **2023**, 24, 3638	O
77	Tidal emersion effects on universal metrics, elemental contents, and health conditions of Pacific oyster (Crassostrea gigas) on artificial reefs in Yellow River Delta, China. **2023**, 42, e02409	O
76	Deficiency of primate-specific SSX1 induced asthenoteratozoospermia in infertile men and cynomolgus monkey and tree shrew models. **2023**, 110, 516-530	O
75	Liver Injury and Metabolic Dysregulation in Largemouth Bass (Micropterus salmoides) after Ammonia Exposure. **2023**, 13, 274	O

74	Influences of chemotype and parental genotype on metabolic fingerprints of tansy plants uncovered by predictive metabolomics.	0
73	Distinct H3K27me3 and H3K27ac Modifications in Neural Tube Defects Induced by Benzo[a]pyrene. **2023**, 13, 334	0
72	Machine learning-enabled retrobiosynthesis of molecules. **2023**, 6, 137-151	1
71	Liver Transcriptome Analysis Reveals Energy Regulation and Functional Impairment of Onychostoma sima´During Starvation.	0
70	In silico Identification of Hypoxic Signature followed by reverse transcription-quantitative PCR Validation in Cancer Cell Lines. **2023**, 27, 23-33	0
69	Artificial intelligence-based clustering and characterization of Parkinson's disease trajectories. **2023**, 13,	0
68	Approaches for sRNA Analysis of Human RNA-Seq Data: Comparison, Benchmarking. **2023**, 24, 4195	0
67	Comparative Transcriptome Profiling Reveals Key MicroRNAs and Regulatory Mechanisms for Aluminum Tolerance in Olive. **2023**, 12, 978	0
66	Integrated transcriptome analysis reveals roles of long non-coding RNAs (lncRNAs) in caprine skeletal muscle mass and meat quality. **2023**, 23,	0
65	Acquired radioresistance in EMT6 mouse mammary carcinoma cell line is mediated by CTLA-4 and PD-1 through JAK/STAT/PI3K pathway. **2023**, 13,	0
64	Transcriptional profiling analysis providing insights into desiccation tolerance mechanisms of the desert moss Syntrichia caninervis. 14,	0
63	Comparative gene regulatory network analysis in Alzheimer□ disease and major depressive disorder.	0
62	PriPath: identifying dysregulated pathways from differential gene expression via grouping, scoring, and modeling with an embedded feature selection approach. **2023**, 24,	1
61	Genome-Wide Landscape of mRNAs, lncRNAs, and circRNAs during Testicular Development of Yak. **2023**, 24, 4420	0
60	A minimal genome design to maximally guarantee fertile inter-subspecific hybrid rice. **2023**, 16, 726-738	1
59	Epi-Brassinolide Regulates ZmC4 NADP-ME Expression through the Transcription Factors ZmbHLH157 and ZmNF-YC2. **2023**, 24, 4614	0
58	Spleen Toxicity of Organophosphorus Flame Retardant TDCPP in Mice and the Related Mechanisms. **2023**, 11, 231	0
57	Interpreting metabolic complexity via isotope-assisted metabolic flux analysis. **2023**,	0

56 Hypoxic Preconditioned Neural Stem Cell-Derived Extracellular Vesicles Contain Distinct Protein Cargo from Their Normal Counterparts. **2023**, 45, 1982-1997 o

55 Small Brown Planthopper Nymph Infestation Regulates Plant Defenses by Affecting Secondary Metabolite Biosynthesis in Rice. **2023**, 24, 4764 o

54 Growing Directed Acyclic Graphs: Optimization Functions for Pathway Reconstruction Algorithms. o

53 Transcriptomics and Proteomics of Haemonchus contortus in Response to Ivermectin Treatment. **2023**, 13, 919 o

52 Metatranscriptomics and metabarcoding reveal spatiotemporal shifts in fungal communities and their activities in Chinese coastal waters. o

51 Genome-Wide Analysis of lncRNA and mRNA Expression in the Uterus of Laying Hens during Aging. **2023**, 14, 639 o

50 A Matrix Factorization-Based Drug-Virus Link Prediction Method for´SARS-CoV-2 Drug Prioritization. **2023**, 35-47 o

49 Dynamic Association of ESCRT-II Proteins with ESCRT-I and ESCRT-III Complexes during Phagocytosis of Entamoeba histolytica. **2023**, 24, 5267 o

48 Transcriptome Analysis During Tetrasporogenesis of Gracilariopsis lemaneiformis and Preliminary Study of the Expressions of Its Meiotic Genes. **2023**, 22, 541-554 o

47 Strategy for the Adaptation to Stressful Conditions of the Novel Isolated Conditional Piezophilic Strain Halomonas titanicae ANRCS81. **2023**, 89, o

46 Comparative Transcriptome and Metabolome Analysis of Rubber Trees (Hevea brasiliensis Muell. Arg.) Response to Aluminum Stress. **2023**, 14, 568 o

45 Peptidome and Transcriptome Analysis of Plant Peptides Involved in Bipolaris maydis Infection of Maize. **2023**, 12, 1307 o

44 Transcriptome analysis reveals defense-related genes and pathways during dodder (Cuscuta australis) parasitism on white clover (Trifolium repens). 14, o

43 Comparative Gut Microbiome Differences between High and Low Aortic Arch Calcification Score in Patients with Chronic Diseases. **2023**, 24, 5673 o

42 Transcriptome Analysis of Pecan (Carya illinoinensis) Differentially Expressed Genes in Response to Drought Stress. **2023**, 14, 608 o

41 Transcriptomic and Metabolomic Profiles Provide Insights into the Red-Stipe Symptom of Morel Fruiting Bodies. **2023**, 9, 373 o

40 Comparative transcriptome analysis of molecular mechanisms underlying adventitious root developments in Huangshan Bitter tea (Camellia gymnogyna Chang) under red light quality. 14, o

39 Transcriptome analysis of Lr19-virulent mutants provides clues for the AvrLr19 of Puccinia triticina. 14, o

38	Heterologous VvDREB2c Expression Improves Heat Tolerance in Arabidopsis by Inducing Photoprotective Responses. **2023**, 24, 5989	0
37	Discovery of a novel bacterial class with the capacity to drive sulfur cycling and microbiome structure in a paleo-ocean analog.	0
36	Integrative Transcriptomic and Metabolomic Analysis Reveals the Molecular Mechanism of Red Maple (Acer rubrum L.) Leaf Coloring. **2023**, 13, 464	0
35	Functional differentiation of the ovine preadipocytes insights from gene expression profiling. **2023**, 23,	0
34	Acetylation of GhCaM7 enhances cotton resistance to Verticillium dahliae.	0
33	Pathogenesis of allergic diseases and implications for therapeutic interventions. **2023**, 8,	0
32	Effects of Starvation on the Physiology and Liver Transcriptome of Yellowcheek (Elopichthys bambusa). **2023**, 8, 175	0
31	Machine Learning-Assisted Approaches in Modernized Plant Breeding Programs. **2023**, 14, 777	0
30	Changes in the Long Noncoding RNA Expression Profile in the Development of the Embryonic External Ear After BMP5 Gene Mutation. Publish Ahead of Print,	0
29	Transcriptome analysis of gene expression profiles reveals wood formation mechanisms in Chinese fir at different stand ages. **2023**, 9, e14861	0
28	Comparative Transcriptomic Analysis Reveals the Functionally Segmented Intestine in Tunicate Ascidian. **2023**, 24, 6270	0
27	Quorum Sensing-Mediated Lipid Oxidation Further Regulating the Environmental Adaptability of Aspergillus ochraceus. **2023**, 13, 491	0
26	Transcriptomic Analysis of Liver in Silver sillago, Sillago sihama Fed with High-Level Low-Gossypol Cottonseed Meal in Replacement of Fishmeal Diet. **2023**, 13, 1194	0
25	A Deep-Sea Bacterium Is Capable of Degrading Polyurethane.	0
24	Nucleolar Protein 56 Deficiency in Zebrafish Leads to Developmental Abnormalities and Anemia via p53 and JAK2-STAT3 Signaling. **2023**, 12, 538	0
23	Human menstrual blood-derived stem cells alleviate autoimmune hepatitis via JNK/MAPK signaling pathway in vivo and in vitro.	0
22	Comprehensive investigation of long non-coding RNAs in an endophytic fungus Calcarisporium arbuscula NRRL 3705. **2023**, 205,	0
21	Auxin participates in regulating the leaf curl development of Wucai (Brassica campestris L.). **2023**, 175,	0

20	Gonadal transcriptomes reveal sex-biased expression genes associated with sex determination and differentiation in red-tail catfish (Hemibagrus wyckioides). **2023**, 24,	0
19	Distinct maternal metabolites are associated with obesity and glucose-insulin axis in the first trimester of pregnancy.	0
18	Identification of Key Functional Genes and LncRNAs Influencing Muscle Growth and Development in Leizhou Black Goats. **2023**, 14, 881	0
17	Combining Cryo-Thermal Therapy with Anti-IL-6 Treatment Promoted the Maturation of MDSCs to Induce Long-Term Survival in a Mouse Model of Breast Cancer. **2023**, 24, 7018	0
16	Integrated Transcriptome and Small RNA Sequencing Analyses Reveals Insights into the Molecular Mechanism of Seed Germination in Mung Bean. **2023**, 92, 1793-1812	0
15	Transcriptomic analysis identified SLC40A1 as a key iron metabolism-related gene in airway macrophages in childhood allergic asthma. 11,	0
14	Integrated Metabolome and Transcriptome Analysis Reveals a Potential Mechanism for Water Accumulation Mediated Translucency in Pineapple (Ananas comosus (L.) Merr.) Fruit. **2023**, 24, 7199	0
13	Integration of mRNA and miRNA Analysis Reveals the Post-Transcriptional Regulation of Salt Stress Response in Hemerocallis fulva. **2023**, 24, 7290	0
12	Moderate Salinity Stress Increases the Seedling Biomass in Oilseed Rape (Brassica napus L.). **2023**, 12, 1650	0
11	The Potential Regulation of A-to-I RNA Editing on Genes in Parkinson’s Disease. **2023**, 14, 919	0
10	A Review of Liquid Chromatography-Mass Spectrometry Strategies for the Analyses of Metabolomics Induced by Microplastics. **2023**, 10, 257	0
9	Effect of Mechanical Tension on the Long-Chain Noncoding RNA Expression Profile of Human Skin Regeneration. Publish Ahead of Print,	0
8	Identification and comparative analysis of miRNA transcriptomes after allograft and xenograft transplantation in Pinctada fucata martensii. **2023**, 108752	0
7	OsJRL40, a Jacalin-Related Lectin Gene, Promotes Salt Stress Tolerance in Rice. **2023**, 24, 7441	0
6	In Ovo Injection of CHIR-99021 Promotes Feather Follicle Development via Modulating the Wnt Signaling Pathway and Transcriptome in Goose Embryos (Anser cygnoides). 13,	0
5	Small molecules vs biologics. **2023**, 179-199	0
4	MTX-211 Inhibits GSH Synthesis through Keap1/NRF2/GCLM Axis and Exerts Antitumor Effects in Bladder Cancer. **2023**, 24, 7608	0
3	Low nitrogen stress-induced transcriptome changes revealed the molecular response and tolerance characteristics in maintaining the C/N balance of sugar beet (Beta vulgaris L.). 14,	0

2	Transcriptomic dissection of termite gut microbiota following entomopathogenic fungal infection. 14,	0
1	Novel players in organogenesis and flavonoid biosynthesis in cucumber glandular trichomes.	0