CITATION REPORT

List of articles citing

Gene ontology: tool for the unification of biology. The Gene Ontology Consortium

DOI: 10.1038/75556

Nature Genetics, 2000, 25, 25-9.

Source: https://exaly.com/paper-pdf/31429726/citation-report.pdf

Version: 2024-04-27

#	Paper	IF	Citations
2188	New approaches to antiviral drug discovery (genomics/proteomics). 1211-1218		1
2187	Bibliography. 255-272		
2186	Magnetite Triggering Enhanced Direct Interspecies Electron Transfer: A Scavenger for the Blockage of Electron Transfer in Anaerobic Digestion of High-Solids Sewage Sludge.		
2185	Deletion of Adipose Triglyceride Lipase Links Triacylglycerol Accumulation to a More-Aggressive Phenotype in A549 Lung Carcinoma Cells.		
2184	Comprehensive Analysis of Lysine Acetylome Reveals a Site-Specific Pattern in Rapamycin-Induced Autophagy.		
2183	.		
2182	Being Positive about Selection. **2006**, 4, e87		
2181	Birthday Honours. **1899**, 1, 1421-1422		
2180	SHORT NOTICES. **1974**, LXXXIX, 927-a-927		
2179	WSC volume 23 issue 6 Cover and Back matter. **1975**, 23, b1-b2		
2178	Book Notes. **1991**, 3, 166-189		
2177	Interprofessional Relationships. **1992**, 28, 49-50		
2176	Integrative database analysis in structural genomics. **2000**, 7 Suppl, 960-3		36
2175	Ets target genes: past, present and future. **2000**, 19, 6533-48		304
2174	Differential gene expression technologies for identifying surrogate markers of drug efficacy and toxicity. **2000**, 5, 560-568		30
2173	The current excitement in bioinformatics-analysis of whole-genome expression data: how does it relate to protein structure and function?. **2000**, 10, 574-84		61
2172	Transcription, genomes, function. **2000**, 16, 409-15		114

2171	Measuring shifts in function and evolutionary opportunity using variability profiles: a case study of the globins. **2000**, 51, 223-33	27
2170	Analysis of molecular profile data using generative and discriminative methods. **2000**, 4, 109-126	68
2169	Bioinformatics. A user's perspective. **2000**, 23, 705-11	23
2168	Supporting Web based biology with ontologies.	2
2167	MultiFun, a multifunctional classification scheme for Escherichia coli K-12 gene products. **2000**, 5, 205-22	108
2166	Representing and analysing molecular and cellular function using the computer. **2000**, 381, 921-35	53
2165	MultiFun, a Multifunctional Classification Scheme forEscherichia coliK-12 Gene Products. **2000**, 5, 205-222	34
2164	The Drosophila genome. **2000**, 10, 612-6	12
2163	Recent developments and future directions in computational genomics. **2000**, 480, 42-8	40
2162	Genomics. The Babel of bioinformatics. **2000**, 290, 471-3	51
2161	Mouse genome informatics in a new age of biological inquiry.	10
2160	. **2001**, 40, 532-551	81
2159	A functional update of the Escherichia coli K-12 genome. **2001**, 2, RESEARCH0035	87
2158	Genome cartography through domain annotation. **2001**, 2, Comment 2006	7
2157	Functional annotation of a full-length mouse cDNA collection. **2001**, 409, 685-90	560
2156	BIND--The Biomolecular Interaction Network Database. **2001**, 29, 242-5	396
2155	PicSNP: a browsable catalog of nonsynonymous single nucleotide polymorphisms in the human genome. **2001**, 287, 288-91	19
2154	Program description: Strategies for biological annotation of mammalian systems: implementing gene ontologies in mouse genome informatics. **2001**, 74, 121-8	41

2153	Fold predictions for bacterial genomes. **2001**, 134, 219-31	22
2152	Review: what can structural classifications reveal about protein evolution?. **2001**, 134, 145-65	38
2151	Spotting the target: microarrays for disease gene discovery. **2001**, 11, 258-63	46
2150	Systematic approaches to mouse mutagenesis. **2001**, 11, 268-73	93
2149	. **2001**, 16, 14-18	18
2148	Information technology tools for efficient SNP studies. **2001**, 1, 303-14	3
2147	Gene classification using expression profiles: a feasibility study. **2001**,	13
2146	An algebra for semantic interoperability of information sources. **2001**,	10
2145	Creating the gene ontology resource: design and implementation. **2001**, 11, 1425-33	788
2144	Analysis of expression patterns: the scope of the problem, the problem of scope. **2001**, 17, 59-65	8
2143	Candidate genes and single nucleotide polymorphisms (SNPs) in the study of human disease. **2001**, 17, 89-98	84
2142	PRECIS: an automated pipeline for producing concise reports about proteins. **2001**,	
2141	Identification and classification of differentially expressed genes in renal cell carcinoma by expression profiling on a global human 31,500-element cDNA array. **2001**, 11, 1861-70	165
2140	Storage, data management, and retrieval in bioinformatics. **2001**, 4676, 248	
2139	Which craft is best in bioinformatics?. **2001**, 25, 329-39	13
2138	Genome comparisons highlight similarity and diversity within the eukaryotic kingdoms. **2001**, 5, 86-9	18
2137	Analysing gene expression data from DNA microarrays to identify candidate genes. **2001**, 195, 53-65	108
2136	Issues in the design of medical ontologies used for knowledge sharing. **2001**, 25, 95-108	12

2135	Community watch. *Nature Genetics*, **2001**, 28, 1-2	36.3	6
2134	Verification and initial annotation of the NIA mouse 15K cDNA clone set. *Nature Genetics*, **2001**, 28, 17-8	36.3	96
2133	A literature network of human genes for high-throughput analysis of gene expression. *Nature Genetics*, **2001**, 28, 21-8	36.3	590
2132	Human disease genes. **2001**, 409, 853-5		286
2131	Bioinformatics beyond sequence: mapping gene function in the embryo. **2001**, 2, 409-17		46
2130	Biology’s name game. **2001**, 411, 631-2		44
2129	Genome annotation: from sequence to biology. **2001**, 2, 493-503		249
2128	A tour of structural genomics. **2001**, 2, 801-9		131
2127	Profiling the malaria genome: a gene survey of three species of malaria parasite with comparison to other apicomplexan species. **2001**, 118, 201-10		31
2126	A status report on the sequencing and annotation of the P. falciparum genome. **2001**, 118, 133-8		9
2125	The human proteomics initiative (HPI). **2001**, 19, 178-81		74
2124	Challenges in bioinformatics: infrastructure, models and analytics. **2001**, 19, 159-60		4
2123	Gene expression microarrays and the integration of biological knowledge. **2001**, 19, 412-5		74
2122	Chromosomes on the move. **2001**, 17, 689-90		3
2121	The morning after. **2001**, 17, 688-9		
2120	Mouse genomics: making sense of the sequence. **2001**, 11, R311-4		3
2119	Novel computational methods in anti-microbial target identification. **2001**, 6, 72-80		20
2118	Clustering and analysis of protein families. **2001**, 11, 334-9		38

2117	Whole-genome analysis: annotations and updates. **2001**, 11, 377-81		29
2116	Parasites are GO. **2001**, 17, 463-4		11
2115	DIAN: a novel algorithm for genome ontological classification. **2001**, 11, 1766-79		11
2114	WormBase: network access to the genome and biology of Caenorhabditis elegans. **2001**, 29, 82-6		238
2113	The Mouse Genome Database (MGD): integration nexus for the laboratory mouse. **2001**, 29, 91-4		54
2112	The Mouse Gene Expression Database (GXD). **2001**, 29, 98-101		46
2111	Changes in global gene expression patterns during development and maturation of the rat kidney. **2001**, 98, 5649-54		155
2110	Amygdala-enriched genes identified by microarray technology are restricted to specific amygdaloid subnuclei. **2001**, 98, 5270-5		140
2109	Microarray probe selection strategies. **2001**, 2, 329-40		48
2108	Proteome Analysis Database: online application of InterPro and CluSTr for the functional classification of proteins in whole genomes. **2001**, 29, 44-8		63
2107	PartsList: a web-based system for dynamically ranking protein folds based on disparate attributes, including whole-genome expression and interaction information. **2001**, 29, 1750-64		37
2106	Recent advances in computational genomics. **2001**, 2, 361-72		5
2105	. *Nature Genetics*, **2001**, 28, 21-28	36.3	227
2104	Mining the bibliome. **2001**, 1, 88-9		11
2103	Detection of cis-element clusters in higher eukaryotic DNA. **2001**, 17, 878-89		202
2102	Interrelating different types of genomic data, from proteome to secretome: ’oming in on function. **2001**, 11, 1463-8		121
2101	The use of animal models in expression pharmacogenomic analyses. **2001**, 1, 48-58		11
2100	Chapter 20. Bioinformatics in the drug discovery process. **2001**, 36, 201-210		1

2099	Agent interaction for bioinformatics data management. **2001**, 15, 917-947		13
2098	Altered cellular mRNA levels in human cytomegalovirus-infected fibroblasts: viral block to the accumulation of antiviral mRNAs. **2001**, 75, 12319-30		237
2097	GENIES: a natural-language processing system for the extraction of molecular pathways from journal articles. **2001**, 17 Suppl 1, S74-82		300
2096	Functional versatility and molecular diversity of the metabolic map of Escherichia coli. **2001**, 11, 1503-10		25
2095	From molecular activities and processes to biological function. **2001**, 2, 81-93		26
2094	Protein function from the perspective of molecular interactions and genetic networks. **2001**, 2, 38-50		18
2093	Evaluating mutant mice: anatomic pathology. **2001**, 38, 1-19		68
2092	PlasmoDB: An integrative database of the Plasmodium falciparum genome. Tools for accessing and analyzing finished and unfinished sequence data. The Plasmodium Genome Database Collaborative. **2001**, 29, 66-9		67
2091	A multi-agent system for automated genomic annotation. **2001**,		9
2090	. *Nature Genetics*, **2001**, 28, 1-2	36.3	1
2089	. *Nature Genetics*, **2001**, 28, 17-18	36.3	38
2088	Prediction of higher order functional networks from genomic data. **2001**, 2, 373-85		10
2087	Comparative genome and proteome analysis of Anopheles gambiae and Drosophila melanogaster. **2002**, 298, 149-59		455
2086	Protein-based analysis of alternative splicing in the human genome.		3
2085	euGenes: a eukaryote genome information system. **2002**, 30, 145-8		34
2084	Ontologies in the life sciences. **2002**, 17, 77-80		1
2083	FANTOM DB: database of Functional Annotation of RIKEN Mouse cDNA Clones. **2002**, 30, 116-8		48
2082	Saccharomyces Genome Database (SGD) provides secondary gene annotation using the Gene Ontology (GO). **2002**, 30, 69-72		265

2081	Proteome map of the chloroplast lumen of Arabidopsis thaliana. **2002**, 277, 8354-65	336
2080	Saccharomyces Genome Database. **2002**, 350, 329-46	96
2079	Rough Sets and Current Trends in Computing. **2002**,	15
2078	Assembly, verification, and initial annotation of the NIA mouse 7.4K cDNA clone set. **2002**, 12, 1999-2003	39
2077	Cross-referencing eukaryotic genomes: TIGR Orthologous Gene Alignments (TOGA). **2002**, 12, 493-502	115
2076	Influence of the period-dependent circadian clock on diurnal, circadian, and aperiodic gene expression in Drosophila melanogaster. **2002**, 99, 9562-7	162
2075	BioMAS: A MULTI-AGENT SYSTEM FOR GENOMIC ANNOTATION. **2002**, 11, 265-292	16
2074	Molecular characterization of lymphatic endothelial cells. **2002**, 99, 16069-74	373
2073	Extension and integration of the gene ontology (GO): combining GO vocabularies with external vocabularies. **2002**, 12, 1982-91	65
2072	Large-scale protein annotation through gene ontology. **2002**, 12, 785-94	73
2071	Rat Genome Database (RGD): mapping disease onto the genome. **2002**, 30, 125-8	69
2070	ARROGANT: an application to manipulate large gene collections. **2002**, 18, 1410-7	9
2069	Molecular fossils in the human genome: identification and analysis of the pseudogenes in chromosomes 21 and 22. **2002**, 12, 272-80	144
2068	Progress in bioinformatics and the importance of being earnest. **2002**, 8, 1-54	8
2067	Extracting functional information from microarrays: a challenge for functional genomics. **2002**, 99, 12509-11	19
2066	Genome-wide transcriptional orchestration of circadian rhythms in Drosophila. **2002**, 277, 14048-52	218
2065	Fly factory. **2002**, 12, 1017-8	2
2064	Using a systems biological approach to develop novel therapeutics. **2002**, 3, 12-4	1

2063	Generation of expressed sequence tags from a normalized porcine skeletal muscle cDNA library. **2002**, 13, 211-22	31
2062	Information management systems for pharmacogenomics. **2002**, 3, 651-67	6
2061	On the efficient evaluation of relaxed queries in biological databases. **2002**,	6
2060	Identification of genes periodically expressed in the human cell cycle and their expression in tumors. **2002**, 13, 1977-2000	1043
2059	Genomics for applied microbiology. **2002**, 51, 201-45	13
2058	Conserved codon composition of ribosomal protein coding genes in Escherichia coli, Mycobacterium tuberculosis and Saccharomyces cerevisiae: lessons from supervised machine learning in functional genomics. **2002**, 30, 2599-607	49
2057	Association of nucleotide patterns with gene function classes: application to human 3' untranslated sequences. **2002**, 18, 182-9	53
2056	Associating genes with gene ontology codes using a maximum entropy analysis of biomedical literature. **2002**, 12, 203-14	120
2055	Advances in Web-Age Information Management. **2002**,	1
2054	An efficient algorithm for large-scale detection of protein families. **2002**, 30, 1575-84	2433
2053	Annotating the human proteome: the Human Proteome Survey Database (HumanPSD) and an in-depth target database for G protein-coupled receptors (GPCR-PD) from Incyte Genomics. **2002**, 30, 137-41	57
2052	Transitive functional annotation by shortest-path analysis of gene expression data. **2002**, 99, 12783-8	250
2051	The Celera Discovery System. **2002**, 30, 129-36	49
2050	Using text analysis to identify functionally coherent gene groups. **2002**, 12, 1582-90	44
2049	Dissection of transient oxidative stress response in Saccharomyces cerevisiae by using DNA microarrays. **2002**, 13, 2783-94	95
2048	MitoNuc: a database of nuclear genes coding for mitochondrial proteins. Update 2002. **2002**, 30, 172-3	11
2047	READ: RIKEN Expression Array Database. **2002**, 30, 211-3	31
2046	PipeOnline 2.0: automated EST processing and functional data sorting. **2002**, 30, 4761-9	40

2045	Profiling patterned transcripts in Drosophila embryos. **2002**, 12, 1040-7	20
2044	GenomeHistory: a software tool and its application to fully sequenced genomes. **2002**, 30, 3378-86	59
2043	Predicting protein cellular localization using a domain projection method. **2002**, 12, 1168-74	81
2042	Impact of the presence of paralogs on sequence divergence in a set of mouse-human orthologs. **2002**, 12, 1370-6	49
2041	Relating whole-genome expression data with protein-protein interactions. **2002**, 12, 37-46	509
2040	Judging the quality of gene expression-based clustering methods using gene annotation. **2002**, 12, 1574-81	210
2039	Proteomics. Integrating interactomes. **2002**, 295, 284-7	65
2038	Functional genomics of the endocrine pancreas: the pancreas clone set and PancChip, new resources for diabetes research. **2002**, 51, 1997-2004	69
2037	Annotation of microbial genomes. **2002**, 33, 3-26	4
2036	Biology-driven Clustering of Microarray Data. **2002**, 65-79	2
2035	Asymmetric functional divergence of duplicate genes in yeast. **2002**, 19, 1760-8	112
2034	An ontology for pharmaceutical ligands and its application for in silico screening and library design. **2002**, 42, 947-55	93
2033	Profiling gene expression using onto-express. **2002**, 79, 266-70	398
2032	Computational analysis of alternative splicing using EST tissue information. **2002**, 80, 326-30	35
2031	Global analysis of gene expression patterns in developing mouse neocortex using serial analysis of gene expression. **2002**, 19, 560-73	25
2030	Genomics Applications That Facilitate the Understanding of Drug Action and Toxicity. 83-125	2
2029	Dietary effects of arachidonate-rich fungal oil and fish oil on murine hepatic and hippocampal gene expression. **2002**, 1, 2	68
2028	Microarray analysis of orthologous genes: conservation of the translational machinery across species at the sequence and expression level. **2003**, 4, R4	19

(2002-2002)

2027	The GRID: The General Repository for Interaction Datasets. **2002**, 3, preprint0013.1	
2026	Osprey: A Network Visualization System. **2002**, 3, preprint0012.1	4
2025	An integrated computational pipeline and database to support whole-genome sequence annotation. **2002**, 3, RESEARCH0081	40
2024	Systematic determination of patterns of gene expression during Drosophila embryogenesis. **2002**, 3, RESEARCH0088	487
2023	Evolutionary conservation of otd/Otx2 transcription factor action: a genome-wide microarray analysis in Drosophila. **2002**, 3, RESEARCH0015	20
2022	Intelligent Data Engineering and Automated Learning IDEAL 2002. **2002**,	1
2021	Computational Methods and Bioinformatic Tools. 769-904	
2020	A draft sequence of the rice genome (Oryza sativa L. ssp. indica). **2002**, 296, 79-92	2356
2019	Interrogating a high-density SNP map for signatures of natural selection. **2002**, 12, 1805-14	678
2018	Spontaneous oxidative stress and liver tumors in mice lacking methionine adenosyltransferase 1A. **2002**, 16, 1292-4	236
2017	Evaluation of computational metabolic-pathway predictions for Helicobacter pylori. **2002**, 18, 715-24	72
2016	MIPS Arabidopsis thaliana Database (MAtDB): an integrated biological knowledge resource based on the first complete plant genome. **2002**, 30, 91-3	141
2015	Perspective: microarray technology, seeing more than spots. **2002**, 143, 1983-9	43
2014	Metabolic pathway analysis in trypanosomes and malaria parasites. **2002**, 357, 101-7	22
2013	Studying genomes through the aeons: protein families, pseudogenes and proteome evolution. **2002**, 318, 1155-74	146
2012	Prediction of human protein function from post-translational modifications and localization features. **2002**, 319, 1257-65	274
2011	. **2002**, 90, 1848-1858	5
2010	Gene expression during the life cycle of Drosophila melanogaster. **2002**, 297, 2270-5	740

2009	Gene expression phenotype in heterozygous carriers of ataxia telangiectasia. **2002**, 71, 791-800	44
2008	The value of microarray techniques for quantitative gene profiling in molecular diagnostics. **2002**, 8, 269-72	32
2007	The systemic paradigm and its relevance to the modelling of biological functions. **2002**, 325, 419-30	4
2006	Expression profiling in stably regenerating skeletal muscle of dystrophin-deficient mdx mice. **2002**, 12 Suppl 1, S118-24	30
2005	Functional genomics of immune responses. **2002**, 22, 891-910	2
2004	Gene expression profiling reveals role for EGF-family ligands in mesangial cell proliferation. **2002**, 283, F1151-9	32
2003	Expression profiling of human renal carcinomas with functional taxonomic analysis. **2002**, 3, 26	39
2002	OILing the way to machine understandable bioinformatics resources. **2002**, 6, 129-34	17
2001	AvGI, an index of genes transcribed in the salivary glands of the ixodid tick Amblyomma variegatum. **2002**, 32, 1447-56	74
2000	Electronic tools to manage gene expression data. **2002**, 18, 108-110	5
1999	The FLEXGene repository: exploiting the fruits of the genome projects by creating a needed resource to face the challenges of the post-genomic era. **2002**, 33, 318-24	36
1998	Conservation and diversification of gene function in plant development. **2002**, 5, 56-61	10
1997	Introducing GeneDB: a generic database. **2002**, 18, 465-467	4
1996	Comparative genomics approaches to study organism similarities and differences. **2002**, 35, 142-50	48
1995	Two biomedical sublanguages: a description based on the theories of Zellig Harris. **2002**, 35, 222-35	128
1994	Genome-wide transcript profiles in aging and calorically restricted Drosophila melanogaster. **2002**, 12, 712-23	455
1993	A comprehensive collection of chicken cDNAs. **2002**, 12, 1965-9	274
1992	Text-based knowledge discovery: search and mining of life-sciences documents. **2002**, 7, S89-98	36

1991	Genome annotation techniques: new approaches and challenges. **2002**, 7, S70-6	21
1990	Functional transcriptomes: comparative analysis of biological pathways and processes in eukaryotes to infer genetic networks among transcripts. **2002**, 12, 355-61	15
1989	TEMBLOR - Perspectives of EBI Database Services. **2002**, 3, 47-50	3
1988	Ontology based document enrichment in bioinformatics. **2002**, 3, 42-6	3
1987	The Plant Ontology Consortium and plant ontologies. **2002**, 3, 137-42	80
1986	Website review: how to get the best from fission yeast genome data. **2002**, 3, 282-8	8
1985	A computational strategy for protein function assignment which addresses the multidomain problem. **2002**, 3, 423-40	7
1984	Functional genomics: high-throughput mRNA, protein, and metabolite analyses. **2002**, 4, 98-106	91
1983	A framework for integrating the songbird brain. **2002**, 188, 961-80	24
1982	Expression profiling in mouse fetal thymus reveals clusters of coordinately expressed genes that mark individual stages of T-cell ontogeny. **2002**, 54, 469-78	3
1981	The genomics of yeast responses to environmental stress and starvation. **2002**, 2, 181-92	309
1980	Yeast genomic databases and the challenge of the post-genomic era. **2002**, 2, 212-37	15
1979	Towards patient-specific tumor antigen selection for vaccination. **2002**, 188, 164-76	61
1978	Functional genomics: tools of the trade. **2002**, 153, 27-36	43
1977	Evidence for large domains of similarly expressed genes in the Drosophila genome. **2002**, 1, 5	361
1976	The need for a standard nomenclature for gene classification (a Nucleotide Function Code) and an automated data-based tool to assist in understanding the molecular associations in cell signalling in plant-pathogen interactions. **2002**, 3, 103-9	1
1975	Gene expression profile of Vitamin D3 treated HL60 cells shows an incomplete molecular phenotypic conversion to monocytes. **2002**, 9, 1185-95	11
1974	Sequence and analysis of chromosome 2 of Dictyostelium discoideum. **2002**, 418, 79-85	158

1973	Sequence of Plasmodium falciparum chromosomes 2, 10, 11 and 14. **2002**, 419, 531-4		146
1972	Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13. **2002**, 419, 527-31		127
1971	Genome sequence of the human malaria parasite Plasmodium falciparum. **2002**, 419, 498-511		3336
1970	Sequence of Plasmodium falciparum chromosome 12. **2002**, 419, 534-7		47
1969	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. **2002**, 420, 563-73		1350
1968	Extensive and divergent circadian gene expression in liver and heart. **2002**, 417, 78-83		1235
1967	Analyzing yeast protein-protein interaction data obtained from different sources. **2002**, 20, 991-7		431
1966	GenMAPP, a new tool for viewing and analyzing microarray data on biological pathways. *Nature Genetics*, **2002**, 31, 19-20	36.3	814
1965	Saving sulfur. *Nature Genetics*, **2002**, 31, 228-30	36.3	14
1964	Reversing Babel with GO. *Nature Genetics*, **2002**, 31, 230	36.3	1
1963	Microarray databases: standards and ontologies. *Nature Genetics*, **2002**, 32 Suppl, 469-73	36.3	123
1962	Options available--from start to finish--for obtaining data from DNA microarrays II. *Nature Genetics*, **2002**, 32 Suppl, 481-9	36.3	221
1961	Association of genes to genetically inherited diseases using data mining. *Nature Genetics*, **2002**, 31, 316-9	36.3	283
1960	Large-scale prediction of Saccharomyces cerevisiae gene function using overlapping transcriptional clusters. *Nature Genetics*, **2002**, 31, 255-65	36.3	281
1959	The use and analysis of microarray data. **2002**, 1, 951-60		346
1958	Genomics and natural language processing. **2002**, 3, 601-10		107
1957	SCOR: a Structural Classification of RNA database. **2002**, 30, 392-4		85
1956	Surviving in a sea of data: a survey of plant genome data resources and issues in building data management systems. **2002**, 48, 59-74		11

1955	Microarray data quality analysis: lessons from the AFGC project. Arabidopsis Functional Genomics Consortium. **2002**, 48, 119-31	64
1954	Gramene: a resource for comparative grass genomics. **2002**, 30, 103-5	168
1953	Gramene, a tool for grass genomics. **2002**, 130, 1606-13	162
1952	EST Sequencing, Annotation and Macroarray Transcriptome Analysis Identify Preferentially Root-Expressed Genes in Sugar Beet. **2002**, 4, 700-710	20
1951	Mining the bibliome: searching for a needle in a haystack? New computing tools are needed to effectively scan the growing amount of scientific literature for useful information. **2002**, 3, 200-3	44
1950	Search and retrieve. Large-scale data generation is becoming increasingly important in biological research. But how good are the tools to make sense of the data?. **2002**, 3, 396-400	17
1949	A guide to building image-centric databases. **2003**, 1, 359-77	7
1948	The cell-centered database: a database for multiscale structural and protein localization data from light and electron microscopy. **2003**, 1, 379-95	84
1947	A protein interaction map of Drosophila melanogaster. **2003**, 302, 1727-36	1914
1946	Inclusion of Textual Documentation in the Analysis of Multidimensional Data Sets: Application to Gene Expression Data. **2003**, 52, 119-145	5
1945	Computational approaches to protein-protein interaction. **2003**, 4, 245-55	8
1944	Structural genomics: computational methods for structure analysis. **2003**, 12, 1813-21	88
1943	Bioinformatics and medical informatics: collaborations on the road to genomic medicine?. **2003**, 10, 515-22	60
1942	Target selection and determination of function in structural genomics. **2003**, 55, 249-55	18
1941	Development of a chemical structure comparison method for integrated analysis of chemical and genomic information in the metabolic pathways. **2003**, 125, 11853-65	348
1940	Revamp a model-status and prospects of the Dictyostelium genome project. **2003**, 44, 59-72	13
1939	Automatic prediction of protein function. **2003**, 60, 2637-50	178
1938	Functional genomics and proteomics: charting a multidimensional map of the yeast cell. **2003**, 13, 344-56	102

1937	Malaria parasite and vector genomes: partners in crime. **2003**, 19, 356-62	7
1936	Target validation through high throughput proteomics analysis. **2003**, 2, 217-223	
1935	Beyond similarity-based methods to associate genes for the inference of function. **2003**, 1, 89-96	
1934	Binformatics: not just for sequences anymore. **2003**, 1, 103-111	2
1933	Designing databases to store biological information. **2003**, 1, 134-142	9
1932	A shallow parser based on closed-class words to capture relations in biomedical text. **2003**, 36, 145-58	66
1931	Plans for HDBase research community website for Huntington's Disease. **2003**, 3, 197-217	6
1930	Reading the fine print of the human genome. **2003**, 22, 105-8	
1929	Organelle proteomics: looking at less to see more. **2003**, 13, 629-38	150
1928	An automated method for finding molecular complexes in large protein interaction networks. **2003**, 4, 2	3136
1927	cDNA2Genome: a tool for mapping and annotating cDNAs. **2003**, 4, 39	10
1926	PubMatrix: a tool for multiplex literature mining. **2003**, 4, 61	153
1925	Differential representation of sunflower ESTs in enriched organ-specific cDNA libraries in a small scale sequencing project. **2003**, 4, 40	32
1924	Genomic characterization of a repetitive motif strongly associated with developmental genes in Drosophila. **2003**, 4, 52	4
1923	Helminth vaccines: from mining genomic information for vaccine targets to systems used for protein expression. **2003**, 33, 621-40	76
1922	Predicting gene function by conserved co-expression. **2003**, 19, 238-42	156
1921	Molecular basis of inherited diseases: a structural perspective. **2003**, 19, 505-13	86
1920	Scaling laws in the functional content of genomes. **2003**, 19, 479-84	235

1919	Model systems in drug discovery: chemical genetics meets genomics. **2003**, 99, 183-220	37
1918	From biological databases to platforms for biomedical discovery. **2003**, 21, 263-8	23
1917	Molecular characterization of acute leukemias by use of microarray technology. **2003**, 37, 396-405	116
1916	Phenotype discovery by gene expression profiling: mapping of biological processes linked to BMP-2-mediated osteoblast differentiation. **2003**, 89, 401-26	152
1915	Dynamic visualization of expressed gene networks. **2003**, 196, 419-29	11
1914	Building ontologies in DAML + OIL. **2003**, 4, 133-41	14
1913	An approach to inferring transcriptional regulation among genes from large-scale expression data. **2003**, 4, 148-54	9
1912	Automatic classification of protein functions from the literature. **2003**, 4, 75-9	1
1911	Developing a protein-interactions ontology. **2003**, 4, 85-9	13
1910	Standards and ontologies for functional genomics: towards unified ontologies for biology and biomedicine. **2003**, 4, 116-20	2
1909	Bringing ontology to the gene ontology. **2003**, 4, 90-3	11
1908	ISMB 2003 Text Mining SIG Meeting Report. **2003**, 4, 667-73	2
1907	Ontology recapitulates physiology. **2003**, 10, 784-6	
1906	Genomic data modeling. **2003**, 28, 287-310	14
1905	Ontologies for proteomics: towards a systematic definition of structure and function that scales to the genome level. **2003**, 7, 44-54	46
1904	Gene profiling of hippocampal neuronal culture. **2003**, 85, 1279-88	30
1903	An ontology of human developmental anatomy. **2003**, 203, 347-55	34
1902	Automatic annotation of protein function based on family identification. **2003**, 53, 683-92	39

1901	Better prediction of sub-cellular localization by combining evolutionary and structural information. **2003**, 53, 917-30		67
1900	The Make 2D-DB II package: conversion of federated two-dimensional gel electrophoresis databases into a relational format and interconnection of distributed databases. **2003**, 3, 1441-4		32
1899	GIMS: an integrated data storage and analysis environment for genomic and functional data. **2003**, 20, 1291-306		35
1898	From genomics to proteomics. **2003**, 422, 193-7		734
1897	Biomedical informatics for proteomics. **2003**, 422, 233-7		173
1896	Righting the wrongs. **2003**, 4, 829-31		8
1895	Pancreatic cancer escape variants that evade immunogene therapy through loss of sensitivity to IFNgamma-induced apoptosis. **2003**, 10, 1067-78		31
1894	Making sense of microarray data to classify cancer. **2003**, 3, 308-11		7
1893	Genomics of the periinfarction cortex after focal cerebral ischemia. **2003**, 23, 786-810		148
1892	A universal legal framework as a prerequisite for database interoperability. **2003**, 21, 979-82		7
1891	An integrated functional genomics screening program reveals a role for BMP-9 in glucose homeostasis. **2003**, 21, 294-301		150
1890	Evolution of gene expression in the Drosophila melanogaster subgroup. *Nature Genetics*, **2003**, 33, 138-44	36.3	293
1889	Natural variation in human gene expression assessed in lymphoblastoid cells. *Nature Genetics*, **2003**, 33, 422-5	36.3	474
1888	Bioinformatics in the post-sequence era. *Nature Genetics*, **2003**, 33 Suppl, 305-10	36.3	128
1887	Treatment-specific changes in gene expression discriminate in vivo drug response in human leukemia cells. *Nature Genetics*, **2003**, 34, 85-90	36.3	220
1886	Module networks: identifying regulatory modules and their condition-specific regulators from gene expression data. *Nature Genetics*, **2003**, 34, 166-76	36.3	1275
1885	Trans-acting regulatory variation in Saccharomyces cerevisiae and the role of transcription factors. *Nature Genetics*, **2003**, 35, 57-64	36.3	505
1884	Evolutionary and biomedical implications of a Schistosoma japonicum complementary DNA resource. *Nature Genetics*, **2003**, 35, 139-47	36.3	261

1883	Integrating biological databases. **2003**, 4, 337-45	229
1882	Classification schemes for protein structure and function. **2003**, 4, 508-19	74
1881	The chicken as a model for large-scale analysis of vertebrate gene function. **2003**, 4, 87-98	128
1880	Prediction of human protein function according to Gene Ontology categories. **2003**, 19, 635-42	203
1879	Predicting gene ontology biological process from temporal gene expression patterns. **2003**, 13, 965-79	76
1878	Amino Acid Properties and Consequences of Substitutions. 289-316	246
1877	Application of microarray technology in environmental and comparative physiology. **2003**, 65, 231-59	141
1876	A gene-coexpression network for global discovery of conserved genetic modules. **2003**, 302, 249-55	1618
1875	Prediction of protein function from protein sequence and structure. **2003**, 36, 307-40	300
1874	Modeling biology using relational databases. **2003**, Chapter 9, Unit9.3	
1873	Sequence analysis of a rainbow trout cDNA library and creation of a gene index. **2003**, 102, 347-54	92
1872	MicroRNA targets in Drosophila. **2003**, 5, R1	2206
1871	The construction of an EST database for Bombyx mori and its application. **2003**, 100, 14121-6	227
1870	Identification of pseudogenes in the Drosophila melanogaster genome. **2003**, 31, 1033-7	72
1869	Initial large-scale exploration of protein-protein interactions in human brain.	2
1868	EMDep: a web-based system for the deposition and validation of high-resolution electron microscopy macromolecular structural information. **2003**, 144, 228-37	44
1867	Zea mays ontology--a database of international terms. **2003**, 8, 517-20	21
1866	Comparative genomics of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: implication for land plant evolution. **2003**, 100, 8007-12	301

1865	Application of eVOC: controlled vocabularies for unifying gene expression data. **2003**, 326, 1089-96	7
1864	A new hybrid approach to predict subcellular localization of proteins by incorporating gene ontology. **2003**, 311, 743-7	121
1863	OrthoMCL: identification of ortholog groups for eukaryotic genomes. **2003**, 13, 2178-89	4048
1862	Functional fingerprints of folds: evidence for correlated structure-function evolution. **2003**, 326, 1-9	48
1861	Inferring functional relationships of proteins from local sequence and spatial surface patterns. **2003**, 332, 505-26	133
1860	Gene expression patterns define pathways correlated with loss of differentiation in lung adenocarcinomas. **2003**, 540, 167-70	14
1859	Gene expression profiling as a tool for the diagnosis of acute leukemias. **2003**, 40, 281-95	30
1858	Use of microarrays for investigating the subtoxic effects of snake venoms: insights into venom-induced apoptosis in human umbilical vein endothelial cells. **2003**, 41, 429-40	36
1857	Building a BRIDGE for the integration of heterogeneous data from functional genomics into a platform for systems biology. **2003**, 106, 157-67	22
1856	EMMA: a platform for consistent storage and efficient analysis of microarray data. **2003**, 106, 135-46	99
1855	Exploring the immunogenome with bioinformatics. **2003**, 15, 233-8	0
1854	ESTs from the basidiomycete Schizophyllum commune grown on nitrogen-replete and nitrogen-limited media. **2003**, 39, 191-8	16
1853	Differential gene expression analysis in fish exposed to endocrine disrupting compounds. **2003**, 136, 149-61	40
1852	Global functional profiling of gene expression. **2003**, 81, 98-104	479
1851	Exploring the salivary gland transcriptome and proteome of the Anopheles stephensi mosquito. **2003**, 33, 717-32	166
1850	A catalogue of Anopheles gambiae transcripts significantly more or less expressed following a blood meal. **2003**, 33, 865-82	63
1849	Bioinformatics: Organisms from Venus, Technology from Jupiter, Algorithms from Mars. **2003**, 9, 237-278	8
1848	Leishmania major chromosome 3 contains two long convergent polycistronic gene clusters separated by a tRNA gene. **2003**, 31, 4201-10	59

1847	A Bayesian networks approach for predicting protein-protein interactions from genomic data. **2003** , 302, 449-53	1007
1846	PANTHER: a browsable database of gene products organized by biological function, using curated protein family and subfamily classification. **2003**, 31, 334-41	486
1845	The environmental stress response: a common yeast response to diverse environmental stresses. **2003**, 11-70	74
1844	Primer on medical genomics part V: bioinformatics. **2003**, 78, 57-64	19
1843	Pilot survey of expressed sequence tags (ESTs) from the asexual blood stages of Plasmodium vivax in human patients. **2003**, 2, 21	6
1842	Challenges Faced in the Integration of Biological Information. **2003**, 11-34	3
1841	Functional classification of proteins for the prediction of cellular function from a protein-protein interaction network. **2003**, 5, R6	205
1840	New methods for finding disease-susceptibility genes: impact and potential. **2003**, 4, 119	30
1839	Identifying biological themes within lists of genes with EASE. **2003**, 4, R70	1473
1838	DAVID: Database for Annotation, Visualization, and Integrated Discovery. **2003**, 4, 1	987
1837	A comparative proteomics resource: proteins of Arabidopsis thaliana. **2003**, 4, R51	19
1836	Profiling of pathway-specific changes in gene expression following growth of human cancer cell lines transplanted into mice. **2003**, 4, R46	38
1835	A method to assess compositional bias in biological sequences and its application to prion-like glutamine/asparagine-rich domains in eukaryotic proteomes. **2003**, 4, R40	111
1834	GeneHopper: a web-based search engine to link gene-expression platforms through GenBank accession numbers. **2003**, 4, R35	9
1833	Clustering gene-expression data with repeated measurements. **2003**, 4, R34	132
1832	Analysis and functional classification of transcripts from the nematode Meloidogyne incognita. **2003**, 4, R26	116
1831	GoMiner: a resource for biological interpretation of genomic and proteomic data. **2003**, 4, R28	934
1830	The GRID: the General Repository for Interaction Datasets. **2003**, 4, R23	181

1829	Osprey: a network visualization system. **2003**, 4, R22	328
1828	Exploiting microarrays to reveal differential gene expression in the nervous system. **2003**, 4, 105	16
1827	Integrating computationally assembled mouse transcript sequences with the Mouse Genome Informatics (MGI) database. **2003**, 4, R16	15
1826	MAPPFinder: using Gene Ontology and GenMAPP to create a global gene-expression profile from microarray data. **2003**, 4, R7	683
1825	PAINT: a promoter analysis and interaction network generation tool for gene regulatory network identification. **2003**, 7, 235-52	112
1824	Using gene ontology on genome-scale studies to find significant associations of biologically relevant terms to groups of genes.	
1823	.	0
1822	A contradiction-based framework for testing gene regulation hypotheses.	1
1821	PANTHER: a library of protein families and subfamilies indexed by function. **2003**, 13, 2129-41	2102
1820	The Nuclear Protein Database (NPD): sub-nuclear localisation and functional annotation of the nuclear proteome. **2003**, 31, 328-30	75
1819	Towards automated derivation of biological pathways using high-throughput biological data.	
1818	Tomato expression database (TED) - an interactive management tool for tomato expression profiling data.	
1817	Genome-wide identification of in vivo Drosophila Engrailed-binding DNA fragments and related target genes. **2003**, 130, 1243-54	38
1816	The TIGRFAMs database of protein families. **2003**, 31, 371-3	602
1815	The sequence and analysis of Trypanosoma brucei chromosome II. **2003**, 31, 4856-63	48
1814	Endoplasmic reticulum stress is a determinant of retrovirus-induced spongiform neurodegeneration. **2003**, 77, 12617-29	72
1813	Predicting gene function from patterns of annotation. **2003**, 13, 896-904	95
1812	Annotation of the Arabidopsis genome. **2003**, 132, 461-8	120

1811	A literature-based method for assessing the functional coherence of a gene group. **2003**, 19, 396-401	41
1810	The phylogenetic diversity of eukaryotic transcription. **2003**, 31, 653-60	36
1809	Genome-wide discovery of transcriptional modules from DNA sequence and gene expression. **2003**, 19 Suppl 1, i273-82	163
1808	The SWISS-PROT protein knowledgebase and its supplement TrEMBL in 2003. **2003**, 31, 365-70	2375
1807	Inductive Logic Programming. **2003**,	1
1806	Assessment of genome-wide protein function classification for Drosophila melanogaster. **2003**, 13, 2118-28	35
1805	OntoBlast function: From sequence similarities directly to potential functional annotations by ontology terms. **2003**, 31, 3799-803	81
1804	The Proteome Analysis database: a tool for the in silico analysis of whole proteomes. **2003**, 31, 414-7	55
1803	Automated Gene Ontology annotation for anonymous sequence data. **2003**, 31, 3712-5	62
1802	From gene networks to gene function. **2003**, 13, 2568-76	125
1801	GPCRDB information system for G protein-coupled receptors. **2003**, 31, 294-7	281
1800	Genome evolution reveals biochemical networks and functional modules. **2003**, 100, 15428-33	123
1799	Public services from the European Bioinformatics Institute. **2003**, 4, 332-40	7
1798	Viewing and annotating sequence data with Artemis. **2003**, 4, 124-32	121
1797	Comparing bacterial genomes through conservation profiles. **2003**, 13, 991-8	20
1796	The DNA sequence of chromosome I of an African trypanosome: gene content, chromosome organisation, recombination and polymorphism. **2003**, 31, 4864-73	47
1795	Inferring higher functional information for RIKEN mouse full-length cDNA clones with FACTS. **2003**, 13, 1520-33	10
1794	Predictive metabolic engineering: a goal for systems biology. **2003**, 132, 420-5	124

1793	INCLUSive: A web portal and service registry for microarray and regulatory sequence analysis. **2003**, 31, 3468-70	40
1792	Exploring alternative transcript structure in the human genome using blocks and InterPro. **2003**, 1, 289-306	8
1791	GoFish finds genes with combinations of Gene Ontology attributes. **2003**, 19, 788-9	13
1790	GATA-1-mediated proliferation arrest during erythroid maturation. **2003**, 23, 5031-42	169
1789	Transcriptional response of lymphoblastoid cells to ionizing radiation. **2003**, 13, 2092-100	113
1788	Connecting sequence and biology in the laboratory mouse. **2003**, 13, 1505-19	14
1787	Cryptococcus neoformans gene expression during experimental cryptococcal meningitis. **2003**, 2, 1336-49	105
1786	Systemic and cell type-specific gene expression patterns in scleroderma skin. **2003**, 100, 12319-24	334
1785	SOURCE: a unified genomic resource of functional annotations, ontologies, and gene expression data. **2003**, 31, 219-23	325
1784	NetAffx: Affymetrix probesets and annotations. **2003**, 31, 82-6	390
1783	Target Explorer: An automated tool for the identification of new target genes for a specified set of transcription factors. **2003**, 31, 3589-92	80
1782	GenePublisher: Automated analysis of DNA microarray data. **2003**, 31, 3471-6	27
1781	The computational analysis of scientific literature to define and recognize gene expression clusters. **2003**, 31, 4553-60	40
1780	Advances in spotted microarray resources for expression profiling. **2003**, 2, 21-30	15
1779	Gene expression data preprocessing. **2003**, 19, 655-6	79
1778	Predicting protein function from protein/protein interaction data: a probabilistic approach. **2003**, 19 Suppl 1, i197-204	269
1777	UniqueProt: Creating representative protein sequence sets. **2003**, 31, 3789-91	88
1776	Sequence Evolution Function. **2003**,	103

1775	The European Bioinformatics Institute's data resources. **2003**, 31, 43-50	38
1774	Handbook on Enterprise Architecture. **2003**,	66
1773	The Drosophila phenotype gap - and how to close it. **2003**, 2, 121-7	11
1772	G protein-coupled receptor genes in the FANTOM2 database. **2003**, 13, 1466-77	28
1771	New evidence for genome-wide duplications at the origin of vertebrates using an amphioxus gene set and completed animal genomes. **2003**, 13, 1056-66	134
1770	In silico tools for signal transduction research. **2003**, 4, 315-24	1
1769	The Schistosoma mansoni gene index: gene discovery and biology by reconstruction and analysis of expressed gene sequences. **2003**, 89, 261-9	27
1768	ELM server: A new resource for investigating short functional sites in modular eukaryotic proteins. **2003**, 31, 3625-30	491
1767	Genome-wide survey of human alternative pre-mRNA splicing with exon junction microarrays. **2003**, 302, 2141-4	1172
1766	Identifying underlying factors in breast cancer using independent component analysis.	3
1765	Statistical and visual morph movie analysis of crystallographic mutant selection bias in protein mutation resource data.	1
1764	Ensembl 2002: accommodating comparative genomics. **2003**, 31, 38-42	180
1763	Large-scale delineation of secreted protein biomarkers overexpressed in cancer tissue and serum. **2003**, 100, 3410-5	363
1762	A Bayesian framework for combining heterogeneous data sources for gene function prediction (in Saccharomyces cerevisiae). **2003**, 100, 8348-53	431
1761	eVOC: a controlled vocabulary for unifying gene expression data. **2003**, 13, 1222-30	132
1760	Whither biological database research?. **2003**, 7, 61-5	
1759	Millions of years of evolution preserved: a comprehensive catalog of the processed pseudogenes in the human genome. **2003**, 13, 2541-58	314
1758	Common objects: think global, act local. **2003**, 7, 103-4	

1757	Transcriptional network controlled by the trithorax-group gene ash2 in Drosophila melanogaster. **2003**, 100, 3293-8	19
1756	PRISM, a generic large scale proteomic investigation strategy for mammals. **2003**, 2, 96-106	133
1755	Genomic binding by the Drosophila Myc, Max, Mad/Mnt transcription factor network. **2003**, 17, 1101-14	315
1754	GEPAS: A web-based resource for microarray gene expression data analysis. **2003**, 31, 3461-7	139
1753	WormBase: a cross-species database for comparative genomics. **2003**, 31, 133-7	90
1752	Mining the biomedical literature in the genomic era: an overview. **2003**, 10, 821-55	157
1751	Genetic expression profiling of six odontogenic tumors. **2003**, 82, 551-7	20
1750	Saccharomyces Genome Database (SGD) provides biochemical and structural information for budding yeast proteins. **2003**, 31, 216-8	45
1749	Integrated mapping, chromosomal sequencing and sequence analysis of Cryptosporidium parvum. **2003**, 13, 1787-99	53
1748	A SUITE OF DAML+OIL ONTOLOGIES TO DESCRIBE BIOINFORMATICS WEB SERVICES AND DATA. **2003**, 12, 197-224	88
1747	Honor thy symbionts. **2003**, 100, 10452-9	687
1746	Distributed Query Processing on the Grid. **2003**, 17, 353-367	19
1745	Gene annotation: prediction and testing. **2003**, 4, 69-88	47
1744	The digital human: towards a unified ontology. **2003**, 7, 421-4	2
1743	Genome-wide in silico identification of transcriptional regulators controlling the cell cycle in human cells. **2003**, 13, 773-80	242
1742	Long-term global gene expression patterns in irradiated human lymphocytes. **2003**, 24, 1837-45	45
1741	Evaluation of annotation strategies using an entire genome sequence. **2003**, 19, 717-26	58
1740	Differentiation of stress, metabolism, communication, and defense responses following transplantation. **2003**, 73, 379-90	9

1739	ChipInfo: Software for extracting gene annotation and gene ontology information for microarray analysis. **2003**, 31, 3483-6	76
1738	caCORE: a common infrastructure for cancer informatics. **2003**, 19, 2404-12	120
1737	Discovering molecular pathways from protein interaction and gene expression data. **2003**, 19 Suppl 1, i264-71	192
1736	ILP for Mathematical Discovery. **2003**, 93-111	6
1735	Managing core resources for genomics and proteomics. **2003**, 4, 343-50	4
1734	Serial analysis of gene expression. **2003**, 226, 271-84	
1733	Analysis of Expression Data: An Overview. **2003**, 38, 11.4.1	1
1732	Global predictions and tests of erythroid regulatory regions. **2003**, 68, 335-44	6
1731	Web-based exchange of biochemical information. **2003**, 19, 1730-1	2
1730	Induction of Enzyme Classes from Biological Databases. **2003**, 269-280	2
1729	Global Functional Profiling of Gene Expression Data. **2003**, 306-325	4
1728	Graphical modeling based gene interaction analysis for microarray data. **2003**, 5, 91-100	3
1727	Gene identification and expression analysis of 86,136 Expressed Sequence Tags (EST) from the rice genome. **2003**, 1, 26-42	17
1726	EST pipeline system: detailed and automated EST data processing and mining. **2003**, 1, 236-42	9
1725	Analysis of Expression Data: An Overview. **2003**, 3, 7.1.1	
1724	The Gene Ontology (GO) project: structured vocabularies for molecular biology and their application to genome and expression analysis. **2002**, Chapter 7, Unit 7.2	20
1723	The graft response to transplantation: a gene expression profile analysis. **2003**, 15, 52-64	11
1722	Bioinformatics. 167-187	

1721	Bovine mammary gene expression profiling using a cDNA microarray enhanced for mammary-specific transcripts. **2003**, 16, 8-18	59
1720	Gene expression profiling of renal cell carcinoma and its implications in diagnosis, prognosis, and therapeutics. **2003**, 89, 157-81	28
1719	Using the TIGR gene index databases for biological discovery. **2003**, Chapter 1, Unit 1.6	3
1718	Linking Technological Change to Business Needs. **2003**, 46, 47-52	29
1717	Integrating functional genomics data. **2003**, 31, 1484-7	9
1716	Mouse and Rat Genome Informatics. 119-142	
1715	Functional Relationship and Gene Ontology Classification of Breast Cancer Biomarkers. **2003**, 18, 241-272	16
1714	The Universal Medical Language System and the Gene Ontology: Some Critical Reflections. **2003**, 135-148	11
1713	Integr8: Enhanced Inter-Operability of European Molecular Biology Databases. **2003**, 42, 154-160	9
1712	Gene expression profile of endothelin-1-induced growth in glomerular mesangial cells. **2003**, 285, C1109-15	16
1711	. **2003**,	29
1710	. **2003**,	3
1709	. **2003**,	1
1708	Genome Projects and Gene Therapy: Gateways to Next Generation Biological Weapons. **2003**, 168, 864-871	6
1707	Bioinformatics Resources for In Silico Proteome Analysis. **2003**, 2003, 231-236	6
1706	Transcriptome analysis of mouse stem cells and early embryos. **2003**, 1, E74	135
1705	ArrayTrack--supporting toxicogenomic research at the U.S. Food and Drug Administration National Center for Toxicological Research. **2003**, 111, 1819-26	183
1704	Expression Profiler. **2003**, 142-162	5

1703	Software packages for quantitative microarray-based gene expression analysis. **2003**, 4, 417-37	17
1702	Open Source Software for the Analysis of Microarray Data. **2003**, 34, S45-S51	172
1701	Gene Expression Databases and Data Mining. **2003**, 34, S36-S44	14
1700	[Some chemicophysical order in living functional exuberance]. **2003**, 19, 643-4	
1699	Integrating Genomic and Proteomic Data: The Integr8 Project. **2004**, 1, 108-115	1
1698	Tools f□ die Proteom-Analyse in silico. **2004**, 46, 20-25	
1697	Transcriptional profiling of in vitro smooth muscle cell differentiation identifies specific patterns of gene and pathway activation. **2004**, 19, 292-302	26
1696	Using Support Vector Machines for Classifying Large Sets of Multi-Represented Objects. **2004**,	10
1695	Annotation and cross-indexing of array elements on multiple platforms. **2004**, 112, 506-10	17
1694	A comprehensive nonredundant expressed sequence tag collection for the developing Rattus norvegicus heart. **2004**, 17, 245-52	6
1693	Database development in toxicogenomics: issues and efforts. **2004**, 112, 495-505	94
1692	Joint analysis of multiple cDNA microarray studies via multivariate mixed models applied to genetic improvement of beef cattle. **2004**, 82, 3430-9	39
1691	EST resources, clone sets, and databases. **2004**,	
1690	Experimental Systems: A Life of Their Own?. **2004**, 127-153	
1689	Preface. **2004**, xiii-xiv	
1688	Introduction. **2004**, 1-17	1
1687	Reductionism and the Nature of Explanations. **2004**, 18-50	
1686	Discovery: Solving Biological Problems. **2004**, 51-87	

1685	Scientific Inference: Testing Hypotheses. **2004**, 88-126	
1684	Model Organisms: Of Flies and Elephants. **2004**, 154-187	
1683	Reference and Conceptual Change: Out of Mendel's Garden?. **2004**, 188-228	
1682	Developmental Biology and the Genetic Program: Explaining Ontogeny. **2004**, 229-265	
1681	Scientific Realism: In Search of the Truth. **2004**, 266-296	
1680	Notes. **2004**, 297-320	
1679	Bibliography. **2004**, 321-348	
1678	Protein Variations: Resources and Tools. **2004**, 389-422	
1677	. **2004**,	2
1676	. **2004**,	10
1675	Ontology-Assisted Database Integration to Support Natural Language Processing and Biomedical Data-mining. **2004**, 1, 1-10	7
1674	Evaluation of the host transcriptional response to human cytomegalovirus infection. **2004**, 18, 51-62	31
1673	Bioinformatics: Towards New Directions for Public Health. **2004**, 43, 208-214	15
1672	Ischemic but not pharmacological preconditioning elicits a gene expression profile similar to unprotected myocardium. **2004**, 20, 117-30	32
1671	Identification of gene expression changes associated with the progression of retinal degeneration in the rd1 mouse. **2004**, 45, 2929-42	79
1670	Interaction networks in yeast define and enumerate the signaling steps of the vertebrate aryl hydrocarbon receptor. **2004**, 2, E65	26
1669	Public Health Implications of Bioinformatics. **2004**, 13, 137-143	
1668	Gene expression profile in thyroid of transgenic mice overexpressing the adenosine receptor 2a. **2004**, 18, 194-213	8

1667	Proteomic informatics. **2004**, 61, 127-57	10
1666	THEA: ontology-driven analysis of microarray data. **2004**, 20, 2636-43	23
1665	Conservation and coevolution in the scale-free human gene coexpression network. **2004**, 21, 2058-70	155
1664	Identification of cathepsin B as a mediator of neuronal death induced by Abeta-activated microglial cells using a functional genomics approach. **2004**, 279, 5565-72	104
1663	YETI: Yeast Exploration Tool Integrator. **2004**, 20, 284-5	2
1662	3did: interacting protein domains of known three-dimensional structure. **2005**, 33, D413-7	127
1661	Cytoskeletal activation and altered gene expression in endothelial barrier regulation by simvastatin. **2004**, 30, 662-70	133
1660	Proteomics: current techniques and potential applications to lung disease. **2004**, 287, L1-23	88
1659	Highly conserved upstream sequences for transcription factor genes and implications for the regulatory network. **2004**, 101, 17156-61	33
1658	An ontology for collaborative construction and analysis of cellular pathways. **2004**, 20, 349-56	40
1657	A discriminative model for identifying spatial cis-regulatory modules. **2004**,	4
1656	Probabilistic discovery of overlapping cellular processes and their regulation. **2004**,	12
1655	Statistically rigorous automated protein annotation. **2004**, 20, 1066-73	8
1654	Learning to cluster using local neighborhood structure. **2004**,	2
1653	The functional genomic distribution of protein divergence in two animal phyla: coevolution, genomic conflict, and constraint. **2004**, 14, 802-11	68
1652	Gender-specific gene expression in post-mortem human brain: localization to sex chromosomes. **2004**, 29, 373-84	172
1651	GFINDer: Genome Function INtegrated Discoverer through dynamic annotation, statistical analysis, and mining. **2004**, 32, W293-300	66
1650	Prediction of protein function in the absence of significant sequence similarity. **2004**, 11, 2135-42	53

1649	Phylogenomic inference of protein molecular function: advances and challenges. **2004**, 20, 170-9	162
1648	Gene expression profiles predict survival and progression of pleural mesothelioma. **2004**, 10, 849-59	108
1647	Parasite Genomics Protocols. **2004**,	2
1646	Integrative biological analysis of the APOE*3-leiden transgenic mouse. **2004**, 8, 3-13	99
1645	Large-scale meta-analysis of cancer microarray data identifies common transcriptional profiles of neoplastic transformation and progression. **2004**, 101, 9309-14	790
1644	Probing microRNAs with microarrays: tissue specificity and functional inference. **2004**, 10, 1813-9	317
1643	GO::TermFinder--open source software for accessing Gene Ontology information and finding significantly enriched Gene Ontology terms associated with a list of genes. **2004**, 20, 3710-5	1381
1642	siRNA-mediated gene silencing: a global genome view. **2004**, 32, 3836-45	53
1641	SCA db: spinocerebellar ataxia candidate gene database. **2004**, 20, 2656-61	3
1640	A mouse model for Finnish variant late infantile neuronal ceroid lipofuscinosis, CLN5, reveals neuropathology associated with early aging. **2004**, 13, 2893-906	65
1639	The initiative role of XPC protein in cisplatin DNA damaging treatment-mediated cell cycle regulation. **2004**, 32, 2231-40	51
1638	Semantic search among heterogeneous biological databases based on gene ontology. **2004**, 36, 365-70	14
1637	Gene-Ontology analysis reveals association of tissue-specific 5' CpG-island genes with development and embryogenesis. **2004**, 13, 1969-78	24
1636	Systematic changes in gene expression in postmortem human brains associated with tissue pH and terminal medical conditions. **2004**, 13, 609-16	218
1635	Génolevures: comparative genomics and molecular evolution of hemiascomycetous yeasts. **2004**, 32, D315-8	59
1634	Annotation transfer between genomes: protein-protein interologs and protein-DNA regulogs. **2004**, 14, 1107-18	400
1633	Broadly altered gene expression in blood leukocytes in essential hypertension is absent during treatment. **2004**, 43, 947-51	66
1632	Host cell gene expression during human immunodeficiency virus type 1 latency and reactivation and effects of targeting genes that are differentially expressed in viral latency. **2004**, 78, 9458-73	93

1631	Different gene expression patterns in invasive lobular and ductal carcinomas of the breast. **2004**, 15, 2523-36	488
1630	Global protein function annotation through mining genome-scale data in yeast Saccharomyces cerevisiae. **2004**, 32, 6414-24	87
1629	FatiGO: a web tool for finding significant associations of Gene Ontology terms with groups of genes. **2004**, 20, 578-80	884
1628	PeerGAD: a peer-review-based and community-centric web application for viewing and annotating prokaryotic genome sequences. **2004**, 32, 3124-35	12
1627	Arginine methyltransferase affects interactions and recruitment of mRNA processing and export factors. **2004**, 18, 2024-35	110
1626	GOstat: find statistically overrepresented Gene Ontologies within a group of genes. **2004**, 20, 1464-5	1029
1625	Discovery Science. **2004**,	3
1624	An ORFeome-based analysis of human transcription factor genes and the construction of a microarray to interrogate their expression. **2004**, 14, 2041-7	111
1623	HyBrow: a prototype system for computer-aided hypothesis evaluation. **2004**, 20 Suppl 1, i257-64	36
1622	Nutritional homeostasis in batch and steady-state culture of yeast. **2004**, 15, 4089-104	139
1621	GermOnline, a cross-species community knowledgebase on germ cell differentiation. **2004**, 32, D560-7	22
1620	Functional genomics of lung disease. Second annual Pittsburgh International Lung Conference, October 2003. **2004**, 31, S1-81	10
1619	ClutrFree: cluster tree visualization and interpretation. **2004**, 20, 2869-71	25
1618	Bayesian integrated functional analysis of microarray data. **2004**, 20, 2943-53	19
1617	Large-scale assessment of the utility of low-resolution protein structures for biochemical function assignment. **2004**, 20, 1087-96	49
1616	Identification of the substrates and interaction proteins of aurora kinases from a protein-protein interaction model. **2004**, 3, 93-104	28
1615	Mouse chromosome 17A3.3 contains 13 genes that encode functional tryptic-like serine proteases with distinct tissue and cell expression patterns. **2004**, 279, 2438-52	55
1614	Ontologizing gene-expression microarray data: characterizing clusters with Gene Ontology. **2004**, 20, 979-81	70

1613	A genomic view of estrogen actions in human breast cancer cells by expression profiling of the hormone-responsive transcriptome. **2004**, 32, 719-75	74
1612	The FunCat, a functional annotation scheme for systematic classification of proteins from whole genomes. **2004**, 32, 5539-45	862
1611	Large-scale generation and analysis of expressed sequence tags from porcine ovary. **2004**, 71, 1991-2002	18
1610	Transcriptional transitions during Dictyostelium spore germination. **2004**, 3, 1101-10	24
1609	Identification of a gene expression signature associated with recurrent disease in squamous cell carcinoma of the head and neck. **2004**, 64, 55-63	331
1608	Coordinated genetic regulation of growth and lignin revealed by quantitative trait locus analysis of cDNA microarray data in an interspecific backcross of eucalyptus. **2004**, 135, 2368-78	176
1607	Expression profiling of t(12;22) positive clear cell sarcoma of soft tissue cell lines reveals characteristic up-regulation of potential new marker genes including ERBB3. **2004**, 64, 3395-405	62
1606	Pattern of genes influenced by conditional expression of the transcription factors HNF6, HNF4alpha and HNF1beta in a pancreatic beta-cell line. **2004**, 32, e150	43
1605	Weight loss regulates inflammation-related genes in white adipose tissue of obese subjects. **2004**, 18, 1657-69	506
1604	Comparative analysis of protein domain organization. **2004**, 14, 343-53	65
1603	Developmental expression of 2489 gene clusters during pig embryogenesis: an expressed sequence tag project. **2004**, 71, 1230-43	47
1602	The human plasma proteome: a nonredundant list developed by combination of four separate sources. **2004**, 3, 311-26	695
1601	BioMap. **2004**,	7
1600	Predicting subcellular localization of proteins in a hybridization space. **2004**, 20, 1151-6	81
1599	Pathbase: a database of mutant mouse pathology. **2004**, 32, D512-5	44
1598	Shared relationship analysis: ranking set cohesion and commonalities within a literature-derived relationship network. **2004**, 20, 191-8	88
1597	Evolutionary expressed sequence tag analysis of Drosophila female reproductive tracts identifies genes subjected to positive selection. **2004**, 168, 1457-65	180
1596	ASD: the Alternative Splicing Database. **2004**, 32, D64-9	152

1595	Expression profiling of T-cell lymphomas differentiates peripheral and lymphoblastic lymphomas and defines survival related genes. **2004**, 10, 4971-82	84
1594	Data exploration tools for the Gene Ontology database. **2004**, 20, 3442-54	13
1593	Global survey of chromatin accessibility using DNA microarrays. **2004**, 14, 1374-81	23
1592	The Ensembl core software libraries. **2004**, 14, 929-33	100
1591	Control of yeast filamentous-form growth by modules in an integrated molecular network. **2004**, 14, 380-90	72
1590	Comparative genomics of transcriptional control in the human malaria parasite Plasmodium falciparum. **2004**, 14, 1548-54	192
1589	The Gene Ontology Annotation (GOA) Database: sharing knowledge in Uniprot with Gene Ontology. **2004**, 32, D262-6	643
1588	SMART 4.0: towards genomic data integration. **2004**, 32, D142-4	764
1587	DBSubLoc: database of protein subcellular localization. **2004**, 32, D122-4	41
1586	RNAiDB and PhenoBlast: web tools for genome-wide phenotypic mapping projects. **2004**, 32, D406-10	49
1585	ArrayXPath: mapping and visualizing microarray gene-expression data with integrated biological pathway resources using Scalable Vector Graphics. **2004**, 32, W460-4	51
1584	Transcription factor binding element detection using functional clustering of mutant expression data. **2004**, 32, 2362-71	9
1583	The effect of stress withdrawal on gene expression and certain biochemical and cell biological properties of peroxide-conditioned cell lines. **2004**, 18, 480-8	35
1582	An orderly retreat: Dedifferentiation is a regulated process. **2004**, 101, 7005-10	42
1581	Incipient Alzheimer's disease: microarray correlation analyses reveal major transcriptional and tumor suppressor responses. **2004**, 101, 2173-8	788
1580	Shared transcriptional signature in Caenorhabditis elegans Dauer larvae and long-lived daf-2 mutants implicates detoxification system in longevity assurance. **2004**, 279, 44533-43	306
1579	MitoP2, an integrated database on mitochondrial proteins in yeast and man. **2004**, 32, D459-62	68
1578	Gene expression profiles of transcripts in amyloid precursor protein transgenic mice: up-regulation of mitochondrial metabolism and apoptotic genes is an early cellular change in Alzheimer's disease. **2004**, 13, 1225-40	259

1577	Computational inference of transcriptional regulatory networks from expression profiling and transcription factor binding site identification. **2004**, 32, 179-88	80
1576	yMGV: a cross-species expression data mining tool. **2004**, 32, D323-5	6
1575	Gene annotation from scientific literature using mappings between keyword systems. **2004**, 20, 2084-91	37
1574	CLENCH: a program for calculating Cluster ENriCHment using the Gene Ontology. **2004**, 20, 1196-7	52
1573	SeqExpress: desktop analysis and visualization tool for gene expression experiments. **2004**, 20, 1649-50	9
1572	Genomic and proteomic determinants of outcome in patients undergoing thoracoabdominal aortic aneurysm repair. **2004**, 172, 7103-9	58
1571	WILMA-automated annotation of protein sequences. **2004**, 20, 127-8	7
1570	Identification of candidate disease genes by EST alignments, synteny, and expression and verification of Ensembl genes on rat chromosome 1q43-54. **2004**, 14, 640-50	16
1569	Genome-wide analysis of mRNA stability using transcription inhibitors and microarrays reveals posttranscriptional control of ribosome biogenesis factors. **2004**, 24, 5534-47	269
1568	Handbook on Ontologies. **2004**,	148
1567	Rough Sets and Current Trends in Computing. **2004**,	16
1566	Comparative genomics of gene expression in the parasitic and free-living nematodes Strongyloides stercoralis and Caenorhabditis elegans. **2004**, 14, 209-20	81
1565	CARRIE web service: automated transcriptional regulatory network inference and interactive analysis. **2004**, 32, W213-6	26
1564	A graph-theoretic approach to testing associations between disparate sources of functional genomics data. **2004**, 20, 3353-62	39
1563	GOblet: a platform for Gene Ontology annotation of anonymous sequence data. **2004**, 32, W313-7	67
1562	Onto-Tools: an ensemble of web-accessible, ontology-based tools for the functional design and interpretation of high-throughput gene expression experiments. **2004**, 32, W449-56	120
1561	New challenges in gene expression data analysis and the extended GEPAS. **2004**, 32, W485-91	44
1560	Calculating the statistical significance of physical clusters of co-regulated genes in the genome: the role of chromatin in domain-wide gene regulation. **2004**, 32, 1798-807	26

1559	The Candida Genome Database (CGD), a community resource for Candida albicans gene and protein information. **2005**, 33, D358-63	82
1558	PFD: a database for the investigation of protein folding kinetics and stability. **2005**, 33, D279-83	20
1557	SIEGE: Smoking Induced Epithelial Gene Expression Database. **2005**, 33, D573-9	21
1556	The Yeast Resource Center Public Data Repository. **2005**, 33, D378-82	25
1555	The PANTHER database of protein families, subfamilies, functions and pathways. **2005**, 33, D284-8	589
1554	PartiGeneDB--collating partial genomes. **2005**, 33, D303-7	8
1553	The Legume Information System (LIS): an integrated information resource for comparative legume biology. **2005**, 33, D660-5	90
1552	Positioning Arabidopsis in plant biology. A key step toward unification of plant research. **2004**, 135, 602-6	7
1551	Sfp1 is a stress- and nutrient-sensitive regulator of ribosomal protein gene expression. **2004**, 101, 14315-22	278
1550	A method for finding communities of related genes. **2004**, 101 Suppl 1, 5241-8	161
1549	Early target genes of IL-12 and STAT4 signaling in th cells. **2004**, 172, 6775-82	72
1548	BRENDA, the enzyme database: updates and major new developments. **2004**, 32, D431-3	529
1547	The Cell Wall Navigator database. A systems-based approach to organism-unrestricted mining of protein families involved in cell wall metabolism. **2004**, 136, 3003-8; discussion 3001	62
1546	Proteomic analysis of the intestinal epithelial cell response to enteropathogenic Escherichia coli. **2004**, 279, 20127-36	67
1545	Saccharomyces genome database: underlying principles and organisation. **2004**, 5, 9-22	73
1544	CYGD: the Comprehensive Yeast Genome Database. **2005**, 33, D364-8	242
1543	Swiss-Prot: juggling between evolution and stability. **2004**, 5, 39-55	287
1542	IntAct: an open source molecular interaction database. **2004**, 32, D452-5	670

1541	Identification of differentially expressed genes in scrapie-infected mouse brains by using global gene expression technology. **2004**, 78, 11051-60	118
1540	The Diatom EST Database. **2005**, 33, D344-7	64
1539	Bioie: retargetable information extraction and ontological annotation of biological interactions from the literature. **2004**, 2, 551-68	16
1538	PupaSNP Finder: a web tool for finding SNPs with putative effect at transcriptional level. **2004**, 32, W242-8	75
1537	Coexpression analysis of human genes across many microarray data sets. **2004**, 14, 1085-94	571
1536	Functional divergence of duplicated genes formed by polyploidy during Arabidopsis evolution. **2004**, 16, 1679-91	793
1535	Statistical and visual morph movie analysis of crystallographic mutant selection bias in protein mutation resource data. **2004**, 2, 61-75	2
1534	Protein databases on the internet. **2004**, Chapter 19, Unit 19.4	11
1533	Protein interaction networks. **2004**, 1, 239-49	52
1532	Cellular responses to ErbB-2 overexpression in human mammary luminal epithelial cells: comparison of mRNA and protein expression. **2004**, 90, 173-81	37
1531	QA/QC: challenges and pitfalls facing the microarray community and regulatory agencies. **2004**, 4, 761-77	92
1530	Integrated analysis of microarray data and gene function information. **2004**, 8, 106-17	11
1529	Knowledge discovery in a microarray data warehouse. **2004**,	
1528	The binding sites for the chromatin insulator protein CTCF map to DNA methylation-free domains genome-wide. **2004**, 14, 1594-602	111
1527	Ruleminer: a knowledge system for supporting high-throughput protein function annotations. **2004**, 2, 615-37	16
1526	Coping with cold: An integrative, multitissue analysis of the transcriptome of a poikilothermic vertebrate. **2004**, 101, 16970-5	339
1525	Sperm-induced modification of the oviductal gene expression profile after natural insemination in mice. **2004**, 71, 60-5	133
1524	Generation of a large gene/protein lexicon by morphological pattern analysis. **2004**, 1, 611-26	16

1523	ORFDB: an information resource linking scientific content to a high-quality Open Reading Frame (ORF) collection. **2004**, 32, D595-9	18
1522	Functional bias and spatial organization of genes in mutational hot and cold regions in the human genome. **2004**, 2, E29	73
1521	Gene expression in juvenile arthritis and spondyloarthropathy: pro-angiogenic ELR+ chemokine genes relate to course of arthritis. **2004**, 43, 973-9	72
1520	Textpresso: an ontology-based information retrieval and extraction system for biological literature. **2004**, 2, e309	403
1519	Molecular signatures of proliferation and quiescence in hematopoietic stem cells. **2004**, 2, e301	260
1518	Pathbase: a new reference resource and database for laboratory mouse pathology. **2004**, 112, 525-8	21
1517	Distinct genomic integration of MLV and SIV vectors in primate hematopoietic stem and progenitor cells. **2004**, 2, e423	213
1516	Highly conserved non-coding sequences are associated with vertebrate development. **2005**, 3, e7	714
1515	Human T lymphotropic virus type-1 p30II alters cellular gene expression to selectively enhance signaling pathways that activate T lymphocytes. **2004**, 1, 39	34
1514	ArchDB: automated protein loop classification as a tool for structural genomics. **2004**, 32, D185-8	54
1513	NetAffx Gene Ontology Mining Tool: a visual approach for microarray data analysis. **2004**, 20, 1462-3	70
1512	Distinctive features of plant organs characterized by global analysis of gene expression in Arabidopsis. **2004**, 11, 11-25	23
1511	Genexpressionsanalysen bei akuten Leuk�mien: Diagnostik der Zukunft? / Gene expression profiling in acute leukemia: diagnostics of the future?. **2004**, 28, 225-232	
1510	The Unified Medical Language System (UMLS): integrating biomedical terminology. **2004**, 32, D267-70	1907
1509	Over 20% of human transcripts might form sense-antisense pairs. **2004**, 32, 4812-20	253
1508	GO-Mapper: functional analysis of gene expression data using the expression level as a score to evaluate Gene Ontology terms. **2004**, 20, 2618-25	40
1507	Analysis of Microarray Gene Expression Data. **2004**,	0
1506	Tailored gene array databases: applications in mechanistic toxicology. **2004**, 20, 507-17	16

1505	Bayesian mixture model based clustering of replicated microarray data. **2004**, 20, 1222-32		153
1504	The distribution and query systems of the RCSB Protein Data Bank. **2004**, 32, D223-5		95
1503	Comparative analysis of amino acid repeats in rodents and humans. **2004**, 14, 549-54		121
1502	VirGen: a comprehensive viral genome resource. **2004**, 32, D289-92		13
1501	A gene expression map for the euchromatic genome of Drosophila melanogaster. **2004**, 306, 655-60		251
1500	Differential gene expression of blood-derived cell lines in familial combined hyperlipidemia. **2004**, 24, 2149-54		27
1499	An update of the HLA genomic region, locus information and disease associations: 2004. **2004**, 64, 631-49		277
1498	Development and evaluation of an Arabidopsis whole genome Affymetrix probe array. **2004**, 38, 545-61		217
1497	The transcriptome of adult female Anopheles darlingi salivary glands. **2004**, 13, 73-88		87
1496	Iron-regulated transcription and capsule formation in the fungal pathogen Cryptococcus neoformans. **2005**, 55, 1452-72		79
1495	Regulation of gene expression by dietary Ca2+ in kidneys of 25-hydroxyvitamin D3-1 alpha-hydroxylase knockout mice. **2004**, 65, 531-9		54
1494	Brain-derived neurotrophic factor signaling modifies hippocampal gene expression during epileptogenesis in transgenic mice. **2004**, 19, 3245-54		25
1493	Targeted cellular process profiling approach for uterine leiomyoma using cDNA microarray, proteomics and gene ontology analysis. **2003**, 84, 267-79		41
1492	AnoXcel: an Anopheles gambiae protein database. **2004**, 13, 449-57		39
1491	The major histocompatibility complex origin. **2004**, 198, 216-32		47
1490	Integration of chemical-genetic and genetic interaction data links bioactive compounds to cellular target pathways. **2004**, 22, 62-9		527
1489	Comparing genomic expression patterns across species identifies shared transcriptional profile in aging. *Nature Genetics*, **2004**, 36, 197-204	36.3	362
1488	Familial combined hyperlipidemia is associated with upstream transcription factor 1 (USF1). *Nature Genetics*, **2004**, 36, 371-6	36.3	268

1487	A probabilistic view of gene function. *Nature Genetics*, **2004**, 36, 559-64	36.3	99
1486	Integrated global profiling of cancer. **2004**, 4, 638-44		116
1485	Chemogenomics: an emerging strategy for rapid target and drug discovery. **2004**, 5, 262-75		285
1484	Human brain evolution: insights from microarrays. **2004**, 5, 850-60		157
1483	Biological robustness. **2004**, 5, 826-37		1647
1482	The involvement of XPC protein in the cisplatin DNA damaging treatment-mediated cellular response. **2004**, 14, 303-14		29
1481	TEAM: a tool for the integration of expression, and linkage and association maps. **2004**, 12, 633-8		22
1480	From microarray data to results. Workshop on genomic approaches to microarray data analysis. **2004**, 5, 459-63		3
1479	Mitochondrial dysfunction in schizophrenia: evidence for compromised brain metabolism and oxidative stress. **2004**, 9, 684-97, 643		703
1478	Independent component analysis of microarray data in the study of endometrial cancer. **2004**, 23, 6677-83		84
1477	Evolutionary changes in cis and trans gene regulation. **2004**, 430, 85-8		577
1476	Comparative analysis of processed pseudogenes in the mouse and human genomes. **2004**, 20, 62-7		176
1475	Transcripts of aging. **2004**, 20, 221-4		25
1474	A common framework for understanding the origin of genetic dominance and evolutionary fates of gene duplications. **2004**, 20, 287-90		163
1473	Genome duplication led to highly selective expansion of the Arabidopsis thaliana proteome. **2004**, 20, 461-4		204
1472	Protein domains enriched in mammalian tissue-specific or widely expressed genes. **2004**, 20, 468-72		29
1471	Gene discovery in the adenophorean nematode Trichinella spiralis: an analysis of transcription from three life cycle stages. **2004**, 137, 277-91		53
1470	The Schistosoma mansoni soluble proteome: a comparison across four life-cycle stages. **2004**, 138, 57-66		129

1469	Development of public toxicogenomics software for microarray data management and analysis. **2004**, 549, 241-53	86
1468	The emerging in-silico scientist: how text-based bioinformatics is bridging biology and artificial intelligence. **2004**, 23, 87-93	10
1467	Herpesvirus of turkeys: microarray analysis of host gene responses to infection. **2004**, 318, 102-11	30
1466	Searching for pathogenic gene functions to cervical cancer. **2004**, 93, 41-8	38
1465	Applying Support Vector Machines for Gene Ontology based gene function prediction. **2004**, 5, 116	55
1464	Handling multiple testing while interpreting microarrays with the Gene Ontology Database. **2004**, 5, 124	26
1463	Extending the mutual information measure to rank inferred literature relationships. **2004**, 5, 145	73
1462	Information assessment on predicting protein-protein interactions. **2004**, 5, 154	111
1461	PASBio: predicate-argument structures for event extraction in molecular biology. **2004**, 5, 155	48
1460	GOTree Machine (GOTM): a web-based platform for interpreting sets of interesting genes using Gene Ontology hierarchies. **2004**, 5, 16	348
1459	Implications for domain fusion protein-protein interactions based on structural information. **2004**, 5, 161	9
1458	VisANT: an online visualization and analysis tool for biological interaction data. **2004**, 5, 17	166
1457	GOtcha: a new method for prediction of protein function assessed by the annotation of seven genomes. **2004**, 5, 178	168
1456	CLOE: identification of putative functional relationships among genes by comparison of expression profiles between two species. **2004**, 5, 179	19
1455	Quantifying the relationship between co-expression, co-regulation and gene function. **2004**, 5, 18	231
1454	Optimal cDNA microarray design using expressed sequence tags for organisms with limited genomic information. **2004**, 5, 191	15
1453	Comparing functional annotation analyses with Catmap. **2004**, 5, 193	67
1452	MiCoViTo: a tool for gene-centric comparison and visualization of yeast transcriptome states. **2004**, 5, 20	3

1451	Defining transcriptional networks through integrative modeling of mRNA expression and transcription factor binding data. **2004**, 5, 31	186
1450	Computational identification of transcription factor binding sites by functional analysis of sets of genes sharing overrepresented upstream motifs. **2004**, 5, 57	26
1449	A molecular 'signature' of primary breast cancer cultures; patterns resembling tumor tissue. **2004**, 5, 47	43
1448	Protein kinases of the human malaria parasite Plasmodium falciparum: the kinome of a divergent eukaryote. **2004**, 5, 79	376
1447	FunnyBase: a systems level functional annotation of Fundulus ESTs for the analysis of gene expression. **2004**, 5, 96	30
1446	Technological advances and genomics in metazoan parasites. **2004**, 34, 139-52	18
1445	GeneWays: a system for extracting, analyzing, visualizing, and integrating molecular pathway data. **2004**, 37, 43-53	196
1444	Bioinformatics integration and agent technology. **2004**, 37, 205-19	46
1443	High coding density on the largest Paramecium tetraurelia somatic chromosome. **2004**, 14, 1397-404	40
1442	Proteomic analysis of post-mitochondrial fractions of young and old rat kidney. **2004**, 39, 1155-68	16
1441	Gene expression profiles of mouse aorta and cultured vascular smooth muscle cells differ widely, yet show common responses to dioxin exposure. **2004**, 4, 385-404	20
1440	Ultraconserved elements in the human genome. **2004**, 304, 1321-5	1275
1439	Expression profiling of the developing testis in wild-type and Dazl knockout mice. **2004**, 67, 26-54	41
1438	Taverna: a tool for the composition and enactment of bioinformatics workflows. **2004**, 20, 3045-54	1055
1437	Gene expression profiling of individual cases reveals consistent transcriptional changes in alcoholic human brain. **2004**, 90, 1050-8	109
1436	Exploring the portability of informatics capabilities from a clinical application to a bioscience application. **2004**, 11, 294-9	1
1435	Design of Genetics Home Reference: a new NLM consumer health resource. **2004**, 11, 439-47	24
1434	Automated encoding of clinical documents based on natural language processing. **2004**, 11, 392-402	352

1433	Muscle plasticity and high throughput gene expression studies. **2004**, 25, 231-4	3
1432	Using the gene ontology for microarray data mining: a comparison of methods and application to age effects in human prefrontal cortex. **2004**, 29, 1213-22	185
1431	SCOR: Structural Classification of RNA, version 2.0. **2004**, 32, D182-4	85
1430	Altered hippocampal transcript profile accompanies an age-related spatial memory deficit in mice. **2004**, 11, 253-60	121
1429	Global mapping of the yeast genetic interaction network. **2004**, 303, 808-13	1700
1428	Bioinformatics strategies for translating genome-wide expression analyses into clinically useful cancer markers. **2004**, 1020, 32-40	49
1427	Bayesian decomposition: analyzing microarray data within a biological context. **2004**, 1020, 212-26	10
1426	A survey of SL1-spliced transcripts from the root-lesion nematode Pratylenchus penetrans. **2004**, 272, 138-48	31
1425	Ontologies for Knowledge Management: An Information Systems Perspective. **2004**, 6, 380-401	118
1424	Visualizing the laboratory mouse: capturing phenotype information. **2004**, 122, 89-97	16
1423	A unigene catalogue of 5700 expressed genes in cassava. **2004**, 56, 541-54	50
1422	Functional genomics of cell elongation in developing cotton fibers. **2004**, 54, 911-29	216
1421	Functional annotation of mouse mutations in embryonic stem cells by use of expression profiling. **2004**, 15, 1-13	9
1420	Global gene expression in human myocardium-oligonucleotide microarray analysis of regional diversity and transcriptional regulation in heart failure. **2004**, 82, 308-16	69
1419	An expression profile of human pancreatic islet mRNAs by Serial Analysis of Gene Expression (SAGE). **2004**, 47, 284-99	36
1418	The TБingen approach: identification, selection, and validation of tumor-associated HLA peptides for cancer therapy. **2004**, 53, 187-95	104
1417	Molecular evolution in large genetic networks: does connectivity equal constraint?. **2004**, 58, 203-11	121
1416	Characterization of the protein processing and secretion pathways in a comprehensive set of expressed sequence tags from Trichoderma reesei. **2004**, 230, 275-82	18

1415	Classification of common functional loops of kinase super-families. **2004**, 56, 539-55	18
1414	A unified representation of multiprotein complex data for modeling interaction networks. **2004**, 57, 99-108	23
1413	Intregrated analysis of the human cardiac transcriptome, proteome and phosphoproteome. **2004**, 4, 1505-16	28
1412	A method of knowledge modeling and its application to gene function analysis. **2004**, 35, 21-30	
1411	Microarray gene expression profiling and analysis in renal cell carcinoma. **2004**, 4, 9	42
1410	All systems GO for understanding mouse gene function. **2004**, 3, 20	3
1409	Use of mass spectrometry to identify protein biomarkers of disease severity in the synovial fluid and serum of patients with rheumatoid arthritis. **2004**, 50, 3792-803	232
1408	Short tandem repeats are associated with diverse mRNAs encoding membrane-targeted proteins. **2004**, 26, 434-44	10
1407	Shared components of protein complexes--versatile building blocks or biochemical artefacts?. **2004** , 26, 1333-43	38
1406	Altered gene expression in acute systemic inflammation detected by complete coverage of the human liver transcriptome. **2004**, 39, 353-64	26
1405	Identification of discriminators of hepatoma by gene expression profiling using a minimal dataset approach. **2004**, 39, 944-53	90
1404	Downregulation of tissue factor by RNA interference in human melanoma LOX-L cells reduces pulmonary metastasis in nude mice. **2004**, 112, 994-1002	35
1403	Screening for control genes in rat global cerebral ischemia using high-density oligonucleotide array. **2004**, 76, 512-8	18
1402	Molecular evolution in the yeast transcriptional regulation network. **2004**, 302, 392-411	30
1401	The PlaNet Consortium: a network of European plant databases connecting plant genome data in an integrated biological knowledge resource. **2004**, 5, 184-9	6
1400	Shaping biological knowledge: applications in proteomics. **2004**, 5, 190-5	5
1399	New computational tools for brassica genome research. **2004**, 5, 276-80	20
1398	A critical and integrated view of the yeast interactome. **2004**, 5, 382-402	14

1397	Comparative analysis of the testis and ovary transcriptomes in zebrafish by combining experimental and computational tools. **2004**, 5, 403-18	41
1396	Biomedical informatics and granularity. **2004**, 5, 501-8	21
1395	Ontologies for the description of mouse phenotypes. **2004**, 5, 545-51	24
1394	Obol: integrating language and meaning in bio-ontologies. **2004**, 5, 509-20	67
1393	Ontology for genome comparison and genomic rearrangements. **2004**, 5, 537-44	2
1392	The Montagues and the Capulets. **2004**, 5, 623-32	8
1391	A short study on the success of the Gene Ontology. **2004**, 1, 235-240	46
1390	BioAmbients: an abstraction for biological compartments. **2004**, 325, 141-167	304
1389	Ontology concepts and tools for statistical genomics. **2004**, 90, 213-228	5
1388	A strategy for identifying putative causes of gene expression variation in human cancers. **2004**, 341, 77-88	18
1387	Identification of related gene/protein names based on an HMM of name variations. **2004**, 28, 97-107	13
1386	INBIOMED: a platform for the integration and sharing of genetic, clinical and epidemiological data oriented to biomedical research.	2
1385	Functional proteomics mapping of a human signaling pathway. **2004**, 14, 1324-32	228
1384	A high-throughput approach for subcellular proteome: identification of rat liver proteins using subcellular fractionation coupled with two-dimensional liquid chromatography tandem mass spectrometry and bioinformatic analysis. **2004**, 3, 441-55	66
1383	Comparative analysis of gene sets in the Gene Ontology space under the multiple hypothesis testing framework. **2004**, 425-35	18
1382	Generation of Attribute Value Taxonomies from Data for Data-Driven Construction of Accurate and Compact Classifiers.	5
1381	UniProt: the Universal Protein knowledgebase. **2004**, 32, D115-9	2195
1380	Linking molecular function and biological process terms in the ontology for gene expression data analysis. **2004**, 2004, 2984-6	2

1379	The 14-3-3 proteins in the teleost fish rainbow trout (Oncorhynchus mykiss). **2004**, 207, 3361-8	22
1378	Genome-scale gene function prediction using multiple sources of high-throughput data in yeast Saccharomyces cerevisiae. **2004**, 8, 322-33	43
1377	Cluster analysis of the p53 genetic regulatory network: topology and biology.	2
1376	Biomedical ontologies in post-genomic information systems.	2
1375	AVT-NBL: an algorithm for learning compact and accurate naive Bayes classifiers from attribute value taxonomies and data.	6
1374	Cellular function prediction and biological pathway discovery in Arabidopsis thaliana using microarray data. **2004**, 2004, 2881-4	4
1373	Gene expression profiling as a diagnostic tool in acute myeloid leukemia. **2004**, 4, 225-37	5
1372	Biomedical literature mining: challenges and solutions in the 'omics' era. **2004**, 4, 383-93	25
1371	Comparative analysis of gene expression for convergent evolution of camera eye between octopus and human. **2004**, 14, 1555-61	59
1370	hMiDas and hMitChip: new opportunities in mitochondrial bioinformatics and genomic medicine.	3
1369	A knowledge-based clustering algorithm driven by Gene Ontology. **2004**, 14, 687-700	84
1368	Inferring cellular networks using probabilistic graphical models. **2004**, 303, 799-805	842
1367	Assigning gene ontology categories (GO) to yeast genes using text-based supervised learning methods.	1
1366	The Contribution of Molecular Informatics to Chemogenomics. Knowledge-Based Discovery of Biological Targets and Chemical Lead Compounds. **2004**, 137-166	1
1365	Comprehensive proteomic analysis of human pancreatic juice. **2004**, 3, 1042-55	173
1364	GENEVESTIGATOR. Arabidopsis microarray database and analysis toolbox. **2004**, 136, 2621-32	2091
1363	Identifying gene ontology concepts in natural-language text. **2004**, 2004, 2821-3	2
1362	Proteomic analysis of post-mitochondrial fractions of young and old rat kidney. **2004**, 39, 1155-1155	

1361	The Gene Ontology (GO) database and informatics resource. **2004**, 32, D258-61	2536
1360	Schistosoma mansoni genome project: an update. **2004**, 53, 183-92	52
1359	HIV-associated dementia, Alzheimer's disease, multiple sclerosis, and schizophrenia: gene expression review. **2004**, 224, 3-17	14
1358	Large-scale isolation of ESTs from medaka embryos and its application to medaka developmental genetics. **2004**, 121, 915-32	85
1357	Alterations in the expression of DEAD-box and other RNA binding proteins during HIV-1 replication. **2004**, 1, 42	41
1356	Phenotype characterisation using integrated gene transcript, protein and metabolite profiling. **2004**, 3, 205-17	55
1355	GoSurfer: a graphical interactive tool for comparative analysis of large gene sets in Gene Ontology space. **2004**, 3, 261-4	89
1354	GeneDB: a resource for prokaryotic and eukaryotic organisms. **2004**, 32, D339-43	190
1353	Structure-Based Partitioning of Large Concept Hierarchies. **2004**, 289-303	65
1352	Gene expression profile of omental adipose tissue in human obesity. **2004**, 18, 215-7	136
1351	Towards ubiquitous bio-information computing: data protocols, middleware, and Web services for heterogeneous biological information integration and retrieval.	
1350	Evolving views of involution. **2004**, 6, 89-92	4
1349	Gene expression profiling of mammary gland development reveals putative roles for death receptors and immune mediators in post-lactational regression. **2004**, 6, R92-109	253
1348	Using ontologies to describe mouse phenotypes. **2005**, 6, R8	156
1347	The Mammalian Phenotype Ontology as a tool for annotating, analyzing and comparing phenotypic information. **2005**, 6, R7	298
1346	A Drosophila protein-interaction map centered on cell-cycle regulators. **2004**, 5, R96	148
1345	GOToolBox: functional analysis of gene datasets based on Gene Ontology. **2004**, 5, R101	279
1344	A scale of functional divergence for yeast duplicated genes revealed from analysis of the protein-protein interaction network. **2004**, 5, R76	30

1343	Genome-wide mutagenesis of Zea mays L. using RescueMu transposons. **2004**, 5, R82	55
1342	An Ambystoma mexicanum EST sequencing project: analysis of 17,352 expressed sequence tags from embryonic and regenerating blastema cDNA libraries. **2004**, 5, R67	64
1341	Function-informed transcriptome analysis of Drosophila renal tubule. **2004**, 5, R69	160
1340	A first-draft human protein-interaction map. **2004**, 5, R63	164
1339	Cross-species comparison of genome-wide expression patterns. **2004**, 5, 232	33
1338	Evolutionary conservation and selection of human disease gene orthologs in the rat and mouse genomes. **2004**, 5, R47	102
1337	A survey of ovary-, testis-, and soma-biased gene expression in Drosophila melanogaster adults. **2004**, 5, R40	224
1336	TXTGate: profiling gene groups with text-based information. **2004**, 5, R43	50
1335	The regulatory content of intergenic DNA shapes genome architecture. **2004**, 5, R25	96
1334	Defining a molecular atlas of the hippocampus using DNA microarrays and high-throughput in situ hybridization. **2004**, 24, 3879-89	230
1333	ONCOMINE: a cancer microarray database and integrated data-mining platform. **2004**, 6, 1-6	2548
1332	Effect of linoleic acid on proliferation and gene expression in the breast cancer cell line T47D. **2004**, 209, 25-35	37
1331	Cluster analysis of genes with significant change in expression in cells conditioned to survive TBOOH. **2004**, 78, 301-8	7
1330	Bioinformatics and Systems Biology, rapidly evolving tools for interpreting plant response to global change. **2004**, 90, 117-131	10
1329	Learning module networks from genome-wide location and expression data. **2004**, 578, 297-304	40
1328	Insight into Trichoderma reesei's genome content, organization and evolution revealed through BAC library characterization. **2004**, 41, 1077-87	22
1327	Response of rainbow trout transcriptome to model chemical contaminants. **2004**, 320, 745-53	114
1326	Prediction of protein subcellular locations by GO-FunD-PseAA predictor. **2004**, 320, 1236-9	143

1325	A genome-wide and nonredundant mouse transcription factor database. **2004**, 322, 787-93	101
1324	Predicting 22 protein localizations in budding yeast. **2004**, 323, 425-8	43
1323	T lymphocyte activation gene identification by coregulated expression on DNA microarrays. **2004**, 83, 989-99	68
1322	Learnability-based further prediction of gene functions in Gene Ontology. **2004**, 84, 922-8	17
1321	Textmining in support of knowledge discovery for vaccine development. **2004**, 34, 488-95	5
1320	Microarray analysis of the effect of diesel exhaust particles on in vitro cultured macrophages. **2004**, 18, 377-91	29
1319	The effect of the phytoestrogen coumestrol on the NZB/W F1 murine model of systemic lupus. **2004**, 23, 323-32	15
1318	The promise of functional genomics: completing the encyclopedia of a cell. **2004**, 7, 546-54	39
1317	From wild wolf to domestic dog: gene expression changes in the brain. **2004**, 126, 198-206	107
1316	Schistosome transcriptomes: new insights into the parasite and schistosomiasis. **2004**, 10, 217-25	57
1315	Exploring the sialome of the blood-sucking bug Rhodnius prolixus. **2004**, 34, 61-79	117
1314	Genes transcribed in the salivary glands of female Rhipicephalus appendiculatus ticks infected with Theileria parva. **2004**, 34, 1117-28	79
1313	Prediction and functional analysis of native disorder in proteins from the three kingdoms of life. **2004**, 337, 635-45	1625
1312	Quantifying structure-function uncertainty: a graph theoretical exploration into the origins and limitations of protein annotation. **2004**, 337, 933-49	14
1311	A description scheme of biological processes based on elementary bricks of action. **2004**, 339, 77-88	9
1310	Comparative genomics. **2004**, 5, 15-56	136
1309	Studying DNA microarray data using independent component analysis.	6
1308	Genome-wide germline-enriched and sex-biased expression profiles in Caenorhabditis elegans. **2004**, 131, 311-23	334

1307	Methods in comparative genomics: genome correspondence, gene identification and regulatory motif discovery. **2004**, 11, 319-55		72
1306	Annotating and mining the ligand-target chemogenomics knowledge space. **2004**, 2, 190-200		23
1305	Codifying bioinformatics processes without programming. **2004**, 2, 164-169		2
1304	PRISM: a new strategy to analyze the mammalian proteome. **2004**, 3, 37-42		
1303	Sister grouping of chimpanzees and humans as revealed by genome-wide phylogenetic analysis of brain gene expression profiles. **2004**, 101, 2957-62		184
1302	Global regulation of erythroid gene expression by transcription factor GATA-1. **2004**, 104, 3136-47		334
1301	Regional patterns of gene expression in human and chimpanzee brains. **2004**, 14, 1462-73		245
1300	A module map showing conditional activity of expression modules in cancer. *Nature Genetics*, **2004**, 36, 1090-1098	36.3	546
1299	Gene and protein profiling of the response of MA-10 Leydig tumor cells to human chorionic gonadotropin. **2004**, 25, 900-13		22
1298	Annotation of parasite genomes. **2004**, 270, 17-44		7
1297	ACLAME: a CLAssification of Mobile genetic Elements. **2004**, 32, D45-9		150
1296	Extracting human protein interactions from MEDLINE using a full-sentence parser. **2004**, 20, 604-11		168
1295	Comparative genomic analysis identifies an ADP-ribosylation factor-like gene as the cause of Bardet-Biedl syndrome (BBS3). **2004**, 75, 475-84		196
1294	Genetic variation in radiation-induced expression phenotypes. **2004**, 75, 885-90		51
1293	A Methodology for Biologically Relevant Pattern Discovery from Gene Expression Data. **2004**, 230-241		16
1292	Genomics and Proteomics: Design and Sources of Annotation. 113-130		
1291	Columba: Multidimensional Data Integration of Protein Annotations. **2004**, 156-171		5
1290	LinkSuiteTM: Formally Robust Ontology-Based Data and Information Integration. **2004**, 124-139		2

1289	Challenges in Genome-Wide Transcription Analysis when Using Microarrays for Non-Model Bacteria. **2004**, 2, 71-78	
1288	Extracting and Explaining Biological Knowledge in Microarray Data. **2004**, 699-703	2
1287	Using GenMAPP and MAPPFinder to view microarray data on biological pathways and identify global trends in the data. **2004**, Chapter 7, Unit 7.5	10
1286	Genomics of preconditioning. **2004**, 35, 2683-6	74
1285	Transcript signatures in experimental asthma: identification of STAT6-dependent and -independent pathways. **2004**, 172, 1815-24	103
1284	Using reasoning to guide annotation with gene ontology terms in GOAT. **2004**, 33, 27-32	14
1283	A three-layer multidatabase system for functional statistical analyses of microarray experiment results. **2004**, 2004, 2805-8	
1282	The Use of Go Terms to Understand the Biological Significance of Microarray Differential Gene Expression Data. **2004**, 233-247	
1281	The RCSB Protein Data Bank: a redesigned query system and relational database based on the mmCIF schema. **2005**, 33, D233-7	259
1280	KARMA: a web server application for comparing and annotating heterogeneous microarray platforms. **2004**, 32, W441-4	15
1279	GOAL: automated Gene Ontology analysis of expression profiles. **2004**, 32, W492-9	36
1278	Clustering Multi-represented Objects with Noise. **2004**, 394-403	31
1277	PSORTdb: a protein subcellular localization database for bacteria. **2005**, 33, D164-8	107
1276	Data mining parasite genomes. **2004**, 128 Suppl 1, S23-31	3
1275	Gene expression profiling of normal and malignant CD34-derived megakaryocytic cells. **2004**, 104, 3126-35	66
1274	Analyzing networks with VisANT. **2004**, Chapter 8, Unit 8.8	9
1273	Gene discovery and gene expression in the rice blast fungus, Magnaporthe grisea: analysis of expressed sequence tags. **2004**, 17, 1337-47	76
1272	Gene expression profile analysis of 4-phenylbutyrate treatment of IB3-1 bronchial epithelial cell line demonstrates a major influence on heat-shock proteins. **2004**, 16, 204-11	68

1271	DNA microarray analysis of neonatal mouse lung connects regulation of KDR with dexamethasone-induced inhibition of alveolar formation. **2004**, 286, L411-9	32
1270	EST-based analysis of gene expression in the porcine brain. **2004**, 2, 237-44	6
1269	Searching the Mouse Genome Informatics (MGI) resources for information on mouse biology from genotype to phenotype. **2004**, Chapter 1, Unit 1.7	3
1268	Integrating whole-genome expression results into metabolic networks with Pathway Processor. **2004**, Chapter 7, Unit 7.6	1
1267	Impact of commensal microbiota on murine gastrointestinal tract gene ontologies. **2004**, 19, 22-31	30
1266	Informatics (Computational Biology). **2004**,	
1265	Bioinformatics: harvesting information for plant and crop science. **2004**, 15, 721-731	3
1264	Bayesian Decomposition Classification of the Project Normal Data Set. **2004**, 211-231	
1263	Genetic Databases: Mining. **2005**,	
1262	Design of KEGG and GO. **2005**,	
1261	A comparison of existing tools for ontological analysis of gene expression data. **2005**,	2
1260	Transcriptional profile of NeuroD expression in a human fetal astroglial cell line. **2005**, 12, 123-36	4
1259	A semantic grid-based data access and integration service for bioinformatics. **2005**,	1
1258	ConsDiff: an algorithm for the detection of conserved differences between protein sequences. **2005**, 53, 31-43	
1257	Gene expression profiling of muscle tissue in Brahman steers during nutritional restriction. **2005**, 83, 1-12	96
1256	Annotation of Gene Products in the Literature with Gene Ontology Terms Using Syntactic Dependencies. **2005**, 787-796	1
1255	Genes Associated with Prognosis in Adenocarcinoma Across Studies at Multiple Institutions. **2005**, 239-253	2
1254	Transcriptome analysis of human colon Caco-2 cells exposed to sulforaphane. **2005**, 135, 1865-72	102

1253	Unsupervised Machine Learning to Support Functional Characterization of Genes: Emphasis on Cluster Description and Class Discovery. **2005**, 175-192	
1252	Protein Interaction Prediction by Integrating Genomic Features and Protein Interaction Network Analysis. **2005**, 61-81	2
1251	Ontologies and Functional Genomics. **2005**, 99-112	6
1250	Mapping complex disease phenotypes. **2005**,	
1249	Interoperability of bioinformatics resources. **2005**, 35, 132-139	1
1248	Automating Literature-Based Lead Discovery. **2005**, 1, 267-286	
1247	Oligo Arrays, Global Transcriptome Analysis. **2005**, 27-81	
1246	Systems Biology: Applications in Drug Discovery. **2005**, 123-183	14
1245	Using the Tools and Resources of the RCSB Protein Data Bank. **2005**, 9, 1.9.1	1
1244	A brief Perl tutorial for bioinformatics. **2005**,	
1243	EVALUATION OF LEXICAL METHODS FOR DETECTING RELATIONSHIPS BETWEEN CONCEPTS FROM MULTIPLE ONTOLOGIES. **2005**,	2
1242	PREDICTING GENE FUNCTIONS FROM TEXT USING A CROSS-SPECIES APPROACH. **2005**,	0
1241	DISCOVERING REGULATED NETWORKS DURING HIV-1 LATENCY AND REACTIVATION. **2005**,	
1240	Proteomic analysis and extensive protein identification from dry, germinating Arabidopsis seeds and young seedlings. **2005**, 38, 650-60	27
1239	Computational Pathology. **2005**, 61-81	5
1238	Professional Use of Mutant Laboratory Mice in Research. **2005**, 185-209	
1237	Gene expression profiling of ovine skin and wool follicle development using a combined ovine - bovine skin cDNA microarray. **2005**, 45, 867	15
1236	The Gene Ontology project. **2005**,	3

1235	Identification of Biological Relationships from Text Documents. **2005**, 449-489	5
1234	EXPLORING IMPORTANT ISSUES IN THE IMPLEMENTATION OF GENE SET ENRICHMENT ANALYSIS. **2005**,	
1233	Leaky ribosomal scanning in mammalian genomes: significance of histone H4 alternative translation in vivo. **2005**, 33, 1298-308	24
1232	Grid Services Complemented by Domain Ontology Supporting Biomedical Community. **2005**, 86-98	
1231	Epistatic and Environmental Control of Genome-Wide Gene Expression. **2005**, 8, 5-15	13
1230	Bioinformatics Challenges and Opportunities. **2005**, 63-94	1
1229	Weaning induces NOS-2 expression through NF-kappaB modulation in the lactating mammary gland: importance of GSH. **2005**, 391, 581-8	22
1228	Protein domains. **2005**,	
1227	Predicting enzyme family classes by hybridizing gene product composition and pseudo-amino acid composition. **2005**, 234, 145-9	80
1226	Contribution of the Saccharomyces cerevisiae transcriptional regulator Leu3p to physiology and gene expression in nitrogen- and carbon-limited chemostat cultures. **2005**, 5, 885-97	36
1225	Expressed sequence tags from life cycle stages of Trichinella spiralis: application to biology and parasite control. **2005**, 132, 13-7	19
1224	Molecular responses to xenoestrogens: mechanistic insights from toxicogenomics. **2005**, 213, 177-93	47
1223	Tri-nucleotide repeats and their association with genes in rice genome. **2005**, 82, 248-56	5
1222	Diagonal reverse-phase chromatography applications in peptide-centric proteomics: ahead of catalogue-omics?. **2005**, 345, 18-29	63
1221	The transcriptional regulator pool of the marine bacterium Rhodopirellula baltica SH 1T as revealed by whole genome comparisons. **2005**, 242, 137-45	15
1220	Unconventional systems analysis problems in molecular biology: a case study in gene regulatory network modeling. **2005**, 29, 547-563	11
1219	Gene expression in stem cell-supporting stromal cell lines. **2005**, 1044, 159-67	27
1218	Complete reannotation of the Arabidopsis genome: methods, tools, protocols and the final release. **2005**, 3, 7	118

1217	Isolation and annotation of 10828 putative full length cDNAs from indica rice. **2005**, 48, 445-51	16
1216	"Beijing Region" (3pter-D3S3397) of the human genome: complete sequence and analysis. **2005**, 48, 311-29	1
1215	Growing applications and advancements in microarray technology and analysis tools. **2005**, 43, 149-66	21
1214	Storage and retrieval of microarray data and open source microarray database software. **2005**, 30, 239-51	9
1213	The impact of the NIH public access policy on literature informatics: What role can the neuroinformaticists play?. **2005**, 3, 81-91	2
1212	Representation and high-quality annotation of the Physcomitrella patens transcriptome demonstrates a high proportion of proteins involved in metabolism in mosses. **2005**, 7, 238-50	77
1211	The search for candidate genes of alcoholism: evidence from expression profiling studies. **2005**, 10, 71-9	28
1210	Transcriptional profiling using a novel cDNA array identifies differential gene expression during porcine embryo elongation. **2005**, 71, 129-39	16
1209	Molecular classification of renal tumors by gene expression profiling. **2005**, 7, 206-18	115
1208	Primary differentiation in the human blastocyst: comparative molecular portraits of inner cell mass and trophectoderm cells. **2005**, 23, 1514-25	180
1207	Functional genomics databases on the web. **2005**, 7, 1053-9	3
1206	Global transcript profiling of potato tuber using LongSAGE. **2005**, 3, 175-85	20
1205	Dynamic changes in developmental gene expression in the basal chordate Ciona intestinalis. **2005**, 47, 187-99	13
1204	Screening for rapidly evolving genes in the ectomycorrhizal fungus Paxillus involutus using cDNA microarrays. **2006**, 15, 535-50	29
1203	The search for genenotype/phenotype associations and the phenome scan. **2005**, 19, 264-75	26
1202	Gene expression profile identifies a rare epithelioid variant case of pleomorphic liposarcoma carrying FUS-CHOP transcript. **2005**, 46, 334-41	16
1201	Midgut and salivary gland transcriptomes of the arbovirus vector Culicoides sonorensis (Diptera: Ceratopogonidae). **2005**, 14, 121-36	71
1200	AnoBase: a genetic and biological database of anophelines. **2005**, 14, 591-7	6

1199	Identification of hemoglobin-alpha and -beta subunits as potential serum biomarkers for the diagnosis and prognosis of ovarian cancer. **2005**, 96, 197-201		60
1198	Highly conserved gene expression profiles in humans with allergic rhinitis altered by immunotherapy. **2005**, 35, 1581-90		8
1197	Exploring functional relationships between components of the gene expression machinery. **2005**, 12, 175-82		88
1196	Gene expression profiling of noninvasive primary urothelial tumours using microarrays. **2005**, 93, 1182-90		50
1195	Reverse engineering gene regulatory networks. **2005**, 23, 554-5		107
1194	Functional annotation and network reconstruction through cross-platform integration of microarray data. **2005**, 23, 238-43		118
1193	Minimum information requested in the annotation of biochemical models (MIRIAM). **2005**, 23, 1509-15		445
1192	Mutation accumulation of the transcriptome. *Nature Genetics*, **2005**, 37, 458-60	36.3	8
1191	Epigenetics of hypertension in pregnancy. *Nature Genetics*, **2005**, 37, 460-1	36.3	15
1190	Complex trait analysis of gene expression uncovers polygenic and pleiotropic networks that modulate nervous system function. *Nature Genetics*, **2005**, 37, 233-42	36.3	588
1189	The transcriptional consequences of mutation and natural selection in Caenorhabditis elegans. *Nature Genetics*, **2005**, 37, 544-8	36.3	207
1188	A function for interleukin 2 in Foxp3-expressing regulatory T cells. **2005**, 6, 1142-51		1390
1187	Expression profiling reveals a distinct transcription signature in follicular thyroid carcinomas with a PAX8-PPAR(gamma) fusion oncogene. **2005**, 24, 1467-76		63
1186	Altered expression of cell cycle genes distinguishes aggressive neuroblastoma. **2005**, 24, 1533-41		53
1185	G1/S transcriptional networks modulated by the HOX11/TLX1 oncogene of T-cell acute lymphoblastic leukemia. **2005**, 24, 5561-75		42
1184	7q deletion mapping and expression profiling in uterine fibroids. **2005**, 24, 6545-54		30
1183	Two subclasses of lung squamous cell carcinoma with different gene expression profiles and prognosis identified by hierarchical clustering and non-negative matrix factorization. **2005**, 24, 7105-13		80
1182	Expression Profiling in Alcoholism Research. **2005**, 29, 1066-1073		6

1181	Cerebellar gene expression profiling and eQTL analysis in inbred mouse strains selected for ethanol sensitivity. **2005**, 29, 1568-79	19
1180	Comparative transcriptome analysis reveals significant differences in gene expression and signalling pathways between developmental and dark/starvation-induced senescence in Arabidopsis. **2005**, 42, 567-85	789
1179	Comparative gene expression profile of mouse carotid body and adrenal medulla under physiological hypoxia. **2005**, 566, 491-503	31
1178	Patient-based cross-platform comparison of oligonucleotide microarray expression profiles. **2005**, 85, 1024-39	52
1177	Highly coupled ATP synthesis by F1-ATPase single molecules. **2005**, 433, 773-7	320
1176	Microarray analysis shows that some microRNAs downregulate large numbers of target mRNAs. **2005**, 433, 769-73	3967
1175	Predictive models of molecular machines involved in Caenorhabditis elegans early embryogenesis. **2005**, 436, 861-5	225
1174	Initial sequence of the chimpanzee genome and comparison with the human genome. **2005**, 437, 69-87	1828
1173	A protein interaction network of the malaria parasite Plasmodium falciparum. **2005**, 438, 103-7	425
1172	The Plasmodium protein network diverges from those of other eukaryotes. **2005**, 438, 108-12	110
1171	A haplotype map of the human genome. **2005**, 437, 1299-320	4818
1170	High-throughput two-hybrid analysis. The promise and the peril. **2005**, 272, 5391-9	151
1169	RATES OF DIVERGENCE IN GENE EXPRESSION PROFILES OF PRIMATES, MICE, AND FLIES: STABILIZING SELECTION AND VARIABILITY AMONG FUNCTIONAL CATEGORIES. **2005**, 59, 126-137	114
1168	EVOLUTION OF INSECT METAMORPHOSIS: A MICROARRAY-BASED STUDY OF LARVAL AND ADULT GENE EXPRESSION IN THE ANT CAMPONOTUS FESTINATUS. **2005**, 59, 858-870	29
1167	Cellular process classification of human papillomavirus-16-positive SiHa cervical carcinoma cell using Gene Ontology. **2005**, 15, 94-106	2
1166	Gene expression of energy and protein metabolism in hearts of hypertensive nitric oxide- or GSH-depleted mice. **2005**, 513, 21-33	8
1165	Integration of tools and resources for display and analysis of genomic data for protozoan parasites. **2005**, 35, 481-93	8
1164	Protozoan genomes: gene identification and annotation. **2005**, 35, 495-512	12

1163	Identification of transcriptional regulatory elements in chemosensory receptor genes by probabilistic segmentation. **2005**, 15, 347-52	35
1162	Knowledge-assisted recognition of cluster boundaries in gene expression data. **2005**, 35, 171-83	14
1161	Computational intelligence in solving bioinformatics problems. **2005**, 35, 1-8	18
1160	Characterization of primitive marrow CD34+ cells that persist after a sublethal dose of total body irradiation. **2005**, 33, 1388-401	9
1159	Text-mining approaches in molecular biology and biomedicine. **2005**, 10, 439-45	101
1158	Biological networks and analysis of experimental data in drug discovery. **2005**, 10, 653-62	93
1157	PAX of mind for pathway researchers. **2005**, 10, 937-42	82
1156	Beyond annotation transfer by homology: novel protein-function prediction methods to assist drug discovery. **2005**, 10, 1475-82	71
1155	Gene expression profiling in murine obliterative airway disease. **2005**, 5, 2170-84	15
1154	From worm to human: bioinformatics approaches to identify FOXO target genes. **2005**, 126, 209-15	44
1153	Text-based analysis of genes, proteins, aging, and cancer. **2005**, 126, 193-208	4
1152	Gene expression profiling in mouse lung following polymeric hexamethylene diisocyanate exposure. **2005**, 205, 53-64	16
1151	Clues to function in gene deserts. **2005**, 23, 269-71	15
1150	Plant conserved non-coding sequences and paralogue evolution. **2005**, 21, 60-5	125
1149	Enhancer sequence conservation between vertebrates is favoured in developmental regulator genes. **2005**, 21, 207-10	49
1148	Transcriptional analysis of in vivo Plasmodium yoelii liver stage gene expression. **2005**, 142, 177-83	40
1147	Restraint stress alters lung gene expression in an experimental influenza A viral infection. **2005**, 162, 103-11	15
1146	Microarray analysis of differential gene expression in temporomandibular joint condylar cartilage after experimentally induced osteoarthritis. **2005**, 13, 1115-25	62

1145	Ontogeny of transcription profiles during mouse early craniofacial development. **2005**, 19, 339-52	5
1144	Mapping molecular responses to xenoestrogens through Gene Ontology and pathway analysis of toxicogenomic data. **2005**, 20, 433-40	29
1143	Predicting protein function from sequence and structural data. **2005**, 15, 275-84	250
1142	The study of metabolic pathways in tumors based on the transcriptome. **2005**, 15, 290-9	12
1141	Ab initio identification of putative human transcription factor binding sites by comparative genomics. **2005**, 6, 110	24
1140	AVID: an integrative framework for discovering functional relationships among proteins. **2005**, 6, 136	32
1139	Satellog: a database for the identification and prioritization of satellite repeats in disease association studies. **2005**, 6, 145	13
1138	Alkahest NuclearBLAST : a user-friendly BLAST management and analysis system. **2005**, 6, 147	6
1137	pSLIP: SVM based protein subcellular localization prediction using multiple physicochemical properties. **2005**, 6, 152	65
1136	Tools enabling the elucidation of molecular pathways active in human disease: application to Hepatitis C virus infection. **2005**, 6, 154	13
1135	Theme discovery from gene lists for identification and viewing of multiple functional groups. **2005**, 6, 162	42
1134	Dissecting systems-wide data using mixture models: application to identify affected cellular processes. **2005**, 6, 177	2
1133	FIGENIX: intelligent automation of genomic annotation: expertise integration in a new software platform. **2005**, 6, 198	103
1132	stam--a Bioconductor compliant R package for structured analysis of microarray data. **2005**, 6, 211	2
1131	Dynamic covariation between gene expression and proteome characteristics. **2005**, 6, 215	9
1130	Pathway level analysis of gene expression using singular value decomposition. **2005**, 6, 225	236
1129	Systematic survey reveals general applicability of "guilt-by-association" within gene coexpression networks. **2005**, 6, 227	294
1128	EXPANDER--an integrative program suite for microarray data analysis. **2005**, 6, 232	242

1127	Alternative splicing and protein function. **2005**, 6, 266	35
1126	ErmineJ: tool for functional analysis of gene expression data sets. **2005**, 6, 269	207
1125	Commensurate distances and similar motifs in genetic congruence and protein interaction networks in yeast. **2005**, 6, 270	18
1124	Automated methods of predicting the function of biological sequences using GO and BLAST. **2005**, 6, 272	36
1123	Probabilistic annotation of protein sequences based on functional classifications. **2005**, 6, 302	21
1122	Atlas - a data warehouse for integrative bioinformatics. **2005**, 6, 34	79
1121	The use of edge-betweenness clustering to investigate biological function in protein interaction networks. **2005**, 6, 39	135
1120	Towards precise classification of cancers based on robust gene functional expression profiles. **2005** , 6, 58	118
1119	Statistical Viewer: a tool to upload and integrate linkage and association data as plots displayed within the Ensembl genome browser. **2005**, 6, 95	10
1118	Overview of BioCreAtIvE: critical assessment of information extraction for biology. **2005**, 6 Suppl 1, S1	282
1117	Learning statistical models for annotating proteins with function information using biomedical text. **2005**, 6 Suppl 1, S18	27
1116	Protein annotation as term categorization in the gene ontology using word proximity networks. **2005**, 6 Suppl 1, S20	20
1115	Data-poor categorization and passage retrieval for gene ontology annotation in Swiss-Prot. **2005**, 6 Suppl 1, S23	21
1114	Automating genomic data mining via a sequence-based matrix format and associative rule set. **2005**, 6 Suppl 2, S2	6
1113	ESTree db: a tool for peach functional genomics. **2005**, 6 Suppl 4, S16	28
1112	ParPEST: a pipeline for EST data analysis based on parallel computing. **2005**, 6 Suppl 4, S9	30
1111	Transcribed Tc1-like transposons in salmonid fish. **2005**, 6, 107	34
1110	Laterally transferred elements and high pressure adaptation in Photobacterium profundum strains. **2005**, 6, 122	77

1109	XenDB: full length cDNA prediction and cross species mapping in Xenopus laevis. **2005**, 6, 123	3
1108	Comparative analyses of six solanaceous transcriptomes reveal a high degree of sequence conservation and species-specific transcripts. **2005**, 6, 124	66
1107	GeneSeer: a sage for gene names and genomic resources. **2005**, 6, 134	6
1106	Genes involved in complex adaptive processes tend to have highly conserved upstream regions in mammalian genomes. **2005**, 6, 168	22
1105	An EST-based approach for identifying genes expressed in the intestine and gills of pre-smolt Atlantic salmon (Salmo salar). **2005**, 6, 171	19
1104	Gene expression in the brain and kidney of rainbow trout in response to handling stress. **2005**, 6, 3	110
1103	Gene expression signature of estrogen receptor alpha status in breast cancer. **2005**, 6, 37	114
1102	Comprehensive in silico functional specification of mouse retina transcripts. **2005**, 6, 40	14
1101	Investigating hookworm genomes by comparative analysis of two Ancylostoma species. **2005**, 6, 58	46
1100	Comparison of array-based comparative genomic hybridization with gene expression-based regional expression biases to identify genetic abnormalities in hepatocellular carcinoma. **2005**, 6, 67	29
1099	Expression profile of immune response genes in patients with Severe Acute Respiratory Syndrome. **2005**, 6, 2	217
1098	Expressed sequence tags from the oomycete fish pathogen Saprolegnia parasitica reveal putative virulence factors. **2005**, 5, 46	70
1097	Floral gene resources from basal angiosperms for comparative genomics research. **2005**, 5, 5	90
1096	Differences in gene expression in prostate cancer, normal appearing prostate tissue adjacent to cancer and prostate tissue from cancer free organ donors. **2005**, 5, 45	113
1095	Response rate of fibrosarcoma cells to cytotoxic drugs on the expression level correlates to the therapeutic response rate of fibrosarcomas and is mediated by regulation of apoptotic pathways. **2005**, 5, 74	11
1094	Integrating biological research through Web services. **2005**, 38, 26-31	6
1093	Data mining in protein interactomics. Six computational research challenges and opportunities. **2005**, 24, 95-102	7
1092	Indicative oligodendrocyte dysfunction in spinal cords of human fetuses suffering from a lethal motoneuron disease. **2005**, 65, 269-81	8

1091	Activation of an energy providing response in human keratinocytes after gamma irradiation. **2005**, 95, 620-31	18
1090	Molecular profile of catabolic versus anabolic treatment regimens of parathyroid hormone (PTH) in rat bone: an analysis by DNA microarray. **2005**, 95, 403-18	84
1089	AML M3 and AML M3 variant each have a distinct gene expression signature but also share patterns different from other genetically defined AML subtypes. **2005**, 43, 113-27	35
1088	Identification of genes involved in the initiation of human Th1 or Th2 cell commitment. **2005**, 35, 3307-19	62
1087	Genome-wide response of the human Hep3B hepatoma cell to proinflammatory cytokines, from transcription to translation. **2005**, 42, 946-55	13
1086	Microarray-based gene expression profiling of benign, atypical and anaplastic meningiomas identifies novel genes associated with meningioma progression. **2005**, 114, 249-56	114
1085	Identification and validation of novel ERBB2 (HER2, NEU) targets including genes involved in angiogenesis. **2005**, 114, 590-7	46
1084	Gene expression differences over a critical period of afferent-dependent neuron survival in the mouse auditory brainstem. **2005**, 493, 460-74	32
1083	Distributed robustness versus redundancy as causes of mutational robustness. **2005**, 27, 176-88	216
1082	Genescene: An ontology-enhanced integration of linguistic and co-occurrence based relations in biomedical texts. **2005**, 56, 457-468	28
1081	Integrated bioinformatics application for automated target discovery. **2005**, 56, 483-492	1
1080	Computational Analysis of Modular Protein Architectures. **2005**, 439-476	2
1079	Cerebral gene expression profiles in sporadic Creutzfeldt-Jakob disease. **2005**, 58, 242-57	48
1078	Genome Sequencing and Analysis. **2005**, 43-73	2
1077	Differential gene expression in epidermis of mice sensitive and resistant to phorbol ester skin tumor promotion. **2005**, 44, 122-36	28
1076	Towards a semantic lexicon for biological language processing. **2005**, 6, 61-6	9
1075	The 8 annual bio-ontologies meeting. **2005**, 6, 370-2	
1074	Protein evolution in the context of Drosophila development. **2005**, 60, 774-85	49

1073	EST Sequencing from Embryogenic Cyclamen persicum Cell Cultures Identifies a High Proportion of Transcripts Homologous to Plant Genes Involved in Somatic Embryogenesis. **2005**, 24, 102-115	31
1072	Bioinformatics and proteomics approaches for aging research. **2005**, 6, 227-32	10
1071	Functional profiling of human atrial and ventricular gene expression. **2005**, 450, 201-8	67
1070	Cycloheximide treatment of cotton ovules alters the abundance of specific classes of mRNAs and generates novel ESTs for microarray expression profiling. **2005**, 274, 477-93	19
1069	The effect of replicate number and image analysis method on sweetpotato [Ipomoea batatas (L.) Lam.] cDNA microarray results. **2005**, 23, 367-381	1
1068	CandiVF □Candida albicans Virulence Factor Database. **2005**, 11, 271-277	6
1067	Expression of copper-responsive genes in HepG2 cells. **2005**, 279, 141-7	25
1066	Towards unraveling ethanol-specific neuro-metabolomics based on ethanol responsive genes in vivo. **2005**, 30, 1179-90	7
1065	Exercise responsive genes measured in peripheral blood of women with chronic fatigue syndrome and matched control subjects. **2005**, 5, 5	43
1064	Genome-wide characterization of gene expression variations and DNA copy number changes in prostate cancer cell lines. **2005**, 63, 187-97	60
1063	Genome analysis and gene expression profiling of neuroblastoma and ganglioneuroblastoma reveal differences between neuroblastic and Schwannian stromal cells. **2005**, 207, 346-57	32
1062	Identification and distribution of protein families in 120 completed genomes using Gene3D. **2005**, 59, 603-15	34
1061	A graph spectral analysis of the structural similarity network of protein chains. **2005**, 61, 152-63	18
1060	Correspondence of function and phylogeny of ABC proteins based on an automated analysis of 20 model protein data sets. **2005**, 61, 888-99	19
1059	Edge-count probabilities for the identification of local protein communities and their organization. **2006**, 62, 800-18	24
1058	Computational reconstruction of the human skeletal muscle secretome. **2006**, 62, 776-92	96
1057	Proteomic analysis of plasma membrane vesicles isolated from the rat renal cortex. **2005**, 5, 101-12	55
1056	Proteome analysis of early somatic embryogenesis in Picea glauca. **2005**, 5, 461-73	141

1055	Changes in the proteomic profile during differentiation and maturation of human monocyte-derived dendritic cells stimulated with granulocyte macrophage colony stimulating factor/interleukin-4 and lipopolysaccharide. **2005**, 5, 1186-98	50
1054	The human platelet proteome mapped by peptide-centric proteomics: a functional protein profile. **2005**, 5, 3193-204	120
1053	A proteomic analysis of cold stress responses in rice seedlings. **2005**, 5, 3162-72	280
1052	A proteomic analysis of salivary glands of female Anopheles gambiae mosquito. **2005**, 5, 3765-77	58
1051	Plasma Proteome Database as a resource for proteomics research. **2005**, 5, 3531-6	118
1050	A functional annotation of subproteomes in human plasma. **2005**, 5, 3506-19	77
1049	Data management and preliminary data analysis in the pilot phase of the HUPO Plasma Proteome Project. **2005**, 5, 3246-61	51
1048	Changes in adipose tissue gene expression with energy-restricted diets in obese women. **2005**, 81, 1275-85	118
1047	microRNA target predictions across seven Drosophila species and comparison to mammalian targets. **2005**, 1, e13	349
1046	Coherent expression chromosome cluster analysis reveals differential regulatory functions of amino-terminal and distal parathyroid hormone-related protein domains in prostate carcinoma. **2005**, 2005, 353-63	4
1045	Functional genomics in Saccharomyces cerevisiae. **2005**,	
1044	Functional inference from probabilistic protein interaction networks. **2005**,	
1043	Microarray Annotation and Biological Information on Function. **2005**, 44, 468-472	5
1042	MEGO: gene functional module expression based on gene ontology. **2005**, 38, 277-83	13
1041	Computational, integrative, and comparative methods for the elucidation of genetic coexpression networks. **2005**, 2005, 172-80	20
1040	A limited autoimmunity to p185neu elicited by DNA and allogeneic cell vaccine hampers the progression of preneoplastic lesions in HER-2/NEU transgenic mice. **2005**, 18, 351-63	7
1039	Hepatic gene expression profiles are altered by genistein supplementation in mice with diet-induced obesity. **2005**, 135, 33-41	74
1038	. **2005**,	4

1037	Gene expression and phenotypic characterization of mouse heart after chronic constant or intermittent hypoxia. **2005**, 22, 292-307	72
1036	Cellular process classification of human papillomavirus-16-positive SiHa cervical carcinoma cell using Gene Ontology. **2005**, 15, 94-106	2
1035	. **2005**,	13
1034	. **2005**,	
1033	Large-scale protein annotation. **2005**,	
1032	Introduction to ontologies in biomedicine: from powertools to assistants. **2005**,	
1031	Ontologies for the life sciences. **2005**,	1
1030	Functional classification of proteins based on protein interaction data. **2005**,	
1029	A Knowledge Integration Framework for Information Visualization. **2005**, 207-220	5
1028	Identify lymphatic metastasis-associated genes in mouse hepatocarcinoma cell lines using gene chip. **2005**, 11, 1463-72	42
1027	Tools and strategies for physiological genomics: the Rat Genome Database. **2005**, 23, 246-56	22
1026	Androgen control of gene expression in the mouse meibomian gland. **2005**, 46, 3666-75	69
1025	Gene Expression in HIV-Associated Dementia. **2005**, 305-318	2
1024	Differentially transcribed genes in skeletal muscle of Duroc and Taoyuan pigs. **2005**, 83, 2075-86	56
1023	Applications of Text Mining in Molecular Biology, from Name Recognition to Protein Interaction Maps. **2005**, 41-59	
1022	Genomic Resources for Cancer Biologists. **2005**, 3-17	
1021	Multi-represented kNN-Classification for Large Class Sets. **2005**, 511-522	2
1020	A latent variable model for chemogenomic profiling. **2005**, 21, 3286-93	50

1019	Information extraction in the life sciences: perspectives for medicinal chemistry, pharmacology and toxicology. **2005**, 5, 785-96	14
1018	Differential expression of novel potential regulators in hematopoietic stem cells. **2005**, 1, e28	217
1017	Improving the precision of the structure-function relationship by considering phylogenetic context. **2005**, 1, e9	11
1016	Automatic extraction of gene/protein biological functions from biomedical text. **2005**, 21, 1227-36	56
1015	Visualizing information across multidimensional post-genomic structured and textual databases. **2005**, 21, 1659-67	12
1014	Steady-state effects of temperature acclimation on the transcriptome of the rainbow trout heart. **2005**, 289, R1177-84	87
1013	Network structures and algorithms in Bioconductor. **2005**, 21, 135-6	72
1012	Inference of transcriptional regulatory network by two-stage constrained space factor analysis. **2005**, 21, 4033-8	50
1011	BarleyExpress: a web-based submission tool for enriched microarray database annotations. **2005**, 21, 399-401	7
1010	GOAnno: GO annotation based on multiple alignment. **2005**, 21, 2095-6	33
1009	Co-occurrence based meta-analysis of scientific texts: retrieving biological relationships between genes. **2005**, 21, 2049-58	44
1008	Microarray Data Analysis Using Neural Network Classifiers and Gene Selection Methods. **2005**, 207-222	4
1007	YeastHub: a semantic web use case for integrating data in the life sciences domain. **2005**, 21 Suppl 1, i85-96	74
1006	Balancing protein similarity and gene co-expression reveals new links between genetic conservation and developmental diversity in invertebrates. **2005**, 21, 1550-8	13
1005	GandrKB--ontological microarray annotation and visualization. **2005**, 21, 2785-6	1
1004	TAMO: a flexible, object-oriented framework for analyzing transcriptional regulation using DNA-sequence motifs. **2005**, 21, 3164-5	66
1003	MeSHer: identifying biological concepts in microarray assays based on PubMed references and MeSH terms. **2005**, 21, 3324-6	15
1002	Butylhydroquinone protects cells genetically deficient in glutathione biosynthesis from arsenite-induced apoptosis without significantly changing their prooxidant status. **2005**, 87, 365-84	45

1001	Study of coordinative gene expression at the biological process level. **2005**, 21, 3651-7	10
1000	Gene ontology mapping as an unbiased method for identifying molecular pathways and processes affected by toxicant exposure: application to acute effects caused by the rodent non-genotoxic carcinogen diethylhexylphthalate. **2005**, 86, 453-69	56
999	Database of mRNA gene expression profiles of multiple human organs. **2005**, 15, 443-50	101
998	BioMOBY successfully integrates distributed heterogeneous bioinformatics Web Services. The PlaNet exemplar case. **2005**, 138, 5-17	71
997	Cytoskeletal rearrangements in synovial fibroblasts as a novel pathophysiological determinant of modeled rheumatoid arthritis. **2005**, 1, e48	45
996	Reduced-order modelling of biochemical networks: application to the GTPase-cycle signalling module. **2005**, 152, 229-42	35
995	Computational Modeling of Biological Processes with Petri Net-Based Architecture. **2005**, 179-242	4
994	Time to organize the bioinformatics resourceome. **2005**, 1, e76	55
993	Genome-wide requirements for resistance to functionally distinct DNA-damaging agents. **2005**, 1, e24	136
992	Genes Induced by Reovirus Infection Have a Distinct Modular Cis-Regulatory Architecture. **2005**, 6, 501-513	1
991	Protein molecular function prediction by Bayesian phylogenomics. **2005**, 1, e45	131
990	Comparative gene expression analysis by differential clustering approach: application to the Candida albicans transcription program. **2005**, 1, e39	113
989	Functional coverage of the human genome by existing structures, structural genomics targets, and homology models. **2005**, 1, e31	51
988	Discovering molecular functions significantly related to phenotypes by combining gene expression data and biological information. **2005**, 21, 2988-93	90
987	Integration of GO annotations in Correspondence Analysis: facilitating the interpretation of microarray data. **2005**, 21, 2424-9	24
986	Formalizing concepts of species, sex and developmental stage in anatomical ontologies. **2005**, 21, 2773-9	13
985	Proteome dynamics during C2C12 myoblast differentiation. **2005**, 4, 887-901	104
984	Significance analysis of functional categories in gene expression studies: a structured permutation approach. **2005**, 21, 1943-9	266

983	On the quality of tree-based protein classification. **2005**, 21, 1876-90	18
982	Predicting protein localization in budding yeast. **2005**, 21, 944-50	92
981	Evidence of a large-scale functional organization of mammalian chromosomes. **2005**, 1, e33	73
980	Functional Genomics of Blood Pressure Determination: Dissecting and Assembling a Polygenic Trait by Experimental Genetics. **2005**, 1, 35-50	14
979	DPDB: a database for the storage, representation and analysis of polymorphism in the Drosophila genus. **2005**, 21 Suppl 2, ii26-30	13
978	GOChase: correcting errors from Gene Ontology-based annotations for gene products. **2005**, 21, 829-31	13
977	Aberrant expression of neutrophil and macrophage-related genes in a murine model for human neutrophil-specific granule deficiency. **2005**, 78, 1153-65	33
976	Comparing the human and chimpanzee genomes: searching for needles in a haystack. **2005**, 15, 1746-58	207
975	There’s more to a model than code. **2005**,	
974	CRAVE: a database, middleware and visualization system for phenotype ontologies. **2005**, 21, 1257-62	8
973	Clusters of co-expressed genes in mammalian genomes are conserved by natural selection. **2005**, 22, 767-75	123
972	It’s all GO for plant scientists. **2005**, 138, 1268-79	31
971	Genetical genomics analysis of a yeast segregant population for transcription network inference. **2005**, 170, 533-42	76
970	Munich information center for protein sequences plant genome resources: a framework for integrative and comparative analyses 1(W). **2005**, 138, 1301-9	8
969	Gene-Expression Omnibus integration and clustering tools in SeqExpress. **2005**, 21, 2550-1	19
968	DNA microarray analysis of nitrogen fixation and Fe(III) reduction in Geobacter sulfurreducens. **2005**, 71, 2530-8	76
967	The Arabidopsis genome: a foundation for plant research. **2005**, 15, 1632-42	89
966	The spatial organization of lipid synthesis in the yeast Saccharomyces cerevisiae derived from large scale green fluorescent protein tagging and high resolution microscopy. **2005**, 4, 662-72	134

965	Mammalian male germ cells are fertile ground for expression profiling of sexual reproduction. **2005** , 129, 1-7	57
964	The bioinformatics resource for oral pathogens. **2005**, 33, W734-40	33
963	Plant protein annotation in the UniProt Knowledgebase. **2005**, 138, 59-66	38
962	RATES OF DIVERGENCE IN GENE EXPRESSION PROFILES OF PRIMATES, MICE, AND FLIES: STABILIZING SELECTION AND VARIABILITY AMONG FUNCTIONAL CATEGORIES. **2005**, 59, 126	24
961	A network of transcriptionally coordinated functional modules in Saccharomyces cerevisiae. **2005**, 15, 1298-306	27
960	Defining the mammalian CArGome. **2006**, 16, 197-207	211
959	Gene expression profiling of gilthead sea bream during early development and detection of stress-related genes by the application of cDNA microarray technology. **2005**, 23, 182-91	64
958	Binding sites for metabolic disease related transcription factors inferred at base pair resolution by chromatin immunoprecipitation and genomic microarrays. **2005**, 14, 3435-47	66
957	Rates of protein evolution are positively correlated with developmental timing of expression during mouse spermatogenesis. **2005**, 22, 1044-52	81
956	Influence of androgens on gene expression in the BALB/c mouse submandibular gland. **2005**, 84, 1187-92	23
955	EVOLUTION OF INSECT METAMORPHOSIS: A MICROARRAY-BASED STUDY OF LARVAL AND ADULT GENE EXPRESSION IN THE ANT CAMPONOTUS FESTINATUS. **2005**, 59, 858	7
954	Inverse relationship between evolutionary rate and age of mammalian genes. **2005**, 22, 598-606	112
953	Gene expression profile studies of human keratoconus cornea for NEIBank: a novel cornea-expressed gene and the absence of transcripts for aquaporin 5. **2005**, 46, 1239-46	87
952	Inferring gene transcriptional modulatory relations: a genetical genomics approach. **2005**, 14, 1119-25	66
951	Identification of transcriptional networks during liver regeneration. **2005**, 280, 3715-22	96
950	Molecular decomposition of complex clinical phenotypes using biologically structured analysis of microarray data. **2005**, 21, 1971-8	34
949	Differential proteomic analysis of bronchoalveolar lavage fluid in asthmatics following segmental antigen challenge. **2005**, 4, 1251-64	131
948	Genome cluster database. A sequence family analysis platform for Arabidopsis and rice. **2005**, 138, 47-54	30

947	Large-scale identification of yeast integral membrane protein interactions. **2005**, 102, 12123-8	224
946	Novel specificities emerge by stepwise duplication of functional modules. **2005**, 15, 552-9	70
945	Proton NMR spectroscopy shows lipids accumulate in skeletal muscle in response to burn trauma-induced apoptosis. **2005**, 19, 1431-40	26
944	Genome-wide regulatory complexity in yeast promoters: separation of functionally conserved and neutral sequence. **2005**, 15, 205-13	39
943	Discovering regulatory binding-site modules using rule-based learning. **2005**, 15, 856-66	34
942	Transcriptome profiles of host gene expression in a monkey model of human malaria. **2005**, 191, 400-9	24
941	Calcineurin triggers reactive/inflammatory processes in astrocytes and is upregulated in aging and Alzheimer's models. **2005**, 25, 4649-58	172
940	Incorporating biological information as a prior in an empirical bayes approach to analyzing microarray data. **2005**, 4, Article12	14
939	A semantic analysis of the annotations of the human genome. **2005**, 21, 3416-21	55
938	Object-oriented biological system integration: a SARS coronavirus example. **2005**, 21, 2502-9	8
937	BioLingua: a programmable knowledge environment for biologists. **2005**, 21, 199-207	27
936	Comparison of non-human primate and human whole blood tissue gene expression profiles. **2005**, 87, 306-14	21
935	The planarian Schmidtea mediterranea as a model for epigenetic germ cell specification: analysis of ESTs from the hermaphroditic strain. **2005**, 102, 18491-6	128
934	GENE CLASSIFICATION USING EXPRESSION PROFILES: A FEASIBILITY STUDY. **2005**, 14, 641-660	21
933	XML for Bioinformatics. **2005**,	2
932	Mapping cis-regulatory domains in the human genome using multi-species conservation of synteny. **2005**, 14, 3057-63	61
931	TO-GO: a Java-based Gene Ontology navigation environment. **2005**, 21, 3580-1	4
930	Widespread correlations between dominance and homozygous effects of mutations: implications for theories of dominance. **2005**, 171, 385-92	72

929	Analysis of ARD1 function in hypoxia response using retroviral RNA interference. **2005**, 280, 17749-57	76
928	A regulatory network analysis of phenotypic plasticity in yeast. **2005**, 165, 515-23	30
927	PACdb: PolyA Cleavage Site and 3’-UTR Database. **2005**, 21, 3691-3	49
926	AnoEST: toward A. gambiae functional genomics. **2005**, 15, 893-9	19
925	Identifying subtle interrelated changes in functional gene categories using continuous measures of gene expression. **2005**, 21, 1129-37	56
924	Learning computer programs with the bayesian optimization algorithm. **2005**,	22
923	Construction of gene interaction and regulatory networks in bovine skeletal muscle from expression data. **2005**, 45, 821	11
922	Recent additions and improvements to the Onto-Tools. **2005**, 33, W762-5	101
921	Large-scale databases in toxicogenomics. **2005**, 6, 749-54	11
920	An information-driven approach to pharmacogenomics. **2005**, 6, 473-80	5
919	Genomics of Basal metazoans. **2005**, 45, 639-48	4
918	A criticality-based framework for task composition in multi-agent bioinformatics integration systems. **2005**, 21, 3155-63	8
917	Computational characterization of proteins. **2005**, 2, 129-38	0
916	A unique role of monocyte chemoattractant protein 1 among chemokines in adipose tissue of obese subjects. **2005**, 90, 5834-40	165
915	Post-Genomic Design of Bioactive Molecules. **2005**, 1, 147-162	
914	Regulation of gene expression in magnocellular neurons in rat supraoptic nucleus during sustained hypoosmolality. **2005**, 146, 1254-67	26
913	Comparative gene expression analysis of blood and brain provides concurrent validation of SELENBP1 up-regulation in schizophrenia. **2005**, 102, 15533-8	271
912	Research in Computational Molecular Biology. **2005**,	2

911	The next generation of literature analysis: integration of genomic analysis into text mining. **2005**, 6, 287-97	82
910	An integrated cancer biomarker information system. **2005**, 2005, 2851-4	2
909	Development of a laboratory information system for cancer collaboration projects. **2005**, 2005, 2859-62	12
908	Functional specificity of shuttling hnRNPs revealed by genome-wide analysis of their RNA binding profiles. **2005**, 11, 383-93	79
907	Response of the lung to pulmonary insulin dosing in the rat model and effects of changes in formulation. **2005**, 7, 516-24	4
906	Differential coexpression analysis using microarray data and its application to human cancer. **2005**, 21, 4348-55	201
905	.	5
904	Lysosomes. **2005**,	1
903	Functional modularity in a large-scale mammalian molecular interaction network.	
902	Intrinsic Disorder and Prote in Modifications: Building an SVM Predictor for Methylation. **2005**,	19
901	Medical Informatics. **2005**,	19
900	Protein structure and evolutionary history determine sequence space topology. **2005**, 15, 385-92	71
899	Algorithms and Software for Collaborative Discovery from Autonomous, Semantically Heterogeneous, Distributed Information Sources. **2005**, 13-44	6
898	Clusters of adjacent and similarly expressed genes across normal human tissues complicate comparative transcriptomic discovery. **2005**, 9, 351-63	5
897	A Novel Bioinformatics Technique For Predicting Condition-Specific Transcription Factor Binding Sites. **2005**,	
896	Gene Ontology Automatic Annotation Using a Domain Based Gene Product Similarity Measure.	2
895	Characterizing the grape transcriptome. Analysis of expressed sequence tags from multiple Vitis species and development of a compendium of gene expression during berry development. **2005**, 139, 574-97	141
894	Bio-ontology construction using object-oriented paradigm. **2005**,	1

893	A discriminative model for identifying spatial cis-regulatory modules. **2005**, 12, 822-34	23
892	Automated genome annotation and pathway identification using the KEGG Orthology (KO) as a controlled vocabulary. **2005**, 21, 3787-93	1941
891	Modeling gene and genome duplications in eukaryotes. **2005**, 102, 5454-9	670
890	Utilizing evolutionary information and gene expression data for estimating gene networks with bayesian network models. **2005**, 3, 1295-313	42
889	The Relationship Between Protein Sequence, Structure and Function. **2005**, 15-29	1
888	Transcriptional response of Saccharomyces cerevisiae to the plasma membrane-perturbing compound chitosan. **2005**, 4, 703-15	119
887	Structure, function, and evolution of transient and obligate protein-protein interactions. **2005**, 102, 10930-5	282
886	Phenotypical enrichment strategies for microarray data analysis applied in a type II diabetes study. **2005**, 9, 251-65	10
885	Comparative plant genomics resources at PlantGDB. **2005**, 139, 610-8	83
884	Pathogenomics analysis of Leishmania spp.: flagellar gene families of putative virulence factors. **2005**, 9, 173-93	7
883	A mouse atlas of gene expression: large-scale digital gene-expression profiles from precisely defined developing C57BL/6J mouse tissues and cells. **2005**, 102, 18485-90	102
882	Algorithmic Learning Theory. **2005**,	4
881	Gene expression profiling reveals multiple protective influences of the peptide alpha-melanocyte-stimulating hormone in experimental heart transplantation. **2005**, 175, 3391-401	22
880	Information-based clustering. **2005**, 102, 18297-302	150
879	KI 2005: Advances in Artificial Intelligence. **2005**,	
878	Simvastatin attenuates vascular leak and inflammation in murine inflammatory lung injury. **2005**, 288, L1026-32	202
877	Drosophila melanogaster: a case study of a model genomic sequence and its consequences. **2005**, 15, 1661-7	59
876	RNA expression profiling of normal and tumor cells following photodynamic therapy with 5-aminolevulinic acid-induced protoporphyrin IX in vitro. **2005**, 4, 516-28	34

875	Expression profiling of rat femur revealed suppression of bone formation genes by treatment with alendronate and estrogen but not raloxifene. **2005**, 68, 1225-38	24
874	Elevated evolutionary rates in the laboratory strain of Saccharomyces cerevisiae. **2005**, 102, 1092-7	85
873	Molecular evidence for arterial repair in atherosclerosis. **2005**, 102, 16789-94	67
872	Building a human kinase gene repository: bioinformatics, molecular cloning, and functional validation. **2005**, 102, 8114-9	36
871	Transactions on Rough Sets IV. **2005**,	3
870	Genes regulated in neurons undergoing transcription-dependent apoptosis belong to signaling pathways rather than the apoptotic machinery. **2005**, 280, 5693-702	35
869	Detecting clusters of different geometrical shapes in microarray gene expression data. **2005**, 21, 1927-34	41
868	Accelerated discovery of novel protein function in cultured human cells. **2005**, 4, 1319-27	20
867	BABELOMICS: a suite of web tools for functional annotation and analysis of groups of genes in high-throughput experiments. **2005**, 33, W460-4	197
866	GEPAS, an experiment-oriented pipeline for the analysis of microarray gene expression data. **2005**, 33, W616-20	79
865	Changing perspectives in yeast research nearly a decade after the genome sequence. **2005**, 15, 1611-9	32
864	A glimpse at the organization of the protein universe. **2005**, 102, 5641-2	18
863	Genome-wide analysis of cAMP-response element binding protein occupancy, phosphorylation, and target gene activation in human tissues. **2005**, 102, 4459-64	756
862	Clustering and re-clustering for pattern discovery in gene expression data. **2005**, 3, 281-301	5
861	An enhanced Java graph applet interface for visualizing interactomes. **2005**, 21, 1741-2	7
860	UBIC2 □TOWARDS UBIQUITOUS BIO-INFORMATION COMPUTING: DATA PROTOCOLS, MIDDLEWARE, AND WEB SERVICES FOR HETEROGENEOUS BIOLOGICAL INFORMATION INTEGRATION AND RETRIEVAL. **2005**, 15, 475-485	1
859	Smart Graphics. **2005**,	1
858	Human T lymphotropic virus type 1 accessory protein p12I modulates calcium-mediated cellular gene expression and enhances p300 expression in T lymphocytes. **2005**, 21, 273-84	13

857	Fractal Clustering and Knowledge-driven Validation Assessment for Gene Expression Profiling. **2005**, 2005, 4814-7	
856	Improving Protein Function Prediction using the Hierarchical Structure of the Gene Ontology. **2005**,	41
855	Pathway Analyst Automated Metabolic Pathway Prediction. **2005**,	4
854	Knowledge-based computational search for genes associated with the metabolic syndrome. **2005**, 21, 3146-54	12
853	The promoters of human cell cycle genes integrate signals from two tumor suppressive pathways during cellular transformation. **2005**, 1, 2005.0022	60
852	Orthotopic growth of human glioma cells quantitatively and qualitatively influences radiation-induced changes in gene expression. **2005**, 65, 10389-93	42
851	In silico analysis of 2085 clones from a normalized rat vestibular periphery 3' cDNA library. **2005**, 10, 310-22	8
850	Structure and function of the human genome. **2005**, 15, 1759-66	26
849	DictyMOLD-a Dictyostelium discoideum genome browser database. **2005**, 21, 696-7	1
848	Multi-way clustering of microarray data using probabilistic sparse matrix factorization. **2005**, 21 Suppl 1, i144-51	41
847	Expression of cardiac myosin-binding protein-C (cMyBP-C) in Drosophila as a model for the study of human cardiomyopathies. **2005**, 14, 7-17	8
846	Assessing the limits of genomic data integration for predicting protein networks. **2005**, 15, 945-53	156
845	Inferring combinatorial regulation of transcription in silico. **2005**, 33, 272-9	45
844	Development of Ewing's sarcoma from primary bone marrow-derived mesenchymal progenitor cells. **2005**, 65, 11459-68	289
843	The predicted impact of coding single nucleotide polymorphisms database. **2005**, 14, 2598-604	28
842	Organ-specific expression of Arabidopsis genome during development. **2005**, 138, 80-91	146
841	FPC Web tools for rice, maize, and distribution. **2005**, 138, 116-26	26
840	Spliced-leader trans-splicing in freshwater planarians. **2005**, 22, 2048-54	30

839	Gene function prediction from congruent synthetic lethal interactions in yeast. **2005**, 1, 2005.0026	101
838	In silico gene function prediction using ontology-based pattern identification. **2005**, 21, 1237-45	65
837	MEPD: a resource for medaka gene expression patterns. **2005**, 21, 3195-7	20
836	Transcriptional profiling reveals complex regulation of the monocyte IL-1 beta system by IL-13. **2005**, 174, 834-45	124
835	Burn injury causes mitochondrial dysfunction in skeletal muscle. **2005**, 102, 5368-73	84
834	Effects of threshold choice on biological conclusions reached during analysis of gene expression by DNA microarrays. **2005**, 102, 8961-5	83
833	Distinctions in the specificity of E2F function revealed by gene expression signatures. **2005**, 102, 15948-53	56
832	Reduced expression of the insulin receptor in mouse insulinoma (MIN6) cells reveals multiple roles of insulin signaling in gene expression, proliferation, insulin content, and secretion. **2005**, 280, 4992-5003	71
831	Genome Databases. **2005**,	1
830	Gene clustering by latent semantic indexing of MEDLINE abstracts. **2005**, 21, 104-15	113
829	COBrA: a bio-ontology editor. **2005**, 21, 825-6	12
828	Network constrained clustering for gene microarray data. **2005**, 21, 4014-20	41
827	The institute for genomic research Osa1 rice genome annotation database. **2005**, 138, 18-26	188
826	Conservation and divergence of light-regulated genome expression patterns during seedling development in rice and Arabidopsis. **2005**, 17, 3239-56	172
825	Electronic data sources for kinetic models of cell signaling. **2005**, 137, 653-7	6
824	ArrayXPath II: mapping and visualizing microarray gene-expression data with biomedical ontologies and integrated biological pathway resources using Scalable Vector Graphics. **2005**, 33, W621-6	48
823	Chlamydia trachomatis variant with nonfusing inclusions: growth dynamic and host-cell transcriptional response. **2005**, 192, 1229-36	16
822	Identification of differentially expressed proteins in oral squamous cell carcinoma using a global proteomic approach. **2005**, 27, 59	6

821	Low-dose irradiation alters the transcript profiles of human lymphoblastoid cells including genes associated with cytogenetic radioadaptive response. **2005**, 164, 369-82	115
820	Resistance to intestinal Entamoeba histolytica infection is conferred by innate immunity and Gr-1+ cells. **2005**, 73, 4522-9	68
819	GenColors: accelerated comparative analysis and annotation of prokaryotic genomes at various stages of completeness. **2005**, 21, 3669-71	14
818	Fragnostic: walking through protein structure space. **2005**, 33, W249-51	19
817	BRIGEP--the BRIDGE-based genome-transcriptome-proteome browser. **2005**, 33, W710-6	18
816	GFINDer: genetic disease and phenotype location statistical analysis and mining of dynamically annotated gene lists. **2005**, 33, W717-23	56
815	T-profiler: scoring the activity of predefined groups of genes using gene expression data. **2005**, 33, W592-5	164
814	Correlation between sequence conservation and the genomic context after gene duplication. **2005**, 33, 6164-71	37
813	Nonsense-mediated mRNA decay factors act in concert to regulate common mRNA targets. **2005**, 11, 1530-44	206
812	Integrating protein annotation resources through the Distributed Annotation System. **2005**, 33, W468-70	19
811	Identifying synonymous regulatory elements in vertebrate genomes. **2005**, 33, W403-7	20
810	Analyzing the potato abiotic stress transcriptome using expressed sequence tags. **2005**, 48, 598-605	49
809	BiNGO: a Cytoscape plugin to assess overrepresentation of gene ontology categories in biological networks. **2005**, 21, 3448-9	3065
808	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. **2005**, 15, 1034-50	2643
807	Genomic analysis of the response of mouse models to high-fat feeding shows a major role of nuclear receptors in the simultaneous regulation of lipid and inflammatory genes. **2005**, 182, 249-57	31
806	Identification of genes with a biocontrol function in Trichoderma harzianum mycelium using the expressed sequence tag approach. **2005**, 156, 416-23	55
805	The Proteomics Protocols Handbook. **2005**,	204
804	Knowledge Management, Data Mining, and Text Mining in Medical Informatics. **2005**, 3-33	25

803	Progress in Artificial Intelligence. **2005**,	4
802	Natural Language Processing ▯JCNLP 2004. **2005**,	1
801	Data Integration in the Life Sciences. **2005**,	3
800	Network constrained clustering for gene microarray data.	
799	Towards interactive exploration of images, meta-data, and analytic results in the open microscopy environment.	
798	A novel approach for prediction of multi-labeled protein subcellular localization for prokaryotic bacteria.	2
797	Predicting Single Genes Related to Immune-Relevant Processes. **2005**,	
796	Hierarchy-regularized latent semantic indexing.	
795	Probabilistic discovery of overlapping cellular processes and their regulation. **2005**, 12, 909-27	19
794	Correcting BLAST e-values for low-complexity segments. **2005**, 12, 980-1003	7
793	Abstracting genes to gene ontology terms allows comparison across multiple species.	1
792	Cell intrinsic alterations underlie hematopoietic stem cell aging. **2005**, 102, 9194-9	824
791	Clustering genes using gene expression and text literature data. **2005**, 329-40	3
790	A Knowledge-Driven Method to Evaluate Multi-source Clustering. **2005**, 196-202	
789	Combining Bayesian Networks and Decision Trees to Predict Drosophila melanogaster Protein-Protein Interactions. **2005**,	
788	Bayesian decomposition analysis of bacterial phylogenomic profiles. **2005**, 5, 63-70	3
787	Associative clustering for exploring dependencies between functional genomics data sets. **2005**, 2, 203-16	12
786	The SOL Genomics Network: a comparative resource for Solanaceae biology and beyond. **2005**, 138, 1310-7	348

785	Direct proteomic mapping of Streptomyces Luteogriseus Strain 103 and cnn1 and insights into antibiotic biosynthesis. **2005**, 4, 1999-2006	10
784	The subsystems approach to genome annotation and its use in the project to annotate 1000 genomes. **2005**, 33, 5691-702	1485
783	CML tools and information flow in atomic scale simulations. **2005**, 31, 315-322	8
782	Functional ontologies for cognition: The systematic definition of structure and function. **2005**, 22, 262-75	234
781	Analyzing gene expression time-courses. **2005**, 2, 179-93	58
780	Autophagy promotes MHC class II presentation of peptides from intracellular source proteins. **2005** , 102, 7922-7	510
779	WebGestalt: an integrated system for exploring gene sets in various biological contexts. **2005**, 33, W741-8	1367
778	Effective pre-processing strategies for functional clustering of a protein-protein interactions network.	5
777	Whole-proteome prediction of protein function via graph-theoretic analysis of interaction maps. **2005**, 21 Suppl 1, i302-10	357
776	Global protein shotgun expression profiling of proliferating mcf-7 breast cancer cells. **2005**, 4, 674-89	31
775	Bioinformatics in Functional Genomics. **2005**,	
774	Advances in toxicogenomics. **2005**, 18, 403-14	50
773	Phosphoproteome analysis of HeLa cells using stable isotope labeling with amino acids in cell culture (SILAC). **2005**, 4, 1661-71	108
772	Blast2GO: a universal tool for annotation, visualization and analysis in functional genomics research. **2005**, 21, 3674-6	8222
771	Compositional characterization of the cytoskeleton of NK-like cells. **2005**, 4, 2081-7	22
770	Analysis of differentially-regulated genes within a regulatory network by GPS genome navigation. **2005**, 21, 4073-83	36
769	Putting microarrays in a context: integrated analysis of diverse biological data. **2005**, 6, 34-43	55
768	Global gene repression in hepatocellular carcinoma and fetal liver, and suppression of dudulin-2 mRNA as a possible marker for the cirrhosis-to-tumor transition. **2005**, 42, 860-9	28

767	Genomic and functional characterization of stellate cells isolated from human cirrhotic livers. **2005**, 43, 272-82	73
766	Mimicking cellular sorting improves prediction of subcellular localization. **2005**, 348, 85-100	253
765	Mice with Ppt1Deltaex4 mutation replicate the INCL phenotype and show an inflammation-associated loss of interneurons. **2005**, 18, 226-41	64
764	PABPN1 overexpression leads to upregulation of genes encoding nuclear proteins that are sequestered in oculopharyngeal muscular dystrophy nuclear inclusions. **2005**, 18, 551-67	63
763	Androgen regulation of gene expression in the mouse lacrimal gland. **2005**, 96, 401-13	27
762	BmiGI: a database of cDNAs expressed in Boophilus microplus, the tropical/southern cattle tick. **2005**, 35, 585-95	62
761	Transcriptional changes during neuronal death and replacement in the olfactory epithelium. **2005**, 30, 90-107	40
760	Prediction of cis-regulatory elements using binding site matrices--the successes, the failures and the reasons for both. **2005**, 15, 395-402	55
759	Simple sequence repeats in proteins and their significance for network evolution. **2005**, 345, 113-8	80
758	The architecture of the protein domain universe. **2005**, 347, 199-206	17
757	Human genome-wide screen of haplotype-like blocks of reduced diversity. **2005**, 349, 219-25	42
756	Broadly predicting specific gene functions with expression similarity and taxonomy similarity. **2005**, 352, 75-81	79
755	List of lists-annotated (LOLA): a database for annotation and comparison of published microarray gene lists. **2005**, 360, 78-82	46
754	A human protein-protein interaction network: a resource for annotating the proteome. **2005**, 122, 957-68	1848
753	Illuminating drug discovery with biological pathways. **2005**, 579, 1872-7	81
752	CO: A chemical ontology for identification of functional groups and semantic comparison of small molecules. **2005**, 579, 4685-91	53
751	2.45 GHz radiofrequency fields alter gene expression in cultured human cells. **2005**, 579, 4829-36	71
750	Comparative analysis of 87,000 expressed sequence tags from the fumonisin-producing fungus Fusarium verticillioides. **2005**, 42, 848-61	89

749	Analysis of orthologous gene expression between human pulmonary adenocarcinoma and a carcinogen-induced murine model. **2005**, 167, 1763-75	243
748	A 7872 cDNA microarray and its use in bovine functional genomics. **2005**, 105, 235-45	49
747	A robust hybrid between genetic algorithm and support vector machine for extracting an optimal feature gene subset. **2005**, 85, 16-23	95
746	Interpreting expression profiles of cancers by genome-wide survey of breadth of expression in normal tissues. **2005**, 86, 127-41	218
745	Nested genes in the human genome. **2005**, 86, 414-22	59
744	Assessment and integration of publicly available SAGE, cDNA microarray, and oligonucleotide microarray expression data for global coexpression analyses. **2005**, 86, 476-88	40
743	Studying phospholipid metabolism using yeast systematic and chemical genetics. **2005**, 36, 102-8	8
742	Transcription factor gene expression profiling after acute intermittent nicotine treatment in the rat cerebral cortex. **2005**, 133, 787-96	32
741	Efficient Algorithms for Detecting Signaling Pathways in Protein Interaction Networks. **2005**, 1-13	11
740	Comparative analysis and characterization of expressed sequence tags in gilthead sea bream (Sparus aurata) liver and embryos. **2005**, 243, 69-81	32
739	Transcriptome responses to carbon tetrachloride and pyrene in the kidney and liver of juvenile rainbow trout (Oncorhynchus mykiss). **2005**, 74, 70-81	68
738	Nutrigenomics: the impact of biomics technology on nutrition research. **2005**, 49, 355-65	77
737	Evidence for a preferential targeting of 3'-UTRs by cis-encoded natural antisense transcripts. **2005**, 33, 5533-43	76
736	Low-dose exposure to gamma rays induces specific gene regulations in normal human keratinocytes. **2005**, 163, 623-35	84
735	Molecular aging in human prefrontal cortex is selective and continuous throughout adult life. **2005**, 57, 549-58	177
734	An atlas of differential gene expression during early Xenopus embryogenesis. **2005**, 122, 365-439	58
733	Chapter 11 Protein bioinformatics. **2005**, 487-500	
732	Protein Identification and Analysis Tools on the ExPASy Server. **2005**, 571-607	3376

731	The Arabidopsis Genome and Its Use in Cereal Genomics. **2004**, 515-534	
730	A global view of pleiotropy and phenotypically derived gene function in yeast. **2005**, 1, 2005.0001	232
729	ProFunc: a server for predicting protein function from 3D structure. **2005**, 33, W89-93	491
728	Constructing and analyzing a large-scale gene-to-gene regulatory network--lasso-constrained inference and biological validation. **2005**, 2, 254-61	55
727	Data integration and visualization system for enabling conceptual biology. **2005**, 21 Suppl 1, i177-85	13
726	Information integration in molecular bioscience. **2005**, 4, 157-73	7
725	An update on the functional molecular immunology (FIMM) database. **2005**, 4, 25-31	12
724	Visualization in Science Education. **2005**,	92
723	Sequence features in regions of weak and strong linkage disequilibrium. **2005**, 15, 1519-34	71
722	In silico reconstruction of the metabolic pathways of Lactobacillus plantarum: comparing predictions of nutrient requirements with those from growth experiments. **2005**, 71, 7253-62	146
721	Reduction of macrophage infiltration and chemoattractant gene expression changes in white adipose tissue of morbidly obese subjects after surgery-induced weight loss. **2005**, 54, 2277-86	870
720	Cereal Genomics. **2005**,	3
719	Multidimensional protein identification technology: current status and future prospects. **2005**, 2, 27-39	32
718	An ontology-driven clustering method for supporting gene expression analysis.	2
717	Bioinformatics Technologies. **2005**,	10
716	Systematic analysis of gene expression in human brains before and after death. **2005**, 6, R112	23
715	Primary and secondary transcriptional effects in the developing human Down syndrome brain and heart. **2005**, 6, R107	118
714	Gene expression and metabolite profiling of Populus euphratica growing in the Negev desert. **2005** , 6, R101	186

713	Searching for differentially expressed gene combinations. **2005**, 6, R88	46
712	L2L: a simple tool for discovering the hidden significance in microarray expression data. **2005**, 6, R81	101
711	Tandem repeat copy-number variation in protein-coding regions of human genes. **2005**, 6, R69	44
710	Analysis of the Macaca mulatta transcriptome and the sequence divergence between Macaca and human. **2005**, 6, R60	78
709	Transcript copy number estimation using a mouse whole-genome oligonucleotide microarray. **2005**, 6, R61	98
708	Consolidating the set of known human protein-protein interactions in preparation for large-scale mapping of the human interactome. **2005**, 6, R40	167
707	Derivation of genetic interaction networks from quantitative phenotype data. **2005**, 6, R38	100
706	Pilot Anopheles gambiae full-length cDNA study: sequencing and initial characterization of 35,575 clones. **2005**, 6, R39	21
705	A DNA microarray survey of gene expression in normal human tissues. **2005**, 6, R22	172
704	Identifying genetic networks underlying myometrial transition to labor. **2005**, 6, R12	50
703	Genomic analysis of early murine mammary gland development using novel probe-level algorithms. **2005**, 6, R20	17
702	Fast and systematic genome-wide discovery of conserved regulatory elements using a non-alignment based approach. **2005**, 6, R18	103
701	Gene expression profiling in murine autoimmune arthritis during the initiation and progression of joint inflammation. **2005**, 7, R196-207	30
700	Inflammatory Disorders of the Nervous System. **2005**,	1
699	Pathway and gene-set activation measurement from mRNA expression data: the tissue distribution of human pathways. **2006**, 7, R93	71
698	PhyloFacts: an online structural phylogenomic encyclopedia for protein functional and structural classification. **2006**, 7, R83	47
697	The human urinary proteome contains more than 1500 proteins, including a large proportion of membrane proteins. **2006**, 7, R80	514
696	Shuffling of cis-regulatory elements is a pervasive feature of the vertebrate lineage. **2006**, 7, R56	40

695	Evolution of candidate transcriptional regulatory motifs since the human-chimpanzee divergence. **2006**, 7, R52	12
694	RNA editing of human microRNAs. **2006**, 7, R27	270
693	Comparative analysis of Saccharomyces cerevisiae WW domains and their interacting proteins. **2006**, 7, R30	48
692	Genes regulated by estrogen in breast tumor cells in vitro are similarly regulated in vivo in tumor xenografts and human breast tumors. **2006**, 7, R28	98
691	Deciphering cellular states of innate tumor drug responses. **2006**, 7, R19	97
690	Modulation of the transcription regulatory program in yeast cells committed to sporulation. **2006**, 7, R20	52
689	Anopheles gambiae genome reannotation through synthesis of ab initio and comparative gene prediction algorithms. **2006**, 7, R24	16
688	Full-Length Transcriptome Characterization and Functional Analysis of Pathogenesis-Related Proteins in Lilium Oriental Hybrid Sorbonne Infected with Botrytis elliptica. **2023**, 24, 425	0
687	Analysis of network pharmacology and experimental verification to explore the mechanism of Modified Guilu Erxian Glue in the treatment of low immune function. **2022**, 100213	0
686	A morphometrics approach for inclusion of localised characteristics from medical imaging studies into genome-wide association studies. **2022**,	0
685	Sympatric or micro-allopatric speciation in a glacial lake? Genomic islands support neither.	0
684	The gold-ringed octopus (Amphioctopus fangsiao)´genome and cerebral single-nucleus transcriptomes provide insights into the evolution of karyotype and neural novelties. **2022**, 20,	0
683	The P450 Sterol Side Chain Cleaving Enzyme (P450scc) for Digoxin Biosynthesis in the Foxglove Plant Belongs to the CYP87A Family.	0
682	KL-RF: Predicting disease-gene associations with model fusion. **2022**,	0
681	Antimicrobial resistance in Klebsiella pneumoniae: identification of bacterial DNA adenine methyltransferase as a novel drug target from hypothetical proteins using subtractive genomics. **2022**, 20, e47	0
680	GCL-GO: A novel sequence-based hierarchy-aware method for protein function prediction. **2022**,	0
679	Mapping variation in the morphological landscape of human cells with optical pooled CRISPRi screening.	0
678	Aortic Stress Activates an Adaptive Program in Thoracic Aortic Smooth Muscle Cells That Maintains Aortic Strength and Protects Against Aneurysm and Dissection in Mice.	0

677	Variation in heat shock protein 40 kDa relates to divergence in thermotolerance among cryptic rotifer species. **2022**, 12,	0
676	Positive Feature Values Prioritized Hierarchical Dependency Constrained Averaged One-dependence Estimators for Gene Ontology Feature Spaces. **2022**,	0
675	Identification of the expression, prognostic value and cancer immunity of Gasdermin E based on multi-omics data, machine learning and gene ontology. **2022**,	0
674	Multi-omics network model reveals key genes associated with p-coumaric acid stress response in an industrial yeast strain. **2022**, 12,	0
673	Diversity of Mixotrophic Neutrophilic Thiosulfate- and Iron-Oxidizing Bacteria from Deep-Sea Hydrothermal Vents. **2023**, 11, 100	0
672	Genome Sequence Resource of Fusarium proliferatum f. sp. malus domestica MR5, the Causative Agent of Apple Replant Disease.	0
671	Zero Gravity is a Factor that Induces Negative Changes in Myelinated Fibers of the Spinal Tracts. **2022**, 174, 265-268	0
670	Chromosome-level genome and the identification of sex chromosomes in Uloborus diversus. **2022**, 12,	0
669	Low-level cadmium exposure induced hormesis in peppermint young plant by constantly activating antioxidant activity based on physiological and transcriptomic analyses. 14,	0
668	Physiological and Transcriptomic Response of Asiatic Hard Clam Meretrix meretrix to the Harmful Alga Heterosigma akashiwo. **2023**, 8, 67	1
667	Modular architecture and functional annotation of human RNA-binding proteins containing RNA recogntion motif. **2023**,	0
666	Exploring the hub mechanisms of ischemic stroke based on protein-protein interaction networks related to ischemic stroke and inflammatory bowel disease. **2023**, 13,	0
665	Genetic responses to adding nitrates to improve hydrophilic yellow pigment in Monascus fermentation. **2023**, 107, 1341-1359	0
664	Identification of molecular signatures and pathways involved in Rett syndrome using a multi-omics approach.	0
663	Binary Colloidal Crystals Promote Cardiac Differentiation of Human Pluripotent Stem Cells via Nuclear Accumulation of SETDB1.	0
662	Influence of sex, age and diabetes on brain transcriptome and proteome modifications following cerebral ischemia. **2023**, 24,	0
661	In silico analysis of NHP2 membrane protein, a novel vaccine candidate present in the RD7 region of Mycobacterium tuberculosis.	0
660	TriTrypDB: An integrated functional genomics resource for kinetoplastida. **2023**, 17, e0011058	0

659	Identification of the egusi seed trait locus (eg) and its suppressor gene associated with the thin seed coat trait in watermelon. 14,	0
658	PyGenePlexus: a Python package for gene discovery using network-based machine learning. **2023**, 39,	0
657	De Novo Transcriptome Assembly and EST-SSR Marker Development and Application in Chrysosplenium macrophyllum. **2023**, 14, 279	0
656	A Network of MicroRNAs and mRNAs Involved in Melanosome Maturation and Trafficking Defines the Lower Response of Pigmentable Melanoma Cells to Targeted Therapy. **2023**, 15, 894	0
655	The memory of pathogenic IgE is contained within CD23+IgG1+memory B cells poised to switch to IgE in food allergy.	0
654	Quiescence-inducing 3D-engineered matrix uncovers mechanosensitive and drug protective FHL2-p21 signaling axis.	0
653	Adriforant is a functional antagonist of histamine receptor 4 and attenuates itch and skin inflammation in mice. **2023**, 175533	0
652	Genomic and proteomic analysis of Bacillus subtilis as microplastic bioremediation agents. **2023**,	0
651	Molecular Characterization and Phylogenetic Analysis of Casein Gene Family in Camelus ferus. **2023** , 14, 256	0
650	Identification of ULK1 as a novel mitophagy-related gene in diabetic nephropathy. 13,	0
649	Single-cell analysis of myeloid cells in HPV+ tonsillar cancer. 13,	0
648	The viral packaging motor potentiates late gene expression in Kaposi's sarcoma-associated herpesvirus.	0
647	Long-term potentiation and depression regulatory microRNAs were highlighted in Bisphenol A induced learning and memory impairment by microRNA sequencing and bioinformatics analysis. **2023**, 18, e0279029	0
646	Maternal diet induces persistent DNA methylation changes in the muscle of beef calves. **2023**, 13,	0
645	Whole-genome comparisons identify repeated regulatory changes underlying convergent appendage evolution in diverse fish lineages.	0
644	Novel Genetic Variants Associated with Chronic Kidney Disease Progression. **2023**, Publish Ahead of Print,	0
643	Transcriptomic response of bioengineered human cartilage to parabolic flight microgravity is sex-dependent. **2023**, 9,	1
642	Immunoreactivity against SLC3A2 in high grade gliomas displays positive correlation with glioblastoma patient survival: Potential target for glioma diagnosis and therapy.	0

641	Melatonin Mitigates iNOS-Related Effects of HEMA and Camphorquinone in Human Dental Pulp Cells: Relevance for Postoperative Sensitivity Mechanism in Type 2 Diabetes. **2023**, 24, 2562	0
640	Protein Representation Learning via Knowledge Enhanced Primary Structure Modeling.	0
639	Comparative Expression Profiling Reveals the Regulatory Effects of Dietary Mannan Oligosaccharides on the Intestinal Immune Response of Juvenile Megalobrama amblycephala against Aeromonas hydrophila Infection. **2023**, 24, 2207	0
638	The Gynandropsis gynandra genome provides insights into whole-genome duplications and the evolution of C4 photosynthesis in Cleomaceae.	0
637	Identification of New Candidate Genes Related to Semen Traits in Duroc Pigs through Weighted Single-Step GWAS. **2023**, 13, 365	0
636	Sample size calculation for a NanoString GeoMx spatial transcriptomics experiment to study predictors of fibrosis progression in non-alcoholic fatty liver disease.	0
635	Unraveling the Relevance of Tissue-Specific Decellularized Extracellular Matrix Hydrogels for Vocal Fold Regenerative Biomaterials: A Comprehensive Proteomic and In Vitro Study. 2200095	0
634	Molecular mechanisms of the Guizhi decoction on osteoarthritis based on an integrated network pharmacology and RNA sequencing approach with experimental validation. 14,	0
633	Integration of proteomic and metabolomic analyses: New insights for mapping informal workers exposed to potentially toxic elements. 10,	0
632	Combined PD-1, BRAF and MEK inhibition in BRAFV600E colorectal cancer: a phase 2 trial.	0
631	Prediction of´Protein Molecular Functions Using Transformers. **2023**, 379-387	0
630	Characterization of proteome-size scaling by integrative omics reveals mechanisms of proliferation control in cancer. **2023**, 9,	0
629	CD200 + cytotoxic T lymphocytes in the tumor microenvironment are crucial for efficacious anti□PD-1/PD-L1 therapy. **2023**, 15,	0
628	Cell Cycle-Related Gene SPC24: A Novel Potential Diagnostic and Prognostic Biomarker for Laryngeal Squamous Cell Cancer. **2023**, 2023, 1-14	0
627	Nematode gene annotation by machine-learning-assisted proteotranscriptomics enables proteome-wide evolutionary analysis. **2023**, 33, 112-128	0
626	Ribosome rescue factor PELOTA modulates translation start site choice and protein isoform levels of transcription factor C/EBP□	0
625	Expression profiles of lncRNAs and their possible regulatory role in monocrotaline-induced HSOS in rats. 14,	0
624	Spatial transcriptomic brain imaging reveals the effects of immunomodulation therapy upon specific regional brain cells in mouse dementia model.	0

623	GOThresher: a program to remove annotation biases from protein function annotation datasets. **2023**, 39,	0
622	Gene Expression Profiles in Cancers and Their Therapeutic Implications. **2023**, 29, 9-14	0
621	CitrusGenome: A Bioinformatics Tool to´Characterize, Visualize, and´Explore Large Citrus Variant Datasets. **2023**, 167-178	0
620	Follicular fluid progesterone down-regulated HPGD and COX2 in granulosa cells via suppressing NF-B in endometriosis.	0
619	Stellettin B Induces Cell Death in Bladder Cancer Via Activating the Autophagy/DAPK2/Apoptosis Signaling Cascade. **2023**, 21, 73	0
618	Systematic comparison of transcriptomes of Caco-2 cells cultured under different cellular and physiological conditions.	1
617	Dbx2, an aging-related homeobox gene, inhibits the proliferation of adult neural progenitors.	0
616	Protein network analysis links the NSL complex to Parkinson's disease and mitochondrial biology.	0
615	Network-based quantitative trait linkage analysis of microbiome composition in inflammatory bowel disease families. 14,	0
614	Uncovering the effects and molecular mechanism of Astragalus membranaceus (Fisch.) Bunge and its bioactive ingredients formononetin and calycosin against colon cancer: An integrated approach based on network pharmacology analysis coupled with experimental validation and molecular docking. 14,	0
613	Transcriptome and metabolome profiling of the medicinal plant Veratrum mengtzeanum reveal key components of the alkaloid biosynthesis. 14,	0
612	Comparative Analyses Reveal the Genetic Mechanism of Ambergris Production in the Sperm Whale Based on the Chromosome-Level Genome. **2023**, 13, 361	0
611	Parkinson's Disease Gene Biomarkers Screened by the LASSO and SVM Algorithms. **2023**, 13, 175	0
610	PlantTribes2: Tools for comparative gene family analysis in plant genomics. 13,	0
609	Analyzing RNA-Protein Interactions by Cross-Link Rates and CLIP-seq Libraries. **2023**, 3,	0
608	Large language models generate functional protein sequences across diverse families.	1
607	A targeted multi-proteomics approach generates a blueprint of the ciliary ubiquitinome. 11,	0
606	Peptidomics analysis of plasma in patients with ankylosing spondylitis. 14,	0

605	Identification of Long Noncoding RNAs That Exert Transcriptional Regulation by Forming RNA▯DNA Triplexes in Prostate Cancer. **2023**, 24, 2035	0
604	Self-assembly and self-delivery of the pure nanodrug dihydroartemisinin for tumor therapy and mechanism analysis.	0
603	Characterization and Application of EST-SSR Markers Developed from Transcriptome Sequences in Elymus breviaristatus (Poaceae: Triticeae). **2023**, 14, 302	0
602	miRinGO: Prediction of Biological Processes Indirectly Targeted by Human microRNAs. **2023**, 9, 11	0
601	Addressing the pervasive scarcity of structural annotation in eukaryotic algae. **2023**, 13,	1
600	Comparative analysis of the chrysanthemum transcriptome with DNA methylation inhibitors treatment and silencing MET1 lines. **2023**, 23,	0
599	DNA Methylation Dynamics During Esophageal Epithelial Regeneration Following Repair with Acellular Silk Fibroin Grafts in Rat. 2200160	0
598	scm6A-seq reveals single-cell landscapes of the dynamic m6A during oocyte maturation and early embryonic development. **2023**, 14,	0
597	Investigating nicotine pathway-related long non-coding RNAs in tobacco. 13,	0
596	RNA sequencing indicates widespread conservation of circadian clocks in marine zooplankton. **2023**, 5,	0
595	Functional synapses between small cell lung cancer and glutamatergic neurons.	0
594	Gene expression of macaques infected with malaria species of zoonotic concern.	0
593	Metrics for RNA Secondary Structure Comparison. **2023**, 79-88	0
592	Genome-wide genetic variation and comparative transcriptome analyses of citrus mutant Jedae-unshiu and wild-type Citrus unshiu.	0
591	Correlated evolution of social organization and lifespan in mammals. **2023**, 14,	0
590	Endothelial cell-derived oxysterol ablation attenuates experimental autoimmune encephalomyelitis.	0
589	Protein interaction studies in human induced neurons indicate convergent biology underlying autism spectrum disorders. **2023**, 100250	0
588	Physiological hypoxia improves growth and functional differentiation of human intestinal epithelial organoids. 14,	0

587	Molecular Influence of Resiniferatoxin on the Urinary Bladder Wall Based on Differential Gene Expression Profiling. **2023**, 12, 462	0
586	Transcriptome analysis reveals the key pathways and candidate genes involved in salt stress responses in Cymbidium ensifolium leaves. **2023**, 23,	0
585	Murine scald models characterize the role of neutrophils and neutrophil extracellular traps in severe burns. 14,	0
584	A Tissue-Specific and Toxicology-Focused Knowledge Graph. **2023**, 14, 91	0
583	Genome-wide screening reveals the genetic basis of mammalian embryonic eye development. **2023** , 21,	0
582	Angiogenesis-relevant lncRNA signature for osteosarcoma: prospects for prediction of clinical outcomes and immunotherapeutic efficacy.	0
581	Using Ontologies to Create Machine-Actionable Datasets: Two Case Studies. **2023**, 3, 65-80	0
580	Integrative pathway and network analysis provide insights on flooding-tolerance genes in soybean. **2023**, 13,	0
579	KRT17 serves as an oncogene biomarker of poor survival in patients with hepatocellular carcinoma. **2023**, 3, 18-25	0
578	Therapeutic effects and mechanisms of Ku-Gan formula on atopic dermatitis: A pilot clinical study and modular pharmacology analysis with animal validation. **2023**, 307, 116194	0
577	Using ontologies for life science text-based resource organization. **2023**, 3, 100059	0
576	Deciphering Macromolecular Interactions Involved in Abiotic Stress Signaling: A Review of Bioinformatics Analysis. **2023**, 257-294	0
575	Utility of proteomics and phosphoproteomics in the tailored medication of cancer. **2023**, 319-332	0
574	Combined analysis of chromatin accessibility and gene expression profiles provide insight into Fucoxanthin biosynthesis in Isochrysis galbana under green light. 14,	0
573	Databases and prospects of dynamic gene regulation in eukaryotes: A mini review. **2023**, 21, 2147-2159	0
572	Physiological and transcriptomic responses to cold waves of the most cold-tolerant mangrove, Kandelia obovata. 14,	0
571	Quantitative analysis of high-throughput biological data.	0
570	Single-cell sequencing of ascites fluid illustrates heterogeneity and therapy-induced evolution during gastric cancer peritoneal metastasis. **2023**, 14,	0

569	High-resolution lac insect genome assembly provides genetic insights into lac synthesis and evolution of scale insects.	0
568	vicR overexpression in Streptococcus mutans causes aggregation and affects interspecies competition.	0
567	Hypothesis-free phenotype prediction within a genetics-first framework.	0
566	Interplay between PLEKHG3-regulated actin dynamics and lysosomal trafficking in cell motility.	0
565	Construction of a searchable database for gene expression changes in spinal cord injury experiments.	0
564	Endocrine Disrupting Chemicals Influence Hub Genes Associated with Aggressive Prostate Cancer. **2023**, 24, 3191	0
563	A novel approach to interrogating the effects of chemical warfare agent exposure using organ-on-a-chip technology and multiomic analysis. **2023**, 18, e0280883	0
562	Large-Scale Quantitative Proteomic Analysis during Different Stages of Somatic Embryogenesis in Larix olgensis. **2023**, 45, 2021-2034	0
561	Spatial transcriptomics using multiplexed deterministic barcoding in tissue. **2023**, 14,	0
560	Full-length transcriptome profiling for fruit development in Diospyros oleifera using nanopore sequencing. **2023**, 24,	0
559	Identification of key genes and imbalance of immune cell infiltration in immunoglobulin A associated vasculitis nephritis by integrated bioinformatic analysis. 14,	0
558	Network Pharmacology and Molecular Modeling to Elucidate the Potential Mechanism of Neem Oil against Acne vulgaris. **2023**, 28, 2849	0
557	Identification of fatty acid metabolism-based molecular subtypes and prognostic signature to predict immune landscape and guide clinical drug treatment in renal clear cell carcinoma. **2023**, 116, 109735	0
556	Non-additive effects of schizophrenia risk genes reflect convergent downstream function.	0
555	Low-dose of caffeine alleviates high altitude pulmonary edema via regulating mitochondrial quality control process in AT1 cells. 14,	0
554	Construction and validation of a hypoxia-related risk signature identified EXO1 as a prognostic biomarker based on 12 genes in lung adenocarcinoma. **2023**, 15, 2293-2307	0
553	Effect of fermented soy beverage in aged female mice model. **2023**, 112745	0
552	Genome graphs detect human polymorphisms in active epigenomic state during influenza infection. **2023**, 100294	0

551	PGC-1s shape epidermal physiology by modulating keratinocyte proliferation and terminal differentiation. **2023**, 26, 106314	0
550	Breast cancer cell secretome analysis to decipher miRNA regulating the tumor microenvironment and discover potential biomarkers. **2023**, e15421	0
549	Whole-genome sequencing and analysis of Apocynum cannabinum.	0
548	Genome-scale CRISPR screen reveals neddylation to contribute to cisplatin resistance of testicular germ cell tumours.	0
547	Developing a Knowledge Graph for Pharmacokinetic Natural Product-Drug Interactions. **2023**, 140, 104341	0
546	Bioinformatics and computational chemistry approaches to explore the mechanism of the anti-depressive effect of ligustilide. **2023**, 13,	0
545	Estradiol cycling drives female obesogenic adipocyte hyperplasia. **2023**, 42, 112390	0
544	Unified access to up-to-date residue-level annotations from UniProtKB and other biological databases for PDB data. **2023**, 10,	0
543	Probe-based bacterial single-cell RNA sequencing predicts toxin regulation.	0
542	Cellular proteomic profiling using proximity labelling by TurboID-NES in microglial and neuronal cell lines. **2023**, 100546	0
541	Comparative- and network-based proteomic analysis of bacterial chondronecrosis with osteomyelitis lesions in broilers’ proximal tibiae identifies new molecular signatures of lameness. **2023**, 13,	0
540	Comparative genomics analyses reveal sequence determinants underlying interspecies variations in injury-responsive enhancers. **2023**, 24,	0
539	A comprehensive transcriptional signature in pancreatic ductal adenocarcinoma reveals new insights into the immune and desmoplastic microenvironment.	0
538	Network pharmacology-integrated molecular docking analysis of phytocompounds of Caesalpinia pulcherrima (peacock flower) as potential anti-metastatic agents. 1-17	0
537	RTEL1 is required for silencing and epigenome stability.	0
536	Introducing multi-dimensional hierarchical classification: Characterization, solving strategies and performance measures. **2023**, 533, 141-160	0
535	Mechanisms of Phaeocystis globosa blooms in the Beibu Gulf revealed by metatranscriptome analysis. **2023**, 124, 102407	0
534	Revealing holistic metabolic responses associated with lipid and docosahexaenoic acid (DHA) production in Aurantiochytrium sp. SW1. **2023**, 1868, 159306	0

533	Whole-genome sequencing of a biocontrol Myxococcus xanthus R31 isolate and comparative genomic analysis. **2023**, 863, 147286	0
532	HER2 as a potential therapeutic target on quiescent prostate cancer cells. **2023**, 31, 101642	0
531	The cotton miR530-SAP6 module activated by systemic acquired resistance mediates plant defense against Verticillium dahliae. **2023**, 330, 111647	0
530	Transcriptome response of Antarctic Phaeodactylum tricornutum ICE-H producing dimethylsulphoniopropionate to hypersaline stress. **2023**, 128, 206-217	0
529	REL-NPMI: Exploring genotype and phenotype relationship of pancreatitis based on improved normalized point-by-point mutual information. **2023**, 158, 106868	0
528	Proteomic and phosphoproteomic analyses of Jurkat T-cell treated with 2?3? cGAMP reveals various signaling axes impacted by cyclic dinucleotides. **2023**, 279, 104869	0
527	Overall mortality risk analysis for rectal cancer using deep learning-based fuzzy systems. **2023**, 157, 106706	0
526	Whole genome sequencing identified candidate genes related to litter size of Qinghai fine wool sheep under artificial selection. **2023**, 223, 106969	0
525	Clustering of multi-layer networks with structural relations and conservation of features. **2023**, 140, 110272	0
524	Rare earth elements detoxification mechanism in the hyperaccumulator Dicranopteris linearis: [silicon-pectin] matrix fixation. **2023**, 452, 131254	0
523	Dietary intake of household cadmium-contaminated rice caused genome-wide DNA methylation changes on gene/hubs related to metabolic disorders and cancers. **2023**, 327, 121553	0
522	A deep transcriptome meta-analysis reveals sex differences in multiple sclerosis. **2023**, 181, 106113	0
521	Identification of genes responsible for the social skill in the earthworm, Eudrilus eugeniae. **2023**, 31, 101774	0
520	Metabolic regulation mechanism of Trametes gibbosa CB1 on lignin. **2023**, 240, 124189	0
519	Role of N6-adenosine-methyltransferase subunits METTL3 and METTL14 in the biological properties of periodontal ligament cells. **2023**, 82, 102081	0
518	Complete genome sequence of Lactobacillus fermentum 9-4, a purine-degrading Lactobacillus probiotic isolated from Chinese fermented rice-flour noodles. **2023**, 3, 169-174	0
517	Saikosaponin A and D attenuate skeletal muscle atrophy in chronic kidney disease by reducing oxidative stress through activation of PI3K/AKT/Nrf2 pathway. **2023**, 114, 154766	0
516	Enantioselectivity effects of energy metabolism in honeybees (Apis mellifera) by triticonazole. **2023**, 877, 162884	0

515	Microglia-containing cerebral organoids derived from induced pluripotent stem cells for the study of neurological diseases. **2023**, 26, 106267	0
514	Morphology-guided transcriptomic analysis of human pancreatic cancer organoids reveals microenvironmental signals that enhance invasion. **2023**, 133,	0
513	NetGO 3.0: Protein Language Model Improves Large-scale Functional Annotations. **2023**,	0
512	Identification of key genes involved in neural regeneration and the repairing effect of BDNF-overexpressed BMSCs on spinal cord ischemia-reperfusion injury in rats. **2023**, 160, 114293	0
511	Combined Study of Transcriptome and Metabolome Reveals Involvement of Metabolites and Candidate Genes in Flavonoid Biosynthesis in Prunus avium L.. **2023**, 9, 463	0
510	The viral packaging motor potentiates Kaposi’s sarcoma-associated herpesvirus gene expression late in infection. **2023**, 19, e1011163	0
509	The genome and transcriptome of Sarocladium terricola provide insight into ergosterol biosynthesis. 13,	0
508	Identification of Candidate Genes Involved in the Determinism of Pollen Grain Aperture Morphology by Comparative Transcriptome Analysis in Papaveraceae. **2023**, 12, 1570	0
507	Understanding the response in Pugionium cornutum (L.) Gaertn. seedling leaves under drought stress using transcriptome and proteome integrated analysis. 11, e15165	0
506	Chromosome-level genome assembly and population genomic resource to accelerate orphan crop lablab breeding. **2023**, 14,	0
505	Regulation of neural stem cell self-renewal, proliferation and differentiation by the RhoA guanine nucleotide exchange factor Arhgef 1. **2023**, 863, 147306	0
504	Insights into identifying resistance genes for cold and disease stresses through chromosome-level reference genome analyses of Poncirus polyandra. **2023**, 115, 110617	0
503	A pathogenic variant in the uncharacterized RNF212B gene results in severe aneuploidy male infertility and repeated IVF failure. **2023**, 4, 100189	0
502	A herbal product inhibits carbon tetrachloride-induced liver fibrosis by suppressing the epidermal growth factor receptor signaling pathway. **2023**, 311, 116419	0
501	The genome of Lignosus tigris: Uncovering its hidden nutraceutical potential. **2023**, 154, 108-119	1
500	Investigation of the keratinocyte transcriptome altered in high-glucose environment: An in-vitro model system for precision medicine. **2023**, 109, 37-46	0
499	Toxicologic effect of short-term enrofloxacin exposure on brain of Carassius auratus var. Pengze. **2023**, 869, 161730	0
498	Systems vaccinology for the design of rational vaccines against protozoan parasites. **2022**, 297-334	0

497	Neuro-immune deconvolution analysis of OAS3 as a transcriptomic central node in HIV-associated neurocognitive disorders. **2023**, 446, 120562	0
496	Prognostic value of nuclear morphometry in myxoid liposarcoma.	0
495	FirmTruss Community Search in Multilayer Networks. **2022**, 16, 505-518	0
494	Mechanistic insights into the interactions between cancer drivers and the tumour immune microenvironment.	0
493	BIRCH: An Automated Workflow for Evaluation, Correction, and Visualization of Batch Effect in Bottom-Up Mass Spectrometry-Based Proteomics Data. **2023**, 22, 471-481	0
492	Identifying molecular targets of Aspiletrein-derived steroidal saponins in lung cancer using network pharmacology and molecular docking-based assessments. **2023**, 13,	0
491	PortPred: exploiting deep learning embeddings of amino acid sequences for the identification of transporter proteins and their substrates.	0
490	Alterations in platelet proteome signature and impaired platelet integrin □b□ activation in patients with COVID-19. **2023**,	0
489	Causal knowledge graph construction and evaluation for clinical decision support of diabetic nephropathy. **2023**, 139, 104298	0
488	Surfaceome Profiling of Cell Lines and Patient-Derived Xenografts Confirm FGFR4, NCAM1, CD276, and Highlight AGRL2, JAM3, and L1CAM as Surface Targets for Rhabdomyosarcoma. **2023**, 24, 2601	0
487	Molecular mechanisms of environmental exposures and human disease. **2023**, 24, 332-344	0
486	Computational Approaches to Enzyme Inhibition by Marine Natural Products in the Search for New Drugs. **2023**, 21, 100	0
485	BPDE, the Migration and Invasion of Human Trophoblast Cells, and Occurrence of Miscarriage in Humans: Roles of a Novel lncRNA-HZ09. **2023**, 131,	1
484	Proteome-Wide Detection and Annotation of Receptor Tyrosine Kinases (RTKs): RTK-PRED and the TyReK Database. **2023**, 13, 270	0
483	CP204L Is a Multifunctional Protein of African Swine Fever Virus That Interacts with the VPS39 Subunit of the Homotypic Fusion and Vacuole Protein Sorting Complex and Promotes Lysosome Clustering. **2023**, 97,	0
482	Upregulation of GALNT7 in prostate cancer modifies O-glycosylation and promotes tumour growth. **2023**, 42, 926-937	0
481	De Novo Assembly of an Allotetraploid Artemisia argyi Genome. **2023**, 13, 436	0
480	Systematic approach to identify therapeutic targets and functional pathways for the cervical cancer. **2023**, 21,	0

479	Elucidating the functional roles of prokaryotic proteins using big data and artificial intelligence. **2023**, 47,	0
478	Transcriptome and methylome dynamics in the gills of large yellow croaker (Larimichthys crocea) during low-salinity adaption. 10,	0
477	Remodeling of the Ribosomal Quality Control and Protein Translation by a Viral Ubiquitin Deconjugase.	0
476	Integrative Analysis of Proteome-wide Association Studies and Functional Enrichment Analysis to Identify Genes and Chemicals Associated with Alcohol Dependence. Publish Ahead of Print,	0
475	Organism-Wide Analysis of Sepsis Reveals Mechanisms of Systemic Inflammation.	0
474	Epstein-Barr Virus Synergizes with BRD7 to Conquer c-Myc-Mediated Viral Latency Maintenance via Chromatin Remodeling. **2023**, 11,	0
473	Pan-cancer molecular subtypes of metastasis reveal distinct and evolving transcriptional programs. **2023**, 4, 100932	1
472	Linking chemicals, genes and morphological perturbations to diseases. **2023**, 461, 116407	0
471	A proteomic analysis of NETosis in trauma: Emergence of serpinB1 as a key player. **2023**, 94, 361-370	0
470	Pan-genome and transcriptome analyses provide insights into genomic variation and differential gene expression profiles related to disease resistance and fatty acid biosynthesis in eastern black walnut (Juglans nigra). **2023**, 10,	0
469	Recent development of machine learning models for the prediction of drug-drug interactions. **2023** , 40, 276-285	0
468	Computer-Aided Screening and Revealing Action Mechanism of Green Tea Polyphenols Intervention in Alzheimer's Disease. **2023**, 12, 635	0
467	A genomic perspective of the aging human and mouse lung with a focus on immune response and cellular senescence.	0
466	Chromosome-Level Assembly of Flowering Cherry (Prunus campanulata) Provides Insight into Anthocyanin Accumulation. **2023**, 14, 389	0
465	Reversal of hyperactive higher-order thalamus attenuates defensiveness in a mouse model of PTSD. **2023**, 9,	0
464	Differentially expression analyses in fruit of cultivated and wild species of grape and peach. **2023**, 13,	0
463	microRNAs profiling of small extracellular vesicles from midbrain tissue of Parkinson's disease. 16,	0
462	Evolved bacterial resistance to the chemotherapy gemcitabine modulates its efficacy in co-cultured cancer cells. 12,	0

461	Sexual dimorphism and the multi-omic response to exercise training in rat subcutaneous white adipose tissue.	0
460	Gene panel selection for targeted spatial transcriptomics.	0
459	Transcriptional survey of ovarian bacteriomes in the cereal weevil,Sitophilus oryzae, shows down-regulation of immune effectors at the onset of sexual maturity.	0
458	Novel integrated computational AMP discovery approaches highlight diversity in the helminth AMP repertoire.	0
457	Genome-Wide Identification of Sweet Orange WRKY Transcription Factors and Analysis of Their Expression in Response to Infection by Penicillium digitatum. **2023**, 45, 1250-1271	2
456	Reading bots: The implication of deep learning on guided reading. 14,	0
455	Comparative proteome analysis of different Saccharomyces cerevisiae strains during growth on sucrose and glucose. **2023**, 13,	0
454	Ageotypes revisited: The brain and central nervous system dysfunction as a major nutritional and lifestyle target for healthy aging. **2023**, 170, 51-57	0
453	YAP/TAZ activation predicts clinical outcomes in mesothelioma and is conserved in in vitro model of driver mutations. **2023**, 13,	0
452	Identification of Hub Genes for Colorectal Cancer with Liver Metastasis Using miRNA-mRNA Network. **2023**, 2023, 1-14	0
451	The association of gene polymorphisms with milk production and mastitis resistance phenotypic traits in dairy cattle. **2023**,	0
450	Identification of SARS-CoV-2 Main Protease (Mpro) Cleavage Sites Using Two-Dimensional Electrophoresis and In Silico Cleavage Site Prediction. **2023**, 24, 3236	0
449	Myocardial Infarction-Induced INSL6 Decrease Contributes to Breast Cancer Progression. **2023**, 2023, 1-33	0
448	A Monoclonal Human Alveolar Epithelial Cell Line (Arlo) with Pronounced Barrier Function for Studying Drug Permeability and Viral Infections. **2023**, 10,	0
447	Proteomic insight into human directed evolution of the domesticated chickenGallus gallus.	0
446	Transcriptome sequencing of Cocos nucifera leaves in response to Rhynchophorus ferrugineus infestation. 14,	0
445	PRSet: Pathway-based polygenic risk score analyses and software. **2023**, 19, e1010624	0
444	The anti-leprosy drug clofazimine reduces polyQ toxicity through activation of PPAR	0

443	Interaction-integrated linear mixed model reveals 3D-genetic basis underlying Autism. **2023**, 115, 110575	0
442	Moesin is an effector of tau-induced actin overstabilization, cell cycle activation, and neurotoxicity in Alzheimer’s disease. **2023**, 26, 106152	0
441	Whole genome sequence of Cryptosphaeria pullmanensis, an important pathogenic fungus potentially threatening crop and forestry production. **2023**, 115, 110576	0
440	The Usher syndrome 1C protein harmonin regulates canonical Wnt signaling. 11,	0
439	The scalable precision medicine open knowledge engine (SPOKE): a massive knowledge graph of biomedical information. **2023**, 39,	0
438	An EMS-induced allele of the brachytic2 gene can reduce plant height in maize. **2023**, 42, 749-761	0
437	N-Linked Glycoproteome Analysis of Diosorea alata Tuber Shows Atypical Glycosylation and Indicates Central Role of Glycosylated Proteins in Tuber Maturation. **2023**, 42, 78-93	0
436	Identification of phenotypic and genotypic properties and cold adaptive mechanisms of novel freeze–thaw stress-resistant strain Pseudomonas mandelii from Antarctica. **2023**, 46, 169-183	0
435	Epitranscriptomic regulation of cortical neurogenesis via Mettl8-dependent mitochondrial tRNA m3C modification. **2023**, 30, 300-311.e11	0
434	Single-cell multi-omic analysis profiles defective genome activation and epigenetic reprogramming associated with human pre-implantation embryo arrest. **2023**, 42, 112100	0
433	Human RSPO1 Mutation Represses Beige Adipocyte Thermogenesis and Contributes to Diet-Induced Adiposity. 2207152	0
432	Artificial Intelligence in the Genetic Diagnosis of Rare Disease. **2023**, 43, 127-143	0
431	684. Genome-wide association studies for maturity rate in grazing dairy cows. **2022**,	0
430	373. Fine-mapping young-stock survival QTL on chromosome 6 in Nordic Red Dairy Cattle. **2022**,	0
429	Responses of carbapenemase-producing and non-producing carbapenem-resistant Pseudomonas aeruginosa strains to meropenem revealed by quantitative tandem mass spectrometry proteomics. 13,	0
428	Genome-wide identification and characterization of parthenocarpic fruit set-related gene homologs in cucumber (Cucumis sativus L.). **2023**, 13,	0
427	Metabolomic and transcriptomic analyses ofFmo5-/-mice reveal roles for flavin-containing monooxygenase 5 (FMO5) in NRF2-mediated oxidative stress, the unfolded protein response, lipid homeostasis, and carbohydrate and one-carbon metabolism.	0
426	Enabling Single-Cell Drug Response Annotations from Bulk RNA-Seq Using SCAD. **2023**, 10,	0

425	Multilingual translation for zero-shot biomedical classification using BioTranslator. **2023**, 14,	0
424	Microbial community succession patterns and drivers of Luxiang-flavor Jiupei during long fermentation. 14,	0
423	Pharmacodynamic model of PARP1 inhibition and global sensitivity analyses can lead to cancer biomarker discovery.	0
422	Transcriptomic and physiological analysis reveal phytohormone and phenylpropanoid biosynthesis in root of Cynanchum auriculatum.	0
421	SARS-CoV-2 leverages airway epithelial protective mechanism for viral infection. **2023**, 26, 106175	0
420	Altered microRNA Transcriptome in Cultured Human Airway Cells upon Infection with SARS-CoV-2. **2023**, 15, 496	0
419	HMM-based profiling identifies the binding to divalent cations and nucleotides as common denominators of suramin targets. 3,	0
418	Identification of potential biomarkers for colorectal cancer by clinical database analysis and Kaplan–Meier curves analysis. **2023**, 102, e32877	0
417	Label-Free Mass Spectrometry Proteomics Reveals Different Pathways Modulated in THP-1 Cells Infected with Therapeutic Failure and Drug Resistance Leishmania infantum Clinical Isolates. **2023**, 9, 470-485	0
416	Comprehensive analysis of genetic risk loci uncovers novel candidate genes and pathways in the comorbidity between depression and Alzheimer’s disease.	0
415	Epistatic Features and Machine Learning Improve Alzheimer’s Risk Prediction Over Polygenic Risk Scores.	0
414	Inferring a directed acyclic graph of phenotypes from GWAS summary statistics*.	0
413	Changes in social behaviour with alterations of MAPK3 and KCTD13/CUL3 pathways in two new outbred rat models for the 16p11.2 syndromes with autism spectrum disorders.	0
412	Integrated transcriptomic and metabolomic analyses reveal key metabolic pathways in response to potassium deficiency in coconut (Cocos nucifera L.) seedlings. 14,	0
411	Exploring conserved and novel MicroRNA-like small RNAs from stress tolerant Trichoderma fusants and parental strains during interaction with fungal phytopathogen Sclerotium rolfsii Sacc.. **2023**, 191, 105368	0
410	Identification of Salt Tolerance Related Candidate Genes in “Sea Rice 86” at the Seedling and Reproductive Stages Using QTL-Seq and BSA-Seq. **2023**, 14, 458	1
409	Modeling Blast Crisis Using Mutagenized Chronic Myeloid Leukemia-Derived Induced Pluripotent Stem Cells (iPSCs). **2023**, 12, 598	0
408	SARSMutOnto: An Ontology for SARS-CoV-2 Lineages and Mutations. **2023**, 15, 505	0

407	GO Bench: shared hub for universal benchmarking of machine learning-based protein functional annotations. **2023**, 39,	0
406	A Hybrid Machine Learning Approach to Screen Optimal Predictors for the Classification of Primary Breast Tumors from Gene Expression Microarray Data. **2023**, 13, 708	0
405	Identification of Hub Genes Associated with Breast Cancer Using Integrated Gene Expression Data with Protein-Protein Interaction Network. **2023**, 13, 2403	0
404	Investigation of distinct gene expression profile patterns that can improve the classification of intermediate-risk prognosis in AML patients. 14,	0
403	Single-nucleus RNA sequencing in ischemic cardiomyopathy reveals common transcriptional profile underlying end-stage heart failure. **2023**, 42, 112086	0
402	Leveraging massively parallel reporter assays for evolutionary questions. **2023**, 24,	0
401	Bronchial epithelial cell transcriptional responses to inhaled corticosteroids dictate severe asthmatic outcomes. **2023**,	0
400	Systematic review and meta-analysis of transcriptomic studies on different brain regions reveals different sex-based profiles in schizophrenic patients.	0
399	Genome-wide analysis of long non-coding RNAs in sugar beet (Beta vulgaris L.) under drought stress. 14,	0
398	SynEcoSys: a multifunctional platform of large-scale single-cell omics data analysis.	0
397	Shared Biological Pathways and Processes in Patients with Intellectual Disability: A Multicenter Study.	0
396	DNA methylation profiling reveals novel pathway implicated in cardiovascular diseases of diabetes. 14,	0
395	Germline variation in RASAL2 may predict survival in patients with RAS -activated colorectal cancer. **2023**, 62, 332-341	0
394	Identification of Key Gene and Pathways Associated with Oxidative Stress in Keloids.	0
393	Phylogeny, transcriptional profile, and auxin-induced phosphorylation modification characteristics of conserved PIN proteins in Moso bamboo (Phyllostachys edulis). **2023**, 234, 123671	0
392	Transcriptome analysis of putative key signaling pathways and genes in the nidamental gland tissue associated with reproductive regulation of golden cuttlefish (Sepia esculenta Hoyle). **2023**, 29, 101494	0
391	Transcriptional dynamics of maize leaves, pollens and ovules to gain insights into heat stress-related responses. 14,	0
390	Processing of carbon-reinforced construction materials releases PM2.5 inducing inflammation and (secondary) genotoxicity in human lung epithelial cells and fibroblasts. **2023**, 98, 104079	0

389	Deficiency of primate-specific SSX1 induced asthenoteratozoospermia in infertile men and cynomolgus monkey and tree shrew models. **2023**, 110, 516-530	0
388	Artificial intelligence assessment of the potential of tocilizumab along with corticosteroids therapy for the management of COVID-19 evoked acute respiratory distress syndrome. **2023**, 18, e0280677	0
387	Post-COVID syndrome is associated with capillary alterations, macrophage infiltration and distinct transcriptomic signatures in skeletal muscles.	0
386	Boldine modulates glial transcription and functional recovery in a murine model of contusion spinal cord injury.	0
385	Identification and validation of a novel ubiquitination-related gene UBE2T in Ewing□ sarcoma. 13,	0
384	Profiling cell envelope-antibiotic interactions reveals vulnerabilities to □lactams in a multidrug-resistant bacterium.	0
383	De Novo Assembly and Characterization of the Transcriptome of an Omnivorous Camel Cricket (Tachycines meditationis). **2023**, 24, 4005	0
382	Chromosome-scale genome assembly and insights into the metabolome and gene regulation of leaf color transition in an important oak species, Quercus dentata.	0
381	Clustering rare diseases within an ontology-enriched knowledge graph.	0
380	IRF4 as a novel target involved in malignant transformation of oral submucous fibrosis into oral squamous cell carcinoma. **2023**, 13,	0
379	CRACD, a gatekeeper restricting proliferation, heterogeneity, and immune evasion of small cell lung cancer.	0
378	Computational identification and systematic classification of cytochrome P450 genes in Pogostemon cablin provide insights into flavonoids biosynthesis. **2023**, 45,	0
377	Transcriptional Profiling Supports the Notochordal Origin of Chordoma and Its Dependence on a TGFB1-TBXT Network. **2023**, 193, 532-547	0
376	Cardiomyocyte Pdk4 response is associated with metabolic maladaptation in aging. **2023**, 22,	0
375	Long noncoding RNA GATA2-AS1 augments endothelial hypoxia inducible factor 1-□induction and regulates hypoxic signaling. **2023**, 299, 103029	0
374	Hypothesis-free phenotype prediction within a genetics-first framework. **2023**, 14,	0
373	Exploration and identification of anoikis-related genes in polycythemia vera. 14,	0
372	Genome-Wide Gene-Set Analysis Identifies Molecular Mechanisms Associated with ALS. **2023**, 24, 4021	0

371	Confusoside from Anneslea fragrans Alleviates Acetaminophen-Induced Liver Injury in HepG2 via PI3K-CASP3 Signaling Pathway. **2023**, 28, 1932	0
370	Population genomics-guided engineering of phenazine biosynthesis inPseudomonas chlororaphis.	0
369	Pulmonary osteoclast-like cells in silica induced pulmonary fibrosis.	0
368	Potential Early Markers for Breast Cancer: A Proteomic Approach Comparing Saliva and Serum Samples in a Pilot Study. **2023**, 24, 4164	0
367	Transcriptome-based variations effectively untangling the intraspecific relationships and selection signals in Xinyang Maojian tea population. 14,	0
366	Transcriptomic analysis reveals differentially expressed genes associated with pine wood nematode resistance in resistantPinus thunbergii.	0
365	Genome Size Changes by Duplication, Divergence, and Insertion inCaenorhabditisWorms. **2023**, 40,	0
364	FLI1 and FRA1 transcription factors drive the transcriptional regulatory networks characterizing muscle invasive bladder cancer. **2023**, 6,	1
363	Interpreting biologically informed neural networks for enhanced biomarker discovery and pathway analysis.	0
362	Comprehensive analysis of PHGDH for predicting prognosis and immunotherapy response in patients with endometrial carcinoma. **2023**, 16,	0
361	A compilation of bioinformatic approaches to identify novel downstream targets for the detection and prophylaxis of cancer. **2023**, 75-113	0
360	Leveraging GWAS data derived from a large cooperative group trial to assess the risk of taxane-induced peripheral neuropathy (TIPN) in patients being treated for breast cancer: Part 2functional implications of a SNP cluster associated with TIPN risk in patients being treated for breast cancer. **2023**, 31,	0
359	Astrocyte-like subpopulation of NG2 glia in the adult mouse cortex exhibits characteristics of neural progenitor cells and is capable of forming neuron-like cells after ischemic injury.	0
358	A proteomics approach to identify COPD-related changes in lung fibroblasts. **2023**, 324, L521-L535	0
357	A guide to current methodology and usage of reverse vaccinology towardsin silicovaccine discovery. **2023**, 47,	0
356	Genome-wide analysis of R2R3-MYB transcription factors in Boehmeria nivea (L.) gaudich revealed potential cadmium tolerance and anthocyanin biosynthesis genes. 14,	0
355	Identification and validation of ferroptosis-related genes and immune infiltration in ischemic cardiomyopathy. 10,	0
354	Genome assembly ofMusa beccariishows extensive chromosomal rearrangements and genome expansion during evolution of Musaceae genomes. **2022**, 12,	0

353	Uncovering the complex genetic architecture of human plasma lipidome using machine learning methods. **2023**, 13,	0
352	Integrated transcriptome analysis reveals roles of long non-coding RNAs (lncRNAs) in caprine skeletal muscle mass and meat quality. **2023**, 23,	0
351	Characterization of the First Turtle Organoids: A Model for Investigating Unique Adaptations with Biomedical Potential.	0
350	Whole-Genome Sequence of Lactiplantibacillus plantarum Mut-3, Isolated from Indonesian Fermented Soybean (Tempeh). **2023**, 12,	0
349	Integrated transcriptomics and metabolomics analyses provide insights into salt-stress response in germination and seedling stage of wheat (Triticum aestivum L.). **2023**, 33, 100274	0
348	PANGEA: A New Gene Set Enrichment Tool forDrosophilaand Common Research Organisms.	0
347	Comparative transcriptome analysis of adult worker bees under short-term heat stress. 11,	0
346	Selection signature analysis reveals RDH5 performed key function in vision during sheep domestication process. **2023**, 66, 81-91	0
345	Radiobacillus kanasensis sp. nov., a halotolerant bacterium isolated from woodland soil. **2023**, 73,	0
344	Comparative gene regulatory network analysis in Alzheimer's disease and major depressive disorder.	0
343	LINC01798/miR-17-5p axis regulates ITGA8 and causes changes in tumor microenvironment and stemness in lung adenocarcinoma. 14,	0
342	BEAR: A Novel Virtual Screening Method Based on Large-Scale Bioactivity Data. **2023**, 63, 1429-1437	0
341	AURKA was identified as a potential lung cancer marker through comprehensive bioinformatics analysis and experimental verification. **2023**,	0
340	Neuroligins facilitate the development of bone cancer pain via regulating synaptic transmission: an experimental study. **2023**,	0
339	Using protein-per-mRNA differences among human tissues in codon optimization. **2023**, 24,	0
338	Clustering of Human Gene Expression Stimulated by Bacterial Infection from Microarray Analysis. **2022**,	0
337	Transcriptomic thermal plasticity underlying gonadal development in a turtle with ZZ / ZW sex chromosomes despite canalized genotypic sex determination. **2023**, 13,	0
336	Glioma genetic profiles associated with electrophysiologic hyperexcitability.	0

335	A genome and single-nucleus cerebral cortex transcriptome atlas of the short-finned pilot whale Globicephala macrorhynchus.	0
334	Transcriptomic changes in single yeast cells under various stress conditions. **2023**, 24,	0
333	Gene profiling reveals the role of inflammation, abnormal uterine muscle contraction and vascularity in recurrent implantation failure. 14,	0
332	Photosynthetic and transcriptomic responses of Chlorella sp. to tigecycline. **2023**, 71, 103033	0
331	Cell migration simulator-based biomarkers for glioblastoma.	0
330	MSC-CSMC: A multi-objective semi-supervised clustering algorithm based on constraints selection and multi-source constraints for gene expression data. 14,	0
329	ProteInfer, deep neural networks for protein functional inference. 12,	1
328	Draft Genome and Biological Characteristics of Fusarium solani and Fusarium oxysporum Causing Black Rot in Gastrodia elata. **2023**, 24, 4545	0
327	Comparative transcriptomic and metabolomic analyses reveal differences in flavonoid biosynthesis between PCNA and PCA persimmon fruit. 14,	1
326	Transcriptomic Analyses of Brains of RBM8A Conditional Knockout Mice at Different Developmental Stages Reveal Conserved Signaling Pathways Contributing to Neurodevelopmental Diseases. **2023**, 24, 4600	0
325	Analysis of proteomes□ **2023**, 111-138	0
324	Functional genomics of Chlamydomonas reinhardtii. **2023**, 65-84	0
323	PrismEXP: gene annotation prediction from stratified gene-gene co-expression matrices. 11, e14927	1
322	Nicotinamide riboside supplementation is not associated with altered methylation homeostasis in Parkinson□ disease. **2023**, 26, 106278	0
321	Damage activatesEVG1to suppress vascular differentiation during regeneration inArabidopsis thaliana.	0
320	Consensus Clustering and Survival-Related Genes of Cuproptosis in Cutaneous Melanoma. **2023**, 2023, 1-15	0
319	Using the Proteomics Toolbox to Resolve Topology and Dynamics of Compartmentalized cAMP Signaling. **2023**, 24, 4667	0
318	The early neutrophil-committed progenitors aberrantly differentiate into immunoregulatory monocytes during emergency myelopoiesis. **2023**, 42, 112165	0

317	MultiGML: Multimodal Graph Machine Learning for Prediction of Adverse Drug Events.	0
316	Evaluation of Genetic Testing in a Cohort of Diverse Pediatric Patients in the United States with Congenital Cataracts. **2023**, 14, 608	0
315	The Alzheimer’s Knowledge Base - A knowledge graph for therapeutic discovery in Alzheimer’s Disease research (Preprint).	0
314	Ontology Assisted Unsupervised Clustering for Interpreting Microarray Gene Expression Profiles. **2022**,	0
313	Role of hypoxia-inducible factor-1□and survivin in breast cancer recurrence and prognosis. **2023**, 9, e14132	0
312	Effects of allicin on human Simpson-Golabi-Behmel syndrome cells in mediating browning phenotype. 14,	0
311	AIMedGraph: a comprehensive multi-relational knowledge graph for precision medicine. **2023**, 2023,	0
310	Construction of a fatty acid metabolism-related gene signature for predicting prognosis and immune response in breast cancer. 14,	0
309	The RNA binding protein DND1 is elevated in a subpopulation of pro-spermatogonia and targets chromatin modifiers and translational machinery during late gestation. **2023**, 19, e1010656	0
308	The ion channel CALHM6 controls bacterial infection-induced cellular cross-talk at the immunological synapse. **2023**, 42,	0
307	Deep origins of eukaryotic multicellularity revealed by the Acrasis kona genome and developmental transcriptomes.	0
306	Pathway-specific polygenic risk scores correlate with clinical status and Alzheimer□-related biomarkers.	0
305	Small Brown Planthopper Nymph Infestation Regulates Plant Defenses by Affecting Secondary Metabolite Biosynthesis in Rice. **2023**, 24, 4764	0
304	Transcriptome Analysis of Differentially Expressed Genes Associated with Salt Stress in Cowpea (Vigna unguiculata L.) during the Early Vegetative Stage. **2023**, 24, 4762	0
303	Pan-Cancer Analysis Reveals Functional Similarity of Three lncRNAs across Multiple Tumors. **2023**, 24, 4796	0
302	Artificial intelligence and machine learning in pain research: a data scientometric analysis. **2022**, 7, e1044	1
301	The enormous repetitive Antarctic krill genome reveals environmental adaptations and population insights. **2023**, 186, 1279-1294.e19	0
300	Comparative Genomic and Transcriptomic Analyses Reveal the Impacts of Genetic Admixture in Kazaks, Uyghurs, and Huis. **2023**, 40,	0

299	Bulk RNA-Sequencing of small airway cell cultures from IPF and post-COVID lung fibrosis patients illustrates disease signatures and differential responses to TGF-β1 treatment.	0
298	From multiallele fish to nonstandard environments, how ZFIN assigns phenotypes, human disease models, and gene expression annotations to genes.	0
297	Hepatic gene expression profiles during fed–fasted–refed state in mice. 14,	0
296	Differentially Expressed Genes Analysis in the Human Small Airway Epithelium of Healthy Smokers Shows Potential Risks of Disease Caused by Oxidative Stress and Inflammation and the Potentiality of Astaxanthin as an Anti-Inflammatory Agent. **2023**, 2023, 1-10	0
295	Identification of GNG7 as a novel biomarker and potential therapeutic target for gastric cancer via bioinformatic analysis and in vitro experiments.	0
294	Primary lung fibroblasts respond to IL-33, IL-13, and IL-17A by secreting factors that activate macrophages.	0
293	A scalable, GMP-compatible, autologous organotypic cell therapy for Dystrophic Epidermolysis Bullosa.	0
292	Gene Functional Networks from Time Expression Profiles: A Constructive Approach Demonstrated in Chili Pepper (Capsicum annuum L.). **2023**, 12, 1148	0
291	Biomedical Knowledge Graphs: Context, Queries and Complexity. **2022**, 529-567	0
290	DIS3Variants are Associated With Primary Ovarian Insufficiency: Importance of Transcription/Translation in Oogenesis.	0
289	Direct link between convergent evolution at sequence level and phenotypic level of septal pore cap in Agaricomycotina.	0
288	Single-cell sequencing reveals peritoneal environment and insights into fibrosis in CAPD patients. **2023**, 26, 106336	0
287	Validation of the new EPIC DNA methylation microarray (900K EPIC v2) for high-throughput profiling of the human DNA methylome. **2023**, 18,	0
286	Metatranscriptomics and metabarcoding reveal spatiotemporal shifts in fungal communities and their activities in Chinese coastal waters.	0
285	Exosomal Mir-3613-3p derived from oxygen–glucose deprivation-treated brain microvascular endothelial cell promotes microglial M1 polarization. **2023**, 28,	0
284	Insights into Online microRNA Bioinformatics Tools. **2023**, 9, 18	0
283	Full-Length Transcriptome of the Great Himalayan Leaf-Nosed Bats (Hipposideros armiger) Optimized Genome Annotation and Revealed the Expression of Novel Genes. **2023**, 24, 4937	0
282	Identification of Selection Signatures and Loci Associated with Important Economic Traits in Yunan Black and Huainan Pigs. **2023**, 14, 655	0

281	Integrating Multi-Omics Analysis Reveals the Regulatory Mechanisms of WhiteViolet Mutant Flowers in Grape Hyacinth (Muscari latifolium). **2023**, 24, 5044	0
280	Proteome profiling of hippocampus reveals the neuroprotective effect of mild hypothermia on global cerebral ischemia-reperfusion injury in rats.	0
279	MFN2 deficiency affects calcium homeostasis in lung adenocarcinoma cells via downregulation of UCP4.	0
278	Genome-wide association study to identify SNPs and candidate genes associated with body size traits in donkeys. 14,	0
277	A Specific High Toxicity of Xinjunan (Dioctyldiethylenetriamine) to Xanthomonas by Affecting the Iron Metabolism. **2023**, 11,	0
276	Transcriptome analysis reveals the crucial function of hyperoside in inhibiting anthocyanin accumulation in grape (Vitis vinifera L.) fruits by inducing VvMYB62. 14,	0
275	Translating Ribosome Affinity Purification (TRAP) and Bioinformatic RNA-Seq Analysis in Post-metamorphic Xenopus laevis. **2023**, 279-310	0
274	CD24-associated ceRNA network reveals prognostic biomarkers in breast carcinoma. **2023**, 13,	0
273	Quantitative Proteomics of Nervous System Regeneration: From Sample Preparation to Functional Data Analyses. **2023**, 343-366	0
272	Simultaneous Analysis of Single-nucleus Transcriptome and Chromatin Accessibility Unveils the Mechanisms of Leaf Cell Development in Arachis hypogaea L..	0
271	Histone H3-wild type diffuse midline gliomas with H3K27me3 loss are a distinct entity with exclusive EGFR or ACVR1 mutation and differential methylation of homeobox genes. **2023**, 13,	0
270	Sex-Specific Effects of Early-Life Iron Deficiency and Prenatal Choline Treatment on Adult Rat Hippocampal Transcriptome. **2023**, 15, 1316	0
269	Interpreting structure in sequence count data with differential expression analysis allowing for grades of membership.	0
268	Exploring the components and mechanism of Solanum nigrum L. for colon cancer treatment based on network pharmacology and molecular docking. 13,	0
267	Transcriptomic analysis of pea plant responses to chitooligosaccharidestreatment revealed stimulation of mitogen-activated protein kinase cascade. 14,	0
266	Spatial analysis reveals distinct immune phenotypes and tertiary lymphoid structure-like aggregates in pediatric acute myeloid leukemia.	0
265	Transcriptomic analysis of the Non-Obstructive Azoospermia (NOA) to address gene expression regulation in human testis. 1-19	0
264	Renal microdissection revisited: Lectin-aided sorting of intact tubular nephron segments as a new tool to study sex-related differences in kidney disease.	0

263	A mitochondrial function-related LncRNA signature predicts prognosis and immune microenvironment for breast cancer. **2023**, 13,	0
262	Clinical and prognostic associations of autoantibodies recognizing adrenergic/muscarinic receptors in patients with heart failure.	0
261	CFAGO: cross-fusion of network and attributes based on attention mechanism for protein function prediction. **2023**, 39,	0
260	Higher-order modular regulation of the human proteome.	0
259	Potential biomarker proteins for aspiration pneumonia detected by shotgun proteomics using buccal mucosa samples: a cross-sectional case□ontrol study. **2023**, 20,	0
258	Analysis of context-specific KRAS□ffector (sub)complexes in Caco-2 cells. **2023**, 6, e202201670	0
257	Prognosis and Characterization of Microenvironment in Cervical Cancer Influenced by Fatty Acid Metabolism-Related Genes. **2023**, 2023, 1-34	0
256	Comprehensive bioinformatic analysis constructs a CXCL model for predicting survival and immunotherapy effectiveness in ovarian cancer. 14,	0
255	Genus-Wide Genomic Characterization ofMacrococcus: Insights into Evolution, Population Structure, and Functional Potential.	0
254	N-MYC regulates Cell Survival via eIF4G1 in inv(16) Acute Myeloid Leukemia.	0
253	Molecular and network-level mechanisms explaining individual differences in autism spectrum disorder. **2023**, 26, 650-663	0
252	A crowdsourcing database for the copy-number variation of the Spanish population. **2023**, 17,	0
251	Telomere-related genes as potential biomarkers to predict endometriosis and immune response: Development of a machine learning-based risk model. 10,	0
250	Engineered allostery in light-regulated LOV-Turbo enables precise spatiotemporal control of proximity labeling in living cells.	0
249	Ginseng-based carbon dots inhibit the growth of squamous cancer cells by increasing ferroptosis. 13,	0
248	An atlas of gene regulatory networks for memory CD4+T cells in youth and old age.	0
247	Bioinformatics analysis and verification of m6A related genes based on the construction of keloid diagnostic model.	0
246	An integrated approach of high-performance liquid chromatography□ass spectrometry-based chemical profiling, network pharmacology, and molecular docking to reveal the potential mechanisms of Qishen Gubiao granules for treating coronavirus disease 2019. 2200953	0

245	Patterns of unwanted biological and technical expression variation across 49 human tissues.	0
244	Dysregulation of Prefrontal Oligodendrocyte Lineage Cells Across Mouse Models of Adversity and Human Major Depressive Disorder.	0
243	Ontology for Cellular Senescence Mechanisms.	0
242	Screening and identification of key biomarkers of depression using bioinformatics. **2023**, 13,	0
241	Content and quality of physical activity ontologies: a systematic review. **2023**, 20,	0
240	Single-cell RNA sequencing of cerebrospinal fluid reveals the expansion of innate lymphoid cells with upregulated transposable elements in multiple sclerosis.	0
239	Integrated analysis and clinical correlation analysis of hub genes, immune infiltration, and potential therapeutic agents related to lupus nephritis. 096120332311615	0
238	Proteomic characterisation of perhexiline treatment on THP-1 M1 macrophage differentiation. 14,	0
237	Lipid extract derived from newly isolated Rhodotorula toruloides LAB-07 for cosmetic applications. **2023**, 21, 2009-2017	0
236	Danger Analysis: Risk-Averse on/off-Target Assessment for CRISPR Editing Without a Reference Genome.	0
235	Analysis of gene expression and use of connectivity mapping to identify drugs for treatment of human glomerulopathies. 10,	0
234	A preliminary study on the root-knot nematode resistance of a cherry plum cultivar Mirabolano 29C.	0
233	Strategy for the Adaptation to Stressful Conditions of the Novel Isolated Conditional Piezophilic Strain Halomonas titanicae ANRCS81. **2023**, 89,	0
232	The potential value of cuprotosis in myocardial immune infiltration that occurs in pediatric congenital heart disease in response to surgery with cardiopulmonary bypass. **2023**, 11,	0
231	Identification of potential biomarkers and therapeutic targets for posttraumatic acute respiratory distress syndrome. **2023**, 16,	0
230	Coupling microdroplet-based sample preparation, multiplexed isobaric labeling, and nanoflow peptide fractionation for deep proteome profiling of tissue microenvironment.	0
229	The Josephin domain (JD) containing proteins are predicted to bind to the same interactors: Implications for spinocerebellar ataxia type 3 (SCA3) studies using Drosophila melanogaster mutants. 16,	0
228	Radical-Scavenging and Subchondral Bone-Regenerating Nanomedicine for Osteoarthritis Treatment. **2023**, 17, 6131-6146	0

227	Growth-dependent gene expression variation influences the strength of codon usage biases.	0
226	PD-1/LAG-3 Dysfunctionality Signatures in Human Cancers.	0
225	RSV infection does not induce EMT.	0
224	Bioinformatics approach to identify the impacts of microgravity on the development of bone and joint diseases. **2023**, 38, 101211	0
223	Clustering Algorithm Based on Dual-Index Nearest Neighbor Similarity Measure and Its Application in Gene Expression Data Analysis.	0
222	Different Resistance Exercise Loading Paradigms Similarly Affect Skeletal Muscle Gene Expression Patterns of Myostatin-Related Targets and mTORC1 Signaling Markers. **2023**, 12, 898	0
221	Convergent Aedes and Drosophila CidB interactomes suggest cytoplasmic incompatibility targets are conserved. **2023**, 155, 103931	0
220	Identification of five hub immune genes and characterization of two immune subtypes of osteoarthritis. 14,	0
219	Using a whole genome co-expression network to inform the functional characterisation of predicted genomic elements from Mycobacterium tuberculosis transcriptomic data. **2023**, 119, 381-400	0
218	Shared Genes of PPARG and NOS2 in Alzheimer□ Disease and Ulcerative Colitis Drive Macrophages and Microglia Polarization: Evidence from Bioinformatics Analysis and Following Validation. **2023**, 24, 5651	0
217	In silico analysis to identify miR-1271-5p/PLCB4 (phospholipase C Beta 4) axis mediated oxaliplatin resistance in metastatic colorectal cancer. **2023**, 13,	0
216	Exogenous L-lactate administration in rat hippocampus increases expression of key regulators of mitochondrial biogenesis and antioxidant defense. 16,	0
215	Polyploidization of Indotyphlops braminus, evidence from Isoform-sequencing.	0
214	Pharmacogenomic and Statistical Analysis. **2023**, 305-330	0
213	The MicroRNA Ame-Bantam-3p Controls Larval Pupal Development by Targeting the Multiple Epidermal Growth Factor-like Domains 8 Gene (megf8) in the Honeybee, Apis mellifera. **2023**, 24, 5726	0
212	spSeudoMap: cell type mapping of spatial transcriptomics using unmatched single-cell RNA-seq data. **2023**, 15,	0
211	Integrin □-Mediated Cell Senescence Associates with Gut Inflammation and Intestinal Degeneration in Models of Alzheimer□ Disease. **2023**, 24, 5697	0
210	Analyzing CRISPR screens in non-conventional microbes. **2023**, 50,	0

209	Susceptibility and Permissivity of Zebrafish (Danio rerio) Larvae to Cypriniviruses. **2023**, 15, 768	0
208	DIAPH1 mediates progression of atherosclerosis and regulates hepatic lipid metabolism in mice. **2023**, 6,	0
207	An informatic workflow for the enhanced annotation of excretory/secretory proteins of Haemonchus contortus. **2023**,	0
206	Phenotypic and spatial heterogeneity of brain myeloid cells after stroke is associated with cell ontogeny, tissue damage, and brain connectivity.	0
205	Identification of new potential downstream transcriptional targets of the strigolactone pathway including glucosinolate biosynthesis. **2023**, 7,	0
204	Resistance in pea (Pisum sativum) genetic resources to the pea aphid, Acyrthosiphon pisum.	0
203	Reduced Transcriptome Analysis of Zebrafish Embryos Prioritizes Environmental Compounds with Adverse Cardiovascular Activities. **2023**, 57, 4959-4970	0
202	Immune Activation following Irbesartan Treatment in a Colorectal Cancer Patient: A Case Study. **2023**, 24, 5869	0
201	De Novo Transcriptome Sequencing of Codonopsis lanceolata for Identification of Triterpene Synthase and Triterpene Acetyltransferase. **2023**, 24, 5769	0
200	Comparative proteome profiles of Polygonatum cyrtonema Hua rhizomes (Rhizoma Ploygonati) in response to different levels of cadmium stress. **2023**, 23,	0
199	Integrative transcriptome and proteome analysis reveals maize responses to Fusarium verticillioides infection inside the stalks.	0
198	Integration of Stemness Gene Signatures Reveals Core Functional Modules of Stem Cells and Potential Novel Stemness Genes. **2023**, 14, 745	0
197	Whole Genome Resequencing Revealed the Effect of Helicase yqhH Gene on Regulating Bacillus thuringiensis LLP29 against Ultraviolet Radiation Stress. **2023**, 24, 5810	1
196	Gene augmentation for autosomal dominant retinitis pigmentosa using rhodopsin genomic loci nanoparticles in the P23H+/knock-in murine model.	0
195	Integrated Multi-Omics Techniques and Network Pharmacology Analysis to Explore the Material Basis and Mechanism of Simiao Pill in the Treatment of Rheumatoid Arthritis. **2023**, 8, 11138-11150	0
194	LINCRNA01094 promotes the renal interstitial fibrosis via miR-513b-5p/MELK/Smad3 axis.	0
193	Integrative comparative analysis of avian chromosome evolution by in-silico mapping of the gene ontology of homologous synteny blocks and evolutionary breakpoint regions.	0
192	Icariin Induces Triple-Negative Breast Cancer Cell Apoptosis and Suppresses Invasion by Inhibiting the JNK/c-Jun Signaling Pathway. Volume 17, 821-836	0

191	Automated assembly of molecular mechanisms at scale from text mining and curated databases.	0
190	Computational Approaches Drive Developments in Immune-Oncology Therapies for PD-1/PD-L1 Immune Checkpoint Inhibitors. **2023**, 24, 5908	0
189	Transcriptome sequencing identifies prognostic genes involved in gastric adenocarcinoma.	0
188	Contingency, Repeatability and Predictability in the Evolution of a Prokaryotic Pangenome.	0
187	Intraspecific Comparative Analysis Reveals Genomic Variation of Didymella arachidicola and Pathogenicity Factors Potentially Related to Lesion Phenotype. **2023**, 12, 476	0
186	Elucidating the patterns of pleiotropy and its biological relevance in maize. **2023**, 19, e1010664	0
185	Endosymbiont-containing germarium transcriptional survey in a cereal weevil depicts downregulation of immune effectors at the onset of sexual maturity. 14,	0
184	Stromal Senescence following Treatment with the CDK4/6 Inhibitor Palbociclib Alters the Lung Metastatic Niche and Increases Metastasis of Drug-Resistant Mammary Cancer Cells. **2023**, 15, 1908	0
183	NaRnEA: An Information Theoretic Framework for Gene Set Analysis. **2023**, 25, 542	0
182	Growth rate-associated transcriptome reorganization in response to genomic, environmental, and evolutionary interruptions. 14,	0
181	Construction and analysis of protein–protein interaction networks based on nuclear proteomics data of the desiccation-tolerant Xerophyta schlechteri leaves subjected to dehydration stress. **2023** , 16,	0
180	Adaptation of the Porcine Pituitary Transcriptome, Spliceosome and Editome during Early Pregnancy. **2023**, 24, 5946	0
179	Assembly and Analysis of Haemonchus contortus Transcriptome as a Tool for the Knowledge of Ivermectin Resistance Mechanisms. **2023**, 12, 499	0
178	Influence of Scaffold Microarchitecture on Angiogenesis and Regulation of Cell Differentiation during the Early Phase of Bone Healing: A Transcriptomics and Histological Analysis. **2023**, 24, 6000	0
177	Primate protein-ligand interfaces exhibit significant conservation and unveil human-specific evolutionary drivers. **2023**, 19, e1010966	0
176	SERPINE1 and its co-expressed genes are associated with the progression of clear cell renal cell carcinoma. **2023**, 23,	0
175	Sex differences of signal complexity at resting-state functional magnetic resonance imaging and their associations with the estrogen-signaling pathway in the brain.	0
174	The m6A methylation landscape, molecular characterization and clinical relevance in prostate adenocarcinoma. 14,	0

173	Enterohemorrhagic Escherichia coli responds to gut microbiota metabolites by altering metabolism and activating stress responses. **2023**, 15,	0
172	Urea cycle activation triggered by host-microbiota maladaptation driving colorectal tumorigenesis. **2023**, 35, 651-666.e7	0
171	Complete genome of Sphingomonas paucimobilis ZJSH1, an endophytic bacterium from Dendrobium officinale with stress resistance and growth promotion potential. **2023**, 205,	0
170	The DREAM complex functions as conserved master regulator of somatic DNA-repair capacities. **2023**, 30, 475-488	0
169	B cell-intrinsic STAT3-mediated support of latency and interferon suppression during murine gammaherpesvirus 68 infection revealed through anin vivocompetition model.	0
168	Upregulation of Biomarker Limd1 Was Correlated with Immune Infiltration in Doxorubicin-Related Cardiotoxicity. **2023**, 2023, 1-23	0
167	Peripheral blood transcriptomic profiling indicates molecular mechanisms commonly regulated by binge-drinking and placebo-effects.	0
166	Identification of two unannotated miRNAs in classic Hodgkin lymphoma cell lines. **2023**, 18, e0283186	0
165	Transcriptomic Analyses of Exercise Training in Alzheimer� Disease Cerebral Cortex. **2023**, 1-15	0
164	A novel method to identify and characterize personalized functional driver lncRNAs in cancer samples. **2023**, 21, 2471-2482	0
163	Integrated analysis of transcriptome, small RNA, and phytohormonal content changes between <i>Artemisia annua</i> Linn. and <i>Nicotiana benthamiana</i> Domin in heterogeneous grafting. **2023**, 2, 0-0	0
162	An explainable deep learning classifier of bovine mastitis based on whole genome sequence data - circumventing the p>>>n problem.	0
161	Duckweed evolution: from land back to water.	0
160	The oncogenic properties of the EWSR1::CREM fusion gene are associated with polyamine metabolism. **2023**, 13,	0
159	Fusion gene 4CL-CCR promotes lignification in tobacco suspension cells.	0
158	Fast and accurate protein function prediction from sequence through pretrained language model and homology-based label diffusion.	0
157	CDH1 loss promotes diffuse-type gastric cancer tumorigenesis via epigenetic reprogramming and immune evasion.	0
156	Downregulation of PSAT1 inhibits cell proliferation and migration in uterine corpus endometrial carcinoma. **2023**, 13,	0

155	Physiological, transcriptome and co-expression network analysis of chlorophyll-deficient mutants in flue-cured tobacco. **2023**, 23,	0
154	Proximity proteome mapping reveals PD-L1-dependent pathways disrupted by anti-PD-L1 antibody specifically in EGFR-mutant lung cancer cells. **2023**, 21,	0
153	PI3K/AKT/mTOR inhibitors as potential extracellular matrix modulators for targeting EMT subtype gastric tumors. **2023**, 40,	0
152	Integrating AI/ML Models for Patient Stratification Leveraging Omics Dataset and Clinical Biomarkers from COVID-19 Patients: A Promising Approach to Personalized Medicine. **2023**, 24, 6250	0
151	Whole-genome sequencing analysis of two heat-evolved Escherichia coli strains. **2023**, 24,	0
150	RAS and PP2A activities converge on epigenetic gene regulation. **2023**, 6, e202301928	0
149	Proteomic Landscape of Human Sperm in Patients with Different Spermatogenic Impairments. **2023**, 12, 1017	0
148	Discovery of SNP Molecular Markers and Candidate Genes Associated with Sacbrood Virus Resistance in Apis cerana cerana Larvae by Whole-Genome Resequencing. **2023**, 24, 6238	0
147	Transcriptomics Reveals the Molecular Basis for Methyl Jasmonate to Promote the Synthesis of Monoterpenoids in Schizonepeta tenuifolia Briq.. **2023**, 45, 2738-2756	0
146	Integrated Physiological and Transcriptomic Analyses Revealed Improved Cold Tolerance in Cucumber (Cucumis sativus L.) by Exogenous Chitosan Oligosaccharide. **2023**, 24, 6202	1
145	Uncovering biomarkers for potential therapeutic targeting for COVID-19-related acute kidney injury: A bioinformatic approach. **2023**, 5,	0
144	Identification of gene networks mediating regional resistance to tauopathy in late-onset Alzheimer's disease. **2023**, 19, e1010681	0
143	BioASQ-QA: A manually curated corpus for Biomedical Question Answering. **2023**, 10,	0
142	Identifying molecular and functional similarities and differences between human primary cardiac valve interstitial cells and ventricular fibroblasts. 11,	0
141	Characterization and Genome Analysis of Cladobotryum mycophilum, the Causal Agent of Cobweb Disease of Morchella sextelata in China. **2023**, 9, 411	0
140	Genetic risk of depression is different in subgroups of dietary ratio of tryptophan to large neutral amino acids. **2023**, 13,	0
139	Identifying potential biomarkers for the diagnosis and treatment of IgA nephropathy based on bioinformatics analysis. **2023**, 16,	0
138	Convergent Within-Host Adaptation of Pseudomonas aeruginosa through the Transcriptional Regulatory Network.	0

137	Single Nucleotide Polymorphism rs9277336 Controls the Nuclear Alpha Actinin 4-Human Leukocyte Antigen-DPA1 Axis and Pulmonary Endothelial Pathophenotypes in Pulmonary Arterial Hypertension. **2023**, 12,	0
136	X chromosome dosage and the genetic impact across human tissues. **2023**, 15,	0
135	Bioinformatics-Based Identification of Tumor Immune Invasion- Related prognostic Biomarkers in pancreatic cancer.	0
134	Identification of transcription factors related to diabetic tubulointerstitial injury. **2023**, 21,	0
133	Whole exome sequencing reveals novel variants associated with diminished ovarian reserve in young women. 14,	0
132	Tracking of activated cTfh cells following sequential influenza vaccinations reveals transcriptional profile of clonotypes driving a vaccine-induced immune response. 14,	0
131	Chromosome-level genome assembly of the critically endangered Baer's pochard (Aythya baeri). **2023**, 10,	0
130	FN (Fibronectin)-Integrin 5 Signaling Promotes Thoracic Aortic Aneurysm in a Mouse Model of Marfan Syndrome.	0
129	Transcriptome Analysis of Resistant and Susceptible Pecan (Carya illinoinensis) Reveals the Mechanism of Resistance to Black Spot Disease (Colletotrichum fioriniae). **2023**, 71, 5812-5822	0
128	Best practices for single-cell analysis across modalities.	0
127	AutophagyNet: High-resolution data source for the analysis of autophagy and its regulation.	0
126	Antibiotic resistance in Neisseria gonorrhoeae: broad-spectrum drug target identification using subtractive genomics. **2023**, 21, e5	0
125	Insight into the mechanism of DNA methylation and miRNA-mRNA regulatory network in ischemic stroke. **2023**, 20, 10264-10283	0
124	Transcriptomic analysis reveals novel age-independent immunomodulatory proteins as a mode of cerebroprotection in P2X4R KO mice after ischemic stroke´´´.	0
123	Transcriptomic data in tumor-adjacent normal tissues harbor prognostic information on multiple cancer types.	0
122	Distinct cervical tissue-adherent and luminal microbiome communities correlate with mucosal host gene expression and protein levels in Kenyan sex workers. **2023**, 11,	0
121	Protein language models can capture protein quaternary state.	0
120	PRMT1 is a critical dependency in clear cell renal cell carcinoma through its role in post-transcriptional regulation of DNA damage response genes.	0

119	Transcriptomic data meta-analysis reveals common and injury model specific gene expression changes in the regenerating zebrafish heart. **2023**, 13,	0
118	Metaboverse enables automated discovery and visualization of diverse metabolic regulatory patterns. **2023**, 25, 616-625	0
117	Profiling proteomics responses to hexokinase-II depletion in terpene-producing Saccharomyces cerevisiae. **2023**, 100079	0
116	Human Adult Astrocyte Extracellular Vesicle Transcriptomics Study Identifies Specific RNAs Which Are Preferentially Secreted as EV Luminal Cargo. **2023**, 14, 853	0
115	SARS-CoV-2 ORF3A interacts with the Clic-like chloride channel-1 (CLCC1) and triggers an unfolded protein response. 11, e15077	0
114	A look under the hood of genomic-estimated breed compositions for brangus cattle: What have we learned?. 14,	0
113	Insights on the Biomarker Potential of Exosomal Non-Coding RNAs in Colorectal Cancer: An In Silico Characterization of Related Exosomal lncRNA/circRNA□miRNA□Target Axis. **2023**, 12, 1081	0
112	A complete gap-free diploid genome in Saccharum complex and the genomic footprints of evolution in the highly polyploid Saccharum genus. **2023**, 9, 554-571	0
111	Single-cell RNA-Seq reveals the pseudo-temporal dynamic evolution characteristics of ADSC-induced differentiation into neurons.	0
110	The discovery of genome-wide mutational dependence in naturally evolving populations.	0
109	PRADclass: Multi-pronged Gleason grade-informed computational strategy identifies consensus biomarker features of prostate adenocarcinoma that predict aggressive cancer.	0
108	Digital research environments: a requirements analysis.	0
107	Pregnancy-specific responses to COVID-19 revealed by high-throughput proteomics of human plasma. **2023**, 3,	0
106	Extensive, transient, and long-lasting gene regulation in a song-controlling brain area during testosterone-induced song development in adult female canaries.	0
105	Identification of candidate genes responsible for chasmogamy in wheat. **2023**, 24,	0
104	Multi-omics analysis reveals a crucial role for Retinoic Acid in promoting epigenetic and transcriptional competence of anin vitromodel of human Pharyngeal Endoderm.	0
103	SEQUENCE VS. STRUCTURE: DELVING DEEP INTO DATA-DRIVEN PROTEIN FUNCTION PREDICTION.	0
102	K-RET: knowledgeable biomedical relation extraction system. **2023**, 39,	0

101	Combining GS-assisted GWAS and transcriptome analysis to mine candidate genes for nitrogen utilization efficiency in Populus cathayana. **2023**, 23,	0
100	clusterMaker2: a major update to clusterMaker, a multi-algorithm clustering app for Cytoscape. **2023**, 24,	0
99	A high-quality chromosome-level Eutrema salsugineum genome, an extremophile plant model. **2023**, 24,	0
98	Identification of new immune subtypes of renal injury associated with anti-neutrophil cytoplasmic antibody□ssociated vasculitis based on integrated bioinformatics analysis. 14,	0
97	Integrated enzymes activity and transcriptome reveal the effect of exogenous melatonin on the strain degeneration of Cordyceps militaris. 14,	0
96	Unraveling astrocyte behavior in the space brain: Radiation response of primary astrocytes. 11,	0
95	Coordination of host and endosymbiont gene expression governs endosymbiont growth and elimination in the cereal weevilSitophilusspp.	0
94	Gonadal transcriptomes reveal sex-biased expression genes associated with sex determination and differentiation in red-tail catfish (Hemibagrus wyckioides). **2023**, 24,	0
93	Combined PacBio Iso-Seq and Illumina RNA-Seq Analysis of the Tuta absoluta (Meyrick) Transcriptome and Cytochrome P450 Genes. **2023**, 14, 363	0
92	Identification of Biomarkers Associated with Diagnosis of Diabetic Nephropathy Patients Based on Bioinformatics and Machine Learning.	0
91	N-arachidonylglycine is a caloric state-dependent circulating metabolite which regulates human CD4+T cell responsiveness. **2023**, 26, 106578	0
90	Modeling of clinical phenotypes in systemic lupus erythematosus based on the platelet transcriptome and FCGR2a genotype. **2023**, 21,	0
89	RNAlysis: analyze your RNA sequencing data without writing a single line of code. **2023**, 21,	0
88	A novel gene signature to predict response to neoadjuvant chemotherapy and endocrine treatment in estrogen receptor-positive breast cancer patients.	0
87	Broad functional profiling of fission yeast proteins using phenomics and machine learning.	0
86	N-glycoproteomics of brain synapses and synaptic vesicles. **2023**, 42, 112368	0
85	MOViDA: Multi-Omics Visible Drug Activity Prediction with a Biologically Informed Neural Network Model.	0
84	The effect of temperature and invasive alien predator on genetic and phenotypic variation in the damselfly Ischnura elegans: cross-latitude comparison. **2023**, 20,	0

83	Characterization of rumen microbiome and immune genes expression of crossbred beef steers with divergent residual feed intake phenotypes.	o
82	Ancestry-related differences in chromatin accessibility and gene expression of APOE 4 are associated with Alzheimer’s disease risk.	o
81	Protein language models can capture protein quaternary state.	o
80	METTL3 enhances dentinogenesis differentiation of dental pulp stem cells via increasing GDF6 and STC1 mRNA stability. **2023**, 23,	o
79	Gender trend of monkeypox virus infection. 1-6	o
78	Single-nucleus gene and gene set expression-based similarity network fusion identifies autism molecular subtypes. **2023**, 24,	o
77	Activation of AMPK promotes cardiac differentiation by stimulating the autophagy pathway.	o
76	Cuprotosis Clusters Predicts Prognosis and Immunotherapy Response in Low-grade glioma.	o
75	Accurate prediction ofin vivoprotein abundances by coupling constraint-based modelling and machine learning.	o
74	RoPE: A robust profile likelihood method for differential gene expression analysis.	o
73	The dcGO domain-centric ontology database in 2023: new website and extended annotations for protein structural domains. **2023**, 168093	o
72	Comprehensive Metabolomic and Transcriptomic Analysis of the Regulatory Network of Volatile Terpenoid Formation during the Growth and Development of Pears (Pyrus spp. Panguxiang) **2023**, 9, 483	o
71	Eta polycaprolactone (PCL) implants appear to cause a partial differentiation of breast cancer lung metastasis in a murine model. **2023**, 23,	o
70	Integrated Metabolome and Transcriptome Analysis Reveals a Potential Mechanism for Water Accumulation Mediated Translucency in Pineapple (Ananas comosus (L.) Merr.) Fruit. **2023**, 24, 7199	o
69	Peptidoglycan Recognition Protein S5 of Bombyx mori Facilitates the Proliferation of Bombyx mori Cypovirus 1.	o
68	Transcriptome analysis reveals the molecular mechanisms of adaptation to high temperatures in Gracilaria bailinae. 14,	o
67	Unveiling DNA damage repair-based molecular subtypes, tumor microenvironment and pharmacogenomic landscape in gastric cancer. 14,	o
66	An Anatomical Ontology for the Class Collembola (Arthropoda: Hexapoda). 66,	o

65	A chromosome-scale genome assembly of Malus domestica, a multi-stress resistant apple variety. **2023**, 115, 110627	0
64	Plant Derived MicroRNA156: A Critical Regulator of Environmental Stress.	0
63	Transcriptomic analysis of Andrias davidianus meat and experimental validation for exploring its bioactive components as functional foods. **2023**, 1-13	0
62	Fe/S Redox-Coupled Mercury Transformation Mediated by Acidithiobacillus ferrooxidans ATCC 23270 under Aerobic and/or Anaerobic Conditions. **2023**, 11, 1028	0
61	AlveolarCapillary Barrier Protection In Vitro: Lung Cell Type-Specific Effects and Molecular Mechanisms Induced by 125-Dihydroxyvitamin D3. **2023**, 24, 7298	0
60	Analysis of Nipah Virus Replication and Host Proteome Response Patterns in Differentiated Porcine Airway Epithelial Cells Cultured at the Airliquid Interface. **2023**, 15, 961	0
59	Investigation of Diagnostic and Prognostic Value of CLEC4M of Non-Small Cell Lung Carcinoma Associated with Immune Microenvironment. Volume 16, 1317-1332	0
58	Drug Discovery in Canine Pyometra Disease Identified by Text Mining and Microarray Data Analysis. **2023**, 2023, 1-11	0
57	SMARCAD1 and TOPBP1 contribute to heterochromatin maintenance at the transition from the 2C-like to the pluripotent state.	0
56	Identification of novel pathways and immune profiles related to sarcopenia. 10,	0
55	Genealyzer: web application for the analysis and comparison of gene expression data. **2023**, 24,	0
54	ANP rescues the preeclamptic symptoms inAxlknockout mice by improving trophoblast function ANP rescues the preeclamptic symptoms.	0
53	Identification of NETs-related biomarkers and molecular clusters in systemic lupus erythematosus. 14,	0
52	Integrative analysis of TP53 mutations in lung adenocarcinoma for immunotherapies and prognosis. **2023**, 24,	0
51	A robust reprogramming strategy for generating hepatocyte-like cells usable in pharmaco-toxicological studies. **2023**, 14,	0
50	Elucidating the role of two types of essential oils in regulating antibiotic resistance in soil. **2023**, 131443	0
49	The Effects of a Multi-Ingredient Supplement Containing Wasabia Japonica Extract, Theacrine, and Copper (I) Niacin Chelate on Peripheral Blood Mononuclear Cell DNA Methylation, Transcriptomics, and Sirtuin Activity. **2023**, 3, 233-246	0
48	Nuciferine Effectively Protects Mice against Acetaminophen-Induced Liver Injury. **2023**, 12, 949	0

47	Cyclic GMP□AMP Synthase (cGAS) Deletion Reduces Severity in Bilateral Nephrectomy Mice through Changes in Neutrophil Extracellular Traps and Mitochondrial Respiration. **2023**, 11, 1208	○
46	Multi-omic underpinnings of epigenetic aging and human longevity. **2023**, 14,	○
45	Mass Spectrometry based identification of site-specific proteomic alterations and potential pathways underlying the pathophysiology of schizophrenia.	○
44	Latent generative landscapes as maps of functional diversity in protein sequence space. **2023**, 14,	○
43	Oncogenic CDK13 mutations impede nuclear RNA surveillance. **2023**, 380,	○
42	CD103+ regulatory T cells underlie resistance to radio-immunotherapy and impair CD8+ T cell activation in glioblastoma.	○
41	Metabolomic and transcriptomic analyses of the flavonoid biosynthetic pathway in blueberry (Vaccinium spp.). 14,	○
40	Novel protein interaction network of human calcitonin receptor-like receptor revealed by label-free quantitative proteomics.	○
39	A systematic pan-cancer analysis reveals the clinical prognosis and immunotherapy value of C-X3-C motif ligand 1 (CX3CL1). 14,	○
38	Effects of Atherogenic Factors on Endothelial Cells: Bioinformatics Analysis of Differentially Expressed Genes and Signaling Pathways. **2023**, 11, 1216	○
37	Clinically Relevant Biology of Hyaluronic Acid in the Desmoplastic Stroma of Pancreatic Ductal Adenocarcinoma. **2022**, 51, 1092-1104	○
36	A non-canonical role of ATG8 in Golgi recovery from heat stress in plants.	○
35	In Ovo Injection of CHIR-99021 Promotes Feather Follicle Development via Modulating the Wnt Signaling Pathway and Transcriptome in Goose Embryos (Anser cygnoides). 13,	○
34	Identification of miRNAs Involved in Male Fertility and Pollen Development in Brassica oleracea var. capitata L. by High-Throughput Sequencing. **2023**, 9, 515	○
33	PRDM1 DNA-binding zinc finger domain is required for normal limb development and is disrupted in split hand/foot malformation. **2023**, 16,	○
32	Informatics and computational methods in natural product drug discovery. **2023**, 147-166	○
31	Systematic elucidation of genetic mechanisms underlying cholesterol uptake. **2023**, 100304	○
30	Deep learning on graphs for multi-omics classification of COPD. **2023**, 18, e0284563	○

29	Cortical glia in SOD1(G93A) mice are subtly affected by ALS-like pathology. **2023**, 13,	0
28	Mitoregulin Contributes to Creatine Shuttling and Cardiolipin Protection in Mice Muscle. **2023**, 24, 7589	0
27	The mechanism of peach kernel and safflower herb-pair for the treatment of liver fibrosis based on network pharmacology and molecular docking technology: A review. **2023**, 102, e33593	0
26	The neurogenetics of functional connectivity alterations in Autism: Insights from subtyping in 657 patients. **2023**,	0
25	Oxylipin biosynthetic gene families of Cannabis sativa. **2023**, 18, e0272893	0
24	Responding to ACL Injury and its Treatments: Comparative Gene Expression between Articular Cartilage and Synovium. **2023**, 10, 527	0
23	A familial natural short sleep mutation promotes healthy aging and extends lifespan inDrosophila.	0
22	Ontology Partitioning for Managing Change Effects. **2023**, 132-146	0
21	Sequence-structure-function relationships in the microbial protein universe. **2023**, 14,	0
20	MORC proteins regulate transcription factor binding by mediating chromatin compaction in active chromatin regions. **2023**, 24,	0
19	MaSS: Model-agnostic, Semantic and Stealthy Data Poisoning Attack on Knowledge Graph Embedding. **2023**,	0
18	An eleven-gene risk model associated with lymph node metastasis predicts overall survival in lung adenocarcinoma. **2023**, 13,	0
17	Identification of lncRNAs involved in response to ionizing radiation in fibroblasts of long-term survivors of childhood cancer and cancer-free controls. 13,	0
16	Systematic Pan-cancer Functional Inference and Validation of Hyper, Hypo and Neomorphic Mutations.	0
15	Evolutionary constraint and innovation across hundreds of placental mammals. **2023**, 380,	0
14	Organelle interactions compartmentalize hepatic fatty acid trafficking and metabolism. **2023**, 42, 112435	0
13	Methadone alters transcriptional programs associated with synapse formation in human cortical organoids. **2023**, 13,	0
12	Temperature and day length drive local adaptation in the Patagonian foundation tree speciesNothofagus pumilio.	0

11	Complete genome sequence of Dickeya dadantii strain XJ12 causing banana bacterial sheath rot in China.	0
10	Differentiation of Large Extracellular Vesicles in Oral Fluid: Combined Protocol of Small Force Centrifugation and Pattern Analysis.	0
9	Identification of potential biological processes and key genes in diabetes-related stroke through Weighted gene co-expression network analysis.	0
8	Lessons learned to enable question answering on knowledge graphs extracted from scientific publications: A case study on the coronavirus literature. **2023**, 142, 104382	0
7	Identification of proteins associated with changes in oligosaccharide metabolism in Lycium barbarum L. fruit by using iTRAQ technology. **2023**, 12, 100612	0
6	Up-regulation of cholesterol synthesis pathways and limited neurodegeneration in a knock-inSod1mutant mouse model of ALS.	0
5	Cell-selective proteomics segregates pancreatic cancer subtypes by extracellular proteins in tumors and circulation. **2023**, 14,	0
4	Molecular signatures of post-traumatic stress disorder in war-zone-exposed veteran and active-duty soldiers. **2023**, 4, 101045	0
3	Bioinformatics analyses suggest that mutations in COL12A1 and its miRNAs promote stomach adenocarcinoma via loss of COL12A1 suppression. **2023**,	0
2	Annotating Macromolecular Complexes in the Protein Data Bank: Improving the FAIRness of Structure Data.	0
1	Basal forebrain cholinergic neurons are vulnerable in a mouse model of Down syndrome and their molecular fingerprint is rescued by maternal choline supplementation. **2023**, 37,	0