CITATION REPORT List of articles citing

Bioconductor: open software development for computational biology and bioinformatics

DOI: 10.1186/gb-2004-5-10-r80 Genome Biology, 2004, 5, R80.

Source: https://exaly.com/paper-pdf/37445196/citation-report.pdf

Version: 2024-04-20

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

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

#	Paper	IF	Citations
2282	Gene expression profiling of hypoxia signaling in human hepatocellular carcinoma cells. 2005 , 22, 308-1	8	57
2281	Epistatic and Environmental Control of Genome-Wide Gene Expression. 2005, 8, 5-15		13
2280	Mutant-specific gene programs in the zebrafish. 2005 , 106, 521-30		69
2279	Algorithms for gene expression analysis. 2005,		6
2278	Epistasis analysis with global transcriptional phenotypes. 2005 , 37, 471-7		89
2277	A function for interleukin 2 in Foxp3-expressing regulatory T cells. 2005 , 6, 1142-51		1390
2276	Multiple-laboratory comparison of microarray platforms. 2005 , 2, 345-50		716
2275	Gene expression profiling of arthritis using a QTL chip reveals a complex gene regulation of the Cia5 region in mice. 2005 , 6, 575-83		14
2274	Expression analysis of genes involved in brain tumor progression driven by retroviral insertional mutagenesis in mice. 2005 , 24, 3896-905		59
2273	Gene expression-based classification of nonseminomatous male germ cell tumors. 2005 , 24, 5101-7		48
2272	Immediate-early and delayed cytokinin response genes of Arabidopsis thaliana identified by genome-wide expression profiling reveal novel cytokinin-sensitive processes and suggest cytokinin action through transcriptional cascades. 2005 , 44, 314-33		293
2271	Patient-based cross-platform comparison of oligonucleotide microarray expression profiles. 2005 , 85, 1024-39		52
2270	A comparison of match-only algorithms for the analysis of Plasmodium falciparum oligonucleotide arrays. 2005 , 35, 523-31		2
2269	Microarray-based classification of diffuse large B-cell lymphoma. 2005, 74, 453-65		38
2268	Microarray-based comparative genomic analyses of the human malaria parasite Plasmodium falciparum using Affymetrix arrays. 2005 , 144, 177-86		45
2267	arrayCGHbase: an analysis platform for comparative genomic hybridization microarrays. 2005, 6, 124		74
2266	FACTa framework for the functional interpretation of high-throughput experiments. 2005 , 6, 161		6

(2005-2005)

2265	Calibration of mass spectrometric peptide mass fingerprint data without specific external or internal calibrants. 2005 , 6, 203	18
2264	stama Bioconductor compliant R package for structured analysis of microarray data. 2005 , 6, 211	2
2263	Sources of variation in Affymetrix microarray experiments. 2005 , 6, 214	93
2262	Optimized between-group classification: a new jackknife-based gene selection procedure for genome-wide expression data. 2005 , 6, 239	7
2261	maxdLoad2 and maxdBrowse: standards-compliant tools for microarray experimental annotation, data management and dissemination. 2005 , 6, 264	23
2260	Transformation and other factors of the peptide mass spectrometry pairwise peak-list comparison process. 2005 , 6, 285	15
2259	ArrayQuest: a web resource for the analysis of DNA microarray data. 2005 , 6, 287	19
2258	Comparison of normalization methods for CodeLink Bioarray data. 2005 , 6, 309	51
2257	Correlation test to assess low-level processing of high-density oligonucleotide microarray data. 2005 , 6, 80	41
2256	ProGenExpress: visualization of quantitative data on prokaryotic genomes. 2005 , 6, 98	5
2255	HomoMINT: an inferred human network based on orthology mapping of protein interactions discovered in model organisms. 2005 , 6 Suppl 4, S21	109
2254	An integrated approach of immunogenomics and bioinformatics to identify new Tumor Associated Antigens (TAA) for mammary cancer immunological prevention. 2005 , 6 Suppl 4, S7	25
2253	Limitations of mRNA amplification from small-size cell samples. 2005 , 6, 147	32
2252	GPX-Macrophage Expression Atlas: a database for expression profiles of macrophages challenged with a variety of pro-inflammatory, anti-inflammatory, benign and pathogen insults. 2005 , 6, 178	15
2251	Increased DNA microarray hybridization specificity using sscDNA targets. 2005 , 6, 57	35
2250	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
2249	Transcriptome analysis in primary neural stem cells using a tag cDNA amplification method. 2005 , 6, 28	10
2248	Epidermal growth factor (EGF) withdrawal masks gene expression differences in the study of pituitary adenylate cyclase-activating polypeptide (PACAP) activation of primary neural stem cell proliferation. 2005 , 6, 55	5

2247	Folate system correlations in DNA microarray data. 2005 , 5, 95	6
2246	Laboratory variability does not preclude identification of biological functions impacted by hydroxyurea. 2005 , 46, 221-35	9
2245	Analysis of chromosome breakpoints in neuroblastoma at sub-kilobase resolution using fine-tiling oligonucleotide array CGH. 2005 , 44, 305-19	236
2244	Genotype-phenotype relationships in hepatocellular tumors from mice and man. 2005, 42, 353-61	82
2243	R Version 2.1.0. 2005 , 20, 197-202	5
2242	Genome-wide expression profiling and identification of gene activities during early flower development in Arabidopsis. 2005 , 58, 401-19	63
2241	Expression profiling reveals COI1 to be a key regulator of genes involved in wound- and methyl jasmonate-induced secondary metabolism, defence, and hormone interactions. 2005 , 58, 497-513	257
2240	Assembly of a gene sequence tag microarray by reversible biotin-streptavidin capture for transcript analysis of Arabidopsis thaliana. 2005 , 5, 5	4
2239	Bleomycin-induced pulmonary fibrosis susceptibility genes in AcB/BcA recombinant congenic mice. 2005 , 23, 54-61	30
2238	MADE4: an R package for multivariate analysis of gene expression data. 2005 , 21, 2789-90	267
2237	Gene expression profiling and phenotype analyses of S. cerevisiae in response to changing copper reveals six genes with new roles in copper and iron metabolism. 2005 , 22, 356-67	59
2236	A global survey of gene regulation during cold acclimation in Arabidopsis thaliana. 2005 , 1, e26	322
2235	MACATmicroarray chromosome analysis tool. 2005 , 21, 2112-3	27
2234	Discovering molecular functions significantly related to phenotypes by combining gene expression data and biological information. 2005 , 21, 2988-93	90
2233	Evidence for widespread degradation of gene control regions in hominid genomes. 2005 , 3, e42	153
2232	Framework for kernel regularization with application to protein clustering. 2005 , 102, 12332-7	31
2231	Gene expression profiling reveals a signaling role of glutathione in redox regulation. 2005, 102, 13998-4003	148
2230	Identification and functional significance of genes regulated by structurally different histone deacetylase inhibitors. 2005 , 102, 3697-702	451

(2005-2006)

2229	Molecular characterisation of non-absorptive and absorptive enterocytes in human small intestine. 2006 , 55, 1084-9	31
2228	OLIN: optimized normalization, visualization and quality testing of two-channel microarray data. 2005 , 21, 1724-6	34
2227	Simpleaffy: a BioConductor package for Affymetrix Quality Control and data analysis. 2005 , 21, 3683-5	331
2226	Variation in gene expression and aberrantly regulated chromosome regions in cloned mice. 2005 , 73, 1302-11	52
2225	Molecular decomposition of complex clinical phenotypes using biologically structured analysis of microarray data. 2005 , 21, 1971-8	34
2224	Coordination of nuclear and mitochondrial genome expression during mitochondrial biogenesis in Arabidopsis. 2005 , 17, 1497-512	122
2223	A novel pathophysiological mechanism for osteoporosis suggested by an in vivo gene expression study of circulating monocytes. 2005 , 280, 29011-6	98
2222	Improved microarray methods for profiling the Yeast Knockout strain collection. 2005, 33, e103	47
2221	Experimental comparison and cross-validation of the Affymetrix and Illumina gene expression analysis platforms. 2005 , 33, 5914-23	195
2220	An expression index for Affymetrix GeneChips based on the generalized logarithm. 2005 , 21, 3983-9	31
2219	A distinctive alveolar macrophage activation state induced by cigarette smoking. 2005 , 172, 1383-92	164
2218	twilight; a Bioconductor package for estimating the local false discovery rate. 2005 , 21, 2921-2	39
2217	Limits of predictive models using microarray data for breast cancer clinical treatment outcome. 2005 , 97, 927-30	104
2216	BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. 2005 , 21, 3439-40	1069
2215	GEPAS, an experiment-oriented pipeline for the analysis of microarray gene expression data. 2005 , 33, W616-20	79
2214	Considerations in making microarray cross-platform correlations.	
2213	A new insight into the cellular regulation of aqueous outflow: how trabecular meshwork endothelial cells drive a mechanism that regulates the permeability of Schlemm's canal endothelial cells. 2005 , 89, 1500-5	99
2212	Global gene expression profiling reveals widespread yet distinctive translational responses to different eukaryotic translation initiation factor 2B-targeting stress pathways. 2005 , 25, 9340-9	84

2211	Gene expression in Huntington's disease skeletal muscle: a potential biomarker. 2005, 14, 1863-76	134
2210	Benchmarking the CATMA microarray. A novel tool for Arabidopsis transcriptome analysis. 2005 , 137, 588-601	84
2209	Plant-based microarray data at the European Bioinformatics Institute. Introducing AtMIAMExpress, a submission tool for Arabidopsis gene expression data to ArrayExpress. 2005 , 139, 632-6	9
2208	Association of valproate-induced teratogenesis with histone deacetylase inhibition in vivo. 2005 , 19, 1166-8	145
2207	Use of within-array replicate spots for assessing differential expression in microarray experiments. 2005 , 21, 2067-75	1079
2206	MIDAW: a web tool for statistical analysis of microarray data. 2005 , 33, W644-9	40
2205	goCluster integrates statistical analysis and functional interpretation of microarray expression data. 2005 , 21, 3575-7	22
2204	CpG Island microarray probe sequences derived from a physical library are representative of CpG Islands annotated on the human genome. 2005 , 33, 2952-61	82
2203	Cell-type-specific transcriptomics in chimeric models using transcriptome-based masks. 2005 , 33, e111	25
2202	Cellular differentiation hierarchies in normal and culture-adapted human embryonic stem cells. 2005 , 14, 3129-40	252
2201	Integrating probe-level expression changes across generations of Affymetrix arrays. 2005, 33, e193	44
2200	Redefinition of Affymetrix probe sets by sequence overlap with cDNA microarray probes reduces cross-platform inconsistencies in cancer-associated gene expression measurements. 2005 , 6, 107	99
2199	CCL5-CCR5 interaction provides antiapoptotic signals for macrophage survival during viral infection. 2005 , 11, 1180-7	230
2198	Comparison of label-free methods for quantifying human proteins by shotgun proteomics. 2005 , 4, 1487-502	986
2197	Gene expression patterns 🗈 tool for bioanalysis. 2005 , 85, 589-608	1
2196	Evolving gene/transcript definitions significantly alter the interpretation of GeneChip data. 2005 , 33, e175	1401
2195	A learned comparative expression measure for affymetrix genechip DNA microarrays. 2005, 144-54	2
2194	cDNA microarray analysis reveals novel candidate genes expressed in human peripheral blood following exhaustive exercise. 2005 , 23, 287-94	54

(2006-2005)

2193	Altered cortical glutamatergic and GABAergic signal transmission with glial involvement in depression. 2005 , 102, 15653-8		482
2192	Molecular mechanisms of steroid hormone signaling in plants. 2005 , 21, 177-201		322
2191	Regulatory T cell lineage specification by the forkhead transcription factor foxp3. 2005 , 22, 329-41		1846
2190	Functional genomics in farm animals - Microarray analysis. 2005 , 71, 128-37		8
2189	Gene expression profiling of the preclinical scrapie-infected hippocampus. 2005 , 334, 86-95		66
2188	O13: Automatic Identification of Chromosomal Aberrations in array-CGH Based Experiments Applying the ChipYard Framework for Microarray Data Analysis. 2005 , 48, 469-470		
2187	Effect of JP-8 jet fuel exposure on protein expression in human keratinocyte cells in culture. 2005 , 160, 8-21		7
2186	GOAT: An R Tool for Analysing Gene Ontologytrade mark Term Enrichment. 2005 , 4, 281-3		17
2185	Microarrays and breast cancer clinical studies: forgetting what we have not yet learnt. 2005 , 7, 96-9		22
2184	Genome-wide gene expression in response to parasitoid attack in Drosophila. <i>Genome Biology</i> , 2005 , 6, R94	18.3	126
2183	Chipper: discovering transcription-factor targets from chromatin immunoprecipitation microarrays using variance stabilization. <i>Genome Biology</i> , 2005 , 6, R96	18.3	37
2182	Transcriptome analysis of antigenic variation in Plasmodium falciparumvar silencing is not dependent on antisense RNA. <i>Genome Biology</i> , 2005 , 6, R93	18.3	57
2181	Searching for differentially expressed gene combinations. <i>Genome Biology</i> , 2005 , 6, R88	18.3	46
2180	A molecular map of mesenchymal tumors. <i>Genome Biology</i> , 2005 , 6, R76	18.3	104
2179	Promoter features related to tissue specificity as measured by Shannon entropy. <i>Genome Biology</i> , 2005 , 6, R33	18.3	311
2178	Weighting by heritability for detection of quantitative trait loci with microarray estimates of gene expression. <i>Genome Biology</i> , 2005 , 6, R27	18.3	10
2177	Gene expression profile and synovial microcirculation at early stages of collagen-induced arthritis. 2005 , 7, R868-76		16
2176	Gene expression signatures of morphologically normal breast tissue identify basal-like tumors. 2006 , 8, R58		107

2175	Intrinsic molecular signature of breast cancer in a population-based cohort of 412 patients. 2006 , 8, R3	4	188
2174	ProCAT: a data analysis approach for protein microarrays. <i>Genome Biology</i> , 2006 , 7, R110	18.3	43
2173	Identification of novel regulatory modules in dicotyledonous plants using expression data and comparative genomics. <i>Genome Biology</i> , 2006 , 7, R103	18.3	50
2172	Comparative genomics of Drosophila and human core promoters. <i>Genome Biology</i> , 2006 , 7, R53	18.3	113
2171	Analysis of cell-based RNAi screens. <i>Genome Biology</i> , 2006 , 7, R66	18.3	234
2170	Nonrandom divergence of gene expression following gene and genome duplications in the flowering plant Arabidopsis thaliana. <i>Genome Biology</i> , 2006 , 7, R13	18.3	134
2169	Effect of infliximab on mRNA expression profiles in synovial tissue of rheumatoid arthritis patients. 2006 , 8, R179		54
2168	A model of anti-angiogenesis: differential transcriptosome profiling of microvascular endothelial cells from diffuse systemic sclerosis patients. 2006 , 8, R115		49
2167	Variability in synovial inflammation in rheumatoid arthritis investigated by microarray technology. 2006 , 8, R47		39
2166	A Hidden Markov model web application for analysing bacterial genomotyping DNA microarray experiments. 2006 , 5, 211-8		4
2165	Comparisons of annotation predictions for affymetrix GeneChips. 2006, 5, 237-48		4
2164	The arginine regulon of Escherichia coli: whole-system transcriptome analysis discovers new genes and provides an integrated view of arginine regulation. 2006 , 152, 3343-3354		58
2163	The dopamine D3 receptor plays an essential role in alcohol-seeking and relapse. 2006 , 20, 2223-33		91
2162	Storage and Processing of Mass Spectrometry Data.		
2161	Comparison of Preprocessing Methods for Affymetrix Microarrays. 2006 , 19, 15-20		
2160	ITTACA: a new database for integrated tumor transcriptome array and clinical data analysis. 2006 , 34, D613-6		47
2159	Some statistical issues in microarray gene expression data. 2006 , 165, 745-8		7
2158	Data storage and analysis in ArrayExpress. 2006 , 411, 370-86		33

(2006-2006)

2157	Comparisons between transcriptional regulation and RNA expression in human embryonic stem cell lines. 2006 , 15, 315-23	31
2156	Characterization of phagosome trafficking and identification of PhoP-regulated genes important for survival of Yersinia pestis in macrophages. 2006 , 74, 3727-41	106
2155	Identification and characterization of genes susceptible to transcriptional cross-talk between the hypoxia and dioxin signaling cascades. 2006 , 19, 1284-93	32
2154	Integrated analysis of metabolite and transcript levels reveals the metabolic shifts that underlie tomato fruit development and highlight regulatory aspects of metabolic network behavior. 2006 , 142, 1380-96	361
2153	APC and oncogenic KRAS are synergistic in enhancing Wnt signaling in intestinal tumor formation and progression. 2006 , 131, 1096-109	226
2152	Pathway-specific differences between tumor cell lines and normal and tumor tissue cells. 2006 , 5, 55	149
2151	Bioconductor: an open source framework for bioinformatics and computational biology. 2006 , 411, 119-34	183
2150	Genetic segregation of airway disease traits despite redundancy of calcium-activated chloride channel family members. 2006 , 25, 502-13	58
2149	Thermoregulatory and metabolic defects in Huntington's disease transgenic mice implicate PGC-1alpha in Huntington's disease neurodegeneration. 2006 , 4, 349-62	466
2148	XCMS: processing mass spectrometry data for metabolite profiling using nonlinear peak alignment, matching, and identification. 2006 , 78, 779-87	3048
2148		3048
2147	matching, and identification. 2006 , 78, 779-87	
2147	matching, and identification. 2006 , 78, 779-87 Co-expressed yeast genes cluster over a long range but are not regularly spaced. 2006 , 359, 825-31	29
2147 2146	matching, and identification. 2006, 78, 779-87 Co-expressed yeast genes cluster over a long range but are not regularly spaced. 2006, 359, 825-31 Experimental Design and Analysis of Microarray Data. 2006, 1-36 Developmental timing in Dictyostelium is regulated by the Set1 histone methyltransferase. 2006,	29
2147 2146 2145	matching, and identification. 2006, 78, 779-87 Co-expressed yeast genes cluster over a long range but are not regularly spaced. 2006, 359, 825-31 Experimental Design and Analysis of Microarray Data. 2006, 1-36 Developmental timing in Dictyostelium is regulated by the Set1 histone methyltransferase. 2006, 292, 519-32	29 2 33
2147 2146 2145 2144	matching, and identification. 2006, 78, 779-87 Co-expressed yeast genes cluster over a long range but are not regularly spaced. 2006, 359, 825-31 Experimental Design and Analysis of Microarray Data. 2006, 1-36 Developmental timing in Dictyostelium is regulated by the Set1 histone methyltransferase. 2006, 292, 519-32 Genetic interactions between Drosophila melanogaster menin and Jun/Fos. 2006, 298, 59-70 Accurate and precise transcriptional profiles from 50 pg of total RNA or 100 flow-sorted primary	29 2 33 10
2147 2146 2145 2144 2143	Co-expressed yeast genes cluster over a long range but are not regularly spaced. 2006, 359, 825-31 Experimental Design and Analysis of Microarray Data. 2006, 1-36 Developmental timing in Dictyostelium is regulated by the Set1 histone methyltransferase. 2006, 292, 519-32 Genetic interactions between Drosophila melanogaster menin and Jun/Fos. 2006, 298, 59-70 Accurate and precise transcriptional profiles from 50 pg of total RNA or 100 flow-sorted primary lymphocytes. 2006, 88, 111-21	29 2 33 10 9

2139	Gene expression profile of B 16(F10) murine melanoma cells exposed to hypoxic conditions in vitro. 2006 , 13, 191-203	30
2138	Microarray expression technology: from start to finish. 2006 , 7, 123-34	24
2137	Metabolome, transcriptome, and bioinformatic cis-element analyses point to HNF-4 as a central regulator of gene expression during enterocyte differentiation. 2006 , 27, 141-55	83
2136	Analysis of Affymetrix GeneChip data using amplified RNA. 2006 , 40, 165-6, 168, 170	17
2135	Genome wide profiling of human embryonic stem cells (hESCs), their derivatives and embryonal carcinoma cells to develop base profiles of U.S. Federal government approved hESC lines. 2006 , 6, 20	79
2134	Expression profiling of clonal lymphocyte cell cultures from Rett syndrome patients. 2006, 7, 61	33
2133	The Shivplot: a graphical display for trend elucidation and exploratory analysis of microarray data. 2006 , 1, 6	
2132	Global analysis of X-chromosome dosage compensation. 2006 , 5, 3	242
2131	Brachyury, a crucial regulator of notochordal development, is a novel biomarker for chordomas. 2006 , 209, 157-65	410
2130	Induction of the skin endogenous protective mitochondrial MnSOD by Vitreoscilla filiformis extract. 2006 , 28, 277-87	15
2129	Transcription levels of invasion-related genes in prostate cancer cells are modified by inhibitors of tyrosine kinase. 2006 , 114, 364-71	10
2128	Genome-wide screening of dioxin-responsive genes in fetal brain: bioinformatic and experimental approaches. 2006 , 46, 135-43	9
2127	Genomic and expression profiling identifies the B-cell associated tyrosine kinase Syk as a possible therapeutic target in mantle cell lymphoma. 2006 , 132, 303-16	152
2126	Comparative genome-wide profiling of post-transplant lymphoproliferative disorders and diffuse large B-cell lymphomas. 2006 , 134, 27-36	52
2125	Gene expression profiling reveals consistent differences between clinical samples of human leukaemias and their model cell lines. 2006 , 135, 520-3	12
2124	Microarray analysis of the transcriptome as a stepping stone towards understanding biological systems: practical considerations and perspectives. 2006 , 45, 630-50	72
2123	ABERRANT TESTA SHAPE encodes a KANADI family member, linking polarity determination to separation and growth of Arabidopsis ovule integuments. 2006 , 46, 522-31	102
2122	Membrane-associated transcripts in Arabidopsis; their isolation and characterization by DNA microarray analysis and bioinformatics. 2006 , 46, 708-21	32

2121	The genetics and genomics of the drought response in Populus. 2006 , 48, 321-41	196
2120	phyA dominates in transduction of red-light signals to rapidly responding genes at the initiation of Arabidopsis seedling de-etiolation. 2006 , 48, 728-42	137
2119	UPSC-BASEPopulus transcriptomics online. 2006 , 48, 806-17	52
2118	Towards a molecular definition of worker sterility: differential gene expression and reproductive plasticity in honey bees. 2006 , 15, 637-44	46
2117	A sequence-oriented comparison of gene expression measurements across different hybridization-based technologies. 2006 , 24, 832-40	133
2116	ChIP-on-chip protocol for genome-wide analysis of transcription factor binding in Drosophila melanogaster embryos. 2006 , 1, 2839-55	79
2115	Standards for systems biology. 2006 , 7, 593-605	114
2114	Exploration of global gene expression in human liver steatosis by high-density oligonucleotide microarray. 2006 , 86, 154-65	76
2113	Gene expression profiling of CD34+ cells identifies a molecular signature of chronic myeloid leukemia blast crisis. 2006 , 20, 1028-34	93
2112	Gene expression analysis of bipolar disorder reveals downregulation of the ubiquitin cycle and alterations in synaptic genes. 2006 , 11, 965-78	155
2111	Protection of glioblastoma cells from cisplatin cytotoxicity via protein kinase Ciota-mediated attenuation of p38 MAP kinase signaling. 2006 , 25, 2909-19	55
2110	Transcriptional profiling suggests that Barrett's metaplasia is an early intermediate stage in esophageal adenocarcinogenesis. 2006 , 25, 3346-56	103
2109	siRNA-mediated AML1/MTG8 depletion affects differentiation and proliferation-associated gene expression in t(8;21)-positive cell lines and primary AML blasts. 2006 , 25, 6067-78	55
2108	Gene expression profiles of Arabidopsis Cvi seeds during dormancy cycling indicate a common underlying dormancy control mechanism. 2006 , 46, 805-22	300
2107	Protein expression changes in the nucleus accumbens and amygdala of inbred alcohol-preferring rats given either continuous or scheduled access to ethanol. 2006 , 40, 3-17	53
2106	Predicting O-glycosylation sites in mammalian proteins by using SVMs. 2006 , 30, 203-8	63
2105	Defining molecular profiles of poor outcome in patients with invasive bladder cancer using oligonucleotide microarrays. 2006 , 24, 778-89	455
2104	Wnt but not BMP signaling is involved in the inhibitory action of sclerostin on BMP-stimulated bone formation. 2007 , 22, 19-28	202

2103	Differential gene expression in cultured osteoblasts and bone marrow stromal cells from patients with Paget's disease of bone. 2007 , 22, 298-309	68
2102	Human spontaneous labor without histologic chorioamnionitis is characterized by an acute inflammation gene expression signature. 2006 , 195, 394.e1-24	169
2101	Analysis of microarray experiments of gene expression profiling. 2006 , 195, 373-88	177
2100	Conversion of MapMan to allow the analysis of transcript data from Solanaceous species: effects of genetic and environmental alterations in energy metabolism in the leaf. 2006 , 60, 773-92	110
2099	Global analysis of gene expression during development and ripening of citrus fruit flesh. A proposed mechanism for citric Acid utilization. 2006 , 62, 513-27	140
2098	One hundred years of high-throughput Drosophila research. 2006 , 14, 349-62	17
2097	Effect of sugar-induced senescence on gene expression and implications for the regulation of senescence in Arabidopsis. 2006 , 224, 556-68	179
2096	A new locus for autosomal dominant amelogenesis imperfecta on chromosome 8q24.3. 2007 , 120, 653-62	19
2095	Novel mechanisms of platinum drug resistance identified in cells selected for resistance to JM118 the active metabolite of satraplatin. 2007 , 59, 301-12	21
2094	Bioinformatics and cancer: an essential alliance. 2006 , 8, 409-15	11
2093	Differential gene expression profiles between tumor biopsies and short-term primary cultures of ovarian serous carcinomas: identification of novel molecular biomarkers for early diagnosis and therapy. 2006 , 103, 405-16	90
2092	Gene expression profiling of acute liver stress during living donor liver transplantation. 2006 , 6, 806-24	33
2091	The challenges of gene expression microarrays for the study of human cancer. 2006 , 9, 333-9	80
2090	Ablation of gap junctional communication in hepatocytes of transgenic mice does not lead to disrupted cellular homeostasis or increased spontaneous tumourigenesis. 2006 , 85, 717-28	12
2089	Biological microarray interpretation: the rules of engagement. 2006 , 1759, 319-27	35
2088	Development of mussel mRNA profiling: Can gene expression trends reveal coastal water pollution?. 2006 , 602, 121-34	96
2087	CARMA: A platform for analyzing microarray datasets that incorporate replicate measures. 2006 , 7, 149	18
2086	An improved procedure for gene selection from microarray experiments using false discovery rate criterion. 2006 , 7, 15	12

(2006-2006)

2085	Empirical validation of the S-Score algorithm in the analysis of gene expression data. 2006 , 7, 154	17
2084	The Gaggle: an open-source software system for integrating bioinformatics software and data sources. 2006 , 7, 176	120
2083	MIMAS: an innovative tool for network-based high density oligonucleotide microarray data management and annotation. 2006 , 7, 190	12
2082	Assessment of the relationship between pre-chip and post-chip quality measures for Affymetrix GeneChip expression data. 2006 , 7, 211	31
2081	Evaluation of methods for oligonucleotide array data via quantitative real-time PCR. 2006, 7, 23	81
2080	Correction of scaling mismatches in oligonucleotide microarray data. 2006 , 7, 251	6
2079	Spatial normalization of array-CGH data. 2006 , 7, 264	67
2078	Hybridization interactions between probesets in short oligo microarrays lead to spurious correlations. 2006 , 7, 276	128
2077	SBEAMS-Microarray: database software supporting genomic expression analyses for systems biology. 2006 , 7, 286	45
2076	Evaluation of microarray data normalization procedures using spike-in experiments. 2006, 7, 300	14
2075	Web-based analysis of the mouse transcriptome using Genevestigator. 2006 , 7, 311	24
2074	AMDA: an R package for the automated microarray data analysis. 2006 , 7, 335	31
2073	Cluster analysis of protein array results via similarity of Gene Ontology annotation. 2006 , 7, 338	22
2072	A powerful method for detecting differentially expressed genes from GeneChip arrays that does not require replicates. 2006 , 7, 353	10
2071	Comparison and evaluation of methods for generating differentially expressed gene lists from microarray data. 2006 , 7, 359	234
2070	Analysis with respect to instrumental variables for the exploration of microarray data structures. 2006 , 7, 422	37
2069	A summarization approach for Affymetrix GeneChip data using a reference training set from a large, biologically diverse database. 2006 , 7, 464	57
2068	Goulphar: rapid access and expertise for standard two-color microarray normalization methods. 2006 , 7, 467	50

2067	Effects of filtering by Present call on analysis of microarray experiments. 2006 , 7, 49	192
2066	CoXpress: differential co-expression in gene expression data. 2006 , 7, 509	114
2065	PageMan: an interactive ontology tool to generate, display, and annotate overview graphs for profiling experiments. 2006 , 7, 535	276
2064	Intensity-based hierarchical Bayes method improves testing for differentially expressed genes in microarray experiments. 2006 , 7, 538	195
2063	Gene expression profiling in the striatum of inbred mouse strains with distinct opioid-related phenotypes. 2006 , 7, 146	43
2062	Inferring direct regulatory targets from expression and genome location analyses: a comparison of transcription factor deletion and overexpression. 2006 , 7, 215	16
2061	MicroArray Facility: a laboratory information management system with extended support for Nylon based technologies. 2006 , 7, 240	4
2060	Microarray analysis after RNA amplification can detect pronounced differences in gene expression using limma. 2006 , 7, 252	377
2059	Simultaneous host and parasite expression profiling identifies tissue-specific transcriptional programs associated with susceptibility or resistance to experimental cerebral malaria. 2006 , 7, 295	58
2058	Specific age-related signatures in Drosophila body parts transcriptome. 2006 , 7, 69	81
2057	Global gene expression analyses of hematopoietic stem cell-like cell lines with inducible Lhx2 expression. 2006 , 7, 75	16
2056	Transcriptomes of human prostate cells. 2006 , 7, 92	56
2055	Transcriptional profiling of mesenchymal stromal cells from young and old rats in response to Dexamethasone. 2006 , 7, 95	10
2054	Effects of dexamethazone on LPS-induced activationand migration of mouse dendritic cells revealed by a genome-wide transcriptional analysis. 2006 , 36, 1504-15	46
2053	Genomic alterations in lobular neoplasia: a microarray comparative genomic hybridization signature for early neoplastic proliferationin the breast. 2006 , 45, 1007-17	75
2052	MicroRNA expression abnormalities in pancreatic endocrine and acinar tumors are associated with distinctive pathologic features and clinical behavior. 2006 , 24, 4677-84	658
2051	Group testing for pathway analysis improves comparability of different microarray datasets. 2006 , 22, 2500-6	119
2050	High-resolution spatial normalization for microarrays containing embedded technical replicates. 2006 , 22, 3054-60	15

2049	The Gene Ontology (GO) project in 2006. 2006 , 34, D322-6	794
2048	TOM: a web-based integrated approach for identification of candidate disease genes. 2006 , 34, W285-92	50
2047	Non-linear analysis of GeneChip arrays. 2006 , 34, e105	16
2046	An open-access long oligonucleotide microarray resource for analysis of the human and mouse transcriptomes. 2006 , 34, e87	82
2045	Zfp206 regulates ES cell gene expression and differentiation. 2006 , 34, 4780-90	42
2044	Identifying functional gene sets from hierarchically clustered expression data: map of abiotic stress regulated genes in Arabidopsis thaliana. 2006 , 34, e124	11
2043	Positional artifacts in microarrays: experimental verification and construction of COP, an automated detection tool. 2007 , 35, e8	9
2042	Combined transcript and metabolite profiling of Arabidopsis leaves reveals fundamental effects of the thiol-disulfide status on plant metabolism. 2006 , 141, 412-22	88
2041	Genistein affects adipose tissue deposition in a dose-dependent and gender-specific manner. 2006 , 147, 5740-51	161
2040	How accurately can we control the FDR in analyzing microarray data?. 2006 , 22, 1730-6	23
2039	High-density haplotyping with microarray-based expression and single feature polymorphism markers in Arabidopsis. 2006 , 16, 787-95	148
2038	Clustering microarray data. 2006 , 411, 194-213	31
2037	Improved prediction of treatment response using microarrays and existing biological knowledge. 2006 , 7, 495-501	7
2036	Microarray analysis of RNA processing and modification. 2006 , 410, 300-16	23
2035	Standards in gene expression microarray experiments. 2006 , 411, 63-78	16
2034	Reproducibility of microarray studies: concordance of current analysis methods. 2006 , 158, 109-25	1
2033	Automatic quality assessment of Affymetrix GeneChip data. 2006,	1
2032	affylmGUI: a graphical user interface for linear modeling of single channel microarray data. 2006 , 22, 897-9	179

2031	Analysis and visualization of DNA spectrograms. 2006,	6
2030	Next station in microarray data analysis: GEPAS. 2006 , 34, W486-91	101
2029	SScore: an R package for detecting differential gene expression without gene expression summaries. 2006 , 22, 1272-4	30
2028	Analysis of gene expression using gene sets discriminates cancer patients with and without late radiation toxicity. 2006 , 3, e422	101
2027	The LCB Data Warehouse. 2006 , 22, 1024-6	34
2026	Transcript mapping with high-density oligonucleotide tiling arrays. 2006 , 22, 1963-70	120
2025	Natural genetic variation of freezing tolerance in Arabidopsis. 2006 , 142, 98-112	330
2024	Maydaya microarray data analysis workbench. 2006 , 22, 1010-2	43
2023	Partition resampling and extrapolation averaging: approximation methods for quantifying gene expression in large numbers of short oligonucleotide arrays. 2006 , 22, 2364-72	5
2022	Genetic regulators of myelopoiesis and leukemic signaling identified by gene profiling and linear modeling. 2006 , 80, 433-47	28
2021	Functional profiling reveals that only a small number of phytochrome-regulated early-response genes in Arabidopsis are necessary for optimal deetiolation. 2006 , 18, 2157-71	81
2020	Oxandrolone enhances skeletal muscle myosin synthesis and alters global gene expression profile in Duchenne muscular dystrophy. 2006 , 290, E530-9	27
2019	Model-based boosting in high dimensions. 2006 , 22, 2828-9	38
2018	OrderedLista bioconductor package for detecting similarity in ordered gene lists. 2006 , 22, 2315-6	56
2017	Meta-analysis of differentiating mouse embryonic stem cell gene expression kinetics reveals early change of a small gene set. 2006 , 2, e158	31
2016	Scientific software development is not an oxymoron. 2006 , 2, e87	55
2015	Expression pattern shifts following duplication indicative of subfunctionalization and neofunctionalization in regulatory genes of Arabidopsis. 2006 , 23, 469-78	238
2014	Gene expression profiling reveals reproducible human lung adenocarcinoma subtypes in multiple independent patient cohorts. 2006 , 24, 5079-90	207

(2006-2006)

2013	RankProd: a bioconductor package for detecting differentially expressed genes in meta-analysis. 2006 , 22, 2825-7	566
2012	Genetic and transcriptional analysis of the siderophore malleobactin biosynthesis and transport genes in the human pathogen Burkholderia pseudomallei K96243. 2006 , 188, 1551-66	49
2011	Transcriptome and phenotypic responses of Vibrio cholerae to increased cyclic di-GMP level. 2006 , 188, 3600-13	146
2010	A survey of essential gene function in the yeast cell division cycle. 2006 , 17, 4736-47	74
2009	COPAcancer outlier profile analysis. 2006 , 22, 2950-1	90
2008	An RNA interference-based screen identifies MAP4K4/NIK as a negative regulator of PPARgamma, adipogenesis, and insulin-responsive hexose transport. 2006 , 103, 2087-92	125
2007	Large expression differences in genes for iron and zinc homeostasis, stress response, and lignin biosynthesis distinguish roots of Arabidopsis thaliana and the related metal hyperaccumulator Thlaspi caerulescens. 2006 , 142, 1127-47	407
2006	Gene expression profiling of nephrotoxicity from the sevoflurane degradation product fluoromethyl-2,2-difluoro-1-(trifluoromethyl)vinyl ether ("compound A") in rats. 2006 , 90, 419-31	54
2005	CARMAweb: comprehensive R- and bioconductor-based web service for microarray data analysis. 2006 , 34, W498-503	187
2004	arrayQCplot: software for checking the quality of microarray data. 2006 , 22, 2305-7	9
2003	Targeted ablation of Arnt in mouse epidermis results in profound defects in desquamation and epidermal barrier function. 2006 , 119, 4901-12	44
2002	Genome-wide differences between microsatellite stable and unstable colorectal tumors. 2006 , 27, 419-28	61
2001	An oligonucleotide microarray for mouse imprinted genes profiling. 2006 , 113, 253-61	5
2 000	Acute myeloid leukemia-associated Mkl1 (Mrtf-a) is a key regulator of mammary gland function. 2006 , 26, 5809-26	130
1999	Testicular gene expression profiling following prepubertal rat mono-(2-ethylhexyl) phthalate exposure suggests a common initial genetic response at fetal and prepubertal ages. 2006 , 93, 369-81	46
1998	Maternal care effects on the hippocampal transcriptome and anxiety-mediated behaviors in the offspring that are reversible in adulthood. 2006 , 103, 3480-5	641
1997	Dry work in a wet world: computation in systems biology. 2006 , 2, 40	14
1996	Transcriptional coordination of the metabolic network in Arabidopsis. 2006 , 142, 762-74	163

1995	Reproducible epidemiologic research. 2006 , 163, 783-9	166
1994	Development of a guinea pig immune response-related microarray and its use to define the host response following Mycobacterium bovis BCG vaccination. 2006 , 74, 1436-41	29
1993	Complex genomic alterations and gene expression in acute lymphoblastic leukemia with intrachromosomal amplification of chromosome 21. 2006 , 103, 8167-72	126
1992	A dominant function of IKK/NF-kappaB signaling in global lipopolysaccharide-induced gene expression. 2006 , 281, 31142-51	54
1991	Differences in gene expression between the classical and El Tor biotypes of Vibrio cholerae O1. 2006 , 74, 3633-42	65
1990	Improving reliability and performance of DNA microarrays. 2006 , 6, 481-92	11
1989	Dynamics of global transcriptome in bovine matured oocytes and preimplantation embryos. 2006 , 103, 18905-10	114
1988	Improving identification of differentially expressed genes by integrative analysis of Affymetrix and Illumina arrays. 2006 , 10, 369-80	6
1987	High-resolution global genomic survey of 178 gliomas reveals novel regions of copy number alteration and allelic imbalances. 2006 , 66, 9428-36	105
1986	STABILIZED1, a stress-upregulated nuclear protein, is required for pre-mRNA splicing, mRNA turnover, and stress tolerance in Arabidopsis. 2006 , 18, 1736-49	155
1985	GALGO: an R package for multivariate variable selection using genetic algorithms. 2006, 22, 1154-6	101
1984	The zinc-finger factor Insm1 (IA-1) is essential for the development of pancreatic beta cells and intestinal endocrine cells. 2006 , 20, 2465-78	157
1983	Identification of novel Th2-associated genes in T memory responses to allergens. 2006 , 176, 4766-77	39
1982	Neurotoxic protein expression reveals connections between the circadian clock and mating behavior in Drosophila. 2006 , 103, 13537-42	29
1981	Gene expression in human thyrocytes and autonomous adenomas reveals suppression of negative feedbacks in tumorigenesis. 2006 , 103, 413-8	51
1980	Analysis of variance of microarray data. 2006 , 411, 214-33	26
1979	Aryl hydrocarbon receptor regulates distinct dioxin-dependent and dioxin-independent gene batteries. 2006 , 69, 140-53	263
1978	The landscape of histone modifications across 1% of the human genome in five human cell lines. 2007 , 17, 691-707	315

1977	A faster circular binary segmentation algorithm for the analysis of array CGH data. 2007 , 23, 657-63	688
1976	An integrated view of gene expression and solute profiles of Arabidopsis tumors: a genome-wide approach. 2006 , 18, 3617-34	92
1975	Single-cell transcript profiling of barley attacked by the powdery mildew fungus. 2007, 20, 235-46	39
1974	Evidence of spatially bound gene regulation in Mus musculus: decreased gene expression proximal to microRNA genomic location. 2007 , 104, 5020-5	2
1973	beadarray: R classes and methods for Illumina bead-based data. 2007 , 23, 2183-4	398
1972	The Stanford Microarray Database: implementation of new analysis tools and open source release of software. 2007 , 35, D766-70	130
1971	Limited capacity of human adult islets expanded in vitro to redifferentiate into insulin-producing beta-cells. 2007 , 56, 703-8	59
1970	Identification of aberrant chromosomal regions from gene expression microarray studies applied to human breast cancer. 2007 , 23, 2273-80	25
1969	Quantitative gene expression deregulation in mantle-cell lymphoma: correlation with clinical and biologic factors. 2007 , 25, 2770-7	48
1968	Genome-wide profiling identifies epithelial cell genes associated with asthma and with treatment response to corticosteroids. 2007 , 104, 15858-63	627
1967	Global transcriptional responses to cisplatin in Dictyostelium discoideum identify potential drug targets. 2007 , 104, 15406-11	16
1966	Transcriptomic and phenotypic analyses suggest a network between the transcriptional regulators HrcA and sigmaB in Listeria monocytogenes. 2007 , 73, 7981-91	54
1965	Functional genomic analysis reveals cross-talk between peroxisome proliferator-activated receptor gamma and calcium signaling in human colorectal cancer cells. 2007 , 282, 23387-401	22
1964	Genome-wide analysis of histone lysine methylation variations caused by diabetic conditions in human monocytes. 2007 , 282, 13854-63	136
1963	Genome-wide analyses of human perisylvian cerebral cortical patterning. 2007 , 104, 17849-54	156
1962	MPP: a microarray-to-phylogeny pipeline for analysis of gene and marker content datasets. 2007 , 23, 1023-5	4
1961	Fundamental differences in cell cycle deregulation in human papillomavirus-positive and human papillomavirus-negative head/neck and cervical cancers. 2007 , 67, 4605-19	351
1960	Gene expression profiling of the human maternal-fetal interface reveals dramatic changes between midgestation and term. 2007 , 148, 1059-79	151

1959	oneChannelGUI: a graphical interface to Bioconductor tools, designed for life scientists who are not familiar with R language. 2007 , 23, 3406-8	89
1958	Strand-specific 5'-O-methylation of siRNA duplexes controls guide strand selection and targeting specificity. 2008 , 14, 263-74	148
1957	Integration of expression profiles and genetic mapping data to identify candidate genes in intracranial aneurysm. 2007 , 32, 45-57	27
1956	Adaptive gene expression divergence inferred from population genomics. 2007 , 3, 2007-13	45
1955	CALIB: a Bioconductor package for estimating absolute expression levels from two-color microarray data. 2007 , 23, 1700-1	3
1954	Annotation-based distance measures for patient subgroup discovery in clinical microarray studies. 2007 , 23, 2256-64	11
1953	Slc7a7 disruption causes fetal growth retardation by downregulating Igf1 in the mouse model of lysinuric protein intolerance. 2007 , 293, C191-8	38
1952	Phenotypic and transcriptomic analyses demonstrate interactions between the transcriptional regulators CtsR and Sigma B in Listeria monocytogenes. 2007 , 73, 7967-80	51
1951	A novel plasmid-based microarray screen identifies suppressors of rrp6Delta in Saccharomyces cerevisiae. 2007 , 27, 1044-55	12
1950	Conservation of regional gene expression in mouse and human brain. 2007 , 3, e59	78
1949	Improved detection of overrepresentation of Gene-Ontology annotations with parent child analysis. 2007 , 23, 3024-31	283
1948	The regulatory code for transcriptional response diversity and its relation to genome structural properties in A. thaliana. 2007 , 3, e11	84
1947	Mediante: a web-based microarray data manager. 2007 , 23, 1304-6	27
1946	Integration of genome and chromatin structure with gene expression profiles to predict c-MYC recognition site binding and function. 2007 , 3, e63	26
1945	Prediction of gene expression in embryonic structures of Drosophila melanogaster. 2007 , 3, e144	13
1944	Genome-wide analysis of PPARalpha activation in murine small intestine. 2007 , 30, 192-204	105
1943	Comparing the DNA hypermethylome with gene mutations in human colorectal cancer. 2007 , 3, 1709-23	272
1942	X:Map: annotation and visualization of genome structure for Affymetrix exon array analysis. 2008 , 36, D780-6	56

1941	2007, 30, 342-53	48
1940	Transcript specificity in yeast pre-mRNA splicing revealed by mutations in core spliceosomal components. 2007 , 5, e90	153
1939	Query-driven module discovery in microarray data. 2007 , 23, 2573-80	19
1938	Bayesian Model-Based Clustering Procedures. 2007 , 16, 526-558	116
1937	A high-resolution map of segmental DNA copy number variation in the mouse genome. 2007 , 3, e3	178
1936	Unbiased gene expression analysis implicates the huntingtin polyglutamine tract in extra-mitochondrial energy metabolism. 2007 , 3, e135	63
1935	Signalling pathways involved in adult heart formation revealed by gene expression profiling in Drosophila. 2007 , 3, 1907-21	57
1934	Intestinal phenotype of variable-weight cystic fibrosis knockout mice. 2007 , 293, G222-9	23
1933	Proteomic and microarray analyses of the Dictyostelium Zak1-GSK-3 signaling pathway reveal a role in early development. 2007 , 6, 245-52	14
1932	Unmasking activation of the zygotic genome using chromosomal deletions in the Drosophila embryo. 2007 , 5, e117	201
1931	Transcript profiling of the anoxic rice coleoptile. 2007 , 144, 218-31	245
1930	Relationships between early inflammatory response to bleomycin and sensitivity to lung fibrosis: a role for dipeptidyl-peptidase I and tissue inhibitor of metalloproteinase-3?. 2007 , 176, 1098-107	16
1929	Differential gene expression of p27Kip1 and Rb knockout pituitary tumors associated with altered growth and angiogenesis. 2007 , 6, 750-7	22
1928	Filtering genes to improve sensitivity in oligonucleotide microarray data analysis. 2007, 35, e102	33
1927	Expression of a tumor-related gene network increases in the mammalian hypothalamus at the time of female puberty. 2007 , 148, 5147-61	73
1926	CoCo: a web application to display, store and curate ChIP-on-chip data integrated with diverse types of gene expression data. 2007 , 23, 771-3	
1925	LPIN2 is associated with type 2 diabetes, glucose metabolism, and body composition. 2007 , 56, 3020-6	42
1924	The high-level similarity of some disparate gene expression measures. 2007 , 23, 3032-8	13

A Review of: DNA Microarrays and Related Genomics Techniques: Design, Analysis, and Interpretation of Experiments Dby D. B. Allison, G. P. Page, T. M. Beasley, and J. W. Edwards (Eds.). **2007**, 17, 187-190

1922	Arabidopsis transcriptome changes in response to phloem-feeding silverleaf whitefly nymphs. Similarities and distinctions in responses to aphids. 2007 , 143, 849-65	279
1921	Evolutionary-conserved gene expression response profiles across mammalian tissues. 2007 , 11, 96-115	6
1920	Mycobacterial lipomannan induces granuloma macrophage fusion via a TLR2-dependent, ADAM9-and beta1 integrin-mediated pathway. 2007 , 178, 3161-9	81
1919	Altered regulation of the PINK1 locus: a link between type 2 diabetes and neurodegeneration?. 2007 , 21, 3653-65	69
1918	VISDA: an open-source caBIG analytical tool for data clustering and beyond. 2007 , 23, 2024-7	15
1917	SNPchip: R classes and methods for SNP array data. 2007 , 23, 627-8	13
1916	Characterization of the VIER F-BOX PROTEINE genes from Arabidopsis reveals their importance for plant growth and development. 2007 , 19, 1163-78	44
1915	The plant signal salicylic acid shuts down expression of the vir regulon and activates quormone-quenching genes in Agrobacterium. 2007 , 104, 11790-5	131
1914	Microarray-based characterization of the Listeria monocytogenes cold regulon in log- and stationary-phase cells. 2007 , 73, 6484-98	91
1913	Regulation of Vibrio polysaccharide synthesis and virulence factor production by CdgC, a GGDEF-EAL domain protein, in Vibrio cholerae. 2007 , 189, 717-29	60
1912	Complement induction in spinal cord microglia results in anaphylatoxin C5a-mediated pain hypersensitivity. 2007 , 27, 8699-708	176
1911	Genome-wide mapping and analysis of active promoters in mouse embryonic stem cells and adult organs. 2008 , 18, 46-59	95
1910	Transcriptomic analysis identifies growth rate modulation as a component of the adaptation of mycobacteria to survival inside the macrophage. 2007 , 189, 3969-76	43
1909	An Arabidopsis gene network based on the graphical Gaussian model. 2007 , 17, 1614-25	194
1908	MAGMA: analysis of two-channel microarrays made easy. 2007 , 35, W86-90	15
1907	Temperature-dependent expression of Listeria monocytogenes internalin and internalin-like genes suggests functional diversity of these proteins among the listeriae. 2007 , 73, 2806-14	55
1906	Extracting biology from high-dimensional biological data. 2007 , 210, 1507-17	38

1905	Antisense artiracts in transcriptome microarray experiments are resolved by actinomycin D. 2007 , 35, e128	162
1902	Changes in gene expression induced by tienilic Acid and sulfamethoxazole: testing the danger hypothesis. 2007 , 4, 253-66	15
1903	Reduced expression of succinyl-coenzyme A ligase can be compensated for by up-regulation of the gamma-aminobutyrate shunt in illuminated tomato leaves. 2007 , 145, 626-39	133
1902	Genomewide and biochemical analyses of DNA-binding activity of Cdc6/Orc1 and Mcm proteins in Pyrococcus sp. 2007 , 35, 3214-22	28
1901	A role for transcriptional repressor methyl-CpG-binding protein 2 and plasticity-related gene serum- and glucocorticoid-inducible kinase 1 in the induction of inflammatory pain states. 2007 , 27, 6163-73	86
1900	Microarray analysis using disiloxyl 70mer oligonucleotides. 2008 , 36, 1334-42	
1899	IFN-gamma alters the response of Borrelia burgdorferi-activated endothelium to favor chronic inflammation. 2007 , 178, 1172-9	32
1898	Influenza virus infection causes global respiratory tract B cell response modulation via innate immune signals. 2007 , 178, 1457-67	56
1897	IlluminaGUI: graphical user interface for analyzing gene expression data generated on the Illumina platform. 2007 , 23, 1431-3	13
1896	Gene expression network analysis and applications to immunology. 2007 , 23, 850-8	116
1895	Increased cortical expression of two synaptogenic thrombospondins in human brain evolution. 2007 , 17, 2312-21	78
1894	Comparison of human protein-protein interaction maps. 2007 , 23, 605-11	75
1893	Maize histone deacetylase hda101 is involved in plant development, gene transcription, and sequence-specific modulation of histone modification of genes and repeats. 2007 , 19, 1145-62	55
1892	CSR1, the sole target of imidazolinone herbicide in Arabidopsis thaliana. 2007 , 48, 1340-58	61
1891	Chromosomal rearrangement interferes with meiotic X chromosome inactivation. 2007 , 17, 1431-7	75
1890	Effect of 21 different nitrogen sources on global gene expression in the yeast Saccharomyces cerevisiae. 2007 , 27, 3065-86	171
1889	Expression profiling of Huntington's disease models suggests that brain-derived neurotrophic factor depletion plays a major role in striatal degeneration. 2007 , 27, 11758-68	183

1887	The fou2 gain-of-function allele and the wild-type allele of Two Pore Channel 1 contribute to different extents or by different mechanisms to defense gene expression in Arabidopsis. 2007 , 48, 1775-89	53
1886	AffyProbeMiner: a web resource for computing or retrieving accurately redefined Affymetrix probe sets. 2007 , 23, 2385-90	62
1885	Temporal and spatial transcriptional profiles of aging in Drosophila melanogaster. 2007, 17, 1236-43	67
1884	Genetic effects of a titanium surface on osteoblasts: a meta-analysis. 2007 , 49, 299-309	11
1883	Random-set methods identify distinct aspects of the enrichment signal in gene-set analysis. 2007 , 1, 85	172
1882	Boosting Algorithms: Regularization, Prediction and Model Fitting. 2007 , 22, 477	484
1881	Transcriptomic analysis of the cardiac left ventricle in a rodent model of diabetic cardiomyopathy: molecular snapshot of a severe myocardial disease. 2007 , 28, 284-93	22
1880	Germinal Center B Cell-Like (GCB) and Activated B Cell-Like (ABC) Type of Diffuse Large B Cell Lymphoma (DLBCL): Analysis of Molecular Predictors, Signatures, Cell Cycle State and Patient Survival. 2007 , 3, 117693510700300	36
1879	The gene expression profile of nodal peripheral T-cell lymphoma demonstrates a molecular link between angioimmunoblastic T-cell lymphoma (AITL) and follicular helper T (TFH) cells. 2007 , 109, 4952-63	445
1878	Lesional gene expression profiling in cutaneous T-cell lymphoma reveals natural clusters associated with disease outcome. 2007 , 110, 3015-27	96
1877	Endothelial progenitor cell derived microvesicles activate an angiogenic program in endothelial cells by a horizontal transfer of mRNA. 2007 , 110, 2440-8	760
1876	Angiogenesis soluble factors as hepatocellular carcinoma noninvasive markers for monitoring hepatitis C virus cirrhotic patients awaiting liver transplantation. 2007 , 84, 1262-71	48
1875	Changes in breast cancer transcriptional profiles after treatment with the aromatase inhibitor, letrozole. 2007 , 17, 813-26	82
1874	Genes associated with progression and recurrence of hepatocellular carcinoma in hepatitis C patients waiting and undergoing liver transplantation: preliminary results. 2007 , 83, 973-81	22
1873	Current molecular techniques for the detection of microbial pathogens. 2007 , 90, 29-50	18
1872	Effects of rifampicin on global gene expression in human small intestine. 2007 , 17, 907-18	20
1871	Establishing the molecular pathways involved in chronic allograft nephropathy for testing new noninvasive diagnostic markers. 2007 , 83, 448-57	65
1870	Understanding sample size: what determines the required number of microarrays for an experiment?. 2007 , 12, 46-50	29

1869	Genomic organization of transcriptomes in mammals: Coregulation and cofunctionality. 2007 , 89, 580-7	•	50
1868	Gene expression profiling in the adult Down syndrome brain. 2007 , 90, 647-60		172
1867	Gene expression shifts during perithecium development in Gibberella zeae (anamorph Fusarium graminearum), with particular emphasis on ion transport proteins. 2007 , 44, 1146-56		71
1866	NEDD4-1 is a proto-oncogenic ubiquitin ligase for PTEN. 2007 , 128, 129-39		524
1865	Gene expression profiles in zebrafish (Danio rerio) liver cells exposed to a mixture of pharmaceuticals at environmentally relevant concentrations. 2007 , 70, 65-73		51
1864	ATF6alpha optimizes long-term endoplasmic reticulum function to protect cells from chronic stress. 2007 , 13, 351-64		504
1863	Control of plant organ size by KLUH/CYP78A5-dependent intercellular signaling. 2007, 13, 843-56		257
1862	DNA microarray analysis reveals a role for lysophosphatidic acid in the regulation of anti-inflammatory genes in MC3T3-E1 cells. 2007 , 41, 833-41		13
1861	Classification of neuroblastoma patients by published gene-expression markers reveals a low sensitivity for unfavorable courses of MYCN non-amplified disease. 2007 , 250, 250-67		22
1860	Phenotypic expansion of the supernumerary derivative (22) chromosome syndrome: VACTERL and Hirschsprung's disease. 2007 , 42, 1928-32		20
1859	Aromatase inhibitorsgene discovery. 2007 , 106, 130-42		22
1858	Resveratrol inhibits pancreatic cancer cell proliferation through transcriptional induction of macrophage inhibitory cytokine-1. 2007 , 138, 163-9		63
1857	Comparative analysis of a 3' end tag PCR and a linear RNA amplification approach for microarray analysis. 2007 , 127, 638-46		6
1856	Gene-expression variation within and among human populations. 2007 , 80, 502-9		259
1855	Identification of the transcriptional targets of FOXP2, a gene linked to speech and language, in developing human brain. 2007 , 81, 1144-57		203
1854	Transcriptional profiling of melanocytes from patients with vitiligo vulgaris. 2008, 21, 162-71		40
1853	Aging impacts transcriptomes but not genomes of hormone-dependent breast cancers. 2007 , 9, R59		53
1852	Gene expression profiling of Hfe-/- liver and duodenum in mouse strains with differing susceptibilities to iron loading: identification of transcriptional regulatory targets of Hfe and potential hemochromatosis modifiers. <i>Genome Biology</i> , 2007 , 8, R221	18.3	15

1851	Perturbation of gene expression of the chromatin remodeling pathway in premature newborns at risk for bronchopulmonary dysplasia. <i>Genome Biology</i> , 2007 , 8, R210	18.3	33
1850	MicroRNA expression profiling of human breast cancer identifies new markers of tumor subtype. <i>Genome Biology</i> , 2007 , 8, R214	18.3	742
1849	Identification of novel stem cell markers using gap analysis of gene expression data. <i>Genome Biology</i> , 2007 , 8, R193	18.3	9
1848	DetectiV: visualization, normalization and significance testing for pathogen-detection microarray data. <i>Genome Biology</i> , 2007 , 8, R190	18.3	20
1847	Reversible and permanent effects of tobacco smoke exposure on airway epithelial gene expression. <i>Genome Biology</i> , 2007 , 8, R201	18.3	169
1846	PyCogent: a toolkit for making sense from sequence. <i>Genome Biology</i> , 2007 , 8, R171	18.3	151
1845	Global analysis of patterns of gene expression during Drosophila embryogenesis. <i>Genome Biology</i> , 2007 , 8, R145	18.3	307
1844	Celsius: a community resource for Affymetrix microarray data. <i>Genome Biology</i> , 2007 , 8, R112	18.3	54
1843	Estimation and correction of non-specific binding in a large-scale spike-in experiment. <i>Genome Biology</i> , 2007 , 8, R126	18.3	15
1842	Morphine effects on striatal transcriptome in mice. <i>Genome Biology</i> , 2007 , 8, R128	18.3	60
1841	Genetic background influences murine prostate gene expression: implications for cancer phenotypes. <i>Genome Biology</i> , 2007 , 8, R117	18.3	18
1840	Correcting for sequence biases in present/absent calls. <i>Genome Biology</i> , 2007 , 8, R125	18.3	25
1839	Global transcriptional responses of fission and budding yeast to changes in copper and iron levels: a comparative study. <i>Genome Biology</i> , 2007 , 8, R73	18.3	44
1838	Tilescope: online analysis pipeline for high-density tiling microarray data. <i>Genome Biology</i> , 2007 , 8, R81	18.3	37
1837	An annotation infrastructure for the analysis and interpretation of Affymetrix exon array data. <i>Genome Biology</i> , 2007 , 8, R79	18.3	38
1836	Characterizing the expression of the human olfactory receptor gene family using a novel DNA microarray. <i>Genome Biology</i> , 2007 , 8, R86	18.3	136
1835	Global analyses of mRNA translational control during early Drosophila embryogenesis. <i>Genome Biology</i> , 2007 , 8, R63	18.3	68
1834	Functional dissection of the ash2 and ash1 transcriptomes provides insights into the transcriptional basis of wing phenotypes and reveals conserved protein interactions. <i>Genome Biology</i> , 2007 , 8, R67	18.3	29

1833	Integration of Arabidopsis thaliana stress-related transcript profiles, promoter structures, and cell-specific expression. <i>Genome Biology</i> , 2007 , 8, R49	18.3	182
1832	Normalization of boutique two-color microarrays with a high proportion of differentially expressed probes. <i>Genome Biology</i> , 2007 , 8, R2	18.3	54
1831	Microarray gene expression profiling of osteoarthritic bone suggests altered bone remodelling, WNT and transforming growth factor-beta/bone morphogenic protein signalling. 2007 , 9, R100		136
1830	Analysis of expression data: an overview. 2007 , Chapter 11, Unit11.4		1
1829	Clustering IClass Discovery in the Post-Genomic Era. 2007, 123-148		1
1828	Blood and lymphatic endothelial cell-specific differentiation programs are stringently controlled by the tissue environment. 2007 , 109, 4777-85		102
1827	Genome-wide expression profiling of lymphoblastoid cell lines distinguishes different forms of autism and reveals shared pathways. 2007 , 16, 1682-98		248
1826	Cancer outlier differential gene expression detection. 2007 , 8, 566-75		71
1825	GridR: An R-Based Grid-Enabled Tool for Data Analysis in ACGT Clinico-Genomics Trials. 2007,		10
1824	Quality Assessment of Affymetrix GeneChip Data using the EM Algorithm and a Naive Bayes Classifier. 2007 ,		1
1823	A blocking strategy to improve gene selection for classification of gene expression data. 2007 , 4, 293-3	00	26
1822	The early response to acid shock in Lactobacillus reuteri involves the ClpL chaperone and a putative cell wall-altering esterase. 2007 , 73, 3924-35		100
1821	Semiparametric RMA Background-Correction for Oligonucleotide Arrays. 2007,		
1820	pcaMethodsa bioconductor package providing PCA methods for incomplete data. 2007 , 23, 1164-7		667
1819	Codelink: an R package for analysis of GE healthcare gene expression bioarrays. 2007 , 23, 1168-9		16
1818	Multicenter study of acetaminophen hepatotoxicity reveals the importance of biological endpoints in genomic analyses. 2007 , 99, 326-37		69
1817	A distribution free summarization method for Affymetrix GeneChip arrays. 2007 , 23, 321-7		76
1816	Comparison of the cytotoxicity of the nitroaromatic drug flutamide to its cyano analogue in the hepatocyte cell line TAMH: evidence for complex I inhibition and mitochondrial dysfunction using toxicogenomic screening. 2007 , 20, 1277-90		47

1815	PANP - a New Method of Gene Detection on Oligonucleotide Expression Arrays. 2007,	13
1814	Gene Expression Profile of Chronic Myeloid Leukemia Innately Resistant to Imatinib. 2007 , 1, 234-242	4
1813	Interferon-alpha resistance associated genes in renal cell carcinoma identified by expression profiling. 2007 , 177, 1264-8; discussion 1268	4
1812	Molecular characterisation of the early response in pigs to experimental infection with Actinobacillus pleuropneumoniae using cDNA microarrays. 2007 , 49, 11	23
1811	Transcriptional profiling of bipotential embryonic liver cells to identify liver progenitor cell surface markers. 2007 , 25, 2476-87	28
1810	Isolation and characterization of mesoangioblasts from facioscapulohumeral muscular dystrophy muscle biopsies. 2007 , 25, 3173-82	37
1809	Diesel exhaust inhalation and assessment of peripheral blood mononuclear cell gene transcription effects: an exploratory study of healthy human volunteers. 2007 , 19, 1107-19	80
1808	Analysis of expression data: an overview. 2007 , Chapter 7, Unit 7.1	7
1807	Genomic and functional studies of Drosophila sex hierarchy regulated gene expression in adult head and nervous system tissues. 2007 , 3, e216	98
1806	An assessment of the role of DNA adenine methyltransferase on gene expression regulation in E coli. 2007 , 2, e273	11
1805	Altered T-cell function in schizophrenia: a cellular model to investigate molecular disease mechanisms. 2007 , 2, e692	73
1804	Detection of novel amplicons in prostate cancer by comprehensive genomic profiling of prostate cancer cell lines using oligonucleotide-based arrayCGH. 2007 , 2, e769	14
1803	Gene expression analysis of in vivo fluorescent cells. 2007 , 2, e1151	31
1802	Rapid changes in gene expression dynamics in response to superoxide reveal SoxRS-dependent and independent transcriptional networks. 2007 , 2, e1186	93
1801	Mapping of trans-acting regulatory factors from microarray data. 2007, 1 Suppl 1, S155	2
1800	Effects on linkage analyses of different Affymetrix expression measures as quantitative trait phenotypes. 2007 , 1 Suppl 1, S158	1
1799	Conjugated linoleic acid alters global gene expression in human intestinal-like Caco-2 cells in an isomer-specific manner. 2007 , 137, 2359-65	24
1798	Up-regulation of tissue factor in human pulmonary artery endothelial cells after ultrafine particle exposure. 2007 , 115, 535-40	51

1797	High correspondence between Affymetrix exon and standard expression arrays. 2007, 42, 181-5	44
1796	Integrating functional knowledge during sample clustering for microarray data using unsupervised decision trees. 2007 , 49, 214-29	4
1795	Functional genome-wide analysis of antibody producing NS0 cell line cultivated at different temperatures. 2007 , 98, 616-30	25
1794	Altered gene expression in mice with lupus treated with edratide, a peptide that ameliorates the disease manifestations. 2007 , 56, 2371-81	11
1793	Salivary proteomic and genomic biomarkers for primary Sjgren's syndrome. 2007 , 56, 3588-600	285
1792	Transforming properties of TC-1 in human breast cancer: interaction with FGFR2 and beta-catenin signaling pathways. 2007 , 121, 1265-73	24
1791	Heterogeneous expression of Wnt/beta-catenin target genes within colorectal cancer. 2007, 121, 1941-8	93
1790	Temporal evolution of gene expression in rat carotid artery following balloon angioplasty. 2007 , 101, 399-410	34
1789	Identification of novel genes expressed during mouse tooth development by microarray gene expression analysis. 2007 , 236, 2245-57	19
1788	Etiology-dependent molecular mechanisms in human hepatocarcinogenesis. 2008, 47, 511-20	140
1787	Multi-group cancer outlier differential gene expression detection. 2007, 31, 65-71	9
1786	Functional gene expression differences between inbred alcohol-preferring and -non-preferring rats in five brain regions. 2007 , 41, 95-132	98
1785	Statistical methods for the analysis of high-throughput data based on functional profiles derived from the Gene Ontology. 2007 , 137, 3975-3989	14
1784	Faced with inequality: chicken do not have a general dosage compensation of sex-linked genes. 2007 , 5, 40	186
1783	DeltaNp63 isoforms regulate CD44 and keratins 4, 6, 14 and 19 in squamous cell carcinoma of head and neck. 2007 , 213, 384-91	48
1782	Proteomic analysis of protein expression changes in a model of gliomagenesis. 2007 , 1, 1485-98	0
1782 1781	Proteomic analysis of protein expression changes in a model of gliomagenesis. 2007, 1, 1485-98 Compensation and specificity of function within the E2F family. 2007, 26, 321-7	74

1779	Effective use of microarrays in neuroendocrine research. 2007 , 19, 145-61	4
1778	Regulatory T cell development in the absence of functional Foxp3. 2007 , 8, 359-68	374
1777	A critical developmental switch defines the kinetics of kidney cyst formation after loss of Pkd1. 2007 , 13, 1490-5	308
1776	Analysis and validation of proteomic data generated by tandem mass spectrometry. 2007 , 4, 787-97	523
1775	Beyond standardization: dynamic software infrastructures for systems biology. 2007 , 8, 235-43	39
1774	Evaluation of STOX1 as a preeclampsia candidate gene in a population-wide sample. 2007 , 15, 494-7	38
1773	Painting of fourth and chromosome-wide regulation of the 4th chromosome in Drosophila melanogaster. 2007 , 26, 2307-16	57
1772	Gene expression shift towards normal B cells, decreased proliferative capacity and distinct surface receptors characterize leukemic blasts persisting during induction therapy in childhood acute lymphoblastic leukemia. 2007 , 21, 897-905	33
1771	Identification of genetic alterations in pancreatic cancer by the combined use of tissue microdissection and array-based comparative genomic hybridisation. 2007 , 96, 373-82	34
1770	Rhythmic growth explained by coincidence between internal and external cues. 2007, 448, 358-61	515
1769	Constraint and turnover in sex-biased gene expression in the genus Drosophila. 2007, 450, 233-7	229
1768	Demasculinization of X chromosomes in the Drosophila genus. 2007 , 450, 238-41	181
1767	Coordinated regulation of maize genes during increasing exposure to ultraviolet radiation: identification of ultraviolet-responsive genes, functional processes and associated potential promoter motifs. 2007 , 5, 677-95	16
1766	Growth-phase-dependent gene expression profiling of poplar (Populus alba x Populus tremula var. glandulosa) suspension cells. 2007 , 131, 599-613	14
1765	Identification of candidate transcriptional modulators involved in successful regeneration after nerve injury. 2007 , 25, 3629-37	101
1764	Pyrethroid tolerance is associated with elevated expression of antioxidants and agricultural practice in Anopheles arabiensis sampled from an area of cotton fields in Northern Cameroon. 2008 , 17, 1145-55	111
1763	Smooth to rugose phase variation in Vibrio cholerae can be mediated by a single nucleotide change that targets c-di-GMP signalling pathway. 2007 , 63, 995-1007	89
1762	Production of trans-Neptunian binaries through chaos-assisted capture. 2007 , 379, 229-246	37

1761	shows common quantitative patterns of gene expression directed by environmentally specific sensing. 2007 , 51, 60-78	225
1760	Mitochondrial type-I prohibitins of Arabidopsis thaliana are required for supporting proficient meristem development. 2007 , 52, 850-64	103
1759	The Arabidopsis her1 mutant implicates GABA in E-2-hexenal responsiveness. 2008, 53, 197-213	72
1758	Integrative functional genomics of salt acclimatization in the model legume Lotus japonicus. 2008 , 53, 973-87	156
1757	Differentially expressed genes between high-risk human papillomavirus types in human cervical cancer cells. 2007 , 17, 484-91	15
1756	Identification of candidate genes for alcohol preference by expression profiling of congenic rat strains. 2007 , 31, 1089-98	34
1755	Transcriptome analysis reveals altered cholesterol metabolism during the neurodegeneration in mouse scrapie model. 2007 , 102, 834-47	38
1754	Transcriptional response to aging and caloric restriction in heart and adipose tissue. 2007 , 6, 673-88	77
1753	Selection for contextual fear conditioning affects anxiety-like behaviors and gene expression. 2007 , 6, 736-49	75
1752	Identification of a robust gene signature that predicts breast cancer outcome in independent data sets. 2007 , 7, 61	29
1751	Cross-study analysis of gene expression data for intermediate neuroblastoma identifies two biological subtypes. 2007 , 7, 89	25
1750	Transcript-based redefinition of grouped oligonucleotide probe sets using AceView: high-resolution annotation for microarrays. 2007 , 8, 108	45
1749	A full Bayesian hierarchical mixture model for the variance of gene differential expression. 2007, 8, 124	6
1748	Interpretation of multiple probe sets mapping to the same gene in Affymetrix GeneChips. 2007, 8, 13	58
1747	Supervised multivariate analysis of sequence groups to identify specificity determining residues. 2007 , 8, 135	19
1746	Ringoan R/Bioconductor package for analyzing ChIP-chip readouts. 2007 , 8, 221	134
1745	A transversal approach to predict gene product networks from ontology-based similarity. 2007 , 8, 235	43
1744	Post hoc pattern matching: assigning significance to statistically defined expression patterns in single channel microarray data. 2007 , 8, 240	15

1743	The utility of MAS5 expression summary and detection call algorithms. 2007, 8, 273	122
1742	A framework for significance analysis of gene expression data using dimension reduction methods. 2007 , 8, 346	30
1741	Linking microarray reporters with protein functions. 2007 , 8, 360	12
1740	Weighted analysis of general microarray experiments. 2007 , 8, 387	13
1739	Bioinformatic identification of novel putative photoreceptor specific cis-elements. 2007, 8, 407	4
1738	Prediction potential of candidate biomarker sets identified and validated on gene expression data from multiple datasets. 2007 , 8, 415	20
1737	Application of a correlation correction factor in a microarray cross-platform reproducibility study. 2007 , 8, 447	6
1736	Transcription factor target prediction using multiple short expression time series from Arabidopsis thaliana. 2007 , 8, 454	25
1735	In situ analysis of cross-hybridisation on microarrays and the inference of expression correlation. 2007 , 8, 461	55
1734	Cross platform microarray analysis for robust identification of differentially expressed genes. 2007 , 8 Suppl 1, S5	45
1733	A Grid-based solution for management and analysis of microarrays in distributed experiments. 2007 , 8 Suppl 1, S7	7
1732	Graphs in molecular biology. 2007 , 8 Suppl 6, S8	76
1731	Putative null distributions corresponding to tests of differential expression in the Golden Spike dataset are intensity dependent. 2007 , 8, 105	14
1730	Sensitive and robust gene expression changes in fish exposed to estrogena microarray approach. 2007 , 8, 149	50
1729	Cartilage-selective genes identified in genome-scale analysis of non-cartilage and cartilage gene expression. 2007 , 8, 165	17
1728	Genome-wide changes accompanying knockdown of fatty acid synthase in breast cancer. 2007 , 8, 168	38
1727	Normalization of low-density microarray using external spike-in controls: analysis of macrophage cell lines expression profile. 2007 , 8, 17	8
1726	Microarray analysis of gene expression induced by sexual contact in Schistosoma mansoni. 2007 , 8, 181	32

	abdominal aortic aneurysms. 2007 , 8, 237	132
1724	Gene expression of transporters and phase I/II metabolic enzymes in murine small intestine during fasting. 2007 , 8, 267	33
1723	Comparison of protein coding gene contents of the fungal phyla Pezizomycotina and Saccharomycotina. 2007 , 8, 325	38
1722	Cadmium triggers an integrated reprogramming of the metabolism of Synechocystis PCC6803, under the control of the Slr1738 regulator. 2007 , 8, 350	76
1721	Vascular microarray profiling in two models of hypertension identifies caveolin-1, Rgs2 and Rgs5 as antihypertensive targets. 2007 , 8, 404	28
1720	Genome-wide transcriptional analysis of grapevine berry ripening reveals a set of genes similarly modulated during three seasons and the occurrence of an oxidative burst at valison. 2007 , 8, 428	190
1719	Variable sexually dimorphic gene expression in laboratory strains of Drosophila melanogaster. 2007 , 8, 454	26
1718	Unravelling the molecular control of calvarial suture fusion in children with craniosynostosis. 2007 , 8, 458	77
1717	Profiling sex-biased gene expression during parthenogenetic reproduction in Daphnia pulex. 2007 , 8, 464	43
1716	Intercenter reliability and validity of the rhesus macaque GeneChip. 2007 , 8, 61	16
1715	Gene expression profiling of aging reveals activation of a p53-mediated transcriptional program. 2007 , 8, 80	142
1714	Gene function in early mouse embryonic stem cell differentiation. 2007, 8, 85	115
1713	A meta-analysis of kidney microarray datasets: investigation of cytokine gene detection and correlation with rt-PCR and detection thresholds. 2007 , 8, 88	32
1713 1712		32
	correlation with rt-PCR and detection thresholds. 2007, 8, 88 Fisher's combined p-value for detecting differentially expressed genes using Affymetrix expression	
1712	correlation with rt-PCR and detection thresholds. 2007 , 8, 88 Fisher's combined p-value for detecting differentially expressed genes using Affymetrix expression arrays. 2007 , 8, 96	41
1712 1711	Fisher's combined p-value for detecting differentially expressed genes using Affymetrix expression arrays. 2007, 8, 96 A comparative genomics approach to identifying the plasticity transcriptome. 2007, 8, 20 Hematopoietic progenitor cells (HPC) from mobilized peripheral blood display enhanced migration and marrow homing compared to steady-state bone marrow HPC. 2007, 35, 326-34	20

1707	Altered phenotype and gene transcription in endothelial cells, induced by Plasmodium falciparum-infected red blood cells: pathogenic or protective?. 2007 , 37, 975-87	34
1706	Genome wide gene amplifications and deletions in Plasmodium falciparum. 2007 , 155, 33-44	66
1705	Fetal growth restriction is associated with reduced FasL expression by decidual cells. 2007, 74, 7-14	20
1704	Microarray analysis reveals overexpression of CD163 and HO-1 in symptomatic carotid plaques. 2007 , 27, 154-60	45
1703	Issues in biomedical research data management and analysis: needs and barriers. 2007, 14, 478-88	104
1702	Development of a yeast biosensor-biocatalyst for the detection and biodegradation of the organophosphate paraoxon. 2007 , 76, 1383-94	15
1701	cDNA microarray analysis of cyclosporin A (CsA)-treated human peripheral blood mononuclear cells reveal modulation of genes associated with apoptosis, cell-cycle regulation and DNA repair. 2007 , 304, 235-41	2
1700	Microarray analysis reveals potential mechanisms of BRMS1-mediated metastasis suppression. 2007 , 24, 551-65	40
1699	Laser capture microdissection (LCM) and comparative microarray expression analysis of syncytial cells isolated from incompatible and compatible soybean (Glycine max) roots infected by the soybean cyst nematode (Heterodera glycines). 2007 , 226, 1389-409	129
1698	A time-course comparative microarray analysis of an incompatible and compatible response by Glycine max (soybean) to Heterodera glycines (soybean cyst nematode) infection. 2007 , 226, 1423-47	93
1697	Comparison of RNA amplification techniques meeting the demands for the expression profiling of clinical cancer samples. 2007 , 451, 1019-29	9
1696	Gene expression profiling of liver cells after copper overload in vivo and in vitro reveals new copper-regulated genes. 2007 , 12, 495-507	62
1695	The class of microarray games and the relevance index for genes. 2007 , 15, 256-280	30
1694	Identification of marker genes for type 2 diabetes. 2007 , 2, 137	
1693	Sharing and reusing gene expression profiling data in neuroscience. 2007 , 5, 161-75	8
1692	GEMMA IA Grid environment for microarray management and analysis in bone marrow stem cells experiments. 2007 , 23, 382-390	4
1691	Improving cluster-based missing value estimation of DNA microarray data. 2007, 24, 273-82	53
1690	Long-term phytosterol treatment alters gene expression in the liver of apo E-deficient mice. 2008 , 19, 545-554	22

1689	Breast cancer: a candidate gene approach across the estrogen metabolic pathway. 2008 , 108, 137-49	68
1688	Gene expression analyses in individual grape (Vitis vinifera L.) berries during ripening initiation reveal that pigmentation intensity is a valid indicator of developmental staging within the cluster. 2008 , 68, 301-15	76
1687	Potato, Solanum tuberosum, defense against Colorado potato beetle, Leptinotarsa decemlineata (Say): microarray gene expression profiling of potato by Colorado potato beetle regurgitant treatment of wounded leaves. 2008 , 34, 1013-25	61
1686	Exposure to radiation from global system for mobile communications at 1,800 MHz significantly changes gene expression in rat hippocampus and cortex. 2008 , 28, 458-465	16
1685	Extending lattice: using generics and methods to implement new visualization methods within the Trellis framework. 2008 , 23, 565-572	1
1684	Aberrant hypomethylation of the cancer-testis antigen PRAME correlates with PRAME expression in acute myeloid leukemia. 2008 , 87, 809-18	46
1683	Tissue-specific induction of ADAMTS2 in monocytes and macrophages by glucocorticoids. 2008 , 86, 323-32	29
1682	Surveying expression level polymorphism and single-feature polymorphism in near-isogenic wheat lines differing for the Yr5 stripe rust resistance locus. 2008 , 117, 401-11	27
1681	Transcriptional profiling of myotubes from patients with type 2 diabetes: no evidence for a primary defect in oxidative phosphorylation genes. 2008 , 51, 2068-77	45
1680	Expression of enzymes involved in the prostanoid metabolism by cortical astrocytes after LPS-induced inflammation. 2008 , 34, 177-85	43
1679	Global correlation analysis for micro-RNA and mRNA expression profiles in human cell lines. 2008 , 53, 515	72
1678	Rapid selection response for contextual fear conditioning in a cross between C57BL/6J and A/J: behavioral, QTL and gene expression analysis. 2008 , 38, 277-91	22
1677	Stable RNA markers for identification of blood and saliva stains revealed from whole genome expression analysis of time-wise degraded samples. 2008 , 122, 135-42	135
1676	Gene expression in human peripheral blood mononuclear cells upon acute ischemic stroke. 2008 , 255, 723-31	52
1675	Transcriptomics and adaptive genomics of the asymptomatic bacteriuria Escherichia coli strain 83972. 2008 , 279, 523-34	27
1674	Small RNAs and the regulation of cis-natural antisense transcripts in Arabidopsis. 2008 , 9, 6	105
1673	Integrating open-source technologies to build low-cost information systems for improved access to public health data. 2008 , 7, 29	27
1672	Gene expression profiles in liver of pigs with extreme high and low levels of androstenone. 2008 , 4, 29	30

1671	Pro-neural transcription factors as cancer markers. 2008 , 1, 17	24
1670	Generation of a genomic tiling array of the human major histocompatibility complex (MHC) and its application for DNA methylation analysis. 2008 , 1, 19	23
1669	Influence of monolayer, spheroid, and tumor growth conditions on chromosome 3 gene expression in tumorigenic epithelial ovarian cancer cell lines. 2008 , 1, 34	20
1668	The removal of multiplicative, systematic bias allows integration of breast cancer gene expression datasets - improving meta-analysis and prediction of prognosis. 2008 , 1, 42	95
1667	Gene expression analysis of glioblastomas identifies the major molecular basis for the prognostic benefit of younger age. 2008 , 1, 52	153
1666	Discovery of DNA methylation markers in cervical cancer using relaxation ranking. 2008, 1, 57	30
1665	Uncovering mechanisms of transcriptional regulations by systematic mining of cis regulatory elements with gene expression profiles. 2008 , 1, 4	9
1664	Phosphatidylinositol 3-kinase signaling in proliferating cells maintains an anti-apoptotic transcriptional program mediated by inhibition of FOXO and non-canonical activation of NFkappaB transcription factors. 2008 , 9, 6	37
1663	Overexpression of Scg5 increases enzymatic activity of PCSK2 and is inversely correlated with body weight in congenic mice. 2008 , 9, 34	10
1662	An approach to handling and interpretation of ambiguous data in transcriptome and proteome comparisons. 2008 , 8, 1165-9	20
1661	Are protein complexes made of cores, modules and attachments?. 2008, 8, 425-34	28
1660	Comparative proteomic and transcriptional profiling of a bread wheat cultivar and its derived transgenic line overexpressing a low molecular weight glutenin subunit gene in the endosperm. 2008 , 8, 2948-66	62
1659	D¶vu in proteomics. A hit parade of repeatedly identified differentially expressed proteins. 2008 , 8, 1744-9	300
1658	Probing genetic algorithms for feature selection in comprehensive metabolic profiling approach. 2008 , 22, 1312-24	22
1657	A disattenuated correlation estimate when variables are measured with error: illustration estimating cross-platform correlations. 2008 , 27, 1026-39	8
1656	Biomarkers for exposure to estrogenic compounds: gene expression analysis in zebrafish (Danio rerio). 2008 , 23, 15-24	48
1655	Identification of proteins in human substantia nigra. 2008 , 2, 776-82	27
1654	Expression of microRNAs and protein-coding genes associated with perineural invasion in prostate cancer. 2008 , 68, 1152-64	127

1653	Transcriptional changes in insulin- and lipid metabolism-related genes in the hippocampus of olfactory bulbectomized mice. 2008 , 86, 3184-93	4
1652	Transcriptome analysis of serous ovarian cancers identifies differentially expressed chromosome 3 genes. 2008 , 47, 56-65	23
1651	Predicting response and resistance to endocrine therapy: profiling patients on aromatase inhibitors. 2008 , 112, 689-694	22
1650	Automated gating of flow cytometry data via robust model-based clustering. 2008, 73, 321-32	185
1649	RNA expression microarray analysis in mouse prospermatogonia: identification of candidate epigenetic modifiers. 2008 , 237, 1082-9	17
1648	Genome-wide expression profiling during protection from colitis by regulatory T cells. 2008, 14, 75-87	14
1647	Muramyl dipeptide-induced differential gene expression in NOD2 mutant and wild-type Crohn's disease patient-derived dendritic cells. 2008 , 14, 186-94	12
1646	Activation of NF-kappaB by extracellular S100A4: analysis of signal transduction mechanisms and identification of target genes. 2008 , 123, 1301-10	62
1645	Defining the molecular action of HDAC inhibitors and synergism with androgen deprivation in ERG-positive prostate cancer. 2008 , 123, 2774-81	57
1644	Modulation of several waves of gene expression during FGF-1 induced epithelial-mesenchymal transition of carcinoma cells. 2008 , 104, 826-39	47
1643	Genome-wide expression analysis of cells expressing gain of function mutant D374Y-PCSK9. 2008 , 217, 459-67	31
1642	Prolyl endopeptidase is revealed following SILAC analysis to be a novel mediator of human microglial and THP-1 cell neurotoxicity. 2008 , 56, 675-85	29
1641	CAVEman: Standardized anatomical context for biomedical data mapping. 2008, 1, 10-8	11
1640	Aurora kinase B is a predictive factor for the aggressive recurrence of hepatocellular carcinoma after curative hepatectomy. 2008 , 95, 611-9	88
1639	Gene expression study on peripheral blood identifies progranulin mutations. 2008, 64, 92-6	83
1638	Empirical characterization of random forest variable importance measures. 2008 , 52, 2249-2260	546
1637	Topographical control of human macrophages by a regularly microstructured polyvinylidene fluoride surface. 2008 , 29, 4056-64	99
1636	Defining pancreatic endocrine precursors and their descendants. 2008 , 57, 654-68	61

1635	Analysis of gene expression identifies differentially expressed genes and pathways associated with lymphatic dissemination in patients with adenocarcinoma of the esophagus. 2008 , 15, 3459-70	26
1634	IFN-beta1b induces transient and variable gene expression in relapsing-remitting multiple sclerosis patients independent of neutralizing antibodies or changes in IFN receptor RNA expression. 2008 , 28, 317-31	39
1633	Pluripotency associated genes are reactivated by chromatin-modifying agents in neurosphere cells. 2008 , 26, 920-6	77
1632	Array-based gene discovery with three unrelated subjects shows SCARB2/LIMP-2 deficiency causes myoclonus epilepsy and glomerulosclerosis. 2008 , 82, 673-84	205
1631	Assessing quality and normalization of microarrays: case studies using neurological genomic data. 2008 , 118, 29-41	5
1630	Differential expression of influx and efflux transport proteins in human antigen presenting cells. 2008 , 17, 739-47	32
1629	Dynamics of the yeast transcriptome during wine fermentation reveals a novel fermentation stress response. 2008 , 8, 35-52	141
1628	Motility-related actinin alpha-4 is associated with advanced and metastatic ovarian carcinoma. 2008 , 88, 602-14	47
1627	Gene expression profiling distinguishes JAK2V617F-negative from JAK2V617F-positive patients in essential thrombocythemia. 2008 , 22, 1368-76	31
1626	The expression of 16 genes related to the cell of origin and immune response predicts survival in elderly patients with diffuse large B-cell lymphoma treated with CHOP and rituximab. 2008 , 22, 1917-24	87
1625	LNA-mediated microRNA silencing in non-human primates. 2008 , 452, 896-9	1373
1624	High-resolution mapping of meiotic crossovers and non-crossovers in yeast. 2008 , 454, 479-85	441
1623	Molecular profiling related to poor prognosis in thyroid carcinoma. Combining gene expression data and biological information. 2008 , 27, 1554-61	68
1622	Molecular effectors and modulators of hypericin-mediated cell death in bladder cancer cells. 2008 , 27, 1916-29	80
1621	Microarray analysis refines classification of non-medullary thyroid tumours of uncertain malignancy. 2008 , 27, 2228-36	28
1620	Genes involved in cell adhesion, cell motility and mitogenic signaling are altered due to HPV 16 E5	50
	protein expression. 2008 , 27, 2532-41	
1619	The atypical Rho GTPase RhoBTB2 is required for expression of the chemokine CXCL14 in normal and cancerous epithelial cells. 2008 , 27, 6856-65	34

1617	Acquisition of biologically relevant gene expression data by Affymetrix microarray analysis of archival formalin-fixed paraffin-embedded tumours. 2008 , 98, 1403-14	72
1616	Trefoil factor 3: a novel serum marker identified by gene expression profiling in high-grade endometrial carcinomas. 2008 , 99, 768-73	34
1615	Direct multiplexed measurement of gene expression with color-coded probe pairs. 2008, 26, 317-25	1526
1614	MicroRNA expression profiling using microarrays. 2008 , 3, 563-78	233
1613	Comparing whole genomes using DNA microarrays. 2008 , 9, 291-302	159
1612	The next generation of microarray research: applications in evolutionary and ecological genomics. 2008 , 100, 141-9	43
1611	HIV-1 activates proinflammatory and interferon-inducible genes in human brain microvascular endothelial cells: putative mechanisms of blood-brain barrier dysfunction. 2008 , 28, 697-711	46
1610	Construction of a chromosome 17 transcriptome in serous ovarian cancer identifies differentially expressed genes. 2008 , 18, 963-75	21
1609	Cholecystokinin-2 receptor mediated gene expression in neuronal PC12 cells. 2008, 104, 1450-65	8
1608	Oxidized low density lipoproteins induce a pathologic response by retinal pigmented epithelial cells. 2008 , 105, 1187-97	78
1607	Temporal and functional dynamics of the transcriptome during nerve growth factor-induced differentiation. 2008 , 105, 2388-403	31
1606	Coexpression characteristics of trehalose-6-phosphate phosphatase subfamily genes reveal different functions in a network context. 2008 , 133, 544-56	16
1605	DNA chip databases, omics, and gene fishing: commentary. 2008 , 99, 829-35	4
1604	mTOR inhibition reverses acquired endocrine therapy resistance of breast cancer cells at the cell proliferation and gene-expression levels. 2008 , 99, 1992-2003	60
1603	Transcriptome analysis of high-temperature adult-plant resistance conditioned by Yr39 during the wheat-Puccinia striiformis f. sp. tritici interaction. 2008 , 9, 479-93	63
1602	Expression profiling of microdissected cell populations selected from basal cells in normal epidermis and basal cell carcinoma. 2008 , 158, 527-38	27
1601	Expression differences for genes involved in lignin, glutathione and sulphate metabolism in response to cadmium in Arabidopsis thaliana and the related Zn/Cd-hyperaccumulator Thlaspi caerulescens. 2008 , 31, 301-24	253
1600	Transcriptional regulation by an NAC (NAM-ATAF1,2-CUC2) transcription factor attenuates ABA signalling for efficient basal defence towards Blumeria graminis f. sp. hordei in Arabidopsis. 2008 , 56, 867-80	172

1599	Gene expression in early stage cervical cancer. 2008 , 108, 520-6	89
1598	Evaluation of time profile reconstruction from complex two-color microarray designs. 2008, 9, 1	395
1597	Exon level integration of proteomics and microarray data. 2008 , 9, 118	26
1596	Empirical Bayes analysis of single nucleotide polymorphisms. 2008 , 9, 144	14
1595	A comprehensive re-analysis of the Golden Spike data: towards a benchmark for differential expression methods. 2008 , 9, 164	30
1594	A probe-treatment-reference (PTR) model for the analysis of oligonucleotide expression microarrays. 2008 , 9, 194	7
1593	Conserved co-expression for candidate disease gene prioritization. 2008 , 9, 208	28
1592	Automating dChip: toward reproducible sharing of microarray data analysis. 2008, 9, 231	57
1591	Cross-species and cross-platform gene expression studies with the Bioconductor-compliant R package 'annotationTools'. 2008 , 9, 26	34
1590	Literature-aided meta-analysis of microarray data: a compendium study on muscle development and disease. 2008 , 9, 291	19
1589	MAID : an effect size based model for microarray data integration across laboratories and platforms. 2008 , 9, 305	11
1588	Methodology capture: discriminating between the "best" and the rest of community practice. 2008 , 9, 359	12
1587	Critical assessment of alignment procedures for LC-MS proteomics and metabolomics measurements. 2008 , 9, 375	137
1586	R/parallelspeeding up bioinformatics analysis with R. 2008 , 9, 390	18
1585	easyExona Java-based GUI tool for processing and visualization of Affymetrix exon array data. 2008 , 9, 432	15
1584	CMA: a comprehensive Bioconductor package for supervised classification with high dimensional data. 2008 , 9, 439	80
1583	Background correction using dinucleotide affinities improves the performance of GCRMA. 2008 , 9, 452	38
1582	minet: A R/Bioconductor package for inferring large transcriptional networks using mutual information. 2008 , 9, 461	357

1581	Learning transcriptional regulatory networks from high throughput gene expression data using continuous three-way mutual information. 2008 , 9, 467	50
1580	Standardized high-throughput evaluation of cell-based compound screens. 2008 , 9, 475	13
1579	A Web-based and Grid-enabled dChip version for the analysis of large sets of gene expression data. 2008 , 9, 480	4
1578	Gene set enrichment analysis for non-monotone association and multiple experimental categories. 2008 , 9, 481	10
1577	Genome-scale study of the importance of binding site context for transcription factor binding and gene regulation. 2008 , 9, 484	15
1576	Identifying differential correlation in gene/pathway combinations. 2008, 9, 488	18
1575	EMAAS: an extensible grid-based rich internet application for microarray data analysis and management. 2008 , 9, 493	12
1574	ExonMiner: Web service for analysis of GeneChip Exon array data. 2008 , 9, 494	3
1573	Microarray-based gene set analysis: a comparison of current methods. 2008 , 9, 502	56
1572	A Bayesian calibration model for combining different pre-processing methods in Affymetrix chips. 2008 , 9, 512	4
1571	Statistical issues in the analysis of Illumina data. 2008 , 9, 85	82
1570	Time-course analysis of genome-wide gene expression data from hormone-responsive human breast cancer cells. 2008 , 9 Suppl 2, S12	25
1569	ArrayWiki: an enabling technology for sharing public microarray data repositories and meta-analyses. 2008 , 9 Suppl 6, S18	28
1568	Coordinated evolution of co-expressed gene clusters in the Drosophila transcriptome. 2008 , 8, 2	26
1567	Can subtle changes in gene expression be consistently detected with different microarray platforms?. 2008 , 9, 124	40
1566	Transcriptional regulation by poly(ADP-ribose) polymerase-1 during T cell activation. 2008 , 9, 171	36
1565	Heterologous microarray experiments allow the identification of the early events associated with potato tuber cold sweetening. 2008 , 9, 176	43
1564	RETINOBASE: a web database, data mining and analysis platform for gene expression data on retina. 2008 , 9, 208	12

1563	Genome-wide transcriptional changes induced by phagocytosis or growth on bacteria in Dictyostelium. 2008 , 9, 291	53
1562	The trypanosome transcriptome is remodelled during differentiation but displays limited responsiveness within life stages. 2008 , 9, 298	82
1561	Performance comparison of two microarray platforms to assess differential gene expression in human monocyte and macrophage cells. 2008 , 9, 302	37
1560	Global mRNA expression analysis in myosin II deficient strains of Saccharomyces cerevisiae reveals an impairment of cell integrity functions. 2008 , 9, 34	12
1559	Structural conservation versus functional divergence of maternally expressed microRNAs in the Dlk1/Gtl2 imprinting region. 2008 , 9, 346	45
1558	Novel functional view of the crocidolite asbestos-treated A549 human lung epithelial transcriptome reveals an intricate network of pathways with opposing functions. 2008 , 9, 376	19
1557	Characterization of hemizygous deletions in citrus using array-comparative genomic hybridization and microsynteny comparisons with the poplar genome. 2008 , 9, 381	24
1556	Dynamic RNA profiling in Plasmodium falciparum synchronized blood stages exposed to lethal doses of artesunate. 2008 , 9, 388	52
1555	Heat stress-responsive transcriptome analysis in heat susceptible and tolerant wheat (Triticum aestivum L.) by using Wheat Genome Array. 2008 , 9, 432	238
1554	Differential gene expression profiles are dependent upon method of peripheral blood collection and RNA isolation. 2008 , 9, 474	75
1553	mtDNA depletion confers specific gene expression profiles in human cells grown in culture and in xenograft. 2008 , 9, 521	40
1552	The transcriptomic signature of fasting murine liver. 2008 , 9, 528	58
1551	A process for analysis of microarray comparative genomics hybridisation studies for bacterial genomes. 2008 , 9, 53	23
1550	Transcriptional response of rat frontal cortex following acute in vivo exposure to the pyrethroid insecticides permethrin and deltamethrin. 2008 , 9, 546	17
1549	Dissecting an alternative splicing analysis workflow for GeneChip Exon 1.0 ST Affymetrix arrays. 2008 , 9, 571	18
1548	Combinatorial control of gene expression by the three yeast repressors Mig1, Mig2 and Mig3. 2008 , 9, 601	71
1547	Transcriptomic dissection of tongue squamous cell carcinoma. 2008 , 9, 69	234
1546	Analysis of the retinal gene expression profile after hypoxic preconditioning identifies candidate genes for neuroprotection. 2008 , 9, 73	48

1545	Predicting transcriptional regulatory interactions with artificial neural networks applied to E. coli multidrug resistance efflux pumps. 2008 , 8, 101	8
1544	Global transcriptional responses of Pseudomonas syringae DC3000 to changes in iron bioavailability in vitro. 2008 , 8, 209	48
1543	Universal ligation-detection-reaction microarray applied for compost microbes. 2008 , 8, 237	29
1542	Performance of a 70-mer oligonucleotide microarray for genotyping of Campylobacter jejuni. 2008 , 8, 73	14
1541	Genome-wide transcriptional analysis of super-embryogenic Medicago truncatula explant cultures. 2008 , 8, 110	38
1540	Transcriptional profiling of Medicago truncatula meristematic root cells. 2008 , 8, 21	39
1539	Global expression profiling in leaves of free-growing aspen. 2008 , 8, 61	23
1538	Transcriptional responses of Arabidopsis thaliana plants to As (V) stress. 2008, 8, 87	157
1537	Explorative data analysis of MCL reveals gene expression networks implicated in survival and prognosis supported by explorative CGH analysis. 2008 , 8, 106	28
1536	Gene-expression of metastasized versus non-metastasized primary head and neck squamous cell carcinomas: a pathway-based analysis. 2008 , 8, 168	32
1535	The cancer translational research informatics platform. 2008 , 8, 60	22
1534	Gene-expression profiles of peripheral blood mononuclear cell subpopulations in acute graft-vs-host disease following cord blood transplantation. 2008 , 36, 1760-1770	18
1533	Schistosoma mansoni: Microarray analysis of gene expression induced by host sex. 2008 , 120, 357-63	11
1532	Gene expression profiling of human liver transplants identifies an early transcriptional signature associated with initial poor graft function. 2008 , 8, 1221-36	24
1531	IFN-beta-regulated genes show abnormal expression in therapy-nalle relapsing-remitting MS mononuclear cells: gene expression analysis employing all reported protein-protein interactions. 2008 , 195, 116-20	39
1530	Molecular targets of 2,3,7,8-tetrachlorodibenzo-p-dioxin (TCDD) within the zebrafish ovary: insights into TCDD-induced endocrine disruption and reproductive toxicity. 2008 , 25, 47-57	44
1529	Differential gene expression in the nucleus accumbens with ethanol self-administration in inbred alcohol-preferring rats. 2008 , 89, 481-98	68
1528	Genome-wide effects of acute progressive feed restriction in liver and white adipose tissue. 2008 , 230, 41-56	19

1527	Promoter analysis of TCDD-inducible genes in a thymic epithelial cell line indicates the potential for cell-specific transcription factor crosstalk in the AhR response. 2008 , 232, 268-79		38
1526	Gene expression profiles of adult peripheral and cord blood mononuclear cells altered by lipopolysaccharide. 2008 , 93, 87-100		11
1525	Clinical uses of microarrays in cancer research. 2008, 141, 87-113		11
1524	Microarrays⊠nalysis of Signaling Pathways. 2008 , 115-130		
1523	Microarrays for the study of viral gene expression during human cytomegalovirus latent infection. 2008 , 141, 153-75		10
1522	Evidence for lifespan extension and delayed age-related biomarkers in insulin receptor substrate 1 null mice. 2008 , 22, 807-18		408
1521	Gene expression microarray data analysis demystified. 2008 , 14, 29-61		20
1520	Regulation of xylose metabolism in recombinant Saccharomyces cerevisiae. 2008 , 7, 18		74
1519	Development and evaluation of a high-throughput, low-cost genotyping platform based on oligonucleotide microarrays in rice. 2008 , 4, 13		33
1518	Network-based global inference of human disease genes. 2008 , 4, 189		475
1518 1517	Network-based global inference of human disease genes. 2008 , 4, 189 A weighted average difference method for detecting differentially expressed genes from microarray data. 2008 , 3, 8		475 89
	A weighted average difference method for detecting differentially expressed genes from		
1517	A weighted average difference method for detecting differentially expressed genes from microarray data. 2008 , 3, 8 Genes responsive to both oxidant stress and loss of estrogen receptor function identify a poor	18.3	89
1517 1516	A weighted average difference method for detecting differentially expressed genes from microarray data. 2008 , 3, 8 Genes responsive to both oxidant stress and loss of estrogen receptor function identify a poor prognosis group of estrogen receptor positive primary breast cancers. 2008 , 10, R61 Prioritizing functional modules mediating genetic perturbations and their phenotypic effects: a	18.3	89 32 4
1517 1516 1515	A weighted average difference method for detecting differentially expressed genes from microarray data. 2008, 3, 8 Genes responsive to both oxidant stress and loss of estrogen receptor function identify a poor prognosis group of estrogen receptor positive primary breast cancers. 2008, 10, R61 Prioritizing functional modules mediating genetic perturbations and their phenotypic effects: a global strategy. <i>Genome Biology</i> , 2008, 9, R174 ArrayPlex: distributed, interactive and programmatic access to genome sequence, annotation,		89 32 4
1517 1516 1515	A weighted average difference method for detecting differentially expressed genes from microarray data. 2008, 3, 8 Genes responsive to both oxidant stress and loss of estrogen receptor function identify a poor prognosis group of estrogen receptor positive primary breast cancers. 2008, 10, R61 Prioritizing functional modules mediating genetic perturbations and their phenotypic effects: a global strategy. Genome Biology, 2008, 9, R174 ArrayPlex: distributed, interactive and programmatic access to genome sequence, annotation, ontology, and analytical toolsets. Genome Biology, 2008, 9, R159 MeV+R: using MeV as a graphical user interface for Bioconductor applications in microarray	18.3	89 32 4 1
1517 1516 1515 1514 1513	A weighted average difference method for detecting differentially expressed genes from microarray data. 2008, 3, 8 Genes responsive to both oxidant stress and loss of estrogen receptor function identify a poor prognosis group of estrogen receptor positive primary breast cancers. 2008, 10, R61 Prioritizing functional modules mediating genetic perturbations and their phenotypic effects: a global strategy. Genome Biology, 2008, 9, R174 ArrayPlex: distributed, interactive and programmatic access to genome sequence, annotation, ontology, and analytical toolsets. Genome Biology, 2008, 9, R159 MeV+R: using MeV as a graphical user interface for Bioconductor applications in microarray analysis. Genome Biology, 2008, 9, R118 Susceptibility to glaucoma: differential comparison of the astrocyte transcriptome from	18.3	89 32 4 1

1509	Gene expression profiling of human prostate cancer stem cells reveals a pro-inflammatory phenotype and the importance of extracellular matrix interactions. <i>Genome Biology</i> , 2008 , 9, R83	18.3	159	
1508	Transcriptome analysis reveals new insight into appressorium formation and function in the rice blast fungus Magnaporthe oryzae. <i>Genome Biology</i> , 2008 , 9, R85	18.3	129	
1507	Validation and extension of an empirical Bayes method for SNP calling on Affymetrix microarrays. <i>Genome Biology</i> , 2008 , 9, R63	18.3	28	
1506	Gene expression variation in African and European populations of Drosophila melanogaster. <i>Genome Biology</i> , 2008 , 9, R12	18.3	80	
1505	XCMS2: processing tandem mass spectrometry data for metabolite identification and structural characterization. 2008 , 80, 6382-9		205	
1504	UNBS5162, a novel naphthalimide that decreases CXCL chemokine expression in experimental prostate cancers. 2008 , 10, 573-86		43	
1503	Array-based multiplex analysis of DNA methylation in breast cancer tissues. 2008, 10, 93-101		32	
1502	Ethylene-induced differential gene expression during abscission of citrus leaves. 2008 , 59, 2717-33		80	
1501	Computational diagnostics with gene expression profiles. 2008 , 453, 281-96		6	
1500	Comparative expression analysis of four breast cancer subtypes versus matched normal tissue from the same patients. 2008 , 109, 207-11		3	
1499	Down-regulation of genes related to the adrenergic system may contribute to splanchnic vasodilation in rat portal hypertension. 2008 , 49, 43-51		25	
1498	Molecular phenotypic descriptors of Dupuytren's disease defined using informatics analysis of the transcriptome. 2008 , 33, 359-72		49	
1497	Gene expression profiling of suppressor mechanisms in tuberculosis. 2008, 45, 1573-86		3	
1496	Exposure to brominated flame retardant PBDE-99 affects cytoskeletal protein expression in the neonatal mouse cerebral cortex. 2008 , 29, 628-37		52	
1495	Translational gene mapping of cognitive decline. 2008 , 29, 524-41		22	
1494	Creatine improves health and survival of mice. 2008 , 29, 1404-11		7 ²	
1493	Gene expression in Citrus sinensis (L.) Osbeck following infection with the bacterial pathogen Candidatus Liberibacter asiaticus causing Huanglongbing in Florida. 2008 , 175, 291-306		148	
1492	An improved vaccine for prevention of respiratory tularemia caused by Francisella tularensis SchuS4 strain. 2008 , 26, 5276-88		63	

1491	SrfB, a member of the Serum Response Factor family of transcription factors, regulates starvation response and early development in Dictyostelium. 2008 , 316, 260-74	13
1490	Disruption of epidermal specific gene expression and delayed skin development in AP-2 gamma mutant mice. 2008 , 317, 187-95	26
1489	A transcriptional network coordinately determines transmitter and peptidergic fate in the dorsal spinal cord. 2008 , 322, 381-93	70
1488	Combinatorial effects of four histone modifications in transcription and differentiation. 2008 , 91, 41-51	38
1487	Expression profiling of signature gene sets with trinucleotide threading. 2008 , 91, 209-17	5
1486	Comparison of normalization methods with microRNA microarray. 2008, 92, 122-8	47
1485	A bioinformatic and transcriptomic approach to identifying positional candidate genes without fine mapping: an example using rice root-growth QTLs. 2008 , 92, 344-52	34
1484	Transcriptome analysis of the normal human mammary cell commitment and differentiation process. 2008 , 3, 109-18	274
1483	Expression microarrays in plant-virus interaction. 2008 , 451, 583-613	3
1482	Statistical challenges in preprocessing in microarray experiments in cancer. 2008 , 14, 5959-66	37
1481	p63 contributes to cell invasion and migration in squamous cell carcinoma of the head and neck. 2008 , 263, 26-34	39
1480	Hepatic expression profiling in smolting and adult coho salmon (Onchorhynchus kisutch). 2008 , 106, 365-78	10
1479	Gene expression profiling of mucolipidosis type IV fibroblasts reveals deregulation of genes with relevant functions in lysosome physiology. 2008 , 1782, 250-8	11
1478	Identification of interleukin-1 and interleukin-6-responsive genes in human monocyte-derived macrophages using microarrays. 2008 , 1779, 383-9	44
1477	Coordinate induction of PPAR alpha and SREBP2 in multifunctional protein 2 deficient mice. 2008 , 1781, 694-702	31
1476	Differential gene expression induced by growth hormone treatment in the uremic rat growth plate. 2008 , 18, 353-9	3
1475	Meta-analysis approach identifies candidate genes and associated molecular networks for type-2 diabetes mellitus. 2008 , 9, 310	45
1474	Translational bioinformatics: coming of age. 2008 , 15, 709-14	101

1473	Molecular characterization of human Argonaute-containing ribonucleoprotein complexes and their bound target mRNAs. 2008 , 14, 2580-96	283
1472	A comparison of meta-analysis methods for detecting differentially expressed genes in microarray experiments. 2008 , 24, 374-82	171
1471	A transcriptome database for astrocytes, neurons, and oligodendrocytes: a new resource for understanding brain development and function. 2008 , 28, 264-78	2239
1470	A segmental maximum a posteriori approach to genome-wide copy number profiling. 2008 , 24, 751-8	28
1469	Barley grain maturation and germination: metabolic pathway and regulatory network commonalities and differences highlighted by new MapMan/PageMan profiling tools. 2008 , 146, 1738-58	222
1468	Cdc7-Dbf4 kinase overexpression in multiple cancers and tumor cell lines is correlated with p53 inactivation. 2008 , 10, 920-31	86
1467	The SWI/SNF chromatin-remodeling complex and glucocorticoid resistance in acute lymphoblastic leukemia. 2008 , 100, 1792-803	50
1466	Interleukin-29 functions cooperatively with interferon to induce antiviral gene expression and inhibit hepatitis C virus replication. 2008 , 283, 30079-89	76
1465	Genomic distribution and functional analyses of potential G-quadruplex-forming sequences in Saccharomyces cerevisiae. 2008 , 36, 144-56	214
1464	Differential regulation of Listeria monocytogenes internalin and internalin-like genes by sigmaB and PrfA as revealed by subgenomic microarray analyses. 2008 , 5, 417-35	31
1463	Examining the molecular interaction between potato (Solanum tuberosum) and Colorado potato beetle Leptinotarsa decemlineata. 2008 , 86, 1080-1091	9
1462	Involvement of Arabidopsis HOS15 in histone deacetylation and cold tolerance. 2008 , 105, 4945-50	230
1461	Platelet protein interactions: map, signaling components, and phosphorylation groundstate. 2008 , 28, 1326-31	63
1460	Whole-genome microarray and targeted analysis of angiogenesis-regulating gene expression (ENG, FLT1, VEGF, PlGF) in placentas from pre-eclamptic and small-for-gestational-age pregnancies. 2008 , 21, 267-73	45
1459	Prediction of cardiac transcription networks based on molecular data and complex clinical phenotypes. 2008 , 4, 589-98	15
1458	Gene expression profiling of porcine alveolar macrophages after antibody-mediated cross-linking of Sialoadhesin (Sn, Siglec-1). 2008 , 28, 185-243	7
1457	Gene network dynamics controlling keratinocyte migration. 2008 , 4, 199	44
1456	Gene Networks for the Integration and Understanding of Gene Expression Characteristics. 2008 , 56, 314-321	4

1455	Gene networks in Arabidopsis thaliana for metabolic and environmental functions. 2008, 4, 199-204	16
1454	The Arabidopsis NFYA5 transcription factor is regulated transcriptionally and posttranscriptionally to promote drought resistance. 2008 , 20, 2238-51	660
1453	BioVLAB-Microarray: Microarray Data Analysis in Virtual Environment. 2008,	11
1452	Liver gene expression analysis reveals endoplasmic reticulum stress and metabolic dysfunction in SCD1-deficient mice fed a very low-fat diet. 2008 , 33, 361-72	66
1451	Ripening and genotype control stilbene accumulation in healthy grapes. 2008 , 56, 11773-85	150
1450	Effect of transgenes on global gene expression in soybean is within the natural range of variation of conventional cultivars. 2008 , 56, 3057-67	58
1449	Effect of starvation on transcriptomes of brain and liver in adult female zebrafish (Danio rerio). 2008 , 35, 283-95	94
1448	Yellow fever vaccine induces integrated multilineage and polyfunctional immune responses. 2008 , 205, 3119-31	454
1447	Effects of short-term growth hormone treatment on liver and muscle transcriptomes in rainbow trout (Oncorhynchus mykiss). 2008 , 32, 380-92	51
1446	Conserved chromosomal clustering of genes governed by chromatin regulators in Drosophila. <i>Genome Biology</i> , 2008 , 9, R134	15
1446 1445		15 72
1445	Genome Biology, 2008, 9, R134 Genome-wide discovery and verification of novel structured RNAs in Plasmodium falciparum. 2008,	
1445	Genome Biology, 2008, 9, R134 Genome-wide discovery and verification of novel structured RNAs in Plasmodium falciparum. 2008, 18, 281-92	72
1445 1444	Genome Biology, 2008, 9, R134 Genome-wide discovery and verification of novel structured RNAs in Plasmodium falciparum. 2008, 18, 281-92 Rice-arsenate interactions in hydroponics: whole genome transcriptional analysis. 2008, 59, 2267-76	72 191
1445 1444 1443	Genome-wide discovery and verification of novel structured RNAs in Plasmodium falciparum. 2008, 18, 281-92 Rice-arsenate interactions in hydroponics: whole genome transcriptional analysis. 2008, 59, 2267-76 Glucocorticoid signaling defines a novel commitment state during adipogenesis in vitro. 2008, 19, 4032-41	72 191 99
1445 1444 1443 1442	Genome Biology, 2008, 9, R134 Genome-wide discovery and verification of novel structured RNAs in Plasmodium falciparum. 2008, 18, 281-92 Rice-arsenate interactions in hydroponics: whole genome transcriptional analysis. 2008, 59, 2267-76 Glucocorticoid signaling defines a novel commitment state during adipogenesis in vitro. 2008, 19, 4032-41 RReportGenerator: automatic reports from routine statistical analysis using R. 2008, 24, 276-8 Identifying functional modules in protein-protein interaction networks: an integrated exact	72 191 99
1445 1444 1443 1442	Genome-Wide discovery and verification of novel structured RNAs in Plasmodium falciparum. 2008, 18, 281-92 Rice-arsenate interactions in hydroponics: whole genome transcriptional analysis. 2008, 59, 2267-76 Glucocorticoid signaling defines a novel commitment state during adipogenesis in vitro. 2008, 19, 4032-41 RReportGenerator: automatic reports from routine statistical analysis using R. 2008, 24, 276-8 Identifying functional modules in protein-protein interaction networks: an integrated exact approach. 2008, 24, i223-31	72 191 99 15 367

1437	The L-type calcium ion channel cch1 affects ascospore discharge and mycelial growth in the filamentous fungus Gibberella zeae (anamorph Fusarium graminearum). 2008 , 7, 415-24	58
1436	Transcriptional responses of Plasmodium falciparum to alpha-difluoromethylornithine-induced polyamine depletion. 2008 , 389, 111-25	14
1435	Tissue-specific splicing factor gene expression signatures. 2008 , 36, 4823-32	128
1434	Microarray analysis of a Chlamydia pneumoniae-infected human epithelial cell line by use of gene ontology hierarchy. 2008 , 197, 156-62	38
1433	Identification of SNP interactions using logic regression. 2008 , 9, 187-98	105
1432	Variations in the progranulin gene affect global gene expression in frontotemporal lobar degeneration. 2008 , 17, 1349-62	96
1431	Distinctive patterns of microRNA expression associated with karyotype in acute myeloid leukaemia. 2008 , 3, e2141	218
1430	Solutions for data integration in functional genomics: a critical assessment and case study. 2008 , 9, 532-44	21
1429	Sex and age dimorphism of myocardial gene expression in nonischemic human heart failure. 2008 , 1, 117-25	37
1428	Temporal transcriptomic microarray analysis of "Dehalococcoides ethenogenes" strain 195 during the transition into stationary phase. 2008 , 74, 2864-72	67
1427	HCGene: a software tool to support the hierarchical classification of genes. 2008, 24, 729-31	12
1426	Region-specific gene expression profiling: novel evidence for biological heterogeneity of the human amnion. 2008 , 79, 954-61	48
1425	Auxin responses in mutants of the Arabidopsis CONSTITUTIVE PHOTOMORPHOGENIC9 signalosome. 2008 , 147, 1369-79	37
1424	AffyGCQC: a web-based interface to detect outlying genechips with extreme studentized deviate tests. 2008 , 6, 317-34	6
1423	Lymphocytes from patients with type 1 diabetes display a distinct profile of chromatin histone H3 lysine 9 dimethylation: an epigenetic study in diabetes. 2008 , 57, 3189-98	207
1422	The transcriptional repressor ARR1-SRDX suppresses pleiotropic cytokinin activities in Arabidopsis. 2008 , 147, 1380-95	68
1421	Origin and pathogenesis of nodular lymphocyte-predominant Hodgkin lymphoma as revealed by global gene expression analysis. 2008 , 205, 2251-68	247
1420	Improved grading and survival prediction of human astrocytic brain tumors by artificial neural network analysis of gene expression microarray data. 2008 , 7, 1013-24	64

1419	Podocyte-selective deletion of dicer induces proteinuria and glomerulosclerosis. 2008 , 19, 2159-69	298
1418	DAnTE: a statistical tool for quantitative analysis of -omics data. 2008 , 24, 1556-8	333
1417	PecS is a global regulator of the symptomatic phase in the phytopathogenic bacterium Erwinia chrysanthemi 3937. 2008 , 190, 7508-22	77
1416	MicroRNA-155 is an Epstein-Barr virus-induced gene that modulates Epstein-Barr virus-regulated gene expression pathways. 2008 , 82, 5295-306	211
1415	Airway epithelial versus immune cell Stat1 function for innate defense against respiratory viral infection. 2008 , 180, 3319-28	63
1414	Genome-wide analysis identifies interleukin-10 mRNA as target of tristetraprolin. 2008 , 283, 11689-99	198
1413	Therapeutic efficacy of ABT-737, a selective inhibitor of BCL-2, in small cell lung cancer. 2008 , 68, 2321-8	166
1412	Interplay between cyclic AMP-cyclic AMP receptor protein and cyclic di-GMP signaling in Vibrio cholerae biofilm formation. 2008 , 190, 6646-59	122
1411	The HDAC inhibitor 4b ameliorates the disease phenotype and transcriptional abnormalities in Huntington's disease transgenic mice. 2008 , 105, 15564-9	240
1410	Genome-wide expression profiling reveals distinct clusters of transcriptional regulation during bovine preimplantation development in vivo. 2008 , 105, 19768-73	124
1409	Phosphatase and tensin homologue deleted on chromosome 10 deficiency accelerates tumor induction in a mouse model of ErbB-2 mammary tumorigenesis. 2008 , 68, 2122-31	42
1408	Analysis of the Drosophila melanogaster testes transcriptome reveals coordinate regulation of paralogous genes. 2008 , 179, 305-15	27
1407	Alternate statistical tools and limitations in genetic marker association studies in single-arm drug cancer trials. 2008 , 26, 1400-1	5
1406	Increasing alpha 7 beta 1-integrin promotes muscle cell proliferation, adhesion, and resistance to apoptosis without changing gene expression. 2008 , 294, C627-40	65
1405	Systematic assessment of the human osteoblast transcriptome in resting and induced primary cells. 2008 , 33, 301-11	27
1404	High-resolution gene expression profiling for simultaneous kinetic parameter analysis of RNA synthesis and decay. 2008 , 14, 1959-72	297
1403	Uncovering a macrophage transcriptional program by integrating evidence from motif scanning and expression dynamics. 2008 , 4, e1000021	139
1402	Novel low abundance and transient RNAs in yeast revealed by tiling microarrays and ultra high-throughput sequencing are not conserved across closely related yeast species. 2008 , 4, e1000299	29

1401	Developmental constraints on vertebrate genome evolution. 2008 , 4, e1000311	84
1400	Analyzing ChIP-chip data using bioconductor. 2008 , 4, e1000227	17
1399	In vivo response to methotrexate forecasts outcome of acute lymphoblastic leukemia and has a distinct gene expression profile. 2008 , 5, e83	60
1398	Parasite burden and CD36-mediated sequestration are determinants of acute lung injury in an experimental malaria model. 2008 , 4, e1000068	69
1397	Integrating global gene expression analysis and genetics. 2008, 60, 571-601	43
1396	Early gene expression in human lymphocytes after gamma-irradiation-a genetic pattern with potential for biodosimetry. 2008 , 84, 375-87	45
1395	Molecular properties of side population-sorted cells from mouse small intestine. 2008 , 294, G286-94	25
1394	Identification of Nrf2-dependent airway epithelial adaptive response to proinflammatory oxidant-hypochlorous acid challenge by transcription profiling. 2008 , 294, L469-77	24
1393	Gene set enrichment in eQTL data identifies novel annotations and pathway regulators. 2008 , 4, e1000070	79
1392	GEOmetadb: powerful alternative search engine for the Gene Expression Omnibus. 2008 , 24, 2798-800	93
1391	The Rcs phosphorelay is a cell envelope stress response activated by peptidoglycan stress and contributes to intrinsic antibiotic resistance. 2008 , 190, 2065-74	177
1390	Regenerative response in the pig liver remnant varies with the degree of resection and rise in portal pressure. 2008 , 294, G819-30	19
1389	Agglomerative epigenetic aberrations are a common event in human breast cancer. 2008 , 68, 8616-25	120
1388	Map of differential transcript expression in the normal human large intestine. 2008, 33, 50-64	64
1387	Context-specific metabolic networks are consistent with experiments. 2008, 4, e1000082	382
1386	Genetic analysis of human traits in vitro: drug response and gene expression in lymphoblastoid cell lines. 2008 , 4, e1000287	182
1385	Involvement of Pinus taeda MYB1 and MYB8 in phenylpropanoid metabolism and secondary cell wall biogenesis: a comparative in planta analysis. 2008 , 59, 3925-39	156
1384	Genome-wide expression patterns and the genetic architecture of a fundamental social trait. 2008 , 4, e1000127	57

1383	Comprehensive analysis of affymetrix exon arrays using BioConductor. 2008 , 4, e6	35
1382	Aerobic capacity-dependent differences in cardiac gene expression. 2008 , 33, 100-9	31
1381	Advanced genomic data mining. 2008, 4, e1000121	11
1380	Somatic pairing of chromosome 19 in renal oncocytoma is associated with deregulated EGLN2-mediated [corrected] oxygen-sensing response. 2008 , 4, e1000176	52
1379	Eight-channel iTRAQ enables comparison of the activity of six leukemogenic tyrosine kinases. 2008 , 7, 853-63	203
1378	Cdc7-Dbf4 regulates NDT80 transcription as well as reductional segregation during budding yeast meiosis. 2008 , 19, 4956-67	30
1377	EWS-FLI1 suppresses NOTCH-activated p53 in Ewing's sarcoma. 2008 , 68, 7100-9	85
1376	GEPAS, a web-based tool for microarray data analysis and interpretation. 2008 , 36, W308-14	58
1375	DNA methylation profile of tissue-dependent and differentially methylated regions (T-DMRs) in mouse promoter regions demonstrating tissue-specific gene expression. 2008 , 18, 1969-78	127
1374	The F-box protein ACRE189/ACIF1 regulates cell death and defense responses activated during pathogen recognition in tobacco and tomato. 2008 , 20, 697-719	116
1373	Transcriptional and metabolic adjustments in ADP-glucose pyrophosphorylase-deficient bt2 maize kernels. 2008 , 146, 1553-70	17
1372	Toxicogenomic analysis of gender, chemical, and dose effects in livers of TCDD- or aroclor 1254-exposed rats using a multifactor linear model. 2008 , 102, 291-309	29
1371	wuHMM: a robust algorithm to detect DNA copy number variation using long oligonucleotide microarray data. 2008 , 36, e41	21
1370	The Cladosporium fulvum virulence protein Avr2 inhibits host proteases required for basal defense. 2008 , 20, 1948-63	195
1369	Key issues in conducting a meta-analysis of gene expression microarray datasets. 2008 , 5, e184	364
1368	Short-term high fat-feeding results in morphological and metabolic adaptations in the skeletal muscle of C57BL/6J mice. 2008 , 32, 360-9	102
1367	MicroRNA regulation and the variability of human cortical gene expression. 2008 , 36, 4621-8	26
1366	RNA interference and retinoblastoma-related genes are required for repression of endogenous siRNA targets in Caenorhabditis elegans. 2008 , 105, 20386-91	26

1365	Flexible informatics for linking experimental data to mathematical models via DataRail. 2008, 24, 840-7	59
1364	Amino acid polymorphisms in Arabidopsis phytochrome B cause differential responses to light. 2008 , 105, 3157-62	85
1363	The highly similar Arabidopsis homologs of trithorax ATX1 and ATX2 encode proteins with divergent biochemical functions. 2008 , 20, 568-79	153
1362	Consolidated strategy for the analysis of microarray spike-in data. 2008 , 36, e108	31
1361	Rintact: enabling computational analysis of molecular interaction data from the IntAct repository. 2008 , 24, 1100-1	9
1360	CREB has a context-dependent role in activity-regulated transcription and maintains neuronal cholesterol homeostasis. 2008 , 22, 2872-9	64
1359	DHA induces ER stress and growth arrest in human colon cancer cells: associations with cholesterol and calcium homeostasis. 2008 , 49, 2089-100	97
1358	Phenotype and functional characterization of long-term gp100-specific memory CD8+ T cells in disease-free melanoma patients before and after boosting immunization. 2008 , 14, 5270-83	27
1357	Assessing the impact of tissue devitalization time on genome-wide gene expression analysis in ovarian tumor samples. 2008 , 17, 200-6	22
1356	Antagonism of microRNA-122 in mice by systemically administered LNA-antimiR leads to up-regulation of a large set of predicted target mRNAs in the liver. 2008 , 36, 1153-62	581
1355	Identification of Arx transcriptional targets in the developing basal forebrain. 2008, 17, 3740-60	104
1354	Transcriptome profiling and functional analysis of Agrobacterium tumefaciens reveals a general conserved response to acidic conditions (pH 5.5) and a complex acid-mediated signaling involved in Agrobacterium-plant interactions. 2008 , 190, 494-507	86
1353	Genome-wide promoter analysis uncovers portions of the cancer methylome. 2008 , 68, 2661-70	120
1352	Genes involved in differentiation, stem cell renewal, and tumorigenesis are modulated in telomerase-immortalized human urothelial cells. 2008 , 6, 1154-68	39
1351	Transcriptome analyses and biofilm-forming characteristics of a clonal Pseudomonas aeruginosa from the cystic fibrosis lung. 2008 , 57, 1454-1465	43
1350	Analyzing gene perturbation screens with nested effects models in R and bioconductor. 2008 , 24, 2549-50	24
1349	Interferon-beta signaling is enhanced in patients with insufficient coronary collateral artery development and inhibits arteriogenesis in mice. 2008 , 102, 1286-94	59
1348	Predicting functional transcription factor binding through alignment-free and affinity-based analysis of orthologous promoter sequences. 2008 , 24, i165-71	49

1347	Optimization of experimental design parameters for high-throughput chromatin immunoprecipitation studies. 2008 , 36, e144	26
1346	Type IV pili in Francisella tularensis: roles of pilF and pilT in fiber assembly, host cell adherence, and virulence. 2008 , 76, 2852-61	64
1345	Gcn4 is required for the response to peroxide stress in the yeast Saccharomyces cerevisiae. 2008 , 19, 2995-3007	76
1344	Microarray-based in vitro test system for the discrimination of contact allergens and irritants: identification of potential marker genes. 2008 , 54, 525-33	21
1343	From genetics to mechanism of disease liability. 2008 , 60, 701-26	2
1342	Comparative analysis of the sigma B-dependent stress responses in Listeria monocytogenes and Listeria innocua strains exposed to selected stress conditions. 2008 , 74, 158-71	130
1341	Gene expression in RET/PTC3 and E7 transgenic mouse thyroids: RET/PTC3 but not E7 tumors are partial and transient models of human papillary thyroid cancers. 2008 , 149, 5107-17	16
1340	MEDME: an experimental and analytical methodology for the estimation of DNA methylation levels based on microarray derived MeDIP-enrichment. 2008 , 18, 1652-9	93
1339	The potato-specific apyrase is apoplastically localized and has influence on gene expression, growth, and development. 2008 , 147, 1092-109	57
1338	Disruption of the Arabidopsis circadian clock is responsible for extensive variation in the cold-responsive transcriptome. 2008 , 147, 263-79	186
1337	Predominance of interferon-related responses in the brain during murine malaria, as identified by microarray analysis. 2008 , 76, 1812-24	26
1336	Cellular cross talk in the small intestinal mucosa: postnatal lymphocytic immigration elicits a specific epithelial transcriptional response. 2008 , 294, G1335-43	9
1335	Genomic expression analysis of rat chromosome 4 for skeletal traits at femoral neck. 2008 , 35, 191-6	11
1334	Gene expression profiling of skeletal muscle in exercise-trained and sedentary rats with inborn high and low VO2max. 2008 , 35, 213-21	24
1333	Genetic analysis of congenital cystic adenomatoid malformation reveals a novel pulmonary gene: fatty acid binding protein-7 (brain type). 2008 , 64, 11-6	36
1332	Thyroid hormone action in the adult brain: gene expression profiling of the effects of single and multiple doses of triiodo-L-thyronine in the rat striatum. 2008 , 149, 3989-4000	55
1331	Genes associated with membrane-initiated signaling of estrogen and energy homeostasis. 2008 , 149, 6113-24	72
1330	Rapid recruitment of temporally distinct vascular gene sets by estrogen. 2008 , 22, 2544-56	21

1329	cyclophosphamide. 2008 , 8, 172-9	28
1328	Parallelized preprocessing algorithms for high-density oligonucleotide arrays. 2008,	4
1327	Information systems for cancer research. 2008 , 26, 1060-7	11
1326	From Microarrays to Promoters: The Visual Story of Stat3. 2008,	
1325	Reproducibility-optimized test statistic for ranking genes in microarray studies. 2008 , 5, 423-431	47
1324	ATF4 is an oxidative stress-inducible, prodeath transcription factor in neurons in vitro and in vivo. 2008 , 205, 1227-42	178
1323	Towards dynamic database infrastructures for mouse genetics. 2008,	
1322	Systemic signaling of the plant nitrogen status triggers specific transcriptome responses depending on the nitrogen source in Medicago truncatula. 2008 , 146, 2020-35	120
1321	Statistical similarities between transcriptomics and quantitative shotgun proteomics data. 2008 , 7, 631-44	134
1320	Transcriptomics and micronutrient research. 2008 , 99 Suppl 3, S59-65	15
1319	Pathways change in expression during replicative aging in Saccharomyces cerevisiae. 2008 , 63, 21-34	36
1318	Overexpression of CDX2 perturbs HOX gene expression in murine progenitors depending on its N-terminal domain and is closely correlated with deregulated HOX gene expression in human acute myeloid leukemia. 2008 , 111, 309-19	53
1317	An 86-probe-set gene-expression signature predicts survival in cytogenetically normal acute myeloid leukemia. 2008 , 112, 4193-201	281
1316	Iron regulates phosphorylation of Smad1/5/8 and gene expression of Bmp6, Smad7, Id1, and Atoh8 in the mouse liver. 2008 , 112, 1503-9	340
1315	Expanded cells in monoclonal TCR-alphabeta+/CD4+/NKa+/CD8-/+dim T-LGL lymphocytosis recognize hCMV antigens. 2008 , 112, 4609-16	48
1314	Transcriptional profiling of VEGF-A and VEGF-C target genes in lymphatic endothelium reveals endothelial-specific molecule-1 as a novel mediator of lymphangiogenesis. 2008 , 112, 2318-26	101
1313	Genome-wide gene expression profiling and mutation analysis of Saudi patients with Canavan disease. 2008 , 10, 675-84	18
1312	Mortalin: a protein associated with progression of Parkinson disease?. 2008 , 67, 117-24	69

1311	Knocking down galectin 1 in human hs683 glioblastoma cells impairs both angiogenesis and endoplasmic reticulum stress responses. 2008 , 67, 456-69	72
1310	In-vivo effects of simvastatin and rosuvastatin on global gene expression in peripheral blood leucocytes in a human inflammation model. 2008 , 18, 109-20	24
1309	Association between a prognostic gene signature and functional gene sets. 2008 , 2, 329-41	3
1308	Unsupervised meta-analysis on diverse gene expression datasets allows insight into gene function and regulation. 2008 , 2, 265-80	2
1307	Bronchoalveolar lavage cell gene expression in acute lung rejection: development of a diagnostic classifier. 2008 , 85, 224-31	31
1306	Tubulocystic carcinoma of the kidney: clinicopathologic and molecular characterization. 2008, 32, 177-87	127
1305	Expression of collagen genes in the cones of skin in the Duroc/Yorkshire porcine model of fibroproliferative scarring. 2008 , 29, 815-27	25
1304	Differential gene profiling in acute lung injury identifies injury-specific gene expression. 2008 , 36, 855-65	44
1303	Renal translocation carcinomas: clinicopathologic, immunohistochemical, and gene expression profiling analysis of 31 cases with a review of the literature. 2008 , 32, 656-70	196
1302	Gene expression patterns in deceased donor kidneys developing delayed graft function after kidney transplantation. 2008 , 85, 626-35	29
1301	The role of particulate matter-associated zinc in cardiac injury in rats. 2008, 116, 13-20	65
1300	Efficient genetic method for establishing Drosophila cell lines unlocks the potential to create lines of specific genotypes. 2008 , 4, e1000142	43
1299	Macrophage and T-cell gene expression in a model of early infection with the protozoan Leishmania chagasi. 2008 , 2, e252	36
1298	Effect of synthetic dietary triglycerides: a novel research paradigm for nutrigenomics. 2008, 3, e1681	81
1297	Plasmodium falciparum transcriptome analysis reveals pregnancy malaria associated gene expression. 2008 , 3, e1855	37
1296	A meta-analysis of microarray gene expression in mouse stem cells: redefining stemness. 2008 , 3, e2712	10
1295	Gene expression and functional studies of the optic nerve head astrocyte transcriptome from normal African Americans and Caucasian Americans donors. 2008 , 3, e2847	16
1294	Microarray analysis of human monocytes infected with Francisella tularensis identifies new targets of host response subversion. 2008 , 3, e2924	101

1293	P68 RNA helicase (DDX5) alters activity of cis- and trans-acting factors of the alternative splicing of H-Ras. 2008 , 3, e2926	44
1292	Identification of functional networks of estrogen- and c-Myc-responsive genes and their relationship to response to tamoxifen therapy in breast cancer. 2008 , 3, e2987	77
1291	A snapshot of CNVs in the pig genome. 2008 , 3, e3916	97
1290	Bioinformatic tools for inferring functional information from plant microarray data: tools for the first steps. 2008 , 2008, 147563	4
1289	Genevestigator v3: a reference expression database for the meta-analysis of transcriptomes. 2008 , 2008, 420747	1382
1288	Comparing quantitative trait Loci and gene expression data. 2008 , 719818	2
1287	Is gene activity in plant cells affected by UMTS-irradiation? A whole genome approach. 2008, 1, 71-83	3
1286	Merging mixture components for cell population identification in flow cytometry. 2009, 247646	72
1285	Microarray gene expression profiles of fasting induced changes in liver and adipose tissues of pigs expressing the melanocortin-4 receptor D298N variant. 2009 , 38, 98-111	34
1284	Genes involved in viral carcinogenesis and tumor initiation in hepatitis C virus-induced hepatocellular carcinoma. 2009 , 15, 85-94	214
1283	GaGa: A parsimonious and flexible model for differential expression analysis. 2009, 3,	13
1282	Automatic clustering of flow cytometry data with density-based merging. 2009, 686759	32
1281	Analysis of High-Throughput Flow Cytometry Data Using plateCore. 2009 , 356141	8
1280	One-month diesel exhaust inhalation produces hypertensive gene expression pattern in healthy rats. 2009 , 117, 38-46	49
1279	Toxicogenomic biomarkers for liver toxicity. 2009 , 22, 35-52	22
1278	Using Free and Open-Source Bioconductor Packages to Analyze Array Comparative Genomics Hybridization (aCGH) Data. 2009 , 10, 60-3	1
1277	D-MaPs - DNA-microarray projects: Web-based software for multi-platform microarray analysis. 2009 , 32, 634-9	2
1276	FlowFP: A Bioconductor Package for Fingerprinting Flow Cytometric Data. 2009 , 193947	39

1275	iFlow: A Graphical User Interface for Flow Cytometry Tools in Bioconductor. 2009 , 103839	7
1274	Comparative analysis of gene regulation by the transcription factor PPARalpha between mouse and human. 2009 , 4, e6796	218
1273	Buffering of segmental and chromosomal aneuploidies in Drosophila melanogaster. 2009 , 5, e1000465	72
1272	Evolution of stress-regulated gene expression in duplicate genes of Arabidopsis thaliana. 2009 , 5, e1000581	87
1271	Rapid changes in transcription profiles of the Plasmodium yoelii yir multigene family in clonal populations: lack of epigenetic memory?. 2009 , 4, e4285	23
1270	The effect of transposable element insertions on gene expression evolution in rodents. 2009 , 4, e4321	27
1269	Age and diet affect gene expression profile in canine skeletal muscle. 2009 , 4, e4481	15
1268	Differences in the tumor microenvironment between African-American and European-American breast cancer patients. 2009 , 4, e4531	143
1267	Role of 3'UTRs in the translation of mRNAs regulated by oncogenic eIF4Ea computational inference. 2009 , 4, e4868	16
1266	Influence of smoking on colonic gene expression profile in Crohn's disease. 2009 , 4, e6210	23
1265	Impact of the TCR signal on regulatory T cell homeostasis, function, and trafficking. 2009 , 4, e6580	44
1264	New Alzheimer amyloid beta responsive genes identified in human neuroblastoma cells by hierarchical clustering. 2009 , 4, e6779	15
1263	Global gene expression profiling of human pleural mesotheliomas: identification of matrix metalloproteinase 14 (MMP-14) as potential tumour target. 2009 , 4, e7016	62
1262	The Warburg effect is genetically determined in inherited pheochromocytomas. 2009, 4, e7094	179
1261	Systems integration of biodefense omics data for analysis of pathogen-host interactions and identification of potential targets. 2009 , 4, e7162	16
1260	Molecular signatures reveal circadian clocks may orchestrate the homeorhetic response to lactation. 2009 , 4, e7395	31
1259	Effect of DLK1 and RTL1 but not MEG3 or MEG8 on muscle gene expression in Callipyge lambs. 2009 , 4, e7399	37
1258	Comprehensive gene and microRNA expression profiling reveals a role for microRNAs in human liver development. 2009 , 4, e7511	95

1257	Regulation of GABA(A) and glutamate receptor expression, synaptic facilitation and long-term potentiation in the hippocampus of prion mutant mice. 2009 , 4, e7592	52
1256	A novel lipidomic strategy reveals plasma phospholipid signatures associated with respiratory disease severity in cystic fibrosis patients. 2009 , 4, e7735	44
1255	Alternative splicing and transcriptome profiling of experimental autoimmune encephalomyelitis using genome-wide exon arrays. 2009 , 4, e7773	18
1254	Rainbow trout resistance to bacterial cold-water disease is moderately heritable and is not adversely correlated with growth. 2009 , 87, 860-7	101
1253	In Silico Enhanced Restriction Enzyme Based Methylation Analysis of the Human Glioblastoma Genome Using Agilent 244K CpG Island Microarrays. 2009 , 3, 57	2
1252	Immunological profiles of Bos taurus and Bos indicus cattle infested with the cattle tick, Rhipicephalus (Boophilus) microplus. 2009 , 16, 1074-86	70
1251	Unsupervised selection of highly coexpressed and noncoexpressed genes using a consensus clustering approach. 2009 , 13, 219-37	20
1250	KiWi: A Scalable Subspace Clustering Algorithm for Gene Expression Analysis. 2009,	6
1249	GRISSOM web based grid portal: Exploiting the power of grid infrastructure for the interpretation and storage of DNA microarray experiments. 2009 ,	1
1248	Transcriptomic profiling of heat-stress response in potato periderm. 2009 , 60, 4411-21	69
1247	Exploratory study on the transcriptional profile of pigs subclinically infected with porcine circovirus type 2. 2009 , 20, 96-109	10
1246	Epigenetic biomarker development. 2009 , 1, 99-110	94
1245	Array-based evolution of DNA aptamers allows modelling of an explicit sequence-fitness landscape. 2009 , 37, e6	85
1244	Transcriptome profile and cytogenetic analysis of immortalized neuronally restricted progenitor cells derived from the porcine olfactory bulb. 2009 , 20, 186-215	1
1243	Striatal alterations of secretogranin-1, somatostatin, prodynorphin, and cholecystokinin peptides in an experimental mouse model of Parkinson disease. 2009 , 8, 1094-104	39
1242	Mesenchymal stem cell-derived microvesicles protect against acute tubular injury. 2009 , 20, 1053-67	949
1241	Data integration for plant genomicsexemplars from the integration of Arabidopsis thaliana databases. 2009 , 10, 676-93	19
1240	Overcoming resistance to conventional drugs in Ewing sarcoma and identification of molecular predictors of outcome. 2009 , 27, 2209-16	93

1239	Statistical estimation of cell-cycle progression and lineage commitment in Plasmodium falciparum reveals a homogeneous pattern of transcription in ex vivo culture. 2009 , 106, 7559-64	64
1238	Normalization and statistical analysis of quantitative proteomics data generated by metabolic labeling. 2009 , 8, 2227-42	99
1237	The Vibrio cholerae flagellar regulatory hierarchy controls expression of virulence factors. 2009 , 191, 6555-70	126
1236	Differences in human and chimpanzee gene expression patterns define an evolving network of transcription factors in brain. 2009 , 106, 22358-63	109
1235	BioconductorBuntu: a Linux distribution that implements a web-based DNA microarray analysis server. 2009 , 25, 1438-9	2
1234	KEGGgraph: a graph approach to KEGG PATHWAY in R and bioconductor. 2009 , 25, 1470-1	221
1233	Mouse models of cystathionine beta-synthase deficiency reveal significant threshold effects of hyperhomocysteinemia. 2009 , 23, 883-93	88
1232	A central role for induced regulatory T cells in tolerance induction in experimental colitis. 2009 , 182, 3461-8	180
1231	T-cell infiltration and signaling in the adult dorsal spinal cord is a major contributor to neuropathic pain-like hypersensitivity. 2009 , 29, 14415-22	286
1230	Inosine alters gene expression and axonal projections in neurons contralateral to a cortical infarct and improves skilled use of the impaired limb. 2009 , 29, 8187-97	82
1229	Nodal points and complexity of Notch-Ras signal integration. 2009 , 106, 2218-23	33
1228	Gene expression profiles in zebrafish brain after acute exposure to domoic acid at symptomatic and asymptomatic doses. 2009 , 107, 65-77	44
1227	T-helper type 2-driven inflammation defines major subphenotypes of asthma. 2009 , 180, 388-95	1234
1226	Anatomical and transcriptomic studies of the coleorhiza reveal the importance of this tissue in regulating dormancy in barley. 2009 , 150, 1006-21	122
1225	Deciphering transcriptional and metabolic networks associated with lysine metabolism during Arabidopsis seed development. 2009 , 151, 2058-72	74
1224	Analysis of differential gene expression in colorectal cancer and stroma using fluorescence-activated cell sorting purification. 2009 , 100, 1452-64	27
1223	AtMyb41 regulates transcriptional and metabolic responses to osmotic stress in Arabidopsis. 2009 , 149, 1761-72	140
1222	Genome-wide screen of promoter methylation identifies novel markers in melanoma. 2009 , 19, 1462-70	144

1221	data. 2009 , 2009, 642524	10
1220	PTEN deficiency in a luminal ErbB-2 mouse model results in dramatic acceleration of mammary tumorigenesis and metastasis. 2009 , 284, 19018-26	61
1219	Outcome prediction in pediatric medulloblastoma based on DNA copy-number aberrations of chromosomes 6q and 17q and the MYC and MYCN loci. 2009 , 27, 1627-36	238
1218	Agrobacterium tumefaciens promotes tumor induction by modulating pathogen defense in Arabidopsis thaliana. 2009 , 21, 2948-62	123
1217	Thymic OX40 expression discriminates cells undergoing strong responses to selection ligands. 2009 , 182, 4581-9	54
1216	In vivo interference with AtTCP20 function induces severe plant growth alterations and deregulates the expression of many genes important for development. 2009 , 149, 1462-77	116
1215	Expansion and diversification of the Populus R2R3-MYB family of transcription factors. 2009 , 149, 981-93	346
1214	The high light response in Arabidopsis involves ABA signaling between vascular and bundle sheath cells. 2009 , 21, 2143-62	211
1213	Posttranscriptional regulation of angiotensin II type 1 receptor expression by glyceraldehyde 3-phosphate dehydrogenase. 2009 , 37, 2346-58	39
1212	SubpathwayMiner: a software package for flexible identification of pathways. 2009 , 37, e131	143
1211	A pipeline for the quantitative analysis of CG dinucleotide methylation using mass spectrometry. 2009 , 25, 2164-70	64
1210	WebArrayDB: cross-platform microarray data analysis and public data repository. 2009 , 25, 2425-9	34
1209	Expression differences by continent of origin point to the immortalization process. 2009, 18, 3864-75	3
1208	CD4+CD25-LAG3+ regulatory T cells controlled by the transcription factor Egr-2. 2009 , 106, 13974-9	166
1207	Development and evaluation of normalization methods for label-free relative quantification of endogenous peptides. 2009 , 8, 2285-95	84
1206	Positive selection for elevated gene expression noise in yeast. 2009 , 5, 299	78
1205	Dissection of a complex transcriptional response using genome-wide transcriptional modelling. 2009 , 5, 327	20
1204	Epigenetic profiling of somatic tissues from human autopsy specimens identifies tissue- and individual-specific DNA methylation patterns. 2009 , 18, 4808-17	206

1203	Metastasis-Associated Gene Expression Changes Predict Poor Outcomes in Patients with Dukes Stage B and C Colorectal Cancer. 2009 , 15, 7642-7651	320
1202	Multiple SET methyltransferases are required to maintain normal heterochromatin domains in the genome of Drosophila melanogaster. 2009 , 181, 1303-19	65
1201	Correlation between biofilm formation and the hypoxic response in Candida parapsilosis. 2009, 8, 550-9	71
1200	A unified mixed effects model for gene set analysis of time course microarray experiments. 2009 , 8, Article 47	27
1199	Detecting Gene Regulatory Networks from Microarray Data Using Fuzzy Logic. 2009 , 141-163	3
1198	Transcript and metabolite profiling of the adaptive response to mild decreases in oxygen concentration in the roots of arabidopsis plants. 2009 , 103, 269-80	174
1197	Conserved principles of mammalian transcriptional regulation revealed by RNA half-life. 2009, 37, e115	167
1196	A quick guide for developing effective bioinformatics programming skills. 2009 , 5, e1000589	34
1195	Identifying genes for establishing a multigenic test for hepatocellular carcinoma surveillance in hepatitis C virus-positive cirrhotic patients. 2009 , 18, 2929-32	26
1194	Nicotine withdrawal sensitivity, linkage to chr6q26, and association of OPRM1 SNPs in the SMOking in FAMilies (SMOFAM) sample. 2009 , 18, 3399-406	16
1193	Pharmacologic unmasking of epigenetically silenced genes in breast cancer. 2009 , 15, 1184-91	54
1192	Molecular response to cetuximab and efficacy of preoperative cetuximab-based chemoradiation in rectal cancer. 2009 , 27, 2751-7	86
1191	Gene expression profiling distinguishes radiation-induced fibrosing alveolitis from alveolitis in mice. 2010 , 173, 512-21	26
1190	Quality assessment and data analysis for microRNA expression arrays. 2009 , 37, e17	41
1189	Indole acts as an extracellular cue regulating gene expression in Vibrio cholerae. 2009, 191, 3504-16	130
1188	DNA replication licensing and progenitor numbers are increased by progesterone in normal human breast. 2009 , 150, 3318-26	108
1187	A Bayesian model for cross-study differential gene expression. 2009 , 104, 1295-1310	27
1186	Longitudinal system-based analysis of transcriptional responses to type I interferons. 2009 , 38, 362-71	25

1185	Relative contribution of sequence and structure features to the mRNA binding of Argonaute/EIF2C-miRNA complexes and the degradation of miRNA targets. 2009 , 19, 2009-20	77
1184	Decreased mitochondrial activities of malate dehydrogenase and fumarase in tomato lead to altered root growth and architecture via diverse mechanisms. 2009 , 149, 653-69	65
1183	Extensive structural renovation of retrogenes in the evolution of the Populus genome. 2009 , 151, 1943-51	50
1182	Conditioning of uropathogenic Escherichia coli for enhanced colonization of host. 2009 , 77, 2104-12	36
1181	Influence of fatty acid diets on gene expression in rat mammary epithelial cells. 2009, 38, 80-8	15
1180	Meta-analysis of gene expression in human pancreatic islets after in vitro expansion. 2009 , 39, 72-81	12
1179	Gene expression profiles in peripheral blood mononuclear cells of chronic heart failure patients. 2009 , 38, 233-40	44
1178	Pleiotropic effects of negative energy balance in the postpartum dairy cow on splenic gene expression: repercussions for innate and adaptive immunity. 2009 , 39, 28-37	41
1177	Severe preeclampsia-related changes in gene expression at the maternal-fetal interface include sialic acid-binding immunoglobulin-like lectin-6 and pappalysin-2. 2009 , 150, 452-62	125
1176	Bevacizumab and chemotherapy for recurrent glioblastoma: a single-institution experience. 2009 , 72, 1217-22	201
1175	A systematic characterization of Cwc21, the yeast ortholog of the human spliceosomal protein SRm300. 2009 , 15, 2174-85	28
1174	Differential gene expression in human conducting airway surface epithelia and submucosal glands. 2009 , 40, 189-99	22
1173	rHVDM: an R package to predict the activity and targets of a transcription factor. 2009 , 25, 419-20	5
1172	Getting started in gene expression microarray analysis. 2009 , 5, e1000543	95
1171	Cryptic variation in the human mutation rate. 2009 , 7, e1000027	84
1170	Cholesterol metabolism: the main pathway acting downstream of cytochrome P450 oxidoreductase in skeletal development of the limb. 2009 , 29, 2716-29	53
1169	KSHV manipulates Notch signaling by DLL4 and JAG1 to alter cell cycle genes in lymphatic endothelia. 2009 , 5, e1000616	49
1168	Gene set analysis methods applied to chicken microarray expression data. 2009 , 3 Suppl 4, S8	5

1167	DETORQUEO, QUIRKY, and ZERZAUST represent novel components involved in organ development mediated by the receptor-like kinase STRUBBELIG in Arabidopsis thaliana. 2009 , 5, e1000355	59
1166	Comparative inference of illegitimate recombination between rice and sorghum duplicated genes produced by polyploidization. 2009 , 19, 1026-32	66
1165	Analysis of array-CGH data using the R and Bioconductor software suite. 2009 , 201325	8
1164	Comparison of three microarray probe annotation pipelines: differences in strategies and their effect on downstream analysis. 2009 , 3 Suppl 4, S1	7
1163	Genome-wide transcriptional profiling of mononuclear phagocytes recruited to mouse lungs in response to alveolar challenge with the TLR2 agonist Pam3CSK4. 2009 , 297, L608-18	9
1162	A quick guide to teaching R programming to computational biology students. 2009 , 5, e1000482	17
1161	p63 and p73 transcriptionally regulate genes involved in DNA repair. 2009 , 5, e1000680	107
1160	ROCK2 allelic variants are not associated with pre-eclampsia susceptibility in the Finnish population. 2009 , 15, 443-9	6
1159	Microarray data mining using Bioconductor packages. 2009 , 3 Suppl 4, S9	7
1158	Sir2 paralogues cooperate to regulate virulence genes and antigenic variation in Plasmodium falciparum. 2009 , 7, e84	181
1157	ShortRead: a bioconductor package for input, quality assessment and exploration of high-throughput sequence data. 2009 , 25, 2607-8	355
1156	Statistical methods for gene set co-expression analysis. 2009 , 25, 2780-6	107
1155	Rank of correlation coefficient as a comparable measure for biological significance of gene coexpression. 2009 , 16, 249-60	167
1154	Comments on the analysis of unbalanced microarray data. 2009 , 25, 2035-41	47
1153	Genome-wide identification of alternative splice forms down-regulated by nonsense-mediated mRNA decay in Drosophila. 2009 , 5, e1000525	68
1152	Importing ArrayExpress datasets into R/Bioconductor. 2009 , 25, 2092-4	68
1151	Regulation of leukemic cell differentiation and retinoid-induced gene expression by statins. 2009 , 8, 615-25	11
1150	Ott1 (Rbm15) is essential for placental vascular branching morphogenesis and embryonic development of the heart and spleen. 2009 , 29, 333-41	29

1149	2009, 25, 1137-44	11
1148	aGEM: an integrative system for analyzing spatial-temporal gene-expression information. 2009 , 25, 2566-72	3
1147	Age-dependent variability in gene expression in male Fischer 344 rat retina. 2009, 107, 281-92	14
1146	Salmonella Typhimurium type III secretion effectors stimulate innate immune responses in cultured epithelial cells. 2009 , 5, e1000538	149
1145	Zebrafish miR-1 and miR-133 shape muscle gene expression and regulate sarcomeric actin organization. 2009 , 23, 619-32	131
1144	Detection of growth hormone doping by gene expression profiling of peripheral blood. 2009 , 94, 4703-9	26
1143	R/Bioconductor software for Illumina's Infinium whole-genome genotyping BeadChips. 2009 , 25, 2621-3	43
1142	SAFEGUI: resampling-based tests of categorical significance in gene expression data made easy. 2009 , 25, 541-2	3
1141	Comparative analyses of gene copy number and mRNA expression in glioblastoma multiforme tumors and xenografts. 2009 , 11, 477-87	99
1140	Population genomics in a disease targeted primary cell model. 2009 , 19, 1942-52	77
1139	Peroxisome proliferator-activated receptor beta/delta (PPARbeta/delta) but not PPARalpha serves as a plasma free fatty acid sensor in liver. 2009 , 29, 6257-67	107
1138	Identification and validation of a gene expression signature that predicts outcome in adult men with germ cell tumors. 2009 , 27, 5240-7	62
1137	Visualization of genomic data with the Hilbert curve. 2009 , 25, 1231-5	47
1136	Transcriptional map of respiratory versatility in the hyperthermophilic crenarchaeon Pyrobaculum aerophilum. 2009 , 191, 782-94	40
1135	The induction of antibody production by IL-6 is indirectly mediated by IL-21 produced by CD4+ T cells. 2009 , 206, 69-78	292
1134	arrayQualityMetricsa bioconductor package for quality assessment of microarray data. 2009 , 25, 415-6	635
1133	Genome-wide association study of alcohol dependence. 2009 , 66, 773-84	318
1132	CHF1/Hey2 promotes physiological hypertrophy in response to pressure overload through selective repression and activation of specific transcriptional pathways. 2009 , 13, 501-11	10

1131	Array-based genotyping in S.cerevisiae using semi-supervised clustering. 2009 , 25, 1056-62	5
1130	Lymphotoxin beta receptor signaling promotes tertiary lymphoid organogenesis in the aorta adventitia of aged ApoE-/- mice. 2009 , 206, 233-48	269
1129	Dynamic plastid redox signals integrate gene expression and metabolism to induce distinct metabolic states in photosynthetic acclimation in Arabidopsis. 2009 , 21, 2715-32	152
1128	Genome-wide analysis of maltose utilization and regulation in aspergilli. 2009 , 155, 3893-3902	30
1127	The cytosolic protein response as a subcomponent of the wider heat shock response in Arabidopsis. 2009 , 21, 642-54	151
1126	Gene expression profiles of tumor biology provide a novel approach to prognosis and may guide the selection of therapeutic targets in multiple myeloma. 2009 , 27, 4197-203	61
1125	High-throughput cell-based screening of 4910 known drugs and drug-like small molecules identifies disulfiram as an inhibitor of prostate cancer cell growth. 2009 , 15, 6070-8	148
1124	Aire-deficient C57BL/6 mice mimicking the common human 13-base pair deletion mutation present with only a mild autoimmune phenotype. 2009 , 182, 3902-18	103
1123	Quality assessment of microarray data in a multicenter study. 2009 , 18, 34-43	11
1122	Re-expression of GATA2 cooperates with peroxisome proliferator-activated receptor-gamma depletion to revert the adipocyte phenotype. 2009 , 284, 9458-64	52
1121	A problem with the correlation coefficient as a measure of gene expression divergence. 2009 , 183, 1597-600	43
1120	Identification and characterization of OscR, a transcriptional regulator involved in osmolarity adaptation in Vibrio cholerae. 2009 , 191, 4082-96	52
1119	BCL9 promotes tumor progression by conferring enhanced proliferative, metastatic, and angiogenic properties to cancer cells. 2009 , 69, 7577-86	139
1118	Developmental stage specificity and the role of mitochondrial metabolism in the response of Arabidopsis leaves to prolonged mild osmotic stress. 2010 , 152, 226-44	223
1117	Impaired uptake and/or utilization of leucine by Saccharomyces cerevisiae is suppressed by the SPT15-300 allele of the TATA-binding protein gene. 2009 , 75, 6055-61	18
1116	Binding sites for ETS family of transcription factors dominate the promoter regions of differentially expressed genes in abdominal aortic aneurysms. 2009 , 2, 565-72	22
1115	Cell envelope perturbation induces oxidative stress and changes in iron homeostasis in Vibrio cholerae. 2009 , 191, 5398-408	39
1114	Valproic acid-induced deregulation in vitro of genes associated in vivo with neural tube defects. 2009 , 108, 132-48	54

1113 Web-queryable large-scale data sets for hypothesis generation in plant biology. 2009 , 21	1, 1034-51 98
1112 PAnnBuilder: an R package for assembling proteomic annotation data. 2009 , 25, 1094-5	4
Gibberellin modulates anther development in rice via the transcriptional regulation of G. 2009 , 21, 1453-72	AMYB. 264
Detection of treatment-induced changes in signaling pathways in gastrointestinal strom using transcriptomic data. 2009 , 69, 9125-32	al tumors 50
Biomarkers of dietary energy restriction in women at increased risk of breast cancer. 200	09 , 2, 720-31 36
Differential effects of ethanol in the nucleus accumbens shell of alcohol-preferring (P), alcohol-non-preferring (NP) and Wistar rats: a proteomics study. 2009 , 92, 304-13	44
Gene expression changes in the nucleus accumbens of alcohol-preferring rats following ethanol consumption. 2009 , 94, 131-47	chronic 87
Genome-wide expression analysis of peripheral blood identifies candidate biomarkers for schizophrenia. 2009 , 43, 1073-7	ог 59
The Characterization Tool: A knowledge-based stem cell, differentiated cell, and tissue of with a web-based analysis front-end. 2009 , 3, 88-95	database 8
Toxicogenomic analysis of N-nitrosomorpholine induced changes in rat liver: comparison genomic and proteomic responses and anchoring to histopathological parameters. 2009	
Convergence of biomarkers, bioinformatics and nanotechnology for individualized cance treatment. 2009 , 27, 350-8	er 68
1102 flowCore: a Bioconductor package for high throughput flow cytometry. 2009 , 10, 106	300
1101 flowClust: a Bioconductor package for automated gating of flow cytometry data. 2009 , 1	10, 145 129
1100 MIMAS 3.0 is a Multiomics Information Management and Annotation System. 2009 , 10, 1	51 13
1099 Differential splicing using whole-transcript microarrays. 2009 , 10, 156	14
1098 PreP+07: improvements of a user friendly tool to preprocess and analyse microarray dat	ta. 2009 , 10, 16 10
The development of a comparison approach for Illumina bead chips unravels unexpected challenges applying newest generation microarrays. 2009 , 10, 186	d 4
1096 Unsupervised assessment of microarray data quality using a Gaussian mixture model. 20	09 , 10, 191 3

1095	CLEAN: CLustering Enrichment ANalysis. 2009 , 10, 234	53
1094	TableButler - a Windows based tool for processing large data tables generated with high-throughput methods. 2009 , 10, 235	4
1093	Identifying differential exon splicing using linear models and correlation coefficients. 2009, 10, 26	19
1092	dictyExpress: a Dictyostelium discoideum gene expression database with an explorative data analysis web-based interface. 2009 , 10, 265	57
1091	EDGE(3): a web-based solution for management and analysis of Agilent two color microarray experiments. 2009 , 10, 280	24
1090	Robust extraction of functional signals from gene set analysis using a generalized threshold free scoring function. 2009 , 10, 307	30
1089	Gene ARMADA: an integrated multi-analysis platform for microarray data implemented in MATLAB. 2009 , 10, 354	30
1088	ArrayMining: a modular web-application for microarray analysis combining ensemble and consensus methods with cross-study normalization. 2009 , 10, 358	77
1087	DFP: a Bioconductor package for fuzzy profile identification and gene reduction of microarray data. 2009 , 10, 37	9
1086	A comprehensive sensitivity analysis of microarray breast cancer classification under feature variability. 2009 , 10, 389	16
1085	Quantitative comparison of microarray experiments with published leukemia related gene expression signatures. 2009 , 10, 422	27
1084	TargetSearcha Bioconductor package for the efficient preprocessing of GC-MS metabolite profiling data. 2009 , 10, 428	153
1083	Classification across gene expression microarray studies. 2009 , 10, 453	13
1082	EMMA 2a MAGE-compliant system for the collaborative analysis and integration of microarray data. 2009 , 10, 50	62
1081	RGG: a general GUI Framework for R scripts. 2009 , 10, 74	4
1080	Development and evaluation of new mask protocols for gene expression profiling in humans and chimpanzees. 2009 , 10, 77	8
1079	Threshold selection in gene co-expression networks using spectral graph theory techniques. 2009 , 10 Suppl 11, S4	52
1078	Survival Online: a web-based service for the analysis of correlations between gene expression and clinical and follow-up data. 2009 , 10 Suppl 12, S10	4

1077	Expression pattern divergence of duplicated genes in rice. 2009 , 10 Suppl 6, S8	35
1076	Mechanism-anchored profiling derived from epigenetic networks predicts outcome in acute lymphoblastic leukemia. 2009 , 10 Suppl 9, S6	6
1075	Evolution of plant senescence. 2009 , 9, 163	48
1074	Detection of genomic deletions in rice using oligonucleotide microarrays. 2009 , 10, 129	34
1073	Expression profile and transcription factor binding site exploration of imprinted genes in human and mouse. 2009 , 10, 144	21
1072	BioMartbiological queries made easy. 2009 , 10, 22	501
1071	Gene expression during Drosophila melanogaster egg development before and after reproductive diapause. 2009 , 10, 242	76
1070	Large-scale analysis of antisense transcription in wheat using the Affymetrix GeneChip Wheat Genome Array. 2009 , 10, 253	24
1069	Host cell transcriptional profiling during malaria liver stage infection reveals a coordinated and sequential set of biological events. 2009 , 10, 270	83
1068	Gene expression profile of rat left ventricles reveals persisting changes following chronic mild exercise protocol: implications for cardioprotection. 2009 , 10, 342	20
1067	Characterization of the Zoarces viviparus liver transcriptome using massively parallel pyrosequencing. 2009 , 10, 345	60
1066	Gene copy number variation throughout the Plasmodium falciparum genome. 2009 , 10, 353	33
1065	Grapevine cell early activation of specific responses to DIMEB, a resveratrol elicitor. 2009 , 10, 363	46
1064	Computational identification of hepatitis C virus associated microRNA-mRNA regulatory modules in human livers. 2009 , 10, 373	147
1063	Molecular mechanisms of tungstate-induced pancreatic plasticity: a transcriptomics approach. 2009 , 10, 406	18
1062	Reciprocal regulation of microRNA and mRNA profiles in neuronal development and synapse formation. 2009 , 10, 419	27
1061	Relative power and sample size analysis on gene expression profiling data. 2009 , 10, 439	53
1060	Oligonucleotide array discovery of polymorphisms in cultivated tomato (Solanum lycopersicum L.) reveals patterns of SNP variation associated with breeding. 2009 , 10, 466	39

1059	An oligo-based microarray offers novel transcriptomic approaches for the analysis of pathogen resistance and fruit quality traits in melon (Cucumis melo L.). 2009 , 10, 467	57
1058	Expulsion of Trichuris muris is associated with increased expression of angiogenin 4 in the gut and increased acidity of mucins within the goblet cell. 2009 , 10, 492	22
1057	Fourmidable: a database for ant genomics. 2009 , 10, 5	34
1056	Endogenous control genes in complex vascular tissue samples. 2009 , 10, 516	12
1055	Differentially expressed genes for aggressive pecking behaviour in laying hens. 2009 , 10, 544	18
1054	Characterisation of microRNA expression in post-natal mouse mammary gland development. 2009 , 10, 548	104
1053	Using transcriptome profiling to characterize QTL regions on chicken chromosome 5. 2009 , 10, 575	12
1052	The expansion of amino-acid repeats is not associated to adaptive evolution in mammalian genes. 2009 , 10, 619	5
1051	Transcriptional adaptations following exercise in thoroughbred horse skeletal muscle highlights molecular mechanisms that lead to muscle hypertrophy. 2009 , 10, 638	38
1050	Somatic, germline and sex hierarchy regulated gene expression during Drosophila metamorphosis. 2009 , 10, 80	44
1049	A Distribution-Free Convolution Model for background correction of oligonucleotide microarray data. 2009 , 10 Suppl 1, S19	8
1048	PutidaNET: interactome database service and network analysis of Pseudomonas putida KT2440. 2009 , 10 Suppl 3, S18	15
1047	The choroid plexus response to a repeated peripheral inflammatory stimulus. 2009, 10, 135	50
1046	Comparative transcriptional survey between laser-microdissected cells from laminar abscission zone and petiolar cortical tissue during ethylene-promoted abscission in citrus leaves. 2009 , 9, 127	69
1045	Five QTL hotspots for yield in short rotation coppice bioenergy poplar: the Poplar Biomass Loci. 2009 , 9, 23	60
1044	Expression-based discovery of candidate ovule development regulators through transcriptional profiling of ovule mutants. 2009 , 9, 29	38
1043	Cbf genes of the Fr-A2 allele are differentially regulated between long-term cold acclimated crown tissue of freeze-resistant and - susceptible, winter wheat mutant lines. 2009 , 9, 34	27
1042	Sequence diversity in three tomato species: SNPs, markers, and molecular evolution. 2009 , 9, 85	36

1041	The direct effect of focal adhesion kinase (FAK), dominant-negative FAK, FAK-CD and FAK siRNA on gene expression and human MCF-7 breast cancer cell tumorigenesis. 2009 , 9, 280	47
1040	QPRT: a potential marker for follicular thyroid carcinoma including minimal invasive variant; a gene expression, RNA and immunohistochemical study. 2009 , 9, 93	19
1039	Small molecule activators of SIRT1 replicate signaling pathways triggered by calorie restriction in vivo. 2009 , 3, 31	172
1038	Recent developments in StemBase: a tool to study gene expression in human and murine stem cells. 2009 , 2, 39	14
1037	Differential gene expression signatures for cell wall integrity found in chitin synthase II (chs2Delta) and myosin II (myo1Delta) deficient cytokinesis mutants of Saccharomyces cerevisiae. 2009 , 2, 87	7
1036	Distributed Reproducible Research Using Cached Computations. 2009 , 11, 28-34	7
1035	Modulation of DNA glycosylase activities in mesenchymal stem cells. 2009 , 315, 2558-67	6
1034	Mycobacteria-induced granuloma necrosis depends on IRF-1. 2009 , 13, 2069-2082	13
1033	Bioinformatics analysis of mass spectrometry-based proteomics data sets. 2009 , 583, 1703-12	123
1032	Diagnosis of ulcerative colitis before onset of inflammation by multivariate modeling of genome-wide gene expression data. 2009 , 15, 1032-8	82
1031	Balancing inflammatory, lipid, and xenobiotic signaling pathways by VSL#3, a biotherapeutic agent, in the treatment of inflammatory bowel disease. 2009 , 15, 1721-36	59
1030	HIF-1alpha and HIF-2alpha have divergent roles in colon cancer. 2009 , 124, 763-71	126
1029	PDGF-B induces a homogeneous class of oligodendrogliomas from embryonic neural progenitors. 2009 , 124, 2251-9	43
1028	Downregulation of connective tissue growth factor by three-dimensional matrix enhances ovarian carcinoma cell invasion. 2009 , 125, 816-25	34
1027	Scalable analysis of flow cytometry data using R/Bioconductor. 2009 , 75, 699-706	14
1026	Automation in high-content flow cytometry screening. 2009 , 75, 789-97	25
1025	Per-channel basis normalization methods for flow cytometry data. 2010 , 77, 121-31	55
1024	A comparison of multiplex suspension array large-panel kits for profiling cytokines and chemokines in rheumatoid arthritis patients. 2009 , 76, 159-68	56

1023	RNA profiling of FAC-sorted neurons from the developing zebrafish spinal cord. 2009 , 238, 150-61	14
1022	Dynamic patterning at the pylorus: formation of an epithelial intestine-stomach boundary in late fetal life. 2009 , 238, 3205-17	31
1021	IL-12 and type I IFN response of neonatal myeloid DC to human CMV infection. 2009 , 39, 2789-99	48
1020	Genomic imbalances in rhabdomyosarcoma cell lines affect expression of genes frequently altered in primary tumors: an approach to identify candidate genes involved in tumor development. 2009 , 48, 455-67	85
1019	Identifying the molecular signature of the interstitial deletion 7q subgroup of uterine leiomyomata using a paired analysis. 2009 , 48, 865-85	26
1018	Characterization of B- and T-lineage acute lymphoblastic leukemia by integrated analysis of MicroRNA and mRNA expression profiles. 2009 , 48, 1069-82	75
1017	Distinct MHC gene expression patterns during progression of melanoma. 2010 , 49, 144-54	21
1016	Reprogramming of the transcriptome in a novel chromosome 3 transfer tumor suppressor ovarian cancer cell line model affected molecular networks that are characteristic of ovarian cancer. 2009 , 48, 648-61	15
1015	Cellular dichotomy between anchorage-independent growth responses to bFGF and TPA reflects molecular switch in commitment to carcinogenesis. 2009 , 48, 1059-69	13
1014	Genes involved in radiation therapy response in head and neck cancers. 2009 , 119, 91-101	31
1013	Methylation profile of circulating plasma DNA in patients with pancreatic cancer. 2009 , 99, 119-22	59
1012	High throughput single cell bioinformatics. 2009 , 25, 1772-9	25
1011	Over-expression of cathepsin E and trefoil factor 1 in sessile serrated adenomas of the colorectum identified by gene expression analysis. 2009 , 454, 291-302	26
1010	Uncovering transcriptional regulation of glycerol metabolism in Aspergilli through genome-wide gene expression data analysis. 2009 , 282, 571-86	30
1009	Transcriptome profiling of selectively bred Pacific oyster Crassostrea gigas families that differ in tolerance of heat shock. 2009 , 11, 650-68	79
1008	Stress-related genes define essential steps in the response of maize seedlings to smoke-water. 2009 , 9, 231-42	22
1007	The neuroprotective effect of dental pulp cells in models of Alzheimer's and Parkinson's disease. 2009 , 116, 71-8	64
1006	Immortalization and transformation of human mammary epithelial cells by a tumor-derived Myc mutant. 2009 , 116, 281-94	23

1005	TRAIL induces apoptosis in triple-negative breast cancer cells with a mesenchymal phenotype. 2009 , 113, 217-30	138
1004	Molecular signatures suggest a major role for stromal cells in development of invasive breast cancer. 2009 , 114, 47-62	164
1003	Gene-expression profiling of grape bud response to two alternative dormancy-release stimuli expose possible links between impaired mitochondrial activity, hypoxia, ethylene-ABA interplay and cell enlargement. 2009 , 71, 403-23	106
1002	Local and systemic transcriptome responses to herbivory and jasmonic acid in Populus. 2009 , 5, 459-474	28
1001	The antiproliferative effect of EPA in HL60 cells is mediated by alterations in calcium homeostasis. 2009 , 44, 103-13	17
1000	Docosahexaenoic acid activates some SREBP-2 targets independent of cholesterol and ER stress in SW620 colon cancer cells. 2009 , 44, 673-83	9
999	The effect of trans-10, cis-12 conjugated linoleic acid on gene expression profiles related to lipid metabolism in human intestinal-like Caco-2 cells. 2009 , 4, 103-12	8
998	Estimation of the Proportion of Differentially Expressed Genes Using Hellinger Distance. 2009 , 1, 246-267	
997	Processing and Analyzing Affymetrix SNP Chips with Bioconductor. 2009 , 1, 160-180	3
996	Differentially expressed genes during malting and correlation with malting quality phenotypes in barley (Hordeum vulgare L.). 2009 , 118, 937-52	36
995	Single feature polymorphisms between two rice cultivars detected using a median polish method. 2009 , 119, 151-64	13
994	Cytokine-mediated induction of anti-apoptotic genes that are linked to nuclear factor kappa-B (NF-kappaB) signalling in human islets and in a mouse beta cell line. 2009 , 52, 1092-101	71
993	Endotoxin-induced gene expression differences in the brain and effects of iNOS inhibition and norepinephrine. 2009 , 35, 730-9	14
992	Transcriptional profiling in response to inhibition of cellulose synthesis by thaxtomin A and isoxaben in Arabidopsis thaliana suspension cells. 2009 , 28, 811-30	31
991	Intra- and inter-individual genetic differences in gene expression. 2009 , 20, 281-95	18
990	A novel approach identified the FOLR1 gene, a putative regulator of milk protein synthesis. 2009 , 20, 498-503	18
989	Biomarkers of human gastrointestinal tract regions. 2009 , 20, 516-27	29
988	ANEXdb: an integrated animal ANnotation and microarray EXpression database. 2009 , 20, 768-77	23

987	Stable XIAP knockdown clones of HCT116 colon cancer cells are more sensitive to TRAIL, taxanes and irradiation in vitro. 2009 , 64, 307-16	28
986	Differentiation of a highly tumorigenic basal cell compartment in urothelial carcinoma. 2009 , 27, 1487-95	96
985	R Graphics. 2009 , 1, 216-220	5
984	Benchmarking currently available SELDI-TOF MS preprocessing techniques. 2009 , 9, 1754-62	16
983	Gold nanoparticles of diameter 1.4 nm trigger necrosis by oxidative stress and mitochondrial damage. 2009 , 5, 2067-76	595
982	Activation of the ERK/MAPK pathway: a signature genetic defect in posterior fossa pilocytic astrocytomas. 2009 , 218, 172-81	231
981	Gene expression in chorionic villous samples at 11 weeks of gestation in women who develop preeclampsia later in pregnancy: implications for screening. 2009 , 29, 1038-44	20
980	Bcl-2 mediated modulation of vascularization in prostate cancer xenografts. 2009 , 69, 459-70	12
979	Mapping of HNF4alpha target genes in intestinal epithelial cells. 2009 , 9, 68	51
978	Genetical genomic determinants of alcohol consumption in rats and humans. 2009, 7, 70	123
977	Environmentally-acquired bacteria influence microbial diversity and natural innate immune responses at gut surfaces. 2009 , 7, 79	171
976	Similar gene expression profiles of sporadic, PGL2-, and SDHD-linked paragangliomas suggest a common pathway to tumorigenesis. 2009 , 2, 25	11
975	Gene expression in the prefrontal cortex during adolescence: implications for the onset of schizophrenia. 2009 , 2, 28	83
974	Detailed transcriptome atlas of the pancreatic beta cell. 2009 , 2, 3	90
973	Identification of gene co-regulatory modules and associated cis-elements involved in degenerative heart disease. 2009 , 2, 31	6
972	Integrated analysis of DNA methylation and gene expression reveals specific signaling pathways associated with platinum resistance in ovarian cancer. 2009 , 2, 34	165
971	Finding exclusively deleted or amplified genomic areas in lung adenocarcinomas using a novel chromosomal pattern analysis. 2009 , 2, 43	6
970	MicroRNA-125a is over-expressed in insulin target tissues in a spontaneous rat model of Type 2 Diabetes. 2009 , 2, 54	96

969	Impact of segmental chromosomal duplications on leaf size in the grandifolia-D mutants of Arabidopsis thaliana. 2009 , 60, 122-33	42
968	Current status of gene expression profiling in the diagnosis and management of acute leukaemia. 2009 , 145, 555-68	17
967	A transcriptomic analysis of land-use impacts on the oyster, Crassostrea virginica, in the South Atlantic bight. 2009 , 18, 2415-25	31
966	Roles of rel(Spn) in stringent response, global regulation and virulence of serotype 2 Streptococcus pneumoniae D39. 2009 , 72, 590-611	61
965	Snf1-independent, glucose-resistant transcription of Adr1-dependent genes in a mediator mutant of Saccharomyces cerevisiae. 2009 , 74, 364-83	5
964	Arabidopsis plant homeodomain finger proteins operate downstream of auxin accumulation in specifying the vasculature and primary root meristem. 2009 , 59, 426-36	25
963	Genotype and time of day shape the Populus drought response. 2009 , 60, 703-15	109
962	Identification, structure, and functional requirement of the Mediator submodule Med7N/31. 2009 , 28, 69-80	45
961	Evaluating dosage compensation on the chicken Z chromosome: should effective dosage compensation eliminate sexual bias?. 2009 , 103, 357-9	12
960	Kinetic profile of the transcriptome changes induced in the choroid plexus by peripheral inflammation. 2009 , 29, 921-32	82
959	PML-RARalpha initiates leukemia by conferring properties of self-renewal to committed promyelocytic progenitors. 2009 , 23, 1462-71	72
958	Frequent in-frame somatic deletions activate gp130 in inflammatory hepatocellular tumours. 2009 , 457, 200-4	393
957	Enhancing CD8 T-cell memory by modulating fatty acid metabolism. 2009 , 460, 103-7	1047
956	CD14 regulates the dendritic cell life cycle after LPS exposure through NFAT activation. 2009 , 460, 264-8	232
955	Mitochondrial dysfunction triggered by loss of HtrA2 results in the activation of a brain-specific transcriptional stress response. 2009 , 16, 449-64	137
954	The human colon cancer methylome shows similar hypo- and hypermethylation at conserved tissue-specific CpG island shores. 2009 , 41, 178-186	1681
953	Genome-wide association study and meta-analysis find that over 40 loci affect risk of type 1 diabetes. 2009 , 41, 703-7	1298
952	Aberrant luminal progenitors as the candidate target population for basal tumor development in BRCA1 mutation carriers. 2009 , 15, 907-13	1034

951	A general pipeline for quality and statistical assessment of protein interaction data using R and Bioconductor. 2009 , 4, 535-46	14
950	Mapping identifiers for the integration of genomic datasets with the R/Bioconductor package biomaRt. 2009 , 4, 1184-91	1626
949	ChIP-seq: advantages and challenges of a maturing technology. 2009 , 10, 669-80	1331
948	A combinatorial mechanism for determining the specificity of E2F activation and repression. 2009 , 28, 2873-81	24
947	Systems biology of innate immunity. 2009 , 227, 264-82	118
946	The pleiotropic effects of the bar gene and glufosinate on the Arabidopsis transcriptome. 2009 , 7, 266-282	42
945	Dissimilar molecular defense responses are elicited in Triticum aestivum after infestation by different Diuraphis noxia biotypes. 2009 , 136, 209-22	17
944	Anaerobic adaptation in Pseudomonas aeruginosa: definition of the Anr and Dnr regulons. 2010 , 12, 1719-33	115
943	Gene expression profiles of meningiomas are associated with tumor cytogenetics and patient outcome. 2009 , 19, 409-20	32
942	Genomic landscape of meningiomas. 2010 , 20, 751-62	97
941	Heterogeneous expression of suppressor of cytokine signalling 2 (SOCS-2) in liver tissue. 2009 , 215, 176-83	8
940	Genome-wide reprogramming of regulatory networks, transport, cell wall and membrane biogenesis during arbuscular mycorrhizal symbiosis in Lotus japonicus. 2009 , 182, 200-212	250
939	Expression profiling and functional analysis of Populus WRKY23 reveals a regulatory role in defense. 2009 , 184, 48-70	67
938	Comparison of dorsal root ganglion gene expression in rat models of traumatic and HIV-associated neuropathic pain. 2009 , 13, 387-98	67
937	GridR: An R-based tool for scientific data analysis in grid environments. 2009, 25, 481-488	11
936		.0
,,	Validation of serum protein profiles by a dual antibody array approach. 2009 , 73, 252-66	18
935	Walidation of serum protein profiles by a dual antibody array approach. 2009 , 73, 252-66 miR-21 as a key regulator of oncogenic processes. 2009 , 37, 918-25	372

933	Improving detection of differentially expressed gene sets by applying cluster enrichment analysis to Gene Ontology. 2009 , 10, 240	9
932	PHOENIX, a web interface for (re)analysis of microarray data. 2009 , 4, 603-618	1
931	Preclinical efficacy of a carboxylesterase 2-activated prodrug of doxazolidine. 2009 , 52, 7678-88	23
930	Systems biology approaches and pathway tools for investigating cardiovascular disease. 2009 , 5, 588-602	82
929	Specific roles for the Ccr4-Not complex subunits in expression of the genome. 2009 , 15, 377-83	50
928	Nonallele-specific silencing of mutant and wild-type huntingtin demonstrates therapeutic efficacy in Huntington's disease mice. 2009 , 17, 1053-63	272
927	Robust-linear-model normalization to reduce technical variability in functional protein microarrays. 2009 , 8, 5451-64	55
926	MUI: A New Functional Similarity Measure for Gene Products Based on Gene Ontology. 2009 ,	
925	Administration of tomato and paprika beverages modifies hepatic glucose and lipid metabolism in mice: a DNA microarray analysis. 2009 , 57, 10964-71	13
924	Quantitative phosphoproteomics of tomato mounting a hypersensitive response reveals a swift suppression of photosynthetic activity and a differential role for hsp90 isoforms. 2009 , 8, 1168-82	42
923	Large scale transcriptome data integration across multiple tissues to decipher stem cell signatures. 2009 , 467, 229-245	2
922	Progesterone-regulated changes in endometrial gene expression contribute to advanced conceptus development in cattle. 2009 , 81, 784-94	226
921	Age-specific differences in oncogenic pathway dysregulation and anthracycline sensitivity in patients with acute myeloid leukemia. 2009 , 27, 5580-6	76
920	SATB1 defines the developmental context for gene silencing by Xist in lymphoma and embryonic cells. 2009 , 16, 507-16	164
919	A hierarchy of H3K4me3 and H3K27me3 acquisition in spatial gene regulation in Xenopus embryos. 2009 , 17, 425-34	187
918	Gene expression profile of the bone microenvironment in human fragility fracture bone. 2009 , 44, 87-101	83
917	A transcriptomic analysis of the EK1.Br strain of human fibroblastoid keratocytes: the effects of growth, quiescence and senescence. 2009 , 88, 277-85	18
916	Genomic response of hypoxic M I ler cells involves the very low density lipoprotein receptor as part of an angiogenic network. 2009 , 88, 928-37	27

915	Differences in gene expression of granulosa cells from women undergoing controlled ovarian hyperstimulation with either recombinant follicle-stimulating hormone or highly purified human menopausal gonadotropin. 2009 , 91, 1820-30	83
914	A humanized version of Foxp2 affects cortico-basal ganglia circuits in mice. 2009 , 137, 961-71	427
913	The IFITM proteins mediate cellular resistance to influenza A H1N1 virus, West Nile virus, and dengue virus. 2009 , 139, 1243-54	921
912	Reduced levels of protein tyrosine phosphatase CD45 protect mice from the lethal effects of Ebola virus infection. 2009 , 6, 162-73	21
911	Multiple pathways of mitochondrial-nuclear communication in yeast: intergenomic signaling involves ABF1 and affects a different set of genes than retrograde regulation. 2009 , 1789, 135-45	29
910	Limited transcriptional response of ovine microglia to prion accumulation. 2009 , 386, 345-50	6
909	Implications of age and diet on canine cerebral cortex transcription. 2009 , 30, 1314-26	29
908	Basic molecular fingerprinting of immature cerebellar cortical inhibitory interneurons and their precursors. 2009 , 159, 69-82	16
907	Intracranial self-stimulation to the lateral hypothalamus, a memory improving treatment, results in hippocampal changes in gene expression. 2009 , 162, 359-74	33
906	Expression of tak1 and tram induces synergistic pro-inflammatory signalling and adjuvants DNA vaccines. 2009 , 27, 5589-98	14
905	Simplet controls cell proliferation and gene transcription during zebrafish caudal fin regeneration. 2009 , 325, 329-40	40
904	E2F4 cooperates with pRB in the development of extra-embryonic tissues. 2009 , 332, 104-15	7
903	Arx acts as a regional key selector gene in the ventral telencephalon mainly through its transcriptional repression activity. 2009 , 334, 59-71	42
902	Construction of a functional network for common DNA damage responses in Escherichia coli. 2009 , 93, 514-24	8
901	Optimizing comparative genomic hybridization probes for genotyping and SNP detection in Plasmodium falciparum. 2009 , 93, 543-50	31
900	Left ventricular global transcriptional profiling in human end-stage dilated cardiomyopathy. 2009 , 94, 20-31	35
899	Suppression of inflammatory signaling in monocytes from patients with coronary artery disease. 2009 , 46, 177-85	38
898	Investigating transcriptional regulation: from analysis of complex networks to discovery of cis-regulatory elements. 2009 , 48, 277-86	2

897	interpretation. 2009 , 49, 42-9	9
896	Analysis of gene expression profiles under water stress in tolerant and sensitive sugarcane plants. 2009 , 176, 286-302	91
895	Genome-wide survey and expression profiling of heat shock proteins and heat shock factors revealed overlapped and stress specific response under abiotic stresses in rice. 2009 , 176, 583-90	212
894	Whole blood genomic biomarkers of acute cardiac allograft rejection. 2009 , 28, 927-35	38
893	Suppression of xenogeneic graft-versus-host disease by treatment with immunoglobulin-like transcript 3-Fc. 2009 , 70, 663-9	17
892	Ectopic recombination of a malaria var gene during mitosis associated with an altered var switch rate. 2009 , 389, 453-69	36
891	Physiologic oxygen concentration enhances the stem-like properties of CD133+ human glioblastoma cells in vitro. 2009 , 7, 489-97	205
890	Transcriptome transfer produces a predictable cellular phenotype. 2009 , 106, 7624-9	63
889	DNA microarray analyses and interactomic predictions for atopic dermatitis. 2009 , 55, 123-5	10
888	Global gene expression analysis reveals specific patterns of cell junctions in non-small cell lung cancer subtypes. 2009 , 63, 32-8	147
887	TWEAK/Fn14 pathway: a nonredundant role in intestinal damage in mice through a TWEAK/intestinal epithelial cell axis. 2009 , 136, 912-23	59
886	c-Met confers protection against chronic liver tissue damage and fibrosis progression after bile duct ligation in mice. 2009 , 137, 297-308, 308.e1-4	58
885	Phenotype and gene expression of human mesenchymal stem cells in alginate scaffolds. 2009 , 15, 1763-73	59
884	Transcriptome profiling of primary murine monocytes, lung macrophages and lung dendritic cells reveals a distinct expression of genes involved in cell trafficking. 2009 , 10, 2	23
883	Differential effects of cytokines and corticosteroids on toll-like receptor 2 expression and activity in human airway epithelia. 2009 , 10, 96	27
882	Meta-analysis of glioblastoma multiforme versus anaplastic astrocytoma identifies robust gene markers. 2009 , 8, 71	46
881	Classification-based comparison of pre-processing methods for interpretation of mass spectrometry generated clinical datasets. 2009 , 7, 19	7
880	A cross-study gene set enrichment analysis identifies critical pathways in endometriosis. 2009 , 7, 94	16

879	MicroRNA and gene expression patterns in the differentiation of human embryonic stem cells. 2009 , 7, 20		138
878	Response of sweet orange (Citrus sinensis) to 'Candidatus Liberibacter asiaticus' infection: microscopy and microarray analyses. 2009 , 99, 50-7		213
877	Modeling and analysis of ChIP-chip experiments. 2009 , 567, 133-43		4
876	MetaboAnalyst: a web server for metabolomic data analysis and interpretation. 2009 , 37, W652-60		1202
875	Differential regulation of immune responses and macrophage/neuron interactions in the dorsal root ganglion in young and adult rats following nerve injury. 2009 , 5, 70		88
874	Ranking differentially expressed genes from Affymetrix gene expression data: methods with reproducibility, sensitivity, and specificity. 2009 , 4, 7		61
873	Genomic profiling of breast tumours in relation to BRCA abnormalities and phenotypes. 2009 , 11, R47		106
872	T-cell metagene predicts a favorable prognosis in estrogen receptor-negative and HER2-positive breast cancers. 2009 , 11, R15		289
871	Gene expression profiling of the tumor microenvironment during breast cancer progression. 2009 , 11, R7		477
870	Correlating measurements across samples improves accuracy of large-scale expression profile experiments. <i>Genome Biology</i> , 2009 , 10, R143	18.3	10
869	Probe-level estimation improves the detection of differential splicing in Affymetrix exon array studies. <i>Genome Biology</i> , 2009 , 10, R77	18.3	23
868	Systemic analysis of the response of Aspergillus niger to ambient pH. <i>Genome Biology</i> , 2009 , 10, R47	18.3	84
867	Insights into the regulation of intrinsically disordered proteins in the human proteome by analyzing sequence and gene expression data. <i>Genome Biology</i> , 2009 , 10, R50	18.3	56
866	Development and application of versatile high density microarrays for genome-wide analysis of Streptomyces coelicolor: characterization of the HspR regulon. <i>Genome Biology</i> , 2009 , 10, R5	18.3	32
865	Software Engineering Education for Bioinformatics. 2009,		8
864	On Selecting the Best Pre-processing Method for Affymetrix Genechips. 2009 , 845-852		1
863	Triacylglyceride metabolism by Fusarium graminearum during colonization and sexual development on wheat. 2009 , 22, 1492-503		48
862	Intimate bacterial-fungal interaction triggers biosynthesis of archetypal polyketides in Aspergillus nidulans. 2009 , 106, 14558-63		483

861	Expansion of highly cytotoxic human natural killer cells for cancer cell therapy. 2009 , 69, 4010-7	421
860	A primary xenograft model of small-cell lung cancer reveals irreversible changes in gene expression imposed by culture in vitro. 2009 , 69, 3364-73	358
859	Exploiting scientific workflows for large-scale gene expression data analysis. 2009,	1
858	HTqPCR: high-throughput analysis and visualization of quantitative real-time PCR data in R. 2009 , 25, 3325-6	173
857	New insights into the biology and origin of mature aggressive B-cell lymphomas by combined epigenomic, genomic, and transcriptional profiling. 2009 , 113, 2488-97	121
856	Pathogenicity of a disease-associated human IL-4 receptor allele in experimental asthma. 2009 , 206, 2191-204	59
855	xIP-seq Platform: An Integrative Framework for High-Throughput Sequencing Data Analysis. 2009 ,	2
854	Identifying Functional Modules Using MST-Based Weighted Gene Co-Expression Networks. 2009,	1
853	An integrative genomics approach identifies Hypoxia Inducible Factor-1 (HIF-1)-target genes that form the core response to hypoxia. 2009 , 37, 4587-602	328
852	Genome-Wide Search for Splicing Defects Associated with Amyotrophic Lateral Sclerosis (ALS). 2009 ,	
851	Adipose tissue gene expression profiles of healthy young adult and geriatric dogs. 2009, 63, 160-71	10
850	Reverse engineering molecular regulatory networks from microarray data with qp-graphs. 2009 , 16, 213-27	56
849	Evolutionary and expression signatures of pseudogenes in Arabidopsis and rice. 2009, 151, 3-15	95
848	Pro-atherogenic effects of probucol in apo E-KO mice may be mediated through alterations in immune system: Parallel alterations in gene expression in the aorta and liver. 2009 , 206, 427-33	3
847	The use of a comprehensive tumour xenograft dataset to validate gene signatures relevant for radiation response. 2009 , 92, 417-22	14
846	Identification of TNF-alpha and MMP-9 as potential baseline predictive serum markers of sunitinib activity in patients with renal cell carcinoma using a human cytokine array. 2009 , 101, 1876-83	71
845	Modulation of the E2F1-driven cancer cell fate by the DNA damage response machinery and potential novel E2F1 targets in osteosarcomas. 2009 , 175, 376-91	42
844	Syk tyrosine kinase acts as a pancreatic adenocarcinoma tumor suppressor by regulating cellular growth and invasion. 2009 , 175, 2625-36	33

843	Identification of direct transcriptional targets of (V600E)BRAF/MEK signalling in melanoma. 2009 , 22, 785-98	53
842	Comparative genomic analyses identify the Vibrio harveyi genome sequenced strains BAA-1116 and HY01 as Vibrio campbellii. 2010 , 2, 81-89	120
841	Differential methylation profile of ovarian cancer in tissues and plasma. 2009 , 11, 60-65	71
840	Adult cystic nephroma and mixed epithelial and stromal tumor of the kidney are the same disease entity: molecular and histologic evidence. 2009 , 33, 72-80	70
839	Functional genomic analysis of peripheral blood during early acute renal allograft rejection. 2009 , 88, 942-51	31
838	Histogenomics: association of gene expression patterns with histological parameters in kidney biopsies. 2009 , 87, 290-5	35
837	Candidate genes associated with malignant pheochromocytomas by genome-wide expression profiling. 2009 , 250, 983-90	16
836	Assessment of transcriptional responses of Bacillus subtilis cells to the antibiotic enduracidin, which interferes with cell wall synthesis, using a high-density tiling chip. 2009 , 84, 253-67	20
835	Transcriptome profiling in hybrid poplar following interactions with Melampsora rust fungi. 2009 , 22, 190-200	68
834	Pattern Recognition and Pathway Analysis with Genetic Algorithms in Mass Spectrometry Based Metabolomics. 2009 , 2, 638-666	14
833	Microarray analysis of high-dose recombinant erythropoietin treatment of unilateral brain injury in neonatal mouse hippocampus. 2009 , 65, 485-92	67
832	MLL5 contributes to hematopoietic stem cell fitness and homeostasis. 2009 , 113, 1455-63	57
831	Inhibition of aurora kinases for tailored risk-adapted treatment of multiple myeloma. 2009 , 113, 4331-40	85
830	Role for MKL1 in megakaryocytic maturation. 2009 , 113, 2826-34	60
829	CS1 promotes multiple myeloma cell adhesion, clonogenic growth, and tumorigenicity via c-maf-mediated interactions with bone marrow stromal cells. 2009 , 113, 4309-18	55
828	Induction of angiogenesis by normal and malignant plasma cells. 2009 , 114, 128-43	114
827	The molecular signature of CD8+ T cells undergoing deletional tolerance. 2009 , 113, 4575-85	60
826	CC chemokine ligand 2 down-modulation by selected Toll-like receptor agonist combinations contributes to T helper 1 polarization in human dendritic cells. 2009 , 114, 796-806	20

825	MDS and secondary AML display unique patterns and abundance of aberrant DNA methylation. 2009 , 114, 3448-58	268
824	Gene expression-based classification and regulatory networks of pediatric acute lymphoblastic leukemia. 2009 , 114, 4486-93	35
823	Using CAGE Data for Quantitative Expression. 2009 , 101-121	
822	A comprehensive transcriptomic analysis of the effect of silicon on wheat plants under control and pathogen stress conditions. 2009 , 22, 1323-30	95
821	References. 2009 , 295-327	
820	Gene expression profiling of endometrial adenocarcinomas reveals increased apolipoprotein E expression in poorly differentiated tumors. 2009 , 19, 1226-31	11
819	affyPara-a Bioconductor Package for Parallelized Preprocessing Algorithms of Affymetrix Microarray Data. 2009 , 3, 83-7	8
818	Evolution of transcriptome profiles during muscle development in Casertana and cosmopolite pig breeds. 2009 , 8, 66-68	
817	R and Bioconductor solutions for alternative splicing detection. 2009 , 4, 131-5	
816	Isolation stress for 30 days alters hepatic gene expression profiles, especially with reference to lipid metabolism in mice. 2009 , 37, 79-87	18
815	ODDSOC2 is a MADS box floral repressor that is down-regulated by vernalization in temperate cereals. 2010 , 153, 1062-73	57
814	Increased leaf size: different means to an end. 2010 , 153, 1261-79	172
813	Transcriptional profiling reveals divergent roles of PPARalpha and PPARbeta/delta in regulation of gene expression in mouse liver. 2010 , 41, 42-52	92
812	Anti-melanoma activity of the 9.2.27PE immunotoxin in dacarbazine resistant cells. 2010 , 33, 272-8	9
811	Characterization of frequency-dependent responses of the vascular system to repetitive vibration. 2010 , 52, 584-94	29
810	Distinctive gene expression profiles characterize donor biopsies from HCV-positive kidney donors. 2010 , 90, 1172-9	4
809	The RON1/FRY1/SAL1 gene is required for leaf morphogenesis and venation patterning in Arabidopsis. 2010 , 152, 1357-72	68
808	Mean, median and tri-mean based statistical detection methods for differential gene expression in microarray data. 2010 ,	

807	Quantifying protein function specificity in the gene ontology. 2010 , 2, 238-44	6
806	Gene expression patterns in anterior pituitary associated with quantitative measure of oestrous behaviour in dairy cows. 2010 , 4, 1297-307	12
805	The Arabidopsis thaliana NAC transcription factor family: structure-function relationships and determinants of ANAC019 stress signalling. 2010 , 426, 183-96	274
804	Tools to identify organ rejection and immune quiescence for biological understanding and personalized medical care. 2010 , 4, 115-21	3
803	Transcriptomics approach to investigate zebrafish heart regeneration. 2010 , 11, 369-80	48
802	Boolean modeling of transcriptome data reveals novel modes of heterotrimeric G-protein action. 2010 , 6, 372	89
801	Sheep category can be classified using machine learning techniques applied to fatty acid profiles derivatised as trimethylsilyl esters. 2010 , 50, 782	1
800	Revealing a signaling role of phytosphingosine-1-phosphate in yeast. 2010 , 6, 349	43
799	A partial chromosomal deletion caused by random plasmid integration resulted in a reduced virulence phenotype in Fusarium graminearum. 2010 , 23, 1083-96	11
798	Similarities and differences between smoking-related gene expression in nasal and bronchial epithelium. 2010 , 41, 1-8	91
797	Genes with relevance for early to late progression of colon carcinoma based on combined genomic and transcriptomic information from the same patients. 2010 , 9, 79-91	14
796	Homeodomain-interacting protein kinase 2 plays an important role in normal terminal erythroid differentiation. 2010 , 115, 4853-61	36
795	Clonal expansions of cytotoxic T cells exist in the blood of patients with Waldenstrom macroglobulinemia but exhibit anergic properties and are eliminated by nucleoside analogue therapy. 2010 , 115, 3580-8	29
794	Diffuse large B-cell lymphomas with CDKN2A deletion have a distinct gene expression signature and a poor prognosis under R-CHOP treatment: a GELA study. 2010 , 116, 1092-104	98
793	Chemical genomic screening reveals synergism between parthenolide and inhibitors of the PI-3 kinase and mTOR pathways. 2010 , 116, 5983-90	66
792	A compendium of myeloma-associated chromosomal copy number abnormalities and their prognostic value. 2010 , 116, e56-65	263
791	MicroRNA expression in maturing murine megakaryocytes. 2010 , 116, e128-38	70
790	Early Career Research Award Lecture. Structure, evolution and dynamics of transcriptional regulatory networks. 2010 , 38, 1155-78	18

(2021-2010)

789	Gene enrichment profiles reveal T-cell development, differentiation, and lineage-specific transcription factors including ZBTB25 as a novel NF-AT repressor. 2010 , 115, 5376-84	103
788	A novel role of IL-17-producing lymphocytes in mediating lytic bone disease in multiple myeloma. 2010 , 116, 3554-63	157
787	Functional Analysis of Genes. 2010 , 2, 1-16	2
786	Identifying genes progressively silenced in preneoplastic and neoplastic liver tissues. 2010 , 3, 52-67	3
785	Disruption of two defensive signaling pathways by a viral RNA silencing suppressor. 2010 , 23, 835-45	144
7 ⁸ 4	Rhinovirus-induced modulation of gene expression in bronchial epithelial cells from subjects with asthma. 2010 , 3, 69-80	228
783	Gene expression profiling in multiple sclerosis: a disease of the central nervous system, but with relapses triggered in the periphery?. 2010 , 37, 613-21	45
782	Identification of novel immunomodulators in lung squamous cell carcinoma based on transcriptomic data 2022 , 19, 1843-1860	
781	Lysyl hydroxylase 2 deficiency promotes filopodia formation and fibroblast migration. 2021 , 587, 146-152	
780	BioInfograph: An Online Tool to Design and Display Multi-Panel Scientific Figure Interactively 2021 , 12, 784531	2
779	MethylScore, a pipeline for accurate and context-aware identification of differentially methylated regions from population-scale plant WGBS data.	0
778	Transcriptional analysis of gasoline engine exhaust particulate matter 2.5-exposed human umbilical vein endothelial cells reveals the different gene expression patterns related to the cardiovascular diseases 2022 , 29, 101190	
777	Uncovering transformation products of four organic contaminants of concern by photodegradation experiments and analysis of real samples from a local river 2021 , 293, 133408	2
776	Registered Report: Transcriptional Analysis of Savings Memory Suggests Forgetting is Due to Retrieval Failure. 2020 , 7, ENEURO.0313-19.2020	
775	Bex1 significantly contributes to the proliferation and invasiveness of malignant tumor cells. 2020 , 20, 1-1	3
774	Cdo Is Required for Efficient Motor Neuron Generation of Embryonic Stem Cells. 2020 , 13, 342-352	2
773	♣hydroxybutyrate does not alter the effects of glucose deprivation on breast cancer cells. 2020, 21, 65	1
772	Transcriptome changes in maternal peripheral blood during term parturition mimic perturbations preceding spontaneous Preterm birth 2021,	O

771 Data Management. **2021**, 169-181

770	Surgical trauma is associated with renal immune cell activation in rats: A microarray study. 2021 , 9, e15142	1
769	Adipose Tissue Dysfunctions in Response to an Obesogenic Diet Are Reduced in Mice after Transgenerational Supplementation with Omega 3 Fatty Acids 2021 , 11,	0
768	An atypical class of non-coding small RNAs is produced in rice leaves upon bacterial infection 2021 , 11, 24141	2
767	Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space 2022 , 2, 100085-100085	6
766	Forecasting Gastric Cancer Diagnosis, Prognosis, and Drug Repurposing with Novel Gene Expression Signatures 2021 ,	1
765	Data Integration Challenges for Machine Learning in Precision Medicine 2021 , 8, 784455	О
764	Differential LysoTracker Uptake Defines Two Populations of Distal Epithelial Cells in Idiopathic Pulmonary Fibrosis 2022 , 11,	2
763	Variations in Plant Growth Characteristics Due to Oxygen Plasma Irradiation on Leaf and Seed. 2022 , 12, 259	1
762	Developing Biliary Atresia-like Model by Treating Human Liver Organoids with Polyinosinic:Polycytidylic Acid (Poly (I:C)). 2022 , 44, 644-653	O
761	KRAB zinc finger protein ZNF676 controls the transcriptional influence of LTR12-related endogenous retrovirus sequences 2022 , 13, 4	1
760	ptairMS: real-time processing and analysis of PTR-TOF-MS data for biomarker discovery in exhaled breath 2022 ,	1
759	In-depth analysis of proteomic and genomic fluctuations during the time course of human embryonic stem cells directed differentiation into beta cells 2022 , e2100265	O
758	Improving bioinformatics software quality through incorporation of software engineering practices 2022 , 8, e839	2
757	Assessing and assuring interoperability of a genomics file format.	
756	InterCellar enables interactive analysis and exploration of cell-cell communication in single-cell transcriptomic data 2022 , 5, 21	O
755	Influence of Fermentation Conditions (Temperature and Time) on the Physicochemical Properties and Bacteria Microbiota of Amasi. 2022 , 8, 57	О
754	Differential microRNA expression profile in blood of children with Down syndrome suggests a role in immunological dysfunction 2022 , 1	O

753	Bioinformatic Analysis Combined With Experimental Validation Reveals Novel Hub Genes and Pathways Associated With Focal Segmental Glomerulosclerosis 2021 , 8, 691966	1
752	Gene Network of Susceptibility to Atypical Femoral Fractures Related to Bisphosphonate Treatment 2022 , 13,	O
751	Comprehensive characterization of the epigenetic landscape in Multiple Myeloma 2022, 12, 1715-1729	О
750	Whole-exome Sequencing Study of Hypospadias.	
749	Bioinformatics Characterization of Candidate Genes Associated with Gene Network and miRNA Regulation in Esophageal Squamous Cell Carcinoma Patients. 2022 , 12, 1083	
748	Overlapping transcriptional programs promote survival and axonal regeneration of injured retinal ganglion cells.	О
747	Integrative epigenomic profiling reveal AP-1 is a key regulator in intrahepatich cholangiocarcinoma 2021 , 114, 241-252	1
746	Metabolomics-Based Frailty Biomarkers in Older Chinese Adults 2021 , 8, 830723	O
745	Plotgardener: Cultivating precise multi-panel figures in R 2022,	1
744	Skeletal muscle transcriptomics identifies common pathways in nerve crush injury and ageing 2022 , 12, 3	1
743	Gene Expression Analysis Platform (GEAP): A highly customizable, fast, versatile and ready-to-use microarray analysis platform 2021 , 45, e20210077	
742	Tumor ENPP1(CD203a)/Haptoglobin Axis Exploits Myeloid-Derived Suppressor Cells to Promote Post-Radiotherapy Local Recurrence in Breast Cancer 2022 ,	О
741	SkewC: Identifying cells with skewed gene body coverage in single-cell RNA sequencing data 2022 , 25, 103777	O
740	Disparities in Lung Cancer: miRNA Isoform Characterization in Lung Adenocarcinoma 2022, 14,	О
739	Human Cardiac Organoids to Model COVID-19 Cytokine Storm Induced Cardiac Injuries 2022,	1
738	Image annotation as a multi-aspect case study. 2022 , 207-231	
737	RNA-Seq Experiment and Data Analysis 2022, 2418, 405-424	1
736	Hyperbaric oxygen therapy after mid-cervical spinal contusion injury 2022,	

735	Integrative OMICS Data-Driven Procedure Using a Derivatized Meta-Analysis Approach 2022 , 13, 828786	0
734	Gene mining of 100-grain weight and the number of four-seed pods in soybean (Glycine max).	O
733	Transient inhibition of the JAK/STAT pathway prevents B-ALL development in genetically predisposed mice 2022 ,	0
732	Live-bearing cockroach genome reveals convergent evolutionary mechanisms linked to viviparity in insects and beyond.	O
731	A Python library for probabilistic analysis of single-cell omics data 2022 , 40, 163-166	9
730	Identifying Significant Genes and Functionally Enriched Pathways in Familial Hypercholesterolemia Using Integrated Gene Co-Expression Network Analysis. 2022 ,	O
729	Ectomycorrhizal fungus supports endogenous rhythmic growth and corresponding resource allocation in oak during various below- and aboveground biotic interactions. 2021 , 11, 23680	2
728	Interleukin-10 receptor signaling promotes the maintenance of a PD-1 TCF-1 CD8 T´cell population that sustains anti-tumor immunity. 2021 ,	8
727	CD137 (4-1BB) costimulation of CD8 T cells is more potent when provided in cis than in trans with respect to CD3-TCR stimulation 2021 , 12, 7296	3
726	Interaction network analysis of YBX1 for identification of therapeutic targets in adenocarcinomas. 2019 , 44,	1
725	Microbiome data science. 2019 , 44,	3
724	Simulation Modelling and Machine Learning Platform for Processing Fluorescence Spectroscopy Data. 2022 , 178-190	
723	High-Content Screening in Cell Biology. 2022,	
722	Discovery of Virus-Host interactions using bioinformatic tools. 2022 ,	O
721	Laser Capture Microdissection-Based mRNA Expression Microarrays and Single-Cell RNA Sequencing in Atherosclerosis Research 2022 , 2419, 715-726	O
720	Analysis of Liver Responses to Non-alcoholic Steatohepatitis by mRNA-Sequencing 2022 , 2455, 163-179	
719	Nutrigenomics in livestock: potential role in physiological regulation and practical applications. 2022 ,	
718	What Is the Transcriptome and How It Is Evaluated. 2022, 3-50	

717	Comprehensive Transcriptomic Analysis of Cultivated on Germinated Soybeans 2022, 50, 1-11	0
716	Emerging Bioinformatics Methods and Resources in Drug Toxicology 2022 , 2425, 133-146	1
715	Healthy aging and muscle function are positively associated with NAD+ abundance in humans. 2022 , 2, 254-263	4
714	Ulcerative colitis is characterized by a plasmablast-skewed humoral response associated with disease activity 2022 ,	2
713	Impaired p53-Mediated DNA Damage Response Contributes to Microcephaly in Nijmegen Breakage Syndrome Patient-Derived Cerebral Organoids 2022 , 11,	О
712	Genome-Wide Identification and Expression Profiles of 13 Key Structural Gene Families Involved in the Biosynthesis of Rice Flavonoid Scaffolds 2022 , 13,	O
711	Probiotic normalization of systemic inflammation in siblings of type 1 diabetes patients: an open-label pilot study 2022 , 12, 3306	6
710	Systematic Analysis of Molecular Characterization and Clinical Relevance of Liquid-Liquid Phase Separation Regulators in Digestive System Neoplasms 2021 , 9, 820174	O
709	The Nephrotoxin Puromycin Aminonucleoside Induces Injury in Kidney Organoids Differentiated from Induced Pluripotent Stem Cells 2022 , 11,	1
708	Comparative Analysis of Seed Transcriptome and Coexpression Analysis Reveal Candidate Genes for Enhancing Seed Size/Weight in 2022 , 13, 814486	1
707	Methylome analysis for prediction of long and short-term survival in glioblastoma patients from the Nordic trial.	
706	The anti-aging protein Klotho affects early postnatal myogenesis by downregulating Jmjd3 and the canonical Wnt pathway 2022 , 36, e22192	O
705	PUCHI represses early meristem formation in developing lateral roots of Arabidopsis thaliana 2022 ,	О
704	Genome-wide investigation of the ZF-HD gene family in two varieties of alfalfa (Medicago sativa L.) and its expression pattern under alkaline stress 2022 , 23, 150	O
703	ETV2 regulates PARP-1 binding protein to induce ER stress-mediated death in tuberin-deficient cells 2022 , 5,	O
702	Fucoidan ()/Polydopamine Composite-Modified Surface Promotes Osteogenic Potential of Periodontal Ligament Stem Cells 2022 , 20,	1
701	Evaluation of Early Biomarkers of Atherosclerosis Associated with Polychlorinated Biphenyl Exposure: An and Study 2022 , 130, 37011	О
700	mRNA expression analysis of the hippocampus in a vervet monkey model of fetal alcohol spectrum disorder 2022 , 14, 21	1

699	Deep Single-Cell-Type Proteome Profiling of Mouse Brain by Nonsurgical AAV-Mediated Proximity Labeling 2022 ,	3
698	Human repair-related Schwann cells adopt functions of antigen-presenting cells in vitro.	
697	LEM domain containing 1 promotes pancreatic cancer growth and metastasis by p53 and mTORC1 signaling pathway 2022 , 13, 7771-7784	2
696	Transcriptome analysis reveals SALL4 as a prognostic key gene in gastric adenocarcinoma 2022 , 34, 11	
695	Activation of the Renin-Angiotensin System Disrupts the Cytoskeletal Architecture of Human Urine-Derived Podocytes 2022 , 11,	0
694	Alevin-fry unlocks rapid, accurate and memory-frugal quantification of single-cell RNA-seq data 2022 , 19, 316-322	1
693	Guitar2: An improved version of the Guitar for sketching the transcriptomic view of RNA-related biological features 2022 ,	0
692	Epigenome-wide association study and epigenetic age acceleration associated with cigarette smoking among Costa Rican adults 2022 , 12, 4277	1
691	Bayesian Random-Effects Meta-Analysis Models in Gene Expression Studies.	
690	Graph theoretical way of understanding protein-protein interaction in ovarian cancer. 2022, 1-10	1
689	Suppressed IFN-Eand TNF-Enduced Inflammation in Human Keratinocytes via Down-Regulation of the NF-B and STAT1 Pathways 2022 , 27,	0
688	Vitamin B Complex and Experimental Autoimmune Encephalomyelitis -Attenuation of the Clinical Signs and Gut Microbiota Dysbiosis 2022 , 14,	1
687	Ten simple rules for finding and selecting R packages 2022, 18, e1009884	0
686	Subtypes in pancreatic ductal adenocarcinoma based on niche factor dependency show distinct drug treatment responses 2022 , 41, 89	1
685	Salmonella enterica subsp. enterica Welikade: guideline for phylogenetic analysis of serovars rarely involved in foodborne outbreaks 2022 , 23, 217	0
684	Convergence of case-specific epigenetic alterations identify a confluence of genetic vulnerabilities tied to opioid overdose 2022 ,	o
683	Immediate perturbation of DNA methylation upon acute prenatal alcohol exposure in the mouse developing brain cortex.	
682	Identification of Common and Distinct Pathways in Inflammatory Bowel Disease and Colorectal Cancer: A Hypothesis Based on Weighted Gene Co-Expression Network Analysis 2022 , 13, 848646	О

681	Pericyte Loss Leads to Capillary Stalling Through Increased Leukocyte-Endothelial Cell Interaction in the Brain 2022 , 16, 848764	O
680	Towards standardized and reproducible research in skin microbiomes 2022,	1
679	Molecular basis of differential adventitious rooting competence in poplar genotypes 2022,	О
678	Gene Expression over Time during Cell Transformation Due to Non-Genotoxic Carcinogen Treatment of Bhas 42 Cells 2022 , 23,	1
677	Metabolic incorporation of electron-rich ribonucleosides enhances APEX-seq for profiling spatially restricted nascent transcriptome 2022 ,	1
676	miR-550a-3p is a prognostic biomarker and exerts tumor-suppressive functions by targeting HSP90AA1 in diffuse malignant peritoneal mesothelioma 2022 ,	1
675	€Cyanoalanine Synthase Protects Mites against Arabidopsis Defenses 2022 ,	1
674	Novel cell lines derived from Chinese hamster kidney tissue 2022 , 17, e0266061	1
673	Guidelines for collaborative development of sustainable data treatment software. 2022, 24, 33-72	0
672	Secreted Protein Acidic and Rich in Cysteine, a Novel Regulator of Vascular Cell Function in Pulmonary Hypertension 2022 ,	2
671	RGMQL: scalable and interoperable computing of heterogeneous omics big data and metadata in R/Bioconductor 2022 , 23, 123	O
670	Exploiting 4-1BB immune checkpoint to enhance the efficacy of oncolytic virotherapy for diffuse intrinsic pontine gliomas 2022 , 7,	O
669	Transcriptional responses of Aurantiochytrium limacinum under light conditions 2022,	1
668	Matrisome alterations in obesity - Adipose tissue transcriptome study on monozygotic weight-discordant twins 2022 ,	1
667	ForkJoinPcc Algorithm for Computing the Pcc Matrix in Gene Co-Expression Networks. 2022 , 11, 1174	О
666	Gene markers of dietary macronutrient composition and growth in the skeletal muscle of gilthead sea bream (Sparus aurata). 2022 , 738221	O
665	Genetic effect of ischemia-reperfusion injury upon primary graft dysfunction and chronic lung allograft dysfunction in lung transplantation: evidence based on transcriptome data 2022 , 71, 101556	O
664	Genome-wide DNA methylation profiling identifies epigenetic changes in CD4+ and CD14+ cells of multiple sclerosis patients 2022 , 60, 103714	O

663	The Danish High-Risk and Resilience Study-VIA 15 - A Study Protocol for the Third Clinical Assessment of a Cohort of 522 Children Born to Parents Diagnosed With Schizophrenia or Bipolar Disorder and Population-Based Controls 2022 , 13, 809807	O
662	Bi-phasic regulation of AIMP2 and its splice variant in PARP-1-dependent neurodegeneration.	
661	Physiological and comparative proteomic analyzes reveal immune defense response of the king scallop Pecten maximus in presence of paralytic shellfish toxin (PST) from Alexandrium minutum. 2022 , 115, 102231	
660	Gene expression and network based study of colorectal adenocarcinoma reveals tankyrase, PIK3CB and cyclin G-associated kinase as potential target candidates. 2022 , 27, 101605	
659	Multi-omic based production strain improvement (MOBpsi) for bio-manufacturing of toxic chemicals 2022 ,	0
658	SBGNview: towards data analysis, integration and visualization on all pathways. 2021 ,	
657	Evaluation of the effect of filtered ultrafine particulate matter on bleomycin-induced lung fibrosis in a rat model using computed tomography, histopathologic analysis, and RNA sequencing. 2021 , 11, 22672	0
656	Epithelial-to-Mesenchymal Transition Mediates Resistance to Maintenance Therapy with Vinflunine in Advanced Urothelial Cell Carcinoma 2021 , 13,	1
655	Machine learning prediction of antiviral-HPV protein interactions for anti-HPV pharmacotherapy 2021 , 11, 24367	O
654	Transposable elements mediate genetic effects altering the expression of nearby genes in colorectal cancer.	
653	Hair growth promoting effect of toothpaste in C57BL/6 mice: Active components and their effects on genomic expression. 2021 , 64, 421-431	
652	Carbon flux through photosynthesis and central carbon metabolism show distinct patterns between algae, C and C plants 2021 ,	2
651	geneExpressionFromGEO: An R Package to Facilitate Data Reading from Gene Expression Omnibus (GEO) 2022 , 2401, 187-194	1
650	Syncytiotrophoblast-derived extracellular vesicles carry apolipoprotein-E and affect lipid synthesis of liver cells in vitro. 2021 ,	2
649	Prediction and Experimental Verification of a Hierarchical Transcription Factor Regulatory Network of Porcine Myoglobin (Mb) 2021 , 11,	О
648	Worldwide diversity, association potential, and natural selection in the superimposed taste genes, CD36 and GNAT3 2022 , 47,	
647	An In Vitro Protocol to Study the Modulatory Effects of a Food or Biocompound on Human Gut Microbiome and Metabolome 2021 , 10,	
646	Oxicam-type non-steroidal anti-inflammatory drugs inhibit NPR1-mediated salicylic acid pathway 2021 , 12, 7303	1

645	Genome-wide characterization, evolution, structure, and expression analysis of the F-box genes in Caenorhabditis 2021 , 22, 889	2
644	Transcriptomic analysis of frontotemporal lobar degeneration with TDP-43 pathology reveals cellular alterations across multiple brain regions 2021 , 143, 383	О
643	ProteoDisco: A flexible R approach to generate customized protein databases for extended search space of novel and variant proteins in proteogenomic studies. 2021 ,	
642	Unique transcriptomic changes underlie hormonal interactions during mammary histomorphogenesis in female pigs 2021 ,	О
641	Unraveling the genotype by environment interaction in a thermosensitive fish with a polygenic sex determination system. 2021 , 118,	3
640	Dynamic transcriptome analysis reveals signatures of paradoxical effect of vemurafenib on human dermal fibroblasts 2021 , 19, 123	О
639	What can cold-induced transcriptomes of Arctic Brassicaceae tell us about the evolution of cold tolerance?.	
638	Polycomb group ring finger protein 6 suppresses Myc-induced lymphomagenesis 2022 , 5,	1
637	Macrophage inflammation resolution requires CPEB4-directed offsetting of mRNA degradation 2022 , 11,	1
636	The gut environment regulates bacterial gene expression which modulates susceptibility to bacteriophage infection 2022 , 30, 556-569.e5	1
635	Malic Enzyme 1 Absence in Synovial Sarcoma Shifts Antioxidant System Dependence and Increases Sensitivity to Ferroptosis Induction with ACXT3102 2022 ,	1
634	A presynaptic phosphosignaling hub for lasting homeostatic plasticity 2022 , 39, 110696	О
633	Recurrent WWTR1 S89W mutations and Hippo pathway deregulation in clear cell carcinomas of the cervix 2022 ,	О
632	Pyrroloquinoline quinone (PQQ) protects mitochondrial function of HEI-OC1 cells under premature senescence. 2022 , 8,	О
631	Radix Bupleuri-Radix Paeoniae Alba Couplet Medicine in the Treatment of Type 2 Diabetes Mellitus - a Network Pharmacology and Cellular Experimental Assessment. 2022 , 102132	О
630	The hepatocyte insulin receptor is required to program the liver clock and rhythmic gene expression 2022 , 39, 110674	О
629	Epigenome-wide DNA Methylation Profiling of Normal Mucosa Reveals HLA-F Hypermethylation as a Biomarker Candidate for Serrated Polyposis Syndrome 2022 ,	
628	Identifying Novel Osteoarthritis-Associated Genes in Human Cartilage Using a Systematic Meta-Analysis and a Multi-Source Integrated Network 2022 , 23,	1

idpr: A package for profiling and analyzing Intrinsically Disordered Proteins in R.. 2022, 17, e0266929 627 О Data_Sheet_1.docx. 2020, 626 625 Table_1.XLSX. 2020, Table_2.xlsx. 2020, 624 Table_3.xlsx. 2020, 623 Table_4.xlsx. 2020, 622 Data_Sheet_1.XLSX. 2018, 621 Data_Sheet_2.XLSX. 2018, 620 Data_Sheet_3.XLSX. 2018, 619 618 Data_Sheet_4.XLSX. 2018, Presentation 1. PDF. 2018, 617 Data_Sheet_1.XLS. 2019, 616 615 Image_1.PDF. 2019, DataSheet_1.docx. 2019, 614 Data_Sheet_1.PDF. 2020, 613 612 Table_1.XLSX. **2018**, Table_1.xlsx. 2018, 611 Table_2.xlsx. 2018, 610

(2020-2018)

609 Table_3.docx. 2018, Table_4.xlsx. **2018**, 608 Table_5.xlsx. 2018, 607 Table_6.xlsx. 2018, 606 605 Data_Sheet_1.pdf. 2020, Data_Sheet_1.docx. 2018, 604 603 Data_Sheet_1.PDF. 2020, Table_1.XLSX. **2020**, 602 601 Table_2.XLSX. 2020, 600 Table_3.XLSX. **2020**, Table_4.XLSX. 2020, 599 Data_Sheet_1.pdf. 2020, 598 Table_1.XLSX. **2020**, 597 Table_2.XLSX. **2020**, 596 Table_3.XLSX. 2020, 595 Table_4.XLSX. **2020**, 594 Table_5.XLSX. 2020, 593 Table_6.XLSX. **2020**, 592



(2018-2018)

Data_Sheet_2.PDF. 2018, 573 Table_1.XLSX. 2018, 572 Data_Sheet_1.ZIP. 2018, 571 Data_Sheet_1.doc. 2018, 570 Data_Sheet_1.PDF. 2021, 569 568 Data_Sheet_1.PDF. 2020, 567 Data_Sheet_1.FASTA. 2018, 566 Data_Sheet_2.xlsx. 2018, Data_Sheet_3.xlsx. 2018, 565 564 Data_Sheet_1.csv. 2019, Data_Sheet_2.csv. 2019, 563 Data_Sheet_3.csv. 2019, 562 561 Data_Sheet_4.csv. 2019, Data_Sheet_5.csv. 2019, 560 Data_Sheet_6.csv. 2019, 559 558 Presentation_1.pdf. **2019**, Data_Sheet_1.docx. 2020, 557 556 Data_Sheet_1.DOCX. 2018,



(2018-2019)

Table_1.XLSX. 2019, 537 Table_2.XLSX. **2019**, 536 Table_3.XLSX. 2019, 535 Table_4.XLSX. **2019**, 534 data_sheet_1.PDF. 2018, 533 DataSheet_1.pdf. 2020, 532 Presentation_1.pdf. 2019, 531 Table_1.docx. **2019**, 530 Table_2.xlsx. 2019, 529 528 Table_3.xlsx. **2019**, Table_4.xlsx. 2019, 527 526 Table_5.docx. 2019, Table_6.xlsx. 2019, 525 Table_1.XLS. 2020, 524 Table_2.XLSX. 2020, 523 522 Presentation_1.PDF. 2018, Table_1.xlsx. 2018, 521 Table_2.xlsx. **2018**, 520



(2018-2019)

```
Image_1.TIF. 2019,
501
500
      Image_2.TIF. 2019,
      Image_3.TIF. 2019,
499
498
      Image_1.TIF. 2018,
      Image_2.TIF. 2018,
497
496
      Image_3.TIF. 2018,
      Image_4.TIF. 2018,
495
      Image_5.TIF. 2018,
494
      Image_6.TIF. 2018,
493
      Table_1.XLSX. 2018,
492
      Table_2.XLSX. 2018,
491
      Table_3.xlsx. 2018,
490
489
      Data_Sheet_1.xlsx. 2018,
488
      Data_Sheet_2.xlsx. 2018,
      Data_Sheet_3.docx. 2018,
487
486
      Image_1.TIF. 2018,
      Image_10.TIF. 2018,
485
      Image_2.TIF. 2018,
484
```



(2019-2019)

Table_1.XLSX. 2019, 465 Table_2.XLSX. **2019**, 464 Table_3.XLSX. 2019, 463 Data_Sheet_1.ZIP. 2018, 462 Data_Sheet_2.ZIP. 2018, 461 Image_1.jpeg. 2020, 460 Table_1.xlsx. 2020, 459 Image_1.PDF. 2018, 458 Image_2.PDF. 2018, 457 456 Table_1.PDF. **2018**, Table_2.PDF. 2018, 455 Data_Sheet_1.xlsx. 2018, 454 Supplementary_Table_1.docx. 2018, 453 Data_Sheet_1.CSV. 2019, 452 Data_Sheet_10.ZIP. 2019, 451 450 Data_Sheet_2.ZIP. **2019**, Data_Sheet_3.ZIP. 2019, 449 Data_Sheet_4.ZIP. 2019, 448



(2020-2020)

Image_2.JPEG. 2020, 429 Table_1.XLSX. **2020**, 428 Table_2.XLSX. 2020, 427 Table_3.XLSX. **2020**, 426 Table_4.XLSX. **2020**, 425 Table_5.XLSX. **2020**, 424 Data_Sheet_1.docx. 2019, 423 Data_Sheet_1.pdf. 2018, 422 Table_5.xlsx. 2018, 421 Table_1.DOCX. **2018**, 420 Table_1.xlsx. 2019, 419 418 Data_Sheet_1.pdf. 2019, Data_Sheet_1.XLSX. 2020, 417 Data_Sheet_2.XLSX. 2020, 416 Data_Sheet_3.XLSX. 2020, 415 Data_Sheet_4.XLSX. 2020, 414 Data_Sheet_1.PDF. 2020, 413 Presentation_1.PPTX. 2020, 412



(2017-2020)

Data_Sheet_1.PDF. 2020, 393 Table_1.xlsx. **2020**, 392 Table_2.xlsx. **2020**, 391 Table_3.xlsx. 2020, 390 389 Table_4.xlsx. **2020**, 388 Table_5.xlsx. **2020**, 387 Table_6.xlsx. 2020, 386 Data_Sheet_1.pdf. 2018, Table_1.XLSX. 2018, 385 384 Table_2.XLSX. 2018, Table_3.XLS. 2018, 383 382 Table_4.XLSX. **2018**, 381 Table_5.XLSX. **2018**, Data_Sheet_1.ZIP. 2018, 380 Data_Sheet_2.ZIP. 2018, 379 378 Data_Sheet_3.ZIP. 2018, Table_1.XLSX. 2017, 377 376 Table_2.XLSX. **2017**,



357	Image_2.TIF. 2020 ,	
356	Image_3.TIF. 2020 ,	
355	lmage_4.TIF. 2020 ,	
354	lmage_5.TIF. 2020 ,	
353	Image_1.PDF. 2018 ,	
352	Table_1.XLSX. 2018 ,	
351	Characterization of a castrate-resistant prostate cancer xenograft derived from a patient of West African ancestry. 2021 ,	O
350	Suppression of MYC by PI3K/AKT/mTOR pathway inhibition in combination with all-trans retinoic acid treatment for therapeutic gain in acute myeloid leukaemia 2022 ,	O
349	Genetic Profiling in Children With Acute Lymphoblastic Leukemia Referred for Allogeneic Hematopoietic Stem Cell Transplantation 2022 , 29, 10732748211064776	
348	Infection of Human Endothelial Cells with Lassa Virus Induces Early but Transient Activation and Low Type I IFN Response Compared to the Closely-Related Nonpathogenic Mopeia Virus 2022 , 14,	O
347	The R Language: An Engine for Bioinformatics and Data Science. 2022 , 12, 648	2
346	Reduced adhesion of aged intestinal stem cells contributes to an accelerated clonal drift 2022, 5,	O
345	Development and Characterization of MYB-NFIB Fusion Expression in Adenoid Cystic Carcinoma 2022 , 14,	
344	Gene Expression Meta-Analysis of Potential Shared and Unique Pathways between Autoimmune Diseases under Anti-TNF herapy. 2022 , 13, 776	3
343	Dissociation of nanosilicates induces downstream endochondral differentiation gene expression program 2022 , 8, eabl9404	1
342	Discovering Common Pathophysiological Processes between COVID-19 and Cystic Fibrosis by Differential Gene Expression Pattern Analysis 2022 , 2022, 8078259	O
341	Transcriptional Profiles Elucidate Differential Host Responses to Infection with Cryptococcus neoformans and Cryptococcus gattii. 2022 , 8, 430	O
340	HiCognition: a visual exploration and hypothesis testing tool for 3D genomics.	

339	A game changer for bipolar disorder diagnosis using RNA editing-based biomarkers 2022 , 12, 182	1
338	Artificial Intelligence Predictor for Alzheimer's Disease Trained on Blood Transcriptome: The Role of Oxidative Stress 2022 , 23,	
337	Evaluation of Thrombotic Thrombocytopenic Purpura and Other Thrombotic Microangiopathies: Lessons Learned from a 14-Year Retrospective Study 2022 ,	
336	Regulatory mechanisms behind the phenotypic plasticity associated with Setaria italica water deficit tolerance 2022 , 1	
335	Genomic characteristics and clinical significance of CD56+ Circulating Tumor Cells in Small Cell Lung Carcinoma.	
334	Disclosing Potential Key Genes, Therapeutic Targets and Agents for Non-Small Cell Lung Cancer: Evidence from Integrative Bioinformatics Analysis. 2022 , 10, 771	O
333	FAIRsoft - A practical implementation of FAIR principles for research software.	0
332	An iron-chelating sulfonamide identified from -based screening for antipathogenic discovery 2022 , 13, 833-843	o
331	PTBP1 promotes hematopoietic stem cell maintenance and red blood cell development by ensuring sufficient availability of ribosomal constituents 2022 , 39, 110793	2
330	Plasma miRNA-214 is a predictive candidate biomarker of progression speed in patients with ALS.	
329	Short Communication: Body weight of newborn and suckling piglets affects their intestinal gene expression 2022 ,	1
328	Screening and In Silico Functional Analysis of MiRNAs Associated with Acute Myeloid Leukemia Relapse 2022 ,	
327	Biobased PET from lignin using an engineered cis, cis-muconate-producing Pseudomonas putida strain with superior robustness, energy and redox properties 2022 , 72, 337-352	1
326	Assessing and assuring interoperability of a genomics file format 2022,	
325	Making Biomedical Research Software FAIR: Actionable Step-by-step Guidelines with a User-support Tool.	
324	Innovative in Silico Approaches for Characterization of Genes and Proteins. 2022, 13,	1
323	Microbial Community Analysis and Food Safety Practice Survey-Based Hazard Identification and Risk Assessment for Controlled Environment Hydroponic/Aquaponic Farming Systems. 2022 , 13,	0
322	The regulatory landscape of retinoblastoma: a pathway analysis perspective. 2022 , 9,	O

321 Multidisipliner Bir Bilim Dal $\tilde{-}$ Olarak Biyoinformati $\tilde{+}$ Genel Bir Bak $\tilde{+}$ e Biyoinformatik Fark $\tilde{+}$ dal $\tilde{+}$.

320	Lactotransferrin promotes intervertebral disc degeneration by regulating Fas and inhibiting human nucleus pulposus cell apoptosis.	
319	Transcription factor GATA2 may potentiate follicle-stimulating hormone production in mice via induction of the BMP antagonist gremlin in gonadotrope cells. 2022 , 102072	O
318	Toxicogenomic Assessment of Organ-specific Responses Following Plutonium Internal Contamination. 2022 , 100245	1
317	The Lysine Demethylases KdmA and KdmB Differently Regulate Asexual Development, Stress Response, and Virulence in Aspergillus fumigatus. 2022 , 8, 590	1
316	Disentangling the Potato Tuber Moth-Induced Early-Defense Response by Simulated Herbivory in Potato Plants. 2022 , 13,	O
315	BioTEA: containerized methods of analysis for microarray-based transcriptomics data.	
314	The proteomic and transcriptomic landscapes altered by Rgg2/3 activity in Streptococcus pyogenes.	
313	Volatile Organic Compounds of Streptomyces sp. TOR3209 Stimulated Tobacco Growth by Up-Regulating the Expression of Genes Related to Plant Growth and Development. 2022 , 13,	1
312	Evolutionary targets of gene expression divergence in a complex of closely related pine species.	
311	Full-Length Transcriptome Sequencing Analysis of Differentially Expressed Genes and Pathways After Treatment of Psoriasis With Oxymatrine. 13,	0
310	Differential cofactor dependencies define distinct types of human enhancers.	2
309	Stable and ancient endocytic structures navigate the complex pellicle of apicomplexan parasites.	O
308	RoPE: a robust profile likelihood method for differential gene expression analysis.	
307	Quantitative analysis of redox proteome reveals oxidation-sensitive protein thiols acting in fundamental processes of developmental hematopoiesis. 2022 , 53, 102343	1
306	Gene Expression Tools from a Technical Perspective: Current Approaches and Alternative Solutions for the KnowSeq Suite. 2022 , 404-414	
305	The c-di-GMP Phosphodiesterase PipA (PA0285) Regulates Autoaggregation and Pf4 Bacteriophage Production in Pseudomonas aeruginosa PAO1.	3
304	Identification and verification of differentially expressed key genes in peripheral blood-derived T cells between chronic immune thrombocytopenia patients and healthy controls. 2022 , 13, 13587-13595	

303	CFTR Rescue by Lumacaftor (VX-809) Induces an Extensive Reorganization of Mitochondria in the Cystic Fibrosis Bronchial Epithelium. 2022 , 11, 1938	0
302	How copper can impact pig growth: comparing the effect of copper sulfate and monovalent copper oxide on oxidative status, inflammation, gene abundance, and microbial modulation as potential mechanisms of action.	0
301	Investigating DNA methylation as a mediator of genetic risk in childhood acute lymphoblastic Leukemia.	
300	Clinical sequencing of soft tissue and bone sarcomas delineates diverse genomic landscapes and potential therapeutic targets. 2022 , 13,	3
299	Gene expression studies of WT1 mutant Wilms tumor cell lines in the frame work of published kidney development data reveals their early stem cell origin.	
298	Signaling through the Dystrophin Glycoprotein Complex affects the stress-dependent transcriptome in Drosophila.	
297	Clinical Values of the Identified Hub Genes in Systemic Lupus Erythematosus. 13,	
296	Enhanced metabolism and negative regulation of ER stress support higher erythropoietin production in HEK293 cells. 2022 , 39, 110936	O
295	Accelerated epigenetic aging in newborns with Down syndrome.	1
294	rprimer: an R/bioconductor package for design of degenerate oligos for sequence variable viruses. 2022 , 23,	
293	A compound directed against S6K1 hampers fat mass expansion and mitigates diet-induced hepatosteatosis.	0
292	Whole transcriptome expression array analysis of human colon fibroblasts culture treated with Helichrysum italicum supports its use in traditional medicine. 2022 , 115505	O
291	Identification and Validation of a Novel Signature Based on NK Cell Marker Genes to Predict Prognosis and Immunotherapy Response in Lung Adenocarcinoma by Integrated Analysis of Single-Cell and Bulk RNA-Sequencing. 13,	1
2 90	High-Intensity Aerobic Exercise Suppresses Cancer Growth by Regulating Skeletal Muscle-Derived Oncogenes and Tumor Suppressors. 9,	O
289	Characterization of naked mole-rat hematopoiesis reveals unique stem and progenitor cell patterns and neotenic traits.	O
288	Loss of MMR and TGFBR2 Increases the Susceptibility to Microbiota-Dependent Inflammation-Associated Colon Cancer. 2022 ,	O
287	Plac1 Remodels the Tumor Immune Evasion Microenvironment and Predicts Therapeutic Response in Head and Neck Squamous Cell Carcinoma. 12,	
286	Introducing R as a smart version of calculators enables beginners to explore it on their own. 10, 859	

285	Species-specific sensitivity to TGFBignaling and changes to the Mmp13 promoter underlie avian jaw development and evolution. 11,	0
284	Advances in understanding Norway spruce natural resistance to needle bladder rust infection: transcriptional and secondary metabolites profiling. 2022 , 23,	
283	FCGBP Is a Promising Prognostic Biomarker and Correlates with Immunotherapy Efficacy in Oral Squamous Cell Carcinoma. 2022 , 2022, 1-11	0
282	Overlapping transcriptional programs promote survival and axonal regeneration of injured retinal ganglion cells. 2022 ,	3
281	Transcriptome analysis of SerpinB2-deficient breast tumors provides insight into deciphering SerpinB2-mediated roles in breast cancer progression. 2022 , 23,	
280	T-bet+ B cells Dominate the Peritoneal Cavity B Cell Response during Murine Intracellular Bacterial Infection. 2022 , 208, 2749-2760	
279	Arabidopsis mutants representing each of the four Mediator modules reveal unique functions in the transcriptional response to salt stress.	
278	A Bayesian hierarchical model for improving measurement of 5mC and 5hmC levels: Toward revealing associations between phenotypes and methylation states.	
277	Mycobacterium intracellulare induces a Th17 immune response via M1-like macrophage polarization in canine peripheral blood mononuclear cells. 2022 , 12,	
276	Ripening of Pomegranate Skin as Revealed by Developmental Transcriptomics. 2022 , 11, 2215	
275	Mitochondrial Respiration in Peripheral Blood Mononuclear Cells Negatively Correlates with Disease Severity in Pulmonary Arterial Hypertension. 2022 , 11, 4132	2
274	Galectin-3 inhibition boosts the therapeutic efficacy of Semliki Forest virus in pediatric osteosarcoma. 2022 ,	
273	How Reproducibility Will Accelerate Discovery Through Collaboration in Physio-Logging. 13,	
272	Pseudouridine-dependent ribosome biogenesis regulates translation of polyglutamine proteins during Drosophila oogenesis.	O
271	Enhanced lignin synthesis and ecotypic variation in defense-related gene expression in response to shade in Norway spruce.	О
270	Cannabinerol and NSC-34 Transcriptomic Analysis: Is the Dose Who Makes Neuronal Differentiation?. 2022 , 23, 7541	
269	What can cold-induced transcriptomes of Arctic Brassicaceae tell us about the evolution of cold tolerance?.	O
268	Nuclear receptor HR3 mediates transcriptional regulation of chitin metabolic genes during molting in Tribolium castaneum.	

267	Acute Myeloid Leukemia: New Multiomics Molecular Signatures and Implications for Systems Medicine Diagnostics and Therapeutics Innovation. 2022 , 26, 392-403	О
266	Expression analysis, molecular characterization and prognostic evaluation on TMED4 and TMED9 gene expression in glioma. 2022 , 78, 103922	
265	Protocol for establishing a protein-protein interaction network using tandem affinity purification followed by mass spectrometry in mammalian cells. 2022 , 3, 101569	О
264	Identifying potential signatures for atherosclerosis in the context of predictive, preventive, and personalized medicine using integrative bioinformatics approaches and machine-learning strategies.	O
263	TFEBexplorer: An integrated tool to study genes regulated by the stress-responsive Transcription Factor EB. 2022 , 1, 295-305	0
262	Transcriptome Dynamics in the Developing Larynx, Trachea, and Esophagus. 10,	
261	Uncovering temporospatial sensitive TBI targeting strategies via in vivo phage display. 2022, 8,	
26 0	Metabolomic association analysis reveals defense related secondary metabolic reprogramming in callus of Scutellaria baicalensis Georgi induced by endophytic Pseudomonas sp. 2B. 2022 , 187, 115409	
259	Proteotranscriptomics of ocular adnexal B-cell lymphoma reveals an oncogenic role of alternative splicing and identifies a diagnostic marker. 2022 , 41,	0
258	Evaluating the Prognostic and Therapeutic Potentials of the Proteasome 26S Subunit, ATPase (PSMC) Family of Genes in Lung Adenocarcinoma: A Database Mining Approach. 13,	o
257	Molecular Framework of Mouse Endothelial Cell Dysfunction during Inflammation: A Proteomics Approach. 2022 , 23, 8399	О
256	MicroRNA-218 instructs proper assembly of hippocampal networks.	
255	Nine best practices for research software registries and repositories. 8, e1023	
254	rTASSEL: An R interface to TASSEL for analyzing genomic diversity. 2022 , 7, 4530	o
253	JNK signalling regulates self-renewal of proliferative urine-derived renal progenitor cells via inhibition of ferroptosis.	
252	Human repair-related Schwann cells adopt functions of antigen-presenting cells in vitro.	1
251	Maternal lead exposure induces sex-dependent cerebellar glial alterations and repetitive behaviors. 16,	0
250	Transposon-activated POU5F1B promotes colorectal cancer growth and metastasis. 2022 , 13,	0

249	Methylation associated with long- or short-term survival in glioblastoma patients from the Nordic phase 3 trial. 13,	1
248	Targeting TRAF3IP2 inhibits angiogenesis in glioblastoma. 12,	O
247	Cuproptosis predicts the risk and clinical outcomes of lung adenocarcinoma. 12,	O
246	Colchicine as a novel drug for the treatment of osteosarcoma through drug repositioning based on an FDA drug library. 12,	
245	Senescent Human Pancreatic Stellate Cells Secrete CXCR2 Agonist CXCLs to Promote Proliferation and Migration of Human Pancreatic Cancer AsPC-1 and MIAPaCa-2 Cell Lines. 2022 , 23, 9275	О
244	matchRanges: Generating null hypothesis genomic ranges via covariate-matched sampling.	O
243	Metabolic engineering of Escherichia coli with electron channelling for the production of natural products. 2022 , 5, 726-737	4
242	Differential gene expression analysis of the resprouting process in Pinus canariensis provides new insights into a rare trait in conifers.	
241	Autophagy-mediated NCOR1 degradation is required for brown fat maturation and thermogenesis. 1-22	О
240	FIND-IT: Accelerated trait development for a green evolution. 2022 , 8,	
239	Epigenome-wide association studies of occupational exposure to benzene and formaldehyde. 1-19	0
238	Role of endoplasmic reticulum stress in impaired neonatal lung growth and bronchopulmonary dysplasia. 2022 , 17, e0269564	O
237	Spatial proteomics reveals differences in the cellular architecture of antibody-producing CHO and plasma cell-derived cells. 2022 , 100278	
236	Nuclear receptor estrogen-related receptor modulates antimicrobial peptide expression for host innate immunity in Tribolium castaneum. 2022 , 148, 103816	2
235	Is the forming of neuronal network activity in human-induced pluripotent stem cells important for the detection of drug-induced seizure risks?. 2022 , 931, 175189	
234	A BET Protein Inhibitor Targeting Mononuclear Myeloid Cells Affects Specific Inflammatory Mediators and Pathways in Crohn Disease. 2022 , 11, 2846	O
233	Prognostic and Therapeutic Value of LSM5 Gene in Human Brain Cancer Glioma: An Omics Database Exploration Approach.	O
232	Ensemble Regularized Logistic Regression for Diagnosing Glioma Subtypes. 2022 , 209-215	O

231	Automatic Detection and Analysis of Technical Debts in Peer-Review Documentation of R Packages. 2022 ,	О
230	Comparison of High-Throughput Technologies in the Classification of Adult-Onset Still's Disease Patients. 2022 ,	O
229	Decoding mechanism of action and sensitivity to drug candidates from integrated transcriptome and chromatin state. 11,	O
228	The RNA helicase DDX5 cooperates with EHMT2 to sustain alveolar rhabdomyosarcoma growth. 2022 , 40, 111267	O
227	Molecular Analysis of Short- versus Long-Term Survivors of High-Grade Serous Ovarian Carcinoma. 2022 , 14, 4198	О
226	A Review on Computational Analysis of Big Data in Breast Cancer for Predicting Potential Biomarkers. 2022 , 22, 1793-1810	1
225	PCRedux: A Quantitative PCR Machine Learning Toolkit. 2022 , 7, 4407	О
224	Nitrogen Transformation Processes in Manure Microbiomes of Earthen Pit and Concrete Storages on Commercial Dairy Farms.	О
223	Whole Genome Sequencing Analysis of Effects of CRISPR/Cas9 in Komagataella phaffii: A Budding Yeast in Distress. 2022 , 8, 992	О
222	Nutritional Evaluation of Black Soldier Fly Frass as an Ingredient in Florida Pompano (Trachinotus carolinus L.) Diets. 2022 , 12, 2407	О
221	A metabolic reprogramming-related prognostic risk model for clear cell renal cell carcinoma: From construction to preliminary application. 12,	О
220	Preadapted to adapt: underpinnings of adaptive plasticity revealed by the downy brome genome.	О
219	BioTEA: Containerized Methods of Analysis for Microarray-Based Transcriptomics Data. 2022 , 11, 1346	О
218	A small molecule RIG-I agonist serves to adjuvant broad multifaceted influenza virus vaccine immunity.	O
217	Epigenetic and transcriptomic alterations in offspring born to women with type 1 diabetes (the EPICOM study). 2022 , 20,	О
216	Adaptive strategies of Scots pine under shade: increase in lignin synthesis and ecotypic variation in defence-related gene expression.	O
215	Identification of pyroptosis-related immune signature and drugs for ischemic stroke. 13,	О
214	Effect of Hypoxia in the Transcriptomic Profile of Lung Fibroblasts from Idiopathic Pulmonary Fibrosis. 2022 , 11, 3014	O

213	MicroRNA-4516 in Urinary Exosomes as a Biomarker of Premature Ovarian Insufficiency. 2022, 11, 2797	0
212	Benchmark data and software for assessing genome-wide CRISPR-Cas9 screening pipelines.	O
211	Differential Timing for Glucose Assimilation in Prochlorococcus and Coexistent Microbial Populations in the North Pacific Subtropical Gyre.	1
210	Gaussian graphical models with applications to omics analyses.	О
209	Cone-setting in spruce is regulated by conserved elements of the age-dependent flowering pathway.	О
208	The RPN12a proteasome subunit is essential for the multiple hormonal homeostasis controlling the progression of leaf senescence. 2022 , 5,	O
207	Mast cell regranulation requires a metabolic switch involving mTORC1 and a glucose-6-phosphate transporter. 2022 , 40, 111346	1
206	Time-series transcriptome of Brachypodium distachyon during bacterial flagellin-induced pattern-triggered immunity. 13,	Ο
205	Impact of food restriction on the medio-basal hypothalamus of intact ewes as revealed by a large-scale transcriptomics study.	1
204	Mouse models of COVID-19 recapitulate inflammatory pathways rather than gene expression. 2022 , 18, e1010867	O
203	Lead-exposure associated miRNAs in humans and Alzheimer disease as potential biomarkers of the disease and disease processes. 2022 , 12,	O
202	Human Plasma Proteome During Normal Pregnancy.	Ο
201	Gene Expression and DNA Methylation in Human Papillomavirus Positive and Negative Head and Neck Squamous Cell Carcinomas. 2022 , 23, 10967	1
200	Polyphyly in widespread Salmonella enterica serovars and using genomic proximity to choose the best reference genome for bioinformatics analyses. 10,	1
199	The AHR target gene Scinderin activates the WNT pathway by facilitating the nuclear translocation of $\#$ catenin.	O
198	Structural basis of SNAPc-dependent snRNA transcription initiation by RNA polymerase II.	Ο
197	Altered CD8+ T cell associated aging gene signature in the peripheral blood of patients with Alzheimer disease []	0
196	Key Elements of Cellular Senescence Involve Transcriptional Repression of Mitotic and DNA Repair Genes Through the p53-p16/pRB-E2F-DREAM Complex.	O

195	Prediction of diabetes mellitus development after kidney transplantation using patient-specific induced pluripotent stem cells.	0
194	Perioral secretions enable complex social signaling in African mole-rats (genus Fukomys).	O
193	Krppel-like factor 7 influences translation and pathways involved in ribosomal biogenesis in breast cancer. 2022 , 24,	О
192	Symptomatic and asymptomatic domoic acid exposure in zebrafish (Danio rerio) revealed distinct non-overlapping gene expression patterns in the brain. 2022 , 252, 106310	O
191	Protocol for fast scRNA-seq raw data processing using scKB and non-arbitrary quality control with COPILOT. 2022 , 3, 101729	1
190	Exploring Protein Interactome Data with IPinquiry: Statistical Analysis and Data Visualization by Spectral Counts. 2023 , 243-265	0
189	Prognostic and therapeutic value of LSM5 gene in human brain cancer Glioma: An omics database exploration approach. 2022 , 34, 101114	О
188	Utility of Network Biology Approaches to Understand the Aluminum Stress Responses in Soybean. 2022 , 109-124	o
187	Mutation of the RelA(p65) Thr505 phosphosite disrupts the DNA replication stress response leading to CHK1 inhibitor resistance. 2022 , 479, 2087-2113	3
186	Genome-Scale Modeling and Systems Metabolic Engineering of Vibrio natriegens for the Production of 1,3-Propanediol. 2023 , 209-220	o
185	Immunomodulatory Cell Therapy Using BalCer-Pulsed Dendritic Cells Ameliorates Heart Failure in a Murine Dilated Cardiomyopathy Model.	1
184	Identification of SNPs and Candidate Genes Associated with Salt Stress in Two Korean Sorghum Cultivars and Understanding Selection Pressures in the Breeding Process. 2022 , 12, 2511	0
183	Encapsulation of MSCs and GDNF in an Injectable Nanoreinforced Supramolecular Hydrogel for Brain Tissue Engineering.	0
182	Urine-based detection of biomarkers indicative of chronic kidney disease in a patient cohort from Ghana.	o
181	MLL1 regulates cytokine-driven cell migration and metastasis.	0
180	Regulation of Genes Related to Cognition after tDCS in an Intermittent Hypoxic Brain Injury Rat Model. 2022 , 13, 1824	O
179	RABC: Rheumatoid Arthritis Bioinformatics Center.	0
178	PTEN Protein Phosphatase Activity Is Not Required for Tumour Suppression in the Mouse Prostate. 2022 , 12, 1511	O

177	HRas and Myc synergistically induce cell cycle progression and apoptosis of murine cardiomyocytes. 9,	Ο
176	Biological characterization of natural peptide BcI-1003 from Boana cordobae (anura): role in Alzheimer Disease and microbial infections	O
175	Combinatorial Analysis of Transcription and Metabolism Reveals the Regulatory Network Associated with Antioxidant Substances in Waxy Corn.	O
174	Inferring differential subcellular localisation in comparative spatial proteomics using BANDLE. 2022 , 13,	O
173	Genome-Wide Scans and Transcriptomic Analyses Characterize Selective Changes as a Result of Chlorantraniliprole Resistance in Plutella xylostella. 2022 , 23, 12245	О
172	MYO10-filopodia support basement membranes at pre-invasive tumor boundaries. 2022 , 57, 2350-2364.e7	O
171	The Application of Metagenomics to Study Microbial Communities and Develop Desirable Traits in Fermented Foods. 2022 , 11, 3297	3
170	Anti-apoptotic Splicing Variant of AIMP2 Recover Mutant SOD1-Induced Neuronal Cell Death.	O
169	Gemcitabine-mediated depletion of immunosuppressive dendritic cells enhances the efficacy of therapeutic vaccination. 13,	О
168	The Proteomic and Transcriptomic Landscapes Altered by Rgg2/3 Activity in Streptococcus pyogenes.	O
167	Epigenomic and transcriptomic landscaping unraveled candidate repositioned therapeutics for non-functioning pituitary neuroendocrine tumors.	Ο
166	Transcriptional noise adjusted for expression levels reveals genes with high transcriptional noise that are highly expressed, functionally related, and co-regulated in yeast.	O
165	Lactiplantibacillus plantarum 299v supplementation modulates tell ER stress and antioxidative defense pathways and prevents type 1 diabetes in gluten-free BioBreeding rats. 2022 , 14,	O
164	Mapping brain gene coexpression in daytime transcriptomes unveils diurnal molecular networks and deciphers perturbation gene signatures. 2022 , 110, 3318-3338.e9	1
163	The BRCT Domain from the Homologue of the Oncogene PES1 in Leishmania major (LmjPES) Promotes Malignancy and Drug Resistance in Mammalian Cells. 2022 , 23, 13203	O
162	Iterative remodeling of the mouse uterus requires Hedgehog signaling.	Ο
161	Pseudomonas sp., Strain L5B5: A Genomic and Transcriptomic Insight into an Airborne Mine Bacterium. 2022 , 12, 10854	O
160	miRNA profile at diagnosis predicts treatment outcome in patients with B-chronic lymphocytic leukemia: A FILO study. 13,	Ο

159	The cell-free DNA methylome captures distinctions between localized and metastatic prostate tumors. 2022 , 13,	2
158	Single-cell Landscape Analysis of the Circulating Human B Cell Pool under Selective Pressure of Allogeneic Stem Cell Transplantation.	О
157	Towards future directions in data-integrative supervised prediction of human aging-related genes.	O
156	Oleic acid-bound FABP7 drives glioma cell proliferation through regulation of nuclear lipid droplet formation.	O
155	Hyaline Cartilage Microtissues Engineered from Adult Dedifferentiated Chondrocytes: Safety and Role of WNT Signaling.	0
154	A comprehensive Bioconductor ecosystem for the design of CRISPR guide RNAs across nucleases and technologies. 2022 , 13,	O
153	Heuristic Pairwise Alignment in Database Environments. 2022 , 13, 2005	O
152	The oxidative phosphorylation inhibitor IM156 suppresses B-cell activation by regulating mitochondrial membrane potential and contributes to the mitigation of systemic lupus erythematosus. 2022 ,	O
151	Colicin E2 expression in Escherichia coli biofilms: Induction and regulation revisited. 2022, 3, 100171	O
150	APPINetwork: an R package for building and computational analysis of proteinBrotein interaction networks. 10, e14204	O
149	Teaching Computational Genomics and Bioinformatics on a High Performance Computing Cluster - A Primer.	O
148	LACTB exerts tumor suppressor properties in epithelial ovarian cancer through regulation of Slug. 2023 , 6, e202201510	O
147	Comparing adventitious root-formation and graft-unification abilities in clones of Argania spinosa. 13,	0
146	Simulated Microgravity Modulates Focal Adhesion Gene Expression in Human Neural Stem Progenitor Cells. 2022 , 12, 1827	O
145	PAIP2 is a potential diagnostic and prognostic biomarker of breast cancer and is associated with immune infiltration. 13,	0
144	Application of Machine Learning in Spatial Proteomics.	O
143	Differential immune transcriptomic profiles between vaccinated and resolved HCV reinfected subjects. 2022 , 18, e1010968	0
142	Peptide-mediated inhibition of the transcriptional regulator Elongin BC induces apoptosis in cancer cells.	O

141	Gene expression related to lung cancer altered by PHMG-p treatment in PBTE cells.	О
140	Deciphering sex-specific miRNAs as heat-recorders in zebrafish. 2022 , 12,	O
139	A systems biology approach towards oral cancer using computational tools and techniques. 2022 , 231, 104709	О
138	Robust identification of regulatory variants (eQTLs) using a differential expression framework developed for RNA-sequencing.	O
137	A pan-cancer analysis of the biological function and clinical value of BTLA in tumors. 2023 , 47, 351-366	О
136	Phenylalanine induces mango fruit resistance against chilling injuries during storage at suboptimal temperature. 2022 , 134909	Ο
135	Regulators of Genetic Risk for the Progression of Non-alcoholic Fatty Liver Disease to Hepatocellular Carcinoma: Reconstruction of Transcriptional Network and Signature-Based Metabolic Profiling. 2022 ,	О
134	Data-driven analysis and druggability assessment methods to accelerate the identification of novel cancer targets. 2023 , 21, 46-57	Ο
133	Identifying transcript-level differential expression in primary human immune cells. 2023, 153, 181-193	0
132	Metagenomics analysis of the morphological aspects and bacterial composition of broiler feces. 2023 , 102, 102401	O
131	Embryogenesis of a calanoid copepod analyzed by transcriptomics. 2023 , 45, 101054	О
130	Data Analysis. 2022 , 171-204	O
129	Interdisciplinary Computing Education: An Introductory Programming and Data Science Course for Postdoctoral Researchers in the Biosciences. 2022 ,	O
128	Primate-specific transposable elements shape transcriptional networks during human development. 2022 , 13,	1
127	Quasispecies Fitness Partition to Characterize the Molecular Status of a Viral Population. Negative Effect of Early Ribavirin Discontinuation in a Chronically Infected HEV Patient. 2022 , 23, 14654	0
126	Differential Expression, Functional and Machine Learning Analysis of High-Throughput D mics Data Using Open-Source Tools. 2023 , 317-351	0
125	Biological Characterization of Natural Peptide BcI-1003 from Boana cordobae (anura): Role in Alzheimer Disease and Microbial Infections. 2023 , 29,	О
124	Proteotranscriptomics Analysis Reveals Signature Pathways Associated with Colorectal Cancer Progression: a Pilot Study. 2022 ,	O

Structural basis of SNAPc-dependent snRNA transcription initiation by RNA polymerase II. 2022, 29, 1159-11690 123 Precise genomic editing of pathogenic mutations in RBM20 rescues dilated cardiomyopathy. 2022, 122 14. EcoEvoApps: Interactive apps for theoretical models in ecology and evolutionary biology. 2022, 12, 121 1 Integrated transcriptome-proteome analyses of human stem cells reveal source-dependent 120 differences in their regenerative signature. 2022, Experimental life history evolution results in sex-specific evolution of gene expression in seed 119 0 beetles. Hatchery tanks induce intense reduction in microbiota diversity associated with gills and guts of 118 two endemic species of the SB Francisco River. 13, Identification of potential pathways and biomarkers linked to progression in ALS. 117 O Toxicoproteomics reveals an effect of clozapine on autophagy in human liver spheroids. 1-10 116 Joint Multi-Ancestry and Admixed GWAS Reveals the Complex Genetics behind Human Cranial \circ 115 Vault Shape. Digital twin demonstrates regeneration after partial liver hepatectomy to require biomechanical 114 growth control. 2022, 105714 Phantasus: web-application for visual and interactive gene expression analysis. 113 O FAM3D as a Prognostic Indicator of Head and Neck Squamous Cell Carcinoma Is Associated with 112 \circ Immune Infiltration. 2022, 2022, 1-29 Antenatal N-acetylcysteine antioxidant therapy relieves lung oxidative stress and related perinatal 111 O lethality in HRas/NRas double-null mutant mice. Deep learning-based multi-drug synergy prediction model for individually tailored anti-cancer 110 therapies. 13, A generalization of moderated statistics to data adaptive semiparametric estimation in 109 \circ high-dimensional biology. 096228022211463 Alternative telomere maintenance mechanism in Alligator sinensis provides insights into aging 108 evolution. **2022**, 105850 Perioral secretions enable complex social signaling in African mole-rats (genus Fukomys). 2022, 12, 107 O Comparative transcriptomics reveals commonalities and differences in the genetic underpinnings 106 of a floral dimorphism. 2022, 12,

105	An alternative pathway to plant cold tolerance in the absence of vacuolar invertase activity.	0
104	Bubble: a fast single-cell RNA-seq imputation using an autoencoder constrained by bulk RNA-seq data.	1
103	HNF1B Alters an Evolutionarily Conserved Nephrogenic Program of Target Genes. ASN.2022010076	O
102	Combination bezafibrate and nivolumab treatment of patients with advanced non@mall cell lung cancer. 2022 , 14,	1
101	Connexin 30 Deficiency Ameliorates Disease Progression at the Early Phase in a Mouse Model of Amyotrophic Lateral Sclerosis by Suppressing Glial Inflammation. 2022 , 23, 16046	1
100	Juvenile zebrafish (Danio rerio) are able to recover from lordosis. 2022 , 12,	1
99	Pan-cancer analysis to provide a reliable basis for the clinical use of TIM-3 immunosuppressants.	O
98	Hybrid volatilomics in cancer diagnosis by HS-GC-FID fingerprinting.	o
97	Signaling through the Dystrophin Glycoprotein Complex affects the stress-dependent transcriptome in Drosophila.	0
96	Intrauterine botulinum toxin A administration promotes endometrial regeneration mediated by IGFBP3-dependent OPN proteolytic cleavage in thin endometrium. 2023 , 80,	o
95	Extracellular matrix inclusion in immunoisolating alginate-based microcapsules promotes longevity, reduces fibrosis, and supports function of islet allografts in vivo. 2023 ,	0
94	FOXM1-mediated regulation of reactive oxygen species and radioresistance in oral squamous cell carcinoma cells. 2023 , 100060	O
93	EpiMix: an integrative tool for epigenomic subtyping using DNA methylation.	O
92	Glycolysis Inhibition of Autophagy Drives Malignancy in Ovarian Cancer: Exacerbation by IL-6 and Attenuation by Resveratrol. 2023 , 24, 1723	0
91	Differential expression analysis in epithelial ovarian cancer using functional genomics and integrated bioinformatics approaches. 2023 , 101172	0
90	Colonic TRPV4 overexpression is related to constipation severity. 2023 , 23,	1
89	RNA-seq analysis of the active chick embryo chorioallantoic membrane reveals genes that encode proteins assigned to ion transport and innate immunity. 2023 , 110564	0
88	Dietary essential amino acids for the treatment of heart failure with reduced ejection fraction.	О

87	Generation of bioactive MSC-EVs for bone tissue regeneration by tauroursodeoxycholic acid treatment. 2023 , 354, 45-56	0
86	Urine-Based Detection of Biomarkers Indicative of Chronic Kidney Disease in a Patient Cohort from Ghana. 2023 , 13, 38	Ο
85	Gene Expression Analysis in gla-Mutant Zebrafish Reveals Enhanced Ca2+ Signaling Similar to Fabry Disease. 2023 , 24, 358	0
84	Expansion of ventral foregut is linked to changes in the enhancer landscape for organ-specific differentiation.	O
83	Ochratoxin A induces endoplasmic reticulum stress and fibrosis in the kidney via the HIF-1∄miR-155-5p link. 2023 , 10, 133-145	O
82	Cytokines in the Urine of AKI patients regulate TP53 and SIRT1 and can be used as biomarkers for the early detection of AKI.	O
81	Differential gene expression analysis of the resprouting process in Pinus canariensis provides new insights into a rare trait in conifers.	0
80	Evaluating the mouse neural precursor line, SN4741, as a suitable proxy for midbrain dopaminergic neurons.	O
79	Inducible TRAP RNA profiling reveals host genes expressed in Arabidopsis cells haustoriated by downy mildew.	0
78	Gene expression studies of WT1 mutant Wilms tumor cell lines in the frame work of published kidney development data reveals their early kidney stem cell origin. 2023 , 18, e0270380	O
77	The H2A.Z and NuRD associated protein HMG20A controls early head and heart developmental transcription programs. 2023 , 14,	0
76	Differential angiogenesis of bone and muscle endothelium in aging and inflammatory processes. 2023 , 6,	O
75	Gene Set Enrichment Analysis and Genetic Experiment Reveal Changes in Cell Signaling Pathways Induced by Esynuclein Overexpression. 2023 , 11, 263	0
74	Dbx2, an aging-related homeobox gene, inhibits the proliferation of adult neural progenitors.	O
73	Drug repositioning via host-pathogen protein-protein interactions for the treatment of cervical cancer. 13,	0
72	VGLL2-NCOA2 leverages developmental programs for pediatric sarcomagenesis. 2023 , 42, 112013	O
71	Tasquinimod suppresses tumor cell growth and bone resorption by targeting immunosuppressive myeloid cells and inhibiting c-MYC expression in multiple myeloma. 2023 , 11, e005319	0
70	Eomes is sufficient to regulate IL-10 expression and cytotoxic effector molecules in murine CD4+ T cells. 14,	O

69	Serum Metabolomics Reveals a Potential Benefit of Methionine in Type 1 Diabetes Patients with Poor Glycemic Control and High Glycemic Variability. 2023 , 15, 518	O
68	Loss of dyskerin facilitates the acquisition of metastatic traits by altering the mevalonate pathway. 2023 , 6, e202201692	O
67	Revealing the mode of action of Phenylalanine application in inducing fruit resistance to fungal pathogens. 2023 , 199, 112298	0
66	Nanopore Direct RNA Sequencing of Monosome- and Polysome-Bound RNA. 2023 , 281-297	О
65	Plasma Exosome Gene Signature Differentiates Colon Cancer from Healthy Controls.	0
64	Dynamic Biobanking for Advancing Breast Cancer Research. 2023 , 13, 360	О
63	Risk factors and actionable molecular signatures in COVID-19-associated lung adenocarcinoma and lung squamous cell carcinoma patients. 2023 , 158, 106855	0
62	At low levels, inorganic mercury interference with antigen signaling is associated with modifications to a panel of novel phosphoserine sites in B cell receptor pathway proteins. 2023 , 89, 105564	О
61	MERR APEX-seq protocol for profiling the subcellular nascent transcriptome in mammalian cells. 2023 , 4, 102057	О
60	diffeRenTES: An R package for computing cell differentiation trees from Boolean networks. 2023 , 15, 100470	О
59	Integrated transcriptomic and metabolomic analyses reveal key genes controlling flavonoid biosynthesis in Citrus grandis II omentosal Fruits. 2023 , 196, 210-221	О
58	Epigenetic signals that direct cell typespecific interferon beta response in mouse cells. 2023 , 6, e202201823	О
57	MicrobiotaProcess: A comprehensive R package for deep mining microbiome. 2023, 4, 100388	0
56	DNA quality evaluation of formalin-fixed paraffin-embedded heart tissue for DNA methylation array analysis. 2023 , 13,	О
55	Landscape of immunocytes infiltration and prognostic immune-related genes in hepatocellular carcinoma. 2023 ,	О
54	The turning point of COVID-19 severity is associated with a unique circulating neutrophil gene signature.	O
53	Macrophages promote anti-androgen resistance in prostate cancer bone disease. 2023 , 220,	1
52	Selective and brain-penetrant lanosterol synthase inhibitors target glioma stem-like cells by inducing 24(S),25-epoxycholesterol production. 2023 , 30, 214-229.e18	О

51	Light-Responsive MicroRNAs in Human Retinal Tissue are Differentially Regulated by Distinct Wavelengths of Light.	0
50	Expression of Selected miRNAs in Normal and Cancer-Associated Fibroblasts and in BxPc3 and MIA PaCa-2 Cell Lines of Pancreatic Ductal Adenocarcinoma. 2023 , 24, 3617	O
49	The human periconceptional maternal-embryonic space in health and disease. 2023 , 103, 1965-2038	О
48	Evaluating the mouse neural precursor line, SN4741, as a suitable proxy for midbrain dopaminergic neurons.	O
47	DUX4 double whammy: The transcription factor that causes a rare muscular dystrophy also kills the precursors of the human nose. 2023 , 9,	О
46	Effects of Cudrania tricuspidata and Sargassum fusiforme extracts on hair growth in C57BL/6 mice. 2023 , 39,	O
45	A Transcriptomic and Reverse-Engineering Strategy Reveals Molecular Signatures of Arachidonic Acid Metabolism in 12 Cancers. 2023 , 27, 127-138	О
44	New RoxS sRNA targets identified inB. subtilisby pulsed SILAC.	O
43	The bi-directional association between bipolar disorder and obesity: Evidence from Meta and bioinformatics analysis.	О
42	CRISPR/Cas9-mediated A4GALT suppression rescues Fabry disease phenotypes in a kidney organoid model. 2023 ,	O
41	Analysis of gene expression profile for identification of novel gene signatures during dengue infection. 2023 , 2, 19-30	0
40	Discovery of multi-state gene cluster switches determining the adaptive mitochondrial and metabolic landscape of breast cancer.	O
39	A compilation of bioinformatic approaches to identify novel downstream targets for the detection and prophylaxis of cancer. 2023 , 75-113	О
38	The Interplay among Glucocorticoid Therapy, Platelet-Activating Factor and Endocannabinoid Release Influences the Inflammatory Response to COVID-19. 2023 , 15, 573	1
37	Pathogenic human variant that dislocates GATA2 zinc fingers disrupts hematopoietic gene expression and signaling networks. 2023 , 133,	0
36	Cardinal v3 - a versatile open source software for mass spectrometry imaging analysis.	O
35	Histone H3K9 methyltransferase SETDB1 overexpression correlates with pediatric high-grade gliomas progression and prognosis. 2023 , 101, 387-401	О
34	Ten simple rules for providing bioinformatics support within a hospital. 2023 , 16,	О

33	Whole genome sequencing ofBorrelia burgdorferiisolates reveals linked clusters of plasmid-borne accessory genome elements associated with virulence.	O
32	Impact of Negative Feedbacks on De Novo Pyrimidines Biosynthesis in Escherichia coli. 2023 , 24, 4806	O
31	Exploring microbial functional biodiversity at the protein family level@rom metagenomic sequence reads to annotated protein clusters. 3,	О
30	Signature literature review reveals AHCY, DPYSL3, and NME1 as the most recurrent prognostic genes for neuroblastoma. 2023 , 16,	O
29	Neutrophil efferocytosis reprograms mitochondrial metabolism to switch alveolar macrophages to a pro-resolution phenotype at the cost of bacterial control.	O
28	Tumor MK2 transcript levels are associated with improved response to chemotherapy and patient survival in non-small cell lung cancer. 2023 , 55, 168-178	O
27	Non-canonical functions of SNAIL drive context-specific cancer progression. 2023, 14,	1
26	KRAB zinc finger proteins ZNF587/ZNF417 protect lymphoma cells from replicative stress-induced inflammation.	O
25	Metabolic and Transcriptomic Changes in the Mouse Brain in Response to Short-Term High-Fat Metabolic Stress. 2023 , 13, 407	O
24	The lysosomal LAMTOR / Ragulator complex is essential for nutrient homeostasis in brown adipose tissue. 2023 , 71, 101705	O
23	A Genetic Engineering Toolbox for the Lignocellulolytic Anaerobic Gut Fungus Neocallimastix frontalis. 2023 , 12, 1034-1045	O
22	Transcriptome analysis of Aurantiochytrium limacinumunder low salt conditions. 2023, 134,	O
21	Metabolic and Transcriptomic Signatures of the Acute Psychological Stress Response in the Mouse Brain. 2023 , 13, 453	O
20	shinyNORRRM: A Cross-Platform Software to Calculate the CIPW Norm. 2023 , 55, 563-577	O
19	Cocktails of NSAIDs and 17Æthinylestradiol at Environmentally Relevant Doses in Drinking Water Alter Puberty Onset in Mice Intergenerationally. 2023 , 24, 5890	O
18	Enabling growth-decoupled Komagataella phaffii recombinant protein production based on the methanol-free PDH promoter. 11,	O
17	Eccentric and concentric exercises induce different adaptions in adipose tissue biology.	0
16	Expression of RSUME is Associated With Poor Prognosis in Clear Cell Renal Carcinoma: Involvement of ROS Related Metabolism. 2023 ,	Ο

15	Preadapted to adapt: underpinnings of adaptive plasticity revealed by the downy brome genome. 2023 , 6,	O
14	Bioinformatics-Based Identification of Tumor Immune Invasion- Related prognostic Biomarkers in pancreatic cancer.	O
13	Different approaches to Imaging Mass Cytometry data analysis. 2023, 3,	O
12	Pregnancy-specific responses to COVID-19 revealed by high-throughput proteomics of human plasma. 2023 , 3,	O
11	The scverse project provides a computational ecosystem for single-cell omics data analysis.	O
10	Nitrogen transformation processes catalyzed by manure microbiomes in earthen pit and concrete storages on commercial dairy farms. 2023 , 18,	O
9	Establishment of an artificial particulate matter-induced lung disease model through analyzing pathological changes and transcriptomic profiles in mice. 2023 , 13,	О
8	RoPE: A robust profile likelihood method for differential gene expression analysis.	O
7	Investigation of changes in DNA methylation associated with alterations in gene expression resulting in differences between lean and obese adipogenesis. 2023 , 115, 110623	O
6	Stable endocytic structures navigate the complex pellicle of apicomplexan parasites. 2023 , 14,	O
5	SynBioTools: a one-stop facility for searching and selecting synthetic biology tools. 2023, 24,	O
4	Bioinformatics analysis of the genes associated with co-occurrence of heart failure and lung cancer. 15	53537022311620
3	Electroconductive and mechano-competent PUCL@CNT nanohybrid scaffolds guiding neuronal specification of neural stem/progenitor cells. 2023 , 466, 143125	О
2	Epigenomic profiling at genome scale: from assays and analysis to clinical insights. 2023 , 143-174	O
1	Multifunctional dendrimer@nanoceria engineered GelMA hydrogel accelerates bone regeneration through orchestrated cellular responses. 2023 , 20, 100664	О