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**Gene Expression Omnibus: NCBI gene expression and hybridization array data repository**

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1461	Methodological framework for functional characterization of plant microRNAs. <b>2010</b> , 61, 2271-80	7
1460	Dysregulation of the mitogen granulin in human cancer through the miR-15/107 microRNA gene group. <b>2010</b> , 70, 9137-42	41
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1457	Aggressive fibromatosis (desmoid tumor) is derived from mesenchymal progenitor cells. <b>2010</b> , 70, 7690-8	88
1456	Elevated cyclic AMP levels in T lymphocytes transformed by human T-cell lymphotropic virus type 1. <b>2010</b> , 84, 8732-42	17
1455	The lytic transcriptome of Kaposi's sarcoma-associated herpesvirus reveals extensive transcription of noncoding regions, including regions antisense to important genes. <b>2010</b> , 84, 7934-42	63
1454	Divergence of human and mouse brain transcriptome highlights Alzheimer disease pathways. <b>2010</b> , 107, 12698-703	341
1453	The correlation pattern of acquired copy number changes in 164 ETV6/RUNX1-positive childhood acute lymphoblastic leukemias. <b>2010</b> , 19, 3150-8	39
1452	Array-based transcript profiling and limiting-dilution reverse transcription-PCR analysis identify additional latent genes in Kaposi's sarcoma-associated herpesvirus. <b>2010</b> , 84, 5565-73	89
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1450	Identification of candidate surface antigens for non-invasive prenatal diagnosis by comparative global gene expression on human fetal mesenchymal stem cells. <b>2010</b> , 16, 472-80	2
1449	Rank-rank hypergeometric overlap: identification of statistically significant overlap between gene-expression signatures. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, e169	20.1 210
1448	Cardiovascular networks: systems-based approaches to cardiovascular disease. <b>2010</b> , 121, 157-70	105
1447	MicroRNA gene evolution in <i>Arabidopsis lyrata</i> and <i>Arabidopsis thaliana</i> . <b>2010</b> , 22, 1074-89	204
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1442	Ontology-based meta-analysis of global collections of high-throughput public data. <b>2010</b> , 5, e13066	273
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1440	Differential gene expression in adipose stem cells cultured in allogeneic human serum versus fetal bovine serum. <b>2010</b> , 16, 2281-94	68
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1438	Giraffe--an R/Bioconductor package for functional exploration of aligned next-generation sequencing reads. <b>2010</b> , 26, 2902-3	10
1437	DigOut: viewing differential expression genes as outliers. <b>2010</b> , 8 Suppl 1, 161-75	5
1436	Effects of reduced frequency of milk removal on gene expression in the bovine mammary gland. <b>2010</b> , 41, 21-32	38
1435	Ubiquitin accumulation in autophagy-deficient mice is dependent on the Nrf2-mediated stress response pathway: a potential role for protein aggregation in autophagic substrate selection. <b>2010</b> , 191, 537-52	137
1434	NF-E2-related factor 2 regulates the stress response to UVA-1-oxidized phospholipids in skin cells. <b>2010</b> , 24, 39-48	66
1433	Ternary complex factors SAP-1 and Elk-1, but not net, are functionally equivalent in thymocyte development. <b>2010</b> , 185, 1082-92	34
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1431	The forkhead transcription factor Hcm1 promotes mitochondrial biogenesis and stress resistance in yeast. <b>2010</b> , 285, 37092-101	25
1430	BAFF receptor signaling aids the differentiation of immature B cells into transitional B cells following tonic BCR signaling. <b>2010</b> , 185, 4570-81	80
1429	Blockade of CCL1 inhibits T regulatory cell suppressive function enhancing tumor immunity without affecting T effector responses. <b>2010</b> , 184, 6833-42	80
1428	Expanded multilocus sequence typing and comparative genomic hybridization of <i>Campylobacter coli</i> isolates from multiple hosts. <b>2010</b> , 76, 1913-25	20
1427	Deletion of genes encoding cytochrome oxidases and quinol monooxygenase blocks the aerobic-anaerobic shift in <i>Escherichia coli</i> K-12 MG1655. <b>2010</b> , 76, 6529-40	41



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1425	Fast integration of heterogeneous data sources for predicting gene function with limited annotation. <b>2010</b> , 26, 1759-65	102
1424	Coexpression analysis of tomato genes and experimental verification of coordinated expression of genes found in a functionally enriched coexpression module. <b>2010</b> , 17, 105-16	40
1423	TreeHugger: A New Test for Enrichment of Gene Ontology Terms. <b>2010</b> , 22, 210-221	4
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1421	Neighborhood rough set reduction-based gene selection and prioritization for gene expression profile analysis and molecular cancer classification. <b>2010</b> , 2010, 726413	5
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1418	Mixture-model based estimation of gene expression variance from public database improves identification of differentially expressed genes in small sized microarray data. <b>2010</b> , 26, 486-92	7
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1416	The relationship among gene expression, the evolution of gene dosage, and the rate of protein evolution. <b>2010</b> , 6, e1000944	132
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1414	An integrative approach for high-throughput screening and characterization of transcriptional regulators in <i>Streptomyces coelicolor</i> . <b>2010</b> , 82, 57-67	1
1413	Using pre-existing microarray datasets to increase experimental power: application to insulin resistance. <b>2010</b> , 6, e1000718	8
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1410	Abundant quantitative trait loci exist for DNA methylation and gene expression in human brain. <b>2010</b> , 6, e1000952	612
1409	Functional genetic diversity among <i>Mycobacterium tuberculosis</i> complex clinical isolates: delineation of conserved core and lineage-specific transcriptomes during intracellular survival. <b>2010</b> , 6, e1000988	185

1408	Finding the right questions: exploratory pathway analysis to enhance biological discovery in large datasets. <b>2010</b> , 8, e1000472	42
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1400	Comparative analysis of biclustering algorithms. <b>2010</b> ,	19
1399	Identification of a novel biomarker, SEMA5A, for non-small cell lung carcinoma in nonsmoking women. <b>2010</b> , 19, 2590-7	213
1398	Genome-wide analysis reveals distinct substrate specificities of Rrp6, Dis3, and core exosome subunits. <b>2010</b> , 16, 781-91	43
1397	RB-pathway disruption in breast cancer: differential association with disease subtypes, disease-specific prognosis and therapeutic response. <b>2010</b> , 9, 4153-63	131
1396	Significance of light, sugar, and amino acid supply for diurnal gene regulation in developing barley caryopses. <b>2010</b> , 153, 14-33	31
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1377	Microarray Meta-Miner (MMM): An integrated method and a web tool to identify genes with similar expression profile. <b>2010</b> ,	
1376	Proliferation and pluripotency of human embryonic stem cells maintained on type I collagen. <b>2010</b> , 19, 1923-35	19
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1365	Genome-wide analysis of expression modes and DNA methylation status at sense-antisense transcript loci in mouse. <b>2010</b> , 96, 333-41	14
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1357	Global and unbiased detection of splice junctions from RNA-seq data. <b>2010</b> , 11, R34	65
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1355	Inferring the functions of longevity genes with modular subnetwork biomarkers of <i>Caenorhabditis elegans</i> aging. <b>2010</b> , 11, R13	35

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1353	Immature cell populations and an erythropoiesis gene-expression signature in systemic juvenile idiopathic arthritis: implications for pathogenesis. <b>2010</b> , 12, R123	41
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1349	Transcriptome analysis of alkali shock and alkali adaptation in <i>Listeria monocytogenes</i> 10403S. <b>2010</b> , 7, 1147-57	19
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1334	Data and knowledge management in cross-Omics research projects. <b>2011</b> , 719, 97-111	3
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1332	Omics and literature mining. <b>2011</b> , 719, 457-77	3
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1330	Microarray analysis of genes associated with cell surface NIS protein levels in breast cancer. <b>2011</b> , 4, 397	7
1329	Identification of biomarkers in breast cancer metastasis by integrating protein-protein interaction network and gene expression data. <b>2011</b> ,	3
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1323	Classification of unknown primary tumors with a data-driven method based on a large microarray reference database. <b>2011</b> , 3, 63	9
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1318	Association of FABP5 expression with poor survival in triple-negative breast cancer: implication for retinoic acid therapy. <b>2011</b> , 178, 997-1008	103
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1315	Early response of bovine alveolar macrophages to infection with live and heat-killed Mycobacterium bovis. <b>2011</b> , 35, 580-91	13
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1311	Morphological, functional and gene expression analysis of the hyperoxic mouse retina. <b>2011</b> , 92, 306-14	4
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1304	Discovery and preclinical validation of drug indications using compendia of public gene expression data. <b>2011</b> , 3, 96a77	542
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1297	Omics technologies, data and bioinformatics principles. <b>2011</b> , 719, 3-30	64
1296	Deciphering the molecular basis of wine yeast fermentation traits using a combined genetic and genomic approach. <b>2011</b> , 1, 263-81	62
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1281	MicroRNA controlled adenovirus mediates anti-cancer efficacy without affecting endogenous microRNA activity. <b>2011</b> , 6, e16152	31
1280	Identification of candidate small-molecule therapeutics to cancer by gene-signature perturbation in connectivity mapping. <b>2011</b> , 6, e16382	29
1279	Brain perihematoma genomic profile following spontaneous human intracerebral hemorrhage. <b>2011</b> , 6, e16750	44
1278	Distinct early molecular responses to mutations causing vLINCL and JNCL presage ATP synthase subunit C accumulation in cerebellar cells. <b>2011</b> , 6, e17118	47
1277	Identification and replication of loci involved in camptothecin-induced cytotoxicity using CEPH pedigrees. <b>2011</b> , 6, e17561	10
1276	Relationship between symptoms and gene expression induced by the infection of three strains of Rice dwarf virus. <b>2011</b> , 6, e18094	46
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1262	Genome-wide binding map of the HIV-1 Tat protein to the human genome. <b>2011</b> , 6, e26894	27
1261	Integrated transcriptome and binding sites analysis implicates E2F in the regulation of self-renewal in human pluripotent stem cells. <b>2011</b> , 6, e27231	20
1260	Small interfering RNA against transcription factor STAT6 leads to increased cholesterol synthesis in lung cancer cell lines. <b>2011</b> , 6, e28509	16
1259	Data Management in Large Collaborative Biology Research Projects. <b>2011</b> , 53, 227-233	
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1256	Repression of the RHOH gene by JunD. <b>2011</b> , 437, 75-88	7
1255	The tumor marker Fascin is strongly induced by the Tax oncoprotein of HTLV-1 through NF-kappaB signals. <b>2011</b> , 117, 3609-12	29
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1253	miRNA expression in diffuse large B-cell lymphoma treated with chemoimmunotherapy. <b>2011</b> , 118, 1034-40	73
1252	Pseudonodule formation by wild-type and symbiotic mutant <i>Medicago truncatula</i> in response to auxin transport inhibitors. <b>2011</b> , 24, 1372-84	62
1251	Histone deacetylase inhibitors in the treatment of muscular dystrophies: epigenetic drugs for genetic diseases. <b>2011</b> , 17, 457-65	56
1250	Boolean Analysis of Gene Expression Datasets. <b>2011</b> , 349-375	
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1248	Generation of chimeric repressors that confer salt tolerance in Arabidopsis and rice. <b>2011</b> , 9, 736-46	42
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1246	Molecular events of apical bud formation in white spruce, <i>Picea glauca</i> . <b>2011</b> , 34, 480-500	71
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1242	Mining Affymetrix microarray data for long non-coding RNAs: altered expression in the nucleus accumbens of heroin abusers. <b>2011</b> , 116, 459-66	134
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1240	Comparative kinetic analyses of gene profiles of naïve CD4+ and CD8+ T cells from young and old animals reveal novel age-related alterations. <b>2011</b> , 10, 853-67	23
1239	Unveiling the transcriptional features associated with coccolithovirus infection of natural <i>Emiliana huxleyi</i> blooms. <b>2011</b> , 78, 555-64	22
1238	Phosphoproteomic analysis reveals an intrinsic pathway for the regulation of histone deacetylase 7 that controls the function of cytotoxic T lymphocytes. <b>2011</b> , 12, 352-61	83
1237	Genome-scale analysis of replication timing: from bench to bioinformatics. <b>2011</b> , 6, 870-95	76
1236	A bioinformatical and functional approach to identify novel strategies for chemoprevention of colorectal cancer. <b>2011</b> , 30, 2026-36	18
1235	Bone morphogenetic protein-7 is a MYC target with prosurvival functions in childhood medulloblastoma. <b>2011</b> , 30, 2823-35	23
1234	Integrative mRNA profiling comparing cultured primary cells with clinical samples reveals PLK1 and C20orf20 as therapeutic targets in cutaneous squamous cell carcinoma. <b>2011</b> , 30, 4666-77	54
1233	The expanded human disease network combining protein-protein interaction information. <b>2011</b> , 19, 783-8	43
1232	Peripheral blood gene expression profiles in metabolic syndrome, coronary artery disease and type 2 diabetes. <b>2011</b> , 12, 341-51	45
1231	Transcriptome response of high- and low-light-adapted <i>Prochlorococcus</i> strains to changing iron availability. <b>2011</b> , 5, 1580-94	90
1230	Discovery of new microRNAs by small RNAome deep sequencing in childhood acute lymphoblastic leukemia. <b>2011</b> , 25, 1389-99	72
1229	Role of camalexin, indole glucosinolates, and side chain modification of glucosinolate-derived isothiocyanates in defense of <i>Arabidopsis</i> against <i>Sclerotinia sclerotiorum</i> . <b>2011</b> , 67, 81-93	130

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1227	Drawing networks of rejection - a systems biological approach to the identification of candidate genes in heart transplantation. <b>2011</b> , 15, 949-56	8
1226	CD47 knockout mice exhibit improved recovery from spinal cord injury. <b>2011</b> , 42, 21-34	32
1225	Brother of CDO (BOC) expression in equine articular cartilage. <b>2011</b> , 19, 435-8	6
1224	Cardiac cell modelling: observations from the heart of the cardiac physiome project. <b>2011</b> , 104, 2-21	122
1223	The knockdown of the maternal estrogen receptor 2a (esr2a) mRNA affects embryo transcript contents and larval development in zebrafish. <b>2011</b> , 172, 120-9	21
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1214	Toward the blood-borne miRNome of human diseases. <b>2011</b> , 8, 841-3	282
1213	Population-genetic properties of differentiated human copy-number polymorphisms. <b>2011</b> , 88, 317-32	69
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1211	Identification of transcriptome profiles and signaling pathways for the allelochemical juglone in rice roots. <b>2011</b> , 77, 591-607	35

1210	Comparative transcript profiling of apricot ( <i>Prunus armeniaca</i> L.) fruit development and on-tree ripening. <b>2011</b> , 7, 609-616	29
1209	Integrative computational biology for cancer research. <b>2011</b> , 130, 465-81	21
1208	Alkaline-stress response in Glycine soja leaf identifies specific transcription factors and ABA-mediated signaling factors. <b>2011</b> , 11, 369-79	21
1207	A ED: -xylosidase and a PR-4B precursor identified as genes accounting for differences in peach cold storage tolerance. <b>2011</b> , 11, 357-68	20
1206	Absence of repellents in <i>Ustilago maydis</i> induces genes encoding small secreted proteins. <b>2011</b> , 100, 219-29	5
1205	Alpha-synuclein deficiency leads to increased glyoxalase I expression and glycation stress. <b>2011</b> , 68, 721-33	64
1204	Biofilm formation in <i>Escherichia coli</i> cra mutants is impaired due to down-regulation of curli biosynthesis. <b>2011</b> , 193, 711-22	17
1203	Deriving and comparing the distribution for the number of false positives in single step methods to control k-FWER. <b>2011</b> , 81, 1695-1705	2
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1195	A gene signature in histologically normal surgical margins is predictive of oral carcinoma recurrence. <b>2011</b> , 11, 437	81
1194	Tat RNA silencing suppressor activity contributes to perturbation of lymphocyte miRNA by HIV-1. <b>2011</b> , 8, 36	44
1193	Effect of L-carnitine on the hepatic transcript profile in piglets as animal model. <b>2011</b> , 8, 76	17

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1190	Meta-analysis of multiple microarray datasets reveals a common gene signature of metastasis in solid tumors. <b>2011</b> , 4, 56	40
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1188	A 44K microarray dataset of the changing transcriptome in developing Atlantic salmon ( <i>Salmo salar</i> L.). <b>2011</b> , 4, 88	39
1187	BioAssay Ontology (BAO): a semantic description of bioassays and high-throughput screening results. <b>2011</b> , 12, 257	89
1186	Discovering biological connections between experimental conditions based on common patterns of differential gene expression. <b>2011</b> , 12, 381	14
1185	eXframe: reusable framework for storage, analysis and visualization of genomics experiments. <b>2011</b> , 12, 452	5
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1183	Meta-analysis of muscle transcriptome data using the MADMuscle database reveals biologically relevant gene patterns. <b>2011</b> , 12, 113	19
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1180	Identification of microRNA-mRNA modules using microarray data. <b>2011</b> , 12, 138	53
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1175	MMP1 bimodal expression and differential response to inflammatory mediators is linked to promoter polymorphisms. <b>2011</b> , 12, 43	17

1174	Differential transcriptomic profiles effected by oil palm phenolics indicate novel health outcomes. <b>2011</b> , 12, 432	16
1173	Spleen transcriptome response to infection with avian pathogenic <i>Escherichia coli</i> in broiler chickens. <b>2011</b> , 12, 469	52
1172	Transcriptome profiling of the rice blast fungus during invasive plant infection and in vitro stresses. <b>2011</b> , 12, 49	61
1171	Skin healing and scale regeneration in fed and unfed sea bream, <i>Sparus auratus</i> . <b>2011</b> , 12, 490	47
1170	Evaluation of the NOD/SCID xenograft model for glucocorticoid-regulated gene expression in childhood B-cell precursor acute lymphoblastic leukemia. <b>2011</b> , 12, 565	24
1169	Relative impact of key sources of systematic noise in Affymetrix and Illumina gene-expression microarray experiments. <b>2011</b> , 12, 589	22
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1167	Characterisation and expression of microRNAs in developing wings of the neotropical butterfly <i>Heliconius melpomene</i> . <b>2011</b> , 12, 62	35
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1165	Regulation of IL-2 gene expression by Siva and FOXP3 in human T cells. <b>2011</b> , 12, 54	5
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1163	Concise review: challenging the pluripotency of human testis-derived ESC-like cells. <b>2011</b> , 29, 1165-9	30
1162	Tympanic membrane wound healing in rats assessed by transcriptome profiling. <b>2011</b> , 121, 2199-213	18
1161	Dietary L-carnitine alters gene expression in skeletal muscle of piglets. <b>2011</b> , 55, 419-29	28
1160	The Forkhead factor FoxQ1 influences epithelial differentiation. <b>2011</b> , 226, 710-9	47
1159	<sup>13</sup> C high-resolution-magic angle spinning MRS reveals differences in glucose metabolism between two breast cancer xenograft models with different gene expression patterns. <b>2011</b> , 24, 1243-52	16
1158	Meta-analysis of heterogeneous data sources for genome-scale identification of risk genes in complex phenotypes. <b>2011</b> , 35, 318-32	28
1157	Developmental profiling of postnatal dentate gyrus progenitors provides evidence for dynamic cell-autonomous regulation. <b>2011</b> , 21, 33-47	35

1156	Knockdown of ovarian cancer amplification target ADRM1 leads to downregulation of GIPC1 and upregulation of RECK. <b>2011</b> , 50, 434-41	13
1155	Identification of genetic disparity between primary and metastatic melanoma in human patients. <b>2011</b> , 50, 680-8	7
1154	t(4;8)(q27;q24) in Hodgkin lymphoma cells targets phosphodiesterase PDE5A and homeobox gene ZHX2. <b>2011</b> , 50, 996-1009	23
1153	The knockdown of maternal glucocorticoid receptor mRNA alters embryo development in zebrafish. <b>2011</b> , 240, 874-89	57
1152	MicroRNA-183 family expression in hair cell development and requirement of microRNAs for hair cell maintenance and survival. <b>2011</b> , 240, 808-19	86
1151	Mutant SOD1 and mitochondrial damage alter expression and splicing of genes controlling neurogenesis in models of neurodegeneration. <b>2011</b> , 32, 168-82	30
1150	Large-scale integration of microarray data reveals genes and pathways common to multiple cancer types. <b>2011</b> , 128, 2881-91	30
1149	A spectral approach to clustering numerical vectors as nodes in a network. <b>2011</b> , 44, 236-251	4
1148	Network-based sparse Bayesian classification. <b>2011</b> , 44, 886-900	12
1147	Diversity of accessory genome of human and livestock-associated ST398 methicillin resistant <i>Staphylococcus aureus</i> strains. <b>2011</b> , 11, 290-9	49
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1145	Tracheal occlusion modulates the gene expression profile of the medial thalamus in anesthetized rats. <b>2011</b> , 111, 117-24	7
1144	Rat diaphragm mitochondria have lower intrinsic respiratory rates than mitochondria in limb muscles. <b>2011</b> , 300, R1311-5	5
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1141	COP1-mediated degradation of BBX22/LZF1 optimizes seedling development in Arabidopsis. <b>2011</b> , 156, 228-39	84
1140	Crosstalk between c-Jun and TAp73alpha/beta contributes to the apoptosis-survival balance. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, 6069-85	20.1 39
1139	The role of indirect connections in gene networks in predicting function. <b>2011</b> , 27, 1860-6	60



1138	Soybean homologs of MPK4 negatively regulate defense responses and positively regulate growth and development. <b>2011</b> , 157, 1363-78	109
1137	Gene expression biomarkers provide sensitive indicators of in planta nitrogen status in maize. <b>2011</b> , 157, 1841-52	70
1136	Nearest hyperplane distance neighbor clustering algorithm applied to gene co-expression analysis in Alzheimer's disease. <b>2011</b> , 2011, 5559-62	4
1135	NCBI GEO: archive for functional genomics data sets--10 years on. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D1005-10	829
1134	KeyPathwayMiner: Detecting Case-Specific Biological Pathways Using Expression Data. <b>2011</b> , 7, 299-313	38
1133	SVS: data and knowledge integration in computational biology. <b>2011</b> , 2011, 6474-8	5
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1129	AtCAST, a tool for exploring gene expression similarities among DNA microarray experiments using networks. <b>2011</b> , 52, 169-80	17
1128	Epigenetic silencing of microRNA-203 dysregulates ABL1 expression and drives Helicobacter-associated gastric lymphomagenesis. <b>2011</b> , 71, 3616-24	89
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1126	High-resolution temporal profiling of transcripts during Arabidopsis leaf senescence reveals a distinct chronology of processes and regulation. <b>2011</b> , 23, 873-94	594
1125	Primosomal proteins DnaD and DnaB are recruited to chromosomal regions bound by DnaA in Bacillus subtilis. <b>2011</b> , 193, 640-8	31
1124	Classifying short gene expression time-courses with Bayesian estimation of piecewise constant functions. <b>2011</b> , 27, 946-52	10
1123	Identification of genes specific to mouse primordial germ cells through dynamic global gene expression. <b>2011</b> , 20, 115-25	36
1122	Influence of 17 $\beta$ -Estradiol on gene expression of Paracoccidioides during mycelia-to-yeast transition. <b>2011</b> , 6, e28402	34
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1120	Transcriptional effect of the LH surge in bovine granulosa cells during the peri-ovulation period. <b>2011</b> , 141, 193-205		37
1119	mir-11 limits the proapoptotic function of its host gene, dE2f1. <b>2011</b> , 25, 1820-34		34
1118	Integrative cancer genomics (IntOGen) in Biomart. <b>2011</b> , 2011, bar039		16
1117	Therapeutics of Ebola hemorrhagic fever: whole-genome transcriptional analysis of successful disease mitigation. <b>2011</b> , 204 Suppl 3, S1043-52		31
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1114	Making sense of cancer genomic data. <b>2011</b> , 25, 534-55		260
1113	Proteomics and transcriptomics characterization of bile stress response in probiotic <i>Lactobacillus rhamnosus</i> GG. <b>2011</b> , 10, M110.002741		122
1112	Bile salts induce resistance to polymyxin in enterohemorrhagic <i>Escherichia coli</i> O157:H7. <b>2011</b> , 193, 4509-15		40
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1110	Analysis of group A <i>Streptococcus</i> gene expression in humans with pharyngitis using a microarray. <b>2011</b> , 60, 1725-1733		3
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1108	The need for the pathology community to sponsor a whole slide imaging repository with technical guidance from the pathology informatics community. <b>2011</b> , 2, 31		6
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1105	A screening assay based on host-pathogen interaction models identifies a set of novel antifungal benzimidazole derivatives. <b>2011</b> , 55, 4789-801		10
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1103	Kaposi's sarcoma-associated herpesvirus viral interferon regulatory factor 3 inhibits gamma interferon and major histocompatibility complex class II expression. <b>2011</b> , 85, 4530-7		41

1102	Loss of subcellular lipid transport due to ARV1 deficiency disrupts organelle homeostasis and activates the unfolded protein response. <b>2011</b> , 286, 11951-9		30
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1094	A Bayesian framework for inference of the genotype-phenotype map for segregating populations. <b>2011</b> , 187, 1163-70		29
1093	Identification of genes involved in cell wall biogenesis in grasses by differential gene expression profiling of elongating and non-elongating maize internodes. <b>2011</b> , 62, 3545-61		94
1092	Biphasic gene expression changes elicited by <i>Phakopsora pachyrhizi</i> in soybean correlate with fungal penetration and haustoria formation. <b>2011</b> , 157, 355-71		38
1091	Molecular profiling of stomatal meristemoids reveals new component of asymmetric cell division and commonalities among stem cell populations in <i>Arabidopsis</i> . <b>2011</b> , 23, 3260-75		120
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1087	Ligand-independent phosphorylation of the glucocorticoid receptor integrates cellular stress pathways with nuclear receptor signaling. <b>2011</b> , 31, 4663-75		112
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1085	Systemic gut microbial modulation of bile acid metabolism in host tissue compartments. <b>2011</b> , 108 Suppl 1, 4523-30		495

1084	Transcriptome analysis of high-temperature stress in developing barley caryopses: early stress responses and effects on storage compound biosynthesis. <b>2011</b> , 4, 97-115	113
1083	Determinants of synonymous and nonsynonymous variability in three species of <i>Drosophila</i> . <b>2011</b> , 28, 1731-43	36
1082	Large-scale prediction of long non-coding RNA functions in a coding-non-coding gene co-expression network. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, 3864-78	20.1 447
1081	An atlas of tissue-specific conserved coexpression for functional annotation and disease gene prediction. <b>2011</b> , 19, 1173-80	44
1080	Open chromatin defined by DNaseI and FAIRE identifies regulatory elements that shape cell-type identity. <b>2011</b> , 21, 1757-67	391
1079	The plant cuticle is required for osmotic stress regulation of abscisic acid biosynthesis and osmotic stress tolerance in <i>Arabidopsis</i> . <b>2011</b> , 23, 1971-84	121
1078	Transcriptional profiling at different sites in lungs of pigs during acute bacterial respiratory infection. <b>2011</b> , 17, 41-53	12
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1072	Global gene expression profiling of a population exposed to a range of benzene levels. <b>2011</b> , 119, 628-34	82
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1063	Reciprocal transcriptional regulation of metabolic and signaling pathways correlates with disease severity in heart failure. <b>2011</b> , 4, 475-83	46
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


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