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Statistical significance for genomewide studies

DOI: 10.1073/pnas.1530509100
Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 9440-5.

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2260	.		
2259	Science and Technology Education and Future Human Needs. **1987**, ii		
2258	Introduction. **1992**, 7-8		
2257	mRNA profiling of pancreatic beta-cells: investigating mechanisms of diabetes. **2001**, 187-211		2
2256	Minding the Ps and Qs of genomewide analysis. **2003**, 8, 912-3		
2255	False discovery or missed discovery?. **2003**, 91, 537-8		23
2254	"Are we there yet?": Deciding when one has demonstrated specific genetic causation in complex diseases and quantitative traits. **2003**, 73, 711-9		159
2253	Search for haplotype interactions that influence susceptibility to type 1 diabetes, through use of unphased genotype data. **2003**, 73, 1385-401		8
2252	Using alpha wisely: improving power to detect multiple QTL. **2004**, 3, Article1		7
2251	. **2004**,		348
2250	Longitudinal transcriptional analysis of developing neointimal vascular occlusion and pulmonary hypertension in rats. **2004**, 17, 150-6		24
2249	Using ANOVA to analyze microarray data. **2004**, 37, 173-5, 177		117
2248	Brain gene expression: genomics and genetics. **2004**, 60, 59-95		15
2247	Microarray analysis of human nervous system gene expression in neurological disease. **2004**, 60, 135-51		1
2246	Gene expression profiling of human lung tissue from smokers with severe emphysema. **2004**, 31, 601-10		136

2245	A conserved transcript pattern in response to a specialist and a generalist herbivore. **2004**, 16, 3132-47		408
2244	Large-scale meta-analysis of cancer microarray data identifies common transcriptional profiles of neoplastic transformation and progression. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 9309-14	11.5	790
2243	Multiple quantitative trait loci mapping with cofactors and application of alternative variants of the false discovery rate in an enlarged granddaughter design. **2004**, 168, 1019-27		31
2242	Widespread RNA editing of embedded alu elements in the human transcriptome. **2004**, 14, 1719-25		389
2241	The genetic architecture of response to long-term artificial selection for oil concentration in the maize kernel. **2004**, 168, 2141-55		173
2240	Betting odds and genetic associations. **2004**, 96, 421-3		134
2239	On the distribution of temporal variations in allele frequency: consequences for the estimation of effective population size and the detection of loci undergoing selection. **2004**, 168, 563-8		28
2238	Decoding human regulatory circuits. **2004**, 14, 1967-74		76
2237	Interaction-dependent gene expression in Mla-specified response to barley powdery mildew. **2004**, 16, 2514-28		174
2236	Microarrays as a tool to investigate the biology of aging: a retrospective and a look to the future. **2004**, 2004, re7		24
2235	Evidence for nucleolus organizer regions as the units of regulation in nucleolar dominance in Arabidopsis thaliana interecotype hybrids. **2004**, 167, 931-9		22
2234	Molecular prediction of response to 5-fluorouracil and interferon-alpha combination chemotherapy in advanced hepatocellular carcinoma. **2004**, 10, 6029-38		48
2233	Microarray profiling for differential gene expression in ovaries and ovarian follicles of pigs selected for increased ovulation rate. **2004**, 168, 1529-37		34
2232	ArrayXPath: mapping and visualizing microarray gene-expression data with integrated biological pathway resources using Scalable Vector Graphics. **2004**, 32, W460-4		51
2231	A mixture model-based strategy for selecting sets of genes in multiclass response microarray experiments. **2004**, 20, 2562-71		54
2230	Identification of hair cycle-associated genes from time-course gene expression profile data by using replicate variance. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 15955-60	11.5	69
2229	Impact of PPARgamma overexpression and activation on pancreatic islet gene expression profile analyzed with oligonucleotide microarrays. **2004**, 287, E390-404		26
2228	SIEGE: Smoking Induced Epithelial Gene Expression Database. **2005**, 33, D573-9		21

2227	Pseudomonas aeruginosa flagellin and alginate elicit very distinct gene expression patterns in airway epithelial cells: implications for cystic fibrosis disease. **2004**, 173, 5659-70	87
2226	Computational definition of sequence motifs governing constitutive exon splicing. **2004**, 18, 1241-50	334
2225	Detecting differential gene expression with a semiparametric hierarchical mixture method. **2004**, 5, 155-76	430
2224	Analysis of Microarray Gene Expression Data. **2004**,	0
2223	A note on the adaptive control of false discovery rates. **2004**, 66, 297-304	35
2222	Gene expression analysis of peripheral T cells in a subgroup of common variable immunodeficiency shows predominance of CCR7(-) effector-memory T cells. **2004**, 138, 278-89	36
2221	Genome-scale expression profiling of Hutchinson-Gilford progeria syndrome reveals widespread transcriptional misregulation leading to mesodermal/mesenchymal defects and accelerated atherosclerosis. **2004**, 3, 235-43	155
2220	Gene expression profiling of anti-GBM glomerulonephritis model: the role of NF-kappaB in immune complex kidney disease. **2004**, 66, 1826-37	40
2219	Heritability, correlations and in silico mapping of locomotor behavior and neurochemistry in inbred strains of mice. **2005**, 4, 209-28	31
2218	DNA microarray technology and its applications in dermatology. **2004**, 13, 593-606	37
2217	Genomic Control to the extreme. **2004**, 36, 1129-30; author reply 1131	130
2216	Reply to "Genomic Control to the extreme". **2004**, 36, 1131-1131	6
2215	The effects of human population structure on large genetic association studies. **2004**, 36, 512-7	686
2214	Kaposi sarcoma herpesvirus-induced cellular reprogramming contributes to the lymphatic endothelial gene expression in Kaposi sarcoma. **2004**, 36, 687-93	379
2213	The use of pedigree, sib-pair and association studies of common diseases for genetic mapping and epidemiology. **2004**, 36, 1045-51	130
2212	The Bayesian revolution in genetics. **2004**, 5, 251-61	328
2211	Quantitative genetic analyses of complex behaviours in Drosophila. **2004**, 5, 838-49	116
2210	Support for EKN1 as the susceptibility locus for dyslexia on 15q21. **2004**, 9, 1111-21	100

2209	Balancing false positives and false negatives for the detection of differential expression in malignancies. **2004**, 91, 1160-5	12
2208	Mapping complex disease loci in whole-genome association studies. **2004**, 429, 446-52	500
2207	Combining genome-wide and targeted gene expression profiling in drug discovery: microarrays and real-time PCR. **2004**, 9, 838-45	17
2206	Determination of the differentially expressed genes in microarray experiments using local FDR. **2004**, 5, 125	67
2205	Rank Difference Analysis of Microarrays (RDAM), a novel approach to statistical analysis of microarray expression profiling data. **2004**, 5, 148	23
2204	A power law global error model for the identification of differentially expressed genes in microarray data. **2004**, 5, 203	82
2203	Cross-species hybridisation of human and bovine orthologous genes on high density cDNA microarrays. **2004**, 5, 83	64
2202	Genes regulated by mating, sperm, or seminal proteins in mated female Drosophila melanogaster. **2004**, 14, 1509-14	248
2201	New developments in cancer-related computational statistics. **2004**, 1020, 22-31	1
2200	New approaches for in silico identification of cytokine-modified beta cell gene networks. **2004**, 1037, 41-58	8
2199	Does haplotype diversity predict power for association mapping of disease susceptibility?. **2004**, 115, 157-64	43
2198	Elucidation of the role of Grr1p in glucose sensing by Saccharomyces cerevisiae through genome-wide transcription analysis. **2004**, 5, 193-204	11
2197	Study of Arabidopsis thaliana resistome in response to cucumber mosaic virus infection using whole genome microarray. **2004**, 55, 501-20	111
2196	Differential expression of immunoregulatory genes in male and female Norway rats following infection with Seoul virus. **2004**, 74, 180-90	41
2195	A case study on choosing normalization methods and test statistics for two-channel microarray data. **2004**, 5, 432-44	13
2194	On estimating the proportion of true null hypotheses for false discovery rate controlling procedures in exploratory DNA microarray studies. **2004**, 47, 611-637	18
2193	Qvalue methods may not always control false discovery rate in genomic applications.	
2192	Comparative analysis of gene sets in the Gene Ontology space under the multiple hypothesis testing framework. **2004**, 425-35	18

2191	Quantitative trait loci for obesity- and diabetes-related traits and their dietary responses to high-fat feeding in LGXSM recombinant inbred mouse strains. **2004**, 53, 3328-36	70
2190	A theoretical analysis of gene selection.	12
2189	A stochastic downhill search algorithm for estimating the local false discovery rate. **2004**, 1, 98-108	26
2188	Genomics, prior probability, and statistical tests of multiple hypotheses. **2004**, 14, 997-1001	61
2187	Genetic architecture of flowering time in maize as inferred from quantitative trait loci meta-analysis and synteny conservation with the rice genome. **2004**, 168, 2169-85	283
2186	Gene expression analysis suggests that 1,25-dihydroxyvitamin D3 reverses experimental autoimmune encephalomyelitis by stimulating inflammatory cell apoptosis. **2004**, 18, 141-51	83
2185	Global transcription profiling reveals multiple sugar signal transduction mechanisms in Arabidopsis. **2004**, 16, 2128-50	432
2184	Statistical model for large-scale peptide identification in databases from tandem mass spectra using SEQUEST. **2004**, 76, 6853-60	95
2183	Processing of data generated by 2-dimensional gel electrophoresis for statistical analysis: missing data, normalization, and statistics. **2004**, 3, 1210-8	49
2182	[Multiple comparison procedures: principles, limits. Applications to microarray phenotype-genotype analysis]. **2004**, 52, 523-37	5
2181	Gene-expression patterns in drug-resistant acute lymphoblastic leukemia cells and response to treatment. **2004**, 351, 533-42	492
2180	New applications of statistical tools in plant pathology. **2004**, 94, 999-1003	63
2179	Exploratory differential gene expression analysis in microarray experiments with no or limited replication. **2004**, 5, R18	38
2178	Gene expression profiles highlight adaptive brain mechanisms in corticotropin releasing factor overexpressing mice. **2004**, 129, 135-50	20
2177	Pbx marks genes for activation by MyoD indicating a role for a homeodomain protein in establishing myogenic potential. **2004**, 14, 465-77	270
2176	A MyoD-generated feed-forward circuit temporally patterns gene expression during skeletal muscle differentiation. **2004**, 18, 2348-53	145
2175	Matching strategies for genetic association studies in structured populations. **2004**, 74, 317-25	88
2174	Efficient computation of significance levels for multiple associations in large studies of correlated data, including genomewide association studies. **2004**, 75, 424-35	133

2173	The future of association studies: gene-based analysis and replication. **2004**, 75, 353-62	510
2172	Hierarchical Bayesian neural network for gene expression temporal patterns. **2004**, 3, Article20	12
2171	History of genetic mapping. **2004**,	1
2170	Expression profiling: toward an application in sepsis diagnostics. **2004**, 22, 29-33	48
2169	CREME: Cis-Regulatory Module Explorer for the human genome. **2004**, 32, W253-6	41
2168	Genome-wide scans for loci under selection in humans. **2005**, 2, 113-25	37
2167	References. **2005**, 361-400	
2166	Histology-based expression profiling yields novel prognostic markers in human glioblastoma. **2005**, 64, 948-55	72
2165	Supervised Methods with Genomic Data: a Review and Cautionary View. **2005**, 193-214	10
2164	The identification of functional motifs in temporal gene expression analysis. **2005**, 1, 117693430500100	0
2163	A perspective on DNA microarray technology in food and nutritional science. **2005**, 8, 516-22	12
2162	A comprehensive analysis of phase I and phase II metabolism gene polymorphisms and risk of colorectal cancer. **2005**, 15, 535-46	115
2161	Using mixture models to detect differentially expressed genes. **2005**, 45, 859	15
2160	Genetic expression profiles during physiological and pathological cardiac hypertrophy and heart failure in rats. **2005**, 21, 34-42	98
2159	Statistical methods for gene expression analysis. **2005**,	
2158	Amplification and overexpression of CKS1B at chromosome band 1q21 is associated with reduced levels of p27Kip1 and an aggressive clinical course in multiple myeloma. **2005**, 10 Suppl 1, 117-26	118
2157	Molecular genetic pathways in Parkinson's disease: a review. **2005**, 109, 355-64	30
2156	Gene expression and thioguanine nucleotide disposition in acute lymphoblastic leukemia after in vivo mercaptopurine treatment. **2005**, 106, 1778-85	46

2155	Nematode-induced changes of transporter gene expression in Arabidopsis roots. **2005**, 18, 1247-57	101
2154	Data analysis methods for detection of differential protein expression in two-dimensional gel electrophoresis. **2005**, 340, 226-30	58
2153	Microarray analysis of postictal transcriptional regulation of neuropeptides. **2005**, 25, 285-98	43
2152	Issues for consideration in the analysis of microarray data in behavioural studies. **2005**, 10, 15-21	3
2151	Statistical analysis of microarray data. **2005**, 10, 23-35	33
2150	Transcriptional profiling using a novel cDNA array identifies differential gene expression during porcine embryo elongation. **2005**, 71, 129-39	16
2149	Judicious Use of Multiple Hypothesis Tests. **2005**, 19, 261-267	107
2148	Estimating the proportion of true null hypotheses, with application to DNA microarray data. **2005**, 67, 555-572	157
2147	Gene expression patterns accompanying a dietary shift in Drosophila melanogaster. **2005**, 14, 3203-8	32
2146	Global transcript profiling of primary stems from Arabidopsis thaliana identifies candidate genes for missing links in lignin biosynthesis and transcriptional regulators of fiber differentiation. **2005**, 42, 618-40	234
2145	Comparative taxonomic structure of the floras of two Mediterranean-climate regions: Iberia and California. **2005**, 11, 399-408	13
2144	Identification of novel growth factor-responsive genes in neuroendocrine gastrointestinal tumour cells. **2005**, 92, 1506-16	18
2143	Prediction of preadipocyte differentiation by gene expression reveals role of insulin receptor substrates and necdin. **2005**, 7, 601-11	179
2142	Widespread and nonrandom distribution of DNA palindromes in cancer cells provides a structural platform for subsequent gene amplification. **2005**, 37, 320-7	87
2141	Complex trait analysis of gene expression uncovers polygenic and pleiotropic networks that modulate nervous system function. **2005**, 37, 233-42	588
2140	Integrative analysis of the cancer transcriptome. **2005**, 37 Suppl, S31-7	385
2139	Efficiency and power in genetic association studies. **2005**, 37, 1217-23	1520
2138	Genome-wide association studies for common diseases and complex traits. **2005**, 6, 95-108	2258

2137	Adjusting multiple testing in multilocus analyses using the eigenvalues of a correlation matrix. **2005**, 95, 221-7	970
2136	New insights into MLL gene rearranged acute leukemias using gene expression profiling: shared pathways, lineage commitment, and partner genes. **2005**, 19, 953-64	73
2135	Controlling false discoveries in candidate gene studies. **2005**, 10, 230-1	26
2134	Evidence for linkage on 21q and 7q in a subset of autism characterized by developmental regression. **2005**, 10, 741-6	69
2133	Meta-analysis of microarray data on pancreatic cancer defines a set of commonly dysregulated genes. **2005**, 24, 5079-88	143
2132	Expression Profiling in Alcoholism Research. **2005**, 29, 1066-1073	6
2131	Complex genetics of interactions of alcohol and CNS function and behavior. **2005**, 29, 1706-19	17
2130	Gene expression profiling of cultured human NF1 heterozygous (NF1+/-) melanocytes reveals downregulation of a transcriptional cis-regulatory network mediating activation of the melanocyte-specific dopachrome tautomerase (DCT) gene. **2005**, 18, 285-99	6
2129	Increased expression of chemokines in the skin of chronic proliferative dermatitis mutant mice. **2005**, 14, 906-13	6
2128	Implementing false discovery rate control: increasing your power. **2005**, 108, 643-647	724
2127	Gene transcripts as potential diagnostic markers for allergic contact dermatitis. **2005**, 53, 100-6	23
2126	Identification of genes associated with chemotherapy crossresistance and treatment response in childhood acute lymphoblastic leukemia. **2005**, 7, 375-86	139
2125	Expression profiling using a tumor-specific cDNA microarray predicts the prognosis of intermediate risk neuroblastomas. **2005**, 7, 337-50	131
2124	Radial glia cells are candidate stem cells of ependymoma. **2005**, 8, 323-35	670
2123	Gene expression microarray studies in polygenic psychiatric disorders: applications and data analysis. **2005**, 50, 142-55	48
2122	Children and adults with acute lymphoblastic leukaemia have similar gene expression profiles. **2005** , 74, 466-80	20
2121	Oligonucleotide-microarray analysis of peripheral-blood lymphocytes in severe asthma. **2005**, 145, 263-74	35
2120	Pathways to the analysis of microarray data. **2005**, 23, 429-35	229

2119	Conventional P-values fail to assure reproducibility for genetic association tests. **2005**, 21, 268-9; author reply 269-71	7
2118	Response to Manly: Statistical stringency in tests of genetic association implications for sample size and study design. **2005**, 21, 269-271	2
2117	Genetical genomics in humans and model organisms. **2005**, 21, 377-81	115
2116	The quantitative genetics of transcription. **2005**, 21, 616-23	225
2115	Non-linear mapping for exploratory data analysis in functional genomics. **2005**, 6, 13	5
2114	High-Throughput GoMiner, an 'industrial-strength' integrative gene ontology tool for interpretation of multiple-microarray experiments, with application to studies of Common Variable Immune Deficiency (CVID). **2005**, 6, 168	237
2113	Dissecting systems-wide data using mixture models: application to identify affected cellular processes. **2005**, 6, 177	2
2112	Nonparametric tests for differential gene expression and interaction effects in multi-factorial microarray experiments. **2005**, 6, 186	10
2111	A comparative review of estimates of the proportion unchanged genes and the false discovery rate. **2005**, 6, 199	58
2110	Two-part permutation tests for DNA methylation and microarray data. **2005**, 6, 35	9
2109	Dual activation of pathways regulated by steroid receptors and peptide growth factors in primary prostate cancer revealed by Factor Analysis of microarray data. **2005**, 6, 109	16
2108	Reverse transcriptional profiling: non-correspondence of transcript level variation and proximal promoter polymorphism. **2005**, 6, 110	12
2107	A gene expression fingerprint of C. elegans embryonic motor neurons. **2005**, 6, 42	95
2106	Genome-wide localization of mobile elements: experimental, statistical and biological considerations. **2005**, 6, 81	2
2105	Enhanced gene expression in the forebrain of hatchling and juvenile male zebra finches. **2005**, 64, 224-38	27
2104	P2P-R expression is genetically coregulated with components of the translation machinery and with PUM2, a translational repressor that associates with the P2P-R mRNA. **2005**, 204, 99-105	10
2103	Pattern robustness of diagnostic gene expression signatures in leukemia. **2005**, 42, 299-307	33
2102	AML M3 and AML M3 variant each have a distinct gene expression signature but also share patterns different from other genetically defined AML subtypes. **2005**, 43, 113-27	35

2101	Association mapping: methodologies, strategies, and issues. **2005**, 29 Suppl 1, S77-85	4
2100	Characterization of genotype-phenotype relationships and stratification by the CARD15 variant genotype for inflammatory bowel disease susceptibility loci using multiple short tandem repeat genetic markers. **2005**, 25, 156-66	8
2099	Transcriptome analysis of the murine forelimb and hindlimb autopod. **2005**, 234, 74-89	35
2098	Molecular and phenotypic characterization of ring chromosome 22. **2005**, 137, 139-47	74
2097	Prediction of functional tertiary interactions and intermolecular interfaces from primary sequence data. **2005**, 304, 50-63	8
2096	Comparison of the PhoPQ regulon in Escherichia coli and Salmonella typhimurium. **2005**, 60, 462-74	89
2095	Gene expression differences in mice divergently selected for methamphetamine sensitivity. **2005**, 16, 291-305	78
2094	The effects of rearing temperature on developmental stability and learning and memory in the honey bee, Apis mellifera. **2005**, 191, 1121-9	128
2093	Functional profiling of human atrial and ventricular gene expression. **2005**, 450, 201-8	67
2092	DNA microarray analysis of Methanosarcina mazei Gö reveals adaptation to different methanogenic substrates. **2005**, 273, 225-39	69
2091	The role of high-throughput transcriptome analysis in metabolic engineering. **2005**, 10, 385-399	13
2090	Genome-wide expression profiling and identification of gene activities during early flower development in Arabidopsis. **2005**, 58, 401-19	63
2089	Linkage and association analyses of microsatellites and single-nucleotide polymorphisms in nuclear families. **2005**, 6 Suppl 1, S25	3
2088	Whole-genome association analysis to identify markers associated with recombination rates using single-nucleotide polymorphisms and microsatellites. **2005**, 6 Suppl 1, S51	1
2087	Will the real disease gene please stand up?. **2005**, 6 Suppl 1, S66	8
2086	Microsatellite linkage analysis, single-nucleotide polymorphisms, and haplotype associations with ECB21 in the COGA data. **2005**, 6 Suppl 1, S94	3
2085	Evaluation of SLC11A1 as an inflammatory bowel disease candidate gene. **2005**, 6, 10	7
2084	On the genetic involvement of apoptosis-related genes in Crohn's disease as revealed by an extended association screen using 245 markers: no evidence for new predisposing factors. **2005**, 4, 8	2

2083	Doxycycline, the drug used to control the tet-regulatable promoter system, has no effect on global gene expression in Saccharomyces cerevisiae. **2005**, 22, 565-9	45
2082	Significance testing for small microarray experiments. **2005**, 24, 2281-98	51
2081	FDR-controlling testing procedures and sample size determination for microarrays. **2005**, 24, 2267-80	46
2080	. **2005**,	5
2079	A temporal study of gene expression in rat lung following fixed-volume hemorrhage. **2005**, 23, 275-86	3
2078	References. **2005**, 267-296	
2077	Evaluating the Predictability of Exchange Rates Using Long-Horizon Regressions: Mind Your p 's and q 's!. **2005**, 37, 473-494	19
2076	. **2005**,	13
2075	Microarrays. **2005**,	
2074	Non-parametric Statistical Tests for Informative Gene Selection. **2005**, 697-702	0
2073	Microarray analysis reveals novel gene expression changes associated with erectile dysfunction in diabetic rats. **2005**, 23, 192-205	41
2072	Classification of AML by DNA-oligonucleotide microarrays. **2006**, 125, 213-40	2
2071	A guide to issues in microarray analysis: application to endometrial biology. **2005**, 130, 1-13	34
2070	Reprogramming of the human atrial transcriptome in permanent atrial fibrillation: expression of a ventricular-like genomic signature. **2005**, 96, 1022-9	152
2069	SNPdetector: a software tool for sensitive and accurate SNP detection. **2005**, 1, e53	95
2068	Experimental design for three-color and four-color gene expression microarrays. **2005**, 21 Suppl 1, i459-67	24
2067	Empirical Bayes screening of many p-values with applications to microarray studies. **2005**, 21, 1987-94	41
2066	Lower bounds for the number of false null hypotheses for multiple testing of associations under general dependence structures. **2005**, 92, 893-907	26

2065	Multiple locus linkage analysis of genomewide expression in yeast. **2005**, 3, e267	144
2064	Effect of pooling samples on the efficiency of comparative studies using microarrays. **2005**, 21, 4378-83	61
2063	Significance analysis of functional categories in gene expression studies: a structured permutation approach. **2005**, 21, 1943-9	266
2062	The 'miss rate' for the analysis of gene expression data. **2005**, 6, 111-7	54
2061	Local regulatory variation in Saccharomyces cerevisiae. **2005**, 1, e25	123
2060	Genome-wide associations of gene expression variation in humans. **2005**, 1, e78	431
2059	Biological complexity and drug discovery: a practical systems biology approach. **2005**, 152, 201-6	19
2058	Sperm competitive ability in Drosophila melanogaster associated with variation in male reproductive proteins. **2005**, 169, 243-57	141
2057	Data-adaptive test statistics for microarray data. **2005**, 21 Suppl 2, ii108-14	19
2056	Genetical genomics analysis of a yeast segregant population for transcription network inference. **2005**, 170, 533-42	76
2055	A note on using permutation-based false discovery rate estimates to compare different analysis methods for microarray data. **2005**, 21, 4280-8	96
2054	DNA microarray analysis of nitrogen fixation and Fe(III) reduction in Geobacter sulfurreducens. **2005**, 71, 2530-8	76
2053	Publication policy or publication bias?. **2005**, 14, 1363	11
2052	A network of transcriptionally coordinated functional modules in Saccharomyces cerevisiae. **2005**, 15, 1298-306	27
2051	A Bayesian method for analysing spotted microarray data. **2005**, 6, 318-30	17
2050	Phytochrome control of the Arabidopsis transcriptome anticipates seedling exposure to light. **2005** , 17, 2507-16	36
2049	Explorative multifactor approach for investigating global survival mechanisms of Campylobacter jejuni under environmental conditions. **2005**, 71, 2086-94	75
2048	Statistical and computational methods for comparative proteomic profiling using liquid chromatography-tandem mass spectrometry. **2005**, 4, 419-34	232

2047	Proteomic profiling of recombinant Escherichia coli in high-cell-density fermentations for improved production of an antibody fragment biopharmaceutical. **2005**, 71, 1717-28		53
2046	Haplotype-based linkage disequilibrium mapping via direct data mining. **2005**, 21, 4384-93		46
2045	Characterization of the genome composition of Bartonella koehlerae by microarray comparative genomic hybridization profiling. **2005**, 187, 6155-65		29
2044	A Heuristic method for assigning a false-discovery rate for protein identifications from Mascot database search results. **2005**, 4, 762-72		162
2043	Incorporating biological information as a prior in an empirical bayes approach to analyzing microarray data. **2005**, 4, Article12		14
2042	Global gene expression as a function of germline genetic variation. **2005**, 14, 1621-9		14
2041	The NAC transcription factors NST1 and NST2 of Arabidopsis regulate secondary wall thickenings and are required for anther dehiscence. **2005**, 17, 2993-3006		514
2040	Guidelines for association studies in Human Molecular Genetics. **2005**, 14, 2481-3		61
2039	An efficient Monte Carlo approach to assessing statistical significance in genomic studies. **2005**, 21, 781-7		141
2038	Methodological aspects of the genetic dissection of gene expression. **2005**, 21, 2383-93		50
2037	Discovering functional transcription-factor combinations in the human cell cycle. **2005**, 15, 848-55		60
2036	A simple procedure for estimating the false discovery rate. **2005**, 21, 660-8		80
2035	Experimental comparison and cross-validation of the Affymetrix and Illumina gene expression analysis platforms. **2005**, 33, 5914-23		195
2034	Cell cycle progression in the pericycle is not sufficient for SOLITARY ROOT/IAA14-mediated lateral root initiation in Arabidopsis thaliana. **2005**, 17, 3035-50		253
2033	TileMap: create chromosomal map of tiling array hybridizations. **2005**, 21, 3629-36		201
2032	Intelligent Data Engineering and Automated Learning - IDEAL 2005. **2005**,		1
2031	Computational Genome Analysis. **2005**,		2
2030	Significance analysis of time course microarray experiments. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 12837-42	11.5	469

2029	An empirical Bayes approach to inferring large-scale gene association networks. **2005**, 21, 754-64		567
2028	Identification of differentially expressed genes in individual bovine preimplantation embryos produced by nuclear transfer: improper reprogramming of genes required for development. **2005**, 72, 546-55		77
2027	Bioinformatics approaches in clinical proteomics. **2005**, 2, 847-62		18
2026	Genome-wide expression analysis indicates that FNR of Escherichia coli K-12 regulates a large number of genes of unknown function. **2005**, 187, 1135-60		215
2025	Discovering statistically significant pathways in expression profiling studies. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 13544-9	11.5	503
2024	Genetics and genomics of Drosophila mating behavior. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102 Suppl 1, 6622-9	11.5	109
2023	Divergent mechanisms of cis9, trans11-and trans10, cis12-conjugated linoleic acid affecting insulin resistance and inflammation in apolipoprotein E knockout mice: a proteomics approach. **2005**, 19, 1746-8		69
2022	Response of apolipoprotein E*3-Leiden transgenic mice to dietary fatty acids: combining liver proteomics with physiological data. **2005**, 19, 813-5		52
2021	Rapid evolution of expression and regulatory divergences after yeast gene duplication. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 707-12	11.5	152
2020	Identification of MMP-15 as an anti-apoptotic factor in cancer cells. **2005**, 280, 34123-32		56
2019	Signatures of reproductive isolation in patterns of single nucleotide diversity across inbred strains of mice. **2005**, 171, 1905-16		32
2018	Transcription in response to physical stress--clues to the molecular mechanisms of exercise-induced asthma. **2005**, 19, 1492-4		33
2017	Altered expression of mitochondria-related genes in postmortem brains of patients with bipolar disorder or schizophrenia, as revealed by large-scale DNA microarray analysis. **2005**, 14, 241-53		377
2016	Cytosolic ascorbate peroxidase 1 is a central component of the reactive oxygen gene network of Arabidopsis. **2005**, 17, 268-81		724
2015	High-resolution genomic profiles of human lung cancer. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 9625-30	11.5	326
2014	Evidence by molecular profiling for a placental origin of infantile hemangioma. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 19097-102	11.5	149
2013	Microarray analysis of differentially expressed genes of primary tumors in the canine central nervous system. **2005**, 42, 550-8		36
2012	MyoD targets chromatin remodeling complexes to the myogenin locus prior to forming a stable DNA-bound complex. **2005**, 25, 3997-4009		222

2011	Using weighted permutation scores to detect differential gene expression with microarray data. **2005**, 3, 989-1006		9
2010	Genetic analysis of variation in gene expression in Arabidopsis thaliana. **2005**, 171, 1267-75		106
2009	Empirical bayes estimation of a sparse vector of gene expression changes. **2005**, 4, Article22		14
2008	The landscape of genetic complexity across 5,700 gene expression traits in yeast. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 1572-7	11.5	469
2007	Genome-wide analysis reveals inositol, not choline, as the major effector of Ino2p-Ino4p and unfolded protein response target gene expression in yeast. **2005**, 280, 9106-18		97
2006	The effect of polymorphisms in the enhancer of split gene complex on bristle number variation in a large wild-caught cohort of Drosophila melanogaster. **2005**, 171, 1741-56		35
2005	Sample size determination for the false discovery rate. **2005**, 21, 4263-71		50
2004	On the utility of pooling biological samples in microarray experiments. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 4252-7	11.5	398
2003	Effects of threshold choice on biological conclusions reached during analysis of gene expression by DNA microarrays. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 8961-5	11.5	83
2002	Statistical methods for identifying yeast cell cycle transcription factors. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 13532-7	11.5	78
2001	Functional genomics and gene expression profiling in sepsis: beyond class prediction. **2005**, 41 Suppl 7, S427-35		29
2000	Benchmarking the CATMA microarray. A novel tool for Arabidopsis transcriptome analysis. **2005**, 137, 588-601		84
1999	Conservation and divergence of light-regulated genome expression patterns during seedling development in rice and Arabidopsis. **2005**, 17, 3239-56		172
1998	A large-scale screen for artificial selection in maize identifies candidate agronomic loci for domestication and crop improvement. **2005**, 17, 2859-72		202
1997	PathwayExplorer: web service for visualizing high-throughput expression data on biological pathways. **2005**, 33, W633-7		105
1996	ArrayXPath II: mapping and visualizing microarray gene-expression data with biomedical ontologies and integrated biological pathway resources using Scalable Vector Graphics. **2005**, 33, W621-6		48
1995	Arginase activity differs with allergen in the effector phase of ovalbumin- versus trimellitic anhydride-induced asthma. **2005**, 88, 420-33		29
1994	Kinesin family member 12 is a candidate polycystic kidney disease modifier in the cpk mouse. **2005**, 16, 905-16		50

1993	Generalized rank tests for replicated microarray data. **2005**, 4, Article3	6
1992	Extraction of transcription regulatory signals from genome-wide DNA-protein interaction data. **2005**, 33, 605-15	31
1991	RACE: Remote Analysis Computation for gene Expression data. **2005**, 33, W638-43	52
1990	Increased power of microarray analysis by use of an algorithm based on a multivariate procedure. **2005**, 21, 3530-4	3
1989	Genetic association studies. **2005**, 366, 1121-31	394
1988	What makes a good genetic association study?. **2005**, 366, 1315-23	408
1987	Optimising two-dye microarray designs for estimating associations with a quantitative trait. **2005**, 118, 1-8	
1986	Recent developments in genomewide association scans: a workshop summary and review. **2005**, 77, 337-45	180
1985	High-resolution whole-genome association study of Parkinson disease. **2005**, 77, 685-93	433
1984	Molecular classification and molecular forecasting of breast cancer: ready for clinical application?. **2005**, 23, 7350-60	696
1983	Transcriptional profile of the Arabidopsis root quiescent center. **2005**, 17, 1908-25	257
1982	Parallel adaptive evolution cultures of Escherichia coli lead to convergent growth phenotypes with different gene expression states. **2005**, 15, 1365-72	202
1981	Statistical development and evaluation of microarray gene expression data filters. **2005**, 12, 482-95	27
1980	Gene expression studies provide clues to the pathogenesis of uterine leiomyoma: new evidence and a systematic review. **2005**, 20, 852-63	156
1979	False discovery rate, sensitivity and sample size for microarray studies. **2005**, 21, 3017-24	340
1978	Comment. **2005**, 100, 796-798	
1977	Comparison of statistical approaches for the analysis of proteome expression data of differentiating neural stem cells. **2005**, 4, 96-100	47
1976	Polymorphisms in the TSHR (thyrotropin receptor) gene on chromosome 14q31 are not associated with mental retardation in the iodine-deficient areas of China. **2005**, 382, 179-84	2

1975	Group A Streptococcus transcriptome dynamics during growth in human blood reveals bacterial adaptive and survival strategies. **2005**, 166, 455-65	123
1974	The genetic dissection of immune response using gene-expression studies and genome mapping. **2005**, 105, 343-52	30
1973	Finite mixture model analysis of microarray expression data on samples of uncertain biological type with application to reproductive efficiency. **2005**, 105, 187-96	3
1972	Mouse ovary developmental RNA and protein markers from gene expression profiling. **2005**, 279, 271-90	49
1971	Sex- and segment-specific modulation of gene expression profiles in Drosophila. **2005**, 288, 528-44	29
1970	Validation of a first-generation long-oligonucleotide microarray for transcriptional profiling in the pig. **2005**, 86, 618-25	57
1969	Computational searches for splicing signals. **2005**, 37, 292-305	37
1968	Gene discovery in neuropharmacological and behavioral studies using Affymetrix microarray data. **2005**, 37, 219-28	21
1967	Transcriptome responses to carbon tetrachloride and pyrene in the kidney and liver of juvenile rainbow trout (Oncorhynchus mykiss). **2005**, 74, 70-81	68
1966	Modifying Microarray Analysis Methods for Categorical Data SAM and PAM for SNPs. **2005**, 370-377	1
1965	Analysis of Gene Expression Data. **2005**, 289-336	
1964	Myeloid Leukemia. **2005**,	
1963	Linkage disequilibrium: ancient history drives the new genetics. **2005**, 59, 118-24	41
1962	Genome-wide gene expression in response to parasitoid attack in Drosophila. **2005**, 6, R94	126
1961	Chipper: discovering transcription-factor targets from chromatin immunoprecipitation microarrays using variance stabilization. **2005**, 6, R96	37
1960	Identification of novel regulatory modules in dicotyledonous plants using expression data and comparative genomics. **2006**, 7, R103	50
1959	Transcriptional response to alcohol exposure in Drosophila melanogaster. **2006**, 7, R95	81
1958	Sex-specific expression of alternative transcripts in Drosophila. **2006**, 7, R79	79

1957	The gain and loss of genes during 600 million years of vertebrate evolution. **2006**, 7, R43	270
1956	Genes regulated by estrogen in breast tumor cells in vitro are similarly regulated in vivo in tumor xenografts and human breast tumors. **2006**, 7, R28	98
1955	A reanalysis of a published Affymetrix GeneChip control dataset. **2006**, 7, 401	45
1954	The contributions of normal variation and genetic background to mammalian gene expression. **2006**, 7, R26	32
1953	Ontology annotation treebrowser : an interactive tool where the complementarity of medical subject headings and gene ontology improves the interpretation of gene lists. **2006**, 5, 225-36	11
1952	A bootstrap test for the analysis of microarray experiments with a very small number of replications. **2006**, 5, 173-9	13
1951	Mass Spectrometry Data Analysis in Proteomics. **2006**,	2
1950	Biomarkers in Breast Cancer. **2006**,	3
1949	A powerful approach for effective finding of significantly differentially expressed genes. **2006**, 3, 220-31	1
1948	Significance of gene ranking for classification of microarray samples. **2006**, 3, 312-20	37
1947	Advances in Health care Technology Care Shaping the Future of Medical. **2006**,	7
1946	Some comments on instability of false discovery rate estimation. **2006**, 4, 1057-68	28
1945	Complex Systems Science in Biomedicine. **2006**,	18
1944	A Simple Diagnostic Plot Connecting Robust Estimation, Outlier Detection, and False Discovery Rates. **2006**, 33, 1131-1147	7
1943	Comparison of spectral counting and metabolic stable isotope labeling for use with quantitative microbial proteomics. **2006**, 131, 1335-41	80
1942	Genetic variation in Drosophila melanogaster resistance to infection: a comparison across bacteria. **2006**, 174, 1539-54	93
1941	Platelet-derived microvesicles induce differential gene expression in monocytic cells: a DNA microarray study. **2006**, 17, 571-6	32
1940	Some statistical issues in microarray gene expression data. **2006**, 165, 745-8	7

1939	Using linkage genome scans to improve power of association in genome scans. **2006**, 78, 243-52	173
1938	Spectrum of CHD7 mutations in 110 individuals with CHARGE syndrome and genotype-phenotype correlation. **2006**, 78, 303-14	306
1937	Paraoxonase cluster polymorphisms are associated with sporadic ALS. **2006**, 67, 771-6	103
1936	An insight-based longitudinal study of visual analytics. **2006**, 12, 1511-22	78
1935	A genome-wide screen reveals functional gene clusters in the cancer genome and identifies EphA2 as a mitogen in glioblastoma. **2006**, 66, 10815-23	96
1934	Number of risk genotypes is a risk factor for major depressive disorder: a case control study. **2006**, 2, 24	28
1933	Nonlinear data alignment for UPLC-MS and HPLC-MS based metabolomics: quantitative analysis of endogenous and exogenous metabolites in human serum. **2006**, 78, 3289-95	252
1932	Analysis of the transcriptome of group A Streptococcus in mouse soft tissue infection. **2006**, 169, 927-42	82
1931	Treating expression levels of different genes as a sample in microarray data analysis: is it worth a risk?. **2006**, 5, Article9	13
1930	Assessment Methods. **2006**, 65-88	2
1929	Gene expression programs during shoot, root, and callus development in Arabidopsis tissue culture. **2006**, 141, 620-37	194
1928	A new type of stochastic dependence revealed in gene expression data. **2006**, 5, Article7	29
1927	Mapping density response in maize: a direct approach for testing genotype and treatment interactions. **2006**, 173, 331-48	18
1926	Thermoregulatory and metabolic defects in Huntington's disease transgenic mice implicate PGC-1alpha in Huntington's disease neurodegeneration. **2006**, 4, 349-62	466
1925	Computational prediction of RpoS and RpoD regulatory sites in Geobacter sulfurreducens using sequence and gene expression information. **2006**, 384, 73-95	21
1924	Engineering yeast transcription machinery for improved ethanol tolerance and production. **2006**, 314, 1565-8	638
1923	Relationships between p63 binding, DNA sequence, transcription activity, and biological function in human cells. **2006**, 24, 593-602	227
1922	Gene expression profiling of the effects of intravenous immunoglobulin in human whole blood. **2006**, 43, 939-49	10

1921	Ranking analysis of microarray data: a powerful method for identifying differentially expressed genes. **2006**, 88, 846-854	20
1920	Application of microarray technology in primate behavioral neuroscience research. **2006**, 38, 227-34	14
1919	Protein identification and expression analysis using mass spectrometry. **2006**, 14, 229-35	31
1918	Molecular profiling of murine sensory neurons in the nodose and dorsal root ganglia labeled from the peritoneal cavity. **2006**, 24, 252-63	38
1917	Central genetic alterations common to all HCV-positive, HBV-positive and non-B, non-C hepatocellular carcinoma: A new approach to identify novel tumor markers. **2006**, 28, 383	
1916	Data Perturbation Independent Diagnosis and Validation of Breast Cancer Subtypes Using Clustering and Patterns. **2006**, 2, 117693510600200	10
1915	Magellan: A Web Based System for the Integrated Analysis of Heterogeneous Biological Data and Annotations; Application to DNA Copy Number and Expression Data in Ovarian Cancer. **2006**, 2, 117693510600200	1
1914	Challenges in the Analysis of Mass-Throughput Data: A Technical Commentary from the Statistical Machine Learning Perspective. **2006**, 2, 117693510600200	16
1913	Bibliography. **2006**, 451-529	
1912	Stage-specific suppression of basal defense discriminates barley plants containing fast- and delayed-acting Mla powdery mildew resistance alleles. **2006**, 19, 939-47	71
1911	Multiple testing in large-scale contingency tables: inferring patterns of pair-wise amino acid association in beta-sheets. **2006**, 2, 193-217	10
1910	Gene Expression Profiling with DNA Microarrays. **2006**, 47-61	
1909	Co-expressed gene groups analysis (CGGA): An automatic tool for the interpretation of microarray experiments. **2006**, 3, 188-198	2
1908	Detecting multiple associations in genome-wide studies. **2006**, 2, 310-7	37
1907	From DNA to RNA to disease and back: the 'central dogma' of regulatory disease variation. **2006**, 2, 383-90	18
1906	Evaluation Models for the Effect of Sample Imbalance on Gene Selection. **2006**,	
1905	Identification of changes in gene expression in dorsal root ganglia in diabetic neuropathy: correlation with functional deficits. **2006**, 65, 722-32	30
1904	Chloroplast-mediated regulation of nuclear genes in Arabidopsis thaliana in the absence of light stress. **2006**, 25, 142-52	137

1903	NOS3 polymorphisms, cigarette smoking, and cardiovascular disease risk: the Atherosclerosis Risk in Communities study. **2006**, 16, 891-9	22
1902	Epidermal growth factor receptor-induced circadian-time-dependent gene regulation in suprachiasmatic nucleus. **2006**, 17, 1437-41	8
1901	Phenotype-genotype association grid: a convenient method for summarizing multiple association analyses. **2006**, 7, 30	3
1900	On the Wegener granulomatosis associated region on chromosome 6p21.3. **2006**, 7, 21	28
1899	A robust meta-classification strategy for cancer detection from MS data. **2006**, 6, 592-604	46
1898	Incorporating gene functional annotations in detecting differential gene expression. **2006**, 55, 301-316	5
1897	Controlling the False Discovery Rate: A New Application to Account for Multiple and Dependent Tests in Local Statistics of Spatial Association. **2006**, 38, 180-208	184
1896	Identifying susceptibility genes for immunological disorders: patterns, power, and proof. **2006**, 210, 40-51	15
1895	Mapping of quantitative trait loci for lactation persistency traits in German Holstein dairy cattle. **2006**, 123, 89-96	35
1894	Significance and impotence: towards a balanced view of the null and the alternative hypotheses in marker selection for plant breeding. **2006**, 169, 61-79	9
1893	Microarray and genetic analysis of electron transfer to electrodes in Geobacter sulfurreducens. **2006**, 8, 1805-15	271
1892	Genetic diversity contribution to errors in short oligonucleotide microarray analysis. **2006**, 4, 489-98	25
1891	Refined association mapping for a quantitative trait: weight in the H19-IGF2-INS-TH region. **2006**, 70, 848-56	17
1890	Molecular analysis of poplar defense against herbivory: comparison of wound- and insect elicitor-induced gene expression. **2006**, 172, 617-35	149
1889	Predicting the clinical behavior of ovarian cancer from gene expression profiles. **2006**, 16 Suppl 1, 147-51	21
1888	Large DNA palindromes as a common form of structural chromosome aberrations in human cancers. **2006**, 19, 17-23	23
1887	Statistical methods for expression quantitative trait loci (eQTL) mapping. **2006**, 62, 19-27	102
1886	Identifying genes associated with a quantitative trait or quantitative trait locus via selective transcriptional profiling. **2006**, 62, 504-14	10

1885	Shrunken p-values for assessing differential expression with applications to genomic data analysis. **2006**, 62, 1099-106	3
1884	Computational biology: toward deciphering gene regulatory information in mammalian genomes. **2006**, 62, 645-63	28
1883	WS11Comprehensive investigation of the transcriptome. **2006**, 29, 36-37	
1882	WS12Measuring biological effects in the target species using proteomics: detection of the illegal treatment of cattle with performance enhancing agents. **2006**, 29, 37-39	21
1881	Natural genetic variation in whole-genome expression in Arabidopsis thaliana: the impact of physiological QTL introgression. **2006**, 15, 1351-65	33
1880	Genomics of hybrid poplar (Populus trichocarpax deltoides) interacting with forest tent caterpillars (Malacosoma disstria): normalized and full-length cDNA libraries, expressed sequence tags, and a cDNA microarray for the study of insect-induced defences in poplar. **2006**, 15, 1275-97	159
1879	A genomic scan for divergent selection in a secondary contact zone between Atlantic and Gulf of Mexico oysters, Crassostrea virginica. **2006**, 15, 4229-42	86
1878	Functional genomics of cactus host shifts in Drosophila mojavensis. **2006**, 15, 4635-43	99
1877	Membrane-associated transcripts in Arabidopsis; their isolation and characterization by DNA microarray analysis and bioinformatics. **2006**, 46, 708-21	32
1876	Transcriptional regulators of stamen development in Arabidopsis identified by transcriptional profiling. **2006**, 46, 984-1008	250
1875	Genome-wide analysis of phenobarbital-inducible genes in Drosophila melanogaster. **2006**, 15, 455-64	48
1874	Creation and implications of a phenome-genome network. **2006**, 24, 55-62	176
1873	The genetics of plant metabolism. **2006**, 38, 842-9	401
1872	Pleiotropic fitness effects of the Tre1-Gr5a region in Drosophila melanogaster. **2006**, 38, 824-9	26
1871	Multiplexed protein measurement: technologies and applications of protein and antibody arrays. **2006**, 5, 310-20	571
1870	A tutorial on statistical methods for population association studies. **2006**, 7, 781-91	963
1869	Genetics of global gene expression. **2006**, 7, 862-72	471
1868	The effective size of the Icelandic population and the prospects for LD mapping: inference from unphased microsatellite markers. **2006**, 14, 1044-53	8

1867	Gene expression signatures associated with the resistance to imatinib. **2006**, 20, 1542-50	25
1866	Association between glutamic acid decarboxylase genes and anxiety disorders, major depression, and neuroticism. **2006**, 11, 752-62	138
1865	Conifer defence against insects: microarray gene expression profiling of Sitka spruce (Picea sitchensis) induced by mechanical wounding or feeding by spruce budworms (Choristoneura occidentalis) or white pine weevils (Pissodes strobi) reveals large-scale changes of the host transcriptome. **2006**, 29, 1545-70	197
1864	Genetic dissection of transcriptional regulation by cDNA-AFLP. **2006**, 45, 439-46	42
1863	Identifying differentially expressed genes in unreplicated multiple-treatment microarray timecourse experiments. **2006**, 50, 518-532	3
1862	A permutation test motivated by microarray data analysis. **2006**, 50, 3619-3628	21
1861	Optimal two-stage genome-wide association designs based on false discovery rate. **2006**, 51, 457-465	7
1860	On the statistical analysis of the GS-NS0 cell proteome: imputation, clustering and variability testing. **2006**, 1764, 1179-87	9
1859	Cross model validated feature selection based on gene clusters. **2006**, 84, 172-176	8
1858	A statistical method for estimating the proportion of differentially expressed genes. **2006**, 30, 193-202	6
1857	Molecular genetics of addiction vulnerability. **2006**, 3, 295-301	44
1856	Normalization and quantification of differential expression in gene expression microarrays. **2006**, 7, 166-77	62
1855	Estimating the number of true null hypotheses from a histogram of p values. **2006**, 11, 337-356	81
1854	Imaging phenotypes and genotypes in schizophrenia. **2006**, 4, 21-49	26
1853	Protein identification by tandem mass spectrometry and sequence database searching. **2007**, 367, 87-119	129
1852	Linkage Disequilibrium Mapping of Morphological, Resistance, and Other Agronomically Relevant Traits in Modern Spring Barley Cultivars. **2006**, 17, 41-58	120
1851	Optimum two-stage designs in case-control association studies using false discovery rate. **2006**, 51, 1046-1054	5
1850	Fifty years of genetic epidemiology, with special reference to Japan. **2006**, 51, 269-277	4

1849	A two-stage design for multiple testing in large-scale association studies. **2006**, 51, 523-532	8
1848	Association study on chromosome 20q11.21-13.13 locus and its contribution to type 2 diabetes susceptibility in Japanese. **2006**, 120, 527-42	18
1847	Gene expression profiling in Salmonella Choleraesuis-infected porcine lung using a long oligonucleotide microarray. **2006**, 17, 777-89	37
1846	Integrated gene expression profiling and linkage analysis in the rat. **2006**, 17, 480-9	17
1845	How replicable are mRNA expression QTL?. **2006**, 17, 643-56	52
1844	A review of statistical methods for expression quantitative trait loci mapping. **2006**, 17, 509-17	83
1843	Genetic variation in human gene expression. **2006**, 17, 503-8	39
1842	Connected populations for detecting quantitative trait loci and testing for epistasis: an application in maize. **2006**, 113, 206-24	204
1841	Assessing the importance of genotype x environment interaction for root traits in rice using a mapping population II: conventional QTL analysis. **2006**, 113, 953-64	97
1840	Global effects of vitamin A deficiency on gene expression in rat liver: evidence for hypoandrogenism. **2006**, 17, 345-55	27
1839	Effects of human TRIM5alpha polymorphisms on antiretroviral function and susceptibility to human immunodeficiency virus infection. **2006**, 354, 15-27	105
1838	Unique microRNA molecular profiles in lung cancer diagnosis and prognosis. **2006**, 9, 189-98	2606
1837	Biological microarray interpretation: the rules of engagement. **2006**, 1759, 319-27	35
1836	Murine central and peripheral nervous system transcriptomes: comparative gene expression. **2006**, 1107, 24-41	16
1835	Thioredoxin interacting protein is increased in sensory neurons in experimental diabetes. **2006**, 1116, 206-14	44
1834	Genome-wide association: a promising start to a long race. **2006**, 22, 350-4	25
1833	Characterization of compound mechanisms and secondary activities by BioMAP analysis. **2006**, 53, 67-74	48
1832	An improved procedure for gene selection from microarray experiments using false discovery rate criterion. **2006**, 7, 15	12

1831	OpWise: operons aid the identification of differentially expressed genes in bacterial microarray experiments. **2006**, 7, 19	17
1830	Profiling alternatively spliced mRNA isoforms for prostate cancer classification. **2006**, 7, 202	78
1829	XcisClique: analysis of regulatory bicliques. **2006**, 7, 218	7
1828	WholePathwayScope: a comprehensive pathway-based analysis tool for high-throughput data. **2006**, 7, 30	177
1827	Genome-wide prediction of transcriptional regulatory elements of human promoters using gene expression and promoter analysis data. **2006**, 7, 330	22
1826	Robust computational reconstitution - a new method for the comparative analysis of gene expression in tissues and isolated cell fractions. **2006**, 7, 369	12
1825	Genome comparison using Gene Ontology (GO) with statistical testing. **2006**, 7, 374	12
1824	miTarget: microRNA target gene prediction using a support vector machine. **2006**, 7, 411	160
1823	Semi-supervised discovery of differential genes. **2006**, 7, 414	2
1822	REEF: searching REgionally Enriched Features in genomes. **2006**, 7, 453	30
1821	Effects of filtering by Present call on analysis of microarray experiments. **2006**, 7, 49	192
1820	Assessing stability of gene selection in microarray data analysis. **2006**, 7, 50	62
1819	Integrated siRNA design based on surveying of features associated with high RNAi effectiveness. **2006**, 7, 516	40
1818	Intensity-based hierarchical Bayes method improves testing for differentially expressed genes in microarray experiments. **2006**, 7, 538	195
1817	Comparative analysis of haplotype association mapping algorithms. **2006**, 7, 61	48
1816	Gene expression profiling in the striatum of inbred mouse strains with distinct opioid-related phenotypes. **2006**, 7, 146	43
1815	Analyzing the dose-dependence of the Saccharomyces cerevisiae global transcriptional response to methyl methanesulfonate and ionizing radiation. **2006**, 7, 305	31
1814	Deep and comparative analysis of the mycelium and appressorium transcriptomes of Magnaporthe grisea using MPSS, RL-SAGE, and oligoarray methods. **2006**, 7, 310	54

1813	Detection of transcriptional difference of porcine imprinted genes using different microarray platforms. **2006**, 7, 328	28
1812	Tests for differential gene expression using weights in oligonucleotide microarray experiments. **2006**, 7, 33	9
1811	Developmental disturbances in early life stage mortality (M74) of Baltic salmon fry as studied by changes in gene expression. **2006**, 7, 56	17
1810	Operon information improves gene expression estimation for cDNA microarrays. **2006**, 7, 87	10
1809	Searching for the regulators of human gene expression. **2006**, 28, 968-72	9
1808	Large-scale gene expression profiling reveals major pathogenetic pathways of cartilage degeneration in osteoarthritis. **2006**, 54, 3533-44	292
1807	Impact of trisomy 8 on expression of genes located on chromosome 8 in different AML subgroups. **2006**, 45, 1164-8	35
1806	Stratified false discovery control for large-scale hypothesis testing with application to genome-wide association studies. **2006**, 30, 519-30	116
1805	Molecular evolution of 5' flanking regions of 87 candidate genes for atherosclerotic cardiovascular disease. **2006**, 30, 557-69	9
1804	Pooled association genome scanning for alcohol dependence using 104,268 SNPs: validation and use to identify alcoholism vulnerability loci in unrelated individuals from the collaborative study on the genetics of alcoholism. **2006**, 141B, 844-53	128
1803	Taxonomy and Evolutionary Relationships in the Saxifraga rivularis Complex. **2006**, 31, 702-729	28
1802	A fast, unbiased and exact allelic test for case-control association studies. **2006**, 61, 210-21	24
1801	A multimarker model to predict outcome in tamoxifen-treated breast cancer patients. **2006**, 12, 1175-83	49
1800	Group testing for pathway analysis improves comparability of different microarray datasets. **2006**, 22, 2500-6	119
1799	Maximum likelihood inference of imprinting and allele-specific expression from EST data. **2006**, 22, 3032-9	10
1798	JProGO: a novel tool for the functional interpretation of prokaryotic microarray data using Gene Ontology information. **2006**, 34, W510-5	23
1797	A graph-based motif detection algorithm models complex nucleotide dependencies in transcription factor binding sites. **2006**, 34, 5730-9	17
1796	'Genome design' model and multicellular complexity: golden middle. **2006**, 34, 5906-14	29

1795	Tissue-specific expression and regulation of sexually dimorphic genes in mice. **2006**, 16, 995-1004	628
1794	Gene induction during differentiation of human pulmonary type II cells in vitro. **2006**, 34, 727-37	65
1793	CYP11B2 -344T/C gene polymorphism and blood pressure in patients with acromegaly. **2006**, 91, 5008-12	21
1792	Microarray RNA transcriptional profiling: part II. Analytical considerations and annotation. **2006**, 6, 703-15	11
1791	Genotyping and mapping with high-density oligonucleotide arrays. **2006**, 323, 137-45	23
1790	Scanning microarrays at multiple intensities enhances discovery of differentially expressed genes. **2006**, 22, 1863-70	22
1789	Statistical challenges with gene expression studies. **2006**, 7, 511-9	2
1788	Genetic Dissection of Complex Traits In Silico: Approaches, Problems and Solutions. **2006**, 1, 359-369	2
1787	Reproducibility of microarray studies: concordance of current analysis methods. **2006**, 158, 109-25	1
1786	Automatic quality assessment of Affymetrix GeneChip data. **2006**,	1
1785	Next station in microarray data analysis: GEPAS. **2006**, 34, W486-91	101
1784	A locally adaptive statistical procedure (LAP) to identify differentially expressed chromosomal regions. **2006**, 22, 2658-66	33
1783	An integrated strategy for analyzing the unique developmental programs of different myoblast subtypes. **2006**, 2, e16	74
1782	Relaxed significance criteria for linkage analysis. **2006**, 173, 2371-81	71
1781	Quantitative trait loci for locomotor behavior in Drosophila melanogaster. **2006**, 174, 271-84	58
1780	Approximate Power and Sample Size Calculations with the Benjamini-Hochberg Method. **2006**, 2,	6
1779	A discussion of statistical methods for design and analysis of microarray experiments for plant scientists. **2006**, 18, 2112-21	52
1778	Analysis of gene expression using gene sets discriminates cancer patients with and without late radiation toxicity. **2006**, 3, e422	101

1777	Evidence of influence of genomic DNA sequence on human X chromosome inactivation. **2006**, 2, e113	72
1776	Extracellular phosphate alters cementoblast gene expression. **2006**, 85, 505-9	27
1775	Genomic environment predicts expression patterns on the human inactive X chromosome. **2006**, 2, e151	69
1774	Agouti-related protein promoter variant associated with leanness and decreased risk for diabetes in West Africans. **2006**, 30, 715-21	23
1773	Construction of null statistics in permutation-based multiple testing for multi-factorial microarray experiments. **2006**, 22, 1486-94	15
1772	Quantitative genomics of aggressive behavior in Drosophila melanogaster. **2006**, 2, e154	141
1771	Multidimensional local false discovery rate for microarray studies. **2006**, 22, 556-65	60
1770	A moment-based method for estimating the proportion of true null hypotheses and its application to microarray gene expression data. **2007**, 8, 744-55	14
1769	Dissection of signaling pathways in fourteen breast cancer cell lines using reverse-phase protein lysate microarray. **2006**, 5, 543-51	21
1768	Genomic and metabolic studies of the impact of probiotics on a model gut symbiont and host. **2006** , 4, e413	299
1767	Combined expression trait correlations and expression quantitative trait locus mapping. **2006**, 2, e6	83
1766	Meiotically stable natural epialleles of Sadhu, a novel Arabidopsis retroposon. **2006**, 2, e36	47
1765	A multivariate approach for integrating genome-wide expression data and biological knowledge. **2006**, 22, 2373-80	106
1764	Meta-analysis of differentiating mouse embryonic stem cell gene expression kinetics reveals early change of a small gene set. **2006**, 2, e158	31
1763	An integrative genomic approach to uncover molecular mechanisms of prokaryotic traits. **2006**, 2, e159	26
1762	Estimation of false discovery proportion under general dependence. **2006**, 22, 3025-31	26
1761	Meta-analysis based on control of false discovery rate: combining yeast ChIP-chip datasets. **2006**, 22, 2516-22	18
1760	Patterns of gene expression in the frontal cortex discriminate alcoholic from nonalcoholic individuals. **2006**, 31, 1574-82	201

1759	Expression of late cell cycle genes and an increased proliferative capacity characterize very early relapse of childhood acute lymphoblastic leukemia. **2006**, 12, 4553-61		39
1758	Expression pattern shifts following duplication indicative of subfunctionalization and neofunctionalization in regulatory genes of Arabidopsis. **2006**, 23, 469-78		238
1757	Genome-wide identification of direct targets of the Drosophila retinal determination protein Eyeless. **2006**, 16, 466-76		96
1756	Integrative genetic analysis of transcription modules: towards filling the gap between genetic loci and inherited traits. **2006**, 15, 481-92		34
1755	The potential for the transcriptome to serve as a clinical biomarker for cardiovascular diseases. **2006**, 98, 1459-61		16
1754	Natural variation in male-induced 'cost-of-mating' and allele-specific association with male reproductive genes in Drosophila melanogaster. **2006**, 361, 355-61		27
1753	Modified Hudson-Kreitman-Aguade test and two-dimensional evaluation of neutrality tests. **2006**, 173, 1725-33		28
1752	An initial map of insertion and deletion (INDEL) variation in the human genome. **2006**, 16, 1182-90		455
1751	Wnt-1 is dominant over neu in specifying mammary tumor expression profiles. **2006**, 5, 565-71		11
1750	Toward understanding the genetics of alcohol drinking through transcriptome meta-analysis. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 6368-73	11.5	298
1749	Blood glucose-lowering nuclear receptor agonists only partially normalize hepatic gene expression in db/db mice. **2006**, 316, 797-804		22
1748	Inferring population parameters from single-feature polymorphism data. **2006**, 173, 2257-67		7
1747	Genome-wide analysis of epigenetic silencing identifies BEX1 and BEX2 as candidate tumor suppressor genes in malignant glioma. **2006**, 66, 6665-74		120
1746	Genetic dissection of intermated recombinant inbred lines using a new genetic map of maize. **2006**, 174, 1671-83		67
1745	DNA microarray and proteomic analyses of the RpoS regulon in Geobacter sulfurreducens. **2006**, 188, 2792-800		48
1744	Phosphate acquisition genes in Prochlorococcus ecotypes: evidence for genome-wide adaptation. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 12552-7	11.5	244
1743	Cholestasis and hypercholesterolemia in SCD1-deficient mice fed a low-fat, high-carbohydrate diet. **2006**, 47, 2668-80		48
1742	Nucleotide polymorphism and linkage disequilibrium in wild populations of the partial selfer Caenorhabditis elegans. **2006**, 172, 171-84		115

1741	Role of positive selection in the retention of duplicate genes in mammalian genomes. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 2232-6	11.5	70
1740	Local similarity analysis reveals unique associations among marine bacterioplankton species and environmental factors. **2006**, 22, 2532-8		183
1739	Robust estimation of the false discovery rate. **2006**, 22, 1979-87		126
1738	Validation in genomics: CpG island methylation revisited. **2006**, 5, Article29		1
1737	A two-step multiple comparison procedure for a large number of tests and multiple treatments. **2006**, 5, Article28		7
1736	Genome-wide expression profiling reveals EBV-associated inhibition of MHC class I expression in nasopharyngeal carcinoma. **2006**, 66, 7999-8006		176
1735	EDGE: extraction and analysis of differential gene expression. **2006**, 22, 507-8		250
1734	Natural isolates of Saccharomyces cerevisiae display complex genetic variation in sporulation efficiency. **2006**, 174, 985-97		82
1733	Analysis of co-aggregation of cancer based on registry data. **2006**, 9, 87-92		3
1732	Genetic regulation of gene expression during shoot development in Arabidopsis. **2006**, 172, 1155-64		107
1731	Are we ready for genome-wide association studies?. **2006**, 15, 595-8		43
1730	Integrating data on DNA copy number with gene expression levels and drug sensitivities in the NCI-60 cell line panel. **2006**, 5, 853-67		140
1729	Acute myeloid leukemia-associated Mkl1 (Mrtf-a) is a key regulator of mammary gland function. **2006**, 26, 5809-26		130
1728	An improved statistical method for detecting heterotachy in nucleotide sequences. **2006**, 23, 1397-405		24
1727	Statistical genetics concepts and approaches in schizophrenia and related neuropsychiatric research. **2007**, 33, 95-104		21
1726	Estimation and control of multiple testing error rates for microarray studies. **2006**, 7, 25-36		67
1725	Histone acetylation and transcriptional regulation in the genome of Saccharomyces cerevisiae. **2006**, 22, 392-9		13
1724	Adaptive linear step-up procedures that control the false discovery rate. **2006**, 93, 491-507		1477

1723	Adaptively inferring human transcriptional subnetworks. **2006**, 2, 2006.0029		49
1722	A simple implementation of a normal mixture approach to differential gene expression in multiclass microarrays. **2006**, 22, 1608-15		126
1721	Comparative gene marker selection suite. **2006**, 22, 1924-5		105
1720	Transcriptional profiling of Mycoplasma hyopneumoniae during iron depletion using microarrays. **2006**, 152, 937-944		38
1719	Survival analysis of longitudinal microarrays. **2006**, 22, 2643-9		7
1718	Genetic variation in soluble epoxide hydrolase (EPHX2) and risk of coronary heart disease: The Atherosclerosis Risk in Communities (ARIC) study. **2006**, 15, 1640-9		152
1717	Compstat 2006 - Proceedings in Computational Statistics. **2006**,		1
1716	Functional interpretation of microarray experiments. **2006**, 10, 398-410		68
1715	Involvement of gonadal steroids and gamma interferon in sex differences in response to blood-stage malaria infection. **2006**, 74, 3190-203		71
1714	Selecting "significant" differentially expressed genes from the combined perspective of the null and the alternative. **2006**, 13, 1513-31		11
1713	Clustering biological annotations and gene expression data to identify putatively co-regulated biological processes. **2006**, 4, 833-52		18
1712	Analysis of gene expression in pathophysiological states: balancing false discovery and false negative rates. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 649-53	11.5	44
1711	Multivariate regression analysis of distance matrices for testing associations between gene expression patterns and related variables. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 19430-5	11.5	183
1710	Comparative evaluation of reverse engineering gene regulatory networks with relevance networks, graphical gaussian models and bayesian networks. **2006**, 22, 2523-31		255
1709	A NEW APPROACH TO DECIPHERING PATHWAYS OF ENTEROVIRUS 71-INFECTED CELLS: AN INTEGRATION OF MICROARRAY DATA, GENE ONTOLOGY, AND PATHWAY DATABASE. **2006**, 18, 337-342		
1708	Adaptive evolution in two large families of ubiquitin-ligase adapters in nematodes and plants. **2006** , 16, 1017-30		106
1707	Neutral and adaptive variation in gene expression. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 5425-30	11.5	308
1706	A comprehensive structure-function analysis of Arabidopsis SNI1 defines essential regions and transcriptional repressor activity. **2006**, 18, 1750-65		104

1705	Global analysis of the human gastric epithelial transcriptome altered by Helicobacter pylori eradication in vivo. **2006**, 55, 1717-24		59
1704	Experimental Methods for Measuring Gene Interactions. **2006**, 37, 289-316		21
1703	Hidden Markov Models for Microarray Time Course Data in Multiple Biological Conditions. **2006**, 101, 1323-1332		58
1702	Statistical analysis of DNA microarray data in cancer research. **2006**, 12, 4469-73		37
1701	CACNA1C polymorphisms are associated with the efficacy of calcium channel blockers in the treatment of hypertension. **2006**, 7, 271-9		35
1700	Transcriptional profiling of Mycoplasma hyopneumoniae during heat shock using microarrays. **2006** , 74, 160-6		52
1699	Identification of novel Th2-associated genes in T memory responses to allergens. **2006**, 176, 4766-77		39
1698	Tumor necrosis factor-alpha-induced protein 3 as a putative regulator of nuclear factor-kappaB-mediated resistance to O6-alkylating agents in human glioblastomas. **2006**, 24, 274-87		117
1697	Identification of candidate alkylator-induced cancer susceptibility genes by whole genome scanning in mice. **2006**, 66, 5029-38		41
1696	Gene expression in human thyrocytes and autonomous adenomas reveals suppression of negative feedbacks in tumorigenesis. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 413-8	11.5	51
1695	Analysis of variance of microarray data. **2006**, 411, 214-33		26
1694	Detecting periodic patterns in unevenly spaced gene expression time series using Lomb-Scargle periodograms. **2006**, 22, 310-6		161
1693	Mixture models for detecting differentially expressed genes in microarrays. **2006**, 16, 353-62		4
1692	Functional genomics of wine yeast Saccharomyces cerevisiae. **2007**, 53, 65-121		25
1691	9 Transcript Analysis: A Microarray Approach. **2007**, 189-703		2
1690	MicroRNA expression signatures accurately discriminate acute lymphoblastic leukemia from acute myeloid leukemia. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 19971-6	11.5	378
1689	Silencing of poly(ADP-ribose) polymerase in plants alters abiotic stress signal transduction. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 15150-5	11.5	134
1688	Cholinergic nicotinic receptor genes implicated in a nicotine dependence association study targeting 348 candidate genes with 3713 SNPs. **2007**, 16, 36-49		710

1687	A mouse model of conditional lipodystrophy. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 16627-32	11.5	26
1686	The effects of IL-20 subfamily cytokines on reconstituted human epidermis suggest potential roles in cutaneous innate defense and pathogenic adaptive immunity in psoriasis. **2007**, 178, 2229-40		398
1685	Characterization of pancreatic transcription factor Pdx-1 binding sites using promoter microarray and serial analysis of chromatin occupancy. **2007**, 282, 32084-92		85
1684	Phenotypic and transcriptomic changes associated with potato autopolyploidization. **2007**, 176, 2055-67		181
1683	Extensive intrasubtype recombination in South African human immunodeficiency virus type 1 subtype C infections. **2007**, 81, 4492-500		55
1682	Identification of promoters recognized by RNA polymerase-sigmaE holoenzyme from Thermus thermophilus HB8. **2007**, 189, 8758-64		9
1681	Regulatory network construction in Arabidopsis by using genome-wide gene expression quantitative trait loci. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 1708-13	11.5	269
1680	Sequence-level population simulations over large genomic regions. **2007**, 177, 1725-31		84
1679	Global transcriptional analysis of Mycoplasma hyopneumoniae following exposure to hydrogen peroxide. **2007**, 153, 3785-3790		31
1678	Experimental and statistical considerations to avoid false conclusions in proteomics studies using differential in-gel electrophoresis. **2007**, 6, 1354-64		142
1677	Oviposition by pierid butterflies triggers defense responses in Arabidopsis. **2007**, 143, 784-800		148
1676	Opportunities and limitations of SELDI-TOF-MS in biomedical research: practical advices. **2007**, 4, 51-65		113
1675	Fundamental differences in cell cycle deregulation in human papillomavirus-positive and human papillomavirus-negative head/neck and cervical cancers. **2007**, 67, 4605-19		351
1674	Heritability of alternative splicing in the human genome. **2007**, 17, 1210-8		93
1673	Electronically subtracting expression patterns from a mixed cell population. **2007**, 23, 3328-34		24
1672	Localizing recent adaptive evolution in the human genome. **2007**, 3, e90		342
1671	Evidence of differential HLA class I-mediated viral evolution in functional and accessory/regulatory genes of HIV-1. **2007**, 3, e94		139
1670	NPHS2 variation in sporadic focal segmental glomerulosclerosis. **2007**, 18, 2987-95		49

1669	NAC transcription factors, NST1 and NST3, are key regulators of the formation of secondary walls in woody tissues of Arabidopsis. **2007**, 19, 270-80	576
1668	Quick calculation for sample size while controlling false discovery rate with application to microarray analysis. **2007**, 23, 739-46	93
1667	An integrative genomics strategy for systematic characterization of genetic loci modulating phenotypes. **2007**, 16, 1381-90	15
1666	Frequent occurrence of uniparental disomy in colorectal cancer. **2007**, 28, 38-48	93
1665	Development of progressive aortic vasculopathy in a rat model of aging. **2007**, 293, H2634-43	31
1664	Genome-wide analysis of PPARalpha activation in murine small intestine. **2007**, 30, 192-204	105
1663	Polymorphisms of CUL5 are associated with CD4+ T cell loss in HIV-1 infected individuals. **2007**, 3, e19	45
1662	Capturing heterogeneity in gene expression studies by surrogate variable analysis. **2007**, 3, 1724-35	1165
1661	GeneChip profiling of transcriptional responses to soybean cyst nematode, Heterodera glycines, colonization of soybean roots. **2007**, 58, 3407-18	51
1660	Gene expression-based molecular diagnostic system for malignant gliomas is superior to histological diagnosis. **2007**, 13, 7341-56	63
1659	Query-driven module discovery in microarray data. **2007**, 23, 2573-80	19
1658	Unbiased gene expression analysis implicates the huntingtin polyglutamine tract in extra-mitochondrial energy metabolism. **2007**, 3, e135	63
1657	Adaptive evolution of conserved noncoding elements in mammals. **2007**, 3, 1572-86	68
1656	Contrasting infection strategies in generalist and specialist wasp parasitoids of Drosophila melanogaster. **2007**, 3, 1486-501	155
1655	A statistical framework for modeling HLA-dependent T cell response data. **2007**, 3, 1879-86	5
1654	Neutrality, compensation, and negative selection during evolution of B-cell development transcriptomes. **2007**, 24, 2610-8	5
1653	Sex-specific regulation of gene expression in the aging monkey aorta. **2007**, 29, 169-80	38
1652	PADGE: analysis of heterogeneous patterns of differential gene expression. **2007**, 32, 154-9	17

1651	A two-stage binomial test approach of gene identification in oligonucleotide arrays. **2007**, 17, 903-18	
1650	Selection and validation of normalization methods for c-DNA microarrays using within-array replications. **2007**, 23, 2391-8	16
1649	SNP@Ethnos: a database of ethnically variant single-nucleotide polymorphisms. **2007**, 35, D711-5	22
1648	Position and distance specificity are important determinants of cis-regulatory motifs in addition to evolutionary conservation. **2007**, 35, 3203-13	49
1647	TREMOR--a tool for retrieving transcriptional modules by incorporating motif covariance. **2007**, 35, 7360-71	6
1646	Genome-wide identification of spliced introns using a tiling microarray. **2007**, 17, 503-9	33
1645	Patterns of selection and tissue-specific expression among maize domestication and crop improvement loci. **2007**, 144, 1642-53	17
1644	Integrating biomedical knowledge to model pathways of prostate cancer progression. **2007**, 6, 1177-87	11
1643	N-Acylethanolamine metabolism interacts with abscisic acid signaling in Arabidopsis thaliana seedlings. **2007**, 19, 2454-69	54
1642	Detection of gene x gene interactions in genome-wide association studies of human population data. **2007**, 63, 67-84	145
1641	A potential biomarker in the cord blood of preterm infants who develop retinopathy of prematurity. **2007**, 61, 215-21	21
1640	Gene Aging Nexus: a web database and data mining platform for microarray data on aging. **2007**, 35, D756-9	42
1639	Organismal complexity, cell differentiation and gene expression: human over mouse. **2007**, 35, 6350-6	39
1638	Expression of genes involved in oxidative stress responses in airway epithelial cells of smokers with chronic obstructive pulmonary disease. **2007**, 175, 577-86	170
1637	Unsupervised Thresholding of Affymetrix Microarray Data. **2007**,	2
1636	Major regulatory genes in maize contribute to standing variation in teosinte (Zea mays ssp. parviglumis). **2007**, 177, 2349-59	60
1635	Compensating for unknown confounders in microarray data analysis using filtered permutations. **2007**, 14, 669-81	4
1634	A consolidated approach to analyzing data from high-throughput protein microarrays with an application to immune response profiling in humans. **2007**, 14, 350-9	11

1633	The optimal discovery procedure for large-scale significance testing, with applications to comparative microarray experiments. **2007**, 8, 414-32		111
1632	Assessing the pulmonary toxicity of single-walled carbon nanohorns. **2007**, 1, 157-166		40
1631	Obesity. **2007**,		11
1630	Differential gene expression patterns and interaction networks in BCR-ABL-positive and -negative adult acute lymphoblastic leukemias. **2007**, 25, 1341-9		88
1629	Searching the genomes of inbred mouse strains for incompatibilities that reproductively isolate their wild relatives. **2007**, 98, 115-22		17
1628	Complement induction in spinal cord microglia results in anaphylatoxin C5a-mediated pain hypersensitivity. **2007**, 27, 8699-708		176
1627	Associations between sperm competition and natural variation in male reproductive genes on the third chromosome of Drosophila melanogaster. **2007**, 176, 1245-60		83
1626	Association genetics in Pinus taeda L. I. Wood property traits. **2007**, 175, 399-409		227
1625	Error-pooling-based statistical methods for identifying novel temporal replication profiles of human chromosomes observed by DNA tiling arrays. **2007**, 35, e69		8
1624	Runs of homozygosity reveal highly penetrant recessive loci in schizophrenia. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 19942-7	11.5	282
1623	Quantitative profiling of ubiquitylated proteins reveals proteasome substrates and the substrate repertoire influenced by the Rpn10 receptor pathway. **2007**, 6, 1885-95		85
1622	Intrastrand annealing leads to the formation of a large DNA palindrome and determines the boundaries of genomic amplification in human cancer. **2007**, 27, 1993-2002		52
1621	Statistical assessment of functional categories of genes deregulated in pathological conditions by using microarray data. **2007**, 23, 2063-72		20
1620	Evolutionary analysis of amino acid repeats across the genomes of 12 Drosophila species. **2007**, 24, 2598-609		59
1619	Dickkopf-1 is an epigenetically silenced candidate tumor suppressor gene in medulloblastoma. **2007**, 9, 135-44		53
1618	Multiple hypothesis testing to detect lineages under positive selection that affects only a few sites. **2007**, 24, 1219-28		154
1617	Extending the pathway analysis framework with a test for transcriptional variance implicates novel pathway modulation during myogenic differentiation. **2007**, 23, 1356-62		6
1616	Gene expression signatures for tumor progression, tumor subtype, and tumor thickness in laser-microdissected melanoma tissues. **2007**, 13, 806-15		189

1615	A correlation with exon expression approach to identify cis-regulatory elements for tissue-specific alternative splicing. **2007**, 35, 4845-57		66
1614	Arabidopsis VIRE2 INTERACTING PROTEIN2 is required for Agrobacterium T-DNA integration in plants. **2007**, 19, 1695-708		86
1613	Testing for trends in dose-response microarray experiments: a comparison of several testing procedures, multiplicity and resampling-based inference. **2007**, 6, Article26		18
1612	Frontiers in nephrology: genomic approaches to understanding the molecular basis of atherosclerosis. **2007**, 18, 2853-62		2
1611	Extracting binary signals from microarray time-course data. **2007**, 35, 3705-12		87
1610	Comprehensive transcriptome profiling in tomato reveals a role for glycosyltransferase in Mi-mediated nematode resistance. **2007**, 144, 1079-92		63
1609	High throughput microscopy: from raw images to discoveries. **2007**, 120, 3715-22		76
1608	Novel neutrophil-derived proteins in bronchoalveolar lavage fluid indicate an exaggerated inflammatory response in pediatric cystic fibrosis patients. **2007**, 53, 1782-91		40
1607	Pre- and postnatal hepatic gene expression profiles of two pig breeds differing in body composition: insight into pathways of metabolic regulation. **2007**, 29, 267-79		33
1606	More genes underwent positive selection in chimpanzee evolution than in human evolution. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 7489-94	11.5	161
1605	Improved method for differential expression proteomics using trypsin-catalyzed 18O labeling with a correction for labeling efficiency. **2007**, 6, 1274-86		72
1604	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
1603	HaploBuild: an algorithm to construct non-contiguous associated haplotypes in family based genetic studies. **2007**, 23, 2190-2		12
1602	Founder effects in the assessment of HIV polymorphisms and HLA allele associations. **2007**, 315, 1583-6		213
1601	Tissue-specific regulatory elements in mammalian promoters. **2007**, 3, 73		47
1600	A downstream mediator in the growth repression limb of the jasmonate pathway. **2007**, 19, 2470-83		491
1599	Association Studies of Complex Diseases. 1375-1426		
1598	Constructing gene association networks for rheumatoid arthritis using the backward genotype-trait association (BGTA) algorithm. **2007**, 1 Suppl 1, S13		10

1597	A COMPUTATIONAL PROCEDURE FOR THE INTEGRATIVE ANALYSIS OF GENOMIC DATA AT THE SINGLE SAMPLE LEVEL. **2007**, 40, 243-248	
1596	Conservative adjustment of permutation p-values when the number of permutations is limited. **2007**, 3, 536-46	4
1595	Analysis of Gene Expression Data. 473-507	
1594	Parallel genome-wide expression profiling of host and pathogen during soybean cyst nematode infection of soybean. **2007**, 20, 293-305	176
1593	Developmental transcript profiling of cyst nematode feeding cells in soybean roots. **2007**, 20, 510-25	201
1592	Kaposi sarcoma herpesvirus-encoded vFLIP and vIRF1 regulate antigen presentation in lymphatic endothelial cells. **2007**, 109, 1550-8	47
1591	A validated gene expression model of high-risk multiple myeloma is defined by deregulated expression of genes mapping to chromosome 1. **2007**, 109, 2276-84	699
1590	CYP2J2 and CYP2C8 polymorphisms and coronary heart disease risk: the Atherosclerosis Risk in Communities (ARIC) study. **2007**, 17, 349-58	74
1589	Comparative and evolutionary pharmacogenetics of ABCB1: complex signatures of positive selection on coding and regulatory regions. **2007**, 17, 667-78	18
1588	Unique, shared, and redundant roles for the Arabidopsis SWI/SNF chromatin remodeling ATPases BRAHMA and SPLAYED. **2007**, 19, 403-16	123
1587	Combination of high-resolution magic angle spinning proton magnetic resonance spectroscopy and microscale genomics to type brain tumor biopsies. **2007**,	4
1586	Special issue on postoperative cognitive dysfunction: selected reports from the journal-sponsored symposium. **2007**, 106, 418-20	8
1585	Identification of differentially expressed genes and false discovery rate in microarray studies. **2007**, 18, 187-93	31
1584	"A razor may be sharper than an ax, but it cannot cut wood". **2007**, 106, 420-2	4
1583	Correction to Frasure-Smith et al. Design and rationale for a randomized, controlled trial of interpersonal psychotherapy and citalopram for depression in coronary artery disease (CREATE) (January/February 2006). **2007**, 69, 216	2
1582	Genetics in psychosomatic medicine: research designs and statistical approaches. **2007**, 69, 206-16	22
1581	Understanding sample size: what determines the required number of microarrays for an experiment?. **2007**, 12, 46-50	29
1580	Genome multiplication as adaptation to tissue survival: evidence from gene expression in mammalian heart and liver. **2007**, 89, 70-80	66

1579	Global transcriptional response of porcine mesenteric lymph nodes to Salmonella enterica serovar Typhimurium. **2007**, 90, 72-84	31
1578	Microarray analyses of pituitary adenylate cyclase activating polypeptide (PACAP)-regulated gene targets in sympathetic neurons. **2007**, 28, 1856-70	33
1577	Polymorphisms in hypoxia inducible factor 1 and the initial clinical presentation of coronary disease. **2007**, 154, 1035-42	72
1576	Estrogen-related receptor alpha is essential for the expression of antioxidant protection genes and mitochondrial function. **2007**, 357, 231-6	53
1575	CHD5 is a tumor suppressor at human 1p36. **2007**, 128, 459-75	268
1574	A common mechanism of cellular death induced by bactericidal antibiotics. **2007**, 130, 797-810	1833
1573	A new approach to intensity-dependent normalization of two-channel microarrays. **2007**, 8, 128-39	20
1572	Applications of Linkage Disequilibrium and Association Mapping in Crop Plants. **2007**, 97-119	75
1571	Exploring design-related bias in clinical studies on receptor genetic polymorphism of hypertension. **2007**, 60, 1-7	9
1570	The -1131 T>C and S19W APOA5 gene polymorphisms are associated with high levels of triglycerides and apolipoprotein C-III, but not with coronary artery disease: an angiographic study. **2007**, 191, 409-17	58
1569	QTL-specific genotype-by-smoking interaction and burden of calcified coronary atherosclerosis: the NHLBI Family Heart Study. **2007**, 193, 11-9	11
1568	Human oncogene tissue-specific expression level significantly correlates with sequence compositional features. **2007**, 581, 4361-5	6
1567	Relations of brain volumes with cognitive function in males 45 years and older with past lead exposure. **2007**, 37, 633-41	33
1566	Genome scanning by composite likelihood. **2007**, 80, 19-28	16
1565	Genotype x adiposity interaction linkage analyses reveal a locus on chromosome 1 for lipoprotein-associated phospholipase A2, a marker of inflammation and oxidative stress. **2007**, 80, 168-77	20
1564	Gene-expression variation within and among human populations. **2007**, 80, 502-9	259
1563	A Bayesian measure of the probability of false discovery in genetic epidemiology studies. **2007**, 81, 208-27	343
1562	Classification of human chromosome 21 gene-expression variations in Down syndrome: impact on disease phenotypes. **2007**, 81, 475-91	187

1561	Transcriptional profiling of non-small cell lung cancer cells with activating EGFR somatic mutations. **2007**, 2, e1226	26
1560	Transcript profiling in host-pathogen interactions. **2007**, 45, 329-69	136
1559	Sample size and replication in 2D gel electrophoresis studies. **2007**, 6, 2884-7	58
1558	The DIURNAL project: DIURNAL and circadian expression profiling, model-based pattern matching, and promoter analysis. **2007**, 72, 353-63	274
1557	Plant Systems Biology. **2007**,	1
1556	PhyloScan: identification of transcription factor binding sites using cross-species evidence. **2007**, 2, 1	20
1555	Transcriptional profiling of MnSOD-mediated lifespan extension in Drosophila reveals a species-general network of aging and metabolic genes. **2007**, 8, R262	108
1554	Application of the comprehensive set of heterozygous yeast deletion mutants to elucidate the molecular basis of cellular chromium toxicity. **2007**, 8, R268	47
1553	Divergent evolution of arrested development in the dauer stage of Caenorhabditis elegans and the infective stage of Heterodera glycines. **2007**, 8, R211	36
1552	High-resolution aCGH and expression profiling identifies a novel genomic subtype of ER negative breast cancer. **2007**, 8, R215	230
1551	Harnessing naturally randomized transcription to infer regulatory relationships among genes. **2007**, 8, R219	83
1550	Phenotypic and transcriptional response to selection for alcohol sensitivity in Drosophila melanogaster. **2007**, 8, R231	63
1549	Genetic subtraction profiling identifies genes essential for Arabidopsis reproduction and reveals interaction between the female gametophyte and the maternal sporophyte. **2007**, 8, R204	113
1548	Dynamic cumulative activity of transcription factors as a mechanism of quantitative gene regulation. **2007**, 8, R181	9
1547	Reversible and permanent effects of tobacco smoke exposure on airway epithelial gene expression. **2007**, 8, R201	169
1546	Quantitative genomics of locomotor behavior in Drosophila melanogaster. **2007**, 8, R172	61
1545	An immune response gene expression module identifies a good prognosis subtype in estrogen receptor negative breast cancer. **2007**, 8, R157	383
1544	A functional map of NFkappaB signaling identifies novel modulators and multiple system controls. **2007**, 8, R104	16

1543	Estimation and correction of non-specific binding in a large-scale spike-in experiment. **2007**, 8, R126	15
1542	Towards the uniform distribution of null P values on Affymetrix microarrays. **2007**, 8, R69	25
1541	A distance difference matrix approach to identifying transcription factors that regulate differential gene expression. **2007**, 8, R83	12
1540	Threshold-free high-power methods for the ontological analysis of genome-wide gene-expression studies. **2007**, 8, R74	19
1539	DNA variation and brain region-specific expression profiles exhibit different relationships between inbred mouse strains: implications for eQTL mapping studies. **2007**, 8, R25	55
1538	Expression and regulation of CCL18 in synovial fluid neutrophils of patients with rheumatoid arthritis. **2007**, 9, R94	40
1537	Bioinformatics. **2007**,	1
1536	Circadian Rhythms. **2007**,	11
1535	Microarray Data Analysis. **2007**,	4
1534	Fundamentals of Data Mining in Genomics and Proteomics. **2007**,	69
1533	Clustering Class Discovery in the Post-Genomic Era. **2007**, 123-148	1
1532	Introduction to Genomic and Proteomic Data Analysis. **2007**, 1-37	4
1531	Gene response of human monocytic cells for the detection of antimigraine activity of feverfew extracts. **2007**, 85, 1108-15	5
1530	Linkage Disequilibrium and Association Mapping. **2007**,	7
1529	Procedures for numerical analysis of circadian rhythms. **2007**, 38, 275-325	451
1528	An Empirical CDF Approach to Estimate the Significance of Gene Ranking for Finding Differentially Expressed Genes. **2007**,	1
1527	The pharmacogenetics of lithium response depends upon clinical co-morbidity. **2007**, 11, 161-70	47
1526	Analyzing Designed Experiments with Multiple Responses. **2007**, 34, 1275-1296	27

1525	Shoot-Root defense signaling and activation of root defense by leaf damage in poplarThis article is one of a selection of papers published in the Special Issue on Poplar Research in Canada.. **2007**, 85, 1171-1181	17
1524	Prediction of individual genetic risk to disease from genome-wide association studies. **2007**, 17, 1520-8	436
1523	Extra virgin olive oils increase hepatic fat accumulation and hepatic antioxidant protein levels in APOE-/- mice. **2007**, 6, 4041-54	48
1522	Genome-wide patterns of gene flow across a house mouse hybrid zone. **2008**, 18, 67-76	193
1521	Amygdala gene expression correlates of social behavior in monkeys experiencing maternal separation. **2007**, 27, 3295-304	100
1520	A Bayesian False Discovery Rate for Multiple Testing. **2007**, 34, 1-9	23
1519	Spatial analysis of arabidopsis thaliana gene expression in response to Turnip mosaic virus infection. **2007**, 20, 358-70	120
1518	Oncomine 3.0: genes, pathways, and networks in a collection of 18,000 cancer gene expression profiles. **2007**, 9, 166-80	1537
1517	Direct tissue analysis by matrix-assisted laser desorption ionization mass spectrometry: application to kidney biology. **2007**, 27, 597-608	58
1516	Critical review of published microarray studies for cancer outcome and guidelines on statistical analysis and reporting. **2007**, 99, 147-57	514
1515	[DNA microarray technology: principles and applications to the study of neurological disorders]. **2007**, 163, 409-20	3
1514	Positive association between SIAT8B and schizophrenia in the Chinese Han population. **2007**, 90, 108-14	83
1513	Complete gene expression profiling of Saccharopolyspora erythraea using GeneChip DNA microarrays. **2007**, 6, 37	23
1512	Analysis of signaling pathways in 90 cancer cell lines by protein lysate array. **2007**, 6, 2753-67	29
1511	Genetic variation in S-nitrosoglutathione reductase (GSNOR) and childhood asthma. **2007**, 120, 322-8	58
1510	Spurious genetic associations. **2007**, 61, 1121-6	268
1509	Combining Quantitative Trait and Gene-Expression Data. 389-411	1
1508	Mapping, fine mapping, and molecular dissection of quantitative trait Loci in domestic animals. **2007**, 8, 131-62	93

1507	ABCB1 genotype and PGP expression, function and therapeutic drug response: a critical review and recommendations for future research. **2007**, 7, 154-79	220
1506	Distinct biphasic mRNA changes in response to Asian soybean rust infection. **2007**, 20, 887-99	94
1505	From Gene Expression to Metabolic Fluxes. **2007**, 37-66	2
1504	The evolution of gene expression QTL in Saccharomyces cerevisiae. **2007**, 2, e678	39
1503	Altered T-cell function in schizophrenia: a cellular model to investigate molecular disease mechanisms. **2007**, 2, e692	73
1502	Basonuclin regulates a subset of ribosomal RNA genes in HaCaT cells. **2007**, 2, e902	16
1501	Significant and systematic expression differentiation in long-lived yeast strains. **2007**, 2, e1095	18
1500	Estimating the number and size of the main effects in genome-wide case-control association studies. **2007**, 1 Suppl 1, S143	5
1499	Rapid and robust association mapping of expression quantitative trait loci. **2007**, 1 Suppl 1, S144	14
1498	Comparison of false-discovery rate for genome-wide and fine mapping regions. **2007**, 1 Suppl 1, S148	4
1497	Different normalization strategies for microarray gene expression traits affect the heritability estimation. **2007**, 1 Suppl 1, S154	5
1496	Sex, age and generation effects on genome-wide linkage analysis of gene expression in transformed lymphoblasts. **2007**, 1 Suppl 1, S92	3
1495	DNA microarrays: a powerful genomic tool for biomedical and clinical research. **2007**, 13, 527-41	155
1494	Bridging Genomics and Genetic Diversity: Linkage Disequilibrium Structure and Association Mapping in Maize and Other Cereals. **2007**, 47, S-60-S-71	18
1493	Estimating the False Discovery Rate Using Mixed Normal Distribution for Identifying Differentially Expressed Genes in Microarray Data Analysis. **2007**, 3, 117693510700300	2
1492	Parental smoking modifies the relation between genetic variation in tumor necrosis factor-alpha (TNF) and childhood asthma. **2007**, 115, 616-22	37
1491	Finding cis-regulatory elements using comparative genomics: some lessons from ENCODE data. **2007**, 17, 775-86	61
1490	Interpretation of microarray data: trudging out of the abyss towards elucidation of biological significance. **2007**, 85, E20-3	19

1489	Reducing the Probability of False Positive Research Findings by Pre-Publication Validation - Experience with a Large Multiple Sclerosis Database. **2007**,	1
1488	Promoter regions of many neural- and nutrition-related genes have experienced positive selection during human evolution. **2007**,	0
1487	Mapping common disease genes. 59-79	
1486	Identifying potential biomarkers in LC-MS data. **2007**, 21, 292-302	17
1485	Combining adaptive designs with control of the false discovery rate--a generalized definition for a global p-value. **2007**, 49, 94-106	13
1484	Empirical Bayes identification [correction of identication] of tumor progression genes from microarray data. **2007**, 49, 68-77	
1483	Identification of novel susceptibility genes in childhood-onset systemic lupus erythematosus using a uniquely designed candidate gene pathway platform. **2007**, 56, 4164-73	64
1482	Disruption of cerebral cortex MET signaling in autism spectrum disorder. **2007**, 62, 243-50	151
1481	Evidence for association between multiple complement pathway genes and AMD. **2007**, 31, 224-37	43
1480	Optimal selection of markers for validation or replication from genome-wide association studies. **2007**, 31, 396-407	15
1479	Summary of contributions to GAW15 Group 13: candidate gene association studies. **2007**, 31 Suppl 1, S110-7	2
1478	Multiple testing in the genomics era: findings from Genetic Analysis Workshop 15, Group 15. **2007**, 31 Suppl 1, S124-31	11
1477	A preliminary metabolomic analysis of older adults with and without depression. **2007**, 22, 418-23	113
1476	Human leukocyte antigen-associated sequence polymorphisms in hepatitis C virus reveal reproducible immune responses and constraints on viral evolution. **2007**, 46, 339-49	85
1475	Evidence for human leukocyte antigen heterozygote advantage against hepatitis C virus infection. **2007**, 46, 1713-21	99
1474	Gene expression in 16q is associated with survival and differs between S□lie breast cancer subtypes. **2007**, 46, 87-97	15
1473	Pathway and single gene analyses of inhibited Caco-2 differentiation by ascorbate-stabilized quercetin suggest enhancement of cellular processes associated with development of colon cancer. **2007**, 51, 1031-45	11
1472	Multivariate and geometric morphometrics in the analysis of sexual dimorphism variation in Podarcis lizards. **2007**, 268, 152-65	92

1471	A semi-parametric approach for mixture models: Application to local false discovery rate estimation. **2007**, 51, 5483-5493	29
1470	A CBS haplotype and a polymorphism at the MSR gene are associated with cardiovascular disease in a Spanish case-control study. **2007**, 40, 864-8	9
1469	Automated reduction and interpretation of multidimensional mass spectra for analysis of complex peptide mixtures. **2007**, 260, 20-30	12
1468	Haplotype-based analysis of genes associated with risk of adverse skin reactions after radiotherapy in breast cancer patients. **2007**, 69, 685-93	57
1467	Statistics for proteomics: experimental design and 2-DE differential analysis. **2007**, 849, 261-72	73
1466	Patterns of population differentiation of candidate genes for cardiovascular disease. **2007**, 8, 48	30
1465	Dynamic resolution of functionally related gene sets in response to acute heat stress. **2007**, 8, 46	8
1464	Dosage compensation is less effective in birds than in mammals. **2007**, 6, 2	255
1463	Incorporating prior information via shrinkage: a combined analysis of genome-wide location data and gene expression data. **2007**, 26, 2258-75	4
1462	Sample size calculation with dependence adjustment for FDR-control in microarray studies. **2007**, 26, 4219-37	29
1461	Transcriptional profiling suggests that secondary and primary large B-cell lymphomas of the gastrointestinal (GI) tract are blastic variants of GI marginal zone lymphoma. **2007**, 211, 305-13	22
1460	Abnormal pathways in the genu of the corpus callosum in schizophrenia pathogenesis: a proteome study. **2007**, 1, 1291-305	63
1459	Proteomic analysis of protein expression changes in a model of gliomagenesis. **2007**, 1, 1485-98	0
1458	Biomarker clustering to address correlations in proteomic data. **2007**, 7, 1037-46	12
1457	Statistical identification of differentially labeled peptides from liquid chromatography tandem mass spectrometry. **2007**, 7, 3681-92	19
1456	Protein abundance ratios for global studies of prokaryotes. **2007**, 7, 2904-19	23
1455	Quantitative proteomics of intracellular Porphyromonas gingivalis. **2007**, 7, 4323-37	60
1454	Design and analysis issues in quantitative proteomics studies. **2007**, 7 Suppl 1, 42-50	128

1453	Using array-comparative genomic hybridization to define molecular portraits of primary breast cancers. **2007**, 26, 1959-70	88
1452	Effective use of microarrays in neuroendocrine research. **2007**, 19, 145-61	4
1451	Salt stress responses in Arabidopsis utilize a signal transduction pathway related to endoplasmic reticulum stress signaling. **2007**, 51, 897-909	321
1450	Dynamic evolution of the innate immune system in Drosophila. **2007**, 39, 1461-8	318
1449	On the design and analysis of gene expression studies in human populations. **2007**, 39, 807-8; author reply 808-9	101
1448	Reply to On the design and analysis of gene expression studies in human populations **2007**, 39, 808-809	37
1447	Conjuring SNPs to detect associations. **2007**, 39, 815-6	24
1446	Integrative molecular concept modeling of prostate cancer progression. **2007**, 39, 41-51	734
1445	Innate partnership of HLA-B and KIR3DL1 subtypes against HIV-1. **2007**, 39, 733-40	579
1444	Promoter regions of many neural- and nutrition-related genes have experienced positive selection during human evolution. **2007**, 39, 1140-4	221
1443	CD8+ T-cell responses to different HIV proteins have discordant associations with viral load. **2007**, 13, 46-53	824
1442	Analysis and validation of proteomic data generated by tandem mass spectrometry. **2007**, 4, 787-97	523
1441	Semi-supervised learning for peptide identification from shotgun proteomics datasets. **2007**, 4, 923-5	1362
1440	MetaNetwork: a computational protocol for the genetic study of metabolic networks. **2007**, 2, 685-94	25
1439	Enrichment of HapMap recombination hotspot predictions around human nervous system genes: evidence for positive selection?. **2007**, 15, 1071-8	12
1438	Gene expression time course in the human skin during elicitation of allergic contact dermatitis. **2007**, 127, 2585-95	30
1437	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
1436	Pediatric acute myeloid leukemia with NPM1 mutations is characterized by a gene expression profile with dysregulated HOX gene expression distinct from MLL-rearranged leukemias. **2007**, 21, 2000-9	133

1435	Converging evidence for a pseudoautosomal cytokine receptor gene locus in schizophrenia. **2007**, 12, 572-80	237
1434	Pharmacogenetics and pharmacogenomics of schizophrenia: a review of last decade of research. **2007**, 12, 707-47	288
1433	No association of trace amine receptor genes with bipolar disorder. **2007**, 12, 979-81	7
1432	Reduced overflow of BDNF from the brain is linked with suicide risk in depressive illness. **2007**, 12, 981-3	44
1431	The effect of ancient population bottlenecks on human phenotypic variation. **2007**, 448, 346-8	233
1430	Genetic variants regulating ORMDL3 expression contribute to the risk of childhood asthma. **2007**, 448, 470-3	1201
1429	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
1428	A hierarchical modelling framework for identifying unusual performance in health care providers. **2007**, 170, 865-890	42
1427	The optimal discovery procedure: a new approach to simultaneous significance testing. **2007**, 69, 347-368	111
1426	Polymorphisms of KCNJ11 (Kir6.2 gene) are associated with Type 2 diabetes and hypertension in the Korean population. **2007**, 24, 178-86	57
1425	Life-history and habitat features influence the within-river genetic structure of Atlantic salmon. **2007**, 16, 2638-54	221
1424	Statistical analysis of amplified fragment length polymorphism data: a toolbox for molecular ecologists and evolutionists. **2007**, 16, 3737-58	436
1423	Conditional oxidative stress responses in the Arabidopsis photorespiratory mutant cat2 demonstrate that redox state is a key modulator of daylength-dependent gene expression, and define photoperiod as a crucial factor in the regulation of H2O2-induced cell death. **2007**, 52, 640-57	327
1422	Tissue-specific expression of a defence-related peroxidase in transgenic wheat potentiates cell death in pathogen-attacked leaf epidermis. **2008**, 9, 45-57	34
1421	Altered gene expression profiles in the frontal cortex of cirrhotic alcoholics. **2007**, 31, 1460-6	55
1420	Interpretation of knockout experiments: the congenic footprint. **2007**, 6, 299-303	43
1419	Periodontal therapy alters gene expression of peripheral blood monocytes. **2007**, 34, 736-47	40
1418	Assessing differential gene expression with small sample sizes in oligonucleotide arrays using a mean-variance model. **2007**, 63, 41-9	18

1417	Exploring the information in p-values for the analysis and planning of multiple-test experiments. **2007**, 63, 483-95	30
1416	Nonparametric bayesian estimation of positive false discovery rates. **2007**, 63, 1126-34	25
1415	A Microarray Based Genomic Hybridization Method for Identification of New Genes in Plants: Case Analyses of Arabidopsis and Oryza. **2007**, 49, 915-926	9
1414	Identification of MSRA gene on chromosome 8p as a candidate metastasis suppressor for human hepatitis B virus-positive hepatocellular carcinoma. **2007**, 7, 172	41
1413	Meta-analysis of several gene lists for distinct types of cancer: a simple way to reveal common prognostic markers. **2007**, 8, 118	23
1412	TagSmart: analysis and visualization for yeast mutant fitness data measured by tag microarrays. **2007**, 8, 128	
1411	Detecting multivariate differentially expressed genes. **2007**, 8, 150	20
1410	Re-sampling strategy to improve the estimation of number of null hypotheses in FDR control under strong correlation structures. **2007**, 8, 157	17
1409	A constrained polynomial regression procedure for estimating the local False Discovery Rate. **2007**, 8, 229	6
1408	A comprehensive evaluation of SAM, the SAM R-package and a simple modification to improve its performance. **2007**, 8, 230	54
1407	Detecting differential expression in microarray data: comparison of optimal procedures. **2007**, 8, 28	8
1406	A framework for significance analysis of gene expression data using dimension reduction methods. **2007**, 8, 346	30
1405	A unified framework for finding differentially expressed genes from microarray experiments. **2007**, 8, 347	13
1404	Inferring activity changes of transcription factors by binding association with sorted expression profiles. **2007**, 8, 452	60
1403	Significance analysis of microarray transcript levels in time series experiments. **2007**, 8 Suppl 1, S10	24
1402	Positive selection for unpreferred codon usage in eukaryotic genomes. **2007**, 7, 119	19
1401	Thermal evolution of gene expression profiles in Drosophila subobscura. **2007**, 7, 42	50
1400	Inference of transcription modification in long-live yeast strains from their expression profiles. **2007**, 8, 219	29

1399	Comparison of the contributions of the nuclear and cytoplasmic compartments to global gene expression in human cells. **2007**, 8, 340	62
1398	Inter- and intra-combinatorial regulation by transcription factors and microRNAs. **2007**, 8, 396	90
1397	Spotted cotton oligonucleotide microarrays for gene expression analysis. **2007**, 8, 81	37
1396	Integrating domain knowledge with statistical and data mining methods for high-density genomic SNP disease association analysis. **2007**, 40, 750-60	20
1395	Gene Ontology analysis in multiple gene clusters under multiple hypothesis testing framework. **2007**, 41, 105-15	5
1394	Bioinformatic approach for cholangiocyte pathophysiology. **2007**, 37 Suppl 3, S444-8	2
1393	Prevalence and risk factors of non-adherence with immunosuppressive medication in kidney transplant patients. **2007**, 7, 108-16	138
1392	Candidate genes affecting Drosophila life span identified by integrating microarray gene expression analysis and QTL mapping. **2007**, 128, 237-49	57
1391	Transcriptional profile of mouse pre-granulosa and Sertoli cells isolated from early-differentiated fetal gonads. **2007**, 7, 113-23	53
1390	Biotechnology. Gene expression and microchips: Problems of the quantitative analysis. **2007**, 77, 2071-2081	
1389	Association of bone morphogenetic proteins with otosclerosis. **2008**, 23, 507-16	51
1388	Mechanisms of disease: The genetic basis of coronary heart disease. **2007**, 4, 558-69	52
1387	Estimating the number of pure chemical components in a mixture by maximum likelihood. **2007**, 21, 24-34	20
1386	Mechanisms of occupational asthma: Not all allergens are equal. **2007**, 12, 165-71	3
1385	Quantitative mass spectrometry in proteomics: a critical review. **2007**, 389, 1017-31	1252
1384	Dysfunction of dysferlin-deficient hearts. **2007**, 85, 1203-14	63
1383	Global profiling of genes modified by endoplasmic reticulum stress in pancreatic beta cells reveals the early degradation of insulin mRNAs. **2007**, 50, 1006-14	95
1382	Social and genetic structure of a supercolonial weaver ant, Polyrhachis robsoni, with dimorphic queens. **2007**, 54, 34-41	10

1381	Statistical strategies for avoiding false discoveries in metabolomics and related experiments. **2007**, 2, 171-196	566
1380	Regulatory gene candidates and gene expression analysis of cold acclimation in winter and spring wheat. **2007**, 64, 409-23	86
1379	CARD15 genotype-phenotype relationships in a small inflammatory bowel disease population with severe disease affection status. **2007**, 52, 2716-24	10
1378	A cDNA microarray for Crassostrea virginica and C. gigas. **2007**, 9, 577-91	60
1377	Differentiation of the two rice subspecies indica and japonica: a Gene Ontology perspective. **2007**, 7, 135-51	6
1376	Developmental steps in acquiring competence for shoot development in Arabidopsis tissue culture. **2007**, 226, 1183-94	139
1375	Genetic polymorphisms in transforming growth factor beta-1 (TGFB1) and childhood asthma and atopy. **2007**, 121, 529-38	45
1374	SNPs in the KCNJ11-ABCC8 gene locus are associated with type 2 diabetes and blood pressure levels in the Japanese population. **2007**, 52, 781-793	70
1373	Differential quantitative proteomics of Porphyromonas gingivalis by linear ion trap mass spectrometry: non-label methods comparison, q-values and LOWESS curve fitting. **2007**, 259, 105-116	34
1372	A compression algorithm for pre-simulated Monte Carlo p-value functions: Application to the ontological analysis of microarray studies. **2008**, 29, 768-772	2
1371	Deciphering transcriptional networks that govern Coffea arabica seed development using combined cDNA array and real-time RT-PCR approaches. **2008**, 66, 105-24	47
1370	The use of general and specific combining abilities in a context of gene expression relevant to plant breeding. **2008**, 161, 115-122	6
1369	A correlation network approach to metabolic data analysis for tomato fruits. **2008**, 161, 181-193	67
1368	Patterns of dioxin-altered mRNA expression in livers of dioxin-sensitive versus dioxin-resistant rats. **2008**, 82, 809-30	33
1367	Ecophysiology of the developing total bacterial and lactobacillus communities in the terminal small intestine of weaning piglets. **2008**, 56, 474-83	65
1366	Combining classical trait and microarray data to dissect transcriptional regulation: a case study. **2008**, 116, 683-90	2
1365	Multi-trait association mapping in sugar beet (Beta vulgaris L.). **2008**, 117, 947-54	50
1364	Association between four SNPs on chromosome 9p21 and myocardial infarction is replicated in an Italian population. **2008**, 53, 144-150	102

1363	Canonical pathways and networks regulated by estrogen in the bovine mammary gland. **2008**, 8, 55-68	34
1362	The t-mixture model approach for detecting differentially expressed genes in microarrays. **2008**, 8, 181-6	8
1361	Onset of lactation in the bovine mammary gland: gene expression profiling indicates a strong inhibition of gene expression in cell proliferation. **2008**, 8, 251-64	82
1360	Evolution and diversity of invertase genes in Populus trichocarpa. **2008**, 227, 565-76	58
1359	Evolutionary analysis of genes of two pathways involved in placental malaria infection. **2008**, 123, 343-57	6
1358	Effects of interacting networks of cardiovascular risk genes on the risk of type 2 diabetes mellitus (the CODAM study). **2008**, 9, 36	3
1357	Multiple interactions between the alpha 2C- and beta1-adrenergic receptors influence heart failure survival. **2008**, 9, 93	13
1356	Duplicate gene expression in allopolyploid Gossypium reveals two temporally distinct phases of expression evolution. **2008**, 6, 16	194
1355	Expression-based Pathway Signature Analysis (EPSA): mining publicly available microarray data for insight into human disease. **2008**, 1, 51	11
1354	Uncovering mechanisms of transcriptional regulations by systematic mining of cis regulatory elements with gene expression profiles. **2008**, 1, 4	9
1353	Identification of potential serum biomarkers of inflammation and lipid modulation that are altered by fish oil supplementation in healthy volunteers. **2008**, 8, 1965-74	61
1352	Comparative LC-MS: a landscape of peaks and valleys. **2008**, 8, 731-49	159
1351	Comprehensive proteomics of Methylobacterium extorquens AM1 metabolism under single carbon and nonmethylotrophic conditions. **2008**, 8, 3494-505	52
1350	Towards functional phosphoproteomics by mapping differential phosphorylation events in signaling networks. **2008**, 8, 4453-65	49
1349	Science, marketing and wishful thinking in quantitative proteomics. **2008**, 8, 4618-23	13
1348	Controlling the False Discovery Rate for Feature Selection in High-resolution NMR Spectra. **2008**, 1, 57-66	16
1347	Expression of microRNAs and protein-coding genes associated with perineural invasion in prostate cancer. **2008**, 68, 1152-64	127
1346	The modulation of endothelial cell gene expression by green tea polyphenol-EGCG. **2008**, 52, 1182-92	29

1345	Genome-wide expression profiling during protection from colitis by regulatory T cells. **2008**, 14, 75-87	14
1344	Evolving strategies for global gene expression analysis of cancer. **2008**, 217, 590-7	9
1343	Identification of genes with abnormal expression changes in acute myeloid leukemia. **2008**, 47, 8-20	130
1342	Genome-wide significance for dense SNP and resequencing data. **2008**, 32, 179-85	164
1341	On multiple-testing correction in genome-wide association studies. **2008**, 32, 567-73	193
1340	Comparison of association methods for dense marker data. **2008**, 32, 791-9	12
1339	Bayesian classification and non-Bayesian label estimation via EM algorithm to identify differentially expressed genes: a comparative study. **2008**, 50, 824-36	1
1338	Resampling-based empirical Bayes multiple testing procedures for controlling generalized tail probability and expected value error rates: focus on the false discovery rate and simulation study. **2008**, 50, 716-44	20
1337	Controlling false discoveries in genetic studies. **2008**, 147B, 637-44	53
1336	Quantitative Trait Loci in Inbred Lines. **2008**, 587-622	6
1335	Statistical Inference for Microarray Studies. **2008**, 231-266	
1334	Genetic variation and haplotype structures of innate immunity genes in eastern India. **2008**, 8, 360-6	11
1333	Simultaneous control of false positives and false negatives in multiple hypotheses testing. **2008**, 99, 437-450	3
1332	Comparability of gene expression in human blood, immune and carcinoma cells. **2008**, 205, 178-184	1
1331	Emergent network topology at seizure onset in humans. **2008**, 79, 173-86	190
1330	A genome-wide association study identifies protein quantitative trait loci (pQTLs). **2008**, 4, e1000072	331
1329	Transcriptomes in healthy and diseased gingival tissues. **2008**, 79, 2112-24	117
1328	Evolution of protein-coding genes in Drosophila. **2008**, 24, 114-23	206

1327	Correspondences between low-energy modes in enzymes: dynamics-based alignment of enzymatic functional families. **2008**, 17, 918-29	56
1326	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
1325	Parallel expression profiling of barley-stem rust interactions. **2008**, 8, 187-98	18
1324	Analysis of the adult human plasma metabolome. **2008**, 9, 383-97	343
1323	Semisupervised model-based validation of peptide identifications in mass spectrometry-based proteomics. **2008**, 7, 254-65	114
1322	Molecular genetics of addiction and related heritable phenotypes: genome-wide association approaches identify "connectivity constellation" and drug target genes with pleiotropic effects. **2008**, 1141, 318-81	106
1321	A haplotype-based analysis of the LRP5 gene in relation to osteoporosis phenotypes in Spanish postmenopausal women. **2008**, 23, 1954-63	17
1320	Evaluation of genetic variation contributing to differences in gene expression between populations. **2008**, 82, 631-40	177
1319	Characterization of the quantitative trait locus for haloperidol-induced catalepsy on distal mouse chromosome 1. **2008**, 7, 214-23	11
1318	Alcohol trait and transcriptional genomic analysis of C57BL/6 substrains. **2008**, 7, 677-89	57
1317	Genetic susceptibility to heroin addiction: a candidate gene association study. **2008**, 7, 720-9	167
1316	Dynamics of the yeast transcriptome during wine fermentation reveals a novel fermentation stress response. **2008**, 8, 35-52	141
1315	Genomewide association for schizophrenia in the CATIE study: results of stage 1. **2008**, 13, 570-84	308
1314	Two levels of protection for the B cell genome during somatic hypermutation. **2008**, 451, 841-5	453
1313	Novel risk stratification of patients with neuroblastoma by genomic signature, which is independent of molecular signature. **2008**, 27, 441-9	68
1312	A gene expression atlas of the model legume Medicago truncatula. **2008**, 55, 504-13	569
1311	Genome-wide association scan identifies a colorectal cancer susceptibility locus on 11q23 and replicates risk loci at 8q24 and 18q21. **2008**, 40, 631-7	486
1310	Regulatory changes underlying expression differences within and between Drosophila species. **2008**, 40, 346-50	280

1309	Cyclooxygenase polymorphisms and risk of cardiovascular events: the Atherosclerosis Risk in Communities (ARIC) study. **2008**, 83, 52-60	69
1308	Association study of CSF2RB with schizophrenia in Irish family and case - control samples. **2008**, 13, 930-8	22
1307	Genotype patterns that contribute to increased risk for or protection from developing heroin addiction. **2008**, 13, 417-28	78
1306	Association of ADH and ALDH genes with alcohol dependence in the Irish Affected Sib Pair Study of alcohol dependence (IASPSAD) sample. **2008**, 32, 785-95	69
1305	Correlation of population parameters leading to power differences in association studies with population stratification. **2008**, 72, 801-11	6
1304	Transcript profiles of the cytokinin response regulator gene family in Populus imply diverse roles in plant development. **2008**, 177, 77-89	58
1303	Changes in tomato ovary transcriptome demonstrate complex hormonal regulation of fruit set. **2008**, 177, 60-76	170
1302	Global monitoring of autumn gene expression within and among phenotypically divergent populations of Sitka spruce (Picea sitchensis). **2008**, 178, 103-122	103
1301	Transcriptional profiling of aluminum toxicity and tolerance responses in maize roots. **2008**, 179, 116-128	111
1300	Comparative analysis of the transcriptomes of Populus trichocarpa and Arabidopsis thaliana suggests extensive evolution of gene expression regulation in angiosperms. **2008**, 180, 408-420	43
1299	Priming defense genes and metabolites in hybrid poplar by the green leaf volatile cis-3-hexenyl acetate. **2008**, 180, 722-734	197
1298	Altered frontostriatal coupling in pre-manifest Huntington's disease: effects of increasing cognitive load. **2008**, 15, 1180-90	63
1297	Common genetic variants associated with plasma fibrin D-dimer concentration in older European- and African-American adults. **2008**, 6, 654-9	20
1296	PROC, PROCR and PROS1 polymorphisms, plasma anticoagulant phenotypes, and risk of cardiovascular disease and mortality in older adults: the Cardiovascular Health Study. **2008**, 6, 1625-32	42
1295	Metabolic and genetic perturbations accompany the modification of galactomannan in seeds of Medicago truncatula expressing mannan synthase from guar (Cyamopsis tetragonoloba L.). **2008**, 6, 619-31	22
1294	Discussion of "Sure Independence Screening for Ultra-High Dimensional Feature Space. **2008**, 70, 903	1262
1293	Associations between cytokine/cytokine receptor single nucleotide polymorphisms and humoral immunity to measles, mumps and rubella in a Somali population. **2008**, 72, 211-20	45
1292	Chromosome copy number analysis in screening for prognosis-related genomic regions in colorectal carcinoma. **2008**, 99, 1835-40	56

1291	Gamma-aminobutyric acid receptor genes and nicotine dependence: evidence for association from a case-control study. **2008**, 103, 1027-38	48
1290	Association of a single nucleotide polymorphism in neuronal acetylcholine receptor subunit alpha 5 (CHRNA5) with smoking status and with 'pleasurable buzz' during early experimentation with smoking. **2008**, 103, 1544-52	118
1289	Fungal contamination of big-bale grass silage on Irish farms: predominant mould and yeast species and features of bales and silage. **2008**, 63, 121-137	28
1288	Identifying the susceptibility genes for coronary artery disease: from hyperbole through doubt to cautious optimism. **2008**, 263, 538-52	37
1287	Genetics and evolution of weedy Helianthus annuus populations: adaptation of an agricultural weed. **2008**, 17, 384-94	55
1286	Soft selective sweep near a gene that increases plant height in wheat. **2008**, 17, 741-56	29
1285	Historical fragmentation of islands and genetic drift in populations of Galþagos lava lizards (Microlophus albemarlensis complex). **2008**, 17, 1224-37	58
1284	Identifying footprints of directional and balancing selection in marine and freshwater three-spined stickleback (Gasterosteus aculeatus) populations. **2008**, 17, 3565-82	116
1283	A gene expression signature of confinement in peripheral blood of red wolves (Canis rufus). **2008**, 17, 2782-91	16
1282	Transcriptomic variation and plasticity in rufous-collared sparrows (Zonotrichia capensis) along an altitudinal gradient. **2008**, 17, 4556-69	96
1281	Population-genomic approach reveals adaptive floral divergence in discrete populations of a hawk moth-pollinated violet. **2008**, 17, 5378-90	60
1280	Gene expression quantitative trait locus analysis of 16 000 barley genes reveals a complex pattern of genome-wide transcriptional regulation. **2008**, 53, 90-101	139
1279	The AtGenExpress hormone and chemical treatment data set: experimental design, data evaluation, model data analysis and data access. **2008**, 55, 526-542	383
1278	The glutathione-deficient mutant pad2-1 accumulates lower amounts of glucosinolates and is more susceptible to the insect herbivore Spodoptera littoralis. **2008**, 55, 774-86	162
1277	Autophagy regulated by day length determines the number of fertile florets in wheat. **2008**, 55, 1010-24	114
1276	Gene expression in early stage cervical cancer. **2008**, 108, 520-6	89
1275	Effects of dependence in high-dimensional multiple testing problems. **2008**, 9, 114	163
1274	Empirical Bayes analysis of single nucleotide polymorphisms. **2008**, 9, 144	14

1273	Mapping gene expression quantitative trait loci by singular value decomposition and independent component analysis. **2008**, 9, 244	32
1272	A simple and robust method for connecting small-molecule drugs using gene-expression signatures. **2008**, 9, 258	77
1271	SNPAnalyzer 2.0: a web-based integrated workbench for linkage disequilibrium analysis and association analysis. **2008**, 9, 290	78
1270	A unified approach to false discovery rate estimation. **2008**, 9, 303	281
1269	Integrative bioinformatics analysis of transcriptional regulatory programs in breast cancer cells. **2008**, 9, 404	27
1268	Gene set enrichment analysis for non-monotone association and multiple experimental categories. **2008**, 9, 481	10
1267	Time-course analysis of genome-wide gene expression data from hormone-responsive human breast cancer cells. **2008**, 9 Suppl 2, S12	25
1266	Comprehensive analysis of circadian periodic pattern in plant transcriptome. **2008**, 9 Suppl 9, S18	10
1265	Coordinated evolution of co-expressed gene clusters in the Drosophila transcriptome. **2008**, 8, 2	26
1264	Genome-wide analyses reveal lineage specific contributions of positive selection and recombination to the evolution of Listeria monocytogenes. **2008**, 8, 233	61
1263	Molecular evolution of synonymous codon usage in Populus. **2008**, 8, 307	61
1262	Comparative analysis of the acute response of the trout, O. mykiss, head kidney to in vivo challenge with virulent and attenuated infectious hematopoietic necrosis virus and LPS-induced inflammation. **2008**, 9, 141	54
1261	A novel method of differential gene expression analysis using multiple cDNA libraries applied to the identification of tumour endothelial genes. **2008**, 9, 153	46
1260	Comparative transcriptome analysis of Arabidopsis thaliana infested by diamond back moth (Plutella xylostella) larvae reveals signatures of stress response, secondary metabolism, and signalling. **2008**, 9, 154	77
1259	Identification of SNPs and INDELS in swine transcribed sequences using short oligonucleotide microarrays. **2008**, 9, 252	10
1258	Genome-wide survey of allele-specific splicing in humans. **2008**, 9, 265	31
1257	Expression profiling of a high-fertility mouse line by microarray analysis and qPCR. **2008**, 9, 307	10
1256	Altered gene expression changes in Arabidopsis leaf tissues and protoplasts in response to Plum pox virus infection. **2008**, 9, 325	75

1255	Transcription factor control of growth rate dependent genes in Saccharomyces cerevisiae: a three factor design. **2008**, 9, 341	43
1254	Trait correlated expression combined with expression QTL analysis reveals biological pathways and candidate genes affecting water holding capacity of muscle. **2008**, 9, 367	66
1253	Analysis of porcine transcriptional response to Salmonella enterica serovar Choleraesuis suggests novel targets of NFkappaB are activated in the mesenteric lymph node. **2008**, 9, 437	38
1252	The rules of gene expression in plants: organ identity and gene body methylation are key factors for regulation of gene expression in Arabidopsis thaliana. **2008**, 9, 438	79
1251	Establishing an adjusted p-value threshold to control the family-wide type 1 error in genome wide association studies. **2008**, 9, 516	178
1250	Gene expression profiling in chicken heterophils with Salmonella enteritidis stimulation using a chicken 44 K Agilent microarray. **2008**, 9, 526	60
1249	Combining gene expression, demographic and clinical data in modeling disease: a case study of bipolar disorder and schizophrenia. **2008**, 9, 531	31
1248	Identifying positioned nucleosomes with epigenetic marks in human from ChIP-Seq. **2008**, 9, 537	103
1247	Comparison of the transcriptomic "stress response" evoked by antimycin A and oxygen deprivation in Saccharomyces cerevisiae. **2008**, 9, 627	16
1246	Meta-analysis of expression signatures of muscle atrophy: gene interaction networks in early and late stages. **2008**, 9, 630	46
1245	Gene expression patterns within cell lines are predictive of chemosensitivity. **2008**, 9, 74	14
1244	Genomic and proteomic analysis of the Alkali-Tolerance Response (AlTR) in Listeria monocytogenes 10403S. **2008**, 8, 102	43
1243	Reducing the probability of false positive research findings by pre-publication validation - experience with a large multiple sclerosis database. **2008**, 8, 18	21
1242	Low-penetrance alleles predisposing to sporadic colorectal cancers: a French case-controlled genetic association study. **2008**, 8, 326	70
1241	Genetic and systems level analysis of Drosophila sticky/citron kinase and dFmr1 mutants reveals common regulation of genetic networks. **2008**, 2, 101	7
1240	Systems analysis of quantitative shRNA-library screens identifies regulators of cell adhesion. **2008**, 2, 49	13
1239	Integrated weighted gene co-expression network analysis with an application to chronic fatigue syndrome. **2008**, 2, 95	127
1238	CLEAR-test: combining inference for differential expression and variability in microarray data analysis. **2008**, 41, 33-45	8

1237	Transcriptional changes in trichothiodystrophy cells. **2008**, 7, 1364-71	8
1236	The chemokine receptor Cxcr3 is not essential for acute cardiac allograft rejection in mice and rats. **2008**, 8, 1604-13	32
1235	Natalizumab alters transcriptional expression profiles of blood cell subpopulations of multiple sclerosis patients. **2008**, 194, 153-64	93
1234	Normalization strategies for mRNA expression data in cartilage research. **2008**, 16, 947-55	22
1233	Gene expression profiling from endomyocardial biopsy tissue allows distinction between subentities of dilated cardiomyopathy. **2008**, 136, 360-369.e1	16
1232	Investigating connectivity between the cerebellum and thalamus in schizophrenia using diffusion tensor tractography: a pilot study. **2008**, 163, 193-200	37
1231	Rapid and accurate peptide identification from tandem mass spectra. **2008**, 7, 3022-7	144
1230	Study Design and Statistical Issues in Pharmacogenetics Research. **2008**, 185-206	
1229	Methodology for profiling the steroid metabolome in animal tissues using ultraperformance liquid chromatography-electrospray-time-of-flight mass spectrometry. **2008**, 80, 8771-9	45
1228	Is the histidine triad nucleotide-binding protein 1 (HINT1) gene a candidate for schizophrenia?. **2008**, 106, 200-7	35
1227	Functional network reconstruction reveals somatic stemness genetic maps and dedifferentiation-like transcriptome reprogramming induced by GATA2. **2008**, 26, 1186-201	39
1226	The cis-regulatory map of Shewanella genomes. **2008**, 36, 5376-90	15
1225	Spectral index for assessment of differential protein expression in shotgun proteomics. **2008**, 7, 845-54	92
1224	Strain differences in the gating-disruptive effects of apomorphine: relationship to gene expression in nucleus accumbens signaling pathways. **2008**, 63, 748-58	34
1223	Catechol-O-methyltransferase contributes to genetic susceptibility shared among anxiety spectrum phenotypes. **2008**, 64, 302-10	83
1222	Application of metabolomics to cardiovascular biomarker and pathway discovery. **2008**, 52, 117-23	176
1221	P-Values are Random Variables. **2008**, 62, 242-245	74
1220	Boolean implication networks derived from large scale, whole genome microarray datasets. **2008**, 9, R157	75

1219	Estrogen, not intrinsic aging, is the major regulator of delayed human wound healing in the elderly. **2008**, 9, R80	79
1218	Adipose tissue transcriptomic signature highlights the pathological relevance of extracellular matrix in human obesity. **2008**, 9, R14	300
1217	A fast SEQUEST cross correlation algorithm. **2008**, 7, 4598-602	173
1216	Methods for handling multiple testing. **2008**, 60, 293-308	125
1215	Using GenePattern for gene expression analysis. **2008**, Chapter 7, Unit 7.12	54
1214	Assigning significance to peptides identified by tandem mass spectrometry using decoy databases. **2008**, 7, 29-34	449
1213	Posterior error probabilities and false discovery rates: two sides of the same coin. **2008**, 7, 40-4	218
1212	Data mining in genomics. **2008**, 28, 145-66, viii	24
1211	Pharmacogenomics and Personalized Medicine. **2008**,	2
1210	Natural variation in gene expression between wild and weedy populations of Helianthus annuus. **2008**, 179, 1881-90	56
1209	A review of modern multiple hypothesis testing, with particular attention to the false discovery proportion. **2008**, 17, 347-88	127
1208	Global transcriptional analysis of Mycoplasma hyopneumoniae following exposure to norepinephrine. **2008**, 154, 2581-2588	46
1207	Lr34-mediated leaf rust resistance in wheat: transcript profiling reveals a high energetic demand supported by transient recruitment of multiple metabolic pathways. **2008**, 21, 1515-27	78
1206	Arabidopsis transcriptome analysis under drought, cold, high-salinity and ABA treatment conditions using a tiling array. **2008**, 49, 1135-49	407
1205	Gene expression analysis of human otosclerotic stapedial footplates. **2008**, 240, 80-6	20
1204	Protein expression profile in the amygdala of rats with methamphetamine-induced behavioral sensitization. **2008**, 435, 113-9	30
1203	Use of the false discovery rate when comparing multiple health care providers. **2008**, 61, 232-240	59
1202	Synthesis of genetic association studies for pertinent gene-disease associations requires appropriate methodological and statistical approaches. **2008**, 61, 634-45	286

1201	Toxicogenomics of water chemistry influence on chronic lead exposure to the fathead minnow (Pimephales promelas). **2008**, 87, 200-9	35
1200	Linkage disequilibrium between STRPs and SNPs across the human genome. **2008**, 82, 1039-50	28
1199	Microarray analysis of gene expression in granulosal cells from persistent follicles in cattle. **2008**, 104, 405-13	7
1198	Translational gene mapping of cognitive decline. **2008**, 29, 524-41	22
1197	Genes are differentially expressed in the epididymal fat of rats rendered obese by a high-fat diet. **2008**, 28, 414-22	53
1196	Polymorphisms in interleukin-1B and its receptor antagonist genes and the risk of chronic obstructive pulmonary disease in a Korean population: a case-control study. **2008**, 102, 1311-20	18
1195	Associations between SNPs in toll-like receptors and related intracellular signaling molecules and immune responses to measles vaccine: preliminary results. **2008**, 26, 1731-6	125
1194	Genomics and genome-wide association studies: an integrative approach to expression QTL mapping. **2008**, 92, 129-33	18
1193	Social correlates of testosterone and ornamentation in male mandrills. **2008**, 54, 365-72	101
1192	Single nucleotide polymorphisms in genes encoding LKB1 (STK11), TORC2 (CRTC2) and AMPK alpha2-subunit (PRKAA2) and risk of type 2 diabetes. **2008**, 93, 200-9	29
1191	Connecting chemosensitivity, gene expression and disease. **2008**, 29, 1-5	10
1190	Size-dependent resistance of protected areas to land-use change. **2008**, 275, 1297-304	88
1189	Functional identification of an anti-sigmaE factor from Thermus thermophilus HB8. **2008**, 423, 153-9	7
1188	Analysis of Sus scrofa liver proteome and identification of proteins differentially expressed between genders, and conventional and genetically enhanced lines. **2008**, 3, 234-42	17
1187	Mistranslation of membrane proteins and two-component system activation trigger antibiotic-mediated cell death. **2008**, 135, 679-90	388
1186	Floret-specific differences in gene expression and support for the hypothesis that tapetal degeneration of Zea mays L. occurs via programmed cell death. **2008**, 35, 603-16	10
1185	Detection of quantitative trait loci in Danish Holstein cattle affecting clinical mastitis, somatic cell score, udder conformation traits, and assessment of associated effects on milk yield. **2008**, 91, 4028-36	50
1184	Quantitative trait loci affecting calving traits in Danish Holstein cattle. **2008**, 91, 2098-105	34

1183	Reporting and interpretation in genome-wide association studies. **2008**, 37, 641-53		53
1182	Alterations in mucosal immunity identified in the colon of patients with irritable bowel syndrome. **2008**, 6, 194-205		103
1181	Comment. **2008**, 50, 268-271		
1180	Efficient control of population structure in model organism association mapping. **2008**, 178, 1709-23		1244
1179	Estimating True and False Positive Rates in Higher Dimensional Problems and Its Data Mining Applications. **2008**,		3
1178	Pathway analysis of microarray data via regression. **2008**, 15, 269-77		23
1177	A bioinformatics tool for linking gene expression profiling results with public databases of microRNA target predictions. **2008**, 14, 2290-6		121
1176	Deriving Kripke structures from time series segmentation results. **2008**,		3
1175	Linear discriminant analysis-based estimation of the false discovery rate for phosphopeptide identifications. **2008**, 7, 2195-203		34
1174	Classification of gene expression data using PCA-based fault detection and identification. **2008**,		1
1173	Sex-specific perceptual spaces for a vertebrate basal social aggregative behavior. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 929-33	11.5	67
1172	Label-free comparative analysis of proteomics mixtures using chromatographic alignment of high-resolution muLC-MS data. **2008**, 80, 961-71		57
1171	RNA-seq: an assessment of technical reproducibility and comparison with gene expression arrays. **2008**, 18, 1509-17		2051
1170	Nonlinear fitting method for determining local false discovery rates from decoy database searches. **2008**, 7, 3661-7		267
1169	Mitochondrial dysfunction, oxidative stress, and apoptosis revealed by proteomic and transcriptomic analyses of the striata in two mouse models of Parkinson's disease. **2008**, 7, 666-77		79
1168	Distinct microRNA expression profiles in acute myeloid leukemia with common translocations. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 15535-40	11.5	375
1167	Osteoporosis. **2008**, 455, v-vi		5
1166	Correlation of peripheral-blood gene expression with the extent of coronary artery stenosis. **2008**, 1, 31-8		141

1165	Genetic royal cheats in leaf-cutting ant societies. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 5150-3	11.5	81
1164	Properties of average score distributions of SEQUEST: the probability ratio method. **2008**, 7, 1135-45		96
1163	Marked epitope- and allele-specific differences in rates of mutation in human immunodeficiency type 1 (HIV-1) Gag, Pol, and Nef cytotoxic T-lymphocyte epitopes in acute/early HIV-1 infection. **2008**, 82, 9216-27		152
1162	A family of Bayes multiple testing procedures. **2008**, 95, 295-305		
1161	Life span extension by calorie restriction depends on Rim15 and transcription factors downstream of Ras/PKA, Tor, and Sch9. **2008**, 4, e13		335
1160	Biomechanics of the bat limb skeleton: scaling, material properties and mechanics. **2008**, 187, 59-84		70
1159	Prospects for epigenetic epidemiology. **2009**, 169, 389-400		183
1158	Into the post-HapMap era. **2008**, 60, 727-42		16
1157	Genome-wide inference of protein interaction sites: lessons from the yeast high-quality negative protein-protein interaction dataset. **2008**, 36, 2002-11		11
1156	Evolutionary constraint and adaptation in the metabolic network of Drosophila. **2008**, 25, 2537-46		43
1155	Genomewide association analysis followed by a replication study implicates a novel candidate gene for neuroticism. **2008**, 65, 1062-71		109
1154	Post-mating gene expression profiles of female Drosophila melanogaster in response to time and to four male accessory gland proteins. **2008**, 179, 1395-408		100
1153	New biomarkers of Crohn's disease: serum biomarkers and development of diagnostic tools. **2008**, 8, 327-37		9
1152	Tumor immunobiological differences in prostate cancer between African-American and European-American men. **2008**, 68, 927-36		378
1151	Association of genetic variation in genes implicated in the beta-catenin destruction complex with risk of breast cancer. **2008**, 17, 2101-8		60
1150	FunNet: an integrative tool for exploring transcriptional interactions. **2008**, 24, 2636-8		72
1149	ExactFDR: exact computation of false discovery rate estimate in case-control association studies. **2008**, 24, 2407-8		3
1148	Identification of transcriptional regulatory cascades in retinoic acid-induced growth arrest of HepG2 cells. **2008**, 36, 3443-54		15

1147	Stamen abscission zone transcriptome profiling reveals new candidates for abscission control: enhanced retention of floral organs in transgenic plants overexpressing Arabidopsis ZINC FINGER PROTEIN2. **2008**, 146, 1305-21		152
1146	Tumor cell gene expression changes following short-term in vivo exposure to single agent chemotherapeutics are related to survival in multiple myeloma. **2008**, 14, 4821-9		37
1145	Dialysis-related systemic microinflammation is associated with specific genomic patterns. **2008**, 23, 1673-81		25
1144	Gene number expansion and contraction in vertebrate genomes with respect to invertebrate genomes. **2008**, 18, 221-32		29
1143	The oncogene c-Myc coordinates regulation of metabolic networks to enable rapid cell cycle entry. **2008**, 7, 1054-66		99
1142	Universal false discovery rate estimation methodology for genome-wide association studies. **2008**, 65, 183-94		13
1141	"Contrasting patterns of selection at Pinus pinaster Ait. Drought stress candidate genes as revealed by genetic differentiation analyses". **2008**, 25, 417-37		165
1140	A Statistical Procedure for Detecting Highly Correlated Genes with a Pre-Specified Candidate Gene in Microarray Analysis. **2008**, 37, 2991-3007		2
1139	A transcript profiling approach reveals an epicatechin-specific glucosyltransferase expressed in the seed coat of Medicago truncatula. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 14210-5	11.5	143
1138	Global analysis of Arabidopsis gene expression uncovers a complex array of changes impacting pathogen response and cell cycle during geminivirus infection. **2008**, 148, 436-54		357
1137	Systemic and intracellular responses to photooxidative stress in Arabidopsis. **2007**, 19, 4091-110		190
1136	Reverse Engineering Gene Regulatory Networks with Various Machine Learning Methods. 101-142		5
1135	MicroRNA 29c is down-regulated in nasopharyngeal carcinomas, up-regulating mRNAs encoding extracellular matrix proteins. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 5874-8	11.5	351
1134	Nucleotide polymorphism and phenotypic associations within and around the phytochrome B2 Locus in European aspen (Populus tremula, Salicaceae). **2008**, 178, 2217-26		141
1133	Statistical methods for examining genetic influences of resistance to anti-epileptic drugs. **2008**, 1, 137-44		1
1132	Tools for interpreting large-scale protein profiling in microbiology. **2008**, 87, 1004-15		21
1131	Oncogenic Ras and transforming growth factor-beta synergistically regulate AU-rich element-containing mRNAs during epithelial to mesenchymal transition. **2008**, 6, 1124-36		35
1130	CmeR functions as a pleiotropic regulator and is required for optimal colonization of Campylobacter jejuni in vivo. **2008**, 190, 1879-90		54

1129	Role of the DksA-like protein in the pathogenesis and diverse metabolic activity of Campylobacter jejuni. **2008**, 190, 4512-20		24
1128	The Importance of Gene-Environment Interaction: Implications for Social Scientists. **2008**, 37, 164-200		12
1127	Global gene expression as a function of the iron status of the bacterial cell: influence of differentially expressed genes in the virulence of the human pathogen Vibrio vulnificus. **2008**, 76, 4019-37		54
1126	A general framework for multiple testing dependence. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 18718-23	11.5	225
1125	Seeder: discriminative seeding DNA motif discovery. **2008**, 24, 2303-7		36
1124	Multilocus patterns of nucleotide polymorphism and the demographic history of Populus tremula. **2008**, 180, 329-40		146
1123	HLA class I-driven evolution of human immunodeficiency virus type 1 subtype c proteome: immune escape and viral load. **2008**, 82, 6434-46		115
1122	Pleiotropic effects of Drosophila neuralized on complex behaviors and brain structure. **2008**, 179, 1327-36		25
1121	Inherited variation in the androgen pathway is associated with the efficacy of androgen-deprivation therapy in men with prostate cancer. **2008**, 26, 842-7		86
1120	Whole-genome analysis reveals molecular innovations and evolutionary transitions in chromalveolate species. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 3427-32	11.5	49
1119	Land ahead: using genome scans to identify molecular markers of adaptive relevance. **2008**, 1, 273-283		67
1118	High parallelism, portability, and broad accessibility. **2008**, 4, 1-39		4
1117	Identification of melatonin-regulated genes in the ovine pituitary pars tuberalis, a target site for seasonal hormone control. **2008**, 149, 5527-39		57
1116	Systematic assessment of the human osteoblast transcriptome in resting and induced primary cells. **2008**, 33, 301-11		27
1115	Genome-wide co-expression based prediction of differential expressions. **2008**, 24, 666-73		11
1114	Can systems biology understand pathway activation? Gene expression signatures as surrogate markers for understanding the complexity of pathway activation. **2008**, 9, 349-60		28
1113	. **2008**, 20, 736-751		22
1112	Effects of cis and trans genetic ancestry on gene expression in African Americans. **2008**, 4, e1000294		75

1111	In vivo response to methotrexate forecasts outcome of acute lymphoblastic leukemia and has a distinct gene expression profile. **2008**, 5, e83	60
1110	Parasite burden and CD36-mediated sequestration are determinants of acute lung injury in an experimental malaria model. **2008**, 4, e1000068	69
1109	Effects and interactions in an environmentally relevant mixture of pharmaceuticals. **2008**, 102, 129-37	167
1108	High-resolution mapping of gene expression using association in an outbred mouse stock. **2008**, 4, e1000149	48
1107	Phylogenetic dependency networks: inferring patterns of CTL escape and codon covariation in HIV-1 Gag. **2008**, 4, e1000225	98
1106	Network discovery pipeline elucidates conserved time-of-day-specific cis-regulatory modules. **2008**, 4, e14	389
1105	Non-parametric estimation of posterior error probabilities associated with peptides identified by tandem mass spectrometry. **2008**, 24, i42-8	84
1104	Enriched random forests. **2008**, 24, 2010-4	117
1103	Improved methods for detecting selection by mutation analysis of Ig V region sequences. **2008**, 20, 683-94	63
1102	Statistical Methods for Mapping Multiple QTL. **2008**, 2008, 286561	14
1101	Regulatory hotspots in the malaria parasite genome dictate transcriptional variation. **2008**, 6, e238	58
1100	Nonadaptive explanations for signatures of partial selective sweeps in Drosophila. **2008**, 25, 1025-42	21
1099	Practical issues in imputation-based association mapping. **2008**, 4, e1000279	144
1098	Integrative analysis reveals the direct and indirect interactions between DNA copy number aberrations and gene expression changes. **2008**, 24, 889-96	62
1097	Proteomic analysis of the winter-protected phenotype of hibernating ground squirrel intestine. **2008**, 295, R316-28	42
1096	Genetic analysis of human traits in vitro: drug response and gene expression in lymphoblastoid cell lines. **2008**, 4, e1000287	182
1095	A note on the false discovery rate and inconsistent comparisons between experiments. **2008**, 24, 1225-8	29
1094	Modeling peptide fragmentation with dynamic Bayesian networks for peptide identification. **2008**, 24, i348-56	46

1093	The recombinational anatomy of a mouse chromosome. **2008**, 4, e1000119		108
1092	Calibrating the performance of SNP arrays for whole-genome association studies. **2008**, 4, e1000109		31
1091	Evaluating statistical methods using plasmode data sets in the age of massive public databases: an illustration using false discovery rates. **2008**, 4, e1000098		34
1090	Accurate discovery of expression quantitative trait loci under confounding from spurious and genuine regulatory hotspots. **2008**, 180, 1909-25		107
1089	Challenges in translating plasma proteomics from bench to bedside: update from the NHLBI Clinical Proteomics Programs. **2008**, 295, L16-22		65
1088	Inflammatory gene haplotype-interaction networks involved in coronary collateral formation. **2008**, 66, 252-64		14
1087	Gene-environment interaction in yeast gene expression. **2008**, 6, e83		278
1086	A genome-wide gene expression signature of environmental geography in leukocytes of Moroccan Amazighs. **2008**, 4, e1000052		83
1085	Variation in MAPT is associated with cerebrospinal fluid tau levels in the presence of amyloid-beta deposition. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 8050-4	11.5	74
1084	Metabolic changes associated with adaptive diversification in Escherichia coli. **2008**, 178, 1049-60		32
1083	Considering dependence among genes and markers for false discovery control in eQTL mapping. **2008**, 24, 2015-22		10
1082	An efficient method to identify differentially expressed genes in microarray experiments. **2008**, 24, 1583-9		13
1081	Efficient p-value estimation in massively parallel testing problems. **2008**, 9, 601-12		2
1080	GEPAS, a web-based tool for microarray data analysis and interpretation. **2008**, 36, W308-14		58
1079	Genomic outlier profile analysis: mixture models, null hypotheses, and nonparametric estimation. **2009**, 10, 60-9		24
1078	Innovative Leukemia and Lymphoma Therapy. **2008**,		
1077	The Cladosporium fulvum virulence protein Avr2 inhibits host proteases required for basal defense. **2008**, 20, 1948-63		195
1076	Adaptive choice of the number of bootstrap samples in large scale multiple testing. **2008**, 7, Article13		17

1075	Experimental estimation of mutation rates in a wheat population with a gene genealogy approach. **2008**, 179, 2195-211		23
1074	Integrated analysis of homozygous deletions, focal amplifications, and sequence alterations in breast and colorectal cancers. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 16224-9	11.5	230
1073	Applying gene expression, proteomics and single-nucleotide polymorphism analysis for complex trait gene identification. **2008**, 178, 1795-805		38
1072	The grainyhead like 2 gene (GRHL2), alias TFCP2L3, is associated with age-related hearing impairment. **2008**, 17, 159-69		104
1071	Oocyte regulation of metabolic cooperativity between mouse cumulus cells and oocytes: BMP15 and GDF9 control cholesterol biosynthesis in cumulus cells. **2008**, 135, 111-21		262
1070	Multiple superoxide dismutase 1/splicing factor serine alanine 15 variants are associated with the development and progression of diabetic nephropathy: the Diabetes Control and Complications Trial/Epidemiology of Diabetes Interventions and Complications Genetics study. **2008**, 57, 218-28		83
1069	Genetic characterization of human immunodeficiency virus type 1 in elite controllers: lack of gross genetic defects or common amino acid changes. **2008**, 82, 8422-30		107
1068	Robustified MANOVA with applications in detecting differentially expressed genes from oligonucleotide arrays. **2008**, 24, 1056-62		26
1067	Use of shotgun proteomics for the identification, confirmation, and correction of C. elegans gene annotations. **2008**, 18, 1660-9		69
1066	Toll-like receptor 1 polymorphisms affect innate immune responses and outcomes in sepsis. **2008**, 178, 710-20		226
1065	Improving 2D-DIGE protein expression analysis by two-stage linear mixed models: assessing experimental effects in a melanoma cell study. **2008**, 24, 2706-12		2
1064	Genome-wide association scans identified CTNNBL1 as a novel gene for obesity. **2008**, 17, 1803-13		152
1063	Generalized method for probability-based peptide and protein identification from tandem mass spectrometry data and sequence database searching. **2008**, 7, 1748-54		39
1062	An epistatic genetic basis for physical activity traits in mice. **2008**, 99, 639-46		41
1061	Whole-genome transcriptional profiling of Bradyrhizobium japonicum during chemoautotrophic growth. **2008**, 190, 6697-705		35
1060	Stress-activated genomic expression changes serve a preparative role for impending stress in yeast. **2008**, 19, 4580-7		214
1059	The genetic architecture of complex traits in teosinte (Zea mays ssp. parviglumis): new evidence from association mapping. **2008**, 180, 1221-32		66
1058	Specific genes expressed in association with progesterone receptors in meningioma. **2008**, 68, 314-22		55

1057	Optimization of experimental design parameters for high-throughput chromatin immunoprecipitation studies. **2008**, 36, e144		26
1056	Gcn4 is required for the response to peroxide stress in the yeast Saccharomyces cerevisiae. **2008**, 19, 2995-3007		76
1055	Microbial genotype-phenotype mapping by class association rule mining. **2008**, 24, 1523-9		31
1054	Polymorphism in the IL18 gene and epithelial ovarian cancer in non-Hispanic white women. **2008**, 17, 3567-72		14
1053	Genomic analysis of adaptive differentiation in Drosophila melanogaster. **2008**, 179, 455-73		124
1052	Factorial microarray analysis of zebrafish retinal development. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 12909-14	11.5	39
1051	A high-density association screen of 155 ion transport genes for involvement with common migraine. **2008**, 17, 3318-31		73
1050	Salicylic acid and systemic acquired resistance play a role in attenuating crown gall disease caused by Agrobacterium tumefaciens. **2008**, 146, 703-15		140
1049	Overexpression of innate immune response genes in a model of recessive polycystic kidney disease. **2008**, 73, 63-76		72
1048	Unequal group variances in microarray data analyses. **2008**, 24, 1168-74		17
1047	On correcting the overestimation of the permutation-based false discovery rate estimator. **2008**, 24, 1655-61		7
1046	High quality catalog of proteotypic peptides from human heart. **2008**, 7, 5055-61		42
1045	Pervasive positive selection on duplicated and nonduplicated vertebrate protein coding genes. **2008**, 18, 1393-402		64
1044	Importance of lineage-specific expansion of plant tandem duplicates in the adaptive response to environmental stimuli. **2008**, 148, 993-1003		299
1043	Characterization of dietary protein-dependent amino acid metabolism by linking free amino acids with transcriptional profiles through analysis of correlation. **2008**, 34, 315-26		28
1042	Gene-environment interactions reveal a homeostatic role for cholesterol metabolism during dietary folate perturbation in mice. **2008**, 35, 182-90		12
1041	Meta-analysis and profiling of cardiac expression modules. **2008**, 35, 305-15		11
1040	MADS: a new and improved method for analysis of differential alternative splicing by exon-tiling microarrays. **2008**, 14, 1470-9		78

1039	Quality Assessment for Short Oligonucleotide Microarray Data. **2008**, 50, 241-264	84
1038	Statistical similarities between transcriptomics and quantitative shotgun proteomics data. **2008**, 7, 631-44	134
1037	Human leukocyte antigen-specific polymorphisms in HIV-1 Gag and their association with viral load in chronic untreated infection. **2008**, 22, 1277-86	60
1036	The genetic variation of the tenomodulin gene (TNMD) is associated with serum levels of systemic immune mediators--the Finnish Diabetes Prevention Study. **2008**, 10, 536-44	11
1035	Genotype by Environment Interaction - Basics and Beyond. **2008**, 155-170	2
1034	Gene-based bin analysis of genome-wide association studies. **2008**, 2 Suppl 4, S6	2
1033	Transcriptome and proteome analyses of drug interactions with natural products. **2008**, 9, 1038-48	16
1032	Lack of association between the amiloride-sensitive cation channel 2 (ACCN2) gene and anxiety spectrum disorders. **2008**, 18, 73-9	13
1031	Normalization and gene p-value estimation: issues in microarray data processing. **2008**, 2, 291-305	13
1030	A new test statistic based on shrunken sample variance for identifying differentially expressed genes in small microarray experiments. **2008**, 2, 145-56	4
1029	Model-based gene selection shows engrailed 1 is associated with antipsychotic response. **2008**, 18, 751-9	11
1028	Correlation of Soil Nutrient Characteristics and Reed Canarygrass (Phalaris Arundinacea: Poaceae) Abundance in Northern Illinois (USA). **2008**, 160, 430-437	11
1027	Molecular population genetics of PCSK9: a signature of recent positive selection. **2008**, 18, 169-79	32
1026	. **2008**,	19
1025	Comprehensive analysis of the candidate genes CCL2, CCR2, and TLR4 in age-related macular degeneration. **2008**, 49, 364-71	50
1024	Biological and functional analysis of statistically significant pathways deregulated in colon cancer by using gene expression profiles. **2008**, 4, 368-78	4
1023	Statistical Measures, Hypotheses, and Tests in Applied Research. **2008**, 37, 74-82	25
1022	Estimating the Proportion of True Null Hypotheses for Multiple Comparisons. **2008**, 6, 117693510800600	15

1021 An integrative analysis of microRNA and mRNA expression--a case study. **2008**, 6, 369-79 19

1020 Macrophage and T-cell gene expression in a model of early infection with the protozoan Leishmania chagasi. **2008**, 2, e252 36

1019 Multiple oncogenic pathway signatures show coordinate expression patterns in human prostate tumors. **2008**, 3, e1816 44

1018 Stochastic resonance reveals "pilot light" expression in mammalian genes. **2008**, 3, e1842 10

1017 Concordant gene expression in leukemia cells and normal leukocytes is associated with germline cis-SNPs. **2008**, 3, e2144 6

1016 Protein expression in the nucleus accumbens of rats exposed to developmental vitamin D deficiency. **2008**, 3, e2383 28

1015 Variations in the ghrelin receptor gene associate with obesity and glucose metabolism in individuals with impaired glucose tolerance. **2008**, 3, e2941 26

1014 A resource for transcriptomic analysis in the mouse brain. **2008**, 3, e3012 11

1013 Genome-wide analysis of natural selection on human cis-elements. **2008**, 3, e3137 23

1012 Genomic analysis of differentiation between soil types reveals candidate genes for local adaptation in Arabidopsis lyrata. **2008**, 3, e3183 39

1011 Genome-wide co-expression analysis in multiple tissues. **2008**, 3, e4033 19

1010 Comparative developmental expression profiling of two C. elegans isolates. **2008**, 3, e4055 27

1009 Integrative genomic data mining for discovery of potential blood-borne biomarkers for early diagnosis of cancer. **2008**, 3, e3661 31

1008 Predicting who will benefit from an Expert Patients Programme self-management course. **2008**, 58, 198-203 45

1007 Statistical analysis of efficient unbalanced factorial designs for two-color microarray experiments. **2008**, 2008, 584360 6

1006 Front Matter. I-XX

1005 . **2009**, 59

1004 References. 231-243

1003	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
1002	Laser capture microdissection and genetic analysis of carbon-labeled Kupffer cells. **2009**, 15, 1708-18	11
1001	Neglect of Multiplicity When Testing Families of Related Hypotheses*. **2009**,	4
1000	Global screening of human cord blood proteomes for biomarkers of toxic exposure and effect. **2009**, 117, 832-8	25
999	Looking at Individual Subjects in Research on Judgment and Decision Making (or Anything). **2009**,	1
998	Structures and Assumptions: Strategies to Harness Gene Gene and Gene Environment Interactions in GWAS. **2009**, 24, 472-488	22
997	Gene Set Enrichment Analyses Revealed Differences in Gene Expression Patterns between Males and Females. **2009**, 9, 55-63	20
996	Tor1/Sch9-regulated carbon source substitution is as effective as calorie restriction in life span extension. **2009**, 5, e1000467	158
995	Clustering of codons with rare cognate tRNAs in human genes suggests an extra level of expression regulation. **2009**, 5, e1000548	47
994	Maize inbreds exhibit high levels of copy number variation (CNV) and presence/absence variation (PAV) in genome content. **2009**, 5, e1000734	389
993	Uncovering the genetic landscape for multiple sleep-wake traits. **2009**, 4, e5161	35
992	Identification of novel genes and pathways regulating SREBP transcriptional activity. **2009**, 4, e5197	26
991	Early cell fate decisions of human embryonic stem cells and mouse epiblast stem cells are controlled by the same signalling pathways. **2009**, 4, e6082	196
990	Human disease-drug network based on genomic expression profiles. **2009**, 4, e6536	219
989	Something old, something new, something borrowed; how the thermoacidophilic archaeon Sulfolobus solfataricus responds to oxidative stress. **2009**, 4, e6964	61
988	Meta-analysis of kindling-induced gene expression changes in the rat hippocampus. **2009**, 3, 53	8
987	Epidemiologic and Population Genetic Studies. **2009**, 289-299	
986	Discovering genetic polymorphism associated with gene expression levels across the whole genome. **2009**, 2009, 5466-9	

985	Application of Biostatistics and Bioinformatics Tools to Identify Putative Transcription Factor-Gene Regulatory Network of Ankylosing Spondylitis and Sarcoidosis. **2009**, 38, 3326-3338		4
984	GRISSOM web based grid portal: Exploiting the power of grid infrastructure for the interpretation and storage of DNA microarray experiments. **2009**,		1
983	Arabidopsis bile acid:sodium symporter family protein 5 is involved in methionine-derived glucosinolate biosynthesis. **2009**, 50, 1579-86		75
982	Fish-oil supplementation induces antiinflammatory gene expression profiles in human blood mononuclear cells. **2009**, 90, 415-24		240
981	Identifying Gene Signatures from Cancer Progression Data Using Ordinal Analysis. **2009**,		1
980	Estimation of gene induction enables a relevance-based ranking of gene sets. **2009**, 16, 959-67		4
979	Network inference with confidence from multivariate time series. **2009**, 79, 061916		90
978	Characterization of the Escherichia coli O157:H7 Sakai GadE regulon. **2009**, 191, 1868-77		45
977	Normalization and statistical analysis of quantitative proteomics data generated by metabolic labeling. **2009**, 8, 2227-42		99
976	Statistical model to analyze quantitative proteomics data obtained by 18O/16O labeling and linear ion trap mass spectrometry: application to the study of vascular endothelial growth factor-induced angiogenesis in endothelial cells. **2009**, 8, 1130-49		54
975	Genomic consequences of background effects on scalloped mutant expressivity in the wing of Drosophila melanogaster. **2009**, 181, 1065-76		46
974	Genetic variations in PI3K-AKT-mTOR pathway and bladder cancer risk. **2009**, 30, 2047-52		70
973	Embryonic diapause highlighted by differential expression of mRNAs for ecdysteroidogenesis, transcription and lipid sparing in the cricket Allonemobius socius. **2009**, 212, 2075-84		53
972	Large-scale detection of ubiquitination substrates using cell extracts and protein microarrays. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 2543-8	11.5	77
971	Population-based genomewide genetic analysis of common clinical chemistry analytes. **2009**, 55, 39-51		9
970	Genome-wide allele- and strand-specific expression profiling. **2009**, 5, 274		28
969	Identification of IRAK1 as a risk gene with critical role in the pathogenesis of systemic lupus erythematosus. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 6256-61	11.5	193
968	Normalization of peak intensities in bottom-up MS-based proteomics using singular value decomposition. **2009**, 25, 2573-80		71

967	Epistatic interactions between Opaque2 transcriptional activator and its target gene CyPPDK1 control kernel trait variation in maize. **2009**, 150, 506-20	38
966	An 8-week high-fat diet induces obesity and insulin resistance with small changes in the muscle transcriptome of C57BL/6J mice. **2009**, 2, 280-91	28
965	HLA-associated alterations in replication capacity of chimeric NL4-3 viruses carrying gag-protease from elite controllers of human immunodeficiency virus type 1. **2009**, 83, 140-9	103
964	Circulating monocytes in HIV-1-infected viremic subjects exhibit an antiapoptosis gene signature and virus- and host-mediated apoptosis resistance. **2009**, 182, 4459-70	74
963	Stress-dependent Daxx-CHIP interaction suppresses the p53 apoptotic program. **2009**, 284, 20649-59	27
962	Evolutionary history and stress regulation of plant receptor-like kinase/pelle genes. **2009**, 150, 12-26	272
961	A behavioral syndrome linking courtship behavior toward males and females predicts reproductive success from a single mating in the hissing cockroach, Gromphadorhina portentosa. **2009**, 20, 781-788	31
960	Gene expression profiles of thymic neuroendocrine tumors (carcinoids) with ectopic ACTH syndrome reveal novel molecular mechanism. **2009**, 16, 1273-82	12
959	Identification of chromosomal regions associated with cranial cruciate ligament rupture in a population of Newfoundlands. **2009**, 70, 1013-7	22
958	Rapid evolution of immune proteins in social insects. **2009**, 26, 1791-801	56
957	Impact of DNA-binding position variants on yeast gene expression. **2009**, 37, 6991-7001	7
956	Functional analysis of transcription factors in Arabidopsis. **2009**, 50, 1232-48	200
955	Graph theoretical approach to study eQTL: a case study of Plasmodium falciparum. **2009**, 25, i15-20	13
954	Estimating the posterior probability that genome-wide association findings are true or false. **2009**, 25, 1807-13	11
953	Disruption of LANA in rhesus rhadinovirus generates a highly lytic recombinant virus. **2009**, 83, 9786-802	18
952	Maribavir inhibits epstein-barr virus transcription in addition to viral DNA replication. **2009**, 83, 12108-17	31
951	Differential response of gray poplar leaves and roots underpins stress adaptation during hypoxia. **2009**, 149, 461-73	196
950	Interrogating 11 fast-evolving genes for signatures of recent positive selection in worldwide human populations. **2009**, 26, 2285-97	20

949	Local false discovery rate facilitates comparison of different microarray experiments. **2009**, 37, 7483-97	9
948	Genomewide association study of a rapid progression cohort identifies new susceptibility alleles for AIDS (ANRS Genomewide Association Study 03). **2009**, 200, 1194-201	88
947	QVALITY: non-parametric estimation of q-values and posterior error probabilities. **2009**, 25, 964-6	76
946	Multiple testing in genome-wide association studies via hidden Markov models. **2009**, 25, 2802-8	36
945	Sample size calculations for controlling the distribution of false discovery proportion in microarray experiments. **2009**, 10, 694-705	8
944	Long-lived Indy induces reduced mitochondrial reactive oxygen species production and oxidative damage. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 2277-82	115 65
943	Positive selection for elevated gene expression noise in yeast. **2009**, 5, 299	78
942	The first T cell response to transmitted/founder virus contributes to the control of acute viremia in HIV-1 infection. **2009**, 206, 1253-72	500
941	Absence of MxA induction by interferon beta in patients with MS reflects complete loss of bioactivity. **2009**, 73, 372-7	82
940	Genomic strategy for targeting therapy in castration-resistant prostate cancer. **2009**, 27, 2022-9	111
939	Global gene expression analysis of reactive stroma in prostate cancer. **2009**, 15, 3979-89	123
938	Genomic determination of the glucocorticoid response reveals unexpected mechanisms of gene regulation. **2009**, 19, 2163-71	374
937	High-throughput chromatin information enables accurate tissue-specific prediction of transcription factor binding sites. **2009**, 37, 14-25	46
936	A comprehensive neuropsychiatric study of elderly twins: the Older Australian Twins Study. **2009**, 12, 573-82	52
935	Nicotine withdrawal sensitivity, linkage to chr6q26, and association of OPRM1 SNPs in the SMOking in FAMilies (SMOFAM) sample. **2009**, 18, 3399-406	16
934	Identification of actively translated mRNA transcripts in a rat model of early-stage colon carcinogenesis. **2009**, 2, 984-94	15
933	MicroRNA-1 negatively regulates expression of the hypertrophy-associated calmodulin and Mef2a genes. **2009**, 29, 2193-204	320
932	Reciprocal silencing, transcriptional bias and functional divergence of homeologs in polyploid cotton (gossypium). **2009**, 182, 503-17	174

931	Transcriptional regulation of metabolism associated with the increased desiccation resistance of the cactophilic Drosophila mojavensis. **2009**, 182, 1279-88	31
930	A multiple testing approach to high-dimensional association studies with an application to the detection of associations between risk factors of heart disease and genetic polymorphisms. **2009**, 8, Article 7	1
929	Statistical screening method for genetic factors influencing susceptibility to common diseases in a two-stage genome-wide association study. **2009**, 8, Article 46	
928	Transcriptional profiling analysis of host response to Clostridium perfringens infection in broilers. **2009**, 88, 1023-32	20
927	Ranking bias in association studies. **2009**, 67, 267-75	9
926	Comment. **2009**, 104, 1310-1314	
925	Comment. **2009**, 104, 1314-1318	
924	A Factor Model Approach to Multiple Testing Under Dependence. **2009**, 104, 1406-1415	80
923	Common regulatory variation impacts gene expression in a cell type-dependent manner. **2009**, 325, 1246-50	607
922	Brain-specific proteins decline in the cerebrospinal fluid of humans with Huntington disease. **2009**, 8, 451-66	56
921	A network model of a cooperative genetic landscape in brain tumors. **2009**, 302, 261-75	144
920	CNR1 gene is associated with high neuroticism and low agreeableness and interacts with recent negative life events to predict current depressive symptoms. **2009**, 34, 2019-27	130
919	Screening of 336 single-nucleotide polymorphisms in 85 obesity-related genes revealed McKusick-Kaufman syndrome gene variants are associated with metabolic syndrome. **2009**, 54, 230-5	6
918	Evolution of sex-dependent gene expression in three recently diverged species of Drosophila. **2009** , 183, 1175-85	44
917	Exploring the effect of sex on empirical fitness landscapes. **2009**, 174 Suppl 1, S15-30	99
916	Selection, epistasis, and parent-of-origin effects on deleterious mutations across environments in Drosophila melanogaster. **2009**, 174, 863-74	25
915	Comparative genomic analyses of the human fungal pathogens Coccidioides and their relatives. **2009**, 19, 1722-31	229
914	Wfs1 gene deletion causes growth retardation in mice and interferes with the growth hormone pathway. **2009**, 37, 249-59	36

913	Elucidating the role of gonadal hormones in sexually dimorphic gene coexpression networks. **2009**, 150, 1235-49	171
912	Macrophage-secreted factors promote a profibrotic phenotype in human preadipocytes. **2009**, 23, 11-24	200
911	Dissecting early differentially expressed genes in a mixture of differentiating embryonic stem cells. **2009**, 5, e1000607	10
910	Genome-wide association analyses identify SPOCK as a key novel gene underlying age at menarche. **2009**, 5, e1000420	55
909	Harmonics of circadian gene transcription in mammals. **2009**, 5, e1000442	490
908	Rapid and accurate multiple testing correction and power estimation for millions of correlated markers. **2009**, 5, e1000456	132
907	Imprinting of the polycomb group gene MEDEA serves as a ploidy sensor in Arabidopsis. **2009**, 5, e1000663	105
906	Pre-micro RNA signatures delineate stages of endothelial cell transformation in Kaposi sarcoma. **2009**, 5, e1000389	57
905	Association of chromosome 8q variants with prostate cancer risk in Caucasian and Hispanic men. **2009**, 30, 1372-9	35
904	Caenorhabditis elegans genomic response to soil bacteria predicts environment-specific genetic effects on life history traits. **2009**, 5, e1000503	84
903	Adjusting for HLA-DRbeta1 in a genome-wide association analysis of rheumatoid arthritis and related biomarkers. **2009**, 3 Suppl 7, S12	1
902	Molecular population genetics of human CYP3A locus: signatures of positive selection and implications for evolutionary environmental medicine. **2009**, 117, 1541-8	32
901	Statistical methods for detecting differentially abundant features in clinical metagenomic samples. **2009**, 5, e1000352	1041
900	CHD3 proteins and polycomb group proteins antagonistically determine cell identity in Arabidopsis. **2009**, 5, e1000605	124
899	Expression quantitative trait loci are highly sensitive to cellular differentiation state. **2009**, 5, e1000692	74
898	HIV evolution in early infection: selection pressures, patterns of insertion and deletion, and the impact of APOBEC. **2009**, 5, e1000414	146
897	Genome-wide approaches to identify pharmacogenetic contributions to adverse drug reactions. **2009**, 9, 23-33	79
896	FastMap: fast eQTL mapping in homozygous populations. **2009**, 25, 482-9	32

895	PROMISE: a tool to identify genomic features with a specific biologically interesting pattern of associations with multiple endpoint variables. **2009**, 25, 2013-9	14
894	The Drosophila foraging gene mediates adult plasticity and gene-environment interactions in behaviour, metabolites, and gene expression in response to food deprivation. **2009**, 5, e1000609	75
893	Statistical methods for gene set co-expression analysis. **2009**, 25, 2780-6	107
892	Prognostic significance of prostate cancer susceptibility variants on prostate-specific antigen recurrence after radical prostatectomy. **2009**, 18, 3068-74	66
891	Comments on the analysis of unbalanced microarray data. **2009**, 25, 2035-41	47
890	Alu and b1 repeats have been selectively retained in the upstream and intronic regions of genes of specific functional classes. **2009**, 5, e1000610	57
889	Strain-dependent differences in several reproductive traits are not accompanied by early postmating transcriptome changes in female Drosophila melanogaster. **2009**, 181, 1273-80	10
888	A flexible rank-based framework for detecting copy number aberrations from array data. **2009**, 25, 722-8	7
887	A functional haplotype implicated in vulnerability to develop cocaine dependence is associated with reduced PDYN expression in human brain. **2009**, 34, 1185-97	63
886	Feature selection from a facial image for distinction of sasang constitution. **2009**, 6 Suppl 1, 65-71	18
885	Identification of gene-gene interaction using principal components. **2009**, 3 Suppl 7, S78	9
884	LRpath: a logistic regression approach for identifying enriched biological groups in gene expression data. **2009**, 25, 211-7	138
883	Genome-wide association study identifies two novel loci containing FLNB and SBF2 genes underlying stature variation. **2009**, 18, 1661-9	24
882	Cytotoxic effect of recombinant Mycobacterium tuberculosis CFP-10/ESAT-6 protein on the crucial pathways of WI-38 cells. **2009**, 2009, 917084	8
881	Trans-regulation of mouse meiotic recombination hotspots by Rcr1. **2009**, 7, e36	44
880	Using network component analysis to dissect regulatory networks mediated by transcription factors in yeast. **2009**, 5, e1000311	26
879	Multiple organ system defects and transcriptional dysregulation in the Nipbl(+/-) mouse, a model of Cornelia de Lange Syndrome. **2009**, 5, e1000650	183
878	Regulation of Cellular Metabolism and Cytokines by the Medicinal Herb Feverfew in the Human Monocytic THP-1 Cells. **2009**, 6, 91-8	18

877	Double error shrinkage method for identifying protein binding sites observed by tiling arrays with limited replication. **2009**, 25, 2486-91	1
876	Running behavior and its energy cost in mice selectively bred for high voluntary locomotor activity. **2009**, 82, 662-79	63
875	Detection of growth hormone doping by gene expression profiling of peripheral blood. **2009**, 94, 4703-9	26
874	Regulatory effect of common promoter polymorphisms on the expression of the 11beta-hydroxysteroid dehydrogenase type 1 gene. **2009**, 72, 25-32	10
873	The PmrA/PmrB two-component system of Legionella pneumophila is a global regulator required for intracellular replication within macrophages and protozoa. **2009**, 77, 374-86	58
872	Using high-density exon arrays to profile gene expression in closely related species. **2009**, 37, e90	17
871	Disruption of the aortic elastic lamina and medial calcification share genetic determinants in mice. **2009**, 2, 573-82	13
870	Hypothesis-driven candidate gene association studies: practical design and analytical considerations. **2009**, 170, 986-93	68
869	Protective HLA class I alleles that restrict acute-phase CD8+ T-cell responses are associated with viral escape mutations located in highly conserved regions of human immunodeficiency virus type 1. **2009**, 83, 1845-55	99
868	Genetic changes accompanying the evolution of host specialization in Drosophila sechellia. **2009**, 181, 721-36	74
867	Psychrobacter arcticus 273-4 uses resource efficiency and molecular motion adaptations for subzero temperature growth. **2009**, 191, 2340-52	86
866	Transcriptome analyses revealed diverse expression changes in ago1 and hyl1 Arabidopsis mutants. **2009**, 50, 1715-20	18
865	Cheater genotypes in the parthenogenetic ant Pristomyrmex punctatus. **2009**, 276, 567-74	32
864	Adaptive social immunity in leaf-cutting ants. **2009**, 5, 446-8	73
863	Automated brain tumor biopsy prediction using single-labeling cDNA microarrays-based gene expression profiling. **2009**, 18, 206-18	13
862	Molecular predictors of response to a humanized anti-insulin-like growth factor-I receptor monoclonal antibody in breast and colorectal cancer. **2009**, 8, 2110-21	70
861	Novel susceptibility loci for second primary tumors/recurrence in head and neck cancer patients: large-scale evaluation of genetic variants. **2009**, 2, 617-24	52
860	A WD40 repeat protein from Medicago truncatula is necessary for tissue-specific anthocyanin and proanthocyanidin biosynthesis but not for trichome development. **2009**, 151, 1114-29	107

859	Estimating equation-based causality analysis with application to microarray time series data. **2009**, 10, 468-80		3
858	Genetics of brain fiber architecture and intellectual performance. **2009**, 29, 2212-24		357
857	Identification of novel susceptibility loci for Guam neurodegenerative disease: challenges of genome scans in genetic isolates. **2009**, 18, 3725-38		31
856	The principled control of false positives in neuroimaging. **2009**, 4, 417-22		307
855	Selectome: a database of positive selection. **2009**, 37, D404-7		32
854	Impact of clock-associated Arabidopsis pseudo-response regulators in metabolic coordination. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 7251-6	11.5	200
853	Dynamic reprogramming of transcription factors to and from the subtelomere. **2009**, 19, 1014-25		15
852	Single and multigenic analysis of the association between variants in 12 steroid hormone metabolism genes and risk of prostate cancer. **2009**, 18, 1869-80		77
851	Disruption of adenosine-5'-phosphosulfate kinase in Arabidopsis reduces levels of sulfated secondary metabolites. **2009**, 21, 910-27		159
850	Aberrant functional connectivity of dorsolateral prefrontal and cingulate networks in patients with major depression during working memory processing. **2009**, 39, 977-87		116
849	Germline expression influences operon organization in the Caenorhabditis elegans genome. **2009**, 181, 1219-28		32
848	Basal subtype and MAPK/ERK kinase (MEK)-phosphoinositide 3-kinase feedback signaling determine susceptibility of breast cancer cells to MEK inhibition. **2009**, 69, 565-72		304
847	Cardiac muscle ring finger-1 increases susceptibility to heart failure in vivo. **2009**, 105, 80-8		80
846	Identifying temporally differentially expressed genes through functional principal components analysis. **2009**, 10, 667-79		16
845	Filtering for increased power for microarray data analysis. **2009**, 10, 11		169
844	Improved ChIP-chip analysis by a mixture model approach. **2009**, 10, 173		4
843	A Bayesian approach to efficient differential allocation for resampling-based significance testing. **2009**, 10, 198		6
842	A new multitest correction (SGoF) that increases its statistical power when increasing the number of tests. **2009**, 10, 209		122

841	Correlating gene and protein expression data using Correlated Factor Analysis. **2009**, 10, 272	12
840	Gene ARMADA: an integrated multi-analysis platform for microarray data implemented in MATLAB. **2009**, 10, 354	30
839	A close examination of double filtering with fold change and T test in microarray analysis. **2009**, 10, 402	29
838	In silico evaluation of predicted regulatory interactions in Arabidopsis thaliana. **2009**, 10, 435	3
837	A statistical framework for integrating two microarray data sets in differential expression analysis. **2009**, 10 Suppl 1, S23	9
836	Graph ranking for exploratory gene data analysis. **2009**, 10 Suppl 11, S19	12
835	Genome wide evolutionary analyses reveal serotype specific patterns of positive selection in selected Salmonella serotypes. **2009**, 9, 264	54
834	Genome scan to assess the respective role of host-plant and environmental constraints on the adaptation of a widespread insect. **2009**, 9, 288	41
833	Missing call bias in high-throughput genotyping. **2009**, 10, 106	13
832	Comparative expression pathway analysis of human and canine mammary tumors. **2009**, 10, 135	117
831	Mapping QTL affecting resistance to Marek's disease in an F6 advanced intercross population of commercial layer chickens. **2009**, 10, 20	32
830	Activation of p53-regulated pro-apoptotic signaling pathways in PrP-mediated myopathy. **2009**, 10, 201	11
829	Detection of differentially expressed genes between Erhualian and Large White placentas on day 75 and 90 of gestation. **2009**, 10, 337	25
828	Genomic analysis of a sexually-selected character: EST sequencing and microarray analysis of eye-antennal imaginal discs in the stalk-eyed fly Teleopsis dalmanni (Diopsidae). **2009**, 10, 361	18
827	Mitochondrial dysregulation and oxidative stress in patients with chronic kidney disease. **2009**, 10, 388	160
826	A whole genome Bayesian scan for adaptive genetic divergence in West African cattle. **2009**, 10, 550	124
825	Sequence mining and transcript profiling to explore cyst nematode parasitism. **2009**, 10, 58	34
824	Filling gaps in PPAR-alpha signaling through comparative nutrigenomics analysis. **2009**, 10, 596	8

823	Comparative genomic analysis of light-regulated transcripts in the Solanaceae. **2009**, 10, 60	26
822	Deep RNA sequencing of L. monocytogenes reveals overlapping and extensive stationary phase and sigma B-dependent transcriptomes, including multiple highly transcribed noncoding RNAs. **2009**, 10, 641	145
821	A model selection approach to discover age-dependent gene expression patterns using quantile regression models. **2009**, 10 Suppl 3, S16	6
820	Quantitative proteomics of nutrient limitation in the hydrogenotrophic methanogen Methanococcus maripaludis. **2009**, 9, 149	40
819	Subgingival bacterial colonization profiles correlate with gingival tissue gene expression. **2009**, 9, 221	62
818	Proteomics of Porphyromonas gingivalis within a model oral microbial community. **2009**, 9, 98	83
817	Sexual differentiation of the zebra finch song system: potential roles for sex chromosome genes. **2009**, 10, 24	54
816	Medicago truncatula and Glomus intraradices gene expression in cortical cells harboring arbuscules in the arbuscular mycorrhizal symbiosis. **2009**, 9, 10	235
815	Expression-based discovery of candidate ovule development regulators through transcriptional profiling of ovule mutants. **2009**, 9, 29	38
814	Uncovering the Arabidopsis thaliana nectary transcriptome: investigation of differential gene expression in floral nectariferous tissues. **2009**, 9, 92	51
813	Combined use of expression and CGH arrays pinpoints novel candidate genes in Ewing sarcoma family of tumors. **2009**, 9, 17	54
812	Specific gene expression profiles and chromosomal abnormalities are associated with infant disseminated neuroblastoma. **2009**, 9, 44	21
811	A systems analysis of the chemosensitivity of breast cancer cells to the polyamine analogue PG-11047. **2009**, 7, 77	28
810	Global transcriptional response of Saccharomyces cerevisiae to the deletion of SDH3. **2009**, 3, 17	21
809	A system biology approach highlights a hormonal enhancer effect on regulation of genes in a nitrate responsive "biomodule". **2009**, 3, 59	43
808	Synergism of red and blue light in the control of Arabidopsis gene expression and development. **2009**, 19, 1216-20	63
807	Spatial differences in molecular characteristics of the pontine parabrachial nucleus. **2009**, 1296, 24-34	10
806	Association of genetic profiles to Crohn's disease by linear combinations of single nucleotide polymorphisms. **2009**, 46, 131-8	3

805	Formulating and testing hypotheses in functional genomics. **2009**, 45, 97-107	20
804	Inflammation and stress-related candidate genes, plasma interleukin-6 levels, and longevity in older adults. **2009**, 44, 350-5	43
803	Association of single nucleotide polymorphisms in a glutamate receptor gene (GRM8) with theta power of event-related oscillations and alcohol dependence. **2009**, 150B, 359-68	57
802	Impaired performance of FDR-based strategies in whole-genome association studies when SNPs are excluded prior to the analysis. **2009**, 33, 45-53	16
801	A note on permutation tests for genetic association analysis of quantitative traits when variances are heterogeneous. **2009**, 33, 710-6	
800	Regional brain activation changes and abnormal functional connectivity of the ventrolateral prefrontal cortex during working memory processing in adults with attention-deficit/hyperactivity disorder. **2009**, 30, 2252-66	112
799	Adaptive control of the false discovery rate in voxel-based morphometry. **2009**, 30, 2304-11	15
798	Divergent adaptation of hepatitis C virus genotypes 1 and 3 to human leukocyte antigen-restricted immune pressure. **2009**, 50, 1017-29	50
797	Searching genetic risk factors for schizophrenia and bipolar disorder: learn from the past and back to the future. **2009**, 30, 1139-52	44
796	Opioid use affects antioxidant activity and purine metabolism: preliminary results. **2009**, 24, 666-75	45
795	Bioinformatics and computational approaches applicable to lipidomics. **2009**, 111, 99-106	19
794	CDKN2A, NF2, and JUN are dysregulated among other genes by miRNAs in malignant mesothelioma -A miRNA microarray analysis. **2009**, 48, 615-23	233
793	Identifying the molecular signature of the interstitial deletion 7q subgroup of uterine leiomyomata using a paired analysis. **2009**, 48, 865-85	26
792	microRNAs in acute myeloid leukemia: expression patterns, correlations with genetic and clinical parameters, and prognostic significance. **2010**, 49, 193-203	14
791	High-density genotyping of STAT4 reveals multiple haplotypic associations with systemic lupus erythematosus in different racial groups. **2009**, 60, 1085-95	73
790	Low-intensity microwave irradiation does not substantially alter gene expression in late larval and adult Caenorhabditis elegans. **2009**, 30, 602-12	12
789	High throughput single cell bioinformatics. **2009**, 25, 1772-9	25
788	Gene expression profiling of ozone-treated Arabidopsis abi1td insertional mutant: protein phosphatase 2C ABI1 modulates biosynthesis ratio of ABA and ethylene. **2009**, 230, 1003-17	35

787	Genome-wide association scan for stature in Chinese: evidence for ethnic specific loci. **2009**, 125, 1-9	37
786	Identification of genomic regions contributing to etoposide-induced cytotoxicity. **2009**, 125, 173-80	47
785	Association of Y chromosome haplogroup I with HIV progression, and HAART outcome. **2009**, 125, 281-94	25
784	Linkage analysis of adult height in a large pedigree from a Dutch genetically isolated population. **2009**, 126, 457-71	14
783	Transcriptome profiling of selectively bred Pacific oyster Crassostrea gigas families that differ in tolerance of heat shock. **2009**, 11, 650-68	79
782	Identifying differentially expressed genes in human acute leukemia and mouse brain microarray datasets utilizing QTModel. **2009**, 9, 59-66	2
781	Porcine muscle sensory attributes associate with major changes in gene networks involving CAPZB, ANKRD1, and CTBP2. **2009**, 9, 455-71	33
780	Linear-mixed effects models for feature selection in high-dimensional NMR spectra. **2009**, 36, 4703-4708	14
779	Enrichment of brain-related genes on the mammalian X chromosome is ancient and predates the divergence of synapsid and sauropsid lineages. **2009**, 17, 811-20	7
778	The genetic architecture of complex behaviors: lessons from Drosophila. **2009**, 136, 295-302	30
777	Linkage disequilibrium based association mapping of fiber quality traits in G. hirsutum L. variety germplasm. **2009**, 136, 401-17	100
776	Multiple interval mapping for gene expression QTL analysis. **2009**, 137, 125-34	16
775	Characterization of the biochemical variability of bovine milk using metabolomics. **2009**, 5, 375-386	74
774	Proteomic Profiling of Cerebrospinal Fluid by 8-Plex iTRAQ Reveals Potential Biomarker Candidates of Alzheimer's Disease. **2009**, 5, 114-124	3
773	Allelic association: linkage disequilibrium structure and gene mapping. **2009**, 41, 83-9	9
772	Medicago truncatula as a Model for Dicot Cell Wall Development. **2009**, 2, 59-76	14
771	Tournament screening cum EBIC for feature selection with high-dimensional feature spaces. **2009**, 52, 1327-1341	15
770	A new era in clinical genetic testing for hypertrophic cardiomyopathy. **2009**, 2, 381-91	21

769	Estimation of the Proportion of Differentially Expressed Genes Using Hellinger Distance. **2009**, 1, 246-267	
768	The null distributions of test statistics in genomewide association studies. **2009**, 1, 214-227	
767	Identifying Differentially Expressed Genes in Time Course Microarray Data. **2009**, 1, 144-159	17
766	Development and assessment of Diversity Arrays Technology for high-throughput DNA analyses in Musa. **2009**, 119, 1093-103	55
765	Additive effects of 19 porcine SNPs on growth rate, meat content and selection index. **2009**, 50, 235-43	3
764	Obesity and genetics regulate microRNAs in islets, liver, and adipose of diabetic mice. **2009**, 20, 476-85	119
763	Global versus local centrality in evolution of yeast protein network. **2009**, 68, 192-6	8
762	Exploring Efficient Linear Mixed Models to Detect Quantitative Trait Locus-by-Environment Interactions.	
761	Cell type-aware analysis of RNA-seq data.	0
760	Estimation procedures for the false discovery rate: a systematic comparison for microarray data. **2006**, 67-79	
759	Signals in DNA. **2005**, 225-262	
758	Gene Selection Strategies in Microarray Expression Data: Applications to Case-Control Studies. **2006**, 679-699	2
757	High-Dimensional Inference and False Discovery. **2008**, 593-631	
756	Considerations When Using Array Technologies for Male Factor Assessment. **2007**, 37-54	
755	Expression Profiling of Prostate Cancer Progression. **2007**, 247-267	
754	Gene Expression Profiling in Leiomyoma in Response to GnRH Therapy and TGF-□**2008**, 67-82	
753	Locally Adaptive Statistical Procedures for the Integrative Analysis on Genomic and Transcriptional Data. **2007**, 682-689	
752	Statistical Assessment of MSigDB Gene Sets in Colon Cancer. **2008**, 206-213	

751	Molecular genetics of addiction vulnerability. **2006**, 3, 295-301	
750	Distributions associated with simultaneous multiple hypothesis testing. **2020**, 7,	
749	Genetic and non-genetic factors affecting the expression of COVID-19 relevant genes in the large airway epithelium.	
748	Parallelized calculation of permutation tests.	
747	Deep Collection of Quantitative Nuclear Division Dynamics Data in RNAi-treated Caenorhabditis elegans Embryos.	1
746	Sex differences in the human brain transcriptome of cases with schizophrenia.	0
745	Managing a Large-Scale Multiomics Project: A Team Science Case Study in Proteogenomics. **2021**, 2194, 187-221	
744	Enrichment of genomic variation in pathways linked to autism.	
743	Cell group analysis reveals changes in upper-layer neurons associated with schizophrenia.	1
742	A configurable model of the synaptic proteome reveals the molecular mechanisms of disease co-morbidity.	1
741	Differentially expressed genes related to oxidoreductase activity and glutathione metabolism underlying the adaptation of from the salt marsh in the Yellow River Delta, China. **2020**, 8, e10024	2
740	An extended catalogue of tandem alternative splice sites in human tissue transcriptomes.	
739	A De Novo Genome Assembly, Gene Annotation, And Expression Atlas For The Monarch Butterfly Danaus plexippus.	1
738	Integrating identification and quantification uncertainty for differential protein abundance analysis with Triqler.	
737	Aryl hydrocarbon receptor and TGF-Inducible early gene mediate a transcriptional axis modulating immune homeostasis in mosquitoes.	
736	Leveraging the Mendelian Disorders of the Epigenetic Machinery to Systematically Map Functional Epigenetic Variation.	
735	Current methods integrating variant functional annotation scores have limited capacity to improve the power of genome-wide association studies.	
734	Heritability of DNA methylation in threespine stickleback (Gasterosteus aculeatus).	

733	Data Analysis for Antibody Arrays. **2021**, 2237, 263-276	
732	Integration of genomics and transcriptomics predicts diabetic retinopathy susceptibility genes. **2020**, 9,	5
731	Changes in the lipidome in type 1 diabetes following low carbohydrate diet: a randomized crossover trial.	
730	A comparison of cDNA, oligonucleotide, and Affymetrix GeneChip gene expression microarray platforms. **2004**, 15, 276-84	79
729	A critical analysis of barriers to the clinical implementation of pharmacogenomics. **2007**, 3, 751-9	45
728	Estimating the proportion of true null hypotheses for multiple comparisons. **2008**, 6, 25-32	12
727	The identification of functional motifs in temporal gene expression analysis. **2007**, 1, 84-96	1
726	Single nucleotide polymorphisms of the tenomodulin gene (TNMD) in age-related macular degeneration. **2009**, 15, 762-70	9
725	Data perturbation independent diagnosis and validation of breast cancer subtypes using clustering and patterns. **2007**, 2, 243-74	9
724	Magellan: a web based system for the integrated analysis of heterogeneous biological data and annotations; application to DNA copy number and expression data in ovarian cancer. **2007**, 2, 10-21	7
723	Challenges in the analysis of mass-throughput data: a technical commentary from the statistical machine learning perspective. **2007**, 2, 133-62	14
722	Estimating the false discovery rate using mixed normal distribution for identifying differentially expressed genes in microarray data analysis. **2008**, 3, 140-8	7
721	Gene set enrichment analyses revealed differences in gene expression patterns between males and females. **2009**, 9, 55-63	13
720	Expression profiles of schizophrenia susceptibility genes during human prefrontal cortical development. **2009**, 34, 450-8	47
719	Application of One Sided t-tests and a Generalized Experiment Wise Error Rate to High-Density Oligonucleotide Microarray Experiments: An Example Using Arabidopsis. **2006**, 4, 323-341	4
718	Immunohistochemistry in diagnostic surgical pathology: contributions of protein life-cycle, use of evidence-based methods and data normalization on interpretation of immunohistochemical stains. **2009**, 3, 169-76	16
717	Gene expression patterns in myelodyplasia underline the role of apoptosis and differentiation in disease initiation and progression. **2008**, 3, 137-49	12
716	An alternative cyclin-D1 splice site is not linked to inflammatory bowel disease-associated neoplasia. **2010**, 25, 27-31	4

715	Comparison between NuGEN's WT-Ovation Pico and one-direct amplification systems. **2010**, 21, 141-7	10
714	Six genes associated with the clinical phenotypes of individuals with deficient and proficient DNA repair. **2008**, 3, 1-13	
713	A Selective Overview of Variable Selection in High Dimensional Feature Space. **2010**, 20, 101-148	265
712	Effect of genome-wide simultaneous hypotheses tests on the discovery rate. **2011**, 2, 163-77	
711	Coanalysis of GWAS with eQTLs reveals disease-tissue associations. **2012**, 2012, 35-41	8
710	A Polygenic Approach to the Study ?of Polygenic Diseases. **2012**, 4, 59-71	17
709	LATENT RANK CHANGE DETECTION FOR ANALYSIS OF SPLICE-JUNCTION MICROARRAYS WITH NONLINEAR EFFECTS. **2011**, 5, 364-380	
708	Proteomic analysis of serum opsonins impacting biodistribution and cellular association of porous silicon microparticles. **2011**, 10, 43-55	8
707	Speeding up Permutation Testing in Neuroimaging. **2013**, 2013, 890-898	3
706	An integrative pipeline for multi-modal discovery of disease relationships. **2015**, 407-18	13
705	R package MVR for Joint Adaptive Mean-Variance Regularization and Variance Stabilization. **2011**, 2011, 3849-3863	5
704	Regularized Variance Estimation and Variance Stabilization of High Dimensional Data. **2010**, 2010, 5295-5309	2
703	PERSONALIZED MEDICINE: FROM GENOTYPES AND MOLECULAR PHENOTYPES TOWARDS COMPUTED THERAPY. **2013**, 18, 171-174	
702	RNA sequencing profiling of the retina in C57BL/6J and DBA/2J mice: Enhancing the retinal microarray data sets from GeneNetwork. **2019**, 25, 345-358	6
701	Metabolic profiles of gastric cancer cell lines with different degrees of differentiation. **2018**, 11, 869-875	5
700	Plasma metabolomic profile in chronic thromboembolic pulmonary hypertension. **2020**, 10, 2045894019890553	7
699	Effect of conjugated estrogens and bazedoxifene on glucose, energy and lipid metabolism in obese postmenopausal women. **2020**, 183, 439-452	3
698	Meta-Analyses of Splicing and Expression Quantitative Trait Loci Identified Susceptibility Genes of Glioma. **2021**, 12, 609657	0

697	Characterization of pathways involved in colorectal cancer using real-time RT-PCR gene expression data. **2021**, 14, 123-131	2
696	Examining brain white matter after pediatric mild traumatic brain injury using neurite orientation dispersion and density imaging: An A-CAP study.. **2021**, 32, 102887	0
695	Global molecular alterations involving recurrence or progression of pediatric brain tumors. **2021**, 24, 22-33	1
694	Genome-Wide Association Studies. **2021**, 205-227	1
693	The differentiation state of the Schwann cell progenitor drives phenotypic variation between two contagious cancers. **2021**, 17, e1010033	1
692	Genomic regions associated with resistance to Fusarium wilt in castor identified through linkage and association mapping approaches. **2021**,	2
691	Metabolomic profiling reveals a differential role for hippocampal glutathione reductase in infantile memory formation. **2021**, 10,	
690	A novel method to identify cell-type specific regulatory variants and their role in cancer risk.	0
689	Transcriptome and microRNA Sequencing Identified miRNAs and Target Genes in Different Developmental Stages of the Vascular Cambium in Hooibrenk. **2021**, 12, 751771	1
688	Chromatin-state barriers enforce an irreversible mammalian cell fate decision. **2021**, 37, 109967	4
687	Oxidized Phospholipids Cause Changes in Jejunum Mucus that Induce Dysbiosis and Systemic Inflammation. **2021**, 100153	2
686	GnRH neurons recruit astrocytes in infancy to facilitate network integration and sexual maturation. **2021**, 24, 1660-1672	7
685	Discriminative feature of cells characterizes cell populations of interest by a small subset of genes. **2021**, 17, e1009579	0
684	Impact of fetal expression quantitative trait loci on transcriptome-wide association study of childhood leukemia. **2021**,	
683	The genetic architecture of DNA replication timing in human pluripotent stem cells. **2021**, 12, 6746	4
682	Duodenal Microbiome and Serum Metabolites Predict Hepatocellular Carcinoma in a Multicenter Cohort of Patients with Cirrhosis. **2021**, 1	0
681	Posttranscriptional Regulation of the Human LDL Receptor by the U2-Spliceosome. **2021**,	2
680	Multiple comparison procedures for discrete uniform and homogeneous tests.	

679	Genetic ancestry effects on the response to viral infection are pervasive but cell type specific. **2021**, 374, 1127-1133	5
678	Rearrangement-mediated cis-regulatory alterations in advanced patient tumors reveal interactions with therapy. **2021**, 37, 110023	0
677	Patterns of Maternal Neutrophil Gene Expression at 30 Weeks of Gestation, but Not DNA Methylation, Distinguish Mild from Severe Preeclampsia. **2021**, 22,	0
676	Accelerating wheat breeding for end-use quality through association mapping and multivariate genomic prediction. **2021**, 14, e20164	1
675	Unravelling the distinctive growth mechanism of proso millet (Panicum miliaceum L.) under salt stress: From root-to-leaf adaptations to molecular response. **2022**, 14, 192	0
674	Genomic Uniqueness of Local Sheep Breeds From Morocco.. **2021**, 12, 723599	0
673	Metabolomic Profiles Associated With Incident Ischemic Stroke. **2021**,	1
672	Whole-brain propagating patterns in human resting-state brain activities. **2021**, 245, 118711	1
671	Adiponectin and Its Effects on Acute Leukemia Cells: An Experimental and Bioinformatics Approach.. **2021**, 1338, 117-127	
670	Development of Resistance Cultivars Techniques. **2021**, 651-771	
669	Techniques for Molecular Mechanism of Host Resistance. **2021**, 677-762	
668	Genome-wide association study reveals white lupin candidate gene involved in anthracnose resistance.. **2022**, 1	0
667	Subcutaneous adipose tissue splice quantitative trait loci reveal differences in isoform usage associated with cardiometabolic traits.. **2022**, 109, 66-80	0
666	MethylScore, a pipeline for accurate and context-aware identification of differentially methylated regions from population-scale plant WGBS data.	0
665	Effect of conjugated estrogens and bazedoxifene on glucose, energy and lipid metabolism in obese postmenopausal women. **2020**, 183, 439-452	3
664	Application of Multiple Test Techniques in Big Data Analysis. **2021**, 10, 3532-3538	
663	Spruce Population Genomics. **2021**, 1	
662	Transition towards Solar-Powered built environment: spatial distributions and impacting factors of Australian solar installations. **2021**, 1196, 012024	

661	Immune disease risk variants regulate gene expression dynamics during CD4+ T cell activation.	0
660	Non-additive QTL mapping of lactation traits in 124,000 cattle reveals novel recessive loci.. **2022**, 54, 5	0
659	Identification of replication fork-associated proteins in Drosophila embryos and cultured cells using iPOND coupled to quantitative mass spectrometry.	
658	Analysis of plasma proteins using 2D gels and novel fluorescent probes: in search of blood based biomarkers for Alzheimer's disease.. **2022**, 20, 2	1
657	SILAC Phosphoproteomics Reveals Unique Signaling Circuits in CAR-T Cells and the Inhibition of B Cell-Activating Phosphorylation in Target Cells.. **2022**,	1
656	The impact of stimulus format on task inhibition during task switching.. **2022**, 1	
655	Multi-ancestry eQTL meta-analysis of human brain identifies candidate causal variants for brain-related traits.. **2022**,	1
654	Evaluation and Genetic Analysis of Parthenocarpic Germplasms in Cucumber.. **2022**, 13,	3
653	Comparing genome scans among species of the stickleback order reveals three different patterns of genetic diversity.. **2022**, 12, e8502	
652	Epigenetics of single-site and multi-site atherosclerosis in African Americans from the Genetic Epidemiology Network of Arteriopathy (GENOA).. **2022**, 14, 10	0
651	Dynamic human liver proteome atlas reveals functional insights into disease pathways.	
650	Phenotypic and Transcriptomic Analyses Reveal the Cell Membrane Damage of Induced by Cinnamic Acid.. **2021**, 12, 796754	0
649	Healthy lifestyle, metabolomics and incident type 2 diabetes in a population-based cohort from Spain.. **2022**, 19, 8	1
648	Specific Turbulence- and Chaoborus-Induced Morphotypes Affect the Streamlining Properties of Daphnia cucullata. **2022**, 9,	0
647	Clenbuterol exerts antidiabetic activity through metabolic reprogramming of skeletal muscle cells.. **2022**, 13, 22	1
646	Non-Targeted Dried Blood Spot-Based Metabolomics Analysis Showed Rice Bran Supplementation Effects Multiple Metabolic Pathways during Infant Weaning and Growth in Mali.. **2022**, 14,	0
645	Differences in peripheral immune system gene expression in frontotemporal degeneration.. **2022**, 101, e28645	1
644	Trans-omic Analysis of Insulin Action Reveals a Sub-Network Required for Cell Growth Through Co-Regulated Gene Expression of Anabolic Processes.	

643	Profiling Secreted miRNA Biomarkers of Chemical-Induced Neurodegeneration in Human iPSC Derived Neurons.. **2022**,	
642	Integrated liver and plasma proteomics in obese mice reveals complex metabolic regulation.. **2022**, 100207	1
641	Regional heritability mapping and genome-wide association identify loci for rice traits.	
640	Pan-Cancer DNA Methylation Analysis and Tumor Origin Identification of Carcinoma of Unknown Primary Site Based on Multi-Omics.. **2021**, 12, 798748	0
639	Genetic regulation of human aortic smooth muscle cell gene expression and splicing predict causal coronary artery disease genes.	0
638	Significant genes in response to low temperature in Penaeus chinensis screened from multiple groups of transcriptome comparison. **2022**, 103198	1
637	The Genomic Consistency of the Loss of Anadromy in an Arctic Fish ().. **2022**, 199, 617-635	0
636	Range-wide genomic scans and tests for selection identify non-neutral spatial patterns of genetic variation in a non-model amphibian species (Pelobates cultripes). **2022**, 23, 387	0
635	Mitochondrial-nuclear epistasis underlying phenotypic variation in breast cancer pathology.. **2022**, 12, 1393	0
634	The impact of the COVID-19 lockdown on human psychology and physical activity; a space analogue research perspective. **2022**, 21, 32-45	1
633	Genetic Regulation of Circular RNA Expression in Human Aortic Smooth Muscle Cells and Vascular Traits.	
632	Pea Grain Protein Content Across Italian Environments: Genetic Relationship With Grain Yield, and Opportunities for Genome-Enabled Selection for Protein Yield.. **2021**, 12, 718713	0
631	Evolution under juvenile malnutrition impacts adult metabolism and fitness.	
630	Massively parallel phenotyping of coding variants in cancer with Perturb-seq.. **2022**,	6
629	Tissue-specific multi-omics analysis of atrial fibrillation.. **2022**, 13, 441	1
628	Missense variants causing Wiedemann-Steiner syndrome preferentially occur in the KMT2A-CXXC domain and are accurately classified using AlphaFold2.	
627	IDEAS: individual level differential expression analysis for single-cell RNA-seq data.. **2022**, 23, 33	2
626	Quantitative metaproteomics and activity-based protein profiling of patient fecal microbiome identifies host and microbial serine-type endopeptidase activity associated with ulcerative colitis.. **2022**, 100197	4

625	Single-cell sequencing reveals lineage-specific dynamic genetic regulation of gene expression during human cardiomyocyte differentiation.. **2022**, 18, e1009666	4
624	Genomic context sensitivity of insulator function.. **2022**,	0
623	ROSIE: RObust Sparse ensemble for outlIEr detection and gene selection in cancer omics data.. **2022**, 9622802211072456	0
622	Pharmacological Inhibition of CETP (Cholesteryl Ester Transfer Protein) Increases HDL (High-Density Lipoprotein) That Contains ApoC3 and Other HDL Subspecies Associated With Higher Risk of Coronary Heart Disease.. **2021**, ATVBAHA121317181	0
621	Metabolic, cellular and defense responses to single and co-exposure to carbamazepine and methylmercury in Dreissena polymorpha.. **2022**, 300, 118933	
620	Quantitative proteomic analysis of serum-purified exosomes identifies putative pre-eclampsia-associated biomarkers.. **2022**, 19, 5	1
619	Comparison between short-term stress and long-term adaptive responses reveal common paths to molecular adaptation.. **2022**, 25, 103899	
618	Selection signatures for heat tolerance in Brazilian horse breeds.. **2022**, 297, 449	0
617	The Biology of Veganism: Plasma Metabolomics Analysis Reveals Distinct Profiles of Vegans and Non-Vegetarians in the Adventist Health Study-2 Cohort.. **2022**, 14,	1
616	Multifaceted Analyses of Isolated Mitochondria Establish the Anticancer Drug 2-Hydroxyoleic Acid as an Inhibitor of Substrate Oxidation and an Activator of Complex IV-Dependent State 3 Respiration.. **2022**, 11,	0
615	Hypoxia stress affects the physiological responses, apoptosis and innate immunity of Kuruma shrimp, Marsupenaeus japonicus.. **2022**,	0
614	Hsp40 Affinity to Identify Proteins Destabilized by Cellular Toxicant Exposure. **2021**,	0
613	Megastudies improve the impact of applied behavioural science. **2021**,	8
612	Rare coding variation illuminates the allelic architecture, risk genes, cellular expression patterns, and phenotypic context of autism.	4
611	A validated analysis pipeline for mass spectrometry-based vitreous proteomics: new insights into proliferative diabetic retinopathy. **2021**, 18, 28	2
610	Lipids and Trehalose Actively Cooperate in Heat Stress Management of .. **2021**, 22,	2
609	Meta-Analyses of Splicing and Expression Quantitative Trait Loci Identified Susceptibility Genes of Glioma. **2021**, 12, 609657	0
608	Regional Disparity of Residential Solar Panel Diffusion in Australia: The Roles of Socio-Economic Factors.	

607	The High-Frequency Factor Zoo.	
606	Identification of Urine Biomarkers to Improve Eligibility for Prostate Biopsy and Detect High-Grade Prostate Cancer.. **2022**, 14,	0
605	A genome-wide scan for signatures of selection in Kurdish horse breed.. **2022**, 103916	0
604	Sustained software development, not number of citations or journal choice, is indicative of accurate bioinformatic software.. **2022**, 23, 56	2
603	Evidence of episodic positive selection in complex of species and its implementations in identification of drug and vaccine targets.. **2022**, 10, e12662	0
602	5-Year Revision Rates After Elective Multilevel Lumbar/Thoracolumbar Instrumented Fusions in Older Patients: An Analysis of State Databases.. **2022**,	0
601	Leveraging Gene-Level Prediction as Informative Covariate in Hypothesis Weighting Improves Power for Rare Variant Association Studies.. **2022**, 13,	
600	Meta-analysis of transcriptional regulatory networks for lipid metabolism in neural cells from schizophrenia patients based on an open-source intelligence approach.. **2021**,	1
599	Gut Microbiome Diversity and Abundance Correlate with Gray Matter Volume (GMV) in Older Adults with Depression.. **2022**, 19,	0
598	Comprehensive Analysis of the Effect of 20()-Ginsenoside Rg3 on Stroke Recovery in Rats via the Integrative miRNA-mRNA Regulatory Network.. **2022**, 27,	0
597	Impact of Notch3 Activation on Aortic Aneurysm Development in Marfan Syndrome.. **2022**, 2022, 7538649	1
596	Profiling the Skeletal Muscle Proteome in Patients on Atypical Antipsychotics and Mood Stabilizers.. **2022**, 12,	0
595	In Silico Study of Superoxide Dismutase Gene Family in Potato and Effects of Elevated Temperature and Salicylic Acid on Gene Expression.. **2022**, 11,	1
594	Functionally prioritised whole-genome sequence variants improve the accuracy of genomic prediction for heat tolerance.. **2022**, 54, 17	0
593	The Association Between Genomic Heterozygosity and Carcass Merit in Cattle.. **2022**, 13, 789270	0
592	Batf-mediated epigenetic control of effector CD8 T cell differentiation.. **2022**, 7, eabi4919	1
591	Pneumococcal within-host diversity during colonisation, transmission and treatment.	0
590	Phenotypic and transcriptional response of Daphnia pulicaria to the combined effects of temperature and predation.	

589	Discovering genomic regions associated with the phenotypic differentiation of European local pig breeds.	
588	A Single Bout of Ultra-Endurance Exercise Reveals Early Signs of Muscle Aging in Master Athletes.. **2022**, 23,	1
587	Drivers of intraspecific differentiation of an alpine cold-tolerant herb, Notopterygium oviforme : roles of isolation by distance and ecological factors.	
586	eQTL mapping using allele-specific count data is computationally feasible, powerful, and provides individual-specific estimates of genetic effects.. **2022**, 18, e1010076	0
585	BRCA1 mutations in high-grade serous ovarian cancer are associated with proteomic changes in DNA repair, splicing, transcription regulation and signaling.. **2022**, 12, 4445	0
584	Resequencing and Signatures of Selective Scans Point to Candidate Genetic Variants for Hair Length Traits in Long-Haired and Normal-Haired Tianzhu White Yak.. **2022**, 13, 798076	1
583	Limitations of principal components in quantitative genetic association models for human studies.	0
582	Evaluating Client Protein Recovery by the Hsp40s DNAJB8 and DNAJB1 with AP-MS.	0
581	Mitogenomics provides new insights into the phylogenetic relationships and evolutionary history of deep-sea sea stars (Asteroidea).. **2022**, 12, 4656	0
580	The effects of gestational diabetes mellitus with maternal age between 35 and 40 years on the metabolite profiles of plasma and urine.. **2022**, 22, 174	1
579	Gestational Perfluoroalkyl Substance Exposure and DNA Methylation at Birth and 12 Years of Age: A Longitudinal Epigenome-Wide Association Study.. **2022**, 130, 37005	1
578	EviCor: Interactive Web Platform for Exploration of Molecular Features and Response to Anti-cancer Drugs. **2022**, 167528	1
577	Illumina-based Whole De Novo Transcriptome Profiling and Diosgenin Biosynthetic pathway of Tribulus terrestris: A Medicinal herb.	
576	Hetero-grafted chrysanthemums enhance salt stress tolerance by integrating the ROS, soluble sugar, and proline.	4
575	Mixed Effects of Soil Compaction on the Nitrogen Cycle Under Pea and Wheat.. **2021**, 12, 822487	0
574	RNAi-Mediated Screen of Primary AML Cells Nominates MDM4 as a Therapeutic Target in NK-AML with Mutations.. **2022**, 11,	1
573	The zinc-finger transcription factor LSL-1 is a major regulator of the germline transcriptional program in C. elegans.. **2022**,	
572	Strain-specific alterations in gut microbiome and host immune responses elicited by Bifidobacterium pseudolongum.	

571	Temporally Regulated Plant-Nematode Gene Networks Implicate Metabolic Pathways.. **2022**,	
570	Survey and Recommendations on the Use of P-Values Driving Decisions in Nonclinical Pharmaceutical Applications. 1-16	
569	Tracking Strain-Specific Morpho- and Angio-genesis of Murine Calvaria with Large-Scale Optoacoustic and Ultrasound Microscopy.. **2022**,	0
568	Noncanonical genomic imprinting in the monoamine system determines naturalistic foraging and brain-adrenal axis functions.. **2022**, 38, 110500	0
567	Genetic associations at regulatory phenotypes improve fine-mapping of causal variants for 12 immune-mediated diseases.. **2022**, 54, 251-262	1
566	Association Mapping for Common Bunt Resistance in Wheat Landraces and Cultivars. **2022**, 12, 642	0
565	Transcriptomic analysis of pea aphids (Acyrthosiphon pisum) treated with plant extracts from endophyte-containing drunken horse grass.	
564	Enrichment analyses identify shared associations for 25 quantitative traits in over 600,000 individuals from seven diverse ancestries.. **2022**,	0
563	Genetics as a key to improving crop photosynthesis.. **2022**,	1
562	Virulome and genome analyses identify associations between antimicrobial resistance genes and virulence factors in highly drug-resistant Escherichia coli isolated from veal calves.. **2022**, 17, e0265445	0
561	A genome-scale screen for synthetic drivers of T cell proliferation.. **2022**, 603, 728-735	3
560	Transcriptome expression profiles reveal response mechanisms to drought and drought-stress mitigation mechanisms by exogenous glycine betaine in maize.. **2022**, 44, 367	2
559	Association of ARRDC3 and NFIA variants with bovine congestive heart failure in feedlot cattle. 11, 385	1
558	MicroRNA-eQTLs in the developing human neocortex link miR-4707-3p expression to brain size.	
557	Functional Biomarkers of Ex-vivo Dental Caries Onset.	1
556	Optimal false discovery rate control for large scale multiple testing with auxiliary information. **2022** , 50,	1
555	Efficient Permutation-based Genome-wide Association Studies for Normal and Skewed Phenotypic Distributions.	0
554	Multi-omics discovery of aroma-active compound formation by Pichia kluyveri during cider production. **2022**, 159, 113233	

553	Comparative transcriptome analyses unravel the response to acute thermal stress in the razor clam, Sinonovacula constricta. **2022**, 23, 101079	1
552	Trans-omics analysis of insulin action reveals a cell growth subnetwork which co-regulates anabolic processes.. **2022**, 25, 104231	0
551	Disparities in Visual Acuity Outcomes after Endothelial Keratoplasty - an IRIS® Registry Analysis.. **2022**,	0
550	New insights into the genetic etiology of Alzheimer's disease and related dementias.. **2022**,	27
549	Susceptibility to epilepsy after traumatic brain injury is associated with preexistent gut microbiome profile.. **2022**,	0
548	Null-free False Discovery Rate Control Using Decoy Permutations.. **2022**, 38, 235-253	0
547	Aryl hydrocarbon receptor and Krüppel like factor 10 mediate a transcriptional axis modulating immune homeostasis in mosquitoes.. **2022**, 12, 6005	
546	Dissecting the genetic control of natural variation in sorghum photosynthetic response to drought stress. **2021**,	0
545	False Discovery in A/B Testing.	0
544	Identification of Cell-Type-Specific Spatially Variable Genes Accounting for Excess Zeros.	
543	Transposable elements mediate genetic effects altering the expression of nearby genes in colorectal cancer.	
542	Plasma metabolomic profiling of hypertrophic cardiomyopathy patients before and after surgical myectomy suggests postoperative improvement in metabolic function.. **2021**, 21, 617	
541	Molecular Basis to Integrate Microgravity Signals into the Photoperiodic Flowering Pathway in under Spaceflight Condition.. **2021**, 23,	1
540	Genetic architecture of microRNA expression and its link to complex diseases in the Japanese population.. **2021**,	0
539	The zinc-finger transcription factor LSL-1 is a major regulator of the germline transcriptional program in C. elegans.	
538	Consequences of a low protein diet on the liver and longissimus dorsi transcriptome of Duroc×Iberian crossbred pigs. **2021**, 15, 100408	
537	Combined Transcriptome and Proteome Profiling for Role of pfEMP1 in Antimalarial Mechanism of Action of Dihydroartemisinin.. **2021**, 9, e0127821	1
536	Integrative genomic analyses in adipocytes implicate DNA methylation in human obesity and diabetes.	0

535	Genetically regulated expression in late-onset Alzheimer's disease implicates risk genes within known and novel loci. **2021**, 11, 618	2
534	A Method for Identifying Environmental Stimuli and Genes Responsible for Genotype-by-Environment Interactions From a Large-Scale Multi-Environment Data Set.. **2021**, 12, 803636	2
533	Single-fiber nucleosome density shapes the regulatory output of a mammalian chromatin remodeling enzyme.	0
532	Unraveling Autocrine Signaling Pathways through Metabolic Fingerprinting in Serous Ovarian Cancer Cells.. **2021**, 9,	0
531	Identification and application of plasmatic microRNA expression quantitative trait loci (miR-QTL) at first trimester of pregnancy.	
530	Population structure and adaptive variation of Helichrysum italicum (Roth) G. Don along eastern Adriatic temperature and precipitation gradient.. **2021**, 11, 24333	2
529	Age-Related Changes of Gene Expression Profiles in .. **2021**, 12,	0
528	Genetic Dissection of Temperament Personality Traits in Italian Isolates.. **2021**, 13,	0
527	The Ovarian Development Genes of Bisexual and Parthenogenetic Evaluated by Transcriptomics and Proteomics.. **2021**, 8, 783404	0
526	Cold Conditioned: Discovery of Novel Alleles for Low-Temperature Tolerance in the Vavilov Barley Collection.. **2021**, 12, 800284	0
525	ExPheWas: a platform for cis-Mendelian randomization and gene-based association scans.. **2022**,	
524	False discovery rate: the Achilles' heel of proteogenomics.. **2022**,	0
523	Differing impact of phosphoglycerate mutase 1-deficiency on brown and white adipose tissue.. **2022**, 25, 104268	
522	Integrative Multi-Omics database (iMOMdb) of Asian Pregnant Women.. **2022**,	0
521	Threshold Values for the Gini Variable Importance A Empirical Bayes Approach.	
520	Distinct immune and transcriptomic profiles in dominant versus subordinate males in mouse social hierarchies.. **2022**, 103, 130-144	2
519	LATENT RANK CHANGE DETECTION FOR ANALYSIS OF SPLICE-JUNCTION MICROARRAYS WITH NONLINEAR EFFECTS. **2011**, 5, 364-380	
518	Table_1.doc. **2019**,	

517 Presentation1.PDF. **2018**,

516 Data_Sheet_1.PDF. **2020**,

515 Table_1.xlsx. **2020**,

514 Table_2.xlsx. **2020**,

513 Table_3.xlsx. **2020**,

512 DataSheet_1.pdf. **2019**,

511 Data_Sheet_1.xlsx. **2019**,

510 Data_Sheet_2.xlsx. **2019**,

509 Data_Sheet_3.docx. **2019**,

508 Presentation_1.PDF. **2018**,

507 Image_1.pdf. **2020**,

506 Image_2.pdf. **2020**,

505 Image_3.pdf. **2020**,

504 Table_1.xlsx. **2020**,

503 Table_2.docx. **2020**,

502 Table_3.xlsx. **2020**,

501 Table_4.docx. **2020**,

500 Table_5.xlsx. **2020**,

499 Table_6.xlsx. **2020**,

498 Table_7.xlsx. **2020**,

497 Data_Sheet_1.xlsx. **2019**,

496 Data_Sheet_2.pdf. **2019**,

495 Image_1.jpeg. **2020**,

494 Table_1.xls. **2020**,

493 Presentation_1.pdf. **2018**,

492 Table_2.XLSX. **2018**,

491 Table_3.XLSX. **2018**,

490 Table_4.XLSX. **2018**,

489 Table_5.XLSX. **2018**,

488 Data_Sheet_1.PDF. **2019**,

487 Image_1.pdf. **2019**,

486 Table_1.docx. **2019**,

485 Presentation_1.PDF. **2018**,

484 Table_1.docx. **2018**,

483 Table_2.docx. **2018**,

482 Table_3.docx. **2018**,

481 Data_Sheet_1.docx. **2018**,

480 Image_1.PDF. **2018**,

479 Table_1.PDF. **2018**,

478 Table_2.pdf. **2018**,

477 Table_3.pdf. **2018**,

476 Data_Sheet_1.docx. **2018**,

475 Image_1.TIF. **2018**,

474 Image_2.TIF. **2018**,

473 Image_3.TIFF. **2018**,

472 Image_4.TIFF. **2018**,

471 Table_1.DOCX. **2019**,

470 image_1.tif. **2018**,

469 image_2.tif. **2018**,

468 table_1.xlsx. **2018**,

467 table_2.xlsx. **2018**,

466 table_3.xlsx. **2018**,

465 table_4.xlsx. **2018**,

464 Data_Sheet_1.PDF. **2018**,

463 Data_Sheet_2.PDF. **2018**,

462 Image_1.TIFF. **2018**,

461 Table_1.DOCX. **2018**,

460 Image_1.TIF. **2019**,

459 Table_1.XLSX. **2019**,

458 Table_2.XLSX. **2019**,

457 Table_3.XLSX. **2019**,

456 Table_4.XLSX. **2019**,

455 Table_5.XLSX. **2019**,

454 Table_6.XLSX. **2019**,

453 DataSheet_1.zip. **2019**,

452 Table_1.xlsx. **2019**,

451 Table_2.docx. **2019**,

450 Video_1.wmv. **2019**,

449 Video_2.wmv. **2019**,

448 Video_3.wmv. **2019**,

447 Data_Sheet_1.pdf. **2019**,

446 Data_Sheet_1.zip. **2020**,

445 Image_1.tif. **2018**,

444 Image_2.TIF. **2018**,

443 Table_1.XLSX. **2018**,

442 Table_2.XLSX. **2018**,

441 Table_3.XLSX. **2018**,

440 Table_4.XLSX. **2018**,

439 Table_5.XLSX. **2018**,

438 Table_6.XLSX. **2018**,

437 Table_7.XLSX. **2018**,

436 Table_8.XLSX. **2018**,

435 Data_Sheet_1.docx. **2019**,

434 Image_1.TIF. **2019**,

433 Image_2.TIF. **2019**,

432 Image_3.TIF. **2019**,

431 Table_1.DOCX. **2019**,

430 Image_1.JPEG. **2019**,

429 Image_2.JPEG. **2019**,

428 Image_3.JPEG. **2019**,

427 Image_4.JPEG. **2019**,

426 Image_5.JPEG. **2019**,

425 Image_6.JPEG. **2019**,

424 Table_1.pdf. **2019**,

423 Image_1.TIF. **2019**,

422 Image_2.TIF. **2019**,

421 Image_3.TIF. **2019**,

420 Image_4.TIF. **2019**,

419 Image_5.TIF. **2019**,

418 Image_6.TIF. **2019**,

417 Image_7.TIF. **2019**,

416 Image_8.TIF. **2019**,

415 Image_9.TIF. **2019**,

414 Table_1.DOCX. **2019**,

413 Table_2.DOCX. **2019**,

412 Table_3.DOCX. **2019**,

411 Table_4.DOCX. **2019**,

410 Image_1.TIFF. **2019**,

409 Image_2.TIFF. **2019**,

408 Image_3.TIFF. **2019**,

407 Image_4.TIFF. **2019**,

406 Image_5.TIFF. **2019**,

405 Table_1.docx. **2019**,

404 Table_2.DOCX. **2019**,

403 Table_3.DOCX. **2019**,

402 Table_4.DOCX. **2019**,

401 Data_Sheet_1.docx. **2019**,

400 Table_1.XLSX. **2018**,

399 Data_Sheet_1.xlsx. **2018**,

398 Data_Sheet_2.docx. **2018**,

397 Image_1.pdf. **2018**,

396 Image_2.pdf. **2018**,

395 Image_3.pdf. **2018**,

394 Image_4.pdf. **2018**,

393 Table_1.docx. **2018**,

392 Table_2.docx. **2018**,

391 Table_3.docx. **2018**,

390 Table_4.docx. **2018**,

389 Image_1.TIF. **2019**,

388 Image_2.TIF. **2019**,

387 Image_3.TIF. **2019**,

386 Image_4.TIF. **2019**,

385 Image_5.TIF. **2019**,

384 Image_6.TIF. **2019**,

383 Image_7.tif. **2019**,

382 Image_8.tif. **2019**,

381 Table_1.pdf. **2019**,

380 Table_2.pdf. **2019**,

379 Table_3.xls. **2019**,

378 Table_4.pdf. **2019**,

377 Data_Sheet_1.pdf. **2018**,

376 Table_1.docx. **2020**,

375 Table_2.pdf. **2020**,

374 Table_3.xlsx. **2020**,

373 Table_4.xlsx. **2020**,

372 Table_5.xlsx. **2020**,

371 Data_Sheet_1.XLSX. **2018**,

370 Data_Sheet_2.XLSX. **2018**,

369 Data_Sheet_3.XLSX. **2018**,

368 Data_Sheet_4.XLSX. **2018**,

367 Data_Sheet_5.XLSX. **2018**,

366 Data_Sheet_6.XLSX. **2018**,

365 Presentation_1.pdf. **2018**,

364 Table_1.XLSX. **2018**,

363 Table_2.XLSX. **2018**,

362 DataSheet_1.zip. **2020**,

361 Image_1.tif. **2020**,

360 Table_1.docx. **2020**,

359 Table_2.xlsx. **2020**,

358 DataSheet_1.docx. **2020**,

357 DataSheet_2.xlsx. **2020**,

356 Image_1.JPEG. **2020**,

355 Table_1.docx. **2020**,

354 Image_1.tiff. **2020**,

353 Image_2.tiff. **2020**,

352 Table_1.docx. **2020**,

351 Table_2.docx. **2020**,

350 Table_3.docx. **2020**,

349 Table_4.docx. **2020**,

348 Table_5.docx. **2020**,

347 DataSheet_1.zip. **2019**,

346 Data_Sheet_1.XLS. **2018**,

345 Image_1.TIFF. **2018**,

344 Image_2.TIFF. **2018**,

343 Image1.TIF. **2018**,

342 DataSheet_1.zip. **2020**,

341 Table_1.DOCX. **2018**,

340 Image_1.PDF. **2018**,

339 Data_Sheet_1.PDF. **2019**,

338 DataSheet_1.xlsx. **2020**,

337	Image_1.pdf. **2020**,	
336	Data_Sheet_1.xlsx. **2018**,	
335	Image_1.TIF. **2018**,	
334	Image_2.TIF. **2018**,	
333	Image_3.tif. **2018**,	
332	Image_4.TIF. **2018**,	
331	Table_1.DOC. **2018**,	
330	Table_2.doc. **2018**,	
329	Table_3.DOC. **2018**,	
328	Table_4.doc. **2018**,	
327	Table_5.DOC. **2018**,	
326	Table_6.DOC. **2018**,	
325	DataSheet_1.docx. **2019**,	
324	DataSheet_2.xlsx. **2019**,	
323	Carry-over effects of dry period heat stress on the mammary gland proteome and phosphoproteome in the subsequent lactation of dairy cows.. **2022**, 12, 6637	1
322	MtEFD and MtEFD2: two transcription factors with distinct neofunctionalization in symbiotic nodule development.. **2022**,	0
321	Confidence, accuracy judgments and feedback in schizophrenia and bipolar disorder: a time series network analysis.. **2022**, 1-10	0
320	Periodontitis promotes the expression of gingival transmembrane serine protease 2 (TMPRSS2), a priming protease for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2).. **2022**,	3

319	The Two Domains of the Avian Double-Defensin AvBD11 Have Different Ancestors, Common with Potential Monodomain Crocodile and Turtle Defensins. **2022**, 11, 690	1
318	Genome wide association study of MAGIC population reveals a novel QTL for salinity and sodicity tolerance in rice.. **2022**, 28, 819-835	0
317	A Unifying Statistical Framework to Discover Disease Genes from GWAS.	
316	Sputum Metabolites Associated with Nontuberculous Mycobacterial Infection in Cystic Fibrosis.. **2022**, e0010422	0
315	Challenges in Metabolomics-Based Tests, Biomarkers Revealed by Metabolomic Analysis, and the Promise of the Application of Metabolomics in Precision Medicine.. **2022**, 23,	3
314	Multi-ancestry genome-wide analysis identifies effector genes and druggable pathways for coronary artery calcification.	0
313	Selenium Nanoparticles (SeNPs) Immunomodulation Is More Than Redox Improvement: Serum Proteomics and Transcriptomic Analyses. **2022**, 11, 964	0
312	ImShot: An open-source software for probabilistic identification of proteins in situ and visualization of proteomics data.. **2022**, 100242	
311	TNFRSF13B is a potential contributor to prostate cancer.. **2022**, 22, 180	
310	Efficient testing and effect size estimation for set-based genetic association inference via semiparametric multilevel mixture modeling.. **2022**,	
309	Identifying predictive signalling networks for Vedolizumab response in ulcerative colitis.. **2022**, 1	1
308	CircRNA expression profiles in deltamethrin-susceptible and -resistant Culex pipiens pallens (Diptera: Culicidae).. **2022**, 261, 110750	0
307	Taxonomic and Functional Fecal Microbiota Signatures Associated With Insulin Resistance in Non-Diabetic Subjects With Overweight/Obesity Within the Frame of the PREDIMED-Plus Study.. **2022**, 13, 804455	0
306	Proteogenomic characterization of 2002 human cancers reveals pan-cancer molecular subtypes and associated pathways.. **2022**, 13, 2669	3
305	Improvements Achieved by Multiple Imputation for Single-Cell RNA-Seq Data in Clustering Analysis and Differential Expression Analysis.. **2022**,	0
304	Dynamic human liver proteome atlas reveals functional insights into disease pathways.. **2022**, 18, e10947	3
303	Statistical analysis of spatially resolved transcriptomic data by incorporating multi-omics auxiliary information.	
302	Distinct Cellular Tools of Mild Hyperthermia-Induced Acquired Stress Tolerance in Chinese Hamster Ovary Cells. **2022**, 10, 1172	

301	Integrating genetic regulation and single-cell expression with GWAS prioritizes causal genes and cell types for glaucoma.	0
300	Connectivity in eQTL networks dictates reproducibility and genomic properties. **2022**, 2, 100218	0
299	Metabolomics in pulmonary medicine - extracting the most from your data. 2200102	0
298	Ensemble classification based signature discovery for cancer diagnosis in RNA expression profiles across different platforms.	0
297	PqsE Expands and Differentially Modulates the RhlR Quorum Sensing Regulon in Pseudomonas aeruginosa.	1
296	Immune disease risk variants regulate gene expression dynamics during CD4+ T cell activation.	2
295	Association of HLA-DQ Heterodimer Residues 18 and 57 With Progression From Islet Autoimmunity to Diabetes in the Diabetes Prevention Trial-Type 1.	0
294	Serine and arginine rich splicing factor 1 deficiency alters pathways involved in IL-17A expression and is implicated in human psoriasis. **2022**, 240, 109041	0
293	The Pandemic Effects on Market Power and Profitability.	
292	Integrating proteomic data with metabolic modelling provides insight into key pathways of Bordetella pertussis biofilms.	
291	An adaptive direction-assisted test for microbiome compositional data.	0
290	An exposome-wide association study on body mass index in adolescents using the National Health and Nutrition Examination Survey (NHANES) 2003–2004 and 2013–2014 data. **2022**, 12,	0
289	Effect of Killed PRRSV Vaccine on Gut Microbiota Diversity in Pigs. **2022**, 14, 1081	1
288	Mutational signatures are markers of drug sensitivity of cancer cells. **2022**, 13,	2
287	MicroRNA Profiling in Melanoma Cells That Are Resistant to Dacarbazine. **2022**, 16, 203-212	0
286	MaLAdapt reveals novel targets of adaptive introgression from Neanderthals and Denisovans in worldwide human populations.	
285	Stromal changes in the aged lung induce an emergence from melanoma dormancy.	2
284	Mapping genomic regulation of kidney disease and traits through high-resolution and interpretable eQTLs.	0

283	Early life microbial exposures shape the Crassostrea gigas immune system for lifelong and intergenerational disease protection. **2022**, 10,	2
282	TDP 2 modulates the expression of estrogen-responsive oncogenes.	
281	SAMBA: A Multicolor Digital Melting PCR Platform for Rapid Microbiome Profiling. 2200185	1
280	Clioquinol as an inhibitor of JmjC-histone demethylase exhibits common and unique histone methylome and transcriptome between clioquinol and hypoxia. **2022**, 104517	1
279	A cross-disease human microglial framework identifies disease-enriched subsets and tool compounds for microglial polarization..	0
278	Comparative analysis of allele frequencies for DNA polymorphisms associated with disease and economically important traits in the genomes of Russian and foreign cattle breeds. **2022**, 26, 298-307	
277	Cellular and immunometabolic mechanisms of inflammation in depression: Preliminary findings from single cell RNA sequencing and a tribute to Bruce McEwen. **2022**, 19, 100462	0
276	fdrci: FDR confidence interval selection and adjustment for large-scale hypothesis testing. **2022**, 2,	1
275	Evaluation of field-based single plant phenotyping for wheat breeding. **2022**, 5,	0
274	Conscientiousness associated with efficiency of the salience/ventral attention network: Replication in three samples using individualized parcellation.	
273	Automated High-Definition MRI Processing Routine Robustly Detects Longitudinal Morphometry Changes in Alzheimer Disease Patients. 14,	
272	Mitochondrial cyclophilin D promotes disease tolerance by licensing NK cell development and IL-22 production against influenza virus. **2022**, 39, 110974	1
271	Resequencing the Yaroslavl cattle genomes reveals signatures of selection and a rare haplotype on BTA28 likely to be related to breed phenotypes.	
270	COLMARq: A Web Server for 2D NMR Peak Picking and Quantitative Comparative Analysis of Cohorts of Metabolomics Samples. **2022**, 94, 8674-8682	2
269	A Comprehensive Metabolomics Analysis of Fecal Samples from Advanced Adenoma and Colorectal Cancer Patients. **2022**, 12, 550	2
268	Human Follicular Mites: Ectoparasites Becoming Symbionts. **2022**, 39,	0
267	Pretransplant Systemic Lipidomic Profiles in Allogeneic Stem Cell Transplant Recipients. **2022**, 14, 2910	0
266	Epigenomic and transcriptomic analyses define core cell types, genes and targetable mechanisms for kidney disease.	0

265	Statistical analysis of spatially resolved transcriptomic data by incorporating multi-omics auxiliary information.	
264	Attenuated HIV-1 Nef But Not Vpu Function in a Cohort of Rwandan Long-Term Survivors. 2,	
263	Searching for signatures of sexually antagonistic selection on stickleback sex chromosomes. **2022**, 377,	1
262	Integrating variant functional annotation scores have varied abilities to improve power of genome-wide association studies. **2022**, 12,	
261	Missense variants causing Wiedemann-Steiner syndrome preferentially occur in the KMT2A-CXXC domain and are accurately classified using AlphaFold2. **2022**, 18, e1010278	0
260	Facing the Green Threat: A Water Flea Defenses against a Carnivorous Plant. **2022**, 23, 6474	0
259	Evolutionary Divergence of Marinobacter Strains in Cryopeg Brines as Revealed by Pangenomics. 13,	0
258	BATF3 Protects Against Metabolic Syndrome and Maintains Intestinal Epithelial Homeostasis. 13,	0
257	The association between aging-related monocyte transcriptional networks and comorbidity burden: the Multi-Ethnic Study of Atherosclerosis (MESA).	0
256	Detection of Embryonic Trisomy 21 in the First Trimester Using Maternal Plasma Cell-Free RNA. **2022**, 12, 1410	0
255	The origin of bladder cancer from mucosal field effects. **2022**, 25, 104551	0
254	Alzheimer's disease is associated with disruption in thiamin transport physiology: A potential role for neuroinflammation. **2022**, 171, 105799	1
253	Transcriptome profiling during double-flower development provides insight into stamen petaloid in cultivated <i>Lilium</i>. **2022**, 2, 1-11	0
252	Advancing understanding of dietary and movement behaviours in an Asian population through real-time monitoring: Protocol of the Continuous Observations of Behavioural Risk Factors in Asia study (COBRA). **2022**, 8, 205520762211105	
251	Lignin-Oxidizing Vibrios Involved in the Mineralization of Plant Detritus in the Continental Slope.	
250	Contribution of schizophrenia polygenic burden to longitudinal phenotypic variance in 22q11.2 deletion syndrome.	0
249	Systemic Discrimination Among Large U.S. Employers.	2
248	Identification of Two Genetic Loci Associated with Leukopenia after Chemotherapy in Patients with Breast Cancer. OF1-OF14	0

247	Hspa13 Regulates Endoplasmic Reticulum and Cytosolic Proteostasis Through Modulation of Protein Translocation.	
246	RUV-III-NB: normalization of single cell RNA-seq data.	0
245	Regulation of HLA class I expression by non-coding gene variations. **2022**, 18, e1010212	0
244	Significant hot hand effect in the game of cricket. **2022**, 12,	
243	Adipose methylome integrative-omic analyses reveal genetic and dietary metabolic health drivers and insulin resistance classifiers. **2022**, 14,	1
242	Mediterranean Diet Reduces Social Isolation and Anxiety in Adult Female Nonhuman Primates. **2022**, 14, 2852	1
241	Multi-Cell-Type Openness-Weighted Association Studies for Trait-Associated Genomic Segments Prioritization. **2022**, 13, 1220	
240	Male mice exposed to chronic intermittent ethanol exposure exhibit significant upregulation or downregulation of circular RNAs. 1-11	0
239	Genetic score omics regression and multi-trait meta-analysis detect widespread cis-regulatory effects shaping bovine complex traits.	1
238	Association of Cardiovascular Health Through Young Adulthood With Genome-Wide DNA Methylation Patterns in Midlife: The CARDIA Study. **2022**, 146, 94-109	0
237	Pathway Analysis Through Mutual Information.	0
236	Genomic signals of local adaptation and hybridization in Asian white birch.	
235	Identification of Cell-Type-Specific Spatially Variable Genes Accounting for Excess Zeros.	
234	Metabolomics-guided discovery of cytochrome P450s involved in pseudotropine-dependent biosynthesis of modified tropane alkaloids. **2022**, 13,	0
233	Whole-body transcriptome analysis provides insights into the cascade of sequential expression events involved in growth, immunity, and metabolism during the molting cycle in Scylla paramamosain. **2022**, 12,	
232	Ecological significance of intraplant variation: epigenetic mosaicism in Lavandula latifolia plants predicts extant and transgenerational variability of fecundity-related traits.	0
231	Detection of Genomic Imprinting for Carcass Traits in Cattle Using Imputed High-Density Genotype Data. 13,	
230	DeCAF: a novel method to identify cell-type specific regulatory variants and their role in cancer risk. **2022**, 23,	

229	Candidate Plasma Biomarkers to Detect Anthracycline-Related Cardiomyopathy in Childhood Cancer Survivors: A Case Control Study in the Dutch Childhood Cancer Survivor Study.	
228	Dynamic Transcriptomic Profiling During Liver Development in Schizothorax Prenanti. 13,	
227	Phenotypic and transcriptional response of Daphnia pulicaria to the combined effects of temperature and predation. **2022**, 17, e0265103	
226	Genetic dissection of the RNA polymerase II transcription cycle. 11,	0
225	Identification and validation of TCONS_00093333 for regulating fertility conversion of thermo-sensitive cytoplasmic male-sterility wheat with Aegilops kotschyi cytoplasm. **2022**, 838, 146707	
224	Effects of air exposure stress on crustaceans: Histopathological changes, antioxidant and immunity of the red swamp crayfish Procambarus clarkii. **2022**, 135, 104480	1
223	Integrative analysis of drug response and clinical outcome in acute myeloid leukemia. **2022**,	4
222	Genetic variation in correlated regulatory region of Immunity.	0
221	Novel Interactions Between Phytoplankton and Bacteria Shape Microbial Seasonal Dynamics in Coastal Ocean Waters. 9,	0
220	Arc Regulates a "Second-Guessing" Cognitive Bias During Naturalistic Foraging.	
219	Multiple Inference: A Python package for comparing multiple parameters. **2022**, 7, 4492	
218	Comparative genomic analysis of Echinococcus multilocularis with other tapeworms.	
217	Probabilistic integration of transcriptome-wide association studies and colocalization analysis prioritizes molecular pathways of complex traits.	
216	VMP1 Regulated by chi-miR-124a Effects Goat Myoblast Proliferation, Autophagy, and Apoptosis through the PI3K/ULK1/mTOR Signaling Pathway. **2022**, 11, 2227	1
215	RNA-seq analysis reveals genes related to photosynthetic carbon partitioning and lipid production in Phaeodactylum tricornutum under alkaline conditions. 13,	
214	Time-resolved transcriptome analysis of Scenedesmus obliquus HTB1 under 10% CO 2 condition.	
213	RNA editing underlies genetic risk of common inflammatory diseases. **2022**, 608, 569-577	2
212	Tbx18 Orchestrates Cytostructural Transdifferentiation of Cardiomyocytes to Pacemaker Cells by Recruiting the Epithelial-Mesenchymal Transition Program.	

211	Exploring the adaptability and robustness of the central carbon metabolism of Mycoplasma pneumoniae.	
210	Comparing mixed models and Random Forest association tests using naturalGWAS and a Striped Bass SNP dataset.	
209	Cardiovascular Image-Derived Phenotypes from Abdominal MRI at a Population Scale.	
208	Tight gene co-expression in BCB positive cattle oocytes and their surrounding cumulus cells. **2022**, 20,	2
207	An investigation of the sex-specific genetic architecture of fitness in Drosophila melanogaster.	
206	Trans-genetic effects of circular RNA expression quantitative trait loci and potential causal mechanisms in autism.	1
205	Metabolomic and transcriptomic signatures of influenza vaccine response in healthy young and older adults.	0
204	Crohn disease in endoscopic remission, obesity, and cases of high genetic risk demonstrate overlapping shifts in the colonic mucosal-luminal interface microbiome. **2022**, 14,	0
203	Alterations in Microbiota and Metabolites Related to Spontaneous Diabetes and Pre-Diabetes in Rhesus Macaques. **2022**, 13, 1513	
202	The genetic basis of transpiration sensitivity to vapor pressure deficit in wheat.	0
201	Depletion of Mdig Changes Proteomic Profiling in Triple Negative Breast Cancer Cells. **2022**, 10, 2021	
200	A robust knockoff filter for sparse regression analysis of microbiome compositional data.	
199	Complex metabolic interactions between ovary, plasma, urine, and hair in ovarian cancer. 12,	
198	Selection against admixture and gene regulatory divergence in a long-term primate field study. **2022**, 377, 635-641	1
197	Impact of sublethal chlorantraniliprole on epidermis of Bombyx mori during prepupal-pupal transition. **2022**, 187, 105200	0
196	Developmentally related and drought-induced shifts in the kale metabolome limited Salmonella enterica association, providing novel insights to enhance food safety. **2022**, 108, 104113	
195	Wavelet Transformations of Tumor Expression Profiles Reveals a Pervasive Genome-Wide Imprinting of Aneuploidy on the Cancer Transcriptome. **2005**, 65, 186-194	4
194	Time and age dependent regulation of neuroinflammation in a rat model of mesial temporal lobe epilepsy: Correlation with human data. 10,	0

193	Lignin-oxidizing and xylan-hydrolyzing Vibrio involved in the mineralization of plant detritus in the continental slope. **2023**, 854, 158714	0
192	Genomic and Bioinformatic Resources for Next-Generation Breeding Approaches Towards Enhanced Stress Tolerance in Cereals. **2022**, 453-493	0
191	A Social Scientist Guide to Multiple Inference.	0
190	Reduce Bioaccumulation of Cd Pollutants Through the Antagonism of Se:Bioaccumulation of Cd and Comparative Transcriptome Analysis in the Hepatopancreas of Estuary Mud Crab (Scylla Paramamosain).	0
189	Understanding Uncertainty Maps in Vision with Statistical Testing. **2022**,	0
188	Impact of a cell cycle and an extracellular matrix remodeling transcriptional signature on tumor progression and correlation with EZH2 expression in meningioma. **2022**, 1-14	0
187	Population-level variation in enhancer expression identifies disease mechanisms in the human brain. **2022**, 54, 1493-1503	0
186	Parallel genomic basis of age at maturity across spatial scales in Atlantic Salmon.	0
185	Characterization of differential expression patterns of the extracellular purinergic enzymes in colorectal cancer.	0
184	Conserved non-coding sequences and de novo Mutator insertion alleles are imprinted in maize.	0
183	Clinico-genomic Characterization of ATM and HRD in Pancreas Cancer: Application for Practice. OF1-OF11	0
182	A Transformative Vision for an Omics-Based Regulatory Chemical Testing Paradigm.	1
181	Integrated bioinformatics analysis and screening of hub genes in polycystic ovary syndrome.	1
180	Functional signatures of ex-vivo dental caries onset. **2022**, 14,	1
179	Noninvasive, low-cost RNA-sequencing enhances discovery potential of transcriptome studies.	0
178	Genetic control of RNA editing in Neurodegenerative disease.	1
177	Effects of uteroplacental insufficiency on growth-restricted rats with altered lung development: A metabolomic analysis. 10,	0
176	Efficient permutation-based genome-wide association studies for normal and skewed phenotypic distributions. **2022**, 38, ii5-ii12	0

175	Association of Whole-Person Eigen-Polygenic Risk Scores with Alzheimer's Disease.	0
174	Comment on: What genes are differentially expressed in individuals with schizophrenia? A systematic review.	0
173	Remodeling of Liver and Plasma Lipidomes in Mice Lacking Cyclophilin D. **2022**, 23, 11274	0
172	Ketogenic diet uncovers differential metabolic plasticity of brain cells. **2022**, 8,	0
171	Boolean implication analysis of single-cell data predicts retinal cell type markers. **2022**, 23,	0
170	Transcriptome and chromatin accessibility landscapes across 25 distinct human brain regions expand the susceptibility gene set for neuropsychiatric disorders.	0
169	An improvement of FDR for edge detection by applying EM method. **2022**, 26, 1161-1184	0
168	Pasture-finishing of Bison Improves Animal Metabolic Health and Potential Health-Promoting Compounds in Meat.	0
167	Associations between forensic loci and expression levels of neighboring genes may compromise medical privacy. **2022**, 119,	0
166	Cellular Biogenetic Law and Its Distortion by Protein Interactions: A Possible Unified Framework for Cancer Biology and Regenerative Medicine. **2022**, 23, 11486	2
165	Orang Asli Health and Lifeways Project (OA HeLP): a cross-sectional cohort study protocol. **2022**, 12, e058660	0
164	Discovering significant evolutionary trajectories in cancer phylogenies. **2022**, 38, ii49-ii55	0
163	Integrated multi-omics analysis of adverse cardiac remodeling and metabolic inflexibility upon ErbB2 and ERRα deficiency. **2022**, 5,	0
162	Leveraging interindividual variability of regulatory activity for refining genetic regulation of gene expression in schizophrenia.	0
161	Facilitating early parent-infant emotional connection improves cortical networks in preterm infants. **2022**, 14,	0
160	Transcriptome sequencing and DEG analysis in different developmental stages of floral buds induced by potassium chlorate in <i>Dimocarpus longan</i>. **2022**, 39, 259-272	0
159	Admixture mapping of severe asthma exacerbations in Hispanic/Latino children and youth. thoraxjnl-2022-218755	0
158	Cognitive theories of autism based on the interactions between brain functional networks. 16,	1

157	Exogenous citrate restores the leaf metabolic profiles of navel orange plants under boron deficiency. **2022**,	1
156	Growth promotion effect of red ginseng dietary fiber to probiotics and transcriptome analysis of Lactiplantibacillus plantarum. **2022**,	1
155	Sex-dependent placental mQTL provide insight into the prenatal origins of childhood-onset traits and conditions.	0
154	Integrating Identification and Quantification Uncertainty for Differential Protein Abundance Analysis with Triqler. **2023**, 91-117	0
153	Genetic Analysis Implicates Dysregulation of SHANK2 in Renal Cell Carcinoma Progression. **2022**, 19, 12471	0
152	Heat Shock Protein Hspa13 Regulates Endoplasmic Reticulum and Cytosolic Proteostasis Through Modulation of Protein Translocation. **2022**, 102597	1
151	Small extravesicular microRNA in head and neck squamous cell carcinoma and its potential as a liquid biopsy for early detection.	1
150	Transcriptome analysis revealed potential genes involved in thermogenesis in muscle tissue in cold-exposed lambs. 13,	1
149	Dissecting the cotranscriptome landscape of plants and their microbiota.	0
148	Genes vary greatly in their propensity for collateral fitness effects of mutations.	0
147	Classification of High-Grade Serous Ovarian Cancer Using Tumor Morphologic Characteristics. **2022**, 5, e2236626	0
146	Pneumococcal within-host diversity during colonization, transmission and treatment. **2022**, 7, 1791-1804	0
145	Genetic variants for prediction of gestational diabetes mellitus and modulation of susceptibility by a nutritional intervention based on a Mediterranean diet. 13,	0
144	Population genomic insights into invasion success in the polyphagous agricultural pest, Halyomorpha halys.	0
143	MicroRNA expression within neuronal-derived small extracellular vesicles in frontotemporal degeneration. **2022**, 101, e30854	0
142	Epigenetic impact of a 1-week intensive multimodal group program for adolescents with multiple adverse childhood experiences. **2022**, 12,	0
141	Metabolomic Profile of Children Conceived With Medically Assisted Technologies.	0
140	Transcriptomics-based network medicine approach identifies metformin as a repurposable drug for atrial fibrillation. **2022**, 3, 100749	1

139	Challenging Targets or Describing Mismatches? A Comment on Common Decoy Distribution by Madej et al..	0
138	Metformin increases natural killer cell functions in head and neck squamous cell carcinoma through CXCL1 inhibition. **2022**, 10, e005632	0
137	OXI1 induces immunity by coordinating N-hydroxypipecolic acid, salicylic acid and camalexin synthesis.	0
136	Analysis of the caudate nucleus transcriptome in individuals with schizophrenia highlights effects of antipsychotics and new risk genes. **2022**, 25, 1559-1568	2
135	A functional analysis of 180 cancer cell lines reveals conserved intrinsic metabolic programs. **2022**, 18,	2
134	Multiple lineages of monkeypox virus detected in the United States, 2021–2022. **2022**, 378, 560-565	7
133	The use of untargeted and widely targeted metabolomics to distinguish between asphyxia and sudden cardiac death as the cause of death in rats: A preliminary study. **2022**, 15, 104322	0
132	Fatty hepatocyte-derived exosomal miR-122 promotes lipid synthesis and reduces immunocompetence in grass carp (Ctenopharyngodon idella). **2023**, 563, 738921	0
131	Human and murine neutrophils share core transcriptional programs in both homeostatic and inflamed contexts.	0
130	Genetic Dissection of Phosphorus Use Efficiency and Genotype-by-Environment Interaction in Maize. **2022**, 23, 13943	0
129	Association between gut microbiota and preeclampsia-eclampsia: a two-sample Mendelian randomization study. **2022**, 20,	1
128	Systematic discovery and functional dissection of enhancers needed for cancer cell fitness and proliferation. **2022**, 41, 111630	0
127	A Type 2 Innate Lymphoid Cell-Interleukin 9 Circuit Induces Paneth Cell Metaplasia and Small Intestinal Remodeling.	0
126	miRNA–mRNA–protein dysregulated network in COPD in women. 13,	0
125	The RNA editing landscape in Acute Myeloid Leukaemia reveals associations with disease mutations and clinical outcome. **2022**, 105622	0
124	Genomic signals of local adaptation and hybridization in Asian white birch.	0
123	Low Temperature Inhibits the Defoliation Efficiency of Thidiazuron in Cotton by Regulating Plant Hormone Synthesis and the Signaling Pathway. **2022**, 23, 14208	1
122	Genetic regulation of circular RNA expression in human aortic smooth muscle cells and vascular traits. **2023**, 4, 100164	0

121	Comparative study on the gonadal development in the diploid and artificially induced triploid olive flounder Paralichthys olivaceus. **2023**, 565, 739106	0
120	Targeted Resequencing of Otosclerosis Patients from Different Populations Replicates Results from a Previous Genome-Wide Association Study. **2022**, 11, 6978	0
119	Salivary microRNA and Metabolic Profiles in a Mouse Model of Subchronic and Mild Social Defeat Stress. **2022**, 23, 14479	0
118	Transection injury differentially alters the proteome of the human sural nerve. **2022**, 17, e0260998	0
117	Genomic signatures of recent convergent transitions to social life in spiders. **2022**, 13,	0
116	Genome-wide association study for resistance in bread wheat (Triticum aestivum L.) to stripe rust (Puccinia striiformis f. sp. tritici) races in Argentina. **2022**, 22,	0
115	Mendelian randomization and genetic colocalization infer the effects of the multi-tissue proteome on 211 complex disease-related phenotypes. **2022**, 14,	1
114	An Approach for Systems-Level Understanding of Prostate Cancer from High-Throughput Data Integration to Pathway Modeling and Simulation. **2022**, 11, 4121	0
113	A combination of molecular and clinical parameters provides a new strategy for high-grade serous ovarian cancer patient management. **2022**, 20,	0
112	Diagnostic metabolomic profiling of Parkinson's disease biospecimens. **2022**, 105962	0
111	G Protein-Coupled Receptor 15 Expression Is Associated with Myocardial Infarction. **2023**, 24, 180	0
110	Gene Expression Linked to Reepithelialization of Human Skin Wounds. **2022**, 23, 15746	0
109	Particulate and dissolved metabolite distributions along a latitudinal transect of the western Atlantic Ocean.	0
108	Integrating age, BMI, and serum N-glycans detected by MALDI mass spectrometry to classify suspicious mammogram findings as benign lesions or breast cancer. **2022**, 12,	0
107	Clinical and functional characterization of germline PIK3CA variants in patients with PIK3CA-related overgrowth Spectrum disorders.	0
106	Weighted kernels improve multi-environment genomic prediction.	0
105	Transcriptomic, histological and biochemical analyses of Macrobrachium nipponense response to acute heat stress.	0
104	Facioscapulohumeral muscular dystrophy is associated with altered myoblast proteome dynamics.	0

103	Ribitol alters multiple metabolic pathways of central carbon metabolism with enhanced glycolysis: A metabolomics and transcriptomics profiling of breast cancer. **2022**, 17, e0278711	0
102	A multi-omics analysis identifies molecular features associated with heifer fertility in a case-control design including Angus and Holstein cattle.	0
101	Plant GWAS. **2022**, 181-189	0
100	Transcriptome sequencing analysis and WGCNA reveal the internal molecular mechanism that triggers programmed cell death in rice mutant zj-lm.	0
99	Dyslipidemia is associated with worse asthma clinical outcomes: a prospective cohort study. **2022**,	0
98	An Exponentially Weighted Moving Average Procedure for Detecting Back Random Responding Behavior.	0
97	PGF 2Facilitates pathological retinal angiogenesis by modulating endothelial FOS -driven ELR + CXC chemokine expression.	0
96	A novel steroid hydroxylase from Nigrospora sphaerica exhibiting broad substrate and stero-specificity. **2022**, 106236	0
95	Brassinosteroid-induced gene repression requires specific and tight promoter binding of BIL1/BZR1 via DNA shape readout. **2022**, 8, 1440-1452	0
94	DNA methylation QTL mapping across diverse human tissues provides molecular links between genetic variation and complex traits.	0
93	Assessing and removing the effect of unwanted technical variations in microbiome data. **2022**, 12,	0
92	Metabolite diversity amongProchlorococcusstrains belonging to divergent ecotypes.	0
91	Identification of salivary microRNA profiles in male mouse model of chronic sleep disorder. **2023**, 26, 21-28	0
90	Quality-controlled LC-ESI-MS food metabolomics of fenugreek (Trigonella foenum-graecum) sprouts: insights into changes in primary and specialized metabolites. **2022**, 112347	0
89	Fecal and Tissue Microbiota Are Associated with Tumor T-Cell Infiltration and Mesenteric Lymph Node Involvement in Colorectal Cancer. **2023**, 15, 316	0
88	Probabilistic integration of transcriptome-wide association studies and colocalization analysis identifies key molecular pathways of complex traits. **2023**, 110, 44-57	0
87	Angiotensin-Converting Enzyme (ACE) Inhibitors May Moderate COVID-19 Hyperinflammatory Response: An Observational Study with Deep Immunophenotyping. **2022**, 2022,	1
86	Genome-wide DNA methylation and mRNA transcription analysis revealed aberrant gene regulation pathways in dermatomyositis and polymyositis patients.	0

85	Evaluation of the Role of Soybean Lecithin, Egg Yolk Lecithin, and Krill Oil in Promoting Ovarian Development in the Female Redclaw Crayfish Cherax quadricarinatus. **2023**, 2023, 1-16	0
84	Competition co-immunoprecipitation reveals interactors of the chloroplast CPN60 chaperonin machinery.	0
83	From SNP to pathway-based GWAS meta-analysis: do current meta-analysis approaches resolve power and replication in genetic association studies?.	0
82	MicroRNA-eQTLs in the developing human neocortex link miR-4707-3p expression to brain size. 12,	0
81	Long-chain polyunsaturated lipids associated with responsiveness to anti-PD-1 therapy are co-localized with immune infiltrates in the tumor microenvironment. **2023**, 102902	0
80	Allele-specific expression analysis for complex genetic phenotypes applied to a unique dilated cardiomyopathy cohort. **2023**, 13,	0
79	Transcriptome analysis reveals flower development and the role of hormones in three flower types of grapevine.	0
78	Sequence analyses of relapsed or refractory diffuse large B-cell lymphomas unravel three genetic subgroups of patients and the GNA13 mutant as poor prognostic biomarker, results of LNH-EP1 study.	0
77	Axl regulated survival/proliferation network and its therapeutic intervention in mouse models of glomerulonephritis. **2022**, 24,	0
76	Association between ustekinumab therapy and changes in specific anti-microbial response, serum biomarkers, and microbiota composition in patients with IBD: A pilot study. **2022**, 17, e0277576	0
75	SHP-2 and PD-1-SHP-2 signaling regulate myeloid cell differentiation and antitumor responses. **2023**, 24, 55-68	0
74	SNEP-DB: An integrated database to associate genomic and pathological aspects of psychiatric disorders. **2022**,	0
73	370. Detecting the presence of genomic imprinting for carcass traits in cattle using imputed high-density genotypes. **2022**,	0
72	Identification of miRNA-mediated gene regulatory networks in L-methionine exposure counteracts cocaine-conditioned place preference in mice. 13,	0
71	Global analysis of aging-related protein structural changes uncovers enzyme polymerization-based control of longevity.	0
70	Strain-specific alterations in gut microbiome and host immune responses elicited by tolerogenic Bifidobacterium pseudolongum. **2023**, 13,	0
69	Sequencing-based fine-mapping and in silico functional characterization of the 10q24.32 arsenic metabolism efficiency locus across multiple arsenic-exposed populations. **2023**, 19, e1010588	0
68	Confidence and Discoveries with E-values. **2023**, -1,	0

67	Genetic control of RNA editing in neurodegenerative disease.	0
66	False discovery rate control in cancer biomarker selection. **2023**,	0
65	Alternative polyadenylation transcriptome-wide association study identifies APA-linked susceptibility genes in brain disorders. **2023**, 14,	0
64	Deciphering Macromolecular Interactions Involved in Abiotic Stress Signaling: A Review of Bioinformatics Analysis. **2023**, 257-294	0
63	Conscientiousness associated with efficiency of the salience/ventral attention network: Replication in three samples using individualized parcellation. **2023**, 272, 120081	0
62	Methodology to identify a gene expression signature by merging microarray datasets. **2023**, 159, 106867	0
61	Plasma lipidomic profile of depressive symptoms: a longitudinal study in a large sample of community-dwelling American Indians in the strong heart study.	1
60	Molecular quantitative trait loci. **2023**, 3,	0
59	The tragedy of the common? A comparative population genomic study of two bumblebee species.	0
58	Differing paths to organizational performance: strategic implications of resource transformation and capability reinforcement. 1-24	0
57	Pan-cancer molecular subtypes of metastasis reveal distinct and evolving transcriptional programs. **2023**, 4, 100932	1
56	Sample multiplexing-based targeted pathway proteomics with real-time analytics reveals the impact of genetic variation on protein expression. **2023**, 14,	0
55	497. Enrichment of causative variants in tissue-specific and shared ATAC-Seq peaks in cattle. **2022**,	0
54	Identification of candidate genes for nicotine withdrawal in C57BL / 6J ⍰DBA / 2J recombinant inbred mice. **2023**, 22,	0
53	Sex Significantly Impacts the Function of Major Depression⍰linked Variants In ́Vivo. **2023**,	0
52	JUMP: replicability analysis of high-throughput experiments with applications to spatial transcriptomic studies.	0
51	ATP8B1 : A prognostic prostate cancer biomarker identified via genetic analysis. **2023**, 83, 602-611	0
50	Comparison of the gut microbiome and resistome in captive African and Asian elephants on the same diet. 10,	0

49	Genes Vary Greatly in Their Propensity for Collateral Fitness Effects of Mutations. **2023**, 40,	0
48	Deciphering local adaptation of native Indian cattle (Bos indicus) breeds using landscape genomics and in-silico prediction of deleterious SNP effects on protein structure and function. **2023**, 13,	0
47	Geographic variation of theforgene reveals signatures of local adaptation inDrosophila melanogaster.	0
46	Screening-Assisted Dynamic Multiple Testing with False Discovery Rate Control. **2023**, 36, 716-754	0
45	Genomic insights into the NPGS intermediate wheatgrass germplasm collection.	0
44	Quantifying the weekly cycle effect of air pollution in cities of China.	0
43	Regional disparity of residential solar panel diffusion in Australia: The roles of socio-economic factors. **2023**, 206, 808-819	0
42	Genetic influences vary by age and sex: Trajectories of the association of cholinergic system variants and theta band event related oscillations.	0
41	Whole-genome sequencing of cryopreserved resources from French Large White pigs at two distinct sampling times reveals strong signatures of convergent and divergent selection between the dam and sire lines. **2023**, 55,	0
40	A field-wide assessment of differential expression profiling by high-throughput sequencing reveals widespread bias. **2023**, 21, e3002007	0
39	Comparative Genomic and Transcriptomic Analyses Reveal the Impacts of Genetic Admixture in Kazaks, Uyghurs, and Huis. **2023**, 40,	0
38	HiPerMAb: a tool for judging the potential of small sample size biomarker pilot studies. **2023**,	0
37	Computational genomics for understanding of DNA-DNA and protein-protein similarity. **2023**, 217-263	0
36	Reduction of mRNA m6A associates with glucose metabolism via YTHDC1 in human and mice. **2023**, 198, 110607	0
35	Geography, environment, and colonization history interact with morph type to shape genomic variation in an Arctic fish.	0
34	Release from sexual selection leads to rapid genome-wide evolution in Aedes aegypti. **2023**, 33, 1351-1357.e5	0
33	Identification of asthma-related genes using asthmatic blood eQTLs of Korean patients.	0
32	Bioinformatic and Statistical Analysis of Microbiome Data. **2023**, 183-229	0

31	The analysis of gut microbiota in patients with bile acid diarrhoea treated with colesevelam. 14,	0
30	Integration of Stemness Gene Signatures Reveals Core Functional Modules of Stem Cells and Potential Novel Stemness Genes. **2023**, 14, 745	0
29	Muscle of obese insulin-resistant humans exhibits losses in proteostasis and attenuated proteome dynamics that are improved by exercise training.	0
28	RNA sequencing-based exploration of the effects of far-red light on microRNAs involved in the shade-avoidance response of D. officinale. 11, e15001	0
27	Universal recording of cell-cell contacts in vivo for interaction-based transcriptomics.	0
26	Pretransplant systemic metabolic profiles in allogeneic hematopoietic stem cell transplant recipients - identification of patient subsets with increased transplant-related mortality. **2023**,	0
25	DIP-MS: A novel ultra-deep interaction proteomics for the deconvolution of protein complexes.	0
24	An integrative framework for circular RNA quantitative trait locus discovery with application in human T cells.	0
23	Change-detection-assisted multiple testing for spatiotemporal data. **2023**,	1
22	Small RNA sequencing identified miR-3180 as a potential prognostic biomarker for Chinese hepatocellular carcinoma patients. 14,	0
21	Evaluation of dynamic differential expressed genes combined with functional enrichment of floral development in Arabidopsis. **2022**,	0
20	Systemic Alterations of Cancer Cells and Their Boost by Polyploidization: Unicellular Attractor (UCA) Model. **2023**, 24, 6196	0
19	Applying T-classifier, binary classifiers, upon high-throughput TCR sequencing output to identify cytomegalovirus exposure history. **2023**, 13,	0
18	Genetic variation in cis-regulatory domains suggests cell type-specific regulatory mechanisms in immunity. **2023**, 6,	0
17	Protein-metabolite interactomics of carbohydrate metabolism reveal regulation of lactate dehydrogenase. **2023**, 379, 996-1003	0
16	Pasture-finishing of bison improves animal metabolic health and potential health-promoting compounds in meat. **2023**, 14,	0
15	HIV-1 subtype C Nef-mediated SERINC5 down-regulation significantly contributes to overall Nef activity. **2023**, 20,	0
14	The transcription regulator ATF4 is a mediator of skeletal muscle aging.	0

13	A nonparametric mixture approach to density and null proportion estimation in large-scale multiple comparison problems. **2023**, 65, 49-75	0
12	Genetic markers and tree properties predicting wood biorefining potential in aspen (Populus tremula) bioenergy feedstock. **2023**, 16,	0
11	The climate changes promoted the chloroplast genomic evolution of Dendrobium orchids among multiple photosynthetic pathways. **2023**, 23,	0
10	Protocol for a nested case-control study design for omics investigations in the Environmental Determinants of Islet Autoimmunity cohort. **2023**, 55,	0
9	Longitudinal lipidomic signatures of all-cause and CVD mortality in American Indians: findings from the Strong Heart Study.	0
8	Gut microbiota-mediated associations of green tea and catechin intakes with glucose metabolism in individuals without type 2 diabetes mellitus: a four-season observational study with mediation analysis. **2023**, 205,	0
7	Exceedance control of the false discovery proportion via high precision inversion method of Berk-Jones statistics. **2023**, 185, 107758	0
6	Comparative Transcriptome Analysis Reveals the Effect of the DHN Melanin Biosynthesis Pathway on the Appressorium Turgor Pressure of the Poplar Anthracnose-Causing Fungus Colletotrichum gloeosporioides. **2023**, 24, 7411	0
5	Identifying novel regulatory effects for clinically relevant genes through the study of the Greek population.	0
4	Mapping genomic regulation of kidney disease and traits through high-resolution and interpretable eQTLs. **2023**, 14,	0
3	The causal relationship between gut microbiota and immune skin diseases: a bidirectional Mendelian randomization.	0
2	Summary and Exploration of Exclusive Hypothesis Test of Pleiotropy. **2023**, 12, 1531-1548	0
1	A study of gene expression in the living human brain.	0