Shawn E Levy

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3051145/publications.pdf

Version: 2024-02-01

153 papers	48,705 citations	7069 78 h-index	6282 158 g-index
167 all docs	167 docs citations	167 times ranked	79005 citing authors

#	Article	IF	Citations
1	System-wide transcriptome damage and tissue identity loss in COVID-19 patients. Cell Reports Medicine, 2022, 3, 100522.	3.3	24
2	Betacoronavirus-specific alternate splicing. Genomics, 2022, 114, 110270.	1.3	12
3	Shotgun transcriptome, spatial omics, and isothermal profiling of SARS-CoV-2 infection reveals unique host responses, viral diversification, and drug interactions. Nature Communications, 2021, 12, 1660.	5.8	132
4	Coordinated interactions between endothelial cells and macrophages in the islet microenvironment promote Î² cell regeneration. Npj Regenerative Medicine, 2021, 6, 22.	2.5	14
5	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. Nature Genetics, 2021, 53, 817-829.	9.4	629
6	Combinatorial transcription factor profiles predict mature and functional human islet Î± and Î² cells. JCI Insight, 2021, 6, .	2.3	22
7	Performance assessment of DNA sequencing platforms in the ABRF Next-Generation Sequencing Study. Nature Biotechnology, 2021, 39, 1129-1140.	9.4	69
8	Identification of canine circulating miRNAs as tumor biospecific markers using Next-Generation Sequencing and Q-RT-PCR. Biochemistry and Biophysics Reports, 2021, 28, 101106.	0.7	7
9	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. Molecular Psychiatry, 2021, 26, 5239-5250.	4.1	15
10	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. Biological Psychiatry, 2020, 88, 169-184.	0.7	137
11	The COVID-19 XPRIZE and the need for scalable, fast, and widespread testing. Nature Biotechnology, 2020, 38, 1021-1024.	9.4	71
12	Single-cell sperm transcriptomes and variants from fathers of children with and without autism spectrum disorder. Npj Genomic Medicine, 2020, 5, 14.	1.7	10
13	Tacrolimus- and sirolimus-induced human Î² cell dysfunction is reversible and preventable. JCI Insight, 2020, 5, .	2.3	41
14	The Airplane Cabin Microbiome. Microbial Ecology, 2019, 77, 87-95.	1.4	19
15	The whole-genome landscape of Burkitt lymphoma subtypes. Blood, 2019, 134, 1598-1607.	0.6	113
16	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
17	The Extracellular RNA Communication Consortium: Establishing Foundational Knowledge and Technologies for Extracellular RNA Research. Cell, 2019, 177, 231-242.	13.5	152
18	AS03-Adjuvanted H5N1 Avian Influenza Vaccine Modulates Early Innate Immune Signatures in Human Peripheral Blood Mononuclear Cells. Journal of Infectious Diseases, 2019, 219, 1786-1798.	1.9	16

#	Article	IF	Citations
19	Ectonucleoside Triphosphate Diphosphohydrolase-3 Antibody Targets Adult Human Pancreatic Î² Cells for InÂVitro and InÂVivo Analysis. Cell Metabolism, 2019, 29, 745-754.e4.	7.2	59
20	Next-Generation Sequencing Strategies. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a025791.	2.9	51
21	Î± Cell Function and Gene Expression Are Compromised in Type 1 Diabetes. Cell Reports, 2018, 22, 2667-2676.	2.9	152
22	Genetic Risk for Subsequent Neoplasms Among Long-Term Survivors of Childhood Cancer. Journal of Clinical Oncology, 2018, 36, 2078-2087.	0.8	105
23	Diverse Long RNAs Are Differentially Sorted into Extracellular Vesicles Secreted by Colorectal Cancer Cells. Cell Reports, 2018, 25, 715-725.e4.	2.9	102
24	Extremely rare variants reveal patterns of germline mutation rate heterogeneity in humans. Nature Communications, 2018, 9, 3753.	5.8	121
25	IRF2BPL Is Associated with Neurological Phenotypes. American Journal of Human Genetics, 2018, 103, 245-260.	2.6	69
26	Spaceflight Modifies Escherichia coli Gene Expression in Response to Antibiotic Exposure and Reveals Role of Oxidative Stress Response. Frontiers in Microbiology, 2018, 9, 310.	1.5	77
27	Functional variants in TBX2 are associated with a syndromic cardiovascular and skeletal developmental disorder. Human Molecular Genetics, 2018, 27, 2454-2465.	1.4	54
28	Human islets expressing HNF1A variant have defective Î² cell transcriptional regulatory networks. Journal of Clinical Investigation, 2018, 129, 246-251.	3.9	65
29	The Undiagnosed Diseases Network: Accelerating Discovery about Health and Disease. American Journal of Human Genetics, 2017, 100, 185-192.	2.6	142
30	The Genetic Basis of Hepatosplenic T-cell Lymphoma. Cancer Discovery, 2017, 7, 369-379.	7.7	163
31	A high-throughput molecular data resource for cutaneous neurofibromas. Scientific Data, 2017, 4, 170045.	2.4	22
32	Enteropathy-associated T cell lymphoma subtypes are characterized by loss of function of SETD2. Journal of Experimental Medicine, 2017, 214, 1371-1386.	4.2	144
33	MARRVEL: Integration of Human and Model Organism Genetic Resources to Facilitate Functional Annotation of the Human Genome. American Journal of Human Genetics, 2017, 100, 843-853.	2.6	181
34	Targeted next-generation sequencing reveals MODY in up to 6.5% of antibody-negative diabetes cases listed in the Norwegian Childhood Diabetes Registry. Diabetologia, 2017, 60, 625-635.	2.9	106
35	Interrupted Glucagon Signaling Reveals Hepatic Î± Cell Axis and Role for L-Glutamine in Î± Cell Proliferation. Cell Metabolism, 2017, 25, 1362-1373.e5.	7.2	153
36	Ecophysiological Examination of the Lake Erie Microcystis Bloom in 2014: Linkages between Biology and the Water Supply Shutdown of Toledo, OH. Environmental Science & Technology, 2017, 51, 6745-6755.	4.6	196

#	Article	IF	Citations
37	A Syndromic Neurodevelopmental Disorder Caused by De Novo Variants in EBF3. American Journal of Human Genetics, 2017, 100, 128-137.	2.6	96
38	Genetic and Functional Drivers of Diffuse Large BÂCell Lymphoma. Cell, 2017, 171, 481-494.e15.	13.5	804
39	International Standards for Genomes, Transcriptomes, and Metagenomes. Journal of Biomolecular Techniques, 2017, 28, 8-18.	0.8	33
40	Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. Genome Biology, 2017, 18, 182.	3.8	260
41	Metagenomic characterization of ambulances across the USA. Microbiome, 2017, 5, 125.	4.9	32
42	Genomic Methods and Microbiological Technologies for Profiling Novel and Extreme Environments for the Extreme Microbiome Project (XMP). Journal of Biomolecular Techniques, 2017, 28, 31-39.	0.8	53
43	Age-dependent human Î² cell proliferation induced by glucagon-like peptide 1 and calcineurin signaling. Journal of Clinical Investigation, 2017, 127, 3835-3844.	3.9	118
44	Cell-Based Systems Biology Analysis of Human AS03-Adjuvanted H5N1 Avian Influenza Vaccine Responses: A Phase I Randomized Controlled Trial. PLoS ONE, 2017, 12, e0167488.	1.1	48
45	Circular RNAs are down-regulated in KRAS mutant colon cancer cells and can be transferred to exosomes. Scientific Reports, 2016, 6, 37982.	1.6	268
46	The mammalian LINC complex regulates genome transcriptional responses to substrate rigidity. Scientific Reports, 2016, 6, 38063.	1.6	121
47	A comparison of microRNA expression profiles from splenic hemangiosarcoma, splenic nodular hyperplasia, and normal spleens of dogs. BMC Veterinary Research, 2016, 12, 272.	0.7	33
48	Exome Sequencing of Familial Bipolar Disorder. JAMA Psychiatry, 2016, 73, 590.	6.0	97
49	De Novo Truncating Variants in ASXL2 Are Associated with a Unique and Recognizable Clinical Phenotype. American Journal of Human Genetics, 2016, 99, 991-999.	2.6	68
50	Next-generation genotype imputation service and methods. Nature Genetics, 2016, 48, 1284-1287.	9.4	2,828
51	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
52	Advancements in Next-Generation Sequencing. Annual Review of Genomics and Human Genetics, 2016, 17, 95-115.	2.5	433
53	Age and Nursing Affect the Neonatal Porcine Uterine Transcriptome1. Biology of Reproduction, 2016, 94, 46.	1.2	13
54	Connecting the Dots: Therapy-Induced Senescence and a Tumor-Suppressive Immune Microenvironment. Journal of the National Cancer Institute, 2016, 108, djv406.	3.0	61

#	Article	IF	Citations
55	A Molecular Genetic Basis Explaining Altered Bacterial Behavior in Space. PLoS ONE, 2016, 11, e0164359.	1.1	61
56	Modern Methods for Delineating Metagenomic Complexity. Cell Systems, 2015, 1, 6-7.	2.9	20
57	KRAS-dependent sorting of miRNA to exosomes. ELife, 2015, 4, e07197.	2.8	296
58	Transcriptome Profiling of Pediatric Core Binding Factor AML. PLoS ONE, 2015, 10, e0138782.	1.1	14
59	Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics. Cell Systems, 2015, 1, 72-87.	2.9	241
60	Exome sequencing in amyotrophic lateral sclerosis identifies risk genes and pathways. Science, 2015, 347, 1436-1441.	6.0	823
61	Defects of CRB2 Cause Steroid-Resistant Nephrotic Syndrome. American Journal of Human Genetics, 2015, 96, 153-161.	2.6	88
62	Deep sequencing of RYR3 gene identifies rare and common variants associated with increased carotid intima-media thickness (cIMT) in HIV-infected individuals. Journal of Human Genetics, 2015, 60, 63-67.	1.1	3
63	KANK deficiency leads to podocyte dysfunction and nephrotic syndrome. Journal of Clinical Investigation, 2015, 125, 2375-2384.	3.9	159
64	A Cell-Based Systems Biology Assessment of Human Blood to Monitor Immune Responses after Influenza Vaccination. PLoS ONE, 2015, 10, e0118528.	1.1	79
65	Vascular endothelial growth factor coordinates islet innervation via vascular scaffolding. Development (Cambridge), 2014, 141, 1480-1491.	1.2	77
66	Progressive increase in mtDNA 3243A>G heteroplasmy causes abrupt transcriptional reprogramming. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4033-42.	3.3	251
67	Differential Gene Expression Landscape of Co-Existing Cervical Pre-Cancer Lesions Using RNA-seq. Frontiers in Oncology, 2014, 4, 339.	1.3	23
68	Diversity and genomic insights into the uncultured <scp>C</scp>hloroflexi from the human microbiota. Environmental Microbiology, 2014, 16, 2635-2643.	1.8	55
69	In search of rare variants: Preliminary results from whole genome sequencing of 1,325 individuals with psychophysiological endophenotypes. Psychophysiology, 2014, 51, 1309-1320.	1.2	25
70	Whole-exome resequencing distinguishes cystic kidney diseases from phenocopies in renal ciliopathies. Kidney International, 2014, 85, 880-887.	2.6	67
71	Islet Microenvironment, Modulated by Vascular Endothelial Growth Factor-A Signaling, Promotes Î² Cell Regeneration. Cell Metabolism, 2014, 19, 498-511.	7.2	177
72	Mutations in EMP2 Cause Childhood-Onset Nephrotic Syndrome. American Journal of Human Genetics, 2014, 94, 884-890.	2.6	101

#	Article	IF	Citations
73	Multi-platform assessment of transcriptome profiling using RNA-seq in the ABRF next-generation sequencing study. Nature Biotechnology, 2014, 32, 915-925.	9.4	217
74	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. Nature Biotechnology, 2014, 32, 903-914.	9.4	883
75	The genomic landscape of mantle cell lymphoma is related to the epigenetically determined chromatin state of normal B cells. Blood, 2014, 123, 2988-2996.	0.6	224
76	Significance of expression of ITGA5 and its splice variants in acute myeloid leukemia: A report from the children's oncology group. American Journal of Hematology, 2013, 88, 694-702.	2.0	11
77	A Neurodegeneration-Specific Gene-Expression Signature of Acutely Isolated Microglia from an Amyotrophic Lateral Sclerosis Mouse Model. Cell Reports, 2013, 4, 385-401.	2.9	552
78	ZMYND10 Is Mutated in Primary Ciliary Dyskinesia and Interacts with LRRC6. American Journal of Human Genetics, 2013, 93, 336-345.	2.6	183
79	Malignant transformation of colonic epithelial cells by a colon-derived long noncoding RNA. Biochemical and Biophysical Research Communications, 2013, 440, 99-104.	1.0	25
80	Novel rare variants in congenital cardiac arrhythmia genes are frequent in drug-induced torsades de pointes. Pharmacogenomics Journal, 2013, 13, 325-329.	0.9	61
81	Genetic heterogeneity of diffuse large B-cell lymphoma. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1398-1403.	3.3	494
82	Gene Signature Distinguishes Patients with Chronic Ulcerative Colitis Harboring Remote Neoplastic Lesions. Inflammatory Bowel Diseases, 2013, 19, 461-470.	0.9	39
83	ADCK4 mutations promote steroid-resistant nephrotic syndrome through CoQ10 biosynthesis disruption. Journal of Clinical Investigation, 2013, 123, 5179-5189.	3.9	275
84	ARHGDIA mutations cause nephrotic syndrome via defective RHO GTPase signaling. Journal of Clinical Investigation, 2013, 123, 3243-3253.	3.9	196
85	Mutations in the colony stimulating factor 1 receptor (CSF1R) gene cause hereditary diffuse leukoencephalopathy with spheroids. Nature Genetics, 2012, 44, 200-205.	9.4	428
86	Increased Protein-Coding Mutations in the Mitochondrial Genome of African American Women With Preeclampsia. Reproductive Sciences, 2012, 19, 1343-1351.	1.1	12
87	Exome Analysis of a Family With Pleiotropic Congenital Heart Disease. Circulation: Cardiovascular Genetics, 2012, 5, 175-182.	5.1	65
88	The genetic landscape of mutations in Burkitt lymphoma. Nature Genetics, 2012, 44, 1321-1325.	9.4	517
89	Exome Capture Reveals ZNF423 and CEP164 Mutations, Linking Renal Ciliopathies to DNA Damage Response Signaling. Cell, 2012, 150, 533-548.	13.5	347
90	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	13.7	15,516

#	Article	IF	Citations
91	RAF265 Inhibits the Growth of Advanced Human Melanoma Tumors. Clinical Cancer Research, 2012, 18, 2184-2198.	3.2	61
92	The use of next generation sequencing technology to study the effect of radiation therapy on mitochondrial DNA mutation. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2012, 744, 154-160.	0.9	49
93	The Pan-ErbB Negative Regulator Lrig1 Is an Intestinal Stem Cell Marker that Functions as a Tumor Suppressor. Cell, 2012, 149, 146-158.	13.5	580
94	De novo gene mutations highlight patterns of genetic and neural complexity in schizophrenia. Nature Genetics, 2012, 44, 1365-1369.	9.4	412
95	Patterns and rates of exonic de novo mutations in autism spectrum disorders. Nature, 2012, 485, 242-245.	13.7	1,597
96	Familial Diarrhea Syndrome Caused by an ActivatingGUCY2CMutation. New England Journal of Medicine, 2012, 366, 1586-1595.	13.9	175
97	Exome Sequencing and Genetic Testing for MODY. PLoS ONE, 2012, 7, e38050.	1.1	91
98	FAN1 mutations cause karyomegalic interstitial nephritis, linking chronic kidney failure to defective DNA damage repair. Nature Genetics, 2012, 44, 910-915.	9.4	205
99	ANKRD7 and CYTL1 are novel risk genes for alcohol drinking behavior. Chinese Medical Journal, 2012, 125, 1127-34.	0.9	11
100	Exome sequencing supports a de novo mutational paradigm for schizophrenia. Nature Genetics, 2011, 43, 864-868.	9.4	435
101	Novel human genetic variants associated with extrapulmonary tuberculosis: a pilot genome wide association study. BMC Research Notes, 2011, 4, 28.	0.6	33
102	Characterizing the Impact of Smoking and Lung Cancer on the Airway Transcriptome Using RNA-Seq. Cancer Prevention Research, 2011, 4, 803-817.	0.7	144
103	Genome-wide association study identifies breast cancer risk variant at 10q21.2: results from the Asia Breast Cancer Consortium. Human Molecular Genetics, 2011, 20, 4991-4999.	1.4	92
104	A genome-wide association analysis implicates SOX6 as a candidate gene for wrist bone mass. Science China Life Sciences, 2010, 53, 1065-1072.	2.3	13
105	Polymorphisms in IL-1Î², vitamin D receptor FokI, and Toll-like receptor 2 are associated with extrapulmonary tuberculosis. BMC Medical Genetics, 2010, 11, 37.	2.1	55
106	Candidate exome capture identifies mutation of SDCCAG8 as the cause of a retinal-renal ciliopathy. Nature Genetics, 2010, 42, 840-850.	9.4	295
107	African Mitochondrial DNA Subhaplogroups and Peripheral Neuropathy during Antiretroviral Therapy. Journal of Infectious Diseases, 2010, 201, 1703-1707.	1.9	38
108	Genome-wide association study of homocysteine levels in Filipinos provides evidence for CPS1 in women and a stronger MTHFR effect in young adults. Human Molecular Genetics, 2010, 19, 2050-2058.	1.4	62

#	Article	IF	Citations
109	Experimentally Derived Metastasis Gene Expression Profile Predicts Recurrence and Death in Patients With Colon Cancer. Gastroenterology, 2010, 138, 958-968.	0.6	576
110	Genome-Wide Association Analyses Identify SPOCK as a Key Novel Gene Underlying Age at Menarche. PLoS Genetics, 2009, 5, e1000420.	1.5	59
111	Genome-wide association study identifies two novel loci containing FLNB and SBF2 genes underlying stature variation. Human Molecular Genetics, 2009, 18, 1661-1669.	1.4	27
112	Powerful Bivariate Genome-Wide Association Analyses Suggest the SOX6 Gene Influencing Both Obesity and Osteoporosis Phenotypes in Males. PLoS ONE, 2009, 4, e6827.	1.1	87
113	Genome-wide association study identifies a new breast cancer susceptibility locus at 6q25.1. Nature Genetics, 2009, 41, 324-328.	9.4	481
114	Genome-wide Association and Follow-Up Replication Studies Identified ADAMTS18 and TGFBR3 as Bone Mass Candidate Genes in Different Ethnic Groups. American Journal of Human Genetics, 2009, 84, 388-398.	2.6	187
115	Genome-wide Association and Replication Studies Identified TRHR as an Important Gene for Lean Body Mass. American Journal of Human Genetics, 2009, 84, 418-423.	2.6	103
116	Genome-Wide Association Study of Exercise Behavior in Dutch and American Adults. Medicine and Science in Sports and Exercise, 2009, 41, 1887-1895.	0.2	105
117	Whole Genome Distribution and Ethnic Differentiation of Copy Number Variation in Caucasian and Asian Populations. PLoS ONE, 2009, 4, e7958.	1.1	51
118	Strong association of de novo copy number mutations with sporadic schizophrenia. Nature Genetics, 2008, 40, 880-885.	9.4	752
119	Complementary RNA amplification methods enhance microarray identification of transcripts expressed in the C. elegans nervous system. BMC Genomics, 2008, 9, 84.	1.2	34
120	MITOCHIP assessment of differential gene expression in the skeletal muscle of Ant1 knockout mice: Coordinate regulation of OXPHOS, antioxidant, and apoptotic genes. Biochimica Et Biophysica Acta - Bioenergetics, 2008, 1777, 666-675.	0.5	28
121	Common MMP-7 Polymorphisms and Breast Cancer Susceptibility: A Multistage Study of Association and Functionality. Cancer Research, 2008, 68, 6453-6459.	0.4	39
122	Oncogenic Ras and Transforming Growth Factor-Î² Synergistically Regulate AU-Rich Elementâ€“Containing mRNAs during Epithelial to Mesenchymal Transition. Molecular Cancer Research, 2008, 6, 1124-1136.	1.5	38
123	Genome-wide association scans identified CTNNBL1 as a novel gene for obesity. Human Molecular Genetics, 2008, 17, 1803-1813.	1.4	168
124	Gene Expression Profiling of a Mouse Model of Pancreatic Islet Dysmorphogenesis. PLoS ONE, 2008, 3, e1611.	1.1	19
125	Identification of PLCL1 Gene for Hip Bone Size Variation in Females in a Genome-Wide Association Study. PLoS ONE, 2008, 3, e3160.	1.1	57
126	A genome-scale map of expression for a mouse brain section obtained using voxelation. Physiological Genomics, 2007, 30, 313-321.	1.0	27

#	Article	IF	Citations
127	Antiproliferative Agents Alter Vascular Plasminogen Activator Inhibitor-1 Expression. Arteriosclerosis, Thrombosis, and Vascular Biology, 2007, 27, 400-406.	1.1	62
128	Transcriptional recapitulation and subversion of embryonic colon development by mouse colon tumor models and human colon cancer. Genome Biology, 2007, 8, R131.	3.8	299
129	Genomics and proteomics: Emerging technologies in clinical cancer research. Critical Reviews in Oncology/Hematology, 2007, 61, 1-25.	2.0	55
130	Gene Expression Profiles as Markers of Aggressive Diseaseâ€"EGFR as a Factor. International Journal of Radiation Oncology Biology Physics, 2007, 69, S102-S105.	0.4	7
131	Ovarian gene expression in the absence of FIGLA, an oocyte-specific transcription factor. BMC Developmental Biology, 2007, 7, 67.	2.1	102
132	The MicroArray Quality Control (MAQC) project shows inter- and intraplatform reproducibility of gene expression measurements. Nature Biotechnology, 2006, 24, 1151-1161.	9.4	1,927
133	Clinical applications of genomics in head and neck cancer. Head and Neck, 2006, 28, 360-368.	0.9	12
134	Gene Expression Differences Associated with Human Papillomavirus Status in Head and Neck Squamous Cell Carcinoma. Clinical Cancer Research, 2006, 12, 701-709.	3.2	269
135	Increased Epidermal Growth Factor Receptor Gene Copy Number Is Associated With Poor Prognosis in Head and Neck Squamous Cell Carcinomas. Journal of Clinical Oncology, 2006, 24, 4170-4176.	0.8	532
136	Analysis of Host- and Tumor-Derived Proteinases Using a Custom Dual Species Microarray Reveals a Protective Role for Stromal Matrix Metalloproteinase-12 in Nonâ€"Small Cell Lung Cancer. Cancer Research, 2006, 66, 7968-7975.	0.4	82
137	Gene Expression Profiles Identify Epithelial-to-Mesenchymal Transition and Activation of Nuclear Factor-ÎºB Signaling as Characteristics of a High-risk Head and Neck Squamous Cell Carcinoma. Cancer Research, 2006, 66, 8210-8218.	0.4	238
138	Gene expression profile analysis of mouse colon embryonic development. Genesis, 2005, 41, 1-12.	0.8	20
139	A comprehensive evaluation of multicategory classification methods for microarray gene expression cancer diagnosis. Bioinformatics, 2005, 21, 631-643.	1.8	750
140	Genomic and Proteomic Analysis of Mammary Tumors Arising in Transgenic Mice. Journal of Proteome Research, 2005, 4, 2088-2098.	1.8	13
141	The ADP/ATP translocator is not essential for the mitochondrial permeability transition pore. Nature, 2004, 427, 461-465.	13.7	986
142	TGF-beta1 induction of the adenine nucleotide translocator 1 in astrocytes occurs through Smads and Sp1 transcription factors. BMC Neuroscience, 2004, 5, 1.	0.8	82
143	Anatomical Methods for Voxelation of the Mammalian Brain. Neurochemical Research, 2004, 29, 1299-1306.	1.6	1
144	Proteome analysis of human colon cancer by two-dimensional difference gel electrophoresis and mass spectrometry. Proteomics, 2004, 4, 793-811.	1.3	352

#	Article	IF	Citations
145	Chaotic mixer improves microarray hybridization. Analytical Biochemistry, 2004, 325, 215-226.	1.1	76
146	Effects of relative humidity and buffer additives on the contact printing of microarrays by quill pins. Analytical Biochemistry, 2003, 320, 281-291.	1.1	48
147	Profiling genes related to mitochondrial function in mice treated with N-methyl-4-phenyl-1,2,3,6-tetrahydropyridine. Biochemical and Biophysical Research Communications, 2003, 308, 197-205.	1.0	13
148	Microarray Analysis in Drug Discovery: An Uplifting View of Depression. Science Signaling, 2003, 2003, pe46-pe46.	1.6	5
149	A training-testing approach to the molecular classification of resected non-small cell lung cancer. Clinical Cancer Research, 2003, 9, 4695-704.	3.2	102
150	Microarray Analysis of Neointima. Arteriosclerosis, Thrombosis, and Vascular Biology, 2002, 22, 1946-1947.	1.1	2
151	Maternal germ-line transmission of mutant mtDNAs from embryonic stem cell-derived chimeric mice. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 14461-14466.	3.3	129
152	Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes. Gene, 2000, 254, 57-66.	1.0	89
153	Transfer of chloramphenicol-resistant mitochondrial DNA into the chimeric mouse. Transgenic Research, 1999, 8, 137-145.	1.3	50