Shawn E Levy

List of Publications by Year
in descending order

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153 papers	48,705 citations	7096 78 h-index	6300 158 g-index
167 all docs	167 docs citations	167 times ranked	79005 citing authors

#	Article	IF	Citations
1	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	27.8	15,516
2	Next-generation genotype imputation service and methods. Nature Genetics, 2016, 48, 1284-1287.	21.4	2,828
3	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	21.4	2,421
4	The MicroArray Quality Control (MAQC) project shows inter- and intraplatform reproducibility of gene expression measurements. Nature Biotechnology, 2006, 24, 1151-1161.	17.5	1,927
5	Patterns and rates of exonic de novo mutations in autism spectrum disorders. Nature, 2012, 485, 242-245.	27.8	1,597
6	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	21.4	1,191
7	The ADP/ATP translocator is not essential for the mitochondrial permeability transition pore. Nature, 2004, 427, 461-465.	27.8	986
8	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. Nature Biotechnology, 2014, 32, 903-914.	17.5	883
9	Exome sequencing in amyotrophic lateral sclerosis identifies risk genes and pathways. Science, 2015, 347, 1436-1441.	12.6	823
10	Genetic and Functional Drivers of Diffuse Large BÂCell Lymphoma. Cell, 2017, 171, 481-494.e15.	28.9	804
11	Strong association of de novo copy number mutations with sporadic schizophrenia. Nature Genetics, 2008, 40, 880-885.	21.4	752
12	A comprehensive evaluation of multicategory classification methods for microarray gene expression cancer diagnosis. Bioinformatics, 2005, 21, 631-643.	4.1	750
13	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.	21.4	629
14	The Pan-ErbB Negative Regulator Lrig1 Is an Intestinal Stem Cell Marker that Functions as a Tumor Suppressor. Cell, 2012, 149, 146-158.	28.9	580
15	Experimentally Derived Metastasis Gene Expression Profile Predicts Recurrence and Death in Patients With Colon Cancer. Gastroenterology, 2010, 138, 958-968.	1.3	576
16	A Neurodegeneration-Specific Gene-Expression Signature of Acutely Isolated Microglia from an Amyotrophic Lateral Sclerosis Mouse Model. Cell Reports, 2013, 4, 385-401.	6.4	552
17	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.	1.6	532
18	The genetic landscape of mutations in Burkitt lymphoma. Nature Genetics, 2012, 44, 1321-1325.	21.4	517

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19	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.	7.1	494
20	Genome-wide association study identifies a new breast cancer susceptibility locus at 6q25.1. Nature Genetics, 2009, 41, 324-328.	21.4	481
21	Exome sequencing supports a de novo mutational paradigm for schizophrenia. Nature Genetics, 2011, 43, 864-868.	21.4	435
22	Advancements in Next-Generation Sequencing. Annual Review of Genomics and Human Genetics, 2016, 17, 95-115.	6.2	433
23	Mutations in the colony stimulating factor 1 receptor (CSF1R) gene cause hereditary diffuse leukoencephalopathy with spheroids. Nature Genetics, 2012, 44, 200-205.	21.4	428
24	De novo gene mutations highlight patterns of genetic and neural complexity in schizophrenia. Nature Genetics, 2012, 44, 1365-1369.	21.4	412
25	Proteome analysis of human colon cancer by two-dimensional difference gel electrophoresis and mass spectrometry. Proteomics, 2004, 4, 793-811.	2.2	352
26	Exome Capture Reveals ZNF423 and CEP164 Mutations, Linking Renal Ciliopathies to DNA Damage Response Signaling. Cell, 2012, 150, 533-548.	28.9	347
27	Transcriptional recapitulation and subversion of embryonic colon development by mouse colon tumor models and human colon cancer. Genome Biology, 2007, 8, R131.	8.8	299
28	KRAS-dependent sorting of miRNA to exosomes. ELife, 2015, 4, e07197.	6.0	296
29	Candidate exome capture identifies mutation of SDCCAG8 as the cause of a retinal-renal ciliopathy. Nature Genetics, 2010, 42, 840-850.	21.4	295
30	ADCK4 mutations promote steroid-resistant nephrotic syndrome through CoQ10 biosynthesis disruption. Journal of Clinical Investigation, 2013, 123, 5179-5189.	8.2	275
31	Gene Expression Differences Associated with Human Papillomavirus Status in Head and Neck Squamous Cell Carcinoma. Clinical Cancer Research, 2006, 12, 701-709.	7.0	269
32	Circular RNAs are down-regulated in KRAS mutant colon cancer cells and can be transferred to exosomes. Scientific Reports, 2016, 6, 37982.	3.3	268
33	Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. Genome Biology, 2017, 18, 182.	8.8	260
34	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.	7.1	251
35	Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics. Cell Systems, 2015, 1, 72-87.	6.2	241
36	Gene Expression Profiles Identify Epithelial-to-Mesenchymal Transition and Activation of Nuclear Factor-Î¹B Signaling as Characteristics of a High-risk Head and Neck Squamous Cell Carcinoma. Cancer Research, 2006, 66, 8210-8218.	0.9	238

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37	The genomic landscape of mantle cell lymphoma is related to the epigenetically determined chromatin state of normal B cells. Blood, 2014, 123, 2988-2996.	1.4	224
38	Multi-platform assessment of transcriptome profiling using RNA-seq in the ABRF next-generation sequencing study. Nature Biotechnology, 2014, 32, 915-925.	17.5	217
39	FAN1 mutations cause karyomegalic interstitial nephritis, linking chronic kidney failure to defective DNA damage repair. Nature Genetics, 2012, 44, 910-915.	21.4	205
40	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.	10.0	196
41	ARHGDIA mutations cause nephrotic syndrome via defective RHO GTPase signaling. Journal of Clinical Investigation, 2013, 123, 3243-3253.	8.2	196
42	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.	6.2	187
43	ZMYND10 Is Mutated in Primary Ciliary Dyskinesia and Interacts with LRRC6. American Journal of Human Genetics, 2013, 93, 336-345.	6.2	183
44	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.	6.2	181
45	Islet Microenvironment, Modulated by Vascular Endothelial Growth Factor-A Signaling, Promotes Î² Cell Regeneration. Cell Metabolism, 2014, 19, 498-511.	16.2	177
46	Familial Diarrhea Syndrome Caused by an ActivatingGUCY2CMutation. New England Journal of Medicine, 2012, 366, 1586-1595.	27.0	175
47	Genome-wide association scans identified CTNNBL1 as a novel gene for obesity. Human Molecular Genetics, 2008, 17, 1803-1813.	2.9	168
48	The Genetic Basis of Hepatosplenic T-cell Lymphoma. Cancer Discovery, 2017, 7, 369-379.	9.4	163
49	KANK deficiency leads to podocyte dysfunction and nephrotic syndrome. Journal of Clinical Investigation, 2015, 125, 2375-2384.	8.2	159
50	Interrupted Glucagon Signaling Reveals Hepatic Î± Cell Axis and Role for L-Glutamine in Î± Cell Proliferation. Cell Metabolism, 2017, 25, 1362-1373.e5.	16.2	153
51	Î± Cell Function and Gene Expression Are Compromised in Type 1 Diabetes. Cell Reports, 2018, 22, 2667-2676.	6.4	152
52	The Extracellular RNA Communication Consortium: Establishing Foundational Knowledge and Technologies for Extracellular RNA Research. Cell, 2019, 177, 231-242.	28.9	152
53	Characterizing the Impact of Smoking and Lung Cancer on the Airway Transcriptome Using RNA-Seq. Cancer Prevention Research, 2011, 4, 803-817.	1.5	144
54	Enteropathy-associated T cell lymphoma subtypes are characterized by loss of function of SETD2. Journal of Experimental Medicine, 2017, 214, 1371-1386.	8.5	144

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55	The Undiagnosed Diseases Network: Accelerating Discovery about Health and Disease. American Journal of Human Genetics, 2017, 100, 185-192.	6.2	142
56	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.	1.3	137
57	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.	12.8	132
58	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.	7.1	129
59	The mammalian LINC complex regulates genome transcriptional responses to substrate rigidity. Scientific Reports, 2016, 6, 38063.	3.3	121
60	Extremely rare variants reveal patterns of germline mutation rate heterogeneity in humans. Nature Communications, 2018, 9, 3753.	12.8	121
61	Age-dependent human Î² cell proliferation induced by glucagon-like peptide 1 and calcineurin signaling. Journal of Clinical Investigation, 2017, 127, 3835-3844.	8.2	118
62	The whole-genome landscape of Burkitt lymphoma subtypes. Blood, 2019, 134, 1598-1607.	1.4	113
63	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.	6.3	106
64	Genome-Wide Association Study of Exercise Behavior in Dutch and American Adults. Medicine and Science in Sports and Exercise, 2009, 41, 1887-1895.	0.4	105
65	Genetic Risk for Subsequent Neoplasms Among Long-Term Survivors of Childhood Cancer. Journal of Clinical Oncology, 2018, 36, 2078-2087.	1.6	105
66	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.	6.2	103
67	Ovarian gene expression in the absence of FIGLA, an oocyte-specific transcription factor. BMC Developmental Biology, 2007, 7, 67.	2.1	102
68	Diverse Long RNAs Are Differentially Sorted into Extracellular Vesicles Secreted by Colorectal Cancer Cells. Cell Reports, 2018, 25, 715-725.e4.	6.4	102
69	A training-testing approach to the molecular classification of resected non-small cell lung cancer. Clinical Cancer Research, 2003, 9, 4695-704.	7.0	102
70	Mutations in EMP2 Cause Childhood-Onset Nephrotic Syndrome. American Journal of Human Genetics, 2014, 94, 884-890.	6.2	101
71	Exome Sequencing of Familial Bipolar Disorder. JAMA Psychiatry, 2016, 73, 590.	11.0	97
72	A Syndromic Neurodevelopmental Disorder Caused by De Novo Variants in EBF3. American Journal of Human Genetics, 2017, 100, 128-137.	6.2	96

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73	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.	2.9	92
74	Exome Sequencing and Genetic Testing for MODY. PLoS ONE, 2012, 7, e38050.	2.5	91
75	Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes. Gene, 2000, 254, 57-66.	2.2	89
76	Defects of CRB2 Cause Steroid-Resistant Nephrotic Syndrome. American Journal of Human Genetics, 2015, 96, 153-161.	6.2	88
77	Powerful Bivariate Genome-Wide Association Analyses Suggest the SOX6 Gene Influencing Both Obesity and Osteoporosis Phenotypes in Males. PLoS ONE, 2009, 4, e6827.	2.5	87
78	TGF-beta1 induction of the adenine nucleotide translocator 1 in astrocytes occurs through Smads and Sp1 transcription factors. BMC Neuroscience, 2004, 5, 1.	1.9	82
79	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.	0.9	82
80	A Cell-Based Systems Biology Assessment of Human Blood to Monitor Immune Responses after Influenza Vaccination. PLoS ONE, 2015, 10, e0118528.	2.5	79
81	Vascular endothelial growth factor coordinates islet innervation via vascular scaffolding. Development (Cambridge), 2014, 141, 1480-1491.	2.5	77
82	Spaceflight Modifies Escherichia coli Gene Expression in Response to Antibiotic Exposure and Reveals Role of Oxidative Stress Response. Frontiers in Microbiology, 2018, 9, 310.	3.5	77
83	Chaotic mixer improves microarray hybridization. Analytical Biochemistry, 2004, 325, 215-226.	2.4	76
84	The COVID-19 XPRIZE and the need for scalable, fast, and widespread testing. Nature Biotechnology, 2020, 38, 1021-1024.	17.5	71
85	IRF2BPL Is Associated with Neurological Phenotypes. American Journal of Human Genetics, 2018, 103, 245-260.	6.2	69
86	Performance assessment of DNA sequencing platforms in the ABRF Next-Generation Sequencing Study. Nature Biotechnology, 2021, 39, 1129-1140.	17.5	69
87	De Novo Truncating Variants in ASXL2 Are Associated with a Unique and Recognizable Clinical Phenotype. American Journal of Human Genetics, 2016, 99, 991-999.	6.2	68
88	Whole-exome resequencing distinguishes cystic kidney diseases from phenocopies in renal ciliopathies. Kidney International, 2014, 85, 880-887.	5.2	67
89	Exome Analysis of a Family With Pleiotropic Congenital Heart Disease. Circulation: Cardiovascular Genetics, 2012, 5, 175-182.	5.1	65
90	Human islets expressing HNF1A variant have defective Î² cell transcriptional regulatory networks. Journal of Clinical Investigation, 2018, 129, 246-251.	8.2	65

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91	Antiproliferative Agents Alter Vascular Plasminogen Activator Inhibitor-1 Expression. Arteriosclerosis, Thrombosis, and Vascular Biology, 2007, 27, 400-406.	2.4	62
92	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.	2.9	62
93	RAF265 Inhibits the Growth of Advanced Human Melanoma Tumors. Clinical Cancer Research, 2012, 18, 2184-2198.	7.0	61
94	Novel rare variants in congenital cardiac arrhythmia genes are frequent in drug-induced torsades de pointes. Pharmacogenomics Journal, 2013, 13, 325-329.	2.0	61
95	Connecting the Dots: Therapy-Induced Senescence and a Tumor-Suppressive Immune Microenvironment. Journal of the National Cancer Institute, 2016, 108, djv406.	6.3	61
96	A Molecular Genetic Basis Explaining Altered Bacterial Behavior in Space. PLoS ONE, 2016, 11, e0164359.	2.5	61
97	Genome-Wide Association Analyses Identify SPOCK as a Key Novel Gene Underlying Age at Menarche. PLoS Genetics, 2009, 5, e1000420.	3.5	59
98	Ectonucleoside Triphosphate Diphosphohydrolase-3 Antibody Targets Adult Human Pancreatic Î² Cells for InÂVitro and InÂVivo Analysis. Cell Metabolism, 2019, 29, 745-754.e4.	16.2	59
99	Identification of PLCL1 Gene for Hip Bone Size Variation in Females in a Genome-Wide Association Study. PLoS ONE, 2008, 3, e3160.	2.5	57
100	Genomics and proteomics: Emerging technologies in clinical cancer research. Critical Reviews in Oncology/Hematology, 2007, 61, 1-25.	4.4	55
101	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
102	Diversity and genomic insights into the uncultured <scp>C</scp>hloroflexi from the human microbiota. Environmental Microbiology, 2014, 16, 2635-2643.	3.8	55
103	Functional variants in TBX2 are associated with a syndromic cardiovascular and skeletal developmental disorder. Human Molecular Genetics, 2018, 27, 2454-2465.	2.9	54
104	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.	1.5	53
105	Next-Generation Sequencing Strategies. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a025791.	6.2	51
106	Whole Genome Distribution and Ethnic Differentiation of Copy Number Variation in Caucasian and Asian Populations. PLoS ONE, 2009, 4, e7958.	2.5	51
107	Transfer of chloramphenicol-resistant mitochondrial DNA into the chimeric mouse. Transgenic Research, 1999, 8, 137-145.	2.4	50
108	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.	1.7	49

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109	Effects of relative humidity and buffer additives on the contact printing of microarrays by quill pins. Analytical Biochemistry, 2003, 320, 281-291.	2.4	48
110	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.	2.5	48
111	Tacrolimus- and sirolimus-induced human Î² cell dysfunction is reversible and preventable. JCI Insight, 2020, 5, .	5.0	41
112	Common MMP-7 Polymorphisms and Breast Cancer Susceptibility: A Multistage Study of Association and Functionality. Cancer Research, 2008, 68, 6453-6459.	0.9	39
113	Gene Signature Distinguishes Patients with Chronic Ulcerative Colitis Harboring Remote Neoplastic Lesions. Inflammatory Bowel Diseases, 2013, 19, 461-470.	1.9	39
114	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.	3.4	38
115	African Mitochondrial DNA Subhaplogroups and Peripheral Neuropathy during Antiretroviral Therapy. Journal of Infectious Diseases, 2010, 201, 1703-1707.	4.0	38
116	Complementary RNA amplification methods enhance microarray identification of transcripts expressed in the C. elegans nervous system. BMC Genomics, 2008, 9, 84.	2.8	34
117	Novel human genetic variants associated with extrapulmonary tuberculosis: a pilot genome wide association study. BMC Research Notes, 2011, 4, 28.	1.4	33
118	A comparison of microRNA expression profiles from splenic hemangiosarcoma, splenic nodular hyperplasia, and normal spleens of dogs. BMC Veterinary Research, 2016, 12, 272.	1.9	33
119	International Standards for Genomes, Transcriptomes, and Metagenomes. Journal of Biomolecular Techniques, 2017, 28, 8-18.	1.5	33
120	Metagenomic characterization of ambulances across the USA. Microbiome, 2017, 5, 125.	11.1	32
121	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.	1.0	28
122	A genome-scale map of expression for a mouse brain section obtained using voxelation. Physiological Genomics, 2007, 30, 313-321.	2.3	27
123	Genome-wide association study identifies two novel loci containing FLNB and SBF2 genes underlying stature variation. Human Molecular Genetics, 2009, 18, 1661-1669.	2.9	27
124	Malignant transformation of colonic epithelial cells by a colon-derived long noncoding RNA. Biochemical and Biophysical Research Communications, 2013, 440, 99-104.	2.1	25
125	In search of rare variants: Preliminary results from whole genome sequencing of 1,325 individuals with psychophysiological endophenotypes. Psychophysiology, 2014, 51, 1309-1320.	2.4	25
126	System-wide transcriptome damage and tissue identity loss in COVID-19 patients. Cell Reports Medicine, 2022, 3, 100522.	6.5	24

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127	Differential Gene Expression Landscape of Co-Existing Cervical Pre-Cancer Lesions Using RNA-seq. Frontiers in Oncology, 2014, 4, 339.	2.8	23
128	A high-throughput molecular data resource for cutaneous neurofibromas. Scientific Data, 2017, 4, 170045.	5.3	22
129	Combinatorial transcription factor profiles predict mature and functional human islet Î± and Î² cells. JCI Insight, 2021, 6, .	5.0	22
130	Gene expression profile analysis of mouse colon embryonic development. Genesis, 2005, 41, 1-12.	1.6	20
131	Modern Methods for Delineating Metagenomic Complexity. Cell Systems, 2015, 1, 6-7.	6.2	20
132	Gene Expression Profiling of a Mouse Model of Pancreatic Islet Dysmorphogenesis. PLoS ONE, 2008, 3, e1611.	2.5	19
133	The Airplane Cabin Microbiome. Microbial Ecology, 2019, 77, 87-95.	2.8	19
134	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.	4.0	16
135	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. Molecular Psychiatry, 2021, 26, 5239-5250.	7.9	15
136	Transcriptome Profiling of Pediatric Core Binding Factor AML. PLoS ONE, 2015, 10, e0138782.	2.5	14
137	Coordinated interactions between endothelial cells and macrophages in the islet microenvironment promote Î² cell regeneration. Npj Regenerative Medicine, 2021, 6, 22.	5.2	14
138	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.	2.1	13
139	Genomic and Proteomic Analysis of Mammary Tumors Arising in Transgenic Mice. Journal of Proteome Research, 2005, 4, 2088-2098.	3.7	13
140	A genome-wide association analysis implicates SOX6 as a candidate gene for wrist bone mass. Science China Life Sciences, 2010, 53, 1065-1072.	4.9	13
141	Age and Nursing Affect the Neonatal Porcine Uterine Transcriptome1. Biology of Reproduction, 2016, 94, 46.	2.7	13
142	Clinical applications of genomics in head and neck cancer. Head and Neck, 2006, 28, 360-368.	2.0	12
143	Increased Protein-Coding Mutations in the Mitochondrial Genome of African American Women With Preeclampsia. Reproductive Sciences, 2012, 19, 1343-1351.	2.5	12
144	Betacoronavirus-specific alternate splicing. Genomics, 2022, 114, 110270.	2.9	12

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145	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.	4.1	11
146	ANKRD7 and CYTL1 are novel risk genes for alcohol drinking behavior. Chinese Medical Journal, 2012, 125, 1127-34.	2.3	11
147	Single-cell sperm transcriptomes and variants from fathers of children with and without autism spectrum disorder. Npj Genomic Medicine, 2020, 5, 14.	3.8	10
148	Gene Expression Profiles as Markers of Aggressive Diseaseâ€"EGFR as a Factor. International Journal of Radiation Oncology Biology Physics, 2007, 69, S102-S105.	0.8	7
149	Identification of canine circulating miRNAs as tumor biospecific markers using Next-Generation Sequencing and Q-RT-PCR. Biochemistry and Biophysics Reports, 2021, 28, 101106.	1.3	7
150	Microarray Analysis in Drug Discovery: An Uplifting View of Depression. Science Signaling, 2003, 2003, pe46-pe46.	3.6	5
151	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.	2.3	3
152	Microarray Analysis of Neointima. Arteriosclerosis, Thrombosis, and Vascular Biology, 2002, 22, 1946-1947.	2.4	2
153	Anatomical Methods for Voxelation of the Mammalian Brain. Neurochemical Research, 2004, 29, 1299-1306.	3.3	1