

Steven J M Jones

List of Publications by Year in descending order

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477
papers

167,384
citations

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487
docs citations

487
times ranked

174180
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive molecular portraits of human breast tumours. <i>Nature</i> , 2012, 490, 61-70.	13.7	10,282
2	Circos: An information aesthetic for comparative genomics. <i>Genome Research</i> , 2009, 19, 1639-1645.	2.4	9,003
3	Comprehensive molecular characterization of human colon and rectal cancer. <i>Nature</i> , 2012, 487, 330-337.	13.7	7,168
4	The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , 2013, 45, 1113-1120.	9.4	6,265
5	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	13.7	5,653
6	Comprehensive molecular characterization of gastric adenocarcinoma. <i>Nature</i> , 2014, 513, 202-209.	13.7	5,055
7	Comprehensive molecular profiling of lung adenocarcinoma. <i>Nature</i> , 2014, 511, 543-550.	13.7	4,572
8	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2013, 368, 2059-2074.	13.9	4,139
9	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013, 497, 67-73.	13.7	4,075
10	The Genome of Black Cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). <i>Science</i> , 2006, 313, 1596-1604.	6.0	3,945
11	Comprehensive genomic characterization of squamous cell lung cancers. <i>Nature</i> , 2012, 489, 519-525.	13.7	3,483
12	Comprehensive genomic characterization of head and neck squamous cell carcinomas. <i>Nature</i> , 2015, 517, 576-582.	13.7	3,209
13	ABYSS: A parallel assembler for short read sequence data. <i>Genome Research</i> , 2009, 19, 1117-1123.	2.4	3,134
14	Comprehensive molecular characterization of clear cell renal cell carcinoma. <i>Nature</i> , 2013, 499, 43-49.	13.7	2,839
15	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.	13.9	2,582
16	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015, 161, 1681-1696.	13.5	2,562
17	Comprehensive molecular characterization of urothelial bladder carcinoma. <i>Nature</i> , 2014, 507, 315-322.	13.7	2,496
18	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	13.5	2,318

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19	The ENCODE (ENCyclopedia Of DNA Elements) Project. <i>Science</i> , 2004, 306, 636-640.	6.0	2,121
20	International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998.	13.7	2,114
21	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943
22	The Genome Sequence of the SARS-Associated Coronavirus. <i>Science</i> , 2003, 300, 1399-1404.	6.0	1,842
23	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	13.5	1,794
24	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. <i>Nature</i> , 2012, 486, 395-399.	13.7	1,778
25	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25.	13.5	1,742
26	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016, 164, 550-563.	13.5	1,695
27	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16899-16903.	3.3	1,610
28	Conserved role of intragenic DNA methylation in regulating alternative promoters. <i>Nature</i> , 2010, 466, 253-257.	13.7	1,568
29	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. <i>Nature Genetics</i> , 2010, 42, 181-185.	9.4	1,504
30	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015, 163, 506-519.	13.5	1,485
31	<i>ARID1A</i> Mutations in Endometriosis-Associated Ovarian Carcinomas. <i>New England Journal of Medicine</i> , 2010, 363, 1532-1543.	13.9	1,460
32	Integrated genomic characterization of oesophageal carcinoma. <i>Nature</i> , 2017, 541, 169-175.	13.7	1,448
33	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. <i>Nature</i> , 2011, 476, 298-303.	13.7	1,428
34	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	7.7	1,428
35	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	6.0	1,283
36	Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. <i>Nature Methods</i> , 2007, 4, 651-657.	9.0	1,254

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37	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. <i>Cell</i> , 2014, 158, 929-944.	13.5	1,242
38	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , 2017, 543, 378-384.	13.7	1,158
39	Mutational Analysis Reveals the Origin and Therapy-Driven Evolution of Recurrent Glioma. <i>Science</i> , 2014, 343, 189-193.	6.0	1,147
40	Tumor-Associated Macrophages and Survival in Classic Hodgkin's Lymphoma. <i>New England Journal of Medicine</i> , 2010, 362, 875-885.	13.9	1,141
41	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016, 374, 135-145.	13.9	1,040
42	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	6.0	1,038
43	The Atlantic salmon genome provides insights into rediploidization. <i>Nature</i> , 2016, 533, 200-205.	13.7	1,021
44	The genetic landscape of high-risk neuroblastoma. <i>Nature Genetics</i> , 2013, 45, 279-284.	9.4	990
45	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. <i>Nature</i> , 2009, 461, 809-813.	13.7	984
46	De novo assembly and analysis of RNA-seq data. <i>Nature Methods</i> , 2010, 7, 909-912.	9.0	886
47	A physical map of the human genome. <i>Nature</i> , 2001, 409, 934-941.	13.7	865
48	Functional genomic analysis of cell division in <i>C. elegans</i> using RNAi of genes on chromosome III. <i>Nature</i> , 2000, 408, 331-336.	13.7	854
49	Full-genome RNAi profiling of early embryogenesis in <i>Caenorhabditis elegans</i> . <i>Nature</i> , 2005, 434, 462-469.	13.7	831
50	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017, 547, 311-317.	13.7	787
51	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018, 362, .	6.0	781
52	Metastasis is regulated via microRNA-200/ZEB1 axis control of tumour cell PD-L1 expression and intratumoral immunosuppression. <i>Nature Communications</i> , 2014, 5, 5241.	5.8	780
53	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. <i>Nature</i> , 2012, 488, 49-56.	13.7	761
54	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	13.5	738

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55	Mutation of <i>FOXL2</i> in Granulosa-Cell Tumors of the Ovary. <i>New England Journal of Medicine</i> , 2009, 360, 2719-2729.	13.9	706
56	Whole-Genome Sequencing and Social-Network Analysis of a Tuberculosis Outbreak. <i>New England Journal of Medicine</i> , 2011, 364, 730-739.	13.9	665
57	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330.	7.7	665
58	The Genome of the Basidiomycetous Yeast and Human Pathogen <i>Cryptococcus neoformans</i> . <i>Science</i> , 2005, 307, 1321-1324.	6.0	664
59	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15.	7.7	642
60	Genetic Alterations Activating Kinase and Cytokine Receptor Signaling in High-Risk Acute Lymphoblastic Leukemia. <i>Cancer Cell</i> , 2012, 22, 153-166.	7.7	621
61	The complete genome of <i>Rhodococcus</i> sp. RHA1 provides insights into a catabolic powerhouse. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15582-15587.	3.3	586
62	MHC class II transactivator CIITA is a recurrent gene fusion partner in lymphoid cancers. <i>Nature</i> , 2011, 471, 377-381.	13.7	551
63	MEG3 long noncoding RNA regulates the TGF- β 2 pathway genes through formation of RNA-DNA triplex structures. <i>Nature Communications</i> , 2015, 6, 7743.	5.8	534
64	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017, 31, 181-193.	7.7	532
65	The Status, Quality, and Expansion of the NIH Full-Length cDNA Project: The Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2004, 14, 2121-2127.	2.4	486
66	CIVIC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. <i>Nature Genetics</i> , 2017, 49, 170-174.	9.4	460
67	DNA Methylation and SETDB1/H3K9me3 Regulate Predominantly Distinct Sets of Genes, Retroelements, and Chimeric Transcripts in mESCs. <i>Cell Stem Cell</i> , 2011, 8, 676-687.	5.2	427
68	Assembling millions of short DNA sequences using SSAKE. <i>Bioinformatics</i> , 2007, 23, 500-501.	1.8	421
69	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	13.5	404
70	Recurrent Somatic <i>DICER1</i> Mutations in Nonepithelial Ovarian Cancers. <i>New England Journal of Medicine</i> , 2012, 366, 234-242.	13.9	401
71	A functional genomic analysis of cell morphology using RNA interference. <i>Journal of Biology</i> , 2003, 2, 27.	2.7	387
72	<i>De novo</i> transcriptome assembly with ABySS. <i>Bioinformatics</i> , 2009, 25, 2872-2877.	1.8	371

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73	ATR-X Syndrome Protein Targets Tandem Repeats and Influences Allele-Specific Expression in a Size-Dependent Manner. <i>Cell</i> , 2010, 143, 367-378.	13.5	365
74	Transcription phenotypes of pancreatic cancer are driven by genomic events during tumor evolution. <i>Nature Genetics</i> , 2020, 52, 231-240.	9.4	365
75	Assembling the 20 Gb white spruce (<i>Picea glauca</i>) genome from whole-genome shotgun sequencing data. <i>Bioinformatics</i> , 2013, 29, 1492-1497.	1.8	356
76	Profiling the HeLa S3 transcriptome using randomly primed cDNA and massively parallel short-read sequencing. <i>BioTechniques</i> , 2008, 45, 81-94.	0.8	355
77	Dynamic Remodeling of Individual Nucleosomes Across a Eukaryotic Genome in Response to Transcriptional Perturbation. <i>PLoS Biology</i> , 2008, 6, e65.	2.6	353
78	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. <i>Blood</i> , 2013, 122, 1256-1265.	0.6	349
79	High-Throughput In Vivo Analysis of Gene Expression in <i>Caenorhabditis elegans</i> . <i>PLoS Biology</i> , 2007, 5, e237.	2.6	346
80	IslandPath: aiding detection of genomic islands in prokaryotes. <i>Bioinformatics</i> , 2003, 19, 418-420.	1.8	344
81	Analysis of the Genome and Transcriptome of <i>Cryptococcus neoformans</i> var. <i>grubii</i> Reveals Complex RNA Expression and Microevolution Leading to Virulence Attenuation. <i>PLoS Genetics</i> , 2014, 10, e1004261.	1.5	336
82	Characterization of HPV and host genome interactions in primary head and neck cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15544-15549.	3.3	317
83	A physical map of the mouse genome. <i>Nature</i> , 2002, 418, 743-750.	13.7	316
84	Transcriptome Analysis of the Normal Human Mammary Cell Commitment and Differentiation Process. <i>Cell Stem Cell</i> , 2008, 3, 109-118.	5.2	310
85	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423.	7.7	309
86	Next-generation tag sequencing for cancer gene expression profiling. <i>Genome Research</i> , 2009, 19, 1825-1835.	2.4	306
87	Alternative expression analysis by RNA sequencing. <i>Nature Methods</i> , 2010, 7, 843-847.	9.0	283
88	Development and Application of a Salmonid EST Database and cDNA Microarray: Data Mining and Interspecific Hybridization Characteristics. <i>Genome Research</i> , 2004, 14, 478-490.	2.4	279
89	Meta-Analysis and Meta-Review of Thyroid Cancer Gene Expression Profiling Studies Identifies Important Diagnostic Biomarkers. <i>Journal of Clinical Oncology</i> , 2006, 24, 5043-5051.	0.8	279
90	Sequencing and analysis of genes involved in the biosynthesis of a vancomycin group antibiotic. <i>Chemistry and Biology</i> , 1998, 5, 155-162.	6.2	278

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91	Concurrent <i>CIC</i> mutations, <i>IDH</i> mutations, and 1p/19q loss distinguish oligodendrogliomas from other cancers. <i>Journal of Pathology</i> , 2012, 226, 7-16.	2.1	272
92	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018, 33, 244-258.e10.	7.7	270
93	Divergent clonal selection dominates medulloblastoma at recurrence. <i>Nature</i> , 2016, 529, 351-357.	13.7	266
94	Oligonucleotide Microarray Analysis of Genomic Imbalance in Children with Mental Retardation. <i>American Journal of Human Genetics</i> , 2006, 79, 500-513.	2.6	261
95	Draft genome of the mountain pine beetle, <i>Dendroctonus ponderosae</i> Hopkins, a major forest pest. <i>Genome Biology</i> , 2013, 14, R27.	13.9	260
96	Mutations in <i>EZH2</i> Cause Weaver Syndrome. <i>American Journal of Human Genetics</i> , 2012, 90, 110-118.	2.6	253
97	FindPeaks 3.1: a tool for identifying areas of enrichment from massively parallel short-read sequencing technology. <i>Bioinformatics</i> , 2008, 24, 1729-1730.	1.8	252
98	Sequencing the genome of the Atlantic salmon (<i>Salmo salar</i>). <i>Genome Biology</i> , 2010, 11, 403.	3.8	250
99	Functional Genomics of the Cilium, a Sensory Organelle. <i>Current Biology</i> , 2005, 15, 935-941.	1.8	245
100	Quiescent Sox2+ Cells Drive Hierarchical Growth and Relapse in Sonic Hedgehog Subgroup Medulloblastoma. <i>Cancer Cell</i> , 2014, 26, 33-47.	7.7	241
101	14-3-3 fusion oncogenes in high-grade endometrial stromal sarcoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 929-934.	3.3	239
102	The genetic basis and cell of origin of mixed phenotype acute leukaemia. <i>Nature</i> , 2018, 562, 373-379.	13.7	236
103	Phosphorylated Caveolin-1 Regulates Rho/ROCK-Dependent Focal Adhesion Dynamics and Tumor Cell Migration and Invasion. <i>Cancer Research</i> , 2008, 68, 8210-8220.	0.4	228
104	ORegAnno: an open-access community-driven resource for regulatory annotation. <i>Nucleic Acids Research</i> , 2007, 36, D107-D113.	6.5	227
105	Conifer defence against insects: microarray gene expression profiling of Sitka spruce (<i>Picea</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj 1 transcriptome. <i>Plant, Cell and Environment</i> , 2006, 29, 1545-1570.	2.8	221
106	FORGE Canada Consortium: Outcomes of a 2-Year National Rare-Disease Gene-Discovery Project. <i>American Journal of Human Genetics</i> , 2014, 94, 809-817.	2.6	219
107	Genome and transcriptome analyses of the mountain pine beetle-fungal symbiont <i>Grosmannia clavigera</i> , a lodgepole pine pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 2504-2509.	3.3	218
108	Reduced adenosine-to-inosine miR-455-5p editing promotes melanoma growth and metastasis. <i>Nature Cell Biology</i> , 2015, 17, 311-321.	4.6	205

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109	Improved white spruce (<i>Picea glauca</i>) genome assemblies and annotation of large gene families of conifer terpenoid and phenolic defense metabolism. <i>Plant Journal</i> , 2015, 83, 189-212.	2.8	200
110	A SAGE Approach to Discovery of Genes Involved in Autophagic Cell Death. <i>Current Biology</i> , 2003, 13, 358-363.	1.8	198
111	Defects in the IFT-B Component IFT172 Cause Jeune and Mainzer-Saldino Syndromes in Humans. <i>American Journal of Human Genetics</i> , 2013, 93, 915-925.	2.6	196
112	LINKS: Scalable, alignment-free scaffolding of draft genomes with long reads. <i>GigaScience</i> , 2015, 4, 35.	3.3	196
113	Locating mammalian transcription factor binding sites: A survey of computational and experimental techniques. <i>Genome Research</i> , 2006, 16, 1455-1464.	2.4	188
114	Hive plots--rational approach to visualizing networks. <i>Briefings in Bioinformatics</i> , 2012, 13, 627-644.	3.2	187
115	Drug repositioning for personalized medicine. <i>Genome Medicine</i> , 2012, 4, 27.	3.6	186
116	The new paradigm of flow cell sequencing: Table 1.. <i>Genome Research</i> , 2008, 18, 839-846.	2.4	185
117	Genomics of hybrid poplar (<i>Populus trichocarpa</i> × <i>deltoides</i>) interacting with forest tent caterpillars (<i>Malacosoma disstria</i>): normalized and full-length cDNA libraries, expressed sequence tags, and a cDNA microarray for the study of insect-induced defences. <i>Molecular Ecology</i> , 2006, 15, 1275-1297.	2.0	183
118	Genome Variation in <i>Cryptococcus gattii</i> , an Emerging Pathogen of Immunocompetent Hosts. <i>MBio</i> , 2011, 2, e00342-10.	1.8	182
119	Novel Avian Influenza H7N3 Strain Outbreak, British Columbia. <i>Emerging Infectious Diseases</i> , 2004, 10, 2192-2195.	2.0	182
120	Analysis of long-lived <i>C. elegans</i> <i>daf-2</i> mutants using serial analysis of gene expression. <i>Genome Research</i> , 2005, 15, 603-615.	2.4	180
121	Analysis of the prostate cancer cell line LNCaP transcriptome using a sequencing-by-synthesis approach. <i>BMC Genomics</i> , 2006, 7, 246.	1.2	173
122	Genome-wide discovery of somatic coding and noncoding mutations in pediatric endemic and sporadic Burkitt lymphoma. <i>Blood</i> , 2019, 133, 1313-1324.	0.6	172
123	Aberrant patterns of H3K4 and H3K27 histone lysine methylation occur across subgroups in medulloblastoma. <i>Acta Neuropathologica</i> , 2013, 125, 373-384.	3.9	169
124	The ELT-2 GATA-factor and the global regulation of transcription in the <i>C. elegans</i> intestine. <i>Developmental Biology</i> , 2007, 302, 627-645.	0.9	165
125	Identification and characterization of Hoxa9 binding sites in hematopoietic cells. <i>Blood</i> , 2012, 119, 388-398.	0.6	165
126	Bromodomain-containing Protein 4 (BRD4) Regulates RNA Polymerase II Serine 2 Phosphorylation in Human CD4+ T Cells. <i>Journal of Biological Chemistry</i> , 2012, 287, 43137-43155.	1.6	164

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127	Insights into Conifer Giga-Genomes. <i>Plant Physiology</i> , 2014, 166, 1724-1732.	2.3	164
128	Genome-wide relationship between histone H3 lysine 4 mono- and tri-methylation and transcription factor binding. <i>Genome Research</i> , 2008, 18, 1906-1917.	2.4	163
129	<i>Salmo salar</i> and <i>Esox lucius</i> full-length cDNA sequences reveal changes in evolutionary pressures on a post-tetraploidization genome. <i>BMC Genomics</i> , 2010, 11, 279.	1.2	163
130	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. <i>Genome Biology</i> , 2010, 11, R82.	13.9	159
131	A novel recurrent mutation in ATP1A3 causes CAPOS syndrome. <i>Orphanet Journal of Rare Diseases</i> , 2014, 9, 15.	1.2	157
132	Mass Spectrometric Characterization of Proteins from the SARS Virus. <i>Molecular and Cellular Proteomics</i> , 2003, 2, 346-356.	2.5	155
133	Distinct roles of KAP1, HP1 and G9a/GLP in silencing of the two-cell-specific retrotransposon MERVL in mouse ES cells. <i>Epigenetics and Chromatin</i> , 2013, 6, 15.	1.8	153
134	The molecular signature and <i>cis</i> -regulatory architecture of a <i>C. elegans</i> gustatory neuron. <i>Genes and Development</i> , 2007, 21, 1653-1674.	2.7	151
135	Homologous Recombination Deficiency and Platinum-Based Therapy Outcomes in Advanced Breast Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 7521-7530.	3.2	144
136	ORegAnno 3.0: a community-driven resource for curated regulatory annotation. <i>Nucleic Acids Research</i> , 2016, 44, D126-D132.	6.5	142
137	Analysis of FOXO1 mutations in diffuse large B-cell lymphoma. <i>Blood</i> , 2013, 121, 3666-3674.	0.6	139
138	CancerMine: a literature-mined resource for drivers, oncogenes and tumor suppressors in cancer. <i>Nature Methods</i> , 2019, 16, 505-507.	9.0	139
139	Global analysis of in vivo Foxa2-binding sites in mouse adult liver using massively parallel sequencing. <i>Nucleic Acids Research</i> , 2008, 36, 4549-4564.	6.5	137
140	Diagnostic Utility of Galectin-3 in Thyroid Cancer. <i>American Journal of Pathology</i> , 2010, 176, 2067-2081.	1.9	137
141	Whole-Genome Profiling of Mutagenesis in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2010, 185, 431-441.	1.2	135
142	Nonmethylated Transposable Elements and Methylated Genes in a Chordate Genome. <i>Science</i> , 1999, 283, 1164-1167.	6.0	134
143	Meta-analysis of Colorectal Cancer Gene Expression Profiling Studies Identifies Consistently Reported Candidate Biomarkers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2008, 17, 543-552.	1.1	132
144	De novo genome sequence assembly of a filamentous fungus using Sanger, 454 and Illumina sequence data. <i>Genome Biology</i> , 2009, 10, R94.	13.9	130

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145	Cryptococcus neoformans Gene Expression during Experimental Cryptococcal Meningitis. Eukaryotic Cell, 2003, 2, 1336-1349.	3.4	129
146	ELT-2 is the predominant transcription factor controlling differentiation and function of the C. elegans intestine, from embryo to adult. Developmental Biology, 2009, 327, 551-565.	0.9	129
147	Retrotransposon-Induced Heterochromatin Spreading in the Mouse Revealed by Insertional Polymorphisms. PLoS Genetics, 2011, 7, e1002301.	1.5	129
148	Gene number in an invertebrate chordate, Ciona intestinalis. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 4437-4440.	3.3	128
149	Recurrent targets of aberrant somatic hypermutation in lymphoma. Oncotarget, 2012, 3, 1308-1319.	0.8	127
150	The completion of the Mammalian Gene Collection (MGC). Genome Research, 2009, 19, 2324-2333.	2.4	125
151	Large-scale profiling of microRNAs for The Cancer Genome Atlas. Nucleic Acids Research, 2016, 44, e3-e3.	6.5	125
152	<i>NRG1</i> Gene Fusions Are Recurrent, Clinically Actionable Gene Rearrangements in <i>KRAS</i> Wild-Type Pancreatic Ductal Adenocarcinoma. Clinical Cancer Research, 2019, 25, 4674-4681.	3.2	121
153	Altered Gene Expression along the Glycolysis-Cholesterol Synthesis Axis Is Associated with Outcome in Pancreatic Cancer. Clinical Cancer Research, 2020, 26, 135-146.	3.2	121
154	A set of BAC clones spanning the human genome. Nucleic Acids Research, 2004, 32, 3651-3660.	6.5	119
155	Population sequencing reveals clonal diversity and ancestral inbreeding in the grapevine cultivar Chardonnay. PLoS Genetics, 2018, 14, e1007807.	1.5	116
156	Development and characterisation of neutralising monoclonal antibody to the SARS-coronavirus. Journal of Virological Methods, 2004, 120, 87-96.	1.0	115
157	Evidence That Plant-Like Genes in Chlamydia Species Reflect an Ancestral Relationship between Chlamydiaceae, Cyanobacteria, and the Chloroplast. Genome Research, 2002, 12, 1159-1167.	2.4	114
158	A conifer genomics resource of 200,000 spruce (<i>Picea</i> spp.) ESTs and 6,464 high-quality, sequence-finished full-length cDNAs for Sitka spruce (<i>Picea sitchensis</i>). BMC Genomics, 2008, 9, 484.	1.2	113
159	A mouse atlas of gene expression: Large-scale digital gene-expression profiles from precisely defined developing C57BL/6J mouse tissues and cells. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 18485-18490.	3.3	112
160	Spatial heterogeneity in medulloblastoma. Nature Genetics, 2017, 49, 780-788.	9.4	112
161	Locus co-occupancy, nucleosome positioning, and H3K4me1 regulate the functionality of FOXA2-, HNF4A-, and PDX1-bound loci in islets and liver. Genome Research, 2010, 20, 1037-1051.	2.4	109
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