

# Steven J M Jones

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

473 papers	125,785 citations	127 h-index	353 g-index
487 ext. papers	151,915 ext. citations	13 avg, IF	9.25 L-index

#	Paper	IF	Citations
473	Comprehensive molecular portraits of human breast tumours. <i>Nature</i> , <b>2012</b> , 490, 61-70	50.4	8025
472	Circos: an information aesthetic for comparative genomics. <i>Genome Research</i> , <b>2009</b> , 19, 1639-45	9.7	6014
471	Comprehensive molecular characterization of human colon and rectal cancer. <i>Nature</i> , <b>2012</b> , 487, 330-7	50.4	5640
470	The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , <b>2013</b> , 45, 1113-20	36.3	3933
469	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , <b>2015</b> , 518, 317-30	50.4	3849
468	Comprehensive molecular characterization of gastric adenocarcinoma. <i>Nature</i> , <b>2014</b> , 513, 202-9	50.4	3659
467	Comprehensive molecular profiling of lung adenocarcinoma. <i>Nature</i> , <b>2014</b> , 511, 543-50	50.4	3310
466	The genome of black cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). <i>Science</i> , <b>2006</b> , 313, 1596-604	33.3	3205
465	Genomic and epigenomic landscapes of adult de novo acute myeloid leukemia. <i>New England Journal of Medicine</i> , <b>2013</b> , 368, 2059-74	59.2	3137
464	Comprehensive genomic characterization of squamous cell lung cancers. <i>Nature</i> , <b>2012</b> , 489, 519-25	50.4	2820
463	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , <b>2013</b> , 497, 67-73	50.4	2800
462	ABYSS: a parallel assembler for short read sequence data. <i>Genome Research</i> , <b>2009</b> , 19, 1117-23	9.7	2508
461	Comprehensive genomic characterization of head and neck squamous cell carcinomas. <i>Nature</i> , <b>2015</b> , 517, 576-82	50.4	2332
460	Comprehensive molecular characterization of clear cell renal cell carcinoma. <i>Nature</i> , <b>2013</b> , 499, 43-9	50.4	2184
459	Comprehensive molecular characterization of urothelial bladder carcinoma. <i>Nature</i> , <b>2014</b> , 507, 315-22	50.4	1963
458	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , <b>2015</b> , 372, 2481-98	59.2	1828
457	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , <b>2015</b> , 161, 1681-96	56.2	1807

456	The ENCODE (ENCyclopedia Of DNA Elements) Project. <i>Science</i> , <b>2004</b> , 306, 636-40	33.3	1692
455	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , <b>2004</b> , 428, 493-521	50.4	1689
454	Integrated genomic characterization of papillary thyroid carcinoma. <i>Cell</i> , <b>2014</b> , 159, 676-90	56.2	1660
453	The Genome sequence of the SARS-associated coronavirus. <i>Science</i> , <b>2003</b> , 300, 1399-404	33.3	1632
452	International network of cancer genome projects. <i>Nature</i> , <b>2010</b> , 464, 993-8	50.4	1613
451	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> , <b>2002</b> , 99, 16899-903	11.5	1457
450	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. <i>Nature</i> , <b>2012</b> , 486, 395-9	50.4	1417
449	Conserved role of intragenic DNA methylation in regulating alternative promoters. <i>Nature</i> , <b>2010</b> , 466, 253-7	50.4	1298
448	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. <i>Nature Genetics</i> , <b>2010</b> , 42, 181-5	36.3	1273
447	ARID1A mutations in endometriosis-associated ovarian carcinomas. <i>New England Journal of Medicine</i> , <b>2010</b> , 363, 1532-43	59.2	1208
446	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. <i>Nature</i> , <b>2011</b> , 476, 298-303	50.4	1180
445	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , <b>2016</b> , 164, 550-63	56.2	1140
444	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , <b>2017</b> , 169, 1327-1341.e23	56.2	1125
443	Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. <i>Nature Methods</i> , <b>2007</b> , 4, 651-7	21.6	1077
442	Evolutionary and biomedical insights from the rhesus macaque genome. <i>Science</i> , <b>2007</b> , 316, 222-34	33.3	1072
441	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , <b>2015</b> , 163, 506-19	56.2	1055
440	Integrated genomic characterization of oesophageal carcinoma. <i>Nature</i> , <b>2017</b> , 541, 169-175	50.4	965
439	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , <b>2017</b> , 171, 540-556.e25	56.2	961

438	Tumor-associated macrophages and survival in classic Hodgkin's lymphoma. <i>New England Journal of Medicine</i> , <b>2010</b> , 362, 875-85	59.2	961
437	Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. <i>Cell</i> , <b>2014</b> , 158, 929-944	56.2	935
436	Mutational analysis reveals the origin and therapy-driven evolution of recurrent glioma. <i>Science</i> , <b>2014</b> , 343, 189-193	33.3	912
435	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , <b>2017</b> , 32, 185-203	21.5	13896
434	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. <i>Nature</i> , <b>2009</b> , 461, 809-13	50.4	879
433	The genome sequence of taurine cattle: a window to ruminant biology and evolution. <i>Science</i> , <b>2009</b> , 324, 522-8	33.3	863
432	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , <b>2017</b> , 543, 378-384	50.4	755
431	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , <b>2016</b> , 374, 135-45	59.2	753
430	Functional genomic analysis of cell division in <i>C. elegans</i> using RNAi of genes on chromosome III. <i>Nature</i> , <b>2000</b> , 408, 331-6	50.4	753
429	A physical map of the human genome. <i>Nature</i> , <b>2001</b> , 409, 934-41	50.4	732
428	The genetic landscape of high-risk neuroblastoma. <i>Nature Genetics</i> , <b>2013</b> , 45, 279-84	36.3	717
427	Full-genome RNAi profiling of early embryogenesis in <i>Caenorhabditis elegans</i> . <i>Nature</i> , <b>2005</b> , 434, 462-9	50.4	717
426	De novo assembly and analysis of RNA-seq data. <i>Nature Methods</i> , <b>2010</b> , 7, 909-12	21.6	701
425	The Atlantic salmon genome provides insights into rediploidization. <i>Nature</i> , <b>2016</b> , 533, 200-5	50.4	606
424	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. <i>Nature</i> , <b>2012</b> , 488, 49-56	50.4	596
423	The genome of the basidiomycetous yeast and human pathogen <i>Cryptococcus neoformans</i> . <i>Science</i> , <b>2005</b> , 307, 1321-4	33.3	580
422	Metastasis is regulated via microRNA-200/ZEB1 axis control of tumour cell PD-L1 expression and intratumoral immunosuppression. <i>Nature Communications</i> , <b>2014</b> , 5, 5241	17.4	573
421	Whole-genome sequencing and social-network analysis of a tuberculosis outbreak. <i>New England Journal of Medicine</i> , <b>2011</b> , 364, 730-9	59.2	561

420	Mutation of FOXL2 in granulosa-cell tumors of the ovary. <i>New England Journal of Medicine</i> , <b>2009</b> , 360, 2719-29	59.2	551
419	The somatic genomic landscape of chromophobe renal cell carcinoma. <i>Cancer Cell</i> , <b>2014</b> , 26, 319-330	24.3	521
418	Genetic alterations activating kinase and cytokine receptor signaling in high-risk acute lymphoblastic leukemia. <i>Cancer Cell</i> , <b>2012</b> , 22, 153-66	24.3	515
417	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> , <b>2006</b> , 103, 15582-7	11.5	515
416	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , <b>2017</b> , 547, 311-317	50.4	472
415	MHC class II transactivator CIITA is a recurrent gene fusion partner in lymphoid cancers. <i>Nature</i> , <b>2011</b> , 471, 377-81	50.4	467
414	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , <b>2017</b> , 171, 950-965.e28	56.2	451
413	MEG3 long noncoding RNA regulates the TGF- $\beta$ pathway genes through formation of RNA-DNA triplex structures. <i>Nature Communications</i> , <b>2015</b> , 6, 7743	17.4	414
412	The status, quality, and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC). <i>Genome Research</i> , <b>2004</b> , 14, 2121-7	9.7	404
411	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , <b>2018</b> , 362,	33.3	392
410	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , <b>2017</b> , 32, 204-220.e15	24.3	391
409	Assembling millions of short DNA sequences using SSAKE. <i>Bioinformatics</i> , <b>2007</b> , 23, 500-1	7.2	357
408	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , <b>2017</b> , 31, 181-193	24.3	350
407	A functional genomic analysis of cell morphology using RNA interference. <i>Journal of Biology</i> , <b>2003</b> , 2, 27		338
406	Recurrent somatic DICER1 mutations in nonepithelial ovarian cancers. <i>New England Journal of Medicine</i> , <b>2012</b> , 366, 234-42	59.2	332
405	De novo transcriptome assembly with ABySS. <i>Bioinformatics</i> , <b>2009</b> , 25, 2872-7	7.2	326
404	Profiling the HeLa S3 transcriptome using randomly primed cDNA and massively parallel short-read sequencing. <i>BioTechniques</i> , <b>2008</b> , 45, 81-94	2.5	322
403	Dynamic remodeling of individual nucleosomes across a eukaryotic genome in response to transcriptional perturbation. <i>PLoS Biology</i> , <b>2008</b> , 6, e65	9.7	315

402	DNA methylation and SETDB1/H3K9me3 regulate predominantly distinct sets of genes, retroelements, and chimeric transcripts in mESCs. <i>Cell Stem Cell</i> , <b>2011</b> , 8, 676-87	18	309
401	CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. <i>Nature Genetics</i> , <b>2017</b> , 49, 170-174	36.3	308
400	ATR-X syndrome protein targets tandem repeats and influences allele-specific expression in a size-dependent manner. <i>Cell</i> , <b>2010</b> , 143, 367-78	56.2	297
399	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. <i>Blood</i> , <b>2013</b> , 122, 1256-65	2.2	289
398	High-throughput in vivo analysis of gene expression in <i>Caenorhabditis elegans</i> . <i>PLoS Biology</i> , <b>2007</b> , 5, e237	9.7	285
397	A physical map of the mouse genome. <i>Nature</i> , <b>2002</b> , 418, 743-50	50.4	282
396	Assembling the 20 Gb white spruce ( <i>Picea glauca</i> ) genome from whole-genome shotgun sequencing data. <i>Bioinformatics</i> , <b>2013</b> , 29, 1492-7	7.2	278
395	Transcriptome analysis of the normal human mammary cell commitment and differentiation process. <i>Cell Stem Cell</i> , <b>2008</b> , 3, 109-18	18	274
394	Next-generation tag sequencing for cancer gene expression profiling. <i>Genome Research</i> , <b>2009</b> , 19, 1825-35	35	271
393	IslandPath: aiding detection of genomic islands in prokaryotes. <i>Bioinformatics</i> , <b>2003</b> , 19, 418-20	7.2	263
392	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> , <b>2014</b> , 10, e1004261 <sup>6</sup>	6	260
391	Sequencing and analysis of genes involved in the biosynthesis of a vancomycin group antibiotic. <i>Chemistry and Biology</i> , <b>1998</b> , 5, 155-62		252
390	Development and application of a salmonid EST database and cDNA microarray: data mining and interspecific hybridization characteristics. <i>Genome Research</i> , <b>2004</b> , 14, 478-90	9.7	251
389	Oligonucleotide microarray analysis of genomic imbalance in children with mental retardation. <i>American Journal of Human Genetics</i> , <b>2006</b> , 79, 500-13	11	247
388	FindPeaks 3.1: a tool for identifying areas of enrichment from massively parallel short-read sequencing technology. <i>Bioinformatics</i> , <b>2008</b> , 24, 1729-30	7.2	234
387	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , <b>2016</b> , 167, 1145-1149	56.2	232
386	Meta-analysis and meta-review of thyroid cancer gene expression profiling studies identifies important diagnostic biomarkers. <i>Journal of Clinical Oncology</i> , <b>2006</b> , 24, 5043-51	2.2	232
385	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> , <b>2014</b> , 111, 15544-9	11.5	229

384	Alternative expression analysis by RNA sequencing. <i>Nature Methods</i> , <b>2010</b> , 7, 843-7	21.6	227
383	Concurrent CIC mutations, IDH mutations, and 1p/19q loss distinguish oligodendrogliomas from other cancers. <i>Journal of Pathology</i> , <b>2012</b> , 226, 7-16	9.4	226
382	Sequencing the genome of the Atlantic salmon ( <i>Salmo salar</i> ). <i>Genome Biology</i> , <b>2010</b> , 11, 403	18.3	216
381	Draft genome of the mountain pine beetle, <i>Dendroctonus ponderosae</i> Hopkins, a major forest pest. <i>Genome Biology</i> , <b>2013</b> , 14, R27	18.3	212
380	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , <b>2017</b> , 31, 411-423	24.3	210
379	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> , <b>2012</b> , 109, 929-34	11.5	208
378	Divergent clonal selection dominates medulloblastoma at recurrence. <i>Nature</i> , <b>2016</b> , 529, 351-7	50.4	206
377	Functional genomics of the cilium, a sensory organelle. <i>Current Biology</i> , <b>2005</b> , 15, 935-41	6.3	206
376	Phosphorylated caveolin-1 regulates Rho/ROCK-dependent focal adhesion dynamics and tumor cell migration and invasion. <i>Cancer Research</i> , <b>2008</b> , 68, 8210-20	10.1	200
375	ORegAnno: an open-access community-driven resource for regulatory annotation. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D107-13	20.1	199
374	Conifer defence against insects: microarray gene expression profiling of Sitka spruce ( <i>Picea sitchensis</i> ) induced by mechanical wounding or feeding by spruce budworms ( <i>Choristoneura occidentalis</i> ) or white pine weevils ( <i>Pissodes strobi</i> ) reveals large-scale changes of the host transcriptome. <i>Plant, Cell and Environment</i> , <b>2006</b> , 29, 1545-70	8.4	197
373	Mutations in EZH2 cause Weaver syndrome. <i>American Journal of Human Genetics</i> , <b>2012</b> , 90, 110-8	11	190
372	Quiescent sox2(+) cells drive hierarchical growth and relapse in sonic hedgehog subgroup medulloblastoma. <i>Cancer Cell</i> , <b>2014</b> , 26, 33-47	24.3	181
371	A SAGE approach to discovery of genes involved in autophagic cell death. <i>Current Biology</i> , <b>2003</b> , 13, 358-63		181
370	FORGE Canada Consortium: outcomes of a 2-year national rare-disease gene-discovery project. <i>American Journal of Human Genetics</i> , <b>2014</b> , 94, 809-17	11	174
369	The new paradigm of flow cell sequencing. <i>Genome Research</i> , <b>2008</b> , 18, 839-46	9.7	165
368	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> , <b>2011</b> , 108, 2504-9	11.5	161
367	Locating mammalian transcription factor binding sites: a survey of computational and experimental techniques. <i>Genome Research</i> , <b>2006</b> , 16, 1455-64	9.7	161

366	Genomics of hybrid poplar ( <i>Populus trichocarpax 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 in poplar. <i>Molecular Ecology</i> , <b>2006</b> , 15, 1275-97	5.7	159
365	Analysis of long-lived <i>C. elegans</i> daf-2 mutants using serial analysis of gene expression. <i>Genome Research</i> , <b>2005</b> , 15, 603-15	9.7	158
364	Defects in the IFT-B component IFT172 cause Jeune and Mainzer-Saldino syndromes in humans. <i>American Journal of Human Genetics</i> , <b>2013</b> , 93, 915-25	11	155
363	Reduced adenosine-to-inosine miR-455-5p editing promotes melanoma growth and metastasis. <i>Nature Cell Biology</i> , <b>2015</b> , 17, 311-21	23.4	155
362	Novel avian influenza H7N3 strain outbreak, British Columbia. <i>Emerging Infectious Diseases</i> , <b>2004</b> , 10, 2192-5	10.2	154
361	<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> , <b>2010</b> , 11, 279	4.5	151
360	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , <b>2018</b> , 33, 244-258.e10	24.3	150
359	Transcription phenotypes of pancreatic cancer are driven by genomic events during tumor evolution. <i>Nature Genetics</i> , <b>2020</b> , 52, 231-240	36.3	148
358	Hive plots--rational approach to visualizing networks. <i>Briefings in Bioinformatics</i> , <b>2012</b> , 13, 627-44	13.4	148
357	Genome-wide relationship between histone H3 lysine 4 mono- and tri-methylation and transcription factor binding. <i>Genome Research</i> , <b>2008</b> , 18, 1906-17	9.7	147
356	Drug repositioning for personalized medicine. <i>Genome Medicine</i> , <b>2012</b> , 4, 27	14.4	144
355	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. <i>Genome Biology</i> , <b>2010</b> , 11, R82	18.3	144
354	The genetic basis and cell of origin of mixed phenotype acute leukaemia. <i>Nature</i> , <b>2018</b> , 562, 373-379	50.4	140
353	Analysis of the prostate cancer cell line LNCaP transcriptome using a sequencing-by-synthesis approach. <i>BMC Genomics</i> , <b>2006</b> , 7, 246	4.5	139
352	Genome variation in <i>Cryptococcus gattii</i> , an emerging pathogen of immunocompetent hosts. <i>MBio</i> , <b>2011</b> , 2, e00342-10	7.8	137
351	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> , <b>2015</b> , 83, 189-212	6.9	136
350	Identification and characterization of Hoxa9 binding sites in hematopoietic cells. <i>Blood</i> , <b>2012</b> , 119, 388-98.2	98.2	132
349	The ELT-2 GATA-factor and the global regulation of transcription in the <i>C. elegans</i> intestine. <i>Developmental Biology</i> , <b>2007</b> , 302, 627-45	3.1	131



348	Mass spectrometric characterization of proteins from the SARS virus: a preliminary report. <i>Molecular and Cellular Proteomics</i> , <b>2003</b> , 2, 346-56	7.6	130
347	Bromodomain-containing protein 4 (BRD4) regulates RNA polymerase II serine 2 phosphorylation in human CD4+ T cells. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 43137-55	5.4	127
346	Global analysis of in vivo Foxa2-binding sites in mouse adult liver using massively parallel sequencing. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, 4549-64	20.1	127
345	Aberrant patterns of H3K4 and H3K27 histone lysine methylation occur across subgroups in medulloblastoma. <i>Acta Neuropathologica</i> , <b>2013</b> , 125, 373-84	14.3	126
344	The molecular signature and cis-regulatory architecture of a C. elegans gustatory neuron. <i>Genes and Development</i> , <b>2007</b> , 21, 1653-74	12.6	125
343	LINKS: Scalable, alignment-free scaffolding of draft genomes with long reads. <i>GigaScience</i> , <b>2015</b> , 4, 35	7.6	124
342	Nonmethylated transposable elements and methylated genes in a chordate genome. <i>Science</i> , <b>1999</b> , 283, 1164-7	33.3	122
341	A novel recurrent mutation in ATP1A3 causes CAPOS syndrome. <i>Orphanet Journal of Rare Diseases</i> , <b>2014</b> , 9, 15	4.2	121
340	Meta-analysis of colorectal cancer gene expression profiling studies identifies consistently reported candidate biomarkers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2008</b> , 17, 543-52	4	120
339	Gene number in an invertebrate chordate, <i>Ciona intestinalis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1998</b> , 95, 4437-40	11.5	120
338	De novo genome sequence assembly of a filamentous fungus using Sanger, 454 and Illumina sequence data. <i>Genome Biology</i> , <b>2009</b> , 10, R94	18.3	119
337	Diagnostic utility of galectin-3 in thyroid cancer. <i>American Journal of Pathology</i> , <b>2010</b> , 176, 2067-81	5.8	118
336	Distinct roles of KAP1, HP1 and G9a/GLP in silencing of the two-cell-specific retrotransposon MERV1 in mouse ES cells. <i>Epigenetics and Chromatin</i> , <b>2013</b> , 6, 15	5.8	107
335	ELT-2 is the predominant transcription factor controlling differentiation and function of the C. elegans intestine, from embryo to adult. <i>Developmental Biology</i> , <b>2009</b> , 327, 551-65	3.1	106
334	Cryptococcus neoformans gene expression during experimental cryptococcal meningitis. <i>Eukaryotic Cell</i> , <b>2003</b> , 2, 1336-49		105
333	Insights into conifer giga-genomes. <i>Plant Physiology</i> , <b>2014</b> , 166, 1724-32	6.6	104
332	Whole-genome profiling of mutagenesis in Caenorhabditis elegans. <i>Genetics</i> , <b>2010</b> , 185, 431-41	4	104
331	Retrotransposon-induced heterochromatin spreading in the mouse revealed by insertional polymorphisms. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002301	6	104

330	A set of BAC clones spanning the human genome. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, 3651-60	20.1	104
329	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> ). <i>BMC Genomics</i> , <b>2008</b> , 9, 484	4.5	102
328	A mouse atlas of gene expression: large-scale digital gene-expression profiles from precisely defined developing C57BL/6J mouse tissues and cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 18485-90	11.5	102
327	Recurrent targets of aberrant somatic hypermutation in lymphoma. <i>Oncotarget</i> , <b>2012</b> , 3, 1308-19	3.3	101
326	Evidence that plant-like genes in <i>Chlamydia</i> species reflect an ancestral relationship between Chlamydiaceae, cyanobacteria, and the chloroplast. <i>Genome Research</i> , <b>2002</b> , 12, 1159-67	9.7	101
325	Analysis of FOXO1 mutations in diffuse large B-cell lymphoma. <i>Blood</i> , <b>2013</b> , 121, 3666-74	2.2	100
324	The completion of the Mammalian Gene Collection (MGC). <i>Genome Research</i> , <b>2009</b> , 19, 2324-33	9.7	98
323	ORegAnno: an open access database and curation system for literature-derived promoters, transcription factor binding sites and regulatory variation. <i>Bioinformatics</i> , <b>2006</b> , 22, 637-40	7.2	97
322	SNP discovery in black cottonwood ( <i>Populus trichocarpa</i> ) by population transcriptome resequencing. <i>Molecular Ecology Resources</i> , <b>2011</b> , 11 Suppl 1, 81-92	8.4	96
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