

Steven J M Jones

List of Publications by Year in Descending Order

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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	A platform for oncogenomic reporting and interpretation.. <i>Nature Communications</i> , 2022 , 13, 756	17.4	1
472	Long-read genome sequencing resolves a complex 13q structural variant associated with syndromic anophthalmia.. <i>American Journal of Medical Genetics, Part A</i> , 2022 ,	2.5	0
471	Optimization of magnetic bead-based nucleic acid extraction for SARS-CoV-2 testing using readily available reagents. <i>Journal of Virological Methods</i> , 2022 , 299, 114339	2.6	3
470	Complex Autism Spectrum Disorder with Epilepsy, Strabismus and Self-Injurious Behaviors in a Patient with a De Novo Heterozygous Variant.. <i>Genes</i> , 2022 , 13,	4.2	1
469	A community approach to the cancer-variant-interpretation bottleneck. <i>Nature Cancer</i> , 2022 , 3, 522-525	15.4	0
468	Clinical response to nivolumab in an INI1-deficient pediatric chordoma correlates with immunogenic recognition of brachyury.. <i>Npj Precision Oncology</i> , 2021 , 5, 103	9.8	2
467	Early-stage economic analysis of research-based comprehensive genomic sequencing for advanced cancer care. <i>Journal of Community Genetics</i> , 2021 , 1	2.5	1
466	GA4GH: International policies and standards for data sharing across genomic research and healthcare.. <i>Cell Genomics</i> , 2021 , 1, 100029-100029		20
465	An infant with congenital respiratory insufficiency and diaphragmatic paralysis: A novel BICD2 phenotype?. <i>American Journal of Medical Genetics, Part A</i> , 2021 ,	2.5	0
464	Rearrangement-mediated cis-regulatory alterations in advanced patient tumors reveal interactions with therapy. <i>Cell Reports</i> , 2021 , 37, 110023	10.6	0
463	Copy-scAT: Deconvoluting single-cell chromatin accessibility of genetic subclones in cancer. <i>Science Advances</i> , 2021 , 7, eabg6045	14.3	0
462	Proteotranscriptomic classification and characterization of pancreatic neuroendocrine neoplasms. <i>Cell Reports</i> , 2021 , 37, 109817	10.6	3
461	The transcriptional landscape of Shh medulloblastoma. <i>Nature Communications</i> , 2021 , 12, 1749	17.4	7
460	A clinical transcriptome approach to patient stratification and therapy selection in acute myeloid leukemia. <i>Nature Communications</i> , 2021 , 12, 2474	17.4	10
459	An approach to rapid characterization of DMD copy number variants for prenatal risk assessment. <i>American Journal of Medical Genetics, Part A</i> , 2021 , 185, 2541-2545	2.5	1
458	Human placental cytotrophoblast epigenome dynamics over gestation and alterations in placental disease. <i>Developmental Cell</i> , 2021 , 56, 1238-1252.e5	10.2	7
457	Deep-learning based classification distinguishes sarcomatoid malignant mesotheliomas from benign spindle cell mesothelial proliferations. <i>Modern Pathology</i> , 2021 , 34, 2028-2035	9.8	2

456	A Scalable Strand-Specific Protocol Enabling Full-Length Total RNA Sequencing From Single Cells. <i>Frontiers in Genetics</i> , 2021 , 12, 665888	4.5	1
455	Clinical and cost outcomes following genomics-informed treatment for advanced cancers. <i>Cancer Medicine</i> , 2021 , 10, 5131-5140	4.8	3
454	Contribution of Multiple Inherited Variants to Autism Spectrum Disorder (ASD) in a Family with 3 Affected Siblings. <i>Genes</i> , 2021 , 12,	4.2	3
453	Rare loss-of-function variants in type I IFN immunity genes are not associated with severe COVID-19. <i>Journal of Clinical Investigation</i> , 2021 , 131,	15.9	25
452	-associated neurodevelopmental disorder. <i>Journal of Medical Genetics</i> , 2021 , 58, 196-204	5.8	4
451	Uncovering Clinically Relevant Gene Fusions with Integrated Genomic and Transcriptomic Profiling of Metastatic Cancers. <i>Clinical Cancer Research</i> , 2021 , 27, 522-531	12.9	4
450	Delving into Early-onset Pancreatic Ductal Adenocarcinoma: How Does Age Fit In?. <i>Clinical Cancer Research</i> , 2021 , 27, 246-254	12.9	4
449	Genome and Transcriptome Biomarkers of Response to Immune Checkpoint Inhibitors in Advanced Solid Tumors. <i>Clinical Cancer Research</i> , 2021 , 27, 202-212	12.9	19
448	Subtype-Discordant Pancreatic Ductal Adenocarcinoma Tumors Show Intermediate Clinical and Molecular Characteristics. <i>Clinical Cancer Research</i> , 2021 , 27, 150-157	12.9	8
447	Matching methods in precision oncology: An introduction and illustrative example. <i>Molecular Genetics & Genomic Medicine</i> , 2021 , 9, e1554	2.3	3
446	Co-expression patterns of chimeric antigen receptor (CAR)-T cell target antigens in primary and recurrent ovarian cancer. <i>Gynecologic Oncology</i> , 2021 , 160, 520-529	4.9	3
445	NTRK2 Fusion driven pediatric glioblastoma: Identification of oncogenic Drivers via integrative Genome and transcriptome profiling. <i>Clinical Case Reports (discontinued)</i> , 2021 , 9, 1472-1477	0.7	2
444	Megabase-scale methylation phasing using nanopore long reads and NanoMethPhase. <i>Genome Biology</i> , 2021 , 22, 68	18.3	9
443	Tumor infiltrating neutrophils and gland formation predict overall survival and molecular subgroups in pancreatic ductal adenocarcinoma. <i>Cancer Medicine</i> , 2021 , 10, 1155-1165	4.8	3
442	The pink salmon genome: Uncovering the genomic consequences of a two-year life cycle.. <i>PLoS ONE</i> , 2021 , 16, e0255752	3.7	3
441	Tumor necrosis factor overcomes immune evasion in p53-mutant medulloblastoma. <i>Nature Neuroscience</i> , 2020 , 23, 842-853	25.5	22
440	Complete Mitochondrial Genome of a Gymnosperm, Sitka Spruce (<i>Picea sitchensis</i>), Indicates a Complex Physical Structure. <i>Genome Biology and Evolution</i> , 2020 , 12, 1174-1179	3.9	13
439	NHJ-1 Is Required for Canonical Nonhomologous End Joining in. <i>Genetics</i> , 2020 , 215, 635-651	4	1

438	Endogenous Retrovirus Transcript Levels Are Associated with Immunogenic Signatures in Multiple Metastatic Cancer Types. <i>Molecular Cancer Therapeutics</i> , 2020 , 19, 1889-1897	6.1	3
437	LIST-S2: taxonomy based sorting of deleterious missense mutations across species. <i>Nucleic Acids Research</i> , 2020 , 48, W154-W161	20.1	13
436	Improved structural variant interpretation for hereditary cancer susceptibility using long-read sequencing. <i>Genetics in Medicine</i> , 2020 , 22, 1892-1897	8.1	15
435	Integration of Whole-Genome Sequencing With Circulating Tumor DNA Analysis Captures Clonal Evolution and Tumor Heterogeneity in Non-V600 BRAF Mutant Colorectal Cancer. <i>Clinical Colorectal Cancer</i> , 2020 , 19, 132-136.e3	3.8	1
434	Transcription phenotypes of pancreatic cancer are driven by genomic events during tumor evolution. <i>Nature Genetics</i> , 2020 , 52, 231-240	36.3	148
433	Fluorouracil sensitivity in a head and neck squamous cell carcinoma with a somatic structural variant. <i>Journal of Physical Education and Sports Management</i> , 2020 , 6,	2.8	3
432	Patient selection for a developmental therapeutics program using whole genome and Transcriptome analysis. <i>Investigational New Drugs</i> , 2020 , 38, 1601-1604	4.3	
431	Pan-cancer analysis of advanced patient tumors reveals interactions between therapy and genomic landscapes.. <i>Nature Cancer</i> , 2020 , 1, 452-468	15.4	34
430	Tumor microRNA profile and prognostic value for lymph node metastasis in oral squamous cell carcinoma patients. <i>Oncotarget</i> , 2020 , 11, 2204-2215	3.3	7
429	Altered Gene Expression along the Glycolysis-Cholesterol Synthesis Axis Is Associated with Outcome in Pancreatic Cancer. <i>Clinical Cancer Research</i> , 2020 , 26, 135-146	12.9	61
428	Establishing a Framework for the Clinical Translation of Germline Findings in Precision Oncology. <i>JNCI Cancer Spectrum</i> , 2020 , 4, pkaa045	4.6	0
427	Complete Chloroplast Genome Sequence of a Black Spruce (<i>Picea mariana</i>) from Eastern Canada. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	1
426	Glioma-derived IL-33 orchestrates an inflammatory brain tumor microenvironment that accelerates glioma progression. <i>Nature Communications</i> , 2020 , 11, 4997	17.4	42
425	Analysis of Ugandan cervical carcinomas identifies human papillomavirus clade-specific epigenome and transcriptome landscapes. <i>Nature Genetics</i> , 2020 , 52, 800-810	36.3	17
424	A Distributed Whole Genome Sequencing Benchmark Study. <i>Frontiers in Genetics</i> , 2020 , 11, 612515	4.5	2
423	Comprehensive genomic profiling of glioblastoma tumors, BTICs, and xenografts reveals stability and adaptation to growth environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 19098-19108	11.5	23
422	Integrated Genomic and Functional microRNA Analysis Identifies miR-30-5p as a Tumor Suppressor and Potential Therapeutic Nanomedicine in Head and Neck Cancer. <i>Clinical Cancer Research</i> , 2019 , 25, 2860-2873	12.9	41
421	Sequencing, Assembly, and Annotation of Four Threespine Stickleback Genomes Based on Microfluidic Partitioned DNA Libraries. <i>Genes</i> , 2019 , 10,	4.2	6

420	Complete Chloroplast Genome Sequence of a White Spruce (<i>Picea glauca</i> , Genotype WS77111) from Eastern Canada. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	2
419	Genomic characterization of a well-differentiated grade 3 pancreatic neuroendocrine tumor. <i>Journal of Physical Education and Sports Management</i> , 2019 , 5,	2.8	8
418	Gene Fusions Are Recurrent, Clinically Actionable Gene Rearrangements in Wild-Type Pancreatic Ductal Adenocarcinoma. <i>Clinical Cancer Research</i> , 2019 , 25, 4674-4681	12.9	63
417	CancerMine: a literature-mined resource for drivers, oncogenes and tumor suppressors in cancer. <i>Nature Methods</i> , 2019 , 16, 505-507	21.6	54
416	ntEdit: scalable genome sequence polishing. <i>Bioinformatics</i> , 2019 , 35, 4430-4432	7.2	29
415	ORCA: a comprehensive bioinformatics container environment for education and research. <i>Bioinformatics</i> , 2019 , 35, 4448-4450	7.2	6
414	Improved measures for evolutionary conservation that exploit taxonomy distances. <i>Nature Communications</i> , 2019 , 10, 1556	17.4	13
413	Application of a Neural Network Whole Transcriptome-Based Pan-Cancer Method for Diagnosis of Primary and Metastatic Cancers. <i>JAMA Network Open</i> , 2019 , 2, e192597	10.4	25
412	Base excision repair deficiency signatures implicate germline and somatic aberrations in pancreatic ductal adenocarcinoma and breast cancer oncogenesis. <i>Journal of Physical Education and Sports Management</i> , 2019 , 5,	2.8	17
411	RTNsurvival: an R/Bioconductor package for regulatory network survival analysis. <i>Bioinformatics</i> , 2019 , 35, 4488-4489	7.2	7
410	Mutations in ILK, encoding integrin-linked kinase, are associated with arrhythmogenic cardiomyopathy. <i>Translational Research</i> , 2019 , 208, 15-29	11	14
409	Whole-Genome Sequencing in Cancer. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2019 , 9,	5.4	14
408	MAVIS: merging, annotation, validation, and illustration of structural variants. <i>Bioinformatics</i> , 2019 , 35, 515-517	7.2	13
407	The pivotal role of sampling recurrent tumors in the precision care of patients with tumors of the central nervous system. <i>Journal of Physical Education and Sports Management</i> , 2019 , 5,	2.8	4
406	The Genome of the Steller Sea Lion (). <i>Genes</i> , 2019 , 10,	4.2	3
405	Complete Chloroplast Genome Sequence of an Engelmann Spruce (, Genotype Se404-851) from Western Canada. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	2
404	RTNduals: an R/Bioconductor package for analysis of co-regulation and inference of dual regulons. <i>Bioinformatics</i> , 2019 , 35, 5357-5358	7.2	2
403	Therapeutic Implication of Genomic Landscape of Adult Metastatic Sarcoma.. <i>JCO Precision Oncology</i> , 2019 , 3, 1-25	3.6	5

402	Evaluation of protocols for rRNA depletion-based RNA sequencing of nanogram inputs of mammalian total RNA. <i>PLoS ONE</i> , 2019 , 14, e0224578	3.7	6
401	Identification and Analyses of Extra-Cranial and Cranial Rhabdoid Tumor Molecular Subgroups Reveal Tumors with Cytotoxic T Cell Infiltration. <i>Cell Reports</i> , 2019 , 29, 2338-2354.e7	10.6	40
400	Expression of Gp78/Autocrine Motility Factor Receptor and Endocytosis of Autocrine Motility Factor in Human Thyroid Cancer Cells. <i>Cureus</i> , 2019 , 11, e4928	1.2	
399	Rare SUZ12 variants commonly cause an overgrowth phenotype. <i>American Journal of Medical Genetics, Part C: Seminars in Medical Genetics</i> , 2019 , 181, 532-547	3.1	8
398	Text-mining clinically relevant cancer biomarkers for curation into the CIViC database. <i>Genome Medicine</i> , 2019 , 11, 78	14.4	19
397	Sources of erroneous sequences and artifact chimeric reads in next generation sequencing of genomic DNA from formalin-fixed paraffin-embedded samples. <i>Nucleic Acids Research</i> , 2019 , 47, e12	20.1	33
396	Genome-wide discovery of somatic coding and noncoding mutations in pediatric endemic and sporadic Burkitt lymphoma. <i>Blood</i> , 2019 , 133, 1313-1324	2.2	75
395	Clinical outcomes after whole-genome sequencing in patients with metastatic non-small-cell lung cancer. <i>Journal of Physical Education and Sports Management</i> , 2019 , 5,	2.8	2
394	A Hematogenous Route for Medulloblastoma Leptomeningeal Metastases. <i>Cell</i> , 2018 , 172, 1050-1062.e14	14.2	46
393	Molecular characterization of -amplified colorectal cancer identifies potential mechanisms of resistance to targeted therapies: a report of two instructive cases. <i>Journal of Physical Education and Sports Management</i> , 2018 , 4,	2.8	9
392	Application of genomics to identify therapeutic targets in recurrent pediatric papillary thyroid carcinoma. <i>Journal of Physical Education and Sports Management</i> , 2018 , 4,	2.8	13
391	Personalized oncogenomic analysis of metastatic adenoid cystic carcinoma: using whole-genome sequencing to inform clinical decision-making. <i>Journal of Physical Education and Sports Management</i> , 2018 , 4,	2.8	14
390	A-to-I miR-378a-3p editing can prevent melanoma progression via regulation of PARVA expression. <i>Nature Communications</i> , 2018 , 9, 461	17.4	39
389	Text-based phenotypic profiles incorporating biochemical phenotypes of inborn errors of metabolism improve phenomics-based diagnosis. <i>Journal of Inherited Metabolic Disease</i> , 2018 , 41, 555-562	5.4	4
388	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018 , 33, 244-258.e10	24.3	150
387	Whole genome and whole transcriptome genomic profiling of a metastatic eccrine porocarcinoma. <i>Npj Precision Oncology</i> , 2018 , 2, 8	9.8	11
386	Opposing Effects of CREBBP Mutations Govern the Phenotype of Rubinstein-Taybi Syndrome and Adult SHH Medulloblastoma. <i>Developmental Cell</i> , 2018 , 44, 709-724.e6	10.2	25
385	A collaborative filtering-based approach to biomedical knowledge discovery. <i>Bioinformatics</i> , 2018 , 34, 652-659	7.2	14

384	Genome-Enhanced Detection and Identification (GEDI) of plant pathogens. <i>PeerJ</i> , 2018 , 6, e4392	3.1	15
383	Molecular characterization of metastatic pancreatic neuroendocrine tumors (PNETs) using whole-genome and transcriptome sequencing. <i>Journal of Physical Education and Sports Management</i> , 2018 , 4,	2.8	20
382	Modern drug design: the implication of using artificial neuronal networks and multiple molecular dynamic simulations. <i>Journal of Computer-Aided Molecular Design</i> , 2018 , 32, 299-311	4.2	4
381	Temporal Dynamics of Genomic Alterations in a Germline-Mutated Pancreatic Cancer With Low Genomic Instability Burden but Exceptional Response to Fluorouracil, Oxaliplatin, Leucovorin, and Irinotecan. <i>JCO Precision Oncology</i> , 2018 , 2,	3.6	0
380	Comparative RNA-Sequencing Analysis Benefits a Pediatric Patient With Relapsed Cancer. <i>JCO Precision Oncology</i> , 2018 , 2,	3.6	6
379	Tigmint: correcting assembly errors using linked reads from large molecules. <i>BMC Bioinformatics</i> , 2018 , 19, 393	3.6	35
378	Whole-genome and transcriptome profiling of a metastatic thyroid-like follicular renal cell carcinoma. <i>Journal of Physical Education and Sports Management</i> , 2018 , 4,	2.8	10
377	Population sequencing reveals clonal diversity and ancestral inbreeding in the grapevine cultivar Chardonnay. <i>PLoS Genetics</i> , 2018 , 14, e1007807	6	54
376	The Genome of the North American Brown Bear or Grizzly: <i>Ursus arctos</i> ssp. <i>horribilis</i> . <i>Genes</i> , 2018 , 9,	4.2	13
375	Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. <i>Nature Communications</i> , 2018 , 9, 4001	17.4	64
374	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018 , 362,	33.3	392
373	The genetic basis and cell of origin of mixed phenotype acute leukaemia. <i>Nature</i> , 2018 , 562, 373-379	50.4	140
372	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , 2017 , 543, 378-384	50.4	755
371	CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. <i>Nature Genetics</i> , 2017 , 49, 170-174	36.3	308
370	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017 , 31, 181-193	24.3	350
369	Hypermethylation signature reveals a slippage and realignment model of translesion synthesis by Rev3 polymerase in cisplatin-treated yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 2663-2668	11.5	13
368	Spatial heterogeneity in medulloblastoma. <i>Nature Genetics</i> , 2017 , 49, 780-788	36.3	80
367	Management of PET diagnosed thyroid incidentalomas in British Columbia Canada: Critical importance of the PET report. <i>American Journal of Surgery</i> , 2017 , 213, 950-957	2.7	3

366	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017 , 169, 1327-1341.e23	56.2	1125
365	Genomic profiling of pelvic genital type leiomyosarcoma in a woman with a germline :c.1100delC mutation and a concomitant diagnosis of metastatic invasive ductal breast carcinoma. <i>Journal of Physical Education and Sports Management</i> , 2017 , 3,	2.8	6
364	Pyruvate Kinase Inhibits Proliferation during Postnatal Cerebellar Neurogenesis and Suppresses Medulloblastoma Formation. <i>Cancer Research</i> , 2017 , 77, 3217-3230	10.1	32
363	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017 , 31, 411-423	24.3	210
362	Integrated genomic characterization of oesophageal carcinoma. <i>Nature</i> , 2017 , 541, 169-175	50.4	965
361	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017 , 171, 540-556.e25	27.5	961
360	RECQ-like helicases Sgs1 and BLM regulate R-loop-associated genome instability. <i>Journal of Cell Biology</i> , 2017 , 216, 3991-4005	7.3	58
359	Clonal expansion and epigenetic reprogramming following deletion or amplification of mutant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 10743-10748	11.5	78
358	Detection and genomic characterization of a mammary-like adenocarcinoma. <i>Journal of Physical Education and Sports Management</i> , 2017 , 3,	2.8	8
357	Compound heterozygous TRPV4 mutations in two siblings with a complex phenotype including severe intellectual disability and neuropathy. <i>American Journal of Medical Genetics, Part A</i> , 2017 , 173, 3087-3092	2.5	7
356	Complete Genome Sequence of SJ42, a Nonoutbreak Strain from an Immunocompromised Patient with Pulmonary Disease. <i>Genome Announcements</i> , 2017 , 5,		2
355	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017 , 547, 311-317	50.4	472
354	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017 , 32, 204-220.e15	24.3	391
353	Characterization of the human thyroid epigenome. <i>Journal of Endocrinology</i> , 2017 , 235, 153-165	4.7	6
352	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017 , 32, 185-203.e13	24.5	13896
351	Homologous Recombination Deficiency and Platinum-Based Therapy Outcomes in Advanced Breast Cancer. <i>Clinical Cancer Research</i> , 2017 , 23, 7521-7530	12.9	82
350	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017 , 171, 950-965.e28	56.2	451
349	Comprehensive whole genome sequence analyses yields novel genetic and structural insights for Intellectual Disability. <i>BMC Genomics</i> , 2017 , 18, 403	4.5	9

348	Differential roles of RET isoforms in medullary and papillary thyroid carcinomas. <i>Endocrine-Related Cancer</i> , 2017 , 24, 53-69	5.7	29
347	Successful targeting of the NRG1 pathway indicates novel treatment strategy for metastatic cancer. <i>Annals of Oncology</i> , 2017 , 28, 3092-3097	10.3	64
346	Increasing quality, throughput and speed of sample preparation for strand-specific messenger RNA sequencing. <i>BMC Genomics</i> , 2017 , 18, 515	4.5	6
345	The Genome of the Beluga Whale (<i>Delphinapterus leucas</i>). <i>Genes</i> , 2017 , 8,	4.2	28
344	The Genome of the Northern Sea Otter (<i>Enhydra lutris kenyoni</i>). <i>Genes</i> , 2017 , 8,	4.2	15
343	Clinical outcomes after whole genome sequencing in patients with metastatic non-small cell lung cancer.. <i>Journal of Clinical Oncology</i> , 2017 , 35, e20563-e20563	2.2	1
342	Automated high throughput nucleic acid purification from formalin-fixed paraffin-embedded tissue samples for next generation sequence analysis. <i>PLoS ONE</i> , 2017 , 12, e0178706	3.7	13
341	A somatic reference standard for cancer genome sequencing. <i>Scientific Reports</i> , 2016 , 6, 24607	4.9	39
340	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016 , 167, 1145-1149	56.2	232
339	Analysis of Normal Human Mammary Epigenomes Reveals Cell-Specific Active Enhancer States and Associated Transcription Factor Networks. <i>Cell Reports</i> , 2016 , 17, 2060-2074	10.6	72
338	rAAV-compatible MiniPromoters for restricted expression in the brain and eye. <i>Molecular Brain</i> , 2016 , 9, 52	4.5	43
337	Divergent clonal selection dominates medulloblastoma at recurrence. <i>Nature</i> , 2016 , 529, 351-7	50.4	206
336	ORegAnno 3.0: a community-driven resource for curated regulatory annotation. <i>Nucleic Acids Research</i> , 2016 , 44, D126-32	20.1	89
335	Large-scale profiling of microRNAs for The Cancer Genome Atlas. <i>Nucleic Acids Research</i> , 2016 , 44, e3	20.1	85
334	Genome-Wide Profiles of Extra-cranial Malignant Rhabdoid Tumors Reveal Heterogeneity and Dysregulated Developmental Pathways. <i>Cancer Cell</i> , 2016 , 29, 394-406	24.3	81
333	Putative BRAF activating fusion in a medullary thyroid cancer. <i>Journal of Physical Education and Sports Management</i> , 2016 , 2, a000729	2.8	11
332	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016 , 164, 550-63	56.2	1140
331	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016 , 374, 135-45	59.2	753

330	Clinical importance of bilateral disease in patients with papillary thyroid cancer. <i>Canadian Journal of Surgery</i> , 2016 , 59, 213-5	2	4
329	Personalized oncogenomics in the management of gastrointestinal carcinomas-early experiences from a pilot study. <i>Current Oncology</i> , 2016 , 23, e571-e575	2.8	6
328	miR-509-3p is clinically significant and strongly attenuates cellular migration and multi-cellular spheroids in ovarian cancer. <i>Oncotarget</i> , 2016 , 7, 25930-48	3.3	39
327	Small molecule epigenetic screen identifies novel EZH2 and HDAC inhibitors that target glioblastoma brain tumor-initiating cells. <i>Oncotarget</i> , 2016 , 7, 59360-59376	3.3	26
326	Genomic Analysis of a Serotype 5 Streptococcus pneumoniae Outbreak in British Columbia, Canada, 2005-2009. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2016 , 2016, 5381871	2.6	4
325	Assembly of the Complete Sitka Spruce Chloroplast Genome Using 10X GenomicsPGemCode Sequencing Data. <i>PLoS ONE</i> , 2016 , 11, e0163059	3.7	27
324	ChAsE: chromatin analysis and exploration tool. <i>Bioinformatics</i> , 2016 , 32, 3324-3326	7.2	23
323	Tumour-suppressor microRNAs regulate ovarian cancer cell physical properties and invasive behaviour. <i>Open Biology</i> , 2016 , 6,	7	24
322	Response to angiotensin blockade with irbesartan in a patient with metastatic colorectal cancer. <i>Annals of Oncology</i> , 2016 , 27, 801-6	10.3	27
321	Molecular etiology of an indolent lymphoproliferative disorder determined by whole-genome sequencing. <i>Journal of Physical Education and Sports Management</i> , 2016 , 2, a000679	2.8	1
320	The Atlantic salmon genome provides insights into rediploidization. <i>Nature</i> , 2016 , 533, 200-5	50.4	606
319	Investigation of PD-L1 Biomarker Testing Methods for PD-1 Axis Inhibition in Non-squamous Non-small Cell Lung Cancer. <i>Journal of Histochemistry and Cytochemistry</i> , 2016 , 64, 587-600	3.4	24
318	Genome sequences of six species threatening forest ecosystems. <i>Genomics Data</i> , 2016 , 10, 85-88		20
317	Epigenetic and transcriptional determinants of the human breast. <i>Nature Communications</i> , 2015 , 6, 6351	17.4	44
316	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015 , 161, 1681-96	56.2	1807
315	Cross-cancer profiling of molecular alterations within the human autophagy interaction network. <i>Autophagy</i> , 2015 , 11, 1668-87	10.2	89
314	MEG3 long noncoding RNA regulates the TGF- β pathway genes through formation of RNA-DNA triplex structures. <i>Nature Communications</i> , 2015 , 6, 7743	17.4	414
313	Precursor States of Brain Tumor Initiating Cell Lines Are Predictive of Survival in Xenografts and Associated with Glioblastoma Subtypes. <i>Stem Cell Reports</i> , 2015 , 5, 1-9	8	51

312	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015 , 372, 2481-98	59.2	1828
311	Prognostic significance of autocrine motility factor receptor expression by colorectal cancer and lymph node metastases. <i>American Journal of Surgery</i> , 2015 , 209, 884-9; discussion 889	2.7	6
310	A novel mutation in EED associated with overgrowth. <i>Journal of Human Genetics</i> , 2015 , 60, 339-42	4.3	46
309	SOX9 modulates the expression of key transcription factors required for heart valve development. <i>Development (Cambridge)</i> , 2015 , 142, 4340-50	6.6	37
308	Retrospective review using targeted deep sequencing reveals mutational differences between gastroesophageal junction and gastric carcinomas. <i>BMC Cancer</i> , 2015 , 15, 32	4.8	28
307	Combined serial analysis of gene expression and transcription factor binding site prediction identifies novel-candidate-target genes of Nr2e1 in neocortex development. <i>BMC Genomics</i> , 2015 , 16, 545	4.5	7
306	LINKS: Scalable, alignment-free scaffolding of draft genomes with long reads. <i>GigaScience</i> , 2015 , 4, 35	7.6	124
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