

# Steven J M Jones

## List of Publications by Year in descending order

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Version: 2024-02-01

477  
papers

167,384  
citations

460

134  
h-index

68

389  
g-index

487  
all docs

487  
docs citations

487  
times ranked

189949  
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	1.0	4
2	Early-stage economic analysis of research-based comprehensive genomic sequencing for advanced cancer care. <i>Journal of Community Genetics</i> , 2022, 13, 523-538.	0.5	4
3	An infant with congenital respiratory insufficiency and diaphragmatic paralysis: A novel <i>BICD2</i> phenotype?. <i>American Journal of Medical Genetics, Part A</i> , 2022, 188, 926-930.	0.7	3
4	A platform for oncogenomic reporting and interpretation. <i>Nature Communications</i> , 2022, 13, 756.	5.8	7
5	Long-read genome sequencing resolves a complex 13q structural variant associated with syndromic anophthalmia. <i>American Journal of Medical Genetics, Part A</i> , 2022, 188, 1589-1594.	0.7	4
6	The genome of the forest insect pest <i>Pissodes strobi</i> reveals genome expansion and evidence of a <i>Wolbachia</i> endosymbiont. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	4
7	Complex Autism Spectrum Disorder with Epilepsy, Strabismus and Self-Injurious Behaviors in a Patient with a De Novo Heterozygous <i>POLR2A</i> Variant. <i>Genes</i> , 2022, 13, 470.	1.0	3
8	cSurvival: a web resource for biomarker interactions in cancer outcomes and in cell lines. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	7
9	Whole-genome and transcriptome analysis of advanced adrenocortical cancer highlights multiple alterations affecting epigenome and DNA repair pathways.. <i>Cold Spring Harbor Molecular Case Studies</i> , 2022, 8, .	0.7	2
10	A community approach to the cancer-variant-interpretation bottleneck. <i>Nature Cancer</i> , 2022, 3, 522-525.	5.7	3
11	Spruce <i>giga</i> genomes: structurally similar yet distinctive with differentially expanding gene families and rapidly evolving genes. <i>Plant Journal</i> , 2022, 111, 1469-1485.	2.8	17
12	<i>SETD1B</i> -associated neurodevelopmental disorder. <i>Journal of Medical Genetics</i> , 2021, 58, 196-204.	1.5	22
13	Uncovering Clinically Relevant Gene Fusions with Integrated Genomic and Transcriptomic Profiling of Metastatic Cancers. <i>Clinical Cancer Research</i> , 2021, 27, 522-531.	3.2	14
14	Delving into Early-onset Pancreatic Ductal Adenocarcinoma: How Does Age Fit In?. <i>Clinical Cancer Research</i> , 2021, 27, 246-254.	3.2	16
15	Genome and Transcriptome Biomarkers of Response to Immune Checkpoint Inhibitors in Advanced Solid Tumors. <i>Clinical Cancer Research</i> , 2021, 27, 202-212.	3.2	50
16	Subtype-Discordant Pancreatic Ductal Adenocarcinoma Tumors Show Intermediate Clinical and Molecular Characteristics. <i>Clinical Cancer Research</i> , 2021, 27, 150-157.	3.2	24
17	Matching methods in precision oncology: An introduction and illustrative example. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2021, 9, e1554.	0.6	13
18	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.	0.6	10

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19	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.	0.2	3
20	Megabase-scale methylation phasing using nanopore long reads and NanoMethPhase. <i>Genome Biology</i> , 2021, 22, 68.	3.8	36
21	The transcriptional landscape of Shh medulloblastoma. <i>Nature Communications</i> , 2021, 12, 1749.	5.8	47
22	A clinical transcriptome approach to patient stratification and therapy selection in acute myeloid leukemia. <i>Nature Communications</i> , 2021, 12, 2474.	5.8	49
23	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.	0.7	3
24	Human placental cytotrophoblast epigenome dynamics over gestation and alterations in placental disease. <i>Developmental Cell</i> , 2021, 56, 1238-1252.e5.	3.1	29
25	Deep-learning based classification distinguishes sarcomatoid malignant mesotheliomas from benign spindle cell mesothelial proliferations. <i>Modern Pathology</i> , 2021, 34, 2028-2035.	2.9	8
26	A Scalable Strand-Specific Protocol Enabling Full-Length Total RNA Sequencing From Single Cells. <i>Frontiers in Genetics</i> , 2021, 12, 665888.	1.1	2
27	Clinical and cost outcomes following genomics-informed treatment for advanced cancers. <i>Cancer Medicine</i> , 2021, 10, 5131-5140.	1.3	8
28	Contribution of Multiple Inherited Variants to Autism Spectrum Disorder (ASD) in a Family with 3 Affected Siblings. <i>Genes</i> , 2021, 12, 1053.	1.0	12
29	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, .	3.9	56
30	Tumor infiltrating neutrophils and gland formation predict overall survival and molecular subgroups in pancreatic ductal adenocarcinoma. <i>Cancer Medicine</i> , 2021, 10, 1155-1165.	1.3	9
31	Copy-scAT: Deconvoluting single-cell chromatin accessibility of genetic subclones in cancer. <i>Science Advances</i> , 2021, 7, eabg6045.	4.7	19
32	Proteotranscriptomic classification and characterization of pancreatic neuroendocrine neoplasms. <i>Cell Reports</i> , 2021, 37, 109817.	2.9	14
33	GA4GH: International policies and standards for data sharing across genomic research and healthcare. <i>Cell Genomics</i> , 2021, 1, 100029.	3.0	94
34	Rearrangement-mediated cis-regulatory alterations in advanced patient tumors reveal interactions with therapy. <i>Cell Reports</i> , 2021, 37, 110023.	2.9	8
35	Clinical response to nivolumab in an INI1-deficient pediatric chordoma correlates with immunogenic recognition of brachyury. <i>Npj Precision Oncology</i> , 2021, 5, 103.	2.3	18
36	The pink salmon genome: Uncovering the genomic consequences of a two-year life cycle. <i>PLoS ONE</i> , 2021, 16, e0255752.	1.1	14

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37	Altered Gene Expression along the Glycolysisâ€“Cholesterol Synthesis Axis Is Associated with Outcome in Pancreatic Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 135-146.	3.2	121
38	Establishing a Framework for the Clinical Translation of Germline Findings in Precision Oncology. <i>JNCI Cancer Spectrum</i> , 2020, 4, pkaa045.	1.4	6
39	Complete Chloroplast Genome Sequence of a Black Spruce ( <i>Picea mariana</i> ) from Eastern Canada. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
40	Glioma-derived IL-33 orchestrates an inflammatory brain tumor microenvironment that accelerates glioma progression. <i>Nature Communications</i> , 2020, 11, 4997.	5.8	109
41	Analysis of Ugandan cervical carcinomas identifies human papillomavirus cladeâ€“specific epigenome and transcriptome landscapes. <i>Nature Genetics</i> , 2020, 52, 800-810.	9.4	40
42	A Distributed Whole Genome Sequencing Benchmark Study. <i>Frontiers in Genetics</i> , 2020, 11, 612515.	1.1	6
43	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.	1.1	49
44	NHJ-1 Is Required for Canonical Nonhomologous End Joining in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2020, 215, 635-651.	1.2	5
45	Endogenous Retrovirus Transcript Levels Are Associated with Immunogenic Signatures in Multiple Metastatic Cancer Types. <i>Molecular Cancer Therapeutics</i> , 2020, 19, 1889-1897.	1.9	10
46	LIST-S2: taxonomy based sorting of deleterious missense mutations across species. <i>Nucleic Acids Research</i> , 2020, 48, W154-W161.	6.5	46
47	Improved structural variant interpretation for hereditary cancer susceptibility using long-read sequencing. <i>Genetics in Medicine</i> , 2020, 22, 1892-1897.	1.1	42
48	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.	1.0	1
49	Transcription phenotypes of pancreatic cancer are driven by genomic events during tumor evolution. <i>Nature Genetics</i> , 2020, 52, 231-240.	9.4	365
50	Fluorouracil sensitivity in a head and neck squamous cell carcinoma with a somatic DPYD structural variant. <i>Journal of Physical Education and Sports Management</i> , 2020, 6, a004713.	0.5	5
51	Patient selection for a developmental therapeutics program using whole genome and Transcriptome analysis. <i>Investigational New Drugs</i> , 2020, 38, 1601-1604.	1.2	0
52	Pan-cancer analysis of advanced patient tumors reveals interactions between therapy and genomic landscapes. <i>Nature Cancer</i> , 2020, 1, 452-468.	5.7	103
53	Tumor microRNA profile and prognostic value for lymph node metastasis in oral squamous cell carcinoma patients. <i>Oncotarget</i> , 2020, 11, 2204-2215.	0.8	8
54	Whole-Genome Sequencing in Cancer. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2019, 9, a034579.	2.9	38

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55	MAVIS: merging, annotation, validation, and illustration of structural variants. <i>Bioinformatics</i> , 2019, 35, 515-517.	1.8	22
56	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, a004143.	0.5	4
57	The Genome of the Steller Sea Lion ( <i>Eumetopias jubatus</i> ). <i>Genes</i> , 2019, 10, 486.	1.0	4
58	Complete Chloroplast Genome Sequence of an Engelmann Spruce ( <i>Picea engelmannii</i> , Genotype) Tj ETQq0,0,0 rgBT /Overlock 1	0.3	4
59	<i>RTNduals</i> : an R/Bioconductor package for analysis of co-regulation and inference of dual regulons. <i>Bioinformatics</i> , 2019, 35, 5357-5358.	1.8	11
60	Therapeutic Implication of Genomic Landscape of Adult Metastatic Sarcoma. <i>JCO Precision Oncology</i> , 2019, 3, 1-25.	1.5	12
61	Evaluation of protocols for rRNA depletion-based RNA sequencing of nanogram inputs of mammalian total RNA. <i>PLoS ONE</i> , 2019, 14, e0224578.	1.1	12
62	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.	2.9	74
63	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.	3.3	42
64	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.	3.2	68
65	De Novo Sequencing, Assembly, and Annotation of Four Threespine Stickleback Genomes Based on Microfluidic Partitioned DNA Libraries. <i>Genes</i> , 2019, 10, 426.	1.0	11
66	Complete Chloroplast Genome Sequence of a White Spruce ( <i>Picea glauca</i> , Genotype WS77111) from Eastern Canada. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	7
67	Genomic characterization of a well-differentiated grade 3 pancreatic neuroendocrine tumor. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a003814.	0.5	17
68	<i>NRG1</i> Gene Fusions Are Recurrent, Clinically Actionable Gene Rearrangements in <i>KRAS</i> Wild-Type Pancreatic Ductal Adenocarcinoma. <i>Clinical Cancer Research</i> , 2019, 25, 4674-4681.	3.2	121
69	CancerMine: a literature-mined resource for drivers, oncogenes and tumor suppressors in cancer. <i>Nature Methods</i> , 2019, 16, 505-507.	9.0	139
70	ntEdit: scalable genome sequence polishing. <i>Bioinformatics</i> , 2019, 35, 4430-4432.	1.8	67
71	ORCA: a comprehensive bioinformatics container environment for education and research. <i>Bioinformatics</i> , 2019, 35, 4448-4450.	1.8	10
72	Improved measures for evolutionary conservation that exploit taxonomy distances. <i>Nature Communications</i> , 2019, 10, 1556.	5.8	21

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73	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.	2.8	67
74	Base excision repair deficiency signatures implicate germline and somatic <i>MUTYH</i> aberrations in pancreatic ductal adenocarcinoma and breast cancer oncogenesis. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a003681.	0.5	33
75	<i>RTNsurvival</i> : an R/Bioconductor package for regulatory network survival analysis. <i>Bioinformatics</i> , 2019, 35, 4488-4489.	1.8	21
76	Mutations in <i>ILK</i> , encoding integrin-linked kinase, are associated with arrhythmogenic cardiomyopathy. <i>Translational Research</i> , 2019, 208, 15-29.	2.2	33
77	Rare <i>SUZ12</i> variants commonly cause an overgrowth phenotype. <i>American Journal of Medical Genetics, Part C: Seminars in Medical Genetics</i> , 2019, 181, 532-547.	0.7	23
78	Text-mining clinically relevant cancer biomarkers for curation into the CIVIC database. <i>Genome Medicine</i> , 2019, 11, 78.	3.6	35
79	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-e12.	6.5	50
80	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
81	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, a002659.	0.5	3
82	Expression of Gp78/Autocrine Motility Factor Receptor and Endocytosis of Autocrine Motility Factor in Human Thyroid Cancer Cells. <i>Cureus</i> , 2019, 11, e4928.	0.2	0
83	A Hematogenous Route for Medulloblastoma Leptomeningeal Metastases. <i>Cell</i> , 2018, 172, 1050-1062.e14.	13.5	85
84	Molecular characterization of <i>ERBB2</i> -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, a002535.	0.5	16
85	Application of genomics to identify therapeutic targets in recurrent pediatric papillary thyroid carcinoma. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002568.	0.5	14
86	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, a002626.	0.5	18
87	A-to-I miR-378a-3p editing can prevent melanoma progression via regulation of <i>PARVA</i> expression. <i>Nature Communications</i> , 2018, 9, 461.	5.8	61
88	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.	1.7	5
89	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018, 33, 244-258.e10.	7.7	270
90	Whole genome and whole transcriptome genomic profiling of a metastatic eccrine porocarcinoma. <i>Npj Precision Oncology</i> , 2018, 2, 8.	2.3	15

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91	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.	3.1	35
92	A collaborative filtering-based approach to biomedical knowledge discovery. <i>Bioinformatics</i> , 2018, 34, 652-659.	1.8	25
93	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, a002329.	0.5	30
94	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.	1.3	6
95	Temporal Dynamics of Genomic Alterations in a BRCA1 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, 1-8.	1.5	1
96	Comparative RNA-Sequencing Analysis Benefits a Pediatric Patient With Relapsed Cancer. <i>JCO Precision Oncology</i> , 2018, 2, 1-16.	1.5	12
97	Tigmint: correcting assembly errors using linked reads from large molecules. <i>BMC Bioinformatics</i> , 2018, 19, 393.	1.2	97
98	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, a003137.	0.5	15
99	Population sequencing reveals clonal diversity and ancestral inbreeding in the grapevine cultivar Chardonnay. <i>PLoS Genetics</i> , 2018, 14, e1007807.	1.5	116
100	The Genome of the North American Brown Bear or Grizzly: <i>Ursus arctos</i> ssp. <i>horribilis</i> . <i>Genes</i> , 2018, 9, 598.	1.0	34
101	Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. <i>Nature Communications</i> , 2018, 9, 4001.	5.8	102
102	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018, 362, .	6.0	781
103	The genetic basis and cell of origin of mixed phenotype acute leukaemia. <i>Nature</i> , 2018, 562, 373-379.	13.7	236
104	Genome-Enhanced Detection and Identification (GEDI) of plant pathogens. <i>PeerJ</i> , 2018, 6, e4392.	0.9	24
105	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , 2017, 543, 378-384.	13.7	1,158
106	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
107	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017, 31, 181-193.	7.7	532
108	Hypermutation 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.	3.3	18

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109	Spatial heterogeneity in medulloblastoma. <i>Nature Genetics</i> , 2017, 49, 780-788.	9.4	112
110	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.	0.9	3
111	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	13.5	1,794
112	Genomic profiling of pelvic genital type leiomyosarcoma in a woman with a germline <i>CHEK2</i> :c.1100delC mutation and a concomitant diagnosis of metastatic invasive ductal breast carcinoma. <i>Journal of Physical Education and Sports Management</i> , 2017, 3, a001628.	0.5	8
113	Pyruvate Kinase Inhibits Proliferation during Postnatal Cerebellar Neurogenesis and Suppresses Medulloblastoma Formation. <i>Cancer Research</i> , 2017, 77, 3217-3230.	0.4	45
114	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423.	7.7	309
115	Integrated genomic characterization of oesophageal carcinoma. <i>Nature</i> , 2017, 541, 169-175.	13.7	1,448
116	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25.	13.5	1,742
117	RECQ-like helicases Sgs1 and BLM regulate R-loop-associated genome instability. <i>Journal of Cell Biology</i> , 2017, 216, 3991-4005.	2.3	90
118	Clonal expansion and epigenetic reprogramming following deletion or amplification of mutant <i>IDH1</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10743-10748.	3.3	109
119	Detection and genomic characterization of a mammary-like adenocarcinoma. <i>Journal of Physical Education and Sports Management</i> , 2017, 3, a002170.	0.5	13
120	Compound heterozygous <i>TRPV4</i> 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.	0.7	13
121	Complete Genome Sequence of <i>Mycobacterium chimaera</i> SJ42, a Nonoutbreak Strain from an Immunocompromised Patient with Pulmonary Disease. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
122	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017, 547, 311-317.	13.7	787
123	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15.	7.7	642
124	Characterization of the human thyroid epigenome. <i>Journal of Endocrinology</i> , 2017, 235, 153-165.	1.2	8
125	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	7.7	1,428
126	Homologous Recombination Deficiency and Platinum-Based Therapy Outcomes in Advanced Breast Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 7521-7530.	3.2	144



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127	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	13.5	738
128	Comprehensive whole genome sequence analyses yields novel genetic and structural insights for Intellectual Disability. <i>BMC Genomics</i> , 2017, 18, 403.	1.2	15
129	Differential roles of RET isoforms in medullary and papillary thyroid carcinomas. <i>Endocrine-Related Cancer</i> , 2017, 24, 53-69.	1.6	38
130	Successful targeting of the NRG1 pathway indicates novel treatment strategy for metastatic cancer. <i>Annals of Oncology</i> , 2017, 28, 3092-3097.	0.6	83
131	Increasing quality, throughput and speed of sample preparation for strand-specific messenger RNA sequencing. <i>BMC Genomics</i> , 2017, 18, 515.	1.2	8
132	The Genome of the Beluga Whale ( <i>Delphinapterus leucas</i> ). <i>Genes</i> , 2017, 8, 378.	1.0	39
133	The Genome of the Northern Sea Otter ( <i>Enhydra lutris kenyoni</i> ). <i>Genes</i> , 2017, 8, 379.	1.0	24
134	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.	0.8	1
135	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.	1.1	18
136	Personalized Oncogenomics in the Management of Gastrointestinal Carcinomasâ€”Early Experiences from a Pilot Study. <i>Current Oncology</i> , 2016, 23, 571-575.	0.9	8
137	miR-509-3p is clinically significant and strongly attenuates cellular migration and multi-cellular spheroids in ovarian cancer. <i>Oncotarget</i> , 2016, 7, 25930-25948.	0.8	49
138	Small molecule epigenetic screen identifies novel EZH2 and HDAC inhibitors that target glioblastoma brain tumor-initiating cells. <i>Oncotarget</i> , 2016, 7, 59360-59376.	0.8	34
139	Genomic Analysis of a Serotype 5<i>i>Streptococcus pneumoniae</i> Outbreak in British Columbia, Canada, 2005â€”2009. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2016, 2016, 1-7.	0.7	6
140	Assembly of the Complete Sitka Spruce Chloroplast Genome Using 10X Genomicsâ€™ GemCode Sequencing Data. <i>PLoS ONE</i> , 2016, 11, e0163059.	1.1	31
141	ChAsE: chromatin analysis and exploration tool. <i>Bioinformatics</i> , 2016, 32, 3324-3326.	1.8	32
142	Tumour-suppressor microRNAs regulate ovarian cancer cell physical properties and invasive behaviour. <i>Open Biology</i> , 2016, 6, 160275.	1.5	29
143	Response to angiotensin blockade with irbesartan in a patient with metastatic colorectal cancer. <i>Annals of Oncology</i> , 2016, 27, 801-806.	0.6	39
144	Molecular etiology of an indolent lymphoproliferative disorder determined by whole-genome sequencing. <i>Journal of Physical Education and Sports Management</i> , 2016, 2, a000679.	0.5	3

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145	The Atlantic salmon genome provides insights into rediploidization. <i>Nature</i> , 2016, 533, 200-205.	13.7	1,021
146	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.	1.3	30
147	Genome sequences of six Phytophthora species threatening forest ecosystems. <i>Genomics Data</i> , 2016, 10, 85-88.	1.3	29
148	A somatic reference standard for cancer genome sequencing. <i>Scientific Reports</i> , 2016, 6, 24607.	1.6	64
149	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	13.5	404
150	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.	2.9	90
151	rAAV-compatible MiniPromoters for restricted expression in the brain and eye. <i>Molecular Brain</i> , 2016, 9, 52.	1.3	69
152	Divergent clonal selection dominates medulloblastoma at recurrence. <i>Nature</i> , 2016, 529, 351-357.	13.7	266
153	ORegAnno 3.0: a community-driven resource for curated regulatory annotation. <i>Nucleic Acids Research</i> , 2016, 44, D126-D132.	6.5	142
154	Large-scale profiling of microRNAs for The Cancer Genome Atlas. <i>Nucleic Acids Research</i> , 2016, 44, e3-e3.	6.5	125
155	Genome-Wide Profiles of Extra-cranial Malignant Rhabdoid Tumors Reveal Heterogeneity and Dysregulated Developmental Pathways. <i>Cancer Cell</i> , 2016, 29, 394-406.	7.7	105
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