

Robert A Holt

List of Publications by Year in descending order

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Version: 2024-02-01

225
papers

152,973
citations

1099

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1347

223
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236
all docs

236
docs citations

236
times ranked

142161
citing authors

#	ARTICLE	IF	CITATIONS
1	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	12.6	12,623
2	Comprehensive molecular portraits of human breast tumours. Nature, 2012, 490, 61-70.	27.8	10,282
3	Comprehensive molecular characterization of human colon and rectal cancer. Nature, 2012, 487, 330-337.	27.8	7,168
4	The Cancer Genome Atlas Pan-Cancer analysis project. Nature Genetics, 2013, 45, 1113-1120.	21.4	6,265
5	The Genome Sequence of <i>Drosophila melanogaster</i> . Science, 2000, 287, 2185-2195.	12.6	5,566
6	Comprehensive molecular characterization of gastric adenocarcinoma. Nature, 2014, 513, 202-209.	27.8	5,055
7	Comprehensive molecular profiling of lung adenocarcinoma. Nature, 2014, 511, 543-550.	27.8	4,572
8	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	27.0	4,139
9	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	27.8	4,075
10	The Genome of Black Cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). Science, 2006, 313, 1596-1604.	12.6	3,945
11	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
12	Comprehensive genomic characterization of squamous cell lung cancers. Nature, 2012, 489, 519-525.	27.8	3,483
13	Comprehensive genomic characterization of head and neck squamous cell carcinomas. Nature, 2015, 517, 576-582.	27.8	3,209
14	Comprehensive molecular characterization of clear cell renal cell carcinoma. Nature, 2013, 499, 43-49.	27.8	2,839
15	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	27.0	2,582
16	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	28.9	2,562
17	Comprehensive molecular characterization of urothelial bladder carcinoma. Nature, 2014, 507, 315-322.	27.8	2,496
18	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	28.9	2,435

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19	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	28.9	2,318
20	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018, 173, 400-416.e11.	28.9	2,277
21	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	28.9	2,111
22	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	27.8	1,966
23	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	27.8	1,943
24	The Genome Sequence of the Malaria Mosquito <i>Anopheles gambiae</i> . <i>Science</i> , 2002, 298, 129-149.	12.6	1,859
25	The Genome Sequence of the SARS-Associated Coronavirus. <i>Science</i> , 2003, 300, 1399-1404.	12.6	1,842
26	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	28.9	1,794
27	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25.	28.9	1,742
28	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018, 173, 291-304.e6.	28.9	1,718
29	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	28.9	1,670
30	<i>Fusobacterium nucleatum</i> infection is prevalent in human colorectal carcinoma. <i>Genome Research</i> , 2012, 22, 299-306.	5.5	1,582
31	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.	21.4	1,504
32	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015, 163, 506-519.	28.9	1,485
33	Integrated genomic characterization of oesophageal carcinoma. <i>Nature</i> , 2017, 541, 169-175.	27.8	1,448
34	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. <i>Nature</i> , 2011, 476, 298-303.	27.8	1,428
35	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	16.8	1,428
36	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	28.9	1,417

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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.	28.9	1,242
38	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , 2017, 543, 378-384.	27.8	1,158
39	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016, 374, 135-145.	27.0	1,040
40	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	12.6	1,038
41	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. <i>Nature</i> , 2009, 461, 809-813.	27.8	984
42	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 239-254.e6.	6.4	801
43	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. <i>Nature</i> , 2012, 488, 49-56.	27.8	761
44	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	16.8	750
45	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	28.9	738
46	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018, 23, 181-193.e7.	6.4	683
47	Whole-Genome Sequencing and Social-Network Analysis of a Tuberculosis Outbreak. <i>New England Journal of Medicine</i> , 2011, 364, 730-739.	27.0	665
48	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330.	16.8	665
49	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15.	16.8	642
50	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	16.8	623
51	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018, 173, 355-370.e14.	28.9	620
52	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018, 6, 271-281.e7.	6.2	605
53	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.	7.1	586
54	Neo-antigens predicted by tumor genome meta-analysis correlate with increased patient survival. <i>Genome Research</i> , 2014, 24, 743-750.	5.5	534

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55	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017, 31, 181-193.	16.8	532
56	Comparative Genome and Proteome Analysis of <i>Anopheles gambiae</i> and <i>Drosophila melanogaster</i> . <i>Science</i> , 2002, 298, 149-159.	12.6	531
57	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018, 23, 313-326.e5.	6.4	523
58	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.	5.5	486
59	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736.	16.8	482
60	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	16.8	478
61	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , 2018, 8, 1548-1565.	9.4	422
62	Assembling millions of short DNA sequences using SSAKE. <i>Bioinformatics</i> , 2007, 23, 500-501.	4.1	421
63	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017, 18, 2780-2794.	6.4	416
64	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.	6.4	407
65	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. <i>Cancer Cell</i> , 2018, 33, 706-720.e9.	16.8	400
66	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8.	16.8	396
67	Profiling the T-cell receptor beta-chain repertoire by massively parallel sequencing. <i>Genome Research</i> , 2009, 19, 1817-1824.	5.5	361
68	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. <i>Blood</i> , 2013, 122, 1256-1265.	1.4	349
69	A Comparison of Whole-Genome Shotgun-Derived Mouse Chromosome 16 and the Human Genome. <i>Science</i> , 2002, 296, 1661-1671.	12.6	344
70	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018, 23, 282-296.e4.	6.4	333
71	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018, 25, 1304-1317.e5.	6.4	329
72	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018, 23, 3392-3406.	6.4	324

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73	Characterization of HPV and host genome interactions in primary head and neck cancers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15544-15549.	7.1	317
74	Exhaustive T-cell repertoire sequencing of human peripheral blood samples reveals signatures of antigen selection and a directly measured repertoire size of at least 1 million clonotypes. Genome Research, 2011, 21, 790-797.	5.5	312
75	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	16.8	309
76	Co-occurrence of anaerobic bacteria in colorectal carcinomas. Microbiome, 2013, 1, 16.	11.1	284
77	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.	6.2	284
78	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272
79	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.	16.8	270
80	Oligonucleotide Microarray Analysis of Genomic Imbalance in Children with Mental Retardation. American Journal of Human Genetics, 2006, 79, 500-513.	6.2	261
81	Interfaces of Malignant and Immunologic Clonal Dynamics in Ovarian Cancer. Cell, 2018, 173, 1755-1769.e22.	28.9	261
82	Functional Genomics of the Cilium, a Sensory Organelle. Current Biology, 2005, 15, 935-941.	3.9	245
83	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	6.4	245
84	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	28.9	228
85	Complete Haplotype Sequence of the Human Immunoglobulin Heavy-Chain Variable, Diversity, and Joining Genes and Characterization of Allelic and Copy-Number Variation. American Journal of Human Genetics, 2013, 92, 530-546.	6.2	223
86	Genome and transcriptome analyses of the mountain pine beetle-fungal symbiont <i>Grosmannia clavigera</i> , a lodgepole pine pathogen. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 2504-2509.	7.1	218
87	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell Reports, 2018, 23, 297-312.e12.	6.4	205
88	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	6.4	204
89	The new paradigm of flow cell sequencing: Table 1.. Genome Research, 2008, 18, 839-846.	5.5	185
90	Genomics of hybrid poplar (<i>Populus trichocarpa</i> × <i>P. 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. Molecular Ecology, 2006, 15, 1275-1297.	3.9	183

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91	Genome Variation in <i>Cryptococcus gattii</i> , an Emerging Pathogen of Immunocompetent Hosts. <i>MBio</i> , 2011, 2, e00342-10.	4.1	182
92	Novel Avian Influenza H7N3 Strain Outbreak, British Columbia. <i>Emerging Infectious Diseases</i> , 2004, 10, 2192-2195.	4.3	182
93	Analysis of long-lived <i>C. elegans</i> daf-2 mutants using serial analysis of gene expression. <i>Genome Research</i> , 2005, 15, 603-615.	5.5	180
94	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018, 23, 270-281.e3.	6.4	177
95	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.	2.0	165
96	Derivation of HLA types from shotgun sequence datasets. <i>Genome Medicine</i> , 2012, 4, 95.	8.2	164
97	<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.	2.8	163
98	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. <i>Genome Biology</i> , 2010, 11, R82.	9.6	159
99	DNA copy-number analysis in bipolar disorder and schizophrenia reveals aberrations in genes involved in glutamate signaling. <i>Human Molecular Genetics</i> , 2006, 15, 743-749.	2.9	158
100	Sequence analysis of T-cell repertoires in health and disease. <i>Genome Medicine</i> , 2013, 5, 98.	8.2	158
101	The molecular signature and cis-regulatory architecture of a <i>C. elegans</i> gustatory neuron. <i>Genes and Development</i> , 2007, 21, 1653-1674.	5.9	151
102	A salmonid EST genomic study: genes, duplications, phylogeny and microarrays. <i>BMC Genomics</i> , 2008, 9, 545.	2.8	145
103	Surveillance of the Tumor Mutanome by T Cells during Progression from Primary to Recurrent Ovarian Cancer. <i>Clinical Cancer Research</i> , 2014, 20, 1125-1134.	7.0	144
104	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- β Superfamily. <i>Cell Systems</i> , 2018, 7, 422-437.e7.	6.2	134
105	De novo genome sequence assembly of a filamentous fungus using Sanger, 454 and Illumina sequence data. <i>Genome Biology</i> , 2009, 10, R94.	9.6	130
106	Brain Microbial Populations in HIV/AIDS: \pm Proteobacteria Predominate Independent of Host Immune Status. <i>PLoS ONE</i> , 2013, 8, e54673.	2.5	127
107	The completion of the Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2009, 19, 2324-2333.	5.5	125
108	Risks and Benefits of Chimeric Antigen Receptor T-Cell (CAR-T) Therapy in Cancer: A Systematic Review and Meta-Analysis. <i>Transfusion Medicine Reviews</i> , 2019, 33, 98-110.	2.0	124

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109	Generation, annotation, analysis and database integration of 16,500 white spruce EST clusters. BMC Genomics, 2005, 6, 144.	2.8	119
110	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.	6.4	119
111	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.	2.8	113
112	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.	7.1	112
113	Low Mutation Burden in Ovarian Cancer May Limit the Utility of Neoantigen-Targeted Vaccines. PLoS ONE, 2016, 11, e0155189.	2.5	112
114	Identification of genes expressed in the hermaphrodite germ line of <i>C. elegans</i> using SAGE. BMC Genomics, 2009, 10, 213.	2.8	105
115	Chronic Treatment with Diazepam or Abecarnil Differentially Affects the Expression of GABA A Receptor Subunit mRNAs in the Rat Cortex. Neuropharmacology, 1996, 35, 1457-1463.	4.1	104
116	Combined immunodeficiency associated with homozygous MALT1 mutations. Journal of Allergy and Clinical Immunology, 2014, 133, 1458-1462.e7.	2.9	103
117	Pan-cancer analysis of advanced patient tumors reveals interactions between therapy and genomic landscapes. Nature Cancer, 2020, 1, 452-468.	13.2	103
118	An Integrated Strategy to Study Muscle Development and Myofilament Structure in <i>Caenorhabditis elegans</i> . PLoS Genetics, 2009, 5, e1000537.	3.5	89
119	Clonal evolution of high-grade serous ovarian carcinoma from primary to recurrent disease. Journal of Pathology, 2013, 229, 515-524.	4.5	88
120	The North American bullfrog draft genome provides insight into hormonal regulation of long noncoding RNA. Nature Communications, 2017, 8, 1433.	12.8	86
121	Brain microbiota disruption within inflammatory demyelinating lesions in multiple sclerosis. Scientific Reports, 2016, 6, 37344.	3.3	85
122	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3.	6.4	83
123	Profiling tissue-resident T cell repertoires by RNA sequencing. Genome Medicine, 2015, 7, 125.	8.2	80
124	CAG-encoded polyglutamine length polymorphism in the human genome. BMC Genomics, 2007, 8, 126.	2.8	78
125	Identification of novel androgen-responsive genes by sequencing of LongSAGE libraries. BMC Genomics, 2009, 10, 476.	2.8	75
126	A regulatory toolbox of MiniPromoters to drive selective expression in the brain. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 16589-16594.	7.1	74

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127	Sequencing and analysis of 10,967 full-length cDNA clones from <i>Xenopus laevis</i> and <i>Xenopus tropicalis</i> reveals post-tetraploidization transcriptome remodeling. <i>Genome Research</i> , 2006, 16, 796-803.	5.5	73
128	A physical map of the bovine genome. <i>Genome Biology</i> , 2007, 8, R165.	9.6	73
129	A physical map of the highly heterozygous <i>Populus</i> genome: integration with the genome sequence and genetic map and analysis of haplotype variation. <i>Plant Journal</i> , 2007, 50, 1063-1078.	5.7	70
130	rAAV-compatible MiniPromoters for restricted expression in the brain and eye. <i>Molecular Brain</i> , 2016, 9, 52.	2.6	69
131	Analysis of 4,664 high-quality sequence-finished poplar full-length cDNA clones and their utility for the discovery of genes responding to insect feeding. <i>BMC Genomics</i> , 2008, 9, 57.	2.8	68
132	Functional Characterization of a Catabolic Plasmid from Polychlorinated- Biphenyl-Degrading <i>Rhodococcus</i> sp. Strain RHA1. <i>Journal of Bacteriology</i> , 2004, 186, 7783-7795.	2.2	65
133	The <i>Anopheles gambiae</i> genome: an update. <i>Trends in Parasitology</i> , 2004, 20, 49-52.	3.3	62
134	A high-throughput screen identifying sequence and promiscuity characteristics of the loxP spacer region in Cre-mediated recombination. <i>BMC Genomics</i> , 2006, 7, 73.	2.8	60
135	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , 2020, 11, 4330.	12.8	60
136	Characteristics of TCR Repertoire Associated With Successful Immune Checkpoint Therapy Responses. <i>Frontiers in Immunology</i> , 2020, 11, 587014.	4.8	56
137	The Sensitivity of Massively Parallel Sequencing for Detecting Candidate Infectious Agents Associated with Human Tissue. <i>PLoS ONE</i> , 2011, 6, e19838.	2.5	55
138	Transcription of foreign DNA in <i>Escherichia coli</i> . <i>Genome Research</i> , 2008, 18, 1798-1805.	5.5	52
139	Nonlinear electrophoretic response yields a unique parameter for separation of biomolecules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 14796-14801.	7.1	50
140	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.	14.5	50
141	Genome and Transcriptome Biomarkers of Response to Immune Checkpoint Inhibitors in Advanced Solid Tumors. <i>Clinical Cancer Research</i> , 2021, 27, 202-212.	7.0	50
142	Identification by full-coverage array CGH of human DNA copy number increases relative to chimpanzee and gorilla. <i>Genome Research</i> , 2006, 16, 173-181.	5.5	48
143	Generation of ESTs in <i>Vitis vinifera</i> wine grape (Cabernet Sauvignon) and table grape (Muscat) Tj ETQq1 1 0.784314 rgBT /Overlock 19 402, 40-50.	2.2	45
144	Activation of an endogenous retrovirus-associated long non-coding RNA in human adenocarcinoma. <i>Genome Medicine</i> , 2015, 7, 22.	8.2	45

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145	Targeted CNS delivery using human MiniPromoters and demonstrated compatibility with adeno-associated viral vectors. <i>Molecular Therapy - Methods and Clinical Development</i> , 2014, 1, 5.	4.1	44
146	Profiling model T-cell metagenomes with short reads. <i>Bioinformatics</i> , 2009, 25, 458-464.	4.1	43
147	Sequencing of the human IG light chain loci from a hydatidiform mole BAC library reveals locus-specific signatures of genetic diversity. <i>Genes and Immunity</i> , 2015, 16, 24-34.	4.1	43
148	Rapid selection and identification of functional CD8+ T cell epitopes from large peptide-coding libraries. <i>Nature Communications</i> , 2019, 10, 4553.	12.8	43
149	Generation and annotation of lodgepole pine and oleoresin-induced expressed sequences from the blue-stain fungus <i>Ophiostoma clavigerum</i> , a Mountain Pine Beetle-associated pathogen. <i>FEMS Microbiology Letters</i> , 2007, 267, 151-158.	1.8	42
150	Targeted Assembly of Short Sequence Reads. <i>PLoS ONE</i> , 2011, 6, e19816.	2.5	41
151	Targeting the undruggable: immunotherapy meets personalized oncology in the genomic era. <i>Annals of Oncology</i> , 2015, 26, 2367-2374.	1.2	40
152	Next generation tools for high-throughput promoter and expression analysis employing single-copy knock-ins at the <i>Hprt1</i> locus. <i>Genomics</i> , 2009, 93, 196-204.	2.9	39
153	Tumor Infiltrating Effector Memory Antigen-Specific CD8+ T Cells Predict Response to Immune Checkpoint Therapy. <i>Frontiers in Immunology</i> , 2020, 11, 584423.	4.8	39
154	A library-based screening method identifies neoantigen-reactive T cells in peripheral blood prior to relapse of ovarian cancer. <i>Oncotmunology</i> , 2018, 7, e1371895.	4.6	35
155	Large-scale production of SAGE libraries from microdissected tissues, flow-sorted cells, and cell lines. <i>Genome Research</i> , 2006, 17, 108-116.	5.5	34
156	Cytosolic protein interactions of the schizophrenia susceptibility gene dysbindin. <i>Journal of Neurochemistry</i> , 2010, 113, 1491-1503.	3.9	33
157	XLF deficiency results in reduced N-nucleotide addition during V(D)J recombination. <i>Blood</i> , 2016, 128, 650-659.	1.4	33
158	Transient Treg depletion enhances therapeutic anti-cancer vaccination. <i>Immunity, Inflammation and Disease</i> , 2017, 5, 16-28.	2.7	33
159	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.	1.2	33
160	Assembly of the Complete Sitka Spruce Chloroplast Genome Using 10X Genomics™ GemCode Sequencing Data. <i>PLoS ONE</i> , 2016, 11, e0163059.	2.5	31
161	Duplication and Divergence of 2 Distinct Pancreatic Ribonuclease Genes in Leaf-Eating African and Asian Colobine Monkeys. <i>Molecular Biology and Evolution</i> , 2006, 23, 1465-1479.	8.9	30
162	Age- and Disease-Dependent HERV-W Envelope Allelic Variation in Brain: Association with Neuroimmune Gene Expression. <i>PLoS ONE</i> , 2011, 6, e19176.	2.5	30

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163	Whole exome sequencing of an asbestos-induced wild-type murine model of malignant mesothelioma. BMC Cancer, 2017, 17, 396.	2.6	30
164	Chronic diazepam exposure decreases transcription of the rat GABAA receptor $\alpha 2$ -subunit gene. Molecular Brain Research, 1997, 48, 164-166.	2.3	29
165	Decreased GABA Enhancement of Benzodiazepine Binding After a Single Dose of Diazepam. Journal of Neurochemistry, 2008, 72, 2219-2222.	3.9	29
166	A Clinically Validated Diagnostic Second-Generation Sequencing Assay for Detection of Hereditary BRCA1 and BRCA2 Mutations. Journal of Molecular Diagnostics, 2013, 15, 796-809.	2.8	29
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