

Robert A Holt

List of Publications by Year in descending order

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Version: 2024-02-01

225
papers

152,973
citations

1094

112
h-index

1341

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. <i>Science</i> , 2001, 291, 1304-1351.	6.0	12,623
2	Comprehensive molecular portraits of human breast tumours. <i>Nature</i> , 2012, 490, 61-70.	13.7	10,282
3	Comprehensive molecular characterization of human colon and rectal cancer. <i>Nature</i> , 2012, 487, 330-337.	13.7	7,168
4	The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , 2013, 45, 1113-1120.	9.4	6,265
5	The Genome Sequence of <i>Drosophila melanogaster</i> . <i>Science</i> , 2000, 287, 2185-2195.	6.0	5,566
6	Comprehensive molecular characterization of gastric adenocarcinoma. <i>Nature</i> , 2014, 513, 202-209.	13.7	5,055
7	Comprehensive molecular profiling of lung adenocarcinoma. <i>Nature</i> , 2014, 511, 543-550.	13.7	4,572
8	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2013, 368, 2059-2074.	13.9	4,139
9	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013, 497, 67-73.	13.7	4,075
10	The Genome of Black Cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). <i>Science</i> , 2006, 313, 1596-1604.	6.0	3,945
11	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	6.6	3,706
12	Comprehensive genomic characterization of squamous cell lung cancers. <i>Nature</i> , 2012, 489, 519-525.	13.7	3,483
13	Comprehensive genomic characterization of head and neck squamous cell carcinomas. <i>Nature</i> , 2015, 517, 576-582.	13.7	3,209
14	Comprehensive molecular characterization of clear cell renal cell carcinoma. <i>Nature</i> , 2013, 499, 43-49.	13.7	2,839
15	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.	13.9	2,582
16	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015, 161, 1681-1696.	13.5	2,562
17	Comprehensive molecular characterization of urothelial bladder carcinoma. <i>Nature</i> , 2014, 507, 315-322.	13.7	2,496
18	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015, 163, 1011-1025.	13.5	2,435

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19	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	13.5	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.	13.5	2,277
21	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	13.5	2,111
22	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	13.7	1,966
23	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943
24	The Genome Sequence of the Malaria Mosquito <i>Anopheles gambiae</i> . <i>Science</i> , 2002, 298, 129-149.	6.0	1,859
25	The Genome Sequence of the SARS-Associated Coronavirus. <i>Science</i> , 2003, 300, 1399-1404.	6.0	1,842
26	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	13.5	1,794
27	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25.	13.5	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.	13.5	1,718
29	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	13.5	1,670
30	<i>Fusobacterium nucleatum</i> infection is prevalent in human colorectal carcinoma. <i>Genome Research</i> , 2012, 22, 299-306.	2.4	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.	9.4	1,504
32	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015, 163, 506-519.	13.5	1,485
33	Integrated genomic characterization of oesophageal carcinoma. <i>Nature</i> , 2017, 541, 169-175.	13.7	1,448
34	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. <i>Nature</i> , 2011, 476, 298-303.	13.7	1,428
35	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	7.7	1,428
36	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	13.5	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.	13.5	1,242
38	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , 2017, 543, 378-384.	13.7	1,158
39	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016, 374, 135-145.	13.9	1,040
40	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	6.0	1,038
41	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. <i>Nature</i> , 2009, 461, 809-813.	13.7	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.	2.9	801
43	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. <i>Nature</i> , 2012, 488, 49-56.	13.7	761
44	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	7.7	750
45	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	13.5	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.	2.9	683
47	Whole-Genome Sequencing and Social-Network Analysis of a Tuberculosis Outbreak. <i>New England Journal of Medicine</i> , 2011, 364, 730-739.	13.9	665
48	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330.	7.7	665
49	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15.	7.7	642
50	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	7.7	623
51	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018, 173, 355-370.e14.	13.5	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.	2.9	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.	3.3	586
54	Neo-antigens predicted by tumor genome meta-analysis correlate with increased patient survival. <i>Genome Research</i> , 2014, 24, 743-750.	2.4	534

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55	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017, 31, 181-193.	7.7	532
56	Comparative Genome and Proteome Analysis of <i>Anopheles gambiae</i> and <i>Drosophila melanogaster</i> . <i>Science</i> , 2002, 298, 149-159.	6.0	531
57	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018, 23, 313-326.e5.	2.9	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.	2.4	486
59	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736.	7.7	482
60	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	7.7	478
61	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , 2018, 8, 1548-1565.	7.7	422
62	Assembling millions of short DNA sequences using SSAKE. <i>Bioinformatics</i> , 2007, 23, 500-501.	1.8	421
63	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017, 18, 2780-2794.	2.9	416
64	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.	2.9	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.	7.7	400
66	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8.	7.7	396
67	Profiling the T-cell receptor beta-chain repertoire by massively parallel sequencing. <i>Genome Research</i> , 2009, 19, 1817-1824.	2.4	361
68	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. <i>Blood</i> , 2013, 122, 1256-1265.	0.6	349
69	A Comparison of Whole-Genome Shotgun-Derived Mouse Chromosome 16 and the Human Genome. <i>Science</i> , 2002, 296, 1661-1671.	6.0	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.	2.9	333
71	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018, 25, 1304-1317.e5.	2.9	329
72	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018, 23, 3392-3406.	2.9	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.	3.3	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.	2.4	312
75	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	7.7	309
76	Co-occurrence of anaerobic bacteria in colorectal carcinomas. Microbiome, 2013, 1, 16.	4.9	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.	2.9	284
78	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	13.5	272
79	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.	7.7	270
80	Oligonucleotide Microarray Analysis of Genomic Imbalance in Children with Mental Retardation. American Journal of Human Genetics, 2006, 79, 500-513.	2.6	261
81	Interfaces of Malignant and Immunologic Clonal Dynamics in Ovarian Cancer. Cell, 2018, 173, 1755-1769.e22.	13.5	261
82	Functional Genomics of the Cilium, a Sensory Organelle. Current Biology, 2005, 15, 935-941.	1.8	245
83	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	2.9	245
84	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	13.5	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.	2.6	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.	3.3	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.	2.9	205
88	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	2.9	204
89	The new paradigm of flow cell sequencing: Table 1.. Genome Research, 2008, 18, 839-846.	2.4	185
90	Genomics of hybrid poplar (<i>Populus trichocarpa</i> × <i>deltoides</i>) interacting with forest tent caterpillars (<i>Malacosoma disstria</i>): normalized and full-length cDNA libraries, expressed sequence tags, and a cDNA microarray for the study of insect-induced defences. Molecular Ecology, 2006, 15, 1275-1297.	2.0	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.	1.8	182
92	Novel Avian Influenza H7N3 Strain Outbreak, British Columbia. <i>Emerging Infectious Diseases</i> , 2004, 10, 2192-2195.	2.0	182
93	Analysis of long-lived <i>C. elegans</i> <i>daf-2</i> mutants using serial analysis of gene expression. <i>Genome Research</i> , 2005, 15, 603-615.	2.4	180
94	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018, 23, 270-281.e3.	2.9	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.	0.9	165
96	Derivation of HLA types from shotgun sequence datasets. <i>Genome Medicine</i> , 2012, 4, 95.	3.6	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.	1.2	163
98	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. <i>Genome Biology</i> , 2010, 11, R82.	13.9	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.	1.4	158
100	Sequence analysis of T-cell repertoires in health and disease. <i>Genome Medicine</i> , 2013, 5, 98.	3.6	158
101	The molecular signature and <i>cis</i> -regulatory architecture of a <i>C. elegans</i> gustatory neuron. <i>Genes and Development</i> , 2007, 21, 1653-1674.	2.7	151
102	A salmonid EST genomic study: genes, duplications, phylogeny and microarrays. <i>BMC Genomics</i> , 2008, 9, 545.	1.2	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.	3.2	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.	2.9	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.	13.9	130
106	Brain Microbial Populations in HIV/AIDS: \pm -Proteobacteria Predominate Independent of Host Immune Status. <i>PLoS ONE</i> , 2013, 8, e54673.	1.1	127
107	The completion of the Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2009, 19, 2324-2333.	2.4	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.	0.9	124

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109	Generation, annotation, analysis and database integration of 16,500 white spruce EST clusters. <i>BMC Genomics</i> , 2005, 6, 144.	1.2	119
110	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 172-180.e3.	2.9	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>). <i>BMC Genomics</i> , 2008, 9, 484.	1.2	113
112	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> , 2005, 102, 18485-18490.	3.3	112
113	Low Mutation Burden in Ovarian Cancer May Limit the Utility of Neoantigen-Targeted Vaccines. <i>PLoS ONE</i> , 2016, 11, e0155189.	1.1	112
114	Identification of genes expressed in the hermaphrodite germ line of <i>C. elegans</i> using SAGE. <i>BMC Genomics</i> , 2009, 10, 213.	1.2	105
115	Chronic Treatment with Diazepam or Abecarnil Differentially Affects the Expression of GABA A Receptor Subunit mRNAs in the Rat Cortex. <i>Neuropharmacology</i> , 1996, 35, 1457-1463.	2.0	104
116	Combined immunodeficiency associated with homozygous MALT1 mutations. <i>Journal of Allergy and Clinical Immunology</i> , 2014, 133, 1458-1462.e7.	1.5	103
117	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
118	An Integrated Strategy to Study Muscle Development and Myofilament Structure in <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , 2009, 5, e1000537.	1.5	89
119	Clonal evolution of high-grade serous ovarian carcinoma from primary to recurrent disease. <i>Journal of Pathology</i> , 2013, 229, 515-524.	2.1	88
120	The North American bullfrog draft genome provides insight into hormonal regulation of long noncoding RNA. <i>Nature Communications</i> , 2017, 8, 1433.	5.8	86
121	Brain microbiota disruption within inflammatory demyelinating lesions in multiple sclerosis. <i>Scientific Reports</i> , 2016, 6, 37344.	1.6	85
122	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018, 23, 213-226.e3.	2.9	83
123	Profiling tissue-resident T cell repertoires by RNA sequencing. <i>Genome Medicine</i> , 2015, 7, 125.	3.6	80
124	CAG-encoded polyglutamine length polymorphism in the human genome. <i>BMC Genomics</i> , 2007, 8, 126.	1.2	78
125	Identification of novel androgen-responsive genes by sequencing of LongSAGE libraries. <i>BMC Genomics</i> , 2009, 10, 476.	1.2	75
126	A regulatory toolbox of MiniPromoters to drive selective expression in the brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 16589-16594.	3.3	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.	2.4	73
128	A physical map of the bovine genome. <i>Genome Biology</i> , 2007, 8, R165.	13.9	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.	2.8	70
130	rAAV-compatible MiniPromoters for restricted expression in the brain and eye. <i>Molecular Brain</i> , 2016, 9, 52.	1.3	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.	1.2	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.	1.0	65
133	The <i>Anopheles gambiae</i> genome: an update. <i>Trends in Parasitology</i> , 2004, 20, 49-52.	1.5	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.	1.2	60
135	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , 2020, 11, 4330.	5.8	60
136	Characteristics of TCR Repertoire Associated With Successful Immune Checkpoint Therapy Responses. <i>Frontiers in Immunology</i> , 2020, 11, 587014.	2.2	56
137	The Sensitivity of Massively Parallel Sequencing for Detecting Candidate Infectious Agents Associated with Human Tissue. <i>PLoS ONE</i> , 2011, 6, e19838.	1.1	55
138	Transcription of foreign DNA in <i>Escherichia coli</i> . <i>Genome Research</i> , 2008, 18, 1798-1805.	2.4	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.	3.3	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.	6.5	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.	3.2	50
142	Identification by full-coverage array CGH of human DNA copy number increases relative to chimpanzee and gorilla. <i>Genome Research</i> , 2005, 16, 173-181.	2.4	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 10 402, 40-50.	1.0	45
144	Activation of an endogenous retrovirus-associated long non-coding RNA in human adenocarcinoma. <i>Genome Medicine</i> , 2015, 7, 22.	3.6	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.	1.8	44
146	Profiling model T-cell metagenomes with short reads. <i>Bioinformatics</i> , 2009, 25, 458-464.	1.8	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.	2.2	43
148	Rapid selection and identification of functional CD8+ T cell epitopes from large peptide-coding libraries. <i>Nature Communications</i> , 2019, 10, 4553.	5.8	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.	0.7	42
150	Targeted Assembly of Short Sequence Reads. <i>PLoS ONE</i> , 2011, 6, e19816.	1.1	41
151	Targeting the undruggable: immunotherapy meets personalized oncology in the genomic era. <i>Annals of Oncology</i> , 2015, 26, 2367-2374.	0.6	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.	1.3	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.	2.2	39
154	A library-based screening method identifies neoantigen-reactive T cells in peripheral blood prior to relapse of ovarian cancer. <i>Oncotmmunology</i> , 2018, 7, e1371895.	2.1	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.	2.4	34
156	Cytosolic protein interactions of the schizophrenia susceptibility gene <i>dysbindin</i> . <i>Journal of Neurochemistry</i> , 2010, 113, 1491-1503.	2.1	33
157	XLF deficiency results in reduced N-nucleotide addition during V(D)J recombination. <i>Blood</i> , 2016, 128, 650-659.	0.6	33
158	Transient Treg depletion enhances therapeutic anti-cancer vaccination. <i>Immunity, Inflammation and Disease</i> , 2017, 5, 16-28.	1.3	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.	0.5	33
160	Assembly of the Complete Sitka Spruce Chloroplast Genome Using 10X Genomics™ GemCode Sequencing Data. <i>PLoS ONE</i> , 2016, 11, e0163059.	1.1	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.	3.5	30
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