Robert A Holt

List of Publications by Year
in descending order

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225 papers	152,973 citations	1296 112 h-index	1551 223 g-index
236 all docs	236 docs citations	236 times ranked	154465 citing authors

#	Article	IF	Citations
1	Fusobacterium nucleatum and Bacteroides fragilis detection in colorectal tumours: Optimal target site and correlation with total bacterial load. PLoS ONE, 2022, 17, e0262416.	1.1	7
2	Selective B cell depletion upon intravenous infusion of replication-incompetent anti-CD19 CAR lentivirus. Molecular Therapy - Methods and Clinical Development, 2022, 26, 4-14.	1.8	5
3	Genome and Transcriptome Biomarkers of Response to Immune Checkpoint Inhibitors in Advanced Solid Tumors. Clinical Cancer Research, 2021, 27, 202-212.	3.2	50
4	Hematologistsâ€™ barriers and enablers to screening and recruiting patients to a chimeric antigen receptor (CAR) T cell therapy trial: a theory-informed interview study. Trials, 2021, 22, 230.	0.7	7
5	Navigating choice in the face of uncertainty: using a theory informed qualitative approach to identifying potential patient barriers and enablers to participating in an early phase chimeric antigen receptor T (CAR-T) cell therapy trial. BMJ Open, 2021, 11, e043929.	0.8	10
6	Improved resolution of phenotypic subsets in human T-ALL by incorporation of RNA-seq based developmental profiling. Leukemia Research, 2021, 110, 106712.	0.4	0
7	Modulation of the Host Cell Transcriptome and Epigenome by Fusobacterium nucleatum. MBio, 2021, 12, e0206221.	1.8	10
8	Clinical response to nivolumab in an INI1-deficient pediatric chordoma correlates with immunogenic recognition of brachyury. Npj Precision Oncology, 2021, 5, 103.	2.3	18
9	Sample Tracking Using Unique Sequence Controls. Journal of Molecular Diagnostics, 2020, 22, 141-146.	1.2	10
10	Identification of a CD8+ T-cell response to a predicted neoantigen in malignant mesothelioma. OncoImmunology, 2020, 9, 1684713.	2.1	12
11	Tumor Infiltrating Effector Memory Antigen-Specific CD8+ T Cells Predict Response to Immune Checkpoint Therapy. Frontiers in Immunology, 2020, 11, 584423.	2.2	39
12	Building Canadian capacity for CARâ€T cells in relapsed/refractory acute lymphoblastic leukaemia: a retrospective cohort study. British Journal of Haematology, 2020, 191, e14-e19.	1.2	1
13	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nature Communications, 2020, 11, 4748.	5.8	27
14	Sex differences in oncogenic mutational processes. Nature Communications, 2020, 11, 4330.	5.8	60
15	Partnering with patients to get better outcomes with chimeric antigen receptor T-cell therapy: towards engagement of patients in early phase trials. Research Involvement and Engagement, 2020, 6, 61.	1.1	12
16	Characteristics of TCR Repertoire Associated With Successful Immune Checkpoint Therapy Responses. Frontiers in Immunology, 2020, 11, 587014.	2.2	56
17	A Rapid and Sensitive Nucleic Acid Amplification Technique for Mycoplasma Screening of Cell Therapy Products. Molecular Therapy - Methods and Clinical Development, 2020, 17, 393-399.	1.8	16
18	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	13.7	1,966

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19	Complementary Methods for de Novo Monoclonal Antibody Sequencing to Achieve Complete Sequence Coverage. Journal of Proteome Research, 2020, 19, 2700-2707.	1.8	12
20	Pan-cancer analysis of advanced patient tumors reveals interactions between therapy and genomic landscapes. Nature Cancer, 2020, 1, 452-468.	5.7	103
21	A survey of Fusobacterium nucleatum genes modulated by host cell infection. Microbial Genomics, 2020, 6, .	1.0	14
22	Synthetic modeling reveals HOXB genes are critical for the initiation and maintenance of human leukemia. Nature Communications, 2019, 10, 2913.	5.8	8
23	Rapid selection and identification of functional CD8+ T cell epitopes from large peptide-coding libraries. Nature Communications, 2019, 10, 4553.	5.8	43
24	Base excision repair deficiency signatures implicate germline and somatic <i>MUTYH</i> aberrations in pancreatic ductal adenocarcinoma and breast cancer oncogenesis. Journal of Physical Education and Sports Management, 2019, 5, a003681.	0.5	33
25	A high-throughput protocol for isolating cell-free circulating tumor DNA from peripheral blood. BioTechniques, 2019, 66, 85-92.	0.8	13
26	Twenty-Seven Tamoxifen-Inducible iCre-Driver Mouse Strains for Eye and Brain, Including Seventeen Carrying a New Inducible-First Constitutive-Ready Allele. Genetics, 2019, 211, 1155-1177.	1.2	17
27	Risks and Benefits of Chimeric Antigen Receptor T-Cell (CAR-T) Therapy in Cancer: A Systematic Review and Meta-Analysis. Transfusion Medicine Reviews, 2019, 33, 98-110.	0.9	124
28	Sources of erroneous sequences and artifact chimeric reads in next generation sequencing of genomic DNA from formalin-fixed paraffin-embedded samples. Nucleic Acids Research, 2019, 47, e12-e12.	6.5	50
29	Neoantigen characteristics in the context of the complete predicted MHC class I self-immunopeptidome. OncoImmunology, 2019, 8, 1556080.	2.1	16
30	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	13.5	2,277
31	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	13.5	1,670
32	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	13.5	1,718
33	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	13.5	228
34	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	13.5	272
35	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	13.5	1,417
36	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	13.5	2,111

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37	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	13.5	620
38	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	2.9	333
39	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	2.9	407
40	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	2.9	245
41	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
42	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	2.9	523
43	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.	2.9	683
44	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	6.6	3,706
45	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.	2.9	119
46	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3.	2.9	83
47	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	2.9	801
48	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	2.9	204
49	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	2.9	177
50	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.	7.7	270
51	A library-based screening method identifies neoantigen-reactive T cells in peripheral blood prior to relapse of ovarian cancer. OncoImmunology, 2018, 7, e1371895.	2.1	35
52	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	2.9	605
53	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
54	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. Cancer Cell, 2018, 33, 706-720.e9.	7.7	400

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55	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	7.7	750
56	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	7.7	396
57	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	7.7	478
58	Malignant cells from pleural fluids in malignant mesothelioma patients reveal novel mutations. Lung Cancer, 2018, 119, 64-70.	0.9	23
59	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-Î² Superfamily. Cell Systems, 2018, 7, 422-437.e7.	2.9	134
60	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. Cancer Discovery, 2018, 8, 1548-1565.	7.7	422
61	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. Cell Reports, 2018, 25, 1304-1317.e5.	2.9	329
62	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	7.7	623
63	Interfaces of Malignant and Immunologic Clonal Dynamics in Ovarian Cancer. Cell, 2018, 173, 1755-1769.e22.	13.5	261
64	Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406.	2.9	324
65	Defining the clonality of peripheral T cell lymphomas using RNA-seq. Bioinformatics, 2017, 33, 1111-1115.	1.8	14
66	Integrated genomic and molecular characterization of cervical cancer. Nature, 2017, 543, 378-384.	13.7	1,158
67	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. Cancer Cell, 2017, 31, 181-193.	7.7	532
68	Cell-Based Therapeutics: Making a Faustian Pact with Biology. Trends in Molecular Medicine, 2017, 23, 104-115.	3.5	9
69	Tumor Potentiating Mechanisms of Fusobacterium nucleatum , AÂMultifaceted Microbe. Gastroenterology, 2017, 152, 694-696.	0.6	20
70	Transient Treg depletion enhances therapeutic antiâ€cancer vaccination. Immunity, Inflammation and Disease, 2017, 5, 16-28.	1.3	33
71	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	13.5	1,794
72	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	7.7	309

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73	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	2.9	416
74	Integrated genomic characterization of oesophageal carcinoma. Nature, 2017, 541, 169-175.	13.7	1,448
75	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.	13.5	1,742
76	Interpreting the T-cell receptor repertoire. Nature Biotechnology, 2017, 35, 829-830.	9.4	3
77	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. Cancer Cell, 2017, 32, 204-220.e15.	7.7	642
78	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	7.7	1,428
79	The North American bullfrog draft genome provides insight into hormonal regulation of long noncoding RNA. Nature Communications, 2017, 8, 1433.	5.8	86
80	Targeted Cell-to-Cell Delivery of Protein Payloads via the Granzyme-Perforin Pathway. Molecular Therapy - Methods and Clinical Development, 2017, 7, 132-145.	1.8	11
81	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	13.5	738
82	Whole exome sequencing of an asbestos-induced wild-type murine model of malignant mesothelioma. BMC Cancer, 2017, 17, 396.	1.1	30
83	RNA-Seq Analysis of Gene Expression, Viral Pathogen, and B-Cell/T-Cell Receptor Signatures in Complex Chronic Disease. Clinical Infectious Diseases, 2017, 64, 476-481.	2.9	21
84	Immunotherapy for Lung Malignancies. Chest, 2017, 151, 891-897.	0.4	17
85	Efficacy and safety of chimeric antigen receptor T-cell (CAR-T) therapy in patients with haematological and solid malignancies: protocol for a systematic review and meta-analysis. BMJ Open, 2017, 7, e019321.	0.8	16
86	Increasing quality, throughput and speed of sample preparation for strand-specific messenger RNA sequencing. BMC Genomics, 2017, 18, 515.	1.2	8
87	Automated high throughput nucleic acid purification from formalin-fixed paraffin-embedded tissue samples for next generation sequence analysis. PLoS ONE, 2017, 12, e0178706.	1.1	18
88	Low Mutation Burden in Ovarian Cancer May Limit the Utility of Neoantigen-Targeted Vaccines. PLoS ONE, 2016, 11, e0155189.	1.1	112
89	Assembly of the Complete Sitka Spruce Chloroplast Genome Using 10X Genomicsâ€™ GemCode Sequencing Data. PLoS ONE, 2016, 11, e0163059.	1.1	31
90	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	7.7	482

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91	XLF deficiency results in reduced N-nucleotide addition during V(D)J recombination. Blood, 2016, 128, 650-659.	0.6	33
92	Brain microbiota disruption within inflammatory demyelinating lesions in multiple sclerosis. Scientific Reports, 2016, 6, 37344.	1.6	85
93	rAAV-compatible MiniPromoters for restricted expression in the brain and eye. Molecular Brain, 2016, 9, 52.	1.3	69
94	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. New England Journal of Medicine, 2016, 374, 135-145.	13.9	1,040
95	Abstract 4136: Properties of the immune microenvironment associated with clonal diversity in high-grade serous ovarian cancer. , 2016, , .		0
96	Immunogenomics: a foundation for intelligent immune design. Genome Medicine, 2015, 7, 116.	3.6	5
97	Profiling tissue-resident T cell repertoires by RNA sequencing. Genome Medicine, 2015, 7, 125.	3.6	80
98	Comprehensive genomic characterization of head and neck squamous cell carcinomas. Nature, 2015, 517, 576-582.	13.7	3,209
99	Sequencing of the human IG light chain loci from a hydatidiform mole BAC library reveals locus-specific signatures of genetic diversity. Genes and Immunity, 2015, 16, 24-34.	2.2	43
100	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	13.5	2,562
101	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	13.9	2,582
102	Activation of an endogenous retrovirus-associated long non-coding RNA in human adenocarcinoma. Genome Medicine, 2015, 7, 22.	3.6	45
103	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	13.5	2,435
104	Targeting the undruggable: immunotherapy meets personalized oncology in the genomic era. Annals of Oncology, 2015, 26, 2367-2374.	0.6	40
105	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.	13.5	1,485
106	Neo-antigens predicted by tumor genome meta-analysis correlate with increased patient survival. Genome Research, 2014, 24, 743-750.	2.4	534
107	Surveillance of the Tumor Mutanome by T Cells during Progression from Primary to Recurrent Ovarian Cancer. Clinical Cancer Research, 2014, 20, 1125-1134.	3.2	144
108	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	13.5	2,318

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109	Comprehensive molecular characterization of urothelial bladder carcinoma. Nature, 2014, 507, 315-322.	13.7	2,496
110	Combined immunodeficiency associated with homozygous MALT1 mutations. Journal of Allergy and Clinical Immunology, 2014, 133, 1458-1462.e7.	1.5	103
111	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
112	Comprehensive molecular characterization of gastric adenocarcinoma. Nature, 2014, 513, 202-209.	13.7	5,055
113	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330.	7.7	665
114	Comprehensive molecular profiling of lung adenocarcinoma. Nature, 2014, 511, 543-550.	13.7	4,572
115	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	13.5	1,242
116	T-cell epitope discovery technologies. Human Immunology, 2014, 75, 514-519.	1.2	13
117	Targeted CNS delivery using human MiniPromoters and demonstrated compatibility with adeno-associated viral vectors. Molecular Therapy - Methods and Clinical Development, 2014, 1, 5.	1.8	44
118	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
119	Co-occurrence of anaerobic bacteria in colorectal carcinomas. Microbiome, 2013, 1, 16.	4.9	284
120	Clonal evolution of highâ€grade serous ovarian carcinoma from primary to recurrent disease. Journal of Pathology, 2013, 229, 515-524.	2.1	88
121	A Clinically Validated Diagnostic Second-Generation Sequencing Assay for Detection of Hereditary BRCA1 and BRCA2 Mutations. Journal of Molecular Diagnostics, 2013, 15, 796-809.	1.2	29
122	The Cancer Genome Atlas Pan-Cancer analysis project. Nature Genetics, 2013, 45, 1113-1120.	9.4	6,265
123	Sequence analysis of T-cell repertoires in health and disease. Genome Medicine, 2013, 5, 98.	3.6	158
124	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	13.7	4,075
125	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	13.9	4,139
126	Comprehensive molecular characterization of clear cell renal cell carcinoma. Nature, 2013, 499, 43-49.	13.7	2,839

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127	Metagenomic and Metabolomic Characterization of Rabies Encephalitis: New Insights into the Treatment of an Ancient Disease. Journal of Infectious Diseases, 2013, 207, 1451-1456.	1.9	15
128	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. Blood, 2013, 122, 1256-1265.	0.6	349
129	Non-coding-regulatory regions of human brain genes delineated by bacterial artificial chromosome knock-in mice. BMC Biology, 2013, 11, 106.	1.7	4
130	Brain Microbial Populations in HIV/AIDS: Î±-Proteobacteria Predominate Independent of Host Immune Status. PLoS ONE, 2013, 8, e54673.	1.1	127
131	Retina Restored and Brain Abnormalities Ameliorated by Single-Copy Knock-In of Human <i>NR2E1</i> in Null Mice. Molecular and Cellular Biology, 2012, 32, 1296-1311.	1.1	14
132	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. Nature, 2012, 488, 49-56.	13.7	761
133	<i>Fusobacterium nucleatum</i> infection is prevalent in human colorectal carcinoma. Genome Research, 2012, 22, 299-306.	2.4	1,582
134	Comprehensive molecular characterization of human colon and rectal cancer. Nature, 2012, 487, 330-337.	13.7	7,168
135	Comprehensive molecular portraits of human breast tumours. Nature, 2012, 490, 61-70.	13.7	10,282
136	Comprehensive genomic characterization of squamous cell lung cancers. Nature, 2012, 489, 519-525.	13.7	3,483
137	Derivation of HLA types from shotgun sequence datasets. Genome Medicine, 2012, 4, 95.	3.6	164
138	Whole-Genome Sequencing and Social-Network Analysis of a Tuberculosis Outbreak. New England Journal of Medicine, 2011, 364, 730-739.	13.9	665
139	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. Nature, 2011, 476, 298-303.	13.7	1,428
140	Targeted Assembly of Short Sequence Reads. Nature Precedings, 2011, , .	0.1	2
141	Age- and Disease-Dependent HERV-W Envelope Allelic Variation in Brain: Association with Neuroimmune Gene Expression. PLoS ONE, 2011, 6, e19176.	1.1	30
142	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
143	Genome Variation in Cryptococcus gattii, an Emerging Pathogen of Immunocompetent Hosts. MBio, 2011, 2, e00342-10.	1.8	182
144	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

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145	Targeted Assembly of Short Sequence Reads. PLoS ONE, 2011, 6, e19816.	1.1	41
146	The Sensitivity of Massively Parallel Sequencing for Detecting Candidate Infectious Agents Associated with Human Tissue. PLoS ONE, 2011, 6, e19838.	1.1	55
147	A quality management system application to investigate and troubleshoot process failures. Clinical Governance, 2010, 15, 102-112.	0.4	0
148	BACE1 Gene Promoter Single-Nucleotide Polymorphisms in Alzheimerâ€™s Disease. Journal of Molecular Neuroscience, 2010, 42, 127-133.	1.1	14
149	Salmo salar and Esox lucius full-length cDNA sequences reveal changes in evolutionary pressures on a post-tetraploidization genome. BMC Genomics, 2010, 11, 279.	1.2	163
150	Gene discovery for the bark beetle-vectored fungal tree pathogen Grosmannia clavigera. BMC Genomics, 2010, 11, 536.	1.2	25
151	Efficient assembly of very short oligonucleotides using T4 DNA Ligase. BMC Research Notes, 2010, 3, 291.	0.6	20
152	Cytosolic protein interactions of the schizophrenia susceptibility gene dysbindin. Journal of Neurochemistry, 2010, 113, 1491-1503.	2.1	33
153	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. Nature Genetics, 2010, 42, 181-185.	9.4	1,504
154	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.	3.3	74
155	A census of predicted mutational epitopes suitable for immunologic cancer control. Human Immunology, 2010, 71, 245-254.	1.2	23
156	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. Genome Biology, 2010, 11, R82.	13.9	159
157	Personalized oncogenomics. Genome Biology, 2010, 11, I5.	13.9	0
158	Identification of Genes Frequently Mutated In FL and DLBCL with Transcriptome, Genome and Exome Sequencing. Blood, 2010, 116, 804-804.	0.6	1
159	The completion of the Mammalian Gene Collection (MGC). Genome Research, 2009, 19, 2324-2333.	2.4	125
160	Nonlinear electrophoretic response yields a unique parameter for separation of biomolecules. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 14796-14801.	3.3	50
161	An Integrated Strategy to Study Muscle Development and Myofilament Structure in Caenorhabditis elegans. PLoS Genetics, 2009, 5, e1000537.	1.5	89
162	Profiling model T-cell metagenomes with short reads. Bioinformatics, 2009, 25, 458-464.	1.8	43

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163	Identification of genes expressed in the hermaphrodite germ line of C. elegans using SAGE. BMC Genomics, 2009, 10, 213.	1.2	105
164	Identification of novel androgen-responsive genes by sequencing of LongSAGE libraries. BMC Genomics, 2009, 10, 476.	1.2	75
165	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. Nature, 2009, 461, 809-813.	13.7	984
166	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science, 2009, 324, 522-528.	6.0	1,038
167	Next generation tools for high-throughput promoter and expression analysis employing single-copy knock-ins at the Hprt1 locus. Genomics, 2009, 93, 196-204.	1.3	39
168	De novo genome sequence assembly of a filamentous fungus using Sanger, 454 and Illumina sequence data. Genome Biology, 2009, 10, R94.	13.9	130
169	Profiling the T-cell receptor beta-chain repertoire by massively parallel sequencing. Genome Research, 2009, 19, 1817-1824.	2.4	361
170	Rainbow Smelt (Osmerus mordax) Genomic Library and EST Resources. Marine Biotechnology, 2008, 10, 487-91.	1.1	21
171	Decreased GABA Enhancement of Benzodiazepine Binding After a Single Dose of Diazepam. Journal of Neurochemistry, 2008, 72, 2219-2222.	2.1	29
172	Synthetic genomes brought closer to life. Nature Biotechnology, 2008, 26, 296-297.	9.4	4
173	SP1 regulates a human SNAP-25 gene expression. Journal of Neurochemistry, 2008, 105, 512-523.	2.1	23
174	A conifer genomics resource of 200,000 spruce (Picea spp.) ESTs and 6,464 high-quality, sequence-finished full-length cDNAs for Sitka spruce (Picea sitchensis). BMC Genomics, 2008, 9, 484.	1.2	113
175	A salmonid EST genomic study: genes, duplications, phylogeny and microarrays. BMC Genomics, 2008, 9, 545.	1.2	145
176	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. BMC Genomics, 2008, 9, 57.	1.2	68
177	Identification of a set of genes showing regionally enriched expression in the mouse brain. BMC Neuroscience, 2008, 9, 66.	0.8	25
178	Transcription of foreign DNA in Escherichia coli. Genome Research, 2008, 18, 1798-1805.	2.4	52
179	The new paradigm of flow cell sequencing: Table 1.. Genome Research, 2008, 18, 839-846.	2.4	185
180	Assembling millions of short DNA sequences using SSAKE. Bioinformatics, 2007, 23, 500-501.	1.8	421

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181	The molecular signature and <i>cis</i>-regulatory architecture of a <i>C. elegans</i> gustatory neuron. Genes and Development, 2007, 21, 1653-1674.	2.7	151
182	The ELT-2 GATA-factor and the global regulation of transcription in the C. elegans intestine. Developmental Biology, 2007, 302, 627-645.	0.9	165
183	Generation of ESTs in Vitis vinifera wine grape (Cabernet Sauvignon) and table grape (Muscat) Tj ETQq1 1 0.784314 rgBT /Overlock 1 402, 40-50.	1.0	45
184	A physical map of the bovine genome. Genome Biology, 2007, 8, R165.	13.9	73
185	LongSAGE profiling of nine human embryonic stem cell lines. Genome Biology, 2007, 8, R113.	13.9	21
186	Rebuilding microbial genomes. BioEssays, 2007, 29, 580-590.	1.2	20
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