

Sean M Grimmond

List of Publications by Year in descending order

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242
papers

47,938
citations

4658

85
h-index

1825

210
g-index

260
all docs

260
docs citations

260
times ranked

65873
citing authors

#	ARTICLE	IF	CITATIONS
1	Signatures of mutational processes in human cancer. <i>Nature</i> , 2013, 500, 415-421.	27.8	8,060
2	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	12.6	3,227
3	Genomic analyses identify molecular subtypes of pancreatic cancer. <i>Nature</i> , 2016, 531, 47-52.	27.8	2,700
4	Whole genomes redefine the mutational landscape of pancreatic cancer. <i>Nature</i> , 2015, 518, 495-501.	27.8	2,132
5	International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998.	27.8	2,114
6	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. <i>Nature</i> , 2012, 491, 399-405.	27.8	1,741
7	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002, 420, 563-573.	27.8	1,548
8	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	16.8	1,428
9	Whole-genome characterization of chemoresistant ovarian cancer. <i>Nature</i> , 2015, 521, 489-494.	27.8	1,206
10	Genome-wide analysis of mammalian promoter architecture and evolution. <i>Nature Genetics</i> , 2006, 38, 626-635.	21.4	1,201
11	Whole-genome landscapes of major melanoma subtypes. <i>Nature</i> , 2017, 545, 175-180.	27.8	1,068
12	Stem cell transcriptome profiling via massive-scale mRNA sequencing. <i>Nature Methods</i> , 2008, 5, 613-619.	19.0	952
13	The regulated retrotransposon transcriptome of mammalian cells. <i>Nature Genetics</i> , 2009, 41, 563-571.	21.4	731
14	Whole-genome landscape of pancreatic neuroendocrine tumours. <i>Nature</i> , 2017, 543, 65-71.	27.8	716
15	Long noncoding RNAs in mouse embryonic stem cell pluripotency and differentiation. <i>Genome Research</i> , 2008, 18, 1433-1445.	5.5	698
16	Assessment of transcript reconstruction methods for RNA-seq. <i>Nature Methods</i> , 2013, 10, 1177-1184.	19.0	679
17	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 140, 744-752.	28.9	667
18	Experimental validation of the regulated expression of large numbers of non-coding RNAs from the mouse genome. <i>Genome Research</i> , 2005, 16, 11-19.	5.5	461

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19	Mutant p53 Drives Pancreatic Cancer Metastasis through Cell-Autonomous PDGF Receptor $\hat{1}^2$ Signaling. <i>Cell</i> , 2014, 157, 382-394.	28.9	412
20	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	21.4	408
21	Conservation and divergence in Toll-like receptor 4-regulated gene expression in primary human versus mouse macrophages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E944-53.	7.1	332
22	Mutational signatures in esophageal adenocarcinoma define etiologically distinct subgroups with therapeutic relevance. <i>Nature Genetics</i> , 2016, 48, 1131-1141.	21.4	332
23	Tiny RNAs associated with transcription start sites in animals. <i>Nature Genetics</i> , 2009, 41, 572-578.	21.4	327
24	PINA v2.0: mining interactome modules. <i>Nucleic Acids Research</i> , 2012, 40, D862-D865.	14.5	321
25	MicroRNAs and their isomiRs function cooperatively to target common biological pathways. <i>Genome Biology</i> , 2011, 12, R126.	9.6	297
26	The deubiquitinase USP9X suppresses pancreatic ductal adenocarcinoma. <i>Nature</i> , 2012, 486, 266-270.	27.8	297
27	The miR-17-5p microRNA is a key regulator of the G1/S phase cell cycle transition. <i>Genome Biology</i> , 2008, 9, R127.	9.6	278
28	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. <i>Nature Communications</i> , 2015, 6, 10001.	12.8	266
29	NRED: a database of long noncoding RNA expression. <i>Nucleic Acids Research</i> , 2009, 37, D122-D126.	14.5	252
30	Mice Lacking the Vascular Endothelial Growth Factor-B Gene (<i>Vegfb</i>) Have Smaller Hearts, Dysfunctional Coronary Vasculature, and Impaired Recovery From Cardiac Ischemia. <i>Circulation Research</i> , 2000, 86, E29-35.	4.5	250
31	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. <i>Nature Communications</i> , 2014, 5, 5224.	12.8	236
32	GLDMAP. <i>Journal of the American Society of Nephrology: JASN</i> , 2008, 19, 667-671.	6.1	225
33	Genome-Wide Identification of Long Noncoding RNAs in CD8+ T Cells. <i>Journal of Immunology</i> , 2009, 182, 7738-7748.	0.8	221
34	Analysis of early nephron patterning reveals a role for distal RV proliferation in fusion to the ureteric tip via a cap mesenchyme-derived connecting segment. <i>Developmental Biology</i> , 2009, 332, 273-286.	2.0	221
35	Precision Medicine for Advanced Pancreas Cancer: The Individualized Molecular Pancreatic Cancer Therapy (IMPaCT) Trial. <i>Clinical Cancer Research</i> , 2015, 21, 2029-2037.	7.0	209
36	Dual targeting of p53 and c-MYC selectively eliminates leukaemic stem cells. <i>Nature</i> , 2016, 534, 341-346.	27.8	204

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37	<i>Sleeping Beauty</i> mutagenesis reveals cooperating mutations and pathways in pancreatic adenocarcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5934-5941.	7.1	201
38	Atlas of Gene Expression in the Developing Kidney at Microanatomic Resolution. <i>Developmental Cell</i> , 2008, 15, 781-791.	7.0	196
39	Characterisation and trophic functions of murine embryonic macrophages based upon the use of a Csf1-EGFP transgene reporter. <i>Developmental Biology</i> , 2007, 308, 232-246.	2.0	194
40	Genome-wide DNA methylation patterns in pancreatic ductal adenocarcinoma reveal epigenetic deregulation of SLIT-ROBO, ITGA2 and MET signaling. <i>International Journal of Cancer</i> , 2014, 135, 1110-1118.	5.1	192
41	The phasevarion: A genetic system controlling coordinated, random switching of expression of multiple genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5547-5551.	7.1	191
42	The Abundance of Short Proteins in the Mammalian Proteome. <i>PLoS Genetics</i> , 2006, 2, e52.	3.5	189
43	Genome-wide characterization of the routes to pluripotency. <i>Nature</i> , 2014, 516, 198-206.	27.8	187
44	A global role for EKLF in definitive and primitive erythropoiesis. <i>Blood</i> , 2006, 107, 3359-3370.	1.4	182
45	A global role for KLF1 in erythropoiesis revealed by CHIP-seq in primary erythroid cells. <i>Genome Research</i> , 2010, 20, 1052-1063.	5.5	180
46	A De Novo Mutation in the β -Tubulin Gene TUBB4A Results in the Leukoencephalopathy Hypomyelination with Atrophy of the Basal Ganglia and Cerebellum. <i>American Journal of Human Genetics</i> , 2013, 92, 767-773.	6.2	174
47	Hypermutation In Pancreatic Cancer. <i>Gastroenterology</i> , 2017, 152, 68-74.e2.	1.3	174
48	Phasevarions Mediate Random Switching of Gene Expression in Pathogenic Neisseria. <i>PLoS Pathogens</i> , 2009, 5, e1000400.	4.7	170
49	Vitamin C Promotes Widespread Yet Specific DNA Demethylation of the Epigenome in Human Embryonic Stem Cells. <i>Stem Cells</i> , 2010, 28, 1848-1855.	3.2	156
50	Mutations in DARS Cause Hypomyelination with Brain Stem and Spinal Cord Involvement and Leg Spasticity. <i>American Journal of Human Genetics</i> , 2013, 92, 774-780.	6.2	151
51	Integration-Free Induced Pluripotent Stem Cells Model Genetic and Neural Developmental Features of Down Syndrome Etiology. <i>Stem Cells</i> , 2013, 31, 467-478.	3.2	144
52	A Continuum of Cell States Spans Pluripotency and Lineage Commitment in Human Embryonic Stem Cells. <i>PLoS ONE</i> , 2009, 4, e7708.	2.5	139
53	miR-139-5p is a regulator of metastatic pathways in breast cancer. <i>Rna</i> , 2013, 19, 1767-1780.	3.5	137
54	Characterization of the mouse Men1 gene and its expression during development. <i>Oncogene</i> , 1998, 17, 2485-2493.	5.9	133

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55	Mutations in the voltage-gated potassium channel gene KCNH1 cause Temple-Baraitser syndrome and epilepsy. <i>Nature Genetics</i> , 2015, 47, 73-77.	21.4	130
56	Identifying the Molecular Phenotype of Renal Progenitor Cells. <i>Journal of the American Society of Nephrology: JASN</i> , 2004, 15, 2344-2357.	6.1	126
57	Targeting enhancer switching overcomes non-genetic drug resistance in acute myeloid leukaemia. <i>Nature Communications</i> , 2019, 10, 2723.	12.8	126
58	Mutation Analysis of the MEN1 Gene in Multiple Endocrine Neoplasia Type 1, Familial Acromegaly and Familial Isolated Hyperparathyroidism. <i>Journal of Clinical Endocrinology and Metabolism</i> , 1998, 83, 2621-2626.	3.6	125
59	Cloning and characterization of a novel human gene related to vascular endothelial growth factor.. <i>Genome Research</i> , 1996, 6, 124-131.	5.5	123
60	Divergent reprogramming routes lead to alternative stem-cell states. <i>Nature</i> , 2014, 516, 192-197.	27.8	123
61	Glioma through the looking GLASS: molecular evolution of diffuse gliomas and the Glioma Longitudinal Analysis Consortium. <i>Neuro-Oncology</i> , 2018, 20, 873-884.	1.2	119
62	A biphasic epigenetic switch controls immunoevasion, virulence and niche adaptation in non-typeable <i>Haemophilus influenzae</i> . <i>Nature Communications</i> , 2015, 6, 7828.	12.8	117
63	Phasevarion Mediated Epigenetic Gene Regulation in <i>Helicobacter pylori</i> . <i>PLoS ONE</i> , 2011, 6, e27569.	2.5	116
64	Whole exome sequencing in patients with white matter abnormalities. <i>Annals of Neurology</i> , 2016, 79, 1031-1037.	5.3	116
65	Transcriptome content and dynamics at single-nucleotide resolution. <i>Genome Biology</i> , 2008, 9, 234.	9.6	112
66	Minimum information specification for in situ hybridization and immunohistochemistry experiments (MISFISHIE). <i>Nature Biotechnology</i> , 2008, 26, 305-312.	17.5	111
67	Imperfect centered miRNA binding sites are common and can mediate repression of target mRNAs. <i>Genome Biology</i> , 2014, 15, R51.	9.6	111
68	Characterization of RasGRP2, a Plasma Membrane-targeted, Dual Specificity Ras/Rap Exchange Factor. <i>Journal of Biological Chemistry</i> , 2000, 275, 32260-32267.	3.4	109
69	Novel genes regulated by Sonic Hedgehog in pluripotent mesenchymal cells. <i>Oncogene</i> , 2002, 21, 8196-8205.	5.9	108
70	MicroRNA-182-5p targets a network of genes involved in DNA repair. <i>Rna</i> , 2013, 19, 230-242.	3.5	108
71	An epigenomic roadmap to induced pluripotency reveals DNA methylation as a reprogramming modulator. <i>Nature Communications</i> , 2014, 5, 5619.	12.8	108
72	Comprehensive transcriptome and immunophenotype analysis of renal and cardiac MSC-like populations supports strong congruence with bone marrow MSC despite maintenance of distinct identities. <i>Stem Cell Research</i> , 2012, 8, 58-73.	0.7	107

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73	Targeting mTOR dependency in pancreatic cancer. <i>Gut</i> , 2014, 63, 1481-1489.	12.1	107
74	Ampullary Cancers Harbor ELF3 Tumor Suppressor Gene Mutations and Exhibit Frequent WNT Dysregulation. <i>Cell Reports</i> , 2016, 14, 907-919.	6.4	107
75	Interaction of c-Myb with p300 is required for the induction of acute myeloid leukemia (AML) by human AML oncogenes. <i>Blood</i> , 2014, 123, 2682-2690.	1.4	103
76	Tailored first-line and second-line CDK4-targeting treatment combinations in mouse models of pancreatic cancer. <i>Gut</i> , 2018, 67, 2142-2155.	12.1	100
77	Integrated genomic and transcriptomic analysis of human brain metastases identifies alterations of potential clinical significance. <i>Journal of Pathology</i> , 2015, 237, 363-378.	4.5	98
78	Clinical and molecular characterization of HER2 amplified-pancreatic cancer. <i>Genome Medicine</i> , 2013, 5, 78.	8.2	97
79	Neuropilin-2 Promotes Extravasation and Metastasis by Interacting with Endothelial $\alpha 5$ Integrin. <i>Cancer Research</i> , 2013, 73, 4579-4590.	0.9	97
80	The Mouse Y Chromosome Interval Necessary for Spermatogonial Proliferation is Gene Dense with Syntenic Homology to the Human AZFa Region. <i>Human Molecular Genetics</i> , 1998, 7, 1713-1724.	2.9	96
81	Sexually dimorphic expression of protease nexin-1 and vanin-1 in the developing mouse gonad prior to overt differentiation suggests a role in mammalian sexual development. <i>Human Molecular Genetics</i> , 2000, 9, 1553-1560.	2.9	95
82	Generation of Diversity in the Innate Immune System: Macrophage Heterogeneity Arises from Gene-Autonomous Transcriptional Probability of Individual Inducible Genes. <i>Journal of Immunology</i> , 2002, 168, 44-50.	0.8	94
83	Reduced mucin sulfonation and impaired intestinal barrier function in the hyposulfataemic NaS1 null mouse. <i>Gut</i> , 2009, 58, 910-919.	12.1	94
84	Ferrets exclusively synthesize Neu5Ac and express naturally humanized influenza A virus receptors. <i>Nature Communications</i> , 2014, 5, 5750.	12.8	94
85	A rescue strategy for multimapping short sequence tags refines surveys of transcriptional activity by CAGE. <i>Genomics</i> , 2008, 91, 281-288.	2.9	92
86	qpure: A Tool to Estimate Tumor Cellularity from Genome-Wide Single-Nucleotide Polymorphism Profiles. <i>PLoS ONE</i> , 2012, 7, e45835.	2.5	92
87	Mouse Proteome Analysis. <i>Genome Research</i> , 2003, 13, 1335-1344.	5.5	91
88	Systematic Characterization of the Zinc-Finger-Containing Proteins in the Mouse Transcriptome. <i>Genome Research</i> , 2003, 13, 1430-1442.	5.5	89
89	Pax9 and Jagged1 act downstream of Gli3 in vertebrate limb development. <i>Mechanisms of Development</i> , 2005, 122, 1218-1233.	1.7	89
90	Subtypes of familial breast tumours revealed by expression and copy number profiling. <i>Breast Cancer Research and Treatment</i> , 2010, 123, 661-677.	2.5	86

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91	Transcriptional analysis of early lineage commitment in human embryonic stem cells. <i>BMC Developmental Biology</i> , 2007, 7, 12.	2.1	84
92	Characterization of the OxyR regulon of <i>Neisseria gonorrhoeae</i> . <i>Molecular Microbiology</i> , 2007, 63, 54-68.	2.5	81
93	Homologous Recombination DNA Repair Pathway Disruption and Retinoblastoma Protein Loss Are Associated with Exceptional Survival in High-Grade Serous Ovarian Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 569-580.	7.0	79
94	Identification of Anchor Genes during Kidney Development Defines Ontological Relationships, Molecular Subcompartments and Regulatory Pathways. <i>PLoS ONE</i> , 2011, 6, e17286.	2.5	78
95	HNF4A and GATA6 Loss Reveals Therapeutically Actionable Subtypes in Pancreatic Cancer. <i>Cell Reports</i> , 2020, 31, 107625.	6.4	78
96	Regulated post-transcriptional RNA cleavage diversifies the eukaryotic transcriptome. <i>Genome Research</i> , 2010, 20, 1639-1650.	5.5	76
97	The Mouse Secretome: Functional Classification of the Proteins Secreted Into the Extracellular Environment. <i>Genome Research</i> , 2003, 13, 1350-1359.	5.5	73
98	Cloning, Mapping, and Expression Analysis of a Gene Encoding a Novel Mammalian EGF-Related Protein (SCUBE1). <i>Genomics</i> , 2000, 70, 74-81.	2.9	72
99	Identification of Human Embryonic Stem Cell Surface Markers by Combined Membrane-Polysome Translation State Array Analysis and Immunotranscriptional Profiling. <i>Stem Cells</i> , 2009, 27, 2446-2456.	3.2	72
100	SOX9 regulates ERBB signalling in pancreatic cancer development. <i>Gut</i> , 2015, 64, 1790-1799.	12.1	71
101	PerR controls Mn-dependent resistance to oxidative stress in <i>Neisseria gonorrhoeae</i> . <i>Molecular Microbiology</i> , 2006, 60, 401-416.	2.5	69
102	Whole Genome Sequence Analysis of the First Australian OXA-48-Producing Outbreak-Associated <i>Klebsiella pneumoniae</i> Isolates: The Resistome and In Vivo Evolution. <i>PLoS ONE</i> , 2013, 8, e59920.	2.5	69
103	MicroRNAs-140-5p/140-3p Modulate Leydig Cell Numbers in the Developing Mouse Testis. <i>Biology of Reproduction</i> , 2013, 88, 143-143.	2.7	68
104	Somatic Point Mutation Calling in Low Cellularity Tumors. <i>PLoS ONE</i> , 2013, 8, e74380.	2.5	67
105	Alternate transcription of the Toll-like receptor signaling cascade. <i>Genome Biology</i> , 2006, 7, R10.	9.6	66
106	Temporal and spatial transcriptional programs in murine kidney development. <i>Physiological Genomics</i> , 2005, 23, 159-171.	2.3	64
107	The uniqueome: a mappability resource for short-tag sequencing. <i>Bioinformatics</i> , 2011, 27, 272-274.	4.1	64
108	Minor class splicing shapes the zebrafish transcriptome during development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 3062-3067.	7.1	64

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109	Dynamic transcription programs during ES cell differentiation towards mesoderm in serum versus serum-freeBMP4 culture. <i>BMC Genomics</i> , 2007, 8, 365.	2.8	63
110	Identification of a Novel de Novo p.Phe932Ile KCNT1 Mutation in a Patient With Leukoencephalopathy and Severe Epilepsy. <i>Pediatric Neurology</i> , 2014, 50, 112-114.	2.1	62
111	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , 2020, 11, 4330.	12.8	60
112	Caveolin-1 Is Necessary for Hepatic Oxidative Lipid Metabolism: Evidence for Crosstalk between Caveolin-1 and Bile Acid Signaling. <i>Cell Reports</i> , 2013, 4, 238-247.	6.4	56
113	<i>EIF1AX</i> and <i>NRAS</i> Mutations Co-occur and Cooperate in Low-Grade Serous Ovarian Carcinomas. <i>Cancer Research</i> , 2017, 77, 4268-4278.	0.9	56
114	Recurrent noncoding regulatory mutations in pancreatic ductal adenocarcinoma. <i>Nature Genetics</i> , 2017, 49, 825-833.	21.4	55
115	Small RNA changes en route to distinct cellular states of induced pluripotency. <i>Nature Communications</i> , 2014, 5, 5522.	12.8	54
116	The phospholipase C $\hat{2}3$ gene located in the MEN1 region shows loss of expression in endocrine tumours. <i>Human Molecular Genetics</i> , 1994, 3, 1775-1781.	2.9	53
117	SnapShot-Seq: A Method for Extracting Genome-Wide, In Vivo mRNA Dynamics from a Single Total RNA Sample. <i>PLoS ONE</i> , 2014, 9, e89673.	2.5	53
118	Clinical and pathologic features of familial pancreatic cancer. <i>Cancer</i> , 2014, 120, 3669-3675.	4.1	53
119	PGTools: A Software Suite for Proteogenomic Data Analysis and Visualization. <i>Journal of Proteome Research</i> , 2015, 14, 2255-2266.	3.7	52
120	Identification of molecular compartments and genetic circuitry in the developing mammalian kidney. <i>Development (Cambridge)</i> , 2012, 139, 1863-1873.	2.5	51
121	Mitochondrial mutations and metabolic adaptation in pancreatic cancer. <i>Cancer & Metabolism</i> , 2017, 5, 2.	5.0	51
122	A global role for zebrafish <i>klf4</i> in embryonic erythropoiesis. <i>Mechanisms of Development</i> , 2007, 124, 762-774.	1.7	50
123	Pancreatic cancer genomics. <i>Current Opinion in Genetics and Development</i> , 2014, 24, 74-81.	3.3	50
124	Subfractionation of Differentiating Human Embryonic Stem Cell Populations Allows the Isolation of a Mesodermal Population Enriched for Intermediate Mesoderm and Putative Renal Progenitors. <i>Stem Cells and Development</i> , 2010, 19, 1637-1648.	2.1	49
125	Genome-wide review of transcriptional complexity in mouse protein kinases and phosphatases. <i>Genome Biology</i> , 2006, 7, R5.	9.6	48
126	Identification of the CIMP-like subtype and aberrant methylation of members of the chromosomal segregation and spindle assembly pathways in esophageal adenocarcinoma. <i>Carcinogenesis</i> , 2016, 37, 356-365.	2.8	46

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127	RNA-MATE: a recursive mapping strategy for high-throughput RNA-sequencing data. <i>Bioinformatics</i> , 2009, 25, 2615-2616.	4.1	45
128	PRMT2 and ROR β Expression Are Associated With Breast Cancer Survival Outcomes. <i>Molecular Endocrinology</i> , 2014, 28, 1166-1185.	3.7	45
129	Proteome adaptation in cell reprogramming proceeds via distinct transcriptional networks. <i>Nature Communications</i> , 2014, 5, 5613.	12.8	45
130	Expression of a novel mammalian epidermal growth factor-related gene during mouse neural development. <i>Mechanisms of Development</i> , 2001, 102, 209-211.	1.7	44
131	Phosphoregulators: Protein Kinases and Protein Phosphatases of Mouse. <i>Genome Research</i> , 2003, 13, 1443-1454.	5.5	43
132	Profiling Gene Expression Induced by Protease-Activated Receptor 2 (PAR2) Activation in Human Kidney Cells. <i>PLoS ONE</i> , 2010, 5, e13809.	2.5	43
133	A High-Throughput Platform for Lentiviral Overexpression Screening of the Human ORFeome. <i>PLoS ONE</i> , 2011, 6, e20057.	2.5	43
134	Identification of Novel Markers of Mouse Fetal Ovary Development. <i>PLoS ONE</i> , 2012, 7, e41683.	2.5	42
135	Recommendations for Accurate Resolution of Gene and Isoform Allele-Specific Expression in RNA-Seq Data. <i>PLoS ONE</i> , 2015, 10, e0126911.	2.5	42
136	Analysis of the Promoter Region of the Human VEGF-Related Factor Gene. <i>Biochemical and Biophysical Research Communications</i> , 1997, 230, 413-418.	2.1	41
137	Probabilistic resolution of multi-mapping reads in massively parallel sequencing data using MuMRRescueLite. <i>Bioinformatics</i> , 2009, 25, 2613-2614.	4.1	41
138	Ascorbate Promotes Epigenetic Activation of CD30 in Human Embryonic Stem Cells. <i>Stem Cells</i> , 2010, 28, 1782-1793.	3.2	41
139	Carriage of an ACME II Variant May Have Contributed to Methicillin-Resistant <i>Staphylococcus aureus</i> Sequence Type 239-Like Strain Replacement in Liverpool Hospital, Sydney, Australia. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 3380-3383.	3.2	41
140	Transcriptional switching in macrophages associated with the peritoneal foreign body response. <i>Immunology and Cell Biology</i> , 2014, 92, 518-526.	2.3	40
141	Telomere sequence content can be used to determine ALT activity in tumours. <i>Nucleic Acids Research</i> , 2018, 46, 4903-4918.	14.5	40
142	Tissue-specific gene expression in soybean (<i>Glycine max</i>) detected by cDNA microarray analysis. <i>Journal of Plant Physiology</i> , 2002, 159, 1361-1374.	3.5	39
143	Proteogenomic Analysis of <i>Bradyrhizobium japonicum</i> USDA110 Using Genosuite, an Automated Multi-algorithmic Pipeline. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3388-3397.	3.8	39
144	Manganese regulation of virulence factors and oxidative stress resistance in <i>Neisseria gonorrhoeae</i> . <i>Journal of Proteomics</i> , 2010, 73, 899-916.	2.4	38

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145	Mining the genomes of exceptional responders. <i>Nature Reviews Cancer</i> , 2014, 14, 291-292.	28.4	38
146	Exome-Wide Association Study of Pancreatic Cancer Risk. <i>Gastroenterology</i> , 2018, 154, 719-722.e3.	1.3	38
147	Spatial gene expression in the T-stage mouse metanephros. <i>Gene Expression Patterns</i> , 2006, 6, 807-825.	0.8	37
148	Recurrent loss of heterozygosity correlates with clinical outcome in pancreatic neuroendocrine cancer. <i>Npj Genomic Medicine</i> , 2018, 3, 18.	3.8	37
149	Integrated genome analysis suggests that most conserved non-coding sequences are regulatory factor binding sites. <i>Nucleic Acids Research</i> , 2012, 40, 7858-7869.	14.5	36
150	Characterization of an <i>ntrX</i> Mutant of <i>Neisseria gonorrhoeae</i> Reveals a Response Regulator That Controls Expression of Respiratory Enzymes in Oxidase-Positive Proteobacteria. <i>Journal of Bacteriology</i> , 2013, 195, 2632-2641.	2.2	36
151	Clinical utility of whole-genome sequencing in precision oncology. <i>Seminars in Cancer Biology</i> , 2022, 84, 32-39.	9.6	35
152	Stromal Protein <i>Ecm1</i> Regulates Ureteric Bud Patterning and Branching. <i>PLoS ONE</i> , 2013, 8, e84155.	2.5	33
153	Gemcitabine and <i>CHK1</i> Inhibition Potentiate <i>EGFR</i> -Directed Radioimmunotherapy against Pancreatic Ductal Adenocarcinoma. <i>Clinical Cancer Research</i> , 2014, 20, 3187-3197.	7.0	32
154	Construction of a 1.2-Mb Sequence-Ready Contig of Chromosome 11q13 Encompassing the Multiple Endocrine Neoplasia Type 1 (<i>MEN1</i>) Gene. <i>Genomics</i> , 1997, 44, 94-100.	2.9	31
155	Understanding pancreatic cancer genomes. <i>Journal of Hepato-Biliary-Pancreatic Sciences</i> , 2013, 20, 549-556.	2.6	31
156	Analysis of the Mouse Transcriptome for Genes Involved in the Function of the Nervous System. <i>Genome Research</i> , 2003, 13, 1395-1401.	5.5	30
157	Gene expression profile of the fibrotic response in the peritoneal cavity. <i>Differentiation</i> , 2010, 79, 232-243.	1.9	30
158	New <i>RAS</i> -Mutant Pancreatic Adenocarcinoma With Combined <i>BRAF</i> and <i>MEK</i> Inhibition for Metastatic Melanoma. <i>Journal of Clinical Oncology</i> , 2015, 33, e52-e56.	1.6	28
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