

Sean M Grimmond

List of Publications by Year in descending order

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Version: 2024-02-01

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	Clinical utility of whole-genome sequencing in precision oncology. <i>Seminars in Cancer Biology</i> , 2022, 84, 32-39.	9.6	35
2	Analytical demands to use whole-genome sequencing in precision oncology. <i>Seminars in Cancer Biology</i> , 2022, 84, 16-22.	9.6	22
3	Clinical interpretation of whole-genome and whole-transcriptome sequencing for precision oncology. <i>Seminars in Cancer Biology</i> , 2022, 84, 23-31.	9.6	10
4	Genomic and Molecular Analyses Identify Molecular Subtypes of Pancreatic Cancer Recurrence. <i>Gastroenterology</i> , 2022, 162, 320-324.e4.	1.3	26
5	qmotif: determination of telomere content from whole-genome sequence data. <i>Bioinformatics Advances</i> , 2022, 2, .	2.4	5
6	Enhancer retargeting of <i>CDX2</i> and <i>UBTF::ATXN7L3</i> define a subtype of high-risk B-progenitor acute lymphoblastic leukemia. <i>Blood</i> , 2022, 139, 3519-3531.	1.4	20
7	Comprehensive genomic and tumour immune profiling reveals potential therapeutic targets in malignant pleural mesothelioma. <i>Genome Medicine</i> , 2022, 14, .	8.2	24
8	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. <i>Communications Biology</i> , 2021, 4, 155.	4.4	26
9	Novel RET Fusion <i>RET-SEPTIN9</i> Predicts Response to Selective RET Inhibition With Selpercatinib in Malignant Pheochromocytoma. <i>JCO Precision Oncology</i> , 2021, 5, 1160-1165.	3.0	7
10	Intravital imaging technology guides FAK-mediated priming in pancreatic cancer precision medicine according to Merlin status. <i>Science Advances</i> , 2021, 7, eabh0363.	10.3	23
11	PRMT5: An Emerging Target for Pancreatic Adenocarcinoma. <i>Cancers</i> , 2021, 13, 5136.	3.7	11
12	The Diverse Applications of Pancreatic Ductal Adenocarcinoma Organoids. <i>Cancers</i> , 2021, 13, 4979.	3.7	9
13	ROR1 and ROR2 expression in pancreatic cancer. <i>BMC Cancer</i> , 2021, 21, 1199.	2.6	4
14	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , 2020, 11, 4330.	12.8	60
15	RAF1 rearrangements are common in pancreatic acinar cell carcinomas. <i>Modern Pathology</i> , 2020, 33, 1811-1821.	5.5	19
16	HNF4A and GATA6 Loss Reveals Therapeutically Actionable Subtypes in Pancreatic Cancer. <i>Cell Reports</i> , 2020, 31, 107625.	6.4	78
17	Targeting enhancer switching overcomes non-genetic drug resistance in acute myeloid leukaemia. <i>Nature Communications</i> , 2019, 10, 2723.	12.8	126
18	Setting CAGE Tags in a Genomic Context. , 2019, , 93-100.		0

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19	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
20	Telomere sequence content can be used to determine ALT activity in tumours. <i>Nucleic Acids Research</i> , 2018, 46, 4903-4918.	14.5	40
21	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
22	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
23	Exome-Wide Association Study of Pancreatic Cancer Risk. <i>Gastroenterology</i> , 2018, 154, 719-722.e3.	1.3	38
24	<i>BRAF</i> Mutations in Low-Grade Serous Ovarian Cancer and Response to BRAF Inhibition. <i>JCO Precision Oncology</i> , 2018, 2, 1-14.	3.0	19
25	Recurrent loss of heterozygosity correlates with clinical outcome in pancreatic neuroendocrine cancer. <i>Npj Genomic Medicine</i> , 2018, 3, 18.	3.8	37
26	Whole-genome landscape of pancreatic neuroendocrine tumours. <i>Nature</i> , 2017, 543, 65-71.	27.8	716
27	Recurrent noncoding regulatory mutations in pancreatic ductal adenocarcinoma. <i>Nature Genetics</i> , 2017, 49, 825-833.	21.4	55
28	Whole-genome landscapes of major melanoma subtypes. <i>Nature</i> , 2017, 545, 175-180.	27.8	1,068
29	Mitochondrial mutations and metabolic adaptation in pancreatic cancer. <i>Cancer & Metabolism</i> , 2017, 5, 2.	5.0	51
30	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	16.8	1,428
31	<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
32	Lost in translation: returning germline genetic results in genome-scale cancer research. <i>Genome Medicine</i> , 2017, 9, 41.	8.2	27
33	Hypermutation In Pancreatic Cancer. <i>Gastroenterology</i> , 2017, 152, 68-74.e2.	1.3	174
34	Whole exome sequencing in patients with white matter abnormalities. <i>Annals of Neurology</i> , 2016, 79, 1031-1037.	5.3	116
35	Mutational signatures in esophageal adenocarcinoma define etiologically distinct subgroups with therapeutic relevance. <i>Nature Genetics</i> , 2016, 48, 1131-1141.	21.4	332
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	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
38	Ampullary Cancers Harbor ELF3 Tumor Suppressor Gene Mutations and Exhibit Frequent WNT Dysregulation. <i>Cell Reports</i> , 2016, 14, 907-919.	6.4	107
39	Genomic analyses identify molecular subtypes of pancreatic cancer. <i>Nature</i> , 2016, 531, 47-52.	27.8	2,700
40	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
41	Whole-genome characterization of chemoresistant ovarian cancer. <i>Nature</i> , 2015, 521, 489-494.	27.8	1,206
42	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. <i>Nature Communications</i> , 2015, 6, 10001.	12.8	266
43	Pancreatic cancer genomics: where can the science take us?. <i>Clinical Genetics</i> , 2015, 88, 213-219.	2.0	13
44	Whole genomes redefine the mutational landscape of pancreatic cancer. <i>Nature</i> , 2015, 518, 495-501.	27.8	2,132
45	PGTools: A Software Suite for Proteogenomic Data Analysis and Visualization. <i>Journal of Proteome Research</i> , 2015, 14, 2255-2266.	3.7	52
46	New <i>RAS</i> -Mutant Pancreatic Adenocarcinoma With Combined BRAF and MEK Inhibition for Metastatic Melanoma. <i>Journal of Clinical Oncology</i> , 2015, 33, e52-e56.	1.6	28
47	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
48	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
49	Mutations in the voltage-gated potassium channel gene <i>KCNH1</i> cause Temple-Baraitser syndrome and epilepsy. <i>Nature Genetics</i> , 2015, 47, 73-77.	21.4	130
50	SOX9 regulates ERBB signalling in pancreatic cancer development. <i>Gut</i> , 2015, 64, 1790-1799.	12.1	71
51	Towards the Systematic Mapping and Engineering of the Protein Prenylation Machinery in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2015, 10, e0120716.	2.5	20
52	Using the MCF10A/MCF10CA1a Breast Cancer Progression Cell Line Model to Investigate the Effect of Active, Mutant Forms of EGFR in Breast Cancer Development and Treatment Using Gefitinib. <i>PLoS ONE</i> , 2015, 10, e0125232.	2.5	27
53	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
54	Abstract PR06: The ampullary adenocarcinoma, its molecular characterization and differentiation from the pancreatic ductal adenocarcinoma, duodenal adenocarcinoma, and cholangiocarcinoma. , 2015, , .		0

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55	SnapShot-Seq: A Method for Extracting Genome-Wide, In Vivo mRNA Dynamics from a Single Total RNA Sample. PLoS ONE, 2014, 9, e89673.	2.5	53
56	Rapid Identification of a Novel Complex I MT-ND3 m.10134C>A Mutation in a Leigh Syndrome Patient. PLoS ONE, 2014, 9, e104879.	2.5	5
57	A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. BioTechniques, 2014, 57, 31-38.	1.8	0
58	PRMT2 and ROR α Expression Are Associated With Breast Cancer Survival Outcomes. Molecular Endocrinology, 2014, 28, 1166-1185.	3.7	45
59	Stratified Medicine for Pancreatic Cancer. , 2014, , 807-814.		0
60	Clinical and pathologic features of familial pancreatic cancer. Cancer, 2014, 120, 3669-3675.	4.1	53
61	Can we move towards personalised pancreatic cancer therapy?. Expert Review of Gastroenterology and Hepatology, 2014, 8, 335-338.	3.0	5
62	Ferrets exclusively synthesize Neu5Ac and express naturally humanized influenza A virus receptors. Nature Communications, 2014, 5, 5750.	12.8	94
63	Small RNA changes en route to distinct cellular states of induced pluripotency. Nature Communications, 2014, 5, 5522.	12.8	54
64	Divergent reprogramming routes lead to alternative stem-cell states. Nature, 2014, 516, 192-197.	27.8	123
65	Genome-wide characterization of the routes to pluripotency. Nature, 2014, 516, 198-206.	27.8	187
66	Genome-wide DNA methylation patterns in pancreatic ductal adenocarcinoma reveal epigenetic deregulation of SLIT α -ROBO, ITGA2 and MET signaling. International Journal of Cancer, 2014, 135, 1110-1118.	5.1	192
67	An epigenomic roadmap to induced pluripotency reveals DNA methylation as a reprogramming modulator. Nature Communications, 2014, 5, 5619.	12.8	108
68	Proteome adaptation in cell reprogramming proceeds via distinct transcriptional networks. Nature Communications, 2014, 5, 5613.	12.8	45
69	Targeting mTOR dependency in pancreatic cancer. Gut, 2014, 63, 1481-1489.	12.1	107
70	Gemcitabine and CHK1 Inhibition Potentiate EGFR-Directed Radioimmunotherapy against Pancreatic Ductal Adenocarcinoma. Clinical Cancer Research, 2014, 20, 3187-3197.	7.0	32
71	Minor class splicing shapes the zebrafish transcriptome during development. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 3062-3067.	7.1	64
72	Imperfect centered miRNA binding sites are common and can mediate repression of target mRNAs. Genome Biology, 2014, 15, R51.	9.6	111

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73	Transcriptional switching in macrophages associated with the peritoneal foreign body response. <i>Immunology and Cell Biology</i> , 2014, 92, 518-526.	2.3	40
74	Mining the genomes of exceptional responders. <i>Nature Reviews Cancer</i> , 2014, 14, 291-292.	28.4	38
75	Mutant p53 Drives Pancreatic Cancer Metastasis through Cell-Autonomous PDGF Receptor β Signaling. <i>Cell</i> , 2014, 157, 382-394.	28.9	412
76	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
77	In vivo evolution of antimicrobial resistance in a series of <i>Staphylococcus aureus</i> patient isolates: the entire picture or a cautionary tale?. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 363-367.	3.0	17
78	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. <i>Nature Communications</i> , 2014, 5, 5224.	12.8	236
79	Returning individual research results for genome sequences of pancreatic cancer. <i>Genome Medicine</i> , 2014, 6, 42.	8.2	25
80	Pancreatic cancer genomics. <i>Current Opinion in Genetics and Development</i> , 2014, 24, 74-81.	3.3	50
81	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
82	10. Clinicopathological features of HER2 amplified pancreatic cancer. <i>Pathology</i> , 2014, 46, S109-S110.	0.6	0
83	Abstract 1715: Elucidating mechanisms of resistance to FGFR inhibitors in endometrial cancer. , 2014, , .		0
84	Abstract LB-73: SOX9 regulates EGFR/ERBB signaling in pancreatic cancer. , 2014, , .		0
85	Understanding pancreatic cancer genomes. <i>Journal of Hepato-Biliary-Pancreatic Sciences</i> , 2013, 20, 549-556.	2.6	31
86	Signatures of mutational processes in human cancer. <i>Nature</i> , 2013, 500, 415-421.	27.8	8,060
87	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
88	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
89	Assessment of transcript reconstruction methods for RNA-seq. <i>Nature Methods</i> , 2013, 10, 1177-1184.	19.0	679
90	Clinical and molecular characterization of HER2 amplified-pancreatic cancer. <i>Genome Medicine</i> , 2013, 5, 78.	8.2	97

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91	Novel cancer drivers: mining the kinome. <i>Genome Medicine</i> , 2013, 5, 19.	8.2	3
92	Neuropilin-2 Promotes Extravasation and Metastasis by Interacting with Endothelial $\alpha 5$ Integrin. <i>Cancer Research</i> , 2013, 73, 4579-4590.	0.9	97
93	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
94	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
95	Identification of Unsafe Human Induced Pluripotent Stem Cell Lines Using a Robust Surrogate Assay for Pluripotency. <i>Stem Cells</i> , 2013, 31, 1498-1510.	3.2	22
96	miR-139-5p is a regulator of metastatic pathways in breast cancer. <i>Rna</i> , 2013, 19, 1767-1780.	3.5	137
97	MicroRNA-182-5p targets a network of genes involved in DNA repair. <i>Rna</i> , 2013, 19, 230-242.	3.5	108
98	Characterization of an α -NtrX 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
99	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
100	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
101	Somatic Point Mutation Calling in Low Cellularity Tumors. <i>PLoS ONE</i> , 2013, 8, e74380.	2.5	67
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	Stromal Protein Ecm1 Regulates Ureteric Bud Patterning and Branching. <i>PLoS ONE</i> , 2013, 8, e84155.	2.5	33
104	Abstract A75: The IMPaCT trial: Individualised Molecular Pancreatic Cancer Therapy. A pilot, randomized, open label Phase II trial assessing first line treatment with gemcitabine or personalized treatment based on tumour molecular signature in patients with metastatic pancreatic cancer.. , 2013, 11		0
105	PINA v2.0: mining interactome modules. <i>Nucleic Acids Research</i> , 2012, 40, D862-D865.	14.5	321
106	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
107	The deubiquitinase USP9X suppresses pancreatic ductal adenocarcinoma. <i>Nature</i> , 2012, 486, 266-270.	27.8	297
108	Identification of molecular compartments and genetic circuitry in the developing mammalian kidney. <i>Development (Cambridge)</i> , 2012, 139, 1863-1873.	2.5	51

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109	<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
110	RON is not a prognostic marker for resectable pancreatic cancer. <i>BMC Cancer</i> , 2012, 12, 395.	2.6	17
111	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. <i>Nature</i> , 2012, 491, 399-405.	27.8	1,741
112	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
113	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
114	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
115	Identification of Novel Markers of Mouse Fetal Ovary Development. <i>PLoS ONE</i> , 2012, 7, e41683.	2.5	42
116	qpure: A Tool to Estimate Tumor Cellularity from Genome-Wide Single-Nucleotide Polymorphism Profiles. <i>PLoS ONE</i> , 2012, 7, e45835.	2.5	92
117	Abstract 5071: The genomic landscape of pancreatic cancer: from discovery to patient care. , 2012, , .		0
118	Abstract LB-404: Genomic analysis reveals roles for chromatin modification and axon guidance in pancreatic cancer. , 2012, , .		0
119	Interaction of c-Myb with p300 Is Required for the Induction of Acute Myeloid Leukemia by Human AML Oncogenes, and Represents a Potential Therapeutic Target.. <i>Blood</i> , 2012, 120, 2402-2402.	1.4	0
120	Sequencing transcriptomes in toto. <i>Integrative Biology (United Kingdom)</i> , 2011, 3, 522.	1.3	16
121	MicroRNAs and their isomiRs function cooperatively to target common biological pathways. <i>Genome Biology</i> , 2011, 12, R126.	9.6	297
122	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
123	A High-Throughput Platform for Lentiviral Overexpression Screening of the Human ORFeome. <i>PLoS ONE</i> , 2011, 6, e20057.	2.5	43
124	Phasevarion Mediated Epigenetic Gene Regulation in <i>Helicobacter pylori</i> . <i>PLoS ONE</i> , 2011, 6, e27569.	2.5	116
125	Analysis of Brca1-deficient mouse mammary glands reveals reciprocal regulation of Brca1 and c-kit. <i>Oncogene</i> , 2011, 30, 1597-1607.	5.9	26
126	Refining transcriptional programs in kidney development by integration of deep RNA-sequencing and array-based spatial profiling. <i>BMC Genomics</i> , 2011, 12, 441.	2.8	27

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127	Deep-transcriptome and ribonome sequencing redefines the molecular networks of pluripotency and the extracellular space in human embryonic stem cells. <i>Genome Research</i> , 2011, 21, 2014-2025.	5.5	23
128	The uniqueome: a mappability resource for short-tag sequencing. <i>Bioinformatics</i> , 2011, 27, 272-274.	4.1	64
129	X-MATE: a flexible system for mapping short read data. <i>Bioinformatics</i> , 2011, 27, 580-581.	4.1	11
130	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
131	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
132	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
133	Ascorbate Promotes Epigenetic Activation of CD30 in Human Embryonic Stem Cells. <i>Stem Cells</i> , 2010, 28, 1782-1793.	3.2	41
134	International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998.	27.8	2,114
135	Simplifying complexity. <i>Nature Methods</i> , 2010, 7, 793-795.	19.0	1
136	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
137	Regulated post-transcriptional RNA cleavage diversifies the eukaryotic transcriptome. <i>Genome Research</i> , 2010, 20, 1639-1650.	5.5	76
138	Use of DNA-Damaging Agents and RNA Pooling to Assess Expression Profiles Associated with BRCA1 and BRCA2 Mutation Status in Familial Breast Cancer Patients. <i>PLoS Genetics</i> , 2010, 6, e1000850.	3.5	9
139	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
140	Redirection of renal mesenchyme to stromal and chondrocytic fates in the presence of TGF- β 2. <i>Differentiation</i> , 2010, 79, 272-284.	1.9	6
141	Gene expression profile of the fibrotic response in the peritoneal cavity. <i>Differentiation</i> , 2010, 79, 232-243.	1.9	30
142	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 140, 744-752.	28.9	667
143	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 141, 369.	28.9	4
144	Comparative gene expression analysis of genital tubercle development reveals a putative appendicular Wnt7 network for the epidermal differentiation. <i>Developmental Biology</i> , 2010, 344, 1071-1087.	2.0	27

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145	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
146	The clinical potential and challenges of sequencing cancer genomes for personalized medical genomics. <i>IDrugs: the Investigational Drugs Journal</i> , 2010, 13, 778-81.	0.7	2
147	Transcriptome-Wide Prediction of miRNA Targets in Human and Mouse Using FASTH. <i>PLoS ONE</i> , 2009, 4, e5745.	2.5	27
148	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
149	Phasevarions Mediate Random Switching of Gene Expression in Pathogenic <i>Neisseria</i> . <i>PLoS Pathogens</i> , 2009, 5, e1000400.	4.7	170
150	GUDMAP - An Online GenitoUrinary Resource. <i>Nature Precedings</i> , 2009, , .	0.1	0
151	Genome-Wide Identification of Long Noncoding RNAs in CD8+ T Cells. <i>Journal of Immunology</i> , 2009, 182, 7738-7748.	0.8	221
152	Probabilistic resolution of multi-mapping reads in massively parallel sequencing data using MuMRRescueLite. <i>Bioinformatics</i> , 2009, 25, 2613-2614.	4.1	41
153	NRED: a database of long noncoding RNA expression. <i>Nucleic Acids Research</i> , 2009, 37, D122-D126.	14.5	252
154	Reduced mucin sulfonation and impaired intestinal barrier function in the hyposulfataemic NaS1 null mouse. <i>Gut</i> , 2009, 58, 910-919.	12.1	94
155	RNA-MATE: a recursive mapping strategy for high-throughput RNA-sequencing data. <i>Bioinformatics</i> , 2009, 25, 2615-2616.	4.1	45
156	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
157	Tiny RNAs associated with transcription start sites in animals. <i>Nature Genetics</i> , 2009, 41, 572-578.	21.4	327
158	The regulated retrotransposon transcriptome of mammalian cells. <i>Nature Genetics</i> , 2009, 41, 563-571.	21.4	731
159	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
160	Atlas of Gene Expression in the Developing Kidney at Microanatomic Resolution. <i>Developmental Cell</i> , 2009, 16, 482.	7.0	2
161	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
162	07-P023 GUDMAP – An online genitourinary resource. <i>Mechanisms of Development</i> , 2009, 126, S143.	1.7	0

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163	Genome Sequencing Approaches and Successes. <i>Methods in Molecular Biology</i> , 2009, 513, 345-358.	0.9	24
164	Setting CAGE Tags in a Genomic Context. , 2009, , 93-100.		0
165	Use of expression data and the CGEMS genome-wide breast cancer association study to identify genes that may modify risk in BRCA1/2 mutation carriers. <i>Breast Cancer Research and Treatment</i> , 2008, 112, 229-236.	2.5	20
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