

Sean M Grimmond

List of Publications by Year in descending order

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Version: 2025-02-01

221
papers

38,388
citations

4704

80
h-index

1983

195
g-index

249
all docs

249
docs citations

249
times ranked

63110
citing authors

#	ARTICLE	IF	CITATIONS
1	Temporally resolved proteomics identifies nidogen-2 as a cotarget in pancreatic cancer that modulates fibrosis and therapy response. <i>Science Advances</i> , 2024, 10, .	11.3	1
2	Description of a novel subtype of acute myeloid leukemia defined by recurrent <i>C/EBFβ</i> insertions. <i>Blood</i> , 2023, 141, 800-805.	1.0	2
3	A first-in-class pan-lysyl oxidase inhibitor impairs stromal remodeling and enhances gemcitabine response and survival in pancreatic cancer. <i>Nature Cancer</i> , 2023, 4, 1326-1344.	13.9	31
4	Clinical utility of whole-genome sequencing in precision oncology. <i>Seminars in Cancer Biology</i> , 2022, 84, 32-39.	14.2	45
5	Analytical demands to use whole-genome sequencing in precision oncology. <i>Seminars in Cancer Biology</i> , 2022, 84, 16-22.	14.2	29
6	Clinical interpretation of whole-genome and whole-transcriptome sequencing for precision oncology. <i>Seminars in Cancer Biology</i> , 2022, 84, 23-31.	14.2	15
7	Genomic and Molecular Analyses Identify Molecular Subtypes of Pancreatic Cancer Recurrence. <i>Gastroenterology</i> , 2022, 162, 320-324.e4.	1.0	26
8	qmotif: determination of telomere content from whole-genome sequence data. <i>Bioinformatics Advances</i> , 2022, 2, .	2.5	8
9	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.	1.0	29
10	Comprehensive genomic and tumour immune profiling reveals potential therapeutic targets in malignant pleural mesothelioma. <i>Genome Medicine</i> , 2022, 14, .	9.9	31
11	Single-nuclei and bulk-tissue gene-expression analysis of pheochromocytoma and paraganglioma links disease subtypes with tumor microenvironment. <i>Nature Communications</i> , 2022, 13, .	14.1	19
12	Implementation of Whole-Genome and Transcriptome Sequencing Into Clinical Cancer Care. <i>JCO Precision Oncology</i> , 2022, , .	2.1	34
13	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. <i>Communications Biology</i> , 2021, 4, .	4.5	28
14	Novel RET Fusion <i>RET-SEPTIN9</i> Predicts Response to Selective RET Inhibition With Selpercatinib in Malignant Pheochromocytoma. <i>JCO Precision Oncology</i> , 2021, , 1160-1165.	2.1	13
15	Intravital imaging technology guides FAK-mediated priming in pancreatic cancer precision medicine according to Merlin status. <i>Science Advances</i> , 2021, 7, .	11.3	31
16	PRMT5: An Emerging Target for Pancreatic Adenocarcinoma. <i>Cancers</i> , 2021, 13, 5136.	4.0	15
17	The Diverse Applications of Pancreatic Ductal Adenocarcinoma Organoids. <i>Cancers</i> , 2021, 13, 4979.	4.0	9
18	ROR1 and ROR2 expression in pancreatic cancer. <i>BMC Cancer</i> , 2021, 21, .	3.0	7

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19	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , 2020, 11, .	14.1	62
20	RAF1 rearrangements are common in pancreatic acinar cell carcinomas. <i>Modern Pathology</i> , 2020, 33, 1811-1821.	5.0	27
21	HNF4A and GATA6 Loss Reveals Therapeutically Actionable Subtypes in Pancreatic Cancer. <i>Cell Reports</i> , 2020, 31, 107625.	6.4	82
22	Targeting enhancer switching overcomes non-genetic drug resistance in acute myeloid leukaemia. <i>Nature Communications</i> , 2019, 10, .	14.1	115
23	Setting CAGE Tags in a Genomic Context. , 2019, , 93-100.		0
24	Glioma through the looking GLASS: molecular evolution of diffuse gliomas and the Glioma Longitudinal Analysis Consortium. <i>Neuro-Oncology</i> , 2018, 20, 873-884.	0.9	118
25	Telomere sequence content can be used to determine ALT activity in tumours. <i>Nucleic Acids Research</i> , 2018, 46, 4903-4918.	16.2	33
26	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.	6.4	69
27	Tailored first-line and second-line CDK4-targeting treatment combinations in mouse models of pancreatic cancer. <i>Gut</i> , 2018, 67, 2142-2155.	14.8	92
28	Exome-Wide Association Study of Pancreatic Cancer Risk. <i>Gastroenterology</i> , 2018, 154, 719-722.e3.	1.0	39
29	<i>BRAF</i> Mutations in Low-Grade Serous Ovarian Cancer and Response to BRAF Inhibition. <i>JCO Precision Oncology</i> , 2018, , 1-14.	2.1	29
30	Recurrent loss of heterozygosity correlates with clinical outcome in pancreatic neuroendocrine cancer. <i>Npj Genomic Medicine</i> , 2018, 3, .	4.5	44
31	Whole-genome landscape of pancreatic neuroendocrine tumours. <i>Nature</i> , 2017, 543, 65-71.	40.1	694
32	Recurrent noncoding regulatory mutations in pancreatic ductal adenocarcinoma. <i>Nature Genetics</i> , 2017, 49, 825-833.	16.3	44
33	Whole-genome landscapes of major melanoma subtypes. <i>Nature</i> , 2017, 545, 175-180.	40.1	1,024
34	Mitochondrial mutations and metabolic adaptation in pancreatic cancer. <i>Cancer & Metabolism</i> , 2017, 5, .	4.8	51
35	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	33.4	1,371
36	<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.	0.6	60

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37	Lost in translation: returning germline genetic results in genome-scale cancer research. <i>Genome Medicine</i> , 2017, 9, .	9.9	25
38	Hypermethylation In Pancreatic Cancer. <i>Gastroenterology</i> , 2017, 152, 68-74.e2.	1.0	176
39	Whole exome sequencing in patients with white matter abnormalities. <i>Annals of Neurology</i> , 2016, 79, 1031-1037.	6.6	120
40	Dual targeting of p53 and c-MYC selectively eliminates leukaemic stem cells. <i>Nature</i> , 2016, 534, 341-346.	40.1	183
41	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.	2.9	42
42	Ampullary Cancers Harbor ELF3 Tumor Suppressor Gene Mutations and Exhibit Frequent WNT Dysregulation. <i>Cell Reports</i> , 2016, 14, 907-919.	6.4	108
43	Genomic analyses identify molecular subtypes of pancreatic cancer. <i>Nature</i> , 2016, 531, 47-52.	40.1	2,593
44	Integrated genomic and transcriptomic analysis of human brain metastases identifies alterations of potential clinical significance. <i>Journal of Pathology</i> , 2015, 237, 363-378.	5.2	100
45	Whole-genome characterization of chemoresistant ovarian cancer. <i>Nature</i> , 2015, 521, 489-494.	40.1	1,161
46	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. <i>Nature Communications</i> , 2015, 6, .	14.1	221
47	Whole genomes redefine the mutational landscape of pancreatic cancer. <i>Nature</i> , 2015, 518, 495-501.	40.1	2,059
48	PGTools: A Software Suite for Proteogenomic Data Analysis and Visualization. <i>Journal of Proteome Research</i> , 2015, 14, 2255-2266.	3.7	47
49	New KRAS-Mutant Pancreatic Adenocarcinoma With Combined BRAF and MEK Inhibition for Metastatic Melanoma. <i>Journal of Clinical Oncology</i> , 2015, 33, e52-e56.	17.1	27
50	Precision Medicine for Advanced Pancreas Cancer: The Individualized Molecular Pancreatic Cancer Therapy (IMPaCT) Trial. <i>Clinical Cancer Research</i> , 2015, 21, 2029-2037.	6.4	203
51	A biphasic epigenetic switch controls immunoevasion, virulence and niche adaptation in non-typeable <i>Haemophilus influenzae</i> . <i>Nature Communications</i> , 2015, 6, .	14.1	98
52	SOX9 regulates ERBB signalling in pancreatic cancer development. <i>Gut</i> , 2015, 64, 1790-1799.	14.8	68
53	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
54	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	24

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55	Recommendations for Accurate Resolution of Gene and Isoform Allele-Specific Expression in RNA-Seq Data. PLoS ONE, 2015, 10, e0126911.	2.5	18
56	Abstract PR06: The ampullary adenocarcinoma, its molecular characterization and differentiation from the pancreatic ductal adenocarcinoma, duodenal adenocarcinoma, and cholangiocarcinoma. , 2015, , .		0
57	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	37
58	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	8
59	A Workflow to Increase Verification Rate of Chromosomal Structural Rearrangements Using High-Throughput Next-Generation Sequencing. BioTechniques, 2014, 57, 31-38.	5.5	0
60	PRMT2 and ROR1 ³ Expression Are Associated With Breast Cancer Survival Outcomes. Molecular Endocrinology, 2014, 28, 1166-1185.	3.6	47
61	Stratified Medicine for Pancreatic Cancer. , 2014, , 807-814.		0
62	Clinical and pathologic features of familial pancreatic cancer. Cancer, 2014, 120, 3669-3675.	4.4	50
63	Can we move towards personalised pancreatic cancer therapy?. Expert Review of Gastroenterology and Hepatology, 2014, 8, 335-338.	2.4	5
64	Ferrets exclusively synthesize Neu5Ac and express naturally humanized influenza A virus receptors. Nature Communications, 2014, 5, .	14.1	95
65	Small RNA changes en route to distinct cellular states of induced pluripotency. Nature Communications, 2014, 5, .	14.1	52
66	Divergent reprogramming routes lead to alternative stem-cell states. Nature, 2014, 516, 192-197.	40.1	105
67	Genome-wide characterization of the routes to pluripotency. Nature, 2014, 516, 198-206.	40.1	175
68	Genome-wide DNA methylation patterns in pancreatic ductal adenocarcinoma reveal epigenetic deregulation of SLIT-ROBO, ITGA2 and MET signaling. International Journal of Cancer, 2014, 135, 1110-1118.	4.5	180
69	An epigenomic roadmap to induced pluripotency reveals DNA methylation as a reprogramming modulator. Nature Communications, 2014, 5, .	14.1	102
70	Proteome adaptation in cell reprogramming proceeds via distinct transcriptional networks. Nature Communications, 2014, 5, .	14.1	40
71	Targeting mTOR dependency in pancreatic cancer. Gut, 2014, 63, 1481-1489.	14.8	101
72	Gemcitabine and CHK1 Inhibition Potentiate EGFR-Directed Radioimmunotherapy against Pancreatic Ductal Adenocarcinoma. Clinical Cancer Research, 2014, 20, 3187-3197.	6.4	35

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73	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.	7.7	53
74	Imperfect centered miRNA binding sites are common and can mediate repression of target mRNAs. Genome Biology, 2014, 15, .	8.4	100
75	Transcriptional switching in macrophages associated with the peritoneal foreign body response. Immunology and Cell Biology, 2014, 92, 518-526.	2.8	35
76	Mining the genomes of exceptional responders. Nature Reviews Cancer, 2014, 14, 291-292.	24.2	35
77	Mutant p53 Drives Pancreatic Cancer Metastasis through Cell-Autonomous PDGF Receptor β Signaling. Cell, 2014, 157, 382-394.	35.1	396
78	Interaction of c-Myb with p300 is required for the induction of acute myeloid leukemia (AML) by human AML oncogenes. Blood, 2014, 123, 2682-2690.	1.0	100
79	In vivo evolution of antimicrobial resistance in a series of Staphylococcus aureus patient isolates: the entire picture or a cautionary tale?. Journal of Antimicrobial Chemotherapy, 2014, 69, 363-367.	3.2	18
80	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. Nature Communications, 2014, 5, .	14.1	217
81	Returning individual research results for genome sequences of pancreatic cancer. Genome Medicine, 2014, 6, .	9.9	17
82	Pancreatic cancer genomics. Current Opinion in Genetics and Development, 2014, 24, 74-81.	3.4	46
83	Identification of a Novel de Novo p.Phe932Ile KCNT1 Mutation in a Patient With Leukoencephalopathy and Severe Epilepsy. Pediatric Neurology, 2014, 50, 112-114.	1.9	55
84	10. Clinicopathological features of HER2 amplified pancreatic cancer. Pathology, 2014, 46, S109-S110.	0.6	0
85	Mutations in the voltage-gated potassium channel gene KCNH1 cause Temple-Baraitser syndrome and epilepsy. Nature Genetics, 2014, 47, 73-77.	16.3	124
86	Abstract 1715: Elucidating mechanisms of resistance to FGFR inhibitors in endometrial cancer. , 2014, , .		0
87	Understanding pancreatic cancer genomes. Journal of Hepato-Biliary-Pancreatic Sciences, 2013, 20, 549-556.	2.5	28
88	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	40.1	7,418
89	Mutations in DARS Cause Hypomyelination with Brain Stem and Spinal Cord Involvement and Leg Spasticity. American Journal of Human Genetics, 2013, 92, 774-780.	6.8	159
90	A De Novo Mutation in the β -Tubulin Gene TUBB4A Results in the Leukoencephalopathy Hypomyelination with Atrophy of the Basal Ganglia and Cerebellum. American Journal of Human Genetics, 2013, 92, 767-773.	6.8	166

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91	Clinical and molecular characterization of HER2 amplified-pancreatic cancer. <i>Genome Medicine</i> , 2013, 5, .	9.9	102
92	Neuropilin-2 Promotes Extravasation and Metastasis by Interacting with Endothelial $\alpha 5$ Integrin. <i>Cancer Research</i> , 2013, 73, 4579-4590.	0.6	86
93	Integration-Free Induced Pluripotent Stem Cells Model Genetic and Neural Developmental Features of Down Syndrome Etiology. <i>Stem Cells</i> , 2013, 31, 467-478.	3.3	118
94	Identification of Unsafe Human Induced Pluripotent Stem Cell Lines Using a Robust Surrogate Assay for Pluripotency. <i>Stem Cells</i> , 2013, 31, 1498-1510.	3.3	20
95	miR-139-5p is a regulator of metastatic pathways in breast cancer. <i>Rna</i> , 2013, 19, 1767-1780.	3.9	125
96	MicroRNA-182-5p targets a network of genes involved in DNA repair. <i>Rna</i> , 2013, 19, 230-242.	3.9	101
97	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.	3.0	28
98	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	64
99	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.	4.8	35
100	Somatic Point Mutation Calling in Low Cellularity Tumors. <i>PLoS ONE</i> , 2013, 8, e74380.	2.5	61
101	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	58
102	Stromal Protein <i>Ecm1</i> Regulates Ureteric Bud Patterning and Branching. <i>PLoS ONE</i> , 2013, 8, e84155.	2.5	31
103	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, .		0
104	PINA v2.0: mining interactome modules. <i>Nucleic Acids Research</i> , 2012, 40, D862-D865.	16.2	279
105	The deubiquitinase USP9X suppresses pancreatic ductal adenocarcinoma. <i>Nature</i> , 2012, 486, 266-270.	40.1	270
106	Identification of molecular compartments and genetic circuitry in the developing mammalian kidney. <i>Development (Cambridge)</i> , 2012, 139, 1863-1873.	3.0	49
107	<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.	7.7	184
108	RON is not a prognostic marker for resectable pancreatic cancer. <i>BMC Cancer</i> , 2012, 12, .	3.0	15

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109	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. <i>Nature</i> , 2012, 491, 399-405.	40.1	1,657
110	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, .	7.7	244
111	Integrated genome analysis suggests that most conserved non-coding sequences are regulatory factor binding sites. <i>Nucleic Acids Research</i> , 2012, 40, 7858-7869.	16.2	33
112	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.	0.6	98
113	Corrigendum to "Comprehensive transcriptome and immunophenotype analysis of renal and cardiac MSC-like populations supports strong congruence with bone marrow MSC despite maintenance of distinct identities" [Stem Cell. 8 (2012) 58-73]. <i>Stem Cell Research</i> , 2012, 9, 58.	0.6	1
114	Identification of Novel Markers of Mouse Fetal Ovary Development. <i>PLoS ONE</i> , 2012, 7, e41683.	2.5	38
115	qpure: A Tool to Estimate Tumor Cellularity from Genome-Wide Single-Nucleotide Polymorphism Profiles. <i>PLoS ONE</i> , 2012, 7, e45835.	2.5	85
116	Abstract 5071: The genomic landscape of pancreatic cancer: from discovery to patient care. <i>Cancer Research</i> , 2012, 72, 5071-5071.	0.6	0
117	Sequencing transcriptomes in toto. <i>Integrative Biology (United Kingdom)</i> , 2011, 3, 522.	1.4	16
118	MicroRNAs and their isomiRs function cooperatively to target common biological pathways. <i>Genome Biology</i> , 2011, 12, .	8.4	280
119	Molecular diagnostics in pancreatic cancer. , 2011, , 20-35.		0
120	Identification of Anchor Genes during Kidney Development Defines Ontological Relationships, Molecular Subcompartments and Regulatory Pathways. <i>PLoS ONE</i> , 2011, 6, e17286.	2.5	70
121	A High-Throughput Platform for Lentiviral Overexpression Screening of the Human ORFeome. <i>PLoS ONE</i> , 2011, 6, e20057.	2.5	41
122	Phasevarion Mediated Epigenetic Gene Regulation in <i>Helicobacter pylori</i> . <i>PLoS ONE</i> , 2011, 6, e27569.	2.5	94
123	Refining transcriptional programs in kidney development by integration of deep RNA-sequencing and array-based spatial profiling. <i>BMC Genomics</i> , 2011, 12, .	3.2	25
124	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.	4.6	23
125	The uniqueome: a mappability resource for short-tag sequencing. <i>Bioinformatics</i> , 2011, 27, 272-274.	5.0	52
126	X-MATE: a flexible system for mapping short read data. <i>Bioinformatics</i> , 2011, 27, 580-581.	5.0	9

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127	Manganese regulation of virulence factors and oxidative stress resistance in <i>Neisseria gonorrhoeae</i> . <i>Journal of Proteomics</i> , 2010, 73, 899-916.	2.5	32
128	Vitamin C Promotes Widespread Yet Specific DNA Demethylation of the Epigenome in Human Embryonic Stem Cells. <i>Stem Cells</i> , 2010, 28, 1848-1855.	3.3	145
129	Ascorbate Promotes Epigenetic Activation of CD30 in Human Embryonic Stem Cells. <i>Stem Cells</i> , 2010, 28, 1782-1793.	3.3	40
130	International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998.	40.1	1,859
131	Simplifying complexity. <i>Nature Methods</i> , 2010, 7, 793-795.	14.5	1
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	Regulated post-transcriptional RNA cleavage diversifies the eukaryotic transcriptome. <i>Genome Research</i> , 2010, 20, 1639-1650.	4.6	71
134	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.	3.3	7
135	A global role for KLF1 in erythropoiesis revealed by ChIP-seq in primary erythroid cells. <i>Genome Research</i> , 2010, 20, 1052-1063.	4.6	174
136	Redirection of renal mesenchyme to stromal and chondrocytic fates in the presence of TGF- β 2. <i>Differentiation</i> , 2010, 79, 272-284.	2.4	6
137	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 140, 744-752.	35.1	584
138	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.	1.9	24
139	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	45
140	Transcriptome-Wide Prediction of miRNA Targets in Human and Mouse Using FASTH. <i>PLoS ONE</i> , 2009, 4, e5745.	2.5	24
141	Phasevarions Mediate Random Switching of Gene Expression in Pathogenic <i>Neisseria</i> . <i>PLoS Pathogens</i> , 2009, 5, e1000400.	4.5	140
142	GUIDMAP - An Online GenitoUrinary Resource. <i>Nature Precedings</i> , 2009, , .	0.1	0
143	Genome-Wide Identification of Long Noncoding RNAs in CD8+ T Cells. <i>Journal of Immunology</i> , 2009, 182, 7738-7748.	0.6	196
144	Probabilistic resolution of multi-mapping reads in massively parallel sequencing data using MuMRRescueLite. <i>Bioinformatics</i> , 2009, 25, 2613-2614.	5.0	32

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145	NRED: a database of long noncoding RNA expression. <i>Nucleic Acids Research</i> , 2009, 37, D122-D126.	16.2	228
146	RNA-MATE: a recursive mapping strategy for high-throughput RNA-sequencing data. <i>Bioinformatics</i> , 2009, 25, 2615-2616.	5.0	38
147	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.	3.3	63
148	Tiny RNAs associated with transcription start sites in animals. <i>Nature Genetics</i> , 2009, 41, 572-578.	16.3	288
149	The regulated retrotransposon transcriptome of mammalian cells. <i>Nature Genetics</i> , 2009, 41, 563-571.	16.3	642
150	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	16.3	362
151	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.	1.9	212
152	07-P023 GUDMAP – An online genitourinary resource. <i>Mechanisms of Development</i> , 2009, 126, S143.	2.6	0
153	Genome Sequencing Approaches and Successes. <i>Methods in Molecular Biology</i> , 2009, , 345-358.	0.0	20
154	Setting CAGE Tags in a Genomic Context. , 2009, , 93-100.		0
155	Subtypes of familial breast tumours revealed by expression and copy number profiling. <i>Breast Cancer Research and Treatment</i> , 2009, 123, 661-677.	2.5	78
156	Minimum information specification for in situ hybridization and immunohistochemistry experiments (MISFISHIE). <i>Nature Biotechnology</i> , 2008, 26, 305-312.	18.1	101
157	Stem cell transcriptome profiling via massive-scale mRNA sequencing. <i>Nature Methods</i> , 2008, 5, 613-619.	14.5	837
158	Transcriptome content and dynamics at single-nucleotide resolution. <i>Genome Biology</i> , 2008, 9, 234.	14.0	104
159	The miR-17-5p microRNA is a key regulator of the G1/S phase cell cycle transition. <i>Genome Biology</i> , 2008, 9, R127.	14.0	249
160	Kidney transcriptome reveals altered steroid homeostasis in NaS1 sulfate transporter null mice. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2008, 112, 55-62.	2.4	16
161	A rescue strategy for multimapping short sequence tags refines surveys of transcriptional activity by CAGE. <i>Genomics</i> , 2008, 91, 281-288.	2.7	76
162	Atlas of Gene Expression in the Developing Kidney at Microanatomic Resolution. <i>Developmental Cell</i> , 2008, 15, 781-791.	7.8	175

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163	Long noncoding RNAs in mouse embryonic stem cell pluripotency and differentiation. <i>Genome Research</i> , 2008, 18, 1433-1445.	4.6	641
164	GUIDMAP. <i>Journal of the American Society of Nephrology: JASN</i> , 2008, 19, 667-671.	0.4	206
165	BRCA1 and BRCA2 Missense Variants of High and Low Clinical Significance Influence Lymphoblastoid Cell Line Post-Irradiation Gene Expression. <i>PLoS Genetics</i> , 2008, 4, e1000080.	3.3	11
166	SEQUENCING THE TRANSCRIPTOME <i>IN TOTO</i> , 2008, , .		0
167	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.	1.9	181
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