

# Sean M Grimmond

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

228  
papers

37,215  
citations

79  
h-index

192  
g-index

260  
ext. papers

43,988  
ext. citations

11.9  
avg, IF

5.94  
L-index

#	Paper	IF	Citations
228	ROR1 and ROR2 expression in pancreatic cancer. <i>BMC Cancer</i> , <b>2021</b> , 21, 1199	4.8	0
227	PRMT5: An Emerging Target for Pancreatic Adenocarcinoma. <i>Cancers</i> , <b>2021</b> , 13,	6.6	1
226	The Diverse Applications of Pancreatic Ductal Adenocarcinoma Organoids. <i>Cancers</i> , <b>2021</b> , 13,	6.6	1
225	Clinical utility of whole-genome sequencing in precision oncology. <i>Seminars in Cancer Biology</i> , <b>2021</b> ,	12.7	7
224	Analytical demands to use whole-genome sequencing in precision oncology. <i>Seminars in Cancer Biology</i> , <b>2021</b> ,	12.7	3
223	Clinical interpretation of whole-genome and whole-transcriptome sequencing for precision oncology. <i>Seminars in Cancer Biology</i> , <b>2021</b> ,	12.7	3
222	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. <i>Communications Biology</i> , <b>2021</b> , 4, 155	6.7	11
221	Novel RET Fusion Predicts Response to Selective RET Inhibition With Selpercatinib in Malignant Pheochromocytoma.. <i>JCO Precision Oncology</i> , <b>2021</b> , 5, 1160-1165	3.6	1
220	Genomic and Molecular Analyses Identify Molecular Subtypes of Pancreatic Cancer Recurrence. <i>Gastroenterology</i> , <b>2021</b> ,	13.3	1
219	Intravital imaging technology guides FAK-mediated priming in pancreatic cancer precision medicine according to Merlin status. <i>Science Advances</i> , <b>2021</b> , 7, eabh0363	14.3	5
218	RAF1 rearrangements are common in pancreatic acinar cell carcinomas. <i>Modern Pathology</i> , <b>2020</b> , 33, 1811-1821	9.8	4
217	HNF4A and GATA6 Loss Reveals Therapeutically Actionable Subtypes in Pancreatic Cancer. <i>Cell Reports</i> , <b>2020</b> , 31, 107625	10.6	34
216	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , <b>2020</b> , 11, 4330	17.4	23
215	Targeting enhancer switching overcomes non-genetic drug resistance in acute myeloid leukaemia. <i>Nature Communications</i> , <b>2019</b> , 10, 2723	17.4	67
214	Setting CAGE Tags in a Genomic Context <b>2019</b> , 93-100		
213	Glioma through the looking GLASS: molecular evolution of diffuse gliomas and the Glioma Longitudinal Analysis Consortium. <i>Neuro-Oncology</i> , <b>2018</b> , 20, 873-884	1	63
212	Telomere sequence content can be used to determine ALT activity in tumours. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 4903-4918	20.1	26

211	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> , <b>2018</b> , 24, 569-580	12.9	46
210	Tailored first-line and second-line CDK4-targeting treatment combinations in mouse models of pancreatic cancer. <i>Gut</i> , <b>2018</b> , 67, 2142-2155	19.2	71
209	Recurrent loss of heterozygosity correlates with clinical outcome in pancreatic neuroendocrine cancer. <i>Npj Genomic Medicine</i> , <b>2018</b> , 3, 18	6.2	23
208	Exome-Wide Association Study of Pancreatic Cancer Risk. <i>Gastroenterology</i> , <b>2018</b> , 154, 719-722.e3	13.3	27
207	Mutations in Low-Grade Serous Ovarian Cancer and Response to BRAF Inhibition.. <i>JCO Precision Oncology</i> , <b>2018</b> , 2, 1-14	3.6	9
206	Whole-genome landscape of pancreatic neuroendocrine tumours. <i>Nature</i> , <b>2017</b> , 543, 65-71	50.4	482
205	Recurrent noncoding regulatory mutations in pancreatic ductal adenocarcinoma. <i>Nature Genetics</i> , <b>2017</b> , 49, 825-833	36.3	41
204	Whole-genome landscapes of major melanoma subtypes. <i>Nature</i> , <b>2017</b> , 545, 175-180	50.4	662
203	Mitochondrial mutations and metabolic adaptation in pancreatic cancer. <i>Cancer &amp; Metabolism</i> , <b>2017</b> , 5, 2	5.4	40
202	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , <b>2017</b> , 32, 185-203.e13	21.5	1396
201	and Mutations Co-occur and Cooperate in Low-Grade Serous Ovarian Carcinomas. <i>Cancer Research</i> , <b>2017</b> , 77, 4268-4278	10.1	32
200	Lost in translation: returning germline genetic results in genome-scale cancer research. <i>Genome Medicine</i> , <b>2017</b> , 9, 41	14.4	18
199	Hypermutation In Pancreatic Cancer. <i>Gastroenterology</i> , <b>2017</b> , 152, 68-74.e2	13.3	130
198	Dual targeting of p53 and c-MYC selectively eliminates leukaemic stem cells. <i>Nature</i> , <b>2016</b> , 534, 341-6	50.4	141
197	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> , <b>2016</b> , 37, 356-65	4.6	30
196	Ampullary Cancers Harbor ELF3 Tumor Suppressor Gene Mutations and Exhibit Frequent WNT Dysregulation. <i>Cell Reports</i> , <b>2016</b> , 14, 907-919	10.6	75
195	Genomic analyses identify molecular subtypes of pancreatic cancer. <i>Nature</i> , <b>2016</b> , 531, 47-52	50.4	1785
194	Whole exome sequencing in patients with white matter abnormalities. <i>Annals of Neurology</i> , <b>2016</b> , 79, 1031-1037	9.4	86

193	Mutational signatures in esophageal adenocarcinoma define etiologically distinct subgroups with therapeutic relevance. <i>Nature Genetics</i> , <b>2016</b> , 48, 1131-41	36.3	233
192	Whole genomes redefine the mutational landscape of pancreatic cancer. <i>Nature</i> , <b>2015</b> , 518, 495-501	50.4	1579
191	PGTools: A Software Suite for Proteogenomic Data Analysis and Visualization. <i>Journal of Proteome Research</i> , <b>2015</b> , 14, 2255-66	5.6	47
190	New RAS-mutant pancreatic adenocarcinoma with combined BRAF and MEK inhibition for metastatic melanoma. <i>Journal of Clinical Oncology</i> , <b>2015</b> , 33, e52-6	2.2	25
189	Precision Medicine for Advanced Pancreas Cancer: The Individualized Molecular Pancreatic Cancer Therapy (IMPaCT) Trial. <i>Clinical Cancer Research</i> , <b>2015</b> , 21, 2029-37	12.9	171
188	A biphasic epigenetic switch controls immunoevasion, virulence and niche adaptation in non-typeable <i>Haemophilus influenzae</i> . <i>Nature Communications</i> , <b>2015</b> , 6, 7828	17.4	81
187	Mutations in the voltage-gated potassium channel gene <i>KCNH1</i> cause Temple-Baraitser syndrome and epilepsy. <i>Nature Genetics</i> , <b>2015</b> , 47, 73-7	36.3	91
186	SOX9 regulates ERBB signalling in pancreatic cancer development. <i>Gut</i> , <b>2015</b> , 64, 1790-9	19.2	57
185	Integrated genomic and transcriptomic analysis of human brain metastases identifies alterations of potential clinical significance. <i>Journal of Pathology</i> , <b>2015</b> , 237, 363-78	9.4	72
184	Whole-genome characterization of chemoresistant ovarian cancer. <i>Nature</i> , <b>2015</b> , 521, 489-94	50.4	890
183	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. <i>Nature Communications</i> , <b>2015</b> , 6, 10001	17.4	199
182	Pancreatic cancer genomics: where can the science take us?. <i>Clinical Genetics</i> , <b>2015</b> , 88, 213-9	4	10
181	Towards the systematic mapping and engineering of the protein prenylation machinery in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , <b>2015</b> , 10, e0120716	3.7	9
180	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> , <b>2015</b> , 10, e0125232	3.7	16
179	Recommendations for Accurate Resolution of Gene and Isoform Allele-Specific Expression in RNA-Seq Data. <i>PLoS ONE</i> , <b>2015</b> , 10, e0126911	3.7	15
178	Transcriptional switching in macrophages associated with the peritoneal foreign body response. <i>Immunology and Cell Biology</i> , <b>2014</b> , 92, 518-26	5	33
177	Mining the genomes of exceptional responders. <i>Nature Reviews Cancer</i> , <b>2014</b> , 14, 291-2	31.3	35
176	Mutant p53 drives pancreatic cancer metastasis through cell-autonomous PDGF receptor $\beta$ signaling. <i>Cell</i> , <b>2014</b> , 157, 382-394	56.2	325

175	Interaction of c-Myb with p300 is required for the induction of acute myeloid leukemia (AML) by human AML oncogenes. <i>Blood</i> , <b>2014</b> , 123, 2682-90	2.2	81
174	In vivo evolution of antimicrobial resistance in a series of Staphylococcus aureus patient isolates: the entire picture or a cautionary tale?. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2014</b> , 69, 363-7	5.1	16
173	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. <i>Nature Communications</i> , <b>2014</b> , 5, 5224	17.4	176
172	Returning individual research results for genome sequences of pancreatic cancer. <i>Genome Medicine</i> , <b>2014</b> , 6, 42	14.4	18
171	Pancreatic cancer genomics. <i>Current Opinion in Genetics and Development</i> , <b>2014</b> , 24, 74-81	4.9	40
170	Identification of a novel de novo p.Phe932Ile KCNT1 mutation in a patient with leukoencephalopathy and severe epilepsy. <i>Pediatric Neurology</i> , <b>2014</b> , 50, 112-4	2.9	49
169	SnapShot-Seq: a method for extracting genome-wide, in vivo mRNA dynamics from a single total RNA sample. <i>PLoS ONE</i> , <b>2014</b> , 9, e89673	3.7	34
168	Rapid identification of a novel complex I MT-ND3 m.10134C>A mutation in a Leigh syndrome patient. <i>PLoS ONE</i> , <b>2014</b> , 9, e104879	3.7	5
167	A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. <i>BioTechniques</i> , <b>2014</b> , 57, 31-8	2.5	
166	PRMT2 and ROR1 expression are associated with breast cancer survival outcomes. <i>Molecular Endocrinology</i> , <b>2014</b> , 28, 1166-85		36
165	Stratified Medicine for Pancreatic Cancer <b>2014</b> , 807-814		
164	Clinical and pathologic features of familial pancreatic cancer. <i>Cancer</i> , <b>2014</b> , 120, 3669-75	6.4	38
163	Ferrets exclusively synthesize Neu5Ac and express naturally humanized influenza A virus receptors. <i>Nature Communications</i> , <b>2014</b> , 5, 5750	17.4	75
162	Small RNA changes en route to distinct cellular states of induced pluripotency. <i>Nature Communications</i> , <b>2014</b> , 5, 5522	17.4	43
161	Divergent reprogramming routes lead to alternative stem-cell states. <i>Nature</i> , <b>2014</b> , 516, 192-7	50.4	98
160	Genome-wide characterization of the routes to pluripotency. <i>Nature</i> , <b>2014</b> , 516, 198-206	50.4	153
159	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> , <b>2014</b> , 135, 1110-8	7.5	149
158	An epigenomic roadmap to induced pluripotency reveals DNA methylation as a reprogramming modulator. <i>Nature Communications</i> , <b>2014</b> , 5, 5619	17.4	85

157	Proteome adaptation in cell reprogramming proceeds via distinct transcriptional networks. <i>Nature Communications</i> , <b>2014</b> , 5, 5613	17.4	37
156	Targeting mTOR dependency in pancreatic cancer. <i>Gut</i> , <b>2014</b> , 63, 1481-9	19.2	93
155	Gemcitabine and CHK1 inhibition potentiate EGFR-directed radioimmunotherapy against pancreatic ductal adenocarcinoma. <i>Clinical Cancer Research</i> , <b>2014</b> , 20, 3187-97	12.9	30
154	Minor class splicing shapes the zebrafish transcriptome during development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 3062-7	11.5	45
153	Imperfect centered miRNA binding sites are common and can mediate repression of target mRNAs. <i>Genome Biology</i> , <b>2014</b> , 15, R51	18.3	90
152	Understanding pancreatic cancer genomes. <i>Journal of Hepato-Biliary-Pancreatic Sciences</i> , <b>2013</b> , 20, 549-568		26
151	Signatures of mutational processes in human cancer. <i>Nature</i> , <b>2013</b> , 500, 415-21	50.4	5895
150	Mutations in DARS cause hypomyelination with brain stem and spinal cord involvement and leg spasticity. <i>American Journal of Human Genetics</i> , <b>2013</b> , 92, 774-80	11	127
149	A de novo mutation in the $\beta$ -tubulin gene TUBB4A results in the leukoencephalopathy hypomyelination with atrophy of the basal ganglia and cerebellum. <i>American Journal of Human Genetics</i> , <b>2013</b> , 92, 767-73	11	133
148	Assessment of transcript reconstruction methods for RNA-seq. <i>Nature Methods</i> , <b>2013</b> , 10, 1177-84	21.6	477
147	Clinical and molecular characterization of HER2 amplified-pancreatic cancer. <i>Genome Medicine</i> , <b>2013</b> , 5, 78	14.4	82
146	Novel cancer drivers: mining the kinome. <i>Genome Medicine</i> , <b>2013</b> , 5, 19	14.4	2
145	Neuropilin-2 promotes extravasation and metastasis by interacting with endothelial $\beta$ integrin. <i>Cancer Research</i> , <b>2013</b> , 73, 4579-4590	10.1	65
144	Caveolin-1 is necessary for hepatic oxidative lipid metabolism: evidence for crosstalk between caveolin-1 and bile acid signaling. <i>Cell Reports</i> , <b>2013</b> , 4, 238-47	10.6	43
143	Integration-free induced pluripotent stem cells model genetic and neural developmental features of down syndrome etiology. <i>Stem Cells</i> , <b>2013</b> , 31, 467-78	5.8	107
142	Identification of unsafe human induced pluripotent stem cell lines using a robust surrogate assay for pluripotency. <i>Stem Cells</i> , <b>2013</b> , 31, 1498-510	5.8	20
141	miR-139-5p is a regulator of metastatic pathways in breast cancer. <i>Rna</i> , <b>2013</b> , 19, 1767-80	5.8	121
140	MicroRNA-182-5p targets a network of genes involved in DNA repair. <i>Rna</i> , <b>2013</b> , 19, 230-42	5.8	95

139	Characterization of an 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> , <b>2013</b> , 195, 2632-41	3.5	22
138	MicroRNAs-140-5p/140-3p modulate Leydig cell numbers in the developing mouse testis. <i>Biology of Reproduction</i> , <b>2013</b> , 88, 143	3.9	55
137	Proteogenomic analysis of <i>Bradyrhizobium japonicum</i> USDA110 using GenoSuite, an automated multi-algorithmic pipeline. <i>Molecular and Cellular Proteomics</i> , <b>2013</b> , 12, 3388-97	7.6	35
136	Somatic point mutation calling in low cellularity tumors. <i>PLoS ONE</i> , <b>2013</b> , 8, e74380	3.7	49
135	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> , <b>2013</b> , 8, e59920	3.7	55
134	Stromal protein Ecm1 regulates ureteric bud patterning and branching. <i>PLoS ONE</i> , <b>2013</b> , 8, e84155	3.7	29
133	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> , <b>2012</b> , 8, 58-73	1.6	99
132	RON is not a prognostic marker for resectable pancreatic cancer. <i>BMC Cancer</i> , <b>2012</b> , 12, 395	4.8	16
131	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. <i>Nature</i> , <b>2012</b> , 491, 399-404	14.27	1427
130	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> , <b>2012</b> , 109, E944-53	11.5	212
129	Integrated genome analysis suggests that most conserved non-coding sequences are regulatory factor binding sites. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, 7858-69	20.1	26
128	PINA v2.0: mining interactome modules. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D862-5	20.1	267
127	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> , <b>2012</b> , 56, 3380-3	5.9	19
126	The deubiquitinase USP9X suppresses pancreatic ductal adenocarcinoma. <i>Nature</i> , <b>2012</b> , 486, 266-70	50.4	253
125	Identification of molecular compartments and genetic circuitry in the developing mammalian kidney. <i>Development (Cambridge)</i> , <b>2012</b> , 139, 1863-73	6.6	47
124	Sleeping Beauty mutagenesis reveals cooperating mutations and pathways in pancreatic adenocarcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 5934-41	11.5	179
123	Identification of novel markers of mouse fetal ovary development. <i>PLoS ONE</i> , <b>2012</b> , 7, e41683	3.7	39
122	qpure: A tool to estimate tumor cellularity from genome-wide single-nucleotide polymorphism profiles. <i>PLoS ONE</i> , <b>2012</b> , 7, e45835	3.7	80

121	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> , <b>2012</b> , 120, 2402-2402	2.2	
120	Sequencing transcriptomes in toto. <i>Integrative Biology (United Kingdom)</i> , <b>2011</b> , 3, 522-8	3.7	16
119	MicroRNAs and their isomiRs function cooperatively to target common biological pathways. <i>Genome Biology</i> , <b>2011</b> , 12, R126	18.3	246
118	Molecular diagnostics in pancreatic cancer <b>2011</b> , 20-35		
117	Identification of anchor genes during kidney development defines ontological relationships, molecular subcompartments and regulatory pathways. <i>PLoS ONE</i> , <b>2011</b> , 6, e17286	3.7	66
116	A high-throughput platform for lentiviral overexpression screening of the human ORFeome. <i>PLoS ONE</i> , <b>2011</b> , 6, e20057	3.7	39
115	Phasevarion mediated epigenetic gene regulation in <i>Helicobacter pylori</i> . <i>PLoS ONE</i> , <b>2011</b> , 6, e27569	3.7	79
114	Analysis of Brca1-deficient mouse mammary glands reveals reciprocal regulation of Brca1 and c-kit. <i>Oncogene</i> , <b>2011</b> , 30, 1597-607	9.2	20
113	Refining transcriptional programs in kidney development by integration of deep RNA-sequencing and array-based spatial profiling. <i>BMC Genomics</i> , <b>2011</b> , 12, 441	4.5	25
112	Deep-transcriptome and ribonome sequencing redefines the molecular networks of pluripotency and the extracellular space in human embryonic stem cells. <i>Genome Research</i> , <b>2011</b> , 21, 2014-25	9.7	22
111	The uniqueome: a mappability resource for short-tag sequencing. <i>Bioinformatics</i> , <b>2011</b> , 27, 272-4	7.2	58
110	X-MATE: a flexible system for mapping short read data. <i>Bioinformatics</i> , <b>2011</b> , 27, 580-1	7.2	10
109	International network of cancer genome projects. <i>Nature</i> , <b>2010</b> , 464, 993-8	50.4	1613
108	Profiling gene expression induced by protease-activated receptor 2 (PAR2) activation in human kidney cells. <i>PLoS ONE</i> , <b>2010</b> , 5, e13809	3.7	37
107	Regulated post-transcriptional RNA cleavage diversifies the eukaryotic transcriptome. <i>Genome Research</i> , <b>2010</b> , 20, 1639-50	9.7	66
106	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> , <b>2010</b> , 6, e1000850	6	7
105	A global role for KLF1 in erythropoiesis revealed by ChIP-seq in primary erythroid cells. <i>Genome Research</i> , <b>2010</b> , 20, 1052-63	9.7	150
104	Redirection of renal mesenchyme to stromal and chondrocytic fates in the presence of TGF-beta2. <i>Differentiation</i> , <b>2010</b> , 79, 272-84	3.5	6



103	Gene expression profile of the fibrotic response in the peritoneal cavity. <i>Differentiation</i> , <b>2010</b> , 79, 232-43,5	43.5	29
102	An atlas of combinatorial transcriptional regulation in mouse and man. <i>Cell</i> , <b>2010</b> , 140, 744-52	56.2	555
101	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , <b>2010</b> , 141, 369	56.2	3
100	Comparative gene expression analysis of genital tubercle development reveals a putative appendicular Wnt7 network for the epidermal differentiation. <i>Developmental Biology</i> , <b>2010</b> , 344, 1071-87 <sup>3,1</sup>	37.1	24
99	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> , <b>2010</b> , 19, 1637-48	4.4	45
98	Subtypes of familial breast tumours revealed by expression and copy number profiling. <i>Breast Cancer Research and Treatment</i> , <b>2010</b> , 123, 661-77	4.4	81
97	Manganese regulation of virulence factors and oxidative stress resistance in <i>Neisseria gonorrhoeae</i> . <i>Journal of Proteomics</i> , <b>2010</b> , 73, 899-916	3.9	26
96	Vitamin C promotes widespread yet specific DNA demethylation of the epigenome in human embryonic stem cells. <i>Stem Cells</i> , <b>2010</b> , 28, 1848-55	5.8	131
95	Ascorbate promotes epigenetic activation of CD30 in human embryonic stem cells. <i>Stem Cells</i> , <b>2010</b> , 28, 1782-93	5.8	40
94	The clinical potential and challenges of sequencing cancer genomes for personalized medical genomics. <i>IDrugs: the Investigational Drugs Journal</i> , <b>2010</b> , 13, 778-81		2
93	Transcriptome-wide prediction of miRNA targets in human and mouse using FASTH. <i>PLoS ONE</i> , <b>2009</b> , 4, e5745	3.7	20
92	A continuum of cell states spans pluripotency and lineage commitment in human embryonic stem cells. <i>PLoS ONE</i> , <b>2009</b> , 4, e7708	3.7	123
91	Phasevarions mediate random switching of gene expression in pathogenic <i>Neisseria</i> . <i>PLoS Pathogens</i> , <b>2009</b> , 5, e1000400	7.6	125
90	Genome-wide identification of long noncoding RNAs in CD8+ T cells. <i>Journal of Immunology</i> , <b>2009</b> , 182, 7738-48	5.3	189
89	Probabilistic resolution of multi-mapping reads in massively parallel sequencing data using MuMRescueLite. <i>Bioinformatics</i> , <b>2009</b> , 25, 2613-4	7.2	32
88	NRED: a database of long noncoding RNA expression. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D122-6	20.1	214
87	Reduced mucin sulfonation and impaired intestinal barrier function in the hyposulfataemic NaS1 null mouse. <i>Gut</i> , <b>2009</b> , 58, 910-9	19.2	77
86	RNA-MATE: a recursive mapping strategy for high-throughput RNA-sequencing data. <i>Bioinformatics</i> , <b>2009</b> , 25, 2615-6	7.2	42

85	Identification of human embryonic stem cell surface markers by combined membrane-polysome translation state array analysis and immunotranscriptional profiling. <i>Stem Cells</i> , <b>2009</b> , 27, 2446-56	5.8	64
84	Tiny RNAs associated with transcription start sites in animals. <i>Nature Genetics</i> , <b>2009</b> , 41, 572-8	36.3	302
83	The regulated retrotransposon transcriptome of mammalian cells. <i>Nature Genetics</i> , <b>2009</b> , 41, 563-71	36.3	601
82	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , <b>2009</b> , 41, 553-62	36.3	356
81	Atlas of Gene Expression in the Developing Kidney at Microanatomic Resolution. <i>Developmental Cell</i> , <b>2009</b> , 16, 482	10.2	2
80	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> , <b>2009</b> , 332, 273-86 <sup>1</sup>	32.1	196
79	Genome sequencing approaches and successes. <i>Methods in Molecular Biology</i> , <b>2009</b> , 513, 345-58	1.4	22
78	Setting CAGE Tags in a Genomic Context <b>2009</b> , 93-100		
77	Minimum information specification for in situ hybridization and immunohistochemistry experiments (MISFISHIE). <i>Nature Biotechnology</i> , <b>2008</b> , 26, 305-12	44.5	97
76	Stem cell transcriptome profiling via massive-scale mRNA sequencing. <i>Nature Methods</i> , <b>2008</b> , 5, 613-9	21.6	841
75	Transcriptome content and dynamics at single-nucleotide resolution. <i>Genome Biology</i> , <b>2008</b> , 9, 234	18.3	97
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