

# Sean M Grimmond

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/6272893/sean-m-grimmond-publications-by-citations.pdf>

**Version:** 2024-04-17

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Signatures of mutational processes in human cancer. <i>Nature</i> , <b>2013</b> , 500, 415-21	50.4	5895
227	The transcriptional landscape of the mammalian genome. <i>Science</i> , <b>2005</b> , 309, 1559-63	33.3	2807
226	Genomic analyses identify molecular subtypes of pancreatic cancer. <i>Nature</i> , <b>2016</b> , 531, 47-52	50.4	1785
225	International network of cancer genome projects. <i>Nature</i> , <b>2010</b> , 464, 993-8	50.4	1613
224	Whole genomes redefine the mutational landscape of pancreatic cancer. <i>Nature</i> , <b>2015</b> , 518, 495-501	50.4	1579
223	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. <i>Nature</i> , <b>2012</b> , 491, 399-404	50.4	1427
222	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , <b>2002</b> , 420, 563-73	50.4	1350
221	Genome-wide analysis of mammalian promoter architecture and evolution. <i>Nature Genetics</i> , <b>2006</b> , 38, 626-35	36.3	1021
220	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , <b>2017</b> , 32, 185-203	50.4	13896
219	Whole-genome characterization of chemoresistant ovarian cancer. <i>Nature</i> , <b>2015</b> , 521, 489-94	50.4	890
218	Stem cell transcriptome profiling via massive-scale mRNA sequencing. <i>Nature Methods</i> , <b>2008</b> , 5, 613-9	21.6	841
217	Whole-genome landscapes of major melanoma subtypes. <i>Nature</i> , <b>2017</b> , 545, 175-180	50.4	662
216	Long noncoding RNAs in mouse embryonic stem cell pluripotency and differentiation. <i>Genome Research</i> , <b>2008</b> , 18, 1433-45	9.7	608
215	The regulated retrotransposon transcriptome of mammalian cells. <i>Nature Genetics</i> , <b>2009</b> , 41, 563-71	36.3	601
214	An atlas of combinatorial transcriptional regulation in mouse and man. <i>Cell</i> , <b>2010</b> , 140, 744-52	56.2	555
213	Whole-genome landscape of pancreatic neuroendocrine tumours. <i>Nature</i> , <b>2017</b> , 543, 65-71	50.4	482
212	Assessment of transcript reconstruction methods for RNA-seq. <i>Nature Methods</i> , <b>2013</b> , 10, 1177-84	21.6	477

211	Experimental validation of the regulated expression of large numbers of non-coding RNAs from the mouse genome. <i>Genome Research</i> , <b>2006</b> , 16, 11-9	9.7	407
210	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
209	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
208	Tiny RNAs associated with transcription start sites in animals. <i>Nature Genetics</i> , <b>2009</b> , 41, 572-8	36.3	302
207	PINA v2.0: mining interactome modules. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D862-5	20.1	267
206	The deubiquitinase USP9X suppresses pancreatic ductal adenocarcinoma. <i>Nature</i> , <b>2012</b> , 486, 266-70	50.4	253
205	MicroRNAs and their isomiRs function cooperatively to target common biological pathways. <i>Genome Biology</i> , <b>2011</b> , 12, R126	18.3	246
204	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
203	The miR-17-5p microRNA is a key regulator of the G1/S phase cell cycle transition. <i>Genome Biology</i> , <b>2008</b> , 9, R127	18.3	228
202	NRED: a database of long noncoding RNA expression. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D122-6	20.1	214
201	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> , <b>2000</b> , 86, E29-35	15.7	214
200	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
199	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
198	GUDMAP: the genitourinary developmental molecular anatomy project. <i>Journal of the American Society of Nephrology: JASN</i> , <b>2008</b> , 19, 667-71	12.7	197
197	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	31	196
196	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
195	Atlas of gene expression in the developing kidney at microanatomic resolution. <i>Developmental Cell</i> , <b>2008</b> , 15, 781-91	10.2	184
194	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

193	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. <i>Nature Communications</i> , <b>2014</b> , 5, 5224	17.4	176
192	Characterisation and trophic functions of murine embryonic macrophages based upon the use of a Csf1r-EGFP transgene reporter. <i>Developmental Biology</i> , <b>2007</b> , 308, 232-46	3.1	173
191	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
190	A global role for EKLF in definitive and primitive erythropoiesis. <i>Blood</i> , <b>2006</b> , 107, 3359-70	2.2	165
189	The abundance of short proteins in the mammalian proteome. <i>PLoS Genetics</i> , <b>2006</b> , 2, e52	6	159
188	Genome-wide characterization of the routes to pluripotency. <i>Nature</i> , <b>2014</b> , 516, 198-206	50.4	153
187	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
186	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
185	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> , <b>2005</b> , 102, 5547-51	11.5	149
184	Dual targeting of p53 and c-MYC selectively eliminates leukaemic stem cells. <i>Nature</i> , <b>2016</b> , 534, 341-6	50.4	141
183	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
182	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
181	Hypermutation In Pancreatic Cancer. <i>Gastroenterology</i> , <b>2017</b> , 152, 68-74.e2	13.3	130
180	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
179	Phasevarions mediate random switching of gene expression in pathogenic <i>Neisseria</i> . <i>PLoS Pathogens</i> , <b>2009</b> , 5, e1000400	7.6	125
178	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
177	Characterization of the mouse Men1 gene and its expression during development. <i>Oncogene</i> , <b>1998</b> , 17, 2485-93	9.2	122
176	miR-139-5p is a regulator of metastatic pathways in breast cancer. <i>Rna</i> , <b>2013</b> , 19, 1767-80	5.8	121

175	Identifying the molecular phenotype of renal progenitor cells. <i>Journal of the American Society of Nephrology: JASN</i> , <b>2004</b> , 15, 2344-57	12.7	110
174	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
173	Characterization of RasGRP2, a plasma membrane-targeted, dual specificity Ras/Rap exchange factor. <i>Journal of Biological Chemistry</i> , <b>2000</b> , 275, 32260-7	5.4	105
172	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> , <b>1998</b> , 83, 2621-2626	5.6	102
171	Novel genes regulated by Sonic Hedgehog in pluripotent mesenchymal cells. <i>Oncogene</i> , <b>2002</b> , 21, 8196-2005	10.5	101
170	Cloning and characterization of a novel human gene related to vascular endothelial growth factor. <i>Genome Research</i> , <b>1996</b> , 6, 124-31	9.7	100
169	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
168	Divergent reprogramming routes lead to alternative stem-cell states. <i>Nature</i> , <b>2014</b> , 516, 192-7	50.4	98
167	Minimum information specification for in situ hybridization and immunohistochemistry experiments (MISFISHIE). <i>Nature Biotechnology</i> , <b>2008</b> , 26, 305-12	44.5	97
166	Transcriptome content and dynamics at single-nucleotide resolution. <i>Genome Biology</i> , <b>2008</b> , 9, 234	18.3	97
165	MicroRNA-182-5p targets a network of genes involved in DNA repair. <i>Rna</i> , <b>2013</b> , 19, 230-42	5.8	95
164	Targeting mTOR dependency in pancreatic cancer. <i>Gut</i> , <b>2014</b> , 63, 1481-9	19.2	93
163	Mutations in the voltage-gated potassium channel gene KCNH1 cause Temple-Baraitser syndrome and epilepsy. <i>Nature Genetics</i> , <b>2015</b> , 47, 73-7	36.3	91
162	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> , <b>1998</b> , 7, 1713-24	5.6	91
161	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
160	Whole exome sequencing in patients with white matter abnormalities. <i>Annals of Neurology</i> , <b>2016</b> , 79, 1031-1037	9.4	86
159	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
158	Pax9 and Jagged1 act downstream of Gli3 in vertebrate limb development. <i>Mechanisms of Development</i> , <b>2005</b> , 122, 1218-33	1.7	84

157	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> , <b>2002</b> , 168, 44-50	5.3	84
156	Clinical and molecular characterization of HER2 amplified-pancreatic cancer. <i>Genome Medicine</i> , <b>2013</b> , 5, 78	14.4	82
155	A rescue strategy for multimapping short sequence tags refines surveys of transcriptional activity by CAGE. <i>Genomics</i> , <b>2008</b> , 91, 281-8	4.3	82
154	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> , <b>2000</b> , 9, 1553-60	5.6	82
153	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
152	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
151	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
150	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
149	Phasevarion mediated epigenetic gene regulation in <i>Helicobacter pylori</i> . <i>PLoS ONE</i> , <b>2011</b> , 6, e27569	3.7	79
148	Systematic characterization of the zinc-finger-containing proteins in the mouse transcriptome. <i>Genome Research</i> , <b>2003</b> , 13, 1430-42	9.7	79
147	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
146	Transcriptional analysis of early lineage commitment in human embryonic stem cells. <i>BMC Developmental Biology</i> , <b>2007</b> , 7, 12	3.1	76
145	Characterization of the OxyR regulon of <i>Neisseria gonorrhoeae</i> . <i>Molecular Microbiology</i> , <b>2007</b> , 63, 54-68	4.1	76
144	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
143	Ferrets exclusively synthesize Neu5Ac and express naturally humanized influenza A virus receptors. <i>Nature Communications</i> , <b>2014</b> , 5, 5750	17.4	75
142	Mouse proteome analysis. <i>Genome Research</i> , <b>2003</b> , 13, 1335-44	9.7	75
141	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
140	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

139	Targeting enhancer switching overcomes non-genetic drug resistance in acute myeloid leukaemia. <i>Nature Communications</i> , <b>2019</b> , 10, 2723	17.4	67
138	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
137	Regulated post-transcriptional RNA cleavage diversifies the eukaryotic transcriptome. <i>Genome Research</i> , <b>2010</b> , 20, 1639-50	9.7	66
136	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
135	The mouse secretome: functional classification of the proteins secreted into the extracellular environment. <i>Genome Research</i> , <b>2003</b> , 13, 1350-9	9.7	65
134	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
133	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
132	Alternate transcription of the Toll-like receptor signaling cascade. <i>Genome Biology</i> , <b>2006</b> , 7, R10	18.3	63
131	Cloning, mapping, and expression analysis of a gene encoding a novel mammalian EGF-related protein (SCUBE1). <i>Genomics</i> , <b>2000</b> , 70, 74-81	4.3	62
130	The uniqueome: a mappability resource for short-tag sequencing. <i>Bioinformatics</i> , <b>2011</b> , 27, 272-4	7.2	58
129	Temporal and spatial transcriptional programs in murine kidney development. <i>Physiological Genomics</i> , <b>2005</b> , 23, 159-71	3.6	58
128	SOX9 regulates ERBB signalling in pancreatic cancer development. <i>Gut</i> , <b>2015</b> , 64, 1790-9	19.2	57
127	Dynamic transcription programs during ES cell differentiation towards mesoderm in serum versus serum-free BMP4 culture. <i>BMC Genomics</i> , <b>2007</b> , 8, 365	4.5	57
126	PerR controls Mn-dependent resistance to oxidative stress in <i>Neisseria gonorrhoeae</i> . <i>Molecular Microbiology</i> , <b>2006</b> , 60, 401-16	4.1	57
125	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
124	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
123	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
122	Somatic point mutation calling in low cellularity tumors. <i>PLoS ONE</i> , <b>2013</b> , 8, e74380	3.7	49



121	The phospholipase C beta 3 gene located in the MEN1 region shows loss of expression in endocrine tumours. <i>Human Molecular Genetics</i> , <b>1994</b> , 3, 1775-81	5.6	48
120	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
119	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
118	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
117	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
116	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
115	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
114	Small RNA changes en route to distinct cellular states of induced pluripotency. <i>Nature Communications</i> , <b>2014</b> , 5, 5522	17.4	43
113	A global role for zebrafish klf4 in embryonic erythropoiesis. <i>Mechanisms of Development</i> , <b>2007</b> , 124, 762-74	7.4	43
112	RNA-MATE: a recursive mapping strategy for high-throughput RNA-sequencing data. <i>Bioinformatics</i> , <b>2009</b> , 25, 2615-6	7.2	42
111	Recurrent noncoding regulatory mutations in pancreatic ductal adenocarcinoma. <i>Nature Genetics</i> , <b>2017</b> , 49, 825-833	36.3	41
110	Genome-wide review of transcriptional complexity in mouse protein kinases and phosphatases. <i>Genome Biology</i> , <b>2006</b> , 7, R5	18.3	41
109	Mitochondrial mutations and metabolic adaptation in pancreatic cancer. <i>Cancer &amp; Metabolism</i> , <b>2017</b> , 5, 2	5.4	40
108	Pancreatic cancer genomics. <i>Current Opinion in Genetics and Development</i> , <b>2014</b> , 24, 74-81	4.9	40
107	Ascorbate promotes epigenetic activation of CD30 in human embryonic stem cells. <i>Stem Cells</i> , <b>2010</b> , 28, 1782-93	5.8	40
106	A high-throughput platform for lentiviral overexpression screening of the human ORFeome. <i>PLoS ONE</i> , <b>2011</b> , 6, e20057	3.7	39
105	Analysis of the promoter region of the human VEGF-related factor gene. <i>Biochemical and Biophysical Research Communications</i> , <b>1997</b> , 230, 413-8	3.4	39
104	Phosphoregulators: protein kinases and protein phosphatases of mouse. <i>Genome Research</i> , <b>2003</b> , 13, 1443-54	9.7	39



103	Expression of a novel mammalian epidermal growth factor-related gene during mouse neural development. <i>Mechanisms of Development</i> , <b>2001</b> , 102, 209-11	1.7	39
102	Identification of novel markers of mouse fetal ovary development. <i>PLoS ONE</i> , <b>2012</b> , 7, e41683	3.7	39
101	Clinical and pathologic features of familial pancreatic cancer. <i>Cancer</i> , <b>2014</b> , 120, 3669-75	6.4	38
100	Proteome adaptation in cell reprogramming proceeds via distinct transcriptional networks. <i>Nature Communications</i> , <b>2014</b> , 5, 5613	17.4	37
99	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
98	PRMT2 and ROR $\alpha$ expression are associated with breast cancer survival outcomes. <i>Molecular Endocrinology</i> , <b>2014</b> , 28, 1166-85		36
97	Tissue-specific gene expression in soybean ( <i>Glycine max</i> ) detected by cDNA microarray analysis. <i>Journal of Plant Physiology</i> , <b>2002</b> , 159, 1361-1374	3.6	36
96	Mining the genomes of exceptional responders. <i>Nature Reviews Cancer</i> , <b>2014</b> , 14, 291-2	31.3	35
95	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
94	HNF4A and GATA6 Loss Reveals Therapeutically Actionable Subtypes in Pancreatic Cancer. <i>Cell Reports</i> , <b>2020</b> , 31, 107625	10.6	34
93	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
92	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
91	Spatial gene expression in the T-stage mouse metanephros. <i>Gene Expression Patterns</i> , <b>2006</b> , 6, 807-25	1.5	33
90	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
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	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
87	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
86	Gene expression profile of the fibrotic response in the peritoneal cavity. <i>Differentiation</i> , <b>2010</b> , 79, 232-43.5		29

85	Stromal protein Ecm1 regulates ureteric bud patterning and branching. <i>PLoS ONE</i> , <b>2013</b> , 8, e84155	3.7	29
84	Exome-Wide Association Study of Pancreatic Cancer Risk. <i>Gastroenterology</i> , <b>2018</b> , 154, 719-722.e3	13.3	27
83	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
82	Understanding pancreatic cancer genomes. <i>Journal of Hepato-Biliary-Pancreatic Sciences</i> , <b>2013</b> , 20, 549-568		26
81	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
80	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
79	Construction of a 1.2-Mb sequence-ready contig of chromosome 11q13 encompassing the multiple endocrine neoplasia type 1 (MEN1) gene. The European Consortium on MEN1. <i>Genomics</i> , <b>1997</b> , 44, 94-100	4.3	26
78	Analysis of the mouse transcriptome for genes involved in the function of the nervous system. <i>Genome Research</i> , <b>2003</b> , 13, 1395-401	9.7	26
77	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
76	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
75	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	3.1	24
74	Characterizing embryonic gene expression patterns in the mouse using nonredundant sequence-based selection. <i>Genome Research</i> , <b>2003</b> , 13, 2609-20	9.7	24
73	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
72	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , <b>2020</b> , 11, 4330	17.4	23
71	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
70	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
69	Genome sequencing approaches and successes. <i>Methods in Molecular Biology</i> , <b>2009</b> , 513, 345-58	1.4	22
68	Transcriptional profile reveals altered hepatic lipid and cholesterol metabolism in hyposulfatemic NaS1 null mice. <i>Physiological Genomics</i> , <b>2006</b> , 26, 116-24	3.6	22

67	Analysis of complementary expression profiles following WT1 induction versus repression reveals the cholesterol/fatty acid synthetic pathways as a possible major target of WT1. <i>Oncogene</i> , <b>2004</b> , 23, 3067-79	9.2	21
66	Expression of the VEGF-related factor gene in pre- and postnatal mouse. <i>Biochemical and Biophysical Research Communications</i> , <b>1996</b> , 220, 147-52	3.4	21
65	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
64	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
63	Transcriptome-wide prediction of miRNA targets in human and mouse using FASTH. <i>PLoS ONE</i> , <b>2009</b> , 4, e5745	3.7	20
62	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
61	Returning individual research results for genome sequences of pancreatic cancer. <i>Genome Medicine</i> , <b>2014</b> , 6, 42	14.4	18
60	Lost in translation: returning germline genetic results in genome-scale cancer research. <i>Genome Medicine</i> , <b>2017</b> , 9, 41	14.4	18
59	Tumour-induced host stromal-cell transformation: induction of mouse spindle-cell fibrosarcoma not mediated by gene transfer. <i>International Journal of Cancer</i> , <b>1990</b> , 46, 299-309	7.5	18
58	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> , <b>2008</b> , 112, 229-36	4.4	17
57	Subcellular localization of mammalian type II membrane proteins. <i>Traffic</i> , <b>2006</b> , 7, 613-25	5.7	17
56	Genomic organization and complete cDNA sequence of the human phosphoinositide-specific phospholipase C beta 3 gene (PLCB3). <i>Genomics</i> , <b>1995</b> , 26, 467-72	4.3	17
55	Characterization of the murine VEGF-related factor gene. <i>Biochemical and Biophysical Research Communications</i> , <b>1996</b> , 220, 922-8	3.4	17
54	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> , <b>2014</b> , 69, 363-7	5.1	16
53	RON is not a prognostic marker for resectable pancreatic cancer. <i>BMC Cancer</i> , <b>2012</b> , 12, 395	4.8	16
52	Sequencing transcriptomes in toto. <i>Integrative Biology (United Kingdom)</i> , <b>2011</b> , 3, 522-8	3.7	16
51	Kidney transcriptome reveals altered steroid homeostasis in NaS1 sulfate transporter null mice. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , <b>2008</b> , 112, 55-62	5.1	16
50	PhosphoregDB: the tissue and sub-cellular distribution of mammalian protein kinases and phosphatases. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 82	3.6	16

49	Development of the Minimum Information Specification for In Situ Hybridization and Immunohistochemistry Experiments (MISFISHIE). <i>OMICS A Journal of Integrative Biology</i> , <b>2006</b> , 10, 205-8	3.8	16
48	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
47	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
46	Characterization of the breast cancer associated ATM 7271T>G (V2424G) mutation by gene expression profiling. <i>Genes Chromosomes and Cancer</i> , <b>2006</b> , 45, 1169-81	5	14
45	Detection of a rare point mutation in Ki-ras of a human bladder cancer xenograft by polymerase chain reaction and direct sequencing. <i>Urological Research</i> , <b>1992</b> , 20, 121-6		14
44	Exploration of the cell-cycle genes found within the RIKEN FANTOM2 data set. <i>Genome Research</i> , <b>2003</b> , 13, 1366-75	9.7	12
43	The search for the MEN1 gene. The European Consortium on MEN-1. <i>Journal of Internal Medicine</i> , <b>1998</b> , 243, 441-6	10.8	11
42	BRCA1 and BRCA2 missense variants of high and low clinical significance influence lymphoblastoid cell line post-irradiation gene expression. <i>PLoS Genetics</i> , <b>2008</b> , 4, e1000080	6	11
41	Identification of three gene candidates for multicellular resistance in colon carcinoma. <i>Cytotechnology</i> , <b>2004</b> , 46, 9-18	2.2	11
40	Exclusion of the 13-kDa rapamycin binding protein gene (FKBP2) as a candidate gene for multiple endocrine neoplasia type 1. <i>Human Genetics</i> , <b>1995</b> , 95, 455-8	6.3	11
39	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. <i>Communications Biology</i> , <b>2021</b> , 4, 155	6.7	11
38	Pancreatic cancer genomics: where can the science take us?. <i>Clinical Genetics</i> , <b>2015</b> , 88, 213-9	4	10
37	X-MATE: a flexible system for mapping short read data. <i>Bioinformatics</i> , <b>2011</b> , 27, 580-1	7.2	10
36	Differential gene expression in the developing mouse ureter. <i>Gene Expression Patterns</i> , <b>2006</b> , 6, 519-38	1.5	10
35	Definition and spatial annotation of the dynamic secretome during early kidney development. <i>Developmental Dynamics</i> , <b>2006</b> , 235, 1709-19	2.9	10
34	Effects of A1 adenosine receptor overexpression on normoxic and post-ischemic gene expression. <i>Cardiovascular Research</i> , <b>2003</b> , 57, 715-26	9.9	10
33	G protein mutations in tumours of the pituitary, parathyroid and endocrine pancreas. <i>Biochemical and Biophysical Research Communications</i> , <b>1995</b> , 211, 1063-70	3.4	10
32	Multiple endocrine neoplasia type 1 (MEN1) in two Asian families. <i>Human Genetics</i> , <b>1994</b> , 94, 468-72	6.3	10

31	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
30	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
29	Confirmation of susceptibility locus on chromosome 13 in Australian breast cancer families. <i>Human Genetics</i> , <b>1996</b> , 98, 80-5	6.3	8
28	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
27	Clinical utility of whole-genome sequencing in precision oncology. <i>Seminars in Cancer Biology</i> , <b>2021</b> ,	12.7	7
26	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
25	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
24	Exclusion of the phosphoinositide-specific phospholipase C beta 3 (PLCB3) gene as a candidate for multiple endocrine neoplasia type 1. <i>Human Genetics</i> , <b>1997</b> , 99, 130-2	6.3	5
23	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
22	RAF1 rearrangements are common in pancreatic acinar cell carcinomas. <i>Modern Pathology</i> , <b>2020</b> , 33, 1811-1821	9.8	4
21	Characterisation of a new human and murine member of the DnaJ family of proteins. <i>Biochemical and Biophysical Research Communications</i> , <b>1998</b> , 243, 273-6	3.4	4
20	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , <b>2010</b> , 141, 369	56.2	3
19	A 500-kb sequence-ready cosmid contig and transcript map of the MEN1 region on 11q13. <i>Genomics</i> , <b>1999</b> , 55, 49-56	4.3	3
18	Analytical demands to use whole-genome sequencing in precision oncology. <i>Seminars in Cancer Biology</i> , <b>2021</b> ,	12.7	3
17	Clinical interpretation of whole-genome and whole-transcriptome sequencing for precision oncology. <i>Seminars in Cancer Biology</i> , <b>2021</b> ,	12.7	3
16	Novel cancer drivers: mining the kinome. <i>Genome Medicine</i> , <b>2013</b> , 5, 19	14.4	2
15	Atlas of Gene Expression in the Developing Kidney at Microanatomic Resolution. <i>Developmental Cell</i> , <b>2009</b> , 16, 482	10.2	2
14	Targeting of TP53-independent cell cycle checkpoints overcomes FOLFOX resistance in Metastatic Colorectal Cancer		2

13	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
12	PRMT5: An Emerging Target for Pancreatic Adenocarcinoma. <i>Cancers</i> , <b>2021</b> , 13,	6.6	1
11	The Diverse Applications of Pancreatic Ductal Adenocarcinoma Organoids. <i>Cancers</i> , <b>2021</b> , 13,	6.6	1
10	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
9	Genomic and Molecular Analyses Identify Molecular Subtypes of Pancreatic Cancer Recurrence. <i>Gastroenterology</i> , <b>2021</b> ,	13.3	1
8	ROR1 and ROR2 expression in pancreatic cancer. <i>BMC Cancer</i> , <b>2021</b> , 21, 1199	4.8	0
7	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	
6	Stratified Medicine for Pancreatic Cancer <b>2014</b> , 807-814		
5	Molecular diagnostics in pancreatic cancer <b>2011</b> , 20-35		
4	Setting CAGE Tags in a Genomic Context <b>2009</b> , 93-100		
3	Expression Profiling with cDNA Microarrays: A User's Perspective and Guide. <i>Principles and Practice</i> , <b>2001</b> , 13-33		
2	Setting CAGE Tags in a Genomic Context <b>2019</b> , 93-100		
1	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