Marcel E Dinger

List of Publications by Year in Descending Order

162 papers	19,457 citations	58 h-index	139 g-index
184 ext. papers	22,944 ext. citations	9.2 avg, IF	7.11 L-index

#	Paper	IF	Citations
162	Interaction between non-coding RNAs, mRNAs and G-quadruplexes.. *Cancer Cell International*, **2022**, 22, 171	6.4	1
161	The Impact of Non-coding RNAs in the Epithelial to Mesenchymal Transition. *Frontiers in Molecular Biosciences*, **2021**, 8, 665199	5.6	5
160	Destination Amyotrophic Lateral Sclerosis. *Frontiers in Neurology*, **2021**, 12, 596006	4.1	6
159	Non-coding RNAs modulate function of extracellular matrix proteins. *Biomedicine and Pharmacotherapy*, **2021**, 136, 111240	7.5	6
158	The role of miRNAs and lncRNAs in conferring resistance to doxorubicin. *Journal of Drug Targeting*, **2021**, 1-21	5.4	2
157	Different types of disease-causing noncoding variants revealed by genomic and gene expression analyses in families with X-linked intellectual disability. *Human Mutation*, **2021**, 42, 835-847	4.7	
156	A Pathway to Precision Medicine for Aboriginal Australians: A Study Protocol. *Methods and Protocols*, **2021**, 4,	2.5	1
155	Genome sequencing in congenital cataracts improves diagnostic yield. *Human Mutation*, **2021**, 42, 1173-1183	4.7	2
154	Identification of miRNA-mRNA Network in Autism Spectrum Disorder Using a Bioinformatics Method. *Journal of Molecular Neuroscience*, **2021**, 71, 761-766	3.3	2
153	LncRNAs and miRNAs participate in determination of sensitivity of cancer cells to cisplatin. *Experimental and Molecular Pathology*, **2021**, 123, 104602	4.4	12
152	Diagnostic Yield of Whole Genome Sequencing After Nondiagnostic Exome Sequencing or Gene Panel in Developmental and Epileptic Encephalopathies. *Neurology*, **2021**, 96, e1770-e1782	6.5	16
151	ClinSV: clinical grade structural and copy number variant detection from whole genome sequencing data. *Genome Medicine*, **2021**, 13, 32	14.4	9
150	Emerging role of non-coding RNAs in response of cancer cells to radiotherapy. *Pathology Research and Practice*, **2021**, 218, 153327	3.4	3
149	Emerging role of circular RNAs in the pathobiology of lung cancer. *Biomedicine and Pharmacotherapy*, **2021**, 141, 111805	7.5	2
148	Genomic diagnostics in polycystic kidney disease: an assessment of real-world use of whole-genome sequencing. *European Journal of Human Genetics*, **2021**, 29, 760-770	5.3	3
147	Revealing hidden genetic diagnoses in the ocular anterior segment disorders. *Genetics in Medicine*, **2020**, 22, 1623-1632	8.1	10
146	Exploring the Role of Non-Coding RNAs in the Pathophysiology of Systemic Lupus Erythematosus. *Biomolecules*, **2020**, 10,	5.9	12

145	Aberrant RAG-mediated recombination contributes to multiple structural rearrangements in lymphoid blast crisis of chronic myeloid leukemia. *Leukemia*, **2020**, 34, 2051-2063	10.7	11
144	The Medical Genome Reference Bank contains whole genome and phenotype data of 2570 healthy elderly. *Nature Communications*, **2020**, 11, 435	17.4	20
143	Non-coding RNAs underlie genetic predisposition to breast cancer. *Genome Biology*, **2020**, 21, 7	18.3	11
142	Overcoming challenges and dogmas to understand the functions of pseudogenes. *Nature Reviews Genetics*, **2020**, 21, 191-201	30.1	63
141	Dysregulation of non-coding RNAs in autoimmune thyroid disease. *Experimental and Molecular Pathology*, **2020**, 117, 104527	4.4	3
140	Emerging roles of non-coding RNAs in the pathogenesis of type 1 diabetes mellitus. *Biomedicine and Pharmacotherapy*, **2020**, 129, 110509	7.5	7
139	Perspectives on the Role of Non-Coding RNAs in the Regulation of Expression and Function of the Estrogen Receptor. *Cancers*, **2020**, 12,	6.6	13
138	Dysregulation of non-coding RNAs in Rheumatoid arthritis. *Biomedicine and Pharmacotherapy*, **2020** , 130, 110617	7.5	12
137	Equitable Expanded Carrier Screening Needs Indigenous Clinical and Population Genomic Data. *American Journal of Human Genetics*, **2020**, 107, 175-182	11	9
136	The critical roles of lncRNAs in the pathogenesis of melanoma. *Experimental and Molecular Pathology*, **2020**, 117, 104558	4.4	10
135	Mutations in the exocyst component EXOC2 cause severe defects in human brain development. *Journal of Experimental Medicine*, **2020**, 217,	16.6	4
134	Attitudes of Australian health professionals towards rapid genomic testing in neonatal and paediatric intensive care. *European Journal of Human Genetics*, **2019**, 27, 1493-1501	5.3	18
133	Pathogenic variants in result in a Stickler syndrome-like connective tissue disorder with vascular complications. *Journal of Medical Genetics*, **2019**, 56, 629-638	5.8	11
132	Lipid Uptake Is an Androgen-Enhanced Lipid Supply Pathway Associated with Prostate Cancer Disease Progression and Bone Metastasis. *Molecular Cancer Research*, **2019**, 17, 1166-1179	6.6	28
131	Mouse Model of Mutated in Colorectal Cancer Gene Deletion Reveals Novel Pathways in Inflammation and Cancer. *Cellular and Molecular Gastroenterology and Hepatology*, **2019**, 7, 819-839	7.9	4
130	Preparing Australia for genomic medicine: data, computing and digital health. *Medical Journal of Australia*, **2019**, 210 Suppl 6, S30-S32	4	4
129	Genomic stratification and liquid biopsy in a rare adrenocortical carcinoma (ACC) case, with dual lung metastases. *Journal of Physical Education and Sports Management*, **2019**, 5,	2.8	7
128	Seave: a comprehensive web platform for storing and interrogating human genomic variation. *Bioinformatics*, **2019**, 35, 122-125	7.2	19

127	Genome sequencing as a first-line genetic test in familial dilated cardiomyopathy. *Genetics in Medicine*, **2019**, 21, 650-662	8.1	36
126	The long noncoding RNA lncNB1 promotes tumorigenesis by interacting with ribosomal protein RPL35. *Nature Communications*, **2019**, 10, 5026	17.4	40
125	De Novo Variants Disrupting the HX Repeat Motif of ATN1 Cause a Recognizable Non-Progressive Neurocognitive Syndrome. *American Journal of Human Genetics*, **2019**, 104, 542-552	11	11
124	Development and validation of a targeted gene sequencing panel for application to disparate cancers. *Scientific Reports*, **2019**, 9, 17052	4.9	10
123	Denisovan, modern human and mouse TNFAIP3 alleles tune A20 phosphorylation and immunity. *Nature Immunology*, **2019**, 20, 1299-1310	19.1	29
122	Reanalysis and optimisation of bioinformatic pipelines is critical for mutation detection. *Human Mutation*, **2019**, 40, 374-379	4.7	6
121	RNAcentral: a hub of information for non-coding RNA sequences. *Nucleic Acids Research*, **2019**, 47, D221-D229	10.2	90
120	Index suffix-prefix overlaps by (w, k)-minimizer to generate long contigs for reads compression. *Bioinformatics*, **2019**, 35, 2066-2074	7.2	11
119	Role and practice evolution for genetic counseling in the genomic era: The experience of Australian and UK genetics practitioners. *Journal of Genetic Counseling*, **2019**, 28, 378-387	2.5	3
118	The Medical Genome Reference Bank: a whole-genome data resource of 4000 healthy elderly individuals. Rationale and cohort design. *European Journal of Human Genetics*, **2019**, 27, 308-316	5.3	17
117	Response to Brodehl et al. *Genetics in Medicine*, **2019**, 21, 1248-1249	8.1	
116	A Mild PUM1 Mutation Is Associated with Adult-Onset Ataxia, whereas Haploinsufficiency Causes Developmental Delay and Seizures. *Cell*, **2018**, 172, 924-936.e11	56.2	65
115	I-motif DNA structures are formed in the nuclei of human cells. *Nature Chemistry*, **2018**, 10, 631-637	17.6	261
114	Evidence that TLR4 Is Not a Receptor for Saturated Fatty Acids but Mediates Lipid-Induced Inflammation by Reprogramming Macrophage Metabolism. *Cell Metabolism*, **2018**, 27, 1096-1110.e5	24.6	210
113	Universal Alternative Splicing of Noncoding Exons. *Cell Systems*, **2018**, 6, 245-255.e5	10.6	58
112	Identification of OAF and PVRL1 as candidate genes for an ocular anomaly characterized by Peters anomaly type 2 and ectopia lentis. *Experimental Eye Research*, **2018**, 168, 161-170	3.7	5
111	Machine learning annotation of human branchpoints. *Bioinformatics*, **2018**, 34, 920-927	7.2	21
110	Integrating exome sequencing into a diagnostic pathway for epileptic encephalopathy: Evidence of clinical utility and cost effectiveness. *Molecular Genetics & Genomic Medicine*, **2018**, 6, 186-199	2.3	46

109	Whole-exome sequencing reanalysis at 12 months boosts diagnosis and is cost-effective when applied early in Mendelian disorders. *Genetics in Medicine*, **2018**, 20, 1564-1574	8.1	76
108	Whole Genome Sequencing Improves Outcomes of Genetic Testing in Patients With Hypertrophic Cardiomyopathy. *Journal of the American College of Cardiology*, **2018**, 72, 419-429	15.1	92
107	Whole genome sequencing provides better diagnostic yield and future value than whole exome sequencing. *Medical Journal of Australia*, **2018**, 209, 197-199	4	22
106	Realizing the significance of noncoding functionality in clinical genomics. *Experimental and Molecular Medicine*, **2018**, 50, 1-8	12.8	52
105	Expanding the spectrum of mutations and novel insights into disease mechanisms. *Molecular Genetics and Metabolism Reports*, **2018**, 16, 46-51	1.8	9
104	NMNAT1 variants cause cone and cone-rod dystrophy. *European Journal of Human Genetics*, **2018**, 26, 428-433	5.3	16
103	Selection of Antibody Fragments Against Structured DNA by Phage Display. *Methods in Molecular Biology*, **2018**, 1827, 197-209	1.4	1
102	The regulatory role of long noncoding RNAs in cancer. *Cancer Letters*, **2017**, 391, 12-19	9.9	75
101	The long non-coding RNA NEAT1 is responsive to neuronal activity and is associated with hyperexcitability states. *Scientific Reports*, **2017**, 7, 40127	4.9	59
100	Germline variants in familial pituitary tumour syndrome genes are common in young patients and families with additional endocrine tumours. *European Journal of Endocrinology*, **2017**, 176, 635-644	6.5	22
99	Benchmarking of RNA-sequencing analysis workflows using whole-transcriptome RT-qPCR expression data. *Scientific Reports*, **2017**, 7, 1559	4.9	129
98	Cancer-associated noncoding mutations affect RNA G-quadruplex-mediated regulation of gene expression. *Scientific Reports*, **2017**, 7, 708	4.9	19
97	Gonadal mosaicism of a novel IQSEC2 variant causing female limited intellectual disability and epilepsy. *European Journal of Human Genetics*, **2017**, 25, 763-767	5.3	14
96	A De Novo Mutation in the Sodium-Activated Potassium Channel KCNT2 Alters Ion Selectivity and Causes Epileptic Encephalopathy. *Cell Reports*, **2017**, 21, 926-933	10.6	20
95	Initiating an undiagnosed diseases program in the Western Australian public health system. *Orphanet Journal of Rare Diseases*, **2017**, 12, 83	4.2	18
94	Intergenic disease-associated regions are abundant in novel transcripts. *Genome Biology*, **2017**, 18, 241	18.3	27
93	Novel Aberrations Uncovered in Barrett's Esophagus and Esophageal Adenocarcinoma Using Whole Transcriptome Sequencing. *Molecular Cancer Research*, **2017**, 15, 1558-1569	6.6	22
92	High resolution temporal transcriptomics of mouse embryoid body development reveals complex expression dynamics of coding and noncoding loci. *Scientific Reports*, **2017**, 7, 6731	4.9	9

91	Long Noncoding RNAs CUPID1 and CUPID2 Mediate Breast Cancer Risk at 11q13 by Modulating the Response to DNA Damage. *American Journal of Human Genetics*, **2017**, 101, 255-266	11	62
90	Improved Diagnosis and Care for Rare Diseases through Implementation of Precision Public Health Framework. *Advances in Experimental Medicine and Biology*, **2017**, 1031, 55-94	3.6	13
89	Widespread promoter methylation of synaptic plasticity genes in long-term potentiation in the adult brain in vivo. *BMC Genomics*, **2017**, 18, 250	4.5	18
88	CCR6 Defines Memory B Cell Precursors in Mouse and Human Germinal Centers, Revealing Light-Zone Location and Predominant Low Antigen Affinity. *Immunity*, **2017**, 47, 1142-1153.e4	32.3	107
87	RNAcentral: a comprehensive database of non-coding RNA sequences. *Nucleic Acids Research*, **2017**, 45, D128-D134	20.1	119
86	Somatic mutations in salivary duct carcinoma and potential therapeutic targets. *Oncotarget*, **2017**, 8, 75893-75903	3.3	19
85	RNA-seq reveals more consistent reference genes for gene expression studies in human non-melanoma skin cancers. *PeerJ*, **2017**, 5, e3631	3.1	24
84	The specificity of long noncoding RNA expression. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2016**, 1859, 16-22	6	115
83	Computational Approaches for Functional Prediction and Characterisation of Long Noncoding RNAs. *Trends in Genetics*, **2016**, 32, 620-637	8.5	70
82	Mutation allele burden remains unchanged in chronic myelomonocytic leukaemia responding to hypomethylating agents. *Nature Communications*, **2016**, 7, 10767	17.4	140
81	Long noncoding RNAs in cancer: mechanisms of action and technological advancements. *Molecular Cancer*, **2016**, 15, 43	42.1	308
80	Comparison of whole-exome sequencing of matched fresh and formalin fixed paraffin embedded melanoma tumours: implications for clinical decision making. *Pathology*, **2016**, 48, 261-6	1.6	28
79	Gonadotropin suppression in men leads to a reduction in claudin-11 at the Sertoli cell tight junction. *Human Reproduction*, **2016**, 31, 875-86	5.7	15
78	The BET bromodomain inhibitor exerts the most potent synergistic anticancer effects with quinone-containing compounds and anti-microtubule drugs. *Oncotarget*, **2016**, 7, 79217-79232	3.3	14
77	The long noncoding RNA MALAT1 promotes tumor-driven angiogenesis by up-regulating pro-angiogenic gene expression. *Oncotarget*, **2016**, 7, 8663-75	3.3	88
76	Claudin-11 and occludin are major contributors to Sertoli cell tight junction function, in vitro. *Asian Journal of Andrology*, **2016**, 18, 620-6	2.8	27
75	The Evx1/Evx1as gene locus regulates anterior-posterior patterning during gastrulation. *Scientific Reports*, **2016**, 6, 26657	4.9	16
74	Identification of a novel fusion transcript between human relaxin-1 (RLN1) and human relaxin-2 (RLN2) in prostate cancer. *Molecular and Cellular Endocrinology*, **2016**, 420, 159-68	4.4	12

73	Endogenous microRNA sponges: evidence and controversy. *Nature Reviews Genetics*, **2016**, 17, 272-83	30.1	1123
72	The Long Noncoding RNA SPRIGHTLY Regulates Cell Proliferation in Primary Human Melanocytes. *Journal of Investigative Dermatology*, **2016**, 136, 819-828	4.3	29
71	Whole-genome sequencing overcomes pseudogene homology to diagnose autosomal dominant polycystic kidney disease. *European Journal of Human Genetics*, **2016**, 24, 1584-1590	5.3	47
70	Improved definition of the mouse transcriptome via targeted RNA sequencing. *Genome Research*, **2016**, 26, 705-16	9.7	23
69	Endometriosis risk alleles at 1p36.12 act through inverse regulation of CDC42 and LINC00339. *Human Molecular Genetics*, **2016**, 25, 5046-5058	5.6	45
68	Defining the genetic basis of early onset hereditary spastic paraplegia using whole genome sequencing. *Neurogenetics*, **2016**, 17, 265-270	3	25
67	Quantitative gene profiling of long noncoding RNAs with targeted RNA sequencing. *Nature Methods*, **2015**, 12, 339-42	21.6	119
66	Cyclin E2 is the predominant E-cyclin associated with NPAT in breast cancer cells. *Cell Division*, **2015** , 10, 1	2.8	12
65	RNAcentral: an international database of ncRNA sequences. *Nucleic Acids Research*, **2015**, 43, D123-9	20.1	89
64	lncRNAdb v2.0: expanding the reference database for functional long noncoding RNAs. *Nucleic Acids Research*, **2015**, 43, D168-73	20.1	398
63	Asparagine Synthetase Deficiency causes reduced proliferation of cells under conditions of limited asparagine. *Molecular Genetics and Metabolism*, **2015**, 116, 178-86	3.7	33
62	Dynamic expression of long noncoding RNAs and repeat elements in synaptic plasticity. *Frontiers in Neuroscience*, **2015**, 9, 351	5.1	34
61	Genome-wide discovery of human splicing branchpoints. *Genome Research*, **2015**, 25, 290-303	9.7	147
60	Abstract 146: The long noncoding RNA MALAT1 promotes hypoxia-driven angiogenesis by upregulating pro-angiogenic gene expression in neuroblastoma cells **2015**,		2
59	The role of microRNAs and long non-coding RNAs in the pathology, diagnosis, and management of melanoma. *Archives of Biochemistry and Biophysics*, **2014**, 563, 60-70	4.1	62
58	IL-21 contributes to fatal inflammatory disease in the absence of Foxp3+ T regulatory cells. *Journal of Immunology*, **2014**, 192, 1404-14	5.3	16
57	Effects of a novel long noncoding RNA, lncUSMycN, on N-Myc expression and neuroblastoma progression. *Journal of the National Cancer Institute*, **2014**, 106,	9.7	81
56	Long non-coding RNAs in disease and development. *Pathology*, **2014**, 46, S26	1.6	

55	The impact of genomics on the future of medicine and health. *Medical Journal of Australia*, **2014**, 201, 17-20	4	19
54	The functional characterization of long noncoding RNA SPRY4-IT1 in human melanoma cells. *Oncotarget*, **2014**, 5, 8959-69	3.3	123
53	Identification of a dinucleotide signature that discriminates coding from non-coding long RNAs. *Frontiers in Genetics*, **2014**, 5, 316	4.5	4
52	Genomics and personalised whole-of-life healthcare. *Trends in Molecular Medicine*, **2014**, 20, 479-86	11.5	13
51	Targeted sequencing for gene discovery and quantification using RNA CaptureSeq. *Nature Protocols*, **2014**, 9, 989-1009	18.8	116
50	The histone demethylase JMJD1A induces cell migration and invasion by up-regulating the expression of the long noncoding RNA MALAT1. *Oncotarget*, **2014**, 5, 1793-804	3.3	91
49	Saccharopolyspora erythraea genome is organised in high-order transcriptional regions mediated by targeted degradation at the metabolic switch. *BMC Genomics*, **2013**, 14, 15	4.5	23
48	Long noncoding RNAs and the genetics of cancer. *British Journal of Cancer*, **2013**, 108, 2419-25	8.7	588
47	The extent of functionality in the human genome. *The HUGO Journal*, **2013**, 7,		19
46	Non-coding RNAs in homeostasis, disease and stress responses: an evolutionary perspective. *Briefings in Functional Genomics*, **2013**, 12, 254-78	4.9	79
45	Genome-wide methylated CpG island profiles of melanoma cells reveal a melanoma coregulation network. *Scientific Reports*, **2013**, 3, 2962	4.9	15
44	Regulated expression of PTPRJ/CD148 and an antisense long noncoding RNA in macrophages by proinflammatory stimuli. *PLoS ONE*, **2013**, 8, e68306	3.7	32
43	Genome-wide analysis of long noncoding RNA stability. *Genome Research*, **2012**, 22, 885-98	9.7	373
42	Pregnancy-induced noncoding RNA (PINC) associates with polycomb repressive complex 2 and regulates mammary epithelial differentiation. *PLoS Genetics*, **2012**, 8, e1002840	6	39
41	Pinstripe: a suite of programs for integrating transcriptomic and proteomic datasets identifies novel proteins and improves differentiation of protein-coding and non-coding genes. *Bioinformatics* , **2012**, 28, 3042-50	7.2	59
40	Expression and function of the protein tyrosine phosphatase receptor J (PTPRJ) in normal mammary epithelial cells and breast tumors. *PLoS ONE*, **2012**, 7, e40742	3.7	14
39	Identification of novel markers of mouse fetal ovary development. *PLoS ONE*, **2012**, 7, e41683	3.7	39
38	Targeted RNA sequencing reveals the deep complexity of the human transcriptome. *Nature Biotechnology*, **2011**, 30, 99-104	44.5	356

37	The melanoma-upregulated long noncoding RNA SPRY4-IT1 modulates apoptosis and invasion. *Cancer Research*, **2011**, 71, 3852-62	10.1	392
36	The human mitochondrial transcriptome. *Cell*, **2011**, 146, 645-58	56.2	561
35	The evolution of RNAs with multiple functions. *Biochimie*, **2011**, 93, 2013-8	4.6	68
34	Expression of distinct RNAs from 3Quntranslated regions. *Nucleic Acids Research*, **2011**, 39, 2393-403	20.1	153
33	SNORD-host RNA Zfas1 is a regulator of mammary development and a potential marker for breast cancer. *Rna*, **2011**, 17, 878-91	5.8	270
32	lncRNAdb: a reference database for long noncoding RNAs. *Nucleic Acids Research*, **2011**, 39, D146-51	20.1	461
31	lncRNAs: finding the forest among the trees?. *Molecular Therapy*, **2011**, 19, 2109-11	11.7	2
30	RNAcentral: A vision for an international database of RNA sequences. *Rna*, **2011**, 17, 1941-6	5.8	54
29	Global analysis of the mammalian RNA degradome reveals widespread miRNA-dependent and miRNA-independent endonucleolytic cleavage. *Nucleic Acids Research*, **2011**, 39, 5658-68	20.1	63
28	The reality of pervasive transcription. *PLoS Biology*, **2011**, 9, e1000625; discussion e1001102	9.7	325
27	A variant of the KLK4 gene is expressed as a cis sense-antisense chimeric transcript in prostate cancer cells. *Rna*, **2010**, 16, 1156-66	5.8	30
26	Regulated post-transcriptional RNA cleavage diversifies the eukaryotic transcriptome. *Genome Research*, **2010**, 20, 1639-50	9.7	66
25	Protein-coding and non-coding gene expression analysis in differentiating human keratinocytes using a three-dimensional epidermal equivalent. *Molecular Genetics and Genomics*, **2010**, 284, 1-9	3.1	25
24	GATExplorer: genomic and transcriptomic explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. *BMC Bioinformatics*, **2010**, 11, 221	3.6	69
23	Long noncoding RNAs in neuronal-glial fate specification and oligodendrocyte lineage maturation. *BMC Neuroscience*, **2010**, 11, 14	3.2	326
22	Non-coding RNAs: regulators of disease. *Journal of Pathology*, **2010**, 220, 126-39	9.4	769
21	Genome-wide identification of long noncoding RNAs in CD8+ T cells. *Journal of Immunology*, **2009**, 182, 7738-48	5.3	189
20	NRED: a database of long noncoding RNA expression. *Nucleic Acids Research*, **2009**, 37, D122-6	20.1	214

19	RNA regulation of epigenetic processes. *BioEssays*, **2009**, 31, 51-9	4.1	295
18	Long non-coding RNAs: insights into functions. *Nature Reviews Genetics*, **2009**, 10, 155-9	30.1	4184
17	Pervasive transcription of the eukaryotic genome: functional indices and conceptual implications. *Briefings in Functional Genomics & Proteomics*, **2009**, 8, 407-23		118
16	MEN epsilon/beta nuclear-retained non-coding RNAs are up-regulated upon muscle differentiation and are essential components of paraspeckles. *Genome Research*, **2009**, 19, 347-59	9.7	469
15	RNAs as extracellular signaling molecules. *Journal of Molecular Endocrinology*, **2008**, 40, 151-9	4.5	157
14	Noncoding RNAs in Long-Term Memory Formation. *Neuroscientist*, **2008**, 14, 434-45	7.6	110
13	The eukaryotic genome as an RNA machine. *Science*, **2008**, 319, 1787-9	33.3	499
12	Long noncoding RNAs in mouse embryonic stem cell pluripotency and differentiation. *Genome Research*, **2008**, 18, 1433-45	9.7	608
11	Differentiating protein-coding and noncoding RNA: challenges and ambiguities. *PLoS Computational Biology*, **2008**, 4, e1000176	5	387
10	Specific expression of long noncoding RNAs in the mouse brain. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 716-21	11.5	928
9	RNAdb 2.0--an expanded database of mammalian non-coding RNAs. *Nucleic Acids Research*, **2007**, 35, D178-82	20.1	134
8	Archaeal genome organization and stress responses: implications for the origin and evolution of cellular life. *Astrobiology*, **2002**, 2, 241-53	3.7	9
7	Growth phase-dependent expression and degradation of histones in the thermophilic archaeon Thermococcus zilligii. *Molecular Microbiology*, **2000**, 36, 876-85	4.1	29
6	Identification of archaeal genes encoding a novel stationary phase-response protein. *Biochimica Et Biophysica Acta Gene Regulatory Mechanisms*, **2000**, 1490, 115-20		4
5	The Medical Genome Reference Bank: Whole genomes and phenotype of 2,570 healthy elderly		1
4	Universal alternative splicing of noncoding exons		2
3	Seave: a comprehensive web platform for storing and interrogating human genomic variation		2
2	mity: A highly sensitive mitochondrial variant analysis pipeline for whole genome sequencing data		8

List of Publications