Marcel E Dinger

List of Publications by Year
in descending order

168 papers	25,139 citations	19657 61 h-index	7160 153 g-index
184 all docs	184 docs citations	184 times ranked	33341 citing authors

#	Article	IF	Citations
1	The role of miRNAs and lncRNAs in conferring resistance to doxorubicin. Journal of Drug Targeting, 2022, 30, 1-21.	4.4	8
2	Whole Genome Sequencing, Focused Assays and Functional Studies Increasing Understanding in Cryptic Inherited Retinal Dystrophies. International Journal of Molecular Sciences, 2022, 23, 3905.	4.1	4
3	Interaction between non-coding RNAs, mRNAs and G-quadruplexes. Cancer Cell International, 2022, 22, 171.	4.1	9
4	Use of Whole-Genome Sequencing for Mitochondrial Disease Diagnosis. Neurology, 2022, 99, .	1.1	33
5	Abstract 6298: The novel long noncoding RNA lncNeur promotes neuroblastoma by up-regulating AURKA and Myc expression. Cancer Research, 2022, 82, 6298-6298.	0.9	0
6	Identification of miRNA-mRNA Network in Autism Spectrum Disorder Using a Bioinformatics Method. Journal of Molecular Neuroscience, 2021, 71, 761-766.	2.3	8
7	LncRNAs and miRNAs participate in determination of sensitivity of cancer cells to cisplatin. Experimental and Molecular Pathology, 2021, 123, 104602.	2.1	26
8	Diagnostic Yield of Whole Genome Sequencing After Nondiagnostic Exome Sequencing or Gene Panel in Developmental and Epileptic Encephalopathies. Neurology, 2021, 96, e1770-e1782.	1.1	53
9	ClinSV: clinical grade structural and copy number variant detection from whole genome sequencing data. Genome Medicine, 2021, 13, 32.	8.2	36
10	Emerging role of non-coding RNAs in response of cancer cells to radiotherapy. Pathology Research and Practice, 2021, 218, 153327.	2.3	14
11	The Impact of Non-coding RNAs in the Epithelial to Mesenchymal Transition. Frontiers in Molecular Biosciences, 2021, 8, 665199.	3.5	17
12	Destination Amyotrophic Lateral Sclerosis. Frontiers in Neurology, 2021, 12, 596006.	2.4	24
13	Non-coding RNAs modulate function of extracellular matrix proteins. Biomedicine and Pharmacotherapy, 2021, 136, 111240.	5.6	35
14	Different types of diseaseâ€causing noncoding variants revealed by genomic and gene expression analyses in families with Xâ€linked intellectual disability. Human Mutation, 2021, 42, 835-847.	2.5	0
15	A Pathway to Precision Medicine for Aboriginal Australians: A Study Protocol. Methods and Protocols, 2021, 4, 42.	2.0	8
16	Genome sequencing in congenital cataracts improves diagnostic yield. Human Mutation, 2021, 42, 1173-1183.	2.5	10
17	Emerging role of circular RNAs in the pathobiology of lung cancer. Biomedicine and Pharmacotherapy, 2021, 141, 111805.	5.6	9
18	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.	2.8	20

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19	Overcoming challenges and dogmas to understand the functions of pseudogenes. Nature Reviews Genetics, 2020, 21, 191-201.	16.3	151
20	Dysregulation of non-coding RNAs in autoimmune thyroid disease. Experimental and Molecular Pathology, 2020, 117, 104527.	2.1	8
21	Emerging roles of non-coding RNAs in the pathogenesis of type 1 diabetes mellitus. Biomedicine and Pharmacotherapy, 2020, 129, 110509.	5.6	21
22	Perspectives on the Role of Non-Coding RNAs in the Regulation of Expression and Function of the Estrogen Receptor. Cancers, 2020, 12, 2162.	3.7	20
23	Dysregulation of non-coding RNAs in Rheumatoid arthritis. Biomedicine and Pharmacotherapy, 2020, 130, 110617.	5.6	33
24	Equitable Expanded Carrier Screening Needs Indigenous Clinical and Population Genomic Data. American Journal of Human Genetics, 2020, 107, 175-182.	6.2	24
25	The critical roles of lncRNAs in the pathogenesis of melanoma. Experimental and Molecular Pathology, 2020, 117, 104558.	2.1	25
26	Mutations in the exocyst component EXOC2 cause severe defects in human brain development. Journal of Experimental Medicine, 2020, 217, .	8.5	17
27	Revealing hidden genetic diagnoses in the ocular anterior segment disorders. Genetics in Medicine, 2020, 22, 1623-1632.	2.4	31
28	Exploring the Role of Non-Coding RNAs in the Pathophysiology of Systemic Lupus Erythematosus. Biomolecules, 2020, 10, 937.	4.0	27
29	Aberrant RAG-mediated recombination contributes to multiple structural rearrangements in lymphoid blast crisis of chronic myeloid leukemia. Leukemia, 2020, 34, 2051-2063.	7.2	27
30	The Medical Genome Reference Bank contains whole genome and phenotype data of 2570 healthy elderly. Nature Communications, 2020, 11, 435.	12.8	47
31	Non-coding RNAs underlie genetic predisposition to breast cancer. Genome Biology, 2020, 21, 7.	8.8	21
32	Abstract 5721: The super-enhancer driven long noncoding RNA lncNB promotes neuroblastoma tumorigenesis. , 2020, , .		0
33	Seave: a comprehensive web platform for storing and interrogating human genomic variation. Bioinformatics, 2019, 35, 122-125.	4.1	26
34	Genome sequencing as a first-line genetic test in familial dilated cardiomyopathy. Genetics in Medicine, 2019, 21, 650-662.	2.4	52
35	The long noncoding RNA lncNB1 promotes tumorigenesis by interacting with ribosomal protein RPL35. Nature Communications, 2019, 10, 5026.	12.8	67
36	Attitudes of Australian health professionals towards rapid genomic testing in neonatal and paediatric intensive care. European Journal of Human Genetics, 2019, 27, 1493-1501.	2.8	29

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37	Pathogenic variants in PLOD3 result in a Stickler syndrome-like connective tissue disorder with vascular complications. Journal of Medical Genetics, 2019, 56, 629-638.	3.2	23
38	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.	3.4	51
39	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.	4.5	11
40	Preparing Australia for genomic medicine: data, computing and digital health. Medical Journal of Australia, 2019, 210, S30-S32.	1.7	4
41	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, a003764.	1.2	7
42	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.	6.2	19
43	Development and validation of a targeted gene sequencing panel for application to disparate cancers. Scientific Reports, 2019, 9, 17052.	3.3	18
44	Denisovan, modern human and mouse TNFAIP3 alleles tune A20 phosphorylation and immunity. Nature Immunology, 2019, 20, 1299-1310.	14.5	53
45	Reanalysis and optimisation of bioinformatic pipelines is critical for mutation detection. Human Mutation, 2019, 40, 374-379.	2.5	7
46	RNAcentral: a hub of information for non-coding RNA sequences. Nucleic Acids Research, 2019, 47, D221-D229.	14.5	153
47	Index suffixâ€“prefix overlaps by (w, k)-minimizer to generate long contigs for reads compression. Bioinformatics, 2019, 35, 2066-2074.	4.1	27
48	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.	1.6	10
49	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.	2.8	28
50	Response to Brodehl et al.. Genetics in Medicine, 2019, 21, 1248-1249.	2.4	0
51	A Mild PUM1 Mutation Is Associated with Adult-Onset Ataxia, whereas Haploinsufficiency Causes Developmental Delay and Seizures. Cell, 2018, 172, 924-936.e11.	28.9	103
52	I-motif DNA structures are formed in the nuclei of human cells. Nature Chemistry, 2018, 10, 631-637.	13.6	407
53	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.	16.2	309
54	Universal Alternative Splicing of Noncoding Exons. Cell Systems, 2018, 6, 245-255.e5.	6.2	110

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55	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.	2.6	5
56	Machine learning annotation of human branchpoints. Bioinformatics, 2018, 34, 920-927.	4.1	52
57	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.	1.2	83
58	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.	2.4	132
59	NMNAT1 variants cause cone and cone-rod dystrophy. European Journal of Human Genetics, 2018, 26, 428-433.	2.8	23
60	Selection of Antibody Fragments Against Structured DNA by Phage Display. Methods in Molecular Biology, 2018, 1827, 197-209.	0.9	1
61	Whole Genome Sequencing Improves Outcomes of Genetic Testing in Patients With Hypertrophic Cardiomyopathy. Journal of the American College of Cardiology, 2018, 72, 419-429.	2.8	138
62	Whole genome sequencing provides better diagnostic yield and future value than whole exome sequencing. Medical Journal of Australia, 2018, 209, 197-199.	1.7	48
63	Realizing the significance of noncoding functionality in clinical genomics. Experimental and Molecular Medicine, 2018, 50, 1-8.	7.7	81
64	Expanding the spectrum of PEX16 mutations and novel insights into disease mechanisms. Molecular Genetics and Metabolism Reports, 2018, 16, 46-51.	1.1	21
65	The regulatory role of long noncoding RNAs in cancer. Cancer Letters, 2017, 391, 12-19.	7.2	94
66	The long non-coding RNA NEAT1 is responsive to neuronal activity and is associated with hyperexcitability states. Scientific Reports, 2017, 7, 40127.	3.3	92
67	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.	3.7	33
68	Benchmarking of RNA-sequencing analysis workflows using whole-transcriptome RT-qPCR expression data. Scientific Reports, 2017, 7, 1559.	3.3	247
69	Somatic mutations in salivary duct carcinoma and potential therapeutic targets. Pathology, 2017, 49, S105.	0.6	1
70	Cancer-associated noncoding mutations affect RNA G-quadruplex-mediated regulation of gene expression. Scientific Reports, 2017, 7, 708.	3.3	37
71	Gonadal mosaicism of a novel IQSEC2 variant causing female limited intellectual disability and epilepsy. European Journal of Human Genetics, 2017, 25, 763-767.	2.8	14
72	A De Novo Mutation in the Sodium-Activated Potassium Channel KCNT2 Alters Ion Selectivity and Causes Epileptic Encephalopathy. Cell Reports, 2017, 21, 926-933.	6.4	40

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73	Novel Aberrations Uncovered in Barrett's Esophagus and Esophageal Adenocarcinoma Using Whole Transcriptome Sequencing. Molecular Cancer Research, 2017, 15, 1558-1569.	3.4	43
74	High resolution temporal transcriptomics of mouse embryoid body development reveals complex expression dynamics of coding and noncoding loci. Scientific Reports, 2017, 7, 6731.	3.3	11
75	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.	6.2	77
76	Improved Diagnosis and Care for Rare Diseases through Implementation of Precision Public Health Framework. Advances in Experimental Medicine and Biology, 2017, 1031, 55-94.	1.6	20
77	Widespread promoter methylation of synaptic plasticity genes in long-term potentiation in the adult brain in vivo. BMC Genomics, 2017, 18, 250.	2.8	26
78	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.	14.3	196
79	RNAcentral: a comprehensive database of non-coding RNA sequences. Nucleic Acids Research, 2017, 45, D128-D134.	14.5	174
80	Initiating an undiagnosed diseases program in the Western Australian public health system. Orphanet Journal of Rare Diseases, 2017, 12, 83.	2.7	24
81	Intergenic disease-associated regions are abundant in novel transcripts. Genome Biology, 2017, 18, 241.	8.8	45
82	Somatic mutations in salivary duct carcinoma and potential therapeutic targets. Oncotarget, 2017, 8, 75893-75903.	1.8	22
83	RNA-seq reveals more consistent reference genes for gene expression studies in human non-melanoma skin cancers. PeerJ, 2017, 5, e3631.	2.0	39
84	Claudin-11 and occludin are major contributors to Sertoli cell tight junction function, in vitro. Asian Journal of Andrology, 2016, 18, 620.	1.6	36
85	The Evx1/Evx1as gene locus regulates anterior-posterior patterning during gastrulation. Scientific Reports, 2016, 6, 26657.	3.3	24
86	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, 159-168.	3.2	18
87	Endogenous microRNA sponges: evidence and controversy. Nature Reviews Genetics, 2016, 17, 272-283.	16.3	1,669
88	The Long Noncoding RNA SPRIGHTLY Regulates Cell Proliferation in Primary Human Melanocytes. Journal of Investigative Dermatology, 2016, 136, 819-828.	0.7	34
89	Whole-genome sequencing overcomes pseudogene homology to diagnose autosomal dominant polycystic kidney disease. European Journal of Human Genetics, 2016, 24, 1584-1590.	2.8	63
90	Improved definition of the mouse transcriptome via targeted RNA sequencing. Genome Research, 2016, 26, 705-716.	5.5	33

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91	Endometriosis risk alleles at 1p36.12 act through inverse regulation ofCDC42andLINC00339. Human Molecular Genetics, 2016, 25, ddw320.	2.9	56
92	Defining the genetic basis of early onset hereditary spastic paraplegia using whole genome sequencing. Neurogenetics, 2016, 17, 265-270.	1.4	32
93	Computational Approaches for Functional Prediction and Characterisation of Long Noncoding RNAs. Trends in Genetics, 2016, 32, 620-637.	6.7	89
94	Mutation allele burden remains unchanged in chronic myelomonocytic leukaemia responding to hypomethylating agents. Nature Communications, 2016, 7, 10767.	12.8	177
95	Long noncoding RNAs in cancer: mechanisms of action and technological advancements. Molecular Cancer, 2016, 15, 43.	19.2	387
96	Tu1135 Whole Transcriptome Sequencing Reveals Previously Unrecognized Alterations in Barrett's Esophagus and Esophageal Adenocarcinoma. Gastroenterology, 2016, 150, S854.	1.3	1
97	Comparison of whole-exome sequencing of matched fresh and formalin fixed paraffin embedded melanoma tumours: implications for clinical decision making. Pathology, 2016, 48, 261-266.	0.6	39
98	Gonadotropin suppression in men leads to a reduction in claudin-11 at the Sertoli cell tight junction. Human Reproduction, 2016, 31, 875-886.	0.9	16
99	The specificity of long noncoding RNA expression. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 16-22.	1.9	167
100	Abstract 2664: Eradication of neuroblastoma by suppressing the expression of a single long noncoding RNA. Cancer Research, 2016, 76, 2664-2664.	0.9	1
101	The BET bromodomain inhibitor exerts the most potent synergistic anticancer effects with quinone-containing compounds and anti-microtubule drugs. Oncotarget, 2016, 7, 79217-79232.	1.8	17
102	The long noncoding RNA MALAT1 promotes tumor-driven angiogenesis by up-regulating pro-angiogenic gene expression. Oncotarget, 2016, 7, 8663-8675.	1.8	97
103	Abstract A09: The long noncoding RNA SPRIGHTLY regulates cell proliferation in primary human melanocytes. , 2016, , .		0
104	Abstract B13: Eradication of neuroblastoma by suppressing the expression of a single long noncoding RNA. , 2016, , .		0
105	Abstract 1598: LncRNA AK001796 as a therapeutic target in aggressive breast cancers. Cancer Research, 2016, 76, 1598-1598.	0.9	2
106	Dynamic expression of long noncoding RNAs and repeat elements in synaptic plasticity. Frontiers in Neuroscience, 2015, 9, 351.	2.8	46
107	Genome-wide discovery of human splicing branchpoints. Genome Research, 2015, 25, 290-303.	5.5	222
108	Quantitative gene profiling of long noncoding RNAs with targeted RNA sequencing. Nature Methods, 2015, 12, 339-342.	19.0	155

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109	Cyclin E2 is the predominant E-cyclin associated with NPAT in breast cancer cells. Cell Division, 2015, 10, 1.	2.4	17
110	RNAcentral: an international database of ncRNA sequences. Nucleic Acids Research, 2015, 43, D123-D129.	14.5	103
111	lncRNAdb v2.0: expanding the reference database for functional long noncoding RNAs. Nucleic Acids Research, 2015, 43, D168-D173.	14.5	474
112	Asparagine Synthetase Deficiency causes reduced proliferation of cells under conditions of limited asparagine. Molecular Genetics and Metabolism, 2015, 116, 178-186.	1.1	47
113	Abstract 146: The long noncoding RNA MALAT1 promotes hypoxia-driven angiogenesis by upregulating pro-angiogenic gene expression in neuroblastoma cells. Cancer Research, 2015, 75, 146-146.	0.9	2
114	The impact of genomics on the future of medicine and health. Medical Journal of Australia, 2014, 201, 17-20.	1.7	30
115	The Functional Characterization of Long Noncoding RNASPRY4-IT1in Human Melanoma Cells. Oncotarget, 2014, 5, 8959-8969.	1.8	142
116	Identification of a dinucleotide signature that discriminates coding from non-coding long RNAs. Frontiers in Genetics, 2014, 5, 316.	2.3	6
117	Genomics and personalised whole-of-life healthcare. Trends in Molecular Medicine, 2014, 20, 479-486.	6.7	18
118	Targeted sequencing for gene discovery and quantification using RNA CaptureSeq. Nature Protocols, 2014, 9, 989-1009.	12.0	171
119	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.	3.0	68
120	IL-21 Contributes to Fatal Inflammatory Disease in the Absence of Foxp3+ T Regulatory Cells. Journal of Immunology, 2014, 192, 1404-1414.	0.8	18
121	Effects of a Novel Long Noncoding RNA, lncUSMycN, on N-Myc Expression and Neuroblastoma Progression. Journal of the National Cancer Institute, 2014, 106, .	6.3	98
122	Long non-coding RNAs in disease and development. Pathology, 2014, 46, S26.	0.6	0
123	The histone demethylase JMJD1A induces cell migration and invasion by up-regulating the expression of the long noncoding RNA MALAT1. Oncotarget, 2014, 5, 1793-1804.	1.8	105
124	Saccharopolyspora erythraeaâ€™sgenome is organised in high-order transcriptional regions mediated by targeted degradation at the metabolic switch. BMC Genomics, 2013, 14, 15.	2.8	33
125	Long noncoding RNAs and the genetics of cancer. British Journal of Cancer, 2013, 108, 2419-2425.	6.4	676
126	The extent of functionality in the human genome. The HUGO Journal, 2013, 7, .	4.1	28

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127	Non-coding RNAs in homeostasis, disease and stress responses: an evolutionary perspective. Briefings in Functional Genomics, 2013, 12, 254-278.	2.7	111
128	Genome-wide methylated CpG island profiles of melanoma cells reveal a melanoma coregulation network. Scientific Reports, 2013, 3, 2962.	3.3	22
129	Regulated Expression of PTPRJ/CD148 and an Antisense Long Noncoding RNA in Macrophages by Proinflammatory Stimuli. PLoS ONE, 2013, 8, e68306.	2.5	48
130	Abstract A039: The role of long noncoding RNAs in epithelial to mesenchymal transition and cancer stem cells. , 2013, , .		0
131	Pregnancy-Induced Noncoding RNA (PINC) Associates with Polycomb Repressive Complex 2 and Regulates Mammary Epithelial Differentiation. PLoS Genetics, 2012, 8, e1002840.	3.5	59
132	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, 3042-3050.	4.1	70
133	Genome-wide analysis of long noncoding RNA stability. Genome Research, 2012, 22, 885-898.	5.5	471
134	Targeted RNA sequencing reveals the deep complexity of the human transcriptome. Nature Biotechnology, 2012, 30, 99-104.	17.5	437
135	Expression and Function of the Protein Tyrosine Phosphatase Receptor J (PTPRJ) in Normal Mammary Epithelial Cells and Breast Tumors. PLoS ONE, 2012, 7, e40742.	2.5	22
136	Identification of Novel Markers of Mouse Fetal Ovary Development. PLoS ONE, 2012, 7, e41683.	2.5	42
137	lncRNAdb: a reference database for long noncoding RNAs. Nucleic Acids Research, 2011, 39, D146-D151.	14.5	508
138	The Melanoma-Upregulated Long Noncoding RNA SPRY4-IT1 Modulates Apoptosis and Invasion. Cancer Research, 2011, 71, 3852-3862.	0.9	432
139	The Human Mitochondrial Transcriptome. Cell, 2011, 146, 645-658.	28.9	716
140	The evolution of RNAs with multiple functions. Biochimie, 2011, 93, 2013-2018.	2.6	75
141	Expression of distinct RNAs from 3â€² untranslated regions. Nucleic Acids Research, 2011, 39, 2393-2403.	14.5	185
142	SNORD-host RNA Zfas1 is a regulator of mammary development and a potential marker for breast cancer. Rna, 2011, 17, 878-891.	3.5	321
143	lncRNAs: Finding the Forest Among the Trees?. Molecular Therapy, 2011, 19, 2109-2111.	8.2	2
144	RNAcentral: A vision for an international database of RNA sequences. Rna, 2011, 17, 1941-1946.	3.5	67

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145	Global analysis of the mammalian RNA degradome reveals widespread miRNA-dependent and miRNA-independent endonucleolytic cleavage. Nucleic Acids Research, 2011, 39, 5658-5668.	14.5	76
146	The Reality of Pervasive Transcription. PLoS Biology, 2011, 9, e1000625.	5.6	380
147	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.	2.1	28
148	GATExplorer: Genomic and Transcriptomic Explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. BMC Bioinformatics, 2010, 11, 221.	2.6	75
149	Long noncoding RNAs in neuronal-glial fate specification and oligodendrocyte lineage maturation. BMC Neuroscience, 2010, 11, 14.	1.9	381
150	Nonâ€coding RNAs: regulators of disease. Journal of Pathology, 2010, 220, 126-139.	4.5	906
151	A variant of the KLK4 gene is expressed as a cis sense-antisense chimeric transcript in prostate cancer cells. Rna, 2010, 16, 1156-1166.	3.5	36
152	Regulated post-transcriptional RNA cleavage diversifies the eukaryotic transcriptome. Genome Research, 2010, 20, 1639-1650.	5.5	76
153	MEN Îµ/Î² nuclear-retained non-coding RNAs are up-regulated upon muscle differentiation and are essential components of paraspeckles. Genome Research, 2009, 19, 347-359.	5.5	570
154	Genome-Wide Identification of Long Noncoding RNAs in CD8+ T Cells. Journal of Immunology, 2009, 182, 7738-7748.	0.8	221
155	NRED: a database of long noncoding RNA expression. Nucleic Acids Research, 2009, 37, D122-D126.	14.5	252
156	RNA regulation of epigenetic processes. BioEssays, 2009, 31, 51-59.	2.5	333
157	Long non-coding RNAs: insights into functions. Nature Reviews Genetics, 2009, 10, 155-159.	16.3	5,105
158	Pervasive transcription of the eukaryotic genome: functional indices and conceptual implications. Briefings in Functional Genomics & Proteomics, 2009, 8, 407-423.	3.8	140
159	RNAs as extracellular signaling molecules. Journal of Molecular Endocrinology, 2008, 40, 151-159.	2.5	195
160	Noncoding RNAs in Long-Term Memory Formation. Neuroscientist, 2008, 14, 434-445.	3.5	116
161	The Eukaryotic Genome as an RNA Machine. Science, 2008, 319, 1787-1789.	12.6	579
162	Long noncoding RNAs in mouse embryonic stem cell pluripotency and differentiation. Genome Research, 2008, 18, 1433-1445.	5.5	698

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163	Differentiating Protein-Coding and Noncoding RNA: Challenges and Ambiguities. PLoS Computational Biology, 2008, 4, e1000176.	3.2	493
164	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, 716-721.	7.1	1,081
165	RNAdb 2.0--an expanded database of mammalian non-coding RNAs. Nucleic Acids Research, 2007, 35, D178-D182.	14.5	149
166	Archaeal Genome Organization and Stress Responses: Implications for the Origin and Evolution of Cellular Life. Astrobiology, 2002, 2, 241-253.	3.0	10
167	Growth phase-dependent expression and degradation of histones in the thermophilic archaeon Thermococcus zilligii. Molecular Microbiology, 2000, 36, 876-885.	2.5	31
168	Identification of archaeal genes encoding a novel stationary phase-response protein. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2000, 1490, 115-120.	2.4	4