

Marcel E Dinger

List of Publications by Year in descending order

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Version: 2024-02-01

168
papers

25,139
citations

19608

61
h-index

7136

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. <i>Journal of Drug Targeting</i> , 2022, 30, 1-21.	2.1	8
2	Whole Genome Sequencing, Focused Assays and Functional Studies Increasing Understanding in Cryptic Inherited Retinal Dysrophies. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3905.	1.8	4
3	Interaction between non-coding RNAs, mRNAs and G-quadruplexes. <i>Cancer Cell International</i> , 2022, 22, 171.	1.8	9
4	Use of Whole-Genome Sequencing for Mitochondrial Disease Diagnosis. <i>Neurology</i> , 2022, 99, .	1.5	33
5	Abstract 6298: The novel long noncoding RNA lncNeur promotes neuroblastoma by up-regulating AURKA and Myc expression. <i>Cancer Research</i> , 2022, 82, 6298-6298.	0.4	0
6	Identification of miRNA-mRNA Network in Autism Spectrum Disorder Using a Bioinformatics Method. <i>Journal of Molecular Neuroscience</i> , 2021, 71, 761-766.	1.1	8
7	lncRNAs and miRNAs participate in determination of sensitivity of cancer cells to cisplatin. <i>Experimental and Molecular Pathology</i> , 2021, 123, 104602.	0.9	26
8	Diagnostic Yield of Whole Genome Sequencing After Nondiagnostic Exome Sequencing or Gene Panel in Developmental and Epileptic Encephalopathies. <i>Neurology</i> , 2021, 96, e1770-e1782.	1.5	53
9	ClinSV: clinical grade structural and copy number variant detection from whole genome sequencing data. <i>Genome Medicine</i> , 2021, 13, 32.	3.6	36
10	Emerging role of non-coding RNAs in response of cancer cells to radiotherapy. <i>Pathology Research and Practice</i> , 2021, 218, 153327.	1.0	14
11	The Impact of Non-coding RNAs in the Epithelial to Mesenchymal Transition. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 665199.	1.6	17
12	Destination Amyotrophic Lateral Sclerosis. <i>Frontiers in Neurology</i> , 2021, 12, 596006.	1.1	24
13	Non-coding RNAs modulate function of extracellular matrix proteins. <i>Biomedicine and Pharmacotherapy</i> , 2021, 136, 111240.	2.5	35
14	Different types of disease-causing noncoding variants revealed by genomic and gene expression analyses in families with X-linked intellectual disability. <i>Human Mutation</i> , 2021, 42, 835-847.	1.1	0
15	A Pathway to Precision Medicine for Aboriginal Australians: A Study Protocol. <i>Methods and Protocols</i> , 2021, 4, 42.	0.9	8
16	Genome sequencing in congenital cataracts improves diagnostic yield. <i>Human Mutation</i> , 2021, 42, 1173-1183.	1.1	10
17	Emerging role of circular RNAs in the pathobiology of lung cancer. <i>Biomedicine and Pharmacotherapy</i> , 2021, 141, 111805.	2.5	9
18	Genomic diagnostics in polycystic kidney disease: an assessment of real-world use of whole-genome sequencing. <i>European Journal of Human Genetics</i> , 2021, 29, 760-770.	1.4	20

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19	Overcoming challenges and dogmas to understand the functions of pseudogenes. <i>Nature Reviews Genetics</i> , 2020, 21, 191-201.	7.7	151
20	Dysregulation of non-coding RNAs in autoimmune thyroid disease. <i>Experimental and Molecular Pathology</i> , 2020, 117, 104527.	0.9	8
21	Emerging roles of non-coding RNAs in the pathogenesis of type 1 diabetes mellitus. <i>Biomedicine and Pharmacotherapy</i> , 2020, 129, 110509.	2.5	21
22	Perspectives on the Role of Non-Coding RNAs in the Regulation of Expression and Function of the Estrogen Receptor. <i>Cancers</i> , 2020, 12, 2162.	1.7	20
23	Dysregulation of non-coding RNAs in Rheumatoid arthritis. <i>Biomedicine and Pharmacotherapy</i> , 2020, 130, 110617.	2.5	33
24	Equitable Expanded Carrier Screening Needs Indigenous Clinical and Population Genomic Data. <i>American Journal of Human Genetics</i> , 2020, 107, 175-182.	2.6	24
25	The critical roles of lncRNAs in the pathogenesis of melanoma. <i>Experimental and Molecular Pathology</i> , 2020, 117, 104558.	0.9	25
26	Mutations in the exocyst component EXOC2 cause severe defects in human brain development. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	17
27	Revealing hidden genetic diagnoses in the ocular anterior segment disorders. <i>Genetics in Medicine</i> , 2020, 22, 1623-1632.	1.1	31
28	Exploring the Role of Non-Coding RNAs in the Pathophysiology of Systemic Lupus Erythematosus. <i>Biomolecules</i> , 2020, 10, 937.	1.8	27
29	Aberrant RAG-mediated recombination contributes to multiple structural rearrangements in lymphoid blast crisis of chronic myeloid leukemia. <i>Leukemia</i> , 2020, 34, 2051-2063.	3.3	27
30	The Medical Genome Reference Bank contains whole genome and phenotype data of 2570 healthy elderly. <i>Nature Communications</i> , 2020, 11, 435.	5.8	47
31	Non-coding RNAs underlie genetic predisposition to breast cancer. <i>Genome Biology</i> , 2020, 21, 7.	3.8	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. <i>Bioinformatics</i> , 2019, 35, 122-125.	1.8	26
34	Genome sequencing as a first-line genetic test in familial dilated cardiomyopathy. <i>Genetics in Medicine</i> , 2019, 21, 650-662.	1.1	52
35	The long noncoding RNA lncNB1 promotes tumorigenesis by interacting with ribosomal protein RPL35. <i>Nature Communications</i> , 2019, 10, 5026.	5.8	67
36	Attitudes of Australian health professionals towards rapid genomic testing in neonatal and paediatric intensive care. <i>European Journal of Human Genetics</i> , 2019, 27, 1493-1501.	1.4	29

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37	Pathogenic variants in <i>PLOD3</i> result in a Stickler syndrome-like connective tissue disorder with vascular complications. <i>Journal of Medical Genetics</i> , 2019, 56, 629-638.	1.5	23
38	Lipid Uptake Is an Androgen-Enhanced Lipid Supply Pathway Associated with Prostate Cancer Disease Progression and Bone Metastasis. <i>Molecular Cancer Research</i> , 2019, 17, 1166-1179.	1.5	51
39	Mouse Model of Mutated in Colorectal Cancer Gene Deletion Reveals Novel Pathways in Inflammation and Cancer. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2019, 7, 819-839.	2.3	11
40	Preparing Australia for genomic medicine: data, computing and digital health. <i>Medical Journal of Australia</i> , 2019, 210, S30-S32.	0.8	4
41	Genomic stratification and liquid biopsy in a rare adrenocortical carcinoma (ACC) case, with dual lung metastases. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a003764.	0.5	7
42	De Novo Variants Disrupting the HX Repeat Motif of ATN1 Cause a Recognizable Non-Progressive Neurocognitive Syndrome. <i>American Journal of Human Genetics</i> , 2019, 104, 542-552.	2.6	19
43	Development and validation of a targeted gene sequencing panel for application to disparate cancers. <i>Scientific Reports</i> , 2019, 9, 17052.	1.6	18
44	Denisovan, modern human and mouse TNFAIP3 alleles tune A20 phosphorylation and immunity. <i>Nature Immunology</i> , 2019, 20, 1299-1310.	7.0	53
45	Reanalysis and optimisation of bioinformatic pipelines is critical for mutation detection. <i>Human Mutation</i> , 2019, 40, 374-379.	1.1	7
46	RNAcentral: a hub of information for non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2019, 47, D221-D229.	6.5	153
47	Index suffix "prefix overlaps by (<i>w</i>), (<i>k</i>)-minimizer to generate long contigs for reads compression. <i>Bioinformatics</i> , 2019, 35, 2066-2074.	1.8	27
48	Role and practice evolution for genetic counseling in the genomic era: The experience of Australian and UK genetics practitioners. <i>Journal of Genetic Counseling</i> , 2019, 28, 378-387.	0.9	10
49	The Medical Genome Reference Bank: a whole-genome data resource of 4000 healthy elderly individuals. Rationale and cohort design. <i>European Journal of Human Genetics</i> , 2019, 27, 308-316.	1.4	28
50	Response to Brodehl et al.. <i>Genetics in Medicine</i> , 2019, 21, 1248-1249.	1.1	0
51	A Mild PUM1 Mutation Is Associated with Adult-Onset Ataxia, whereas Haploinsufficiency Causes Developmental Delay and Seizures. <i>Cell</i> , 2018, 172, 924-936.e11.	13.5	103
52	I-motif DNA structures are formed in the nuclei of human cells. <i>Nature Chemistry</i> , 2018, 10, 631-637.	6.6	407
53	Evidence that TLR4 Is Not a Receptor for Saturated Fatty Acids but Mediates Lipid-Induced Inflammation by Reprogramming Macrophage Metabolism. <i>Cell Metabolism</i> , 2018, 27, 1096-1110.e5.	7.2	309
54	Universal Alternative Splicing of Noncoding Exons. <i>Cell Systems</i> , 2018, 6, 245-255.e5.	2.9	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. <i>Experimental Eye Research</i> , 2018, 168, 161-170.	1.2	5
56	Machine learning annotation of human branchpoints. <i>Bioinformatics</i> , 2018, 34, 920-927.	1.8	52
57	Integrating exome sequencing into a diagnostic pathway for epileptic encephalopathy: Evidence of clinical utility and cost effectiveness. <i>Molecular Genetics & Genomic Medicine</i> , 2018, 6, 186-199.	0.6	83
58	Whole-exome sequencing reanalysis at 12 months boosts diagnosis and is cost-effective when applied early in Mendelian disorders. <i>Genetics in Medicine</i> , 2018, 20, 1564-1574.	1.1	132
59	NMNAT1 variants cause cone and cone-rod dystrophy. <i>European Journal of Human Genetics</i> , 2018, 26, 428-433.	1.4	23
60	Selection of Antibody Fragments Against Structured DNA by Phage Display. <i>Methods in Molecular Biology</i> , 2018, 1827, 197-209.	0.4	1
61	Whole Genome Sequencing Improves Outcomes of Genetic Testing in Patients With Hypertrophic Cardiomyopathy. <i>Journal of the American College of Cardiology</i> , 2018, 72, 419-429.	1.2	138
62	Whole genome sequencing provides better diagnostic yield and future value than whole exome sequencing. <i>Medical Journal of Australia</i> , 2018, 209, 197-199.	0.8	48
63	Realizing the significance of noncoding functionality in clinical genomics. <i>Experimental and Molecular Medicine</i> , 2018, 50, 1-8.	3.2	81
64	Expanding the spectrum of PEX16 mutations and novel insights into disease mechanisms. <i>Molecular Genetics and Metabolism Reports</i> , 2018, 16, 46-51.	0.4	21
65	The regulatory role of long noncoding RNAs in cancer. <i>Cancer Letters</i> , 2017, 391, 12-19.	3.2	94
66	The long non-coding RNA NEAT1 is responsive to neuronal activity and is associated with hyperexcitability states. <i>Scientific Reports</i> , 2017, 7, 40127.	1.6	92
67	Germline variants in familial pituitary tumour syndrome genes are common in young patients and families with additional endocrine tumours. <i>European Journal of Endocrinology</i> , 2017, 176, 635-644.	1.9	33
68	Benchmarking of RNA-sequencing analysis workflows using whole-transcriptome RT-qPCR expression data. <i>Scientific Reports</i> , 2017, 7, 1559.	1.6	247
69	Somatic mutations in salivary duct carcinoma and potential therapeutic targets. <i>Pathology</i> , 2017, 49, S105.	0.3	1
70	Cancer-associated noncoding mutations affect RNA G-quadruplex-mediated regulation of gene expression. <i>Scientific Reports</i> , 2017, 7, 708.	1.6	37
71	Gonadal mosaicism of a novel IQSEC2 variant causing female limited intellectual disability and epilepsy. <i>European Journal of Human Genetics</i> , 2017, 25, 763-767.	1.4	14
72	A De Novo Mutation in the Sodium-Activated Potassium Channel KCNT2 Alters Ion Selectivity and Causes Epileptic Encephalopathy. <i>Cell Reports</i> , 2017, 21, 926-933.	2.9	40

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73	Novel Aberrations Uncovered in Barrett's Esophagus and Esophageal Adenocarcinoma Using Whole Transcriptome Sequencing. <i>Molecular Cancer Research</i> , 2017, 15, 1558-1569.	1.5	43
74	High resolution temporal transcriptomics of mouse embryoid body development reveals complex expression dynamics of coding and noncoding loci. <i>Scientific Reports</i> , 2017, 7, 6731.	1.6	11
75	Long Noncoding RNAs CUPID1 and CUPID2 Mediate Breast Cancer Risk at 11q13 by Modulating the Response to DNA Damage. <i>American Journal of Human Genetics</i> , 2017, 101, 255-266.	2.6	77
76	Improved Diagnosis and Care for Rare Diseases through Implementation of Precision Public Health Framework. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1031, 55-94.	0.8	20
77	Widespread promoter methylation of synaptic plasticity genes in long-term potentiation in the adult brain in vivo. <i>BMC Genomics</i> , 2017, 18, 250.	1.2	26
78	CCR6 Defines Memory B Cell Precursors in Mouse and Human Germinal Centers, Revealing Light-Zone Location and Predominant Low Antigen Affinity. <i>Immunity</i> , 2017, 47, 1142-1153.e4.	6.6	196
79	RNAcentral: a comprehensive database of non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2017, 45, D128-D134.	6.5	174
80	Initiating an undiagnosed diseases program in the Western Australian public health system. <i>Orphanet Journal of Rare Diseases</i> , 2017, 12, 83.	1.2	24
81	Intergenic disease-associated regions are abundant in novel transcripts. <i>Genome Biology</i> , 2017, 18, 241.	3.8	45
82	Somatic mutations in salivary duct carcinoma and potential therapeutic targets. <i>Oncotarget</i> , 2017, 8, 75893-75903.	0.8	22
83	RNA-seq reveals more consistent reference genes for gene expression studies in human non-melanoma skin cancers. <i>PeerJ</i> , 2017, 5, e3631.	0.9	39
84	Claudin-11 and occludin are major contributors to Sertoli cell tight junction function, in vitro. <i>Asian Journal of Andrology</i> , 2016, 18, 620.	0.8	36
85	The <i>Evx1/Evx1as</i> gene locus regulates anterior-posterior patterning during gastrulation. <i>Scientific Reports</i> , 2016, 6, 26657.	1.6	24
86	Identification of a novel fusion transcript between human relaxin-1 (RLN1) and human relaxin-2 (RLN2) in prostate cancer. <i>Molecular and Cellular Endocrinology</i> , 2016, 420, 159-168.	1.6	18
87	Endogenous microRNA sponges: evidence and controversy. <i>Nature Reviews Genetics</i> , 2016, 17, 272-283.	7.7	1,669
88	The Long Noncoding RNA SPRIGHTLY Regulates Cell Proliferation in Primary Human Melanocytes. <i>Journal of Investigative Dermatology</i> , 2016, 136, 819-828.	0.3	34
89	Whole-genome sequencing overcomes pseudogene homology to diagnose autosomal dominant polycystic kidney disease. <i>European Journal of Human Genetics</i> , 2016, 24, 1584-1590.	1.4	63
90	Improved definition of the mouse transcriptome via targeted RNA sequencing. <i>Genome Research</i> , 2016, 26, 705-716.	2.4	33

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91	Endometriosis risk alleles at 1p36.12 act through inverse regulation of CDC42 and LINC00339. <i>Human Molecular Genetics</i> , 2016, 25, ddw320.	1.4	56
92	Defining the genetic basis of early onset hereditary spastic paraplegia using whole genome sequencing. <i>Neurogenetics</i> , 2016, 17, 265-270.	0.7	32
93	Computational Approaches for Functional Prediction and Characterisation of Long Noncoding RNAs. <i>Trends in Genetics</i> , 2016, 32, 620-637.	2.9	89
94	Mutation allele burden remains unchanged in chronic myelomonocytic leukaemia responding to hypomethylating agents. <i>Nature Communications</i> , 2016, 7, 10767.	5.8	177
95	Long noncoding RNAs in cancer: mechanisms of action and technological advancements. <i>Molecular Cancer</i> , 2016, 15, 43.	7.9	387
96	Tu1135 Whole Transcriptome Sequencing Reveals Previously Unrecognized Alterations in Barrett's Esophagus and Esophageal Adenocarcinoma. <i>Gastroenterology</i> , 2016, 150, S854.	0.6	1
97	Comparison of whole-exome sequencing of matched fresh and formalin fixed paraffin embedded melanoma tumours: implications for clinical decision making. <i>Pathology</i> , 2016, 48, 261-266.	0.3	39
98	Gonadotropin suppression in men leads to a reduction in claudin-11 at the Sertoli cell tight junction. <i>Human Reproduction</i> , 2016, 31, 875-886.	0.4	16
99	The specificity of long noncoding RNA expression. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 16-22.	0.9	167
100	Abstract 2664: Eradication of neuroblastoma by suppressing the expression of a single long noncoding RNA. <i>Cancer Research</i> , 2016, 76, 2664-2664.	0.4	1
101	The BET bromodomain inhibitor exerts the most potent synergistic anticancer effects with quinone-containing compounds and anti-microtubule drugs. <i>Oncotarget</i> , 2016, 7, 79217-79232.	0.8	17
102	The long noncoding RNA MALAT1 promotes tumor-driven angiogenesis by up-regulating pro-angiogenic gene expression. <i>Oncotarget</i> , 2016, 7, 8663-8675.	0.8	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. <i>Cancer Research</i> , 2016, 76, 1598-1598.	0.4	2
106	Dynamic expression of long noncoding RNAs and repeat elements in synaptic plasticity. <i>Frontiers in Neuroscience</i> , 2015, 9, 351.	1.4	46
107	Genome-wide discovery of human splicing branchpoints. <i>Genome Research</i> , 2015, 25, 290-303.	2.4	222
108	Quantitative gene profiling of long noncoding RNAs with targeted RNA sequencing. <i>Nature Methods</i> , 2015, 12, 339-342.	9.0	155

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109	Cyclin E2 is the predominant E-cyclin associated with NPAT in breast cancer cells. <i>Cell Division</i> , 2015, 10, 1.	1.1	17
110	RNAcentral: an international database of ncRNA sequences. <i>Nucleic Acids Research</i> , 2015, 43, D123-D129.	6.5	103
111	lncRNAdb v2.0: expanding the reference database for functional long noncoding RNAs. <i>Nucleic Acids Research</i> , 2015, 43, D168-D173.	6.5	474
112	Asparagine Synthetase Deficiency causes reduced proliferation of cells under conditions of limited asparagine. <i>Molecular Genetics and Metabolism</i> , 2015, 116, 178-186.	0.5	47
113	Abstract 146: The long noncoding RNA MALAT1 promotes hypoxia-driven angiogenesis by upregulating pro-angiogenic gene expression in neuroblastoma cells. <i>Cancer Research</i> , 2015, 75, 146-146.	0.4	2
114	The impact of genomics on the future of medicine and health. <i>Medical Journal of Australia</i> , 2014, 201, 17-20.	0.8	30
115	The Functional Characterization of Long Noncoding RNA <i>SPRY4-IT1</i> in Human Melanoma Cells. <i>Oncotarget</i> , 2014, 5, 8959-8969.	0.8	142
116	Identification of a dinucleotide signature that discriminates coding from non-coding long RNAs. <i>Frontiers in Genetics</i> , 2014, 5, 316.	1.1	6
117	Genomics and personalised whole-of-life healthcare. <i>Trends in Molecular Medicine</i> , 2014, 20, 479-486.	3.5	18
118	Targeted sequencing for gene discovery and quantification using RNA CaptureSeq. <i>Nature Protocols</i> , 2014, 9, 989-1009.	5.5	171
119	The role of microRNAs and long non-coding RNAs in the pathology, diagnosis, and management of melanoma. <i>Archives of Biochemistry and Biophysics</i> , 2014, 563, 60-70.	1.4	68
120	IL-21 Contributes to Fatal Inflammatory Disease in the Absence of Foxp3+ T Regulatory Cells. <i>Journal of Immunology</i> , 2014, 192, 1404-1414.	0.4	18
121	Effects of a Novel Long Noncoding RNA, lncUSMycN, on N-Myc Expression and Neuroblastoma Progression. <i>Journal of the National Cancer Institute</i> , 2014, 106, .	3.0	98
122	Long non-coding RNAs in disease and development. <i>Pathology</i> , 2014, 46, S26.	0.3	0
123	The histone demethylase JMJD1A induces cell migration and invasion by up-regulating the expression of the long noncoding RNA MALAT1. <i>Oncotarget</i> , 2014, 5, 1793-1804.	0.8	105
124	<i>Saccharopolyspora erythraea</i> genome is organised in high-order transcriptional regions mediated by targeted degradation at the metabolic switch. <i>BMC Genomics</i> , 2013, 14, 15.	1.2	33
125	Long noncoding RNAs and the genetics of cancer. <i>British Journal of Cancer</i> , 2013, 108, 2419-2425.	2.9	676
126	The extent of functionality in the human genome. <i>The HUGO Journal</i> , 2013, 7, .	4.1	28

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127	Non-coding RNAs in homeostasis, disease and stress responses: an evolutionary perspective. <i>Briefings in Functional Genomics</i> , 2013, 12, 254-278.	1.3	111
128	Genome-wide methylated CpG island profiles of melanoma cells reveal a melanoma coregulation network. <i>Scientific Reports</i> , 2013, 3, 2962.	1.6	22
129	Regulated Expression of PTPRJ/CD148 and an Antisense Long Noncoding RNA in Macrophages by Proinflammatory Stimuli. <i>PLoS ONE</i> , 2013, 8, e68306.	1.1	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. <i>PLoS Genetics</i> , 2012, 8, e1002840.	1.5	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. <i>Bioinformatics</i> , 2012, 28, 3042-3050.	1.8	70
133	Genome-wide analysis of long noncoding RNA stability. <i>Genome Research</i> , 2012, 22, 885-898.	2.4	471
134	Targeted RNA sequencing reveals the deep complexity of the human transcriptome. <i>Nature Biotechnology</i> , 2012, 30, 99-104.	9.4	437
135	Expression and Function of the Protein Tyrosine Phosphatase Receptor J (PTPRJ) in Normal Mammary Epithelial Cells and Breast Tumors. <i>PLoS ONE</i> , 2012, 7, e40742.	1.1	22
136	Identification of Novel Markers of Mouse Fetal Ovary Development. <i>PLoS ONE</i> , 2012, 7, e41683.	1.1	42
137	lncRNADB: a reference database for long noncoding RNAs. <i>Nucleic Acids Research</i> , 2011, 39, D146-D151.	6.5	508
138	The Melanoma-Upregulated Long Noncoding RNA <i>SPRY4-IT1</i> Modulates Apoptosis and Invasion. <i>Cancer Research</i> , 2011, 71, 3852-3862.	0.4	432
139	The Human Mitochondrial Transcriptome. <i>Cell</i> , 2011, 146, 645-658.	13.5	716
140	The evolution of RNAs with multiple functions. <i>Biochimie</i> , 2011, 93, 2013-2018.	1.3	75
141	Expression of distinct RNAs from 3' untranslated regions. <i>Nucleic Acids Research</i> , 2011, 39, 2393-2403.	6.5	185
142	SNORD-host RNA <i>Zfas1</i> is a regulator of mammary development and a potential marker for breast cancer. <i>Rna</i> , 2011, 17, 878-891.	1.6	321
143	lncRNAs: Finding the Forest Among the Trees?. <i>Molecular Therapy</i> , 2011, 19, 2109-2111.	3.7	2
144	RNAcentral: A vision for an international database of RNA sequences. <i>Rna</i> , 2011, 17, 1941-1946.	1.6	67

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145	Global analysis of the mammalian RNA degradome reveals widespread miRNA-dependent and miRNA-independent endonucleolytic cleavage. <i>Nucleic Acids Research</i> , 2011, 39, 5658-5668.	6.5	76
146	The Reality of Pervasive Transcription. <i>PLoS Biology</i> , 2011, 9, e1000625.	2.6	380
147	Protein-coding and non-coding gene expression analysis in differentiating human keratinocytes using a three-dimensional epidermal equivalent. <i>Molecular Genetics and Genomics</i> , 2010, 284, 1-9.	1.0	28
148	GATEExplorer: Genomic and Transcriptomic Explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. <i>BMC Bioinformatics</i> , 2010, 11, 221.	1.2	75
149	Long noncoding RNAs in neuronal-glia fate specification and oligodendrocyte lineage maturation. <i>BMC Neuroscience</i> , 2010, 11, 14.	0.8	381
150	Non-coding RNAs: regulators of disease. <i>Journal of Pathology</i> , 2010, 220, 126-139.	2.1	906
151	A variant of the KLK4 gene is expressed as a cis sense-antisense chimeric transcript in prostate cancer cells. <i>Rna</i> , 2010, 16, 1156-1166.	1.6	36
152	Regulated post-transcriptional RNA cleavage diversifies the eukaryotic transcriptome. <i>Genome Research</i> , 2010, 20, 1639-1650.	2.4	76
153	<i>MEN1</i> nuclear-retained non-coding RNAs are up-regulated upon muscle differentiation and are essential components of paraspeckles. <i>Genome Research</i> , 2009, 19, 347-359.	2.4	570
154	Genome-Wide Identification of Long Noncoding RNAs in CD8+ T Cells. <i>Journal of Immunology</i> , 2009, 182, 7738-7748.	0.4	221
155	NRED: a database of long noncoding RNA expression. <i>Nucleic Acids Research</i> , 2009, 37, D122-D126.	6.5	252
156	RNA regulation of epigenetic processes. <i>BioEssays</i> , 2009, 31, 51-59.	1.2	333
157	Long non-coding RNAs: insights into functions. <i>Nature Reviews Genetics</i> , 2009, 10, 155-159.	7.7	5,105
158	Pervasive transcription of the eukaryotic genome: functional indices and conceptual implications. <i>Briefings in Functional Genomics & Proteomics</i> , 2009, 8, 407-423.	3.8	140
159	RNAs as extracellular signaling molecules. <i>Journal of Molecular Endocrinology</i> , 2008, 40, 151-159.	1.1	195
160	Noncoding RNAs in Long-Term Memory Formation. <i>Neuroscientist</i> , 2008, 14, 434-445.	2.6	116
161	The Eukaryotic Genome as an RNA Machine. <i>Science</i> , 2008, 319, 1787-1789.	6.0	579
162	Long noncoding RNAs in mouse embryonic stem cell pluripotency and differentiation. <i>Genome Research</i> , 2008, 18, 1433-1445.	2.4	698

#	ARTICLE	IF	CITATIONS
163	Differentiating Protein-Coding and Noncoding RNA: Challenges and Ambiguities. <i>PLoS Computational Biology</i> , 2008, 4, e1000176.	1.5	493
164	Specific expression of long noncoding RNAs in the mouse brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 716-721.	3.3	1,081
165	RNAdb 2.0—an expanded database of mammalian non-coding RNAs. <i>Nucleic Acids Research</i> , 2007, 35, D178-D182.	6.5	149
166	Archaeal Genome Organization and Stress Responses: Implications for the Origin and Evolution of Cellular Life. <i>Astrobiology</i> , 2002, 2, 241-253.	1.5	10
167	Growth phase-dependent expression and degradation of histones in the thermophilic archaeon <i>Thermococcus zilligii</i> . <i>Molecular Microbiology</i> , 2000, 36, 876-885.	1.2	31
168	Identification of archaeal genes encoding a novel stationary phase-response protein. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2000, 1490, 115-120.	2.4	4