Marcel E Dinger

List of Publications by Year
in descending order

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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	Long non-coding RNAs: insights into functions. Nature Reviews Genetics, 2009, 10, 155-159.	7.7	5,105
2	Endogenous microRNA sponges: evidence and controversy. Nature Reviews Genetics, 2016, 17, 272-283.	7.7	1,669
3	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.	3.3	1,081
4	Nonâ€coding RNAs: regulators of disease. Journal of Pathology, 2010, 220, 126-139.	2.1	906
5	The Human Mitochondrial Transcriptome. Cell, 2011, 146, 645-658.	13.5	716
6	Long noncoding RNAs in mouse embryonic stem cell pluripotency and differentiation. Genome Research, 2008, 18, 1433-1445.	2.4	698
7	Long noncoding RNAs and the genetics of cancer. British Journal of Cancer, 2013, 108, 2419-2425.	2.9	676
8	The Eukaryotic Genome as an RNA Machine. Science, 2008, 319, 1787-1789.	6.0	579
9	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.	2.4	570
10	lncRNAdb: a reference database for long noncoding RNAs. Nucleic Acids Research, 2011, 39, D146-D151.	6.5	508
11	Differentiating Protein-Coding and Noncoding RNA: Challenges and Ambiguities. PLoS Computational Biology, 2008, 4, e1000176.	1.5	493
12	lncRNAdb v2.0: expanding the reference database for functional long noncoding RNAs. Nucleic Acids Research, 2015, 43, D168-D173.	6.5	474
13	Genome-wide analysis of long noncoding RNA stability. Genome Research, 2012, 22, 885-898.	2.4	471
14	Targeted RNA sequencing reveals the deep complexity of the human transcriptome. Nature Biotechnology, 2012, 30, 99-104.	9.4	437
15	The Melanoma-Upregulated Long Noncoding RNA SPRY4-IT1 Modulates Apoptosis and Invasion. Cancer Research, 2011, 71, 3852-3862.	0.4	432
16	I-motif DNA structures are formed in the nuclei of human cells. Nature Chemistry, 2018, 10, 631-637.	6.6	407
17	Long noncoding RNAs in cancer: mechanisms of action and technological advancements. Molecular Cancer, 2016, 15, 43.	7.9	387
18	Long noncoding RNAs in neuronal-glial fate specification and oligodendrocyte lineage maturation. BMC Neuroscience, 2010, 11, 14.	0.8	381

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19	The Reality of Pervasive Transcription. PLoS Biology, 2011, 9, e1000625.	2.6	380
20	RNA regulation of epigenetic processes. BioEssays, 2009, 31, 51-59.	1.2	333
21	SNORD-host RNA Zfas1 is a regulator of mammary development and a potential marker for breast cancer. Rna, 2011, 17, 878-891.	1.6	321
22	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.	7.2	309
23	NRED: a database of long noncoding RNA expression. Nucleic Acids Research, 2009, 37, D122-D126.	6.5	252
24	Benchmarking of RNA-sequencing analysis workflows using whole-transcriptome RT-qPCR expression data. Scientific Reports, 2017, 7, 1559.	1.6	247
25	Genome-wide discovery of human splicing branchpoints. Genome Research, 2015, 25, 290-303.	2.4	222
26	Genome-Wide Identification of Long Noncoding RNAs in CD8+ T Cells. Journal of Immunology, 2009, 182, 7738-7748.	0.4	221
27	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.	6.6	196
28	RNAs as extracellular signaling molecules. Journal of Molecular Endocrinology, 2008, 40, 151-159.	1.1	195
29	Expression of distinct RNAs from 3â€² untranslated regions. Nucleic Acids Research, 2011, 39, 2393-2403.	6.5	185
30	Mutation allele burden remains unchanged in chronic myelomonocytic leukaemia responding to hypomethylating agents. Nature Communications, 2016, 7, 10767.	5.8	177
31	RNAcentral: a comprehensive database of non-coding RNA sequences. Nucleic Acids Research, 2017, 45, D128-D134.	6.5	174
32	Targeted sequencing for gene discovery and quantification using RNA CaptureSeq. Nature Protocols, 2014, 9, 989-1009.	5.5	171
33	The specificity of long noncoding RNA expression. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 16-22.	0.9	167
34	Quantitative gene profiling of long noncoding RNAs with targeted RNA sequencing. Nature Methods, 2015, 12, 339-342.	9.0	155
35	RNAcentral: a hub of information for non-coding RNA sequences. Nucleic Acids Research, 2019, 47, D221-D229.	6.5	153
36	Overcoming challenges and dogmas to understand the functions of pseudogenes. Nature Reviews Genetics, 2020, 21, 191-201.	7.7	151

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37	RNAdb 2.0--an expanded database of mammalian non-coding RNAs. Nucleic Acids Research, 2007, 35, D178-D182.	6.5	149
38	The Functional Characterization of Long Noncoding RNASPRY4-IT1in Human Melanoma Cells. Oncotarget, 2014, 5, 8959-8969.	0.8	142
39	Pervasive transcription of the eukaryotic genome: functional indices and conceptual implications. Briefings in Functional Genomics & Proteomics, 2009, 8, 407-423.	3.8	140
40	Whole Genome Sequencing Improves Outcomes of Genetic Testing in Patients With Hypertrophic Cardiomyopathy. Journal of the American College of Cardiology, 2018, 72, 419-429.	1.2	138
41	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.	1.1	132
42	Noncoding RNAs in Long-Term Memory Formation. Neuroscientist, 2008, 14, 434-445.	2.6	116
43	Non-coding RNAs in homeostasis, disease and stress responses: an evolutionary perspective. Briefings in Functional Genomics, 2013, 12, 254-278.	1.3	111
44	Universal Alternative Splicing of Noncoding Exons. Cell Systems, 2018, 6, 245-255.e5.	2.9	110
45	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.	0.8	105
46	RNAcentral: an international database of ncRNA sequences. Nucleic Acids Research, 2015, 43, D123-D129.	6.5	103
47	A Mild PUM1 Mutation Is Associated with Adult-Onset Ataxia, whereas Haploinsufficiency Causes Developmental Delay and Seizures. Cell, 2018, 172, 924-936.e11.	13.5	103
48	Effects of a Novel Long Noncoding RNA, lncUSMycN, on N-Myc Expression and Neuroblastoma Progression. Journal of the National Cancer Institute, 2014, 106, .	3.0	98
49	The long noncoding RNA MALAT1 promotes tumor-driven angiogenesis by up-regulating pro-angiogenic gene expression. Oncotarget, 2016, 7, 8663-8675.	0.8	97
50	The regulatory role of long noncoding RNAs in cancer. Cancer Letters, 2017, 391, 12-19.	3.2	94
51	The long non-coding RNA NEAT1 is responsive to neuronal activity and is associated with hyperexcitability states. Scientific Reports, 2017, 7, 40127.	1.6	92
52	Computational Approaches for Functional Prediction and Characterisation of Long Noncoding RNAs. Trends in Genetics, 2016, 32, 620-637.	2.9	89
53	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.	0.6	83
54	Realizing the significance of noncoding functionality in clinical genomics. Experimental and Molecular Medicine, 2018, 50, 1-8.	3.2	81

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55	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.	2.6	77
56	Regulated post-transcriptional RNA cleavage diversifies the eukaryotic transcriptome. Genome Research, 2010, 20, 1639-1650.	2.4	76
57	Global analysis of the mammalian RNA degradome reveals widespread miRNA-dependent and miRNA-independent endonucleolytic cleavage. Nucleic Acids Research, 2011, 39, 5658-5668.	6.5	76
58	GATExplorer: Genomic and Transcriptomic Explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. BMC Bioinformatics, 2010, 11, 221.	1.2	75
59	The evolution of RNAs with multiple functions. Biochimie, 2011, 93, 2013-2018.	1.3	75
60	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.	1.8	70
61	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.	1.4	68
62	RNAcentral: A vision for an international database of RNA sequences. Rna, 2011, 17, 1941-1946.	1.6	67
63	The long noncoding RNA lncNB1 promotes tumorigenesis by interacting with ribosomal protein RPL35. Nature Communications, 2019, 10, 5026.	5.8	67
64	Whole-genome sequencing overcomes pseudogene homology to diagnose autosomal dominant polycystic kidney disease. European Journal of Human Genetics, 2016, 24, 1584-1590.	1.4	63
65	Pregnancy-Induced Noncoding RNA (PINC) Associates with Polycomb Repressive Complex 2 and Regulates Mammary Epithelial Differentiation. PLoS Genetics, 2012, 8, e1002840.	1.5	59
66	Endometriosis risk alleles at 1p36.12 act through inverse regulation ofCDC42andLINC00339. Human Molecular Genetics, 2016, 25, ddw320.	1.4	56
67	Denisovan, modern human and mouse TNFAIP3 alleles tune A20 phosphorylation and immunity. Nature Immunology, 2019, 20, 1299-1310.	7.0	53
68	Diagnostic Yield of Whole Genome Sequencing After Nondiagnostic Exome Sequencing or Gene Panel in Developmental and Epileptic Encephalopathies. Neurology, 2021, 96, e1770-e1782.	1.5	53
69	Machine learning annotation of human branchpoints. Bioinformatics, 2018, 34, 920-927.	1.8	52
70	Genome sequencing as a first-line genetic test in familial dilated cardiomyopathy. Genetics in Medicine, 2019, 21, 650-662.	1.1	52
71	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.	1.5	51
72	Regulated Expression of PTPRJ/CD148 and an Antisense Long Noncoding RNA in Macrophages by Proinflammatory Stimuli. PLoS ONE, 2013, 8, e68306.	1.1	48

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73	Whole genome sequencing provides better diagnostic yield and future value than whole exome sequencing. Medical Journal of Australia, 2018, 209, 197-199.	0.8	48
74	Asparagine Synthetase Deficiency causes reduced proliferation of cells under conditions of limited asparagine. Molecular Genetics and Metabolism, 2015, 116, 178-186.	0.5	47
75	The Medical Genome Reference Bank contains whole genome and phenotype data of 2570 healthy elderly. Nature Communications, 2020, 11, 435.	5.8	47
76	Dynamic expression of long noncoding RNAs and repeat elements in synaptic plasticity. Frontiers in Neuroscience, 2015, 9, 351.	1.4	46
77	Intergenic disease-associated regions are abundant in novel transcripts. Genome Biology, 2017, 18, 241.	3.8	45
78	Novel Aberrations Uncovered in Barrett's Esophagus and Esophageal Adenocarcinoma Using Whole Transcriptome Sequencing. Molecular Cancer Research, 2017, 15, 1558-1569.	1.5	43
79	Identification of Novel Markers of Mouse Fetal Ovary Development. PLoS ONE, 2012, 7, e41683.	1.1	42
80	A De Novo Mutation in the Sodium-Activated Potassium Channel KCNT2 Alters Ion Selectivity and Causes Epileptic Encephalopathy. Cell Reports, 2017, 21, 926-933.	2.9	40
81	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.	0.3	39
82	RNA-seq reveals more consistent reference genes for gene expression studies in human non-melanoma skin cancers. PeerJ, 2017, 5, e3631.	0.9	39
83	Cancer-associated noncoding mutations affect RNA G-quadruplex-mediated regulation of gene expression. Scientific Reports, 2017, 7, 708.	1.6	37
84	A variant of the KLK4 gene is expressed as a cis sense-antisense chimeric transcript in prostate cancer cells. Rna, 2010, 16, 1156-1166.	1.6	36
85	Claudin-11 and occludin are major contributors to Sertoli cell tight junction function, in vitro. Asian Journal of Andrology, 2016, 18, 620.	0.8	36
86	ClinSV: clinical grade structural and copy number variant detection from whole genome sequencing data. Genome Medicine, 2021, 13, 32.	3.6	36
87	Non-coding RNAs modulate function of extracellular matrix proteins. Biomedicine and Pharmacotherapy, 2021, 136, 111240.	2.5	35
88	The Long Noncoding RNA SPRIGHTLY Regulates Cell Proliferation in Primary Human Melanocytes. Journal of Investigative Dermatology, 2016, 136, 819-828.	0.3	34
89	Saccharopolyspora erythraeaâ€™sgenome is organised in high-order transcriptional regions mediated by targeted degradation at the metabolic switch. BMC Genomics, 2013, 14, 15.	1.2	33
90	Improved definition of the mouse transcriptome via targeted RNA sequencing. Genome Research, 2016, 26, 705-716.	2.4	33

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91	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.	1.9	33
92	Dysregulation of non-coding RNAs in Rheumatoid arthritis. Biomedicine and Pharmacotherapy, 2020, 130, 110617.	2.5	33
93	Use of Whole-Genome Sequencing for Mitochondrial Disease Diagnosis. Neurology, 2022, 99, .	1.5	33
94	Defining the genetic basis of early onset hereditary spastic paraplegia using whole genome sequencing. Neurogenetics, 2016, 17, 265-270.	0.7	32
95	Growth phase-dependent expression and degradation of histones in the thermophilic archaeon Thermococcus zilligii. Molecular Microbiology, 2000, 36, 876-885.	1.2	31
96	Revealing hidden genetic diagnoses in the ocular anterior segment disorders. Genetics in Medicine, 2020, 22, 1623-1632.	1.1	31
97	The impact of genomics on the future of medicine and health. Medical Journal of Australia, 2014, 201, 17-20.	0.8	30
98	Attitudes of Australian health professionals towards rapid genomic testing in neonatal and paediatric intensive care. European Journal of Human Genetics, 2019, 27, 1493-1501.	1.4	29
99	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.	1.0	28
100	The extent of functionality in the human genome. The HUGO Journal, 2013, 7, .	4.1	28
101	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.	1.4	28
102	Index suffixâ€“prefix overlaps by (w, k)-minimizer to generate long contigs for reads compression. Bioinformatics, 2019, 35, 2066-2074.	1.8	27
103	Exploring the Role of Non-Coding RNAs in the Pathophysiology of Systemic Lupus Erythematosus. Biomolecules, 2020, 10, 937.	1.8	27
104	Aberrant RAG-mediated recombination contributes to multiple structural rearrangements in lymphoid blast crisis of chronic myeloid leukemia. Leukemia, 2020, 34, 2051-2063.	3.3	27
105	Widespread promoter methylation of synaptic plasticity genes in long-term potentiation in the adult brain in vivo. BMC Genomics, 2017, 18, 250.	1.2	26
106	Seave: a comprehensive web platform for storing and interrogating human genomic variation. Bioinformatics, 2019, 35, 122-125.	1.8	26
107	LncRNAs and miRNAs participate in determination of sensitivity of cancer cells to cisplatin. Experimental and Molecular Pathology, 2021, 123, 104602.	0.9	26
108	The critical roles of lncRNAs in the pathogenesis of melanoma. Experimental and Molecular Pathology, 2020, 117, 104558.	0.9	25

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109	The Evx1/Evx1as gene locus regulates anterior-posterior patterning during gastrulation. Scientific Reports, 2016, 6, 26657.	1.6	24
110	Initiating an undiagnosed diseases program in the Western Australian public health system. Orphanet Journal of Rare Diseases, 2017, 12, 83.	1.2	24
111	Equitable Expanded Carrier Screening Needs Indigenous Clinical and Population Genomic Data. American Journal of Human Genetics, 2020, 107, 175-182.	2.6	24
112	Destination Amyotrophic Lateral Sclerosis. Frontiers in Neurology, 2021, 12, 596006.	1.1	24
113	NMNAT1 variants cause cone and cone-rod dystrophy. European Journal of Human Genetics, 2018, 26, 428-433.	1.4	23
114	Pathogenic variants in PLOD3 result in a Stickler syndrome-like connective tissue disorder with vascular complications. Journal of Medical Genetics, 2019, 56, 629-638.	1.5	23
115	Genome-wide methylated CpG island profiles of melanoma cells reveal a melanoma coregulation network. Scientific Reports, 2013, 3, 2962.	1.6	22
116	Expression and Function of the Protein Tyrosine Phosphatase Receptor J (PTPRJ) in Normal Mammary Epithelial Cells and Breast Tumors. PLoS ONE, 2012, 7, e40742.	1.1	22
117	Somatic mutations in salivary duct carcinoma and potential therapeutic targets. Oncotarget, 2017, 8, 75893-75903.	0.8	22
118	Expanding the spectrum of PEX16 mutations and novel insights into disease mechanisms. Molecular Genetics and Metabolism Reports, 2018, 16, 46-51.	0.4	21
119	Emerging roles of non-coding RNAs in the pathogenesis of type 1 diabetes mellitus. Biomedicine and Pharmacotherapy, 2020, 129, 110509.	2.5	21
120	Non-coding RNAs underlie genetic predisposition to breast cancer. Genome Biology, 2020, 21, 7.	3.8	21
121	Improved Diagnosis and Care for Rare Diseases through Implementation of Precision Public Health Framework. Advances in Experimental Medicine and Biology, 2017, 1031, 55-94.	0.8	20
122	Perspectives on the Role of Non-Coding RNAs in the Regulation of Expression and Function of the Estrogen Receptor. Cancers, 2020, 12, 2162.	1.7	20
123	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.	1.4	20
124	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.	2.6	19
125	Genomics and personalised whole-of-life healthcare. Trends in Molecular Medicine, 2014, 20, 479-486.	3.5	18
126	IL-21 Contributes to Fatal Inflammatory Disease in the Absence of Foxp3+ T Regulatory Cells. Journal of Immunology, 2014, 192, 1404-1414.	0.4	18

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127	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.	1.6	18
128	Development and validation of a targeted gene sequencing panel for application to disparate cancers. Scientific Reports, 2019, 9, 17052.	1.6	18
129	Cyclin E2 is the predominant E-cyclin associated with NPAT in breast cancer cells. Cell Division, 2015, 10, 1.	1.1	17
130	Mutations in the exocyst component EXOC2 cause severe defects in human brain development. Journal of Experimental Medicine, 2020, 217, .	4.2	17
131	The Impact of Non-coding RNAs in the Epithelial to Mesenchymal Transition. Frontiers in Molecular Biosciences, 2021, 8, 665199.	1.6	17
132	The BET bromodomain inhibitor exerts the most potent synergistic anticancer effects with quinone-containing compounds and anti-microtubule drugs. Oncotarget, 2016, 7, 79217-79232.	0.8	17
133	Gonadotropin suppression in men leads to a reduction in claudin-11 at the Sertoli cell tight junction. Human Reproduction, 2016, 31, 875-886.	0.4	16
134	Gonadal mosaicism of a novel IQSEC2 variant causing female limited intellectual disability and epilepsy. European Journal of Human Genetics, 2017, 25, 763-767.	1.4	14
135	Emerging role of non-coding RNAs in response of cancer cells to radiotherapy. Pathology Research and Practice, 2021, 218, 153327.	1.0	14
136	High resolution temporal transcriptomics of mouse embryoid body development reveals complex expression dynamics of coding and noncoding loci. Scientific Reports, 2017, 7, 6731.	1.6	11
137	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.	2.3	11
138	Archaeal Genome Organization and Stress Responses: Implications for the Origin and Evolution of Cellular Life. Astrobiology, 2002, 2, 241-253.	1.5	10
139	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.	0.9	10
140	Genome sequencing in congenital cataracts improves diagnostic yield. Human Mutation, 2021, 42, 1173-1183.	1.1	10
141	Emerging role of circular RNAs in the pathobiology of lung cancer. Biomedicine and Pharmacotherapy, 2021, 141, 111805.	2.5	9
142	Interaction between non-coding RNAs, mRNAs and G-quadruplexes. Cancer Cell International, 2022, 22, 171.	1.8	9
143	Dysregulation of non-coding RNAs in autoimmune thyroid disease. Experimental and Molecular Pathology, 2020, 117, 104527.	0.9	8
144	Identification of miRNA-mRNA Network in Autism Spectrum Disorder Using a Bioinformatics Method. Journal of Molecular Neuroscience, 2021, 71, 761-766.	1.1	8

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145	The role of miRNAs and lncRNAs in conferring resistance to doxorubicin. Journal of Drug Targeting, 2022, 30, 1-21.	2.1	8
146	A Pathway to Precision Medicine for Aboriginal Australians: A Study Protocol. Methods and Protocols, 2021, 4, 42.	0.9	8
147	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.	0.5	7
148	Reanalysis and optimisation of bioinformatic pipelines is critical for mutation detection. Human Mutation, 2019, 40, 374-379.	1.1	7
149	Identification of a dinucleotide signature that discriminates coding from non-coding long RNAs. Frontiers in Genetics, 2014, 5, 316.	1.1	6
150	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.	1.2	5
151	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
152	Preparing Australia for genomic medicine: data, computing and digital health. Medical Journal of Australia, 2019, 210, S30-S32.	0.8	4
153	Whole Genome Sequencing, Focused Assays and Functional Studies Increasing Understanding in Cryptic Inherited Retinal Dystrophies. International Journal of Molecular Sciences, 2022, 23, 3905.	1.8	4
154	lncRNAs: Finding the Forest Among the Trees?. Molecular Therapy, 2011, 19, 2109-2111.	3.7	2
155	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.	0.4	2
156	Abstract 1598: LncRNA AK001796 as a therapeutic target in aggressive breast cancers. Cancer Research, 2016, 76, 1598-1598.	0.4	2
157	Tu1135 Whole Transcriptome Sequencing Reveals Previously Unrecognized Alterations in Barrett's Esophagus and Esophageal Adenocarcinoma. Gastroenterology, 2016, 150, S854.	0.6	1
158	Somatic mutations in salivary duct carcinoma and potential therapeutic targets. Pathology, 2017, 49, S105.	0.3	1
159	Selection of Antibody Fragments Against Structured DNA by Phage Display. Methods in Molecular Biology, 2018, 1827, 197-209.	0.4	1
160	Abstract 2664: Eradication of neuroblastoma by suppressing the expression of a single long noncoding RNA. Cancer Research, 2016, 76, 2664-2664.	0.4	1
161	Long non-coding RNAs in disease and development. Pathology, 2014, 46, S26.	0.3	0
162	Response to Brodehl et al.. Genetics in Medicine, 2019, 21, 1248-1249.	1.1	0

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163	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.	1.1	0
164	Abstract A039: The role of long noncoding RNAs in epithelial to mesenchymal transition and cancer stem cells. , 2013, , .		0
165	Abstract A09: The long noncoding RNA SPRIGHTLY regulates cell proliferation in primary human melanocytes. , 2016, , .		0
166	Abstract B13: Eradication of neuroblastoma by suppressing the expression of a single long noncoding RNA. , 2016, , .		0
167	Abstract 5721: The super-enhancer driven long noncoding RNA lncNB promotes neuroblastoma tumorigenesis. , 2020, , .		0
168	Abstract 6298: The novel long noncoding RNA lncNeur promotes neuroblastoma by up-regulating AURKA and Myc expression. Cancer Research, 2022, 82, 6298-6298.	0.4	0