## John S Mattick

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6071275/publications.pdf Version: 2024-02-01

	950	631
71,579	115	257
citations	h-index	g-index
323	323	69948
docs citations	times ranked	citing authors
	citations 323	71,579 115   citations h-index   323 323

#	Article	IF	CITATIONS
1	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	13.7	5,653
2	Long non-coding RNAs: insights into functions. Nature Reviews Genetics, 2009, 10, 155-159.	7.7	5,105
3	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	13.7	4,709
4	The Transcriptional Landscape of the Mammalian Genome. Science, 2005, 309, 1559-1563.	6.0	3,227
5	â€~Touchdown' PCR to circumvent spurious priming during gene amplification. Nucleic Acids Research, 1991, 19, 4008-4008.	6.5	2,342
6	Non-coding RNA. Human Molecular Genetics, 2006, 15, R17-R29.	1.4	2,052
7	Extracellular DNA Required for Bacterial Biofilm Formation. Science, 2002, 295, 1487-1487.	6.0	1,754
8	Antisense Transcription in the Mammalian Transcriptome. Science, 2005, 309, 1564-1566.	6.0	1,553
9	Ultraconserved Elements in the Human Genome. Science, 2004, 304, 1321-1325.	6.0	1,496
10	Structure and function of long noncoding RNAs in epigenetic regulation. Nature Structural and Molecular Biology, 2013, 20, 300-307.	3.6	1,325
11	The rise of regulatory RNA. Nature Reviews Genetics, 2014, 15, 423-437.	7.7	1,120
12	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
13	Type IV Pili and Twitching Motility. Annual Review of Microbiology, 2002, 56, 289-314.	2.9	1,059
14	Non oding RNAs: regulators of disease. Journal of Pathology, 2010, 220, 126-139.	2.1	906
15	Nonâ€coding RNAs: the architects of eukaryotic complexity. EMBO Reports, 2001, 2, 986-991.	2.0	728
16	The Human Mitochondrial Transcriptome. Cell, 2011, 146, 645-658.	13.5	716
17	Long noncoding RNAs in mouse embryonic stem cell pluripotency and differentiation. Genome Research, 2008, 18, 1433-1445.	2.4	698
18	Long noncoding RNAs and the genetics of cancer. British Journal of Cancer, 2013, 108, 2419-2425.	2.9	676

#	Article	IF	CITATIONS
19	RNA regulation: a new genetics?. Nature Reviews Genetics, 2004, 5, 316-323.	7.7	647
20	The Genetic Signatures of Noncoding RNAs. PLoS Genetics, 2009, 5, e1000459.	1.5	639
21	Somatic retrotransposition alters the genetic landscape of the human brain. Nature, 2011, 479, 534-537.	13.7	621
22	Rapid evolution of noncoding RNAs: lack of conservation does not mean lack of function. Trends in Genetics, 2006, 22, 1-5.	2.9	581
23	Discovery and annotation of long noncoding RNAs. Nature Structural and Molecular Biology, 2015, 22, 5-7.	3.6	581
24	The Eukaryotic Genome as an RNA Machine. Science, 2008, 319, 1787-1789.	6.0	579
25	The relationship between non-protein-coding DNA and eukaryotic complexity. BioEssays, 2007, 29, 288-299.	1.2	578
26	<i>MEN Îμ/β</i> 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
27	RNA Duplex Map in Living Cells Reveals Higher-Order Transcriptome Structure. Cell, 2016, 165, 1267-1279.	13.5	520
28	IncRNAdb: a reference database for long noncoding RNAs. Nucleic Acids Research, 2011, 39, D146-D151.	6.5	508
29	Differentiating Protein-Coding and Noncoding RNA: Challenges and Ambiguities. PLoS Computational Biology, 2008, 4, e1000176.	1.5	493
30	Challenging the dogma: the hidden layer of non-protein-coding RNAs in complex organisms. BioEssays, 2003, 25, 930-939.	1.2	492
31	Touchdown PCR for increased specificity and sensitivity in PCR amplification. Nature Protocols, 2008, 3, 1452-1456.	5.5	480
32	Genome-wide analysis of long noncoding RNA stability. Genome Research, 2012, 22, 885-898.	2.4	471
33	Experimental validation of the regulated expression of large numbers of non-coding RNAs from the mouse genome. Genome Research, 2005, 16, 11-19.	2.4	461
34	Small regulatory RNAs in mammals. Human Molecular Genetics, 2005, 14, R121-R132.	1.4	444
35	Targeted RNA sequencing reveals the deep complexity of the human transcriptome. Nature Biotechnology, 2012, 30, 99-104.	9.4	437
36	The Melanoma-Upregulated Long Noncoding RNA <i>SPRY4-IT1</i> Modulates Apoptosis and Invasion. Cancer Research, 2011, 71, 3852-3862.	0.4	432

#	Article	lF	CITATIONS
37	The Evolution of Controlled Multitasked Gene Networks: The Role of Introns and Other Noncoding RNAs in the Development of Complex Organisms. Molecular Biology and Evolution, 2001, 18, 1611-1630.	3.5	429
38	Long non-coding RNAs in nervous system function and disease. Brain Research, 2010, 1338, 20-35.	1.1	427
39	The RNA modification landscape in human disease. Rna, 2017, 23, 1754-1769.	1.6	427
40	Noncoding RNA in development. Mammalian Genome, 2008, 19, 454-492.	1.0	423
41	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. Nature Genetics, 2009, 41, 553-562.	9.4	408
42	Regulation of Epidermal Growth Factor Receptor Signaling in Human Cancer Cells by MicroRNA-7. Journal of Biological Chemistry, 2009, 284, 5731-5741.	1.6	399
43	The conservation of dinucleotide microsatellites among mammalian genomes allows the use of heterologous PCR primer pairs in closely related species. Genomics, 1991, 10, 654-660.	1.3	393
44	Small RNAs derived from snoRNAs. Rna, 2009, 15, 1233-1240.	1.6	384
45	Long noncoding RNAs in neuronal-glial fate specification and oligodendrocyte lineage maturation. BMC Neuroscience, 2010, 11, 14.	0.8	381
46	The Reality of Pervasive Transcription. PLoS Biology, 2011, 9, e1000625.	2.6	380
47	Analysis of 13 cell types reveals evidence for the expression of numerous novel primate- and tissue-specific microRNAs. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1106-15.	3.3	376
48	Common components in the assembly of type 4 fimbriae, DNA transfer systems, filamentous phage and protein-secretion apparatus: a general system for the formation of surface-associated protein complexes. Molecular Microbiology, 1993, 10, 233-243.	1.2	369
49	Mechanisms of Long Non-coding RNAs in Mammalian Nervous System Development, Plasticity, Disease, and Evolution. Neuron, 2015, 88, 861-877.	3.8	366
50	The long non-coding RNA Gomafu is acutely regulated in response to neuronal activation and involved in schizophrenia-associated alternative splicing. Molecular Psychiatry, 2014, 19, 486-494.	4.1	356
51	RNA regulation of epigenetic processes. BioEssays, 2009, 31, 51-59.	1.2	333
52	Tiny RNAs associated with transcription start sites in animals. Nature Genetics, 2009, 41, 572-578.	9.4	327
53	Accurate detection of m6A RNA modifications in native RNA sequences. Nature Communications, 2019, 10, 4079.	5.8	322
54	SNORD-host RNA <i>Zfas1</i> is a regulator of mammary development and a potential marker for breast cancer. Rna, 2011, 17, 878-891.	1.6	321

#	Article	IF	CITATIONS
55	Long noncoding RNAs in cell biology. Seminars in Cell and Developmental Biology, 2011, 22, 366-376.	2.3	301
56	Characterisation of a Pseudomonas aeruginosa twitching motility gene and evidence for a specialised protein export system widespread in eubacteria. Gene, 1991, 101, 33-44.	1.0	286
57	The Functional Genomics of Noncoding RNA. Science, 2005, 309, 1527-1528.	6.0	281
58	Introns: evolution and function. Current Opinion in Genetics and Development, 1994, 4, 823-831.	1.5	278
59	Noncoding RNAs and RNA Editing in Brain Development, Functional Diversification, and Neurological Disease. Physiological Reviews, 2007, 87, 799-823.	13.1	275
60	Conservation of the regulatory subunit for the Clp ATP-dependent protease in prokaryotes and eukaryotes Proceedings of the National Academy of Sciences of the United States of America, 1990, 87, 3513-3517.	3.3	274
61	Extracellular Vesicles from Neural Stem Cells Transfer IFN-Î <sup>3</sup> via Ifngr1 to Activate Stat1 Signaling in Target Cells. Molecular Cell, 2014, 56, 193-204.	4.5	258
62	NRED: a database of long noncoding RNA expression. Nucleic Acids Research, 2009, 37, D122-D126.	6.5	252
63	Long noncoding RNAs are generated from the mitochondrial genome and regulated by nuclear-encoded proteins. Rna, 2011, 17, 2085-2093.	1.6	251
64	Mechanisms of Thermal Adaptation Revealed From the Genomes of the Antarctic Archaea Methanogenium frigidum and Methanococcoides burtonii. Genome Research, 2003, 13, 1580-1588.	2.4	246
65	A re-examination of twitching motility in Pseudomonas aeruginosa. Microbiology (United Kingdom), 1999, 145, 2863-2873.	0.7	231
66	RNA processing in human mitochondria. Cell Cycle, 2011, 10, 2904-2916.	1.3	226
67	Genome-wide discovery of human splicing branchpoints. Genome Research, 2015, 25, 290-303.	2.4	222
68	Genome-Wide Identification of Long Noncoding RNAs in CD8+ T Cells. Journal of Immunology, 2009, 182, 7738-7748.	0.4	221
69	Long Noncoding RNAs in Cardiac Development and Pathophysiology. Circulation Research, 2012, 111, 1349-1362.	2.0	220
70	<i>Pseudomonas aeruginosa</i> Gene Products PilT and PilU Are Required for Cytotoxicity In Vitro and Virulence in a Mouse Model of Acute Pneumonia. Infection and Immunity, 1999, 67, 3625-3630.	1.0	219
71	Raising the estimate of functional human sequences: Figure 1 Genome Research, 2007, 17, 1245-1253.	2.4	217
72	A new paradigm for developmental biology. Journal of Experimental Biology, 2007, 210, 1526-1547.	0.8	212

#	Article	IF	CITATIONS
73	The central role of RNA in human development and cognition. FEBS Letters, 2011, 585, 1600-1616.	1.3	212
74	Characterization of a complex chemosensory signal transduction system which controls twitching motility in Pseudomonas aeruginosa. Molecular Microbiology, 2004, 52, 873-893.	1.2	208
75	A global view of genomic information – moving beyond the gene and the master regulator. Trends in Genetics, 2010, 26, 21-28.	2.9	208
76	A transcriptional sketch of a primary human breast cancer by 454 deep sequencing. BMC Genomics, 2009, 10, 163.	1.2	205
77	Complex architecture and regulated expression of the <i>Sox2ot</i> locus during vertebrate development. Rna, 2009, 15, 2013-2027.	1.6	200
78	ISIS, the intron information system, reveals the high frequency of alternative splicing in the human genome. Nature Genetics, 2000, 24, 340-341.	9.4	197
79	PilS and PilR, a two-component transcriptional regulatory system controlling expression of type 4 fimbriae in Pseudomonas aeruginosa. Molecular Microbiology, 1993, 7, 669-682.	1.2	196
80	RNAs as extracellular signaling molecules. Journal of Molecular Endocrinology, 2008, 40, 151-159.	1.1	195
81	MicroRNAs in β-Cell Biology, Insulin Resistance, Diabetes and Its Complications. Diabetes, 2011, 60, 1825-1831.	0.3	195
82	Expression of distinct RNAs from 3′ untranslated regions. Nucleic Acids Research, 2011, 39, 2393-2403.	6.5	185
83	Dynamic isomiR regulation in <i>Drosophila</i> development. Rna, 2010, 16, 1881-1888.	1.6	184
84	Triplexator: Detecting nucleic acid triple helices in genomic and transcriptomic data. Genome Research, 2012, 22, 1372-1381.	2.4	181
85	The Dimensions, Dynamics, and Relevance of the Mammalian Noncoding Transcriptome. Trends in Genetics, 2017, 33, 464-478.	2.9	181
86	Differential Regulation of Twitching Motility and Elastase Production by Vfr in Pseudomonas aeruginosa. Journal of Bacteriology, 2002, 184, 3605-3613.	1.0	175
87	Genomics: The amazing complexity of the human transcriptome. European Journal of Human Genetics, 2005, 13, 894-897.	1.4	171
88	Targeted sequencing for gene discovery and quantification using RNA CaptureSeq. Nature Protocols, 2014, 9, 989-1009.	5.5	171
89	FimX, a Multidomain Protein Connecting EnvironmentalSignals to Twitching Motility in Pseudomonasaeruginosa. Journal of Bacteriology, 2003, 185, 7068-7076.	1.0	168
90	Potential in vivo roles of nucleic acid triple-helices. RNA Biology, 2011, 8, 427-439.	1.5	166

#	Article	IF	CITATIONS
91	Genes involved in the biogenesis and function of type-4 fimbriae in Pseudomonas aeruginosa. Gene, 1997, 192, 89-98.	1.0	159
92	MicroRNA regulation of neural plasticity and memory. Neurobiology of Learning and Memory, 2011, 96, 89-94.	1.0	158
93	Quantitative gene profiling of long noncoding RNAs with targeted RNA sequencing. Nature Methods, 2015, 12, 339-342.	9.0	155
94	Identification of a gene, pilV, required for type 4 fimbrial biogenesis in Pseudomonas aeruginosa, whose product possesses a pre-pilin-like leader sequence. Molecular Microbiology, 1995, 16, 485-496.	1.2	152
95	The molecular genetics of type-4 fimbriae in Pseudomonas aeruginosa - a review. Gene, 1996, 179, 147-155.	1.0	152
96	Characterization of a gene, pilU, required for twitching motility but not phage sensitivity in Pseudomonas aeruginosa. Molecular Microbiology, 1994, 13, 1079-1091.	1.2	149
97	RNAdb 2.0an expanded database of mammalian non-coding RNAs. Nucleic Acids Research, 2007, 35, D178-D182.	6.5	149
98	Clusters of Internally Primed Transcripts Reveal Novel Long Noncoding RNAs. PLoS Genetics, 2006, 2, e37.	1.5	148
99	Nuclear-localized tiny RNAs are associated with transcription initiation and splice sites in metazoans. Nature Structural and Molecular Biology, 2010, 17, 1030-1034.	3.6	146
100	The alginate regulator AlgR and an associated sensor FimS are required for twitching motility in Pseudomonas aeruginosa Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 9839-9843.	3.3	145
101	Non-coding RNAs in the nervous system. Journal of Physiology, 2006, 575, 333-341.	1.3	144
102	RNA editing, DNA recoding and the evolution of human cognition. Trends in Neurosciences, 2008, 31, 227-233.	4.2	144
103	Widespread purifying selection on RNA structure in mammals. Nucleic Acids Research, 2013, 41, 8220-8236.	6.5	144
104	Quantitative profiling of pseudouridylation dynamics in native RNAs with nanopore sequencing. Nature Biotechnology, 2021, 39, 1278-1291.	9.4	144
105	The Functional Characterization of Long Noncoding RNA <i>SPRY4-IT1</i> in Human Melanoma Cells. Oncotarget, 2014, 5, 8959-8969.	0.8	142
106	Proteome analysis of extracellular proteins regulated by the las and rhl quorum sensing systems in Pseudomonas aeruginosa PAO1. Microbiology (United Kingdom), 2003, 149, 1311-1322.	0.7	141
107	Pervasive transcription of the eukaryotic genome: functional indices and conceptual implications. Briefings in Functional Genomics & Proteomics, 2009, 8, 407-423.	3.8	140
108	Fimbrial biogenesis genes of Pseudomonas aeruginosa: pilW and pilX increase the similarity of type 4 fimbriae to the GSP protein-secretion systems and pilY1 encodes a gonococcal PilC homologue. Molecular Microbiology, 1996, 22, 161-173.	1.2	136

#	Article	IF	CITATIONS
109	Characterization of pilQ, a new gene required for the biogenesis of type 4 fimbriae in Pseudomonas aeruginosa. Molecular Microbiology, 1993, 9, 857-868.	1.2	135
110	A meta-analysis of the genomic and transcriptomic composition of complex life. Cell Cycle, 2013, 12, 2061-2072.	1.3	134
111	Identification of a novel gene, pilZ, essential for type 4 fimbrial biogenesis in Pseudomonas aeruginosa. Journal of Bacteriology, 1996, 178, 46-53.	1.0	131
112	Identification of vaccine candidate antigens from a genomic analysis of Porphyromonas gingivalis. Vaccine, 2001, 19, 4135-4142.	1.7	127
113	RNAdba comprehensive mammalian noncoding RNA database. Nucleic Acids Research, 2004, 33, D125-D130.	6.5	127
114	Cross-mapping and the identification of editing sites in mature microRNAs in high-throughput sequencing libraries. Genome Research, 2010, 20, 257-264.	2.4	126
115	Spliced synthetic genes as internal controls in RNA sequencing experiments. Nature Methods, 2016, 13, 792-798.	9.0	123
116	The Hidden Genetic Program of Complex Organisms. Scientific American, 2004, 291, 60-67.	1.0	122
117	MicroRNAs Regulate Tumor Angiogenesis Modulated by Endothelial Progenitor Cells. Cancer Research, 2013, 73, 341-352.	0.4	122
118	Quorum Sensing Is Not Required for Twitching Motility in Pseudomonas aeruginosa. Journal of Bacteriology, 2002, 184, 3598-3604.	1.0	121
119	Discrimination of Non-Protein-Coding Transcripts from Protein-Coding mRNA. RNA Biology, 2006, 3, 40-48.	1.5	118
120	Morphogenetic expression of Bacteroides nodosus fimbriae in Pseudomonas aeruginosa. Journal of Bacteriology, 1987, 169, 33-41.	1.0	117
121	Noncoding RNAs in Long-Term Memory Formation. Neuroscientist, 2008, 14, 434-445.	2.6	116
122	Long Noncoding RNA-Directed Epigenetic Regulation of Gene Expression Is Associated With Anxiety-like Behavior in Mice. Biological Psychiatry, 2015, 78, 848-859.	0.7	114
123	Serotype-specific glycoprotein of simian 11 rotavirus: coding assignment and gene sequence Proceedings of the National Academy of Sciences of the United States of America, 1983, 80, 3091-3095.	3.3	113
124	Ultraconserved elements in insect genomes: A highly conserved intronic sequence implicated in the control of homothorax mRNA splicing. Genome Research, 2005, 15, 800-808.	2.4	112
125	DNase l–hypersensitive exons colocalize with promoters and distal regulatory elements. Nature Genetics, 2013, 45, 852-859.	9.4	112
126	Non-coding RNAs in homeostasis, disease and stress responses: an evolutionary perspective. Briefings in Functional Genomics, 2013, 12, 254-278.	1.3	111

#	Article	IF	CITATIONS
127	Differential intron retention in <i>Jumonji</i> chromatin modifier genes is implicated in reptile temperature-dependent sex determination. Science Advances, 2017, 3, e1700731.	4.7	111
128	Universal Alternative Splicing of Noncoding Exons. Cell Systems, 2018, 6, 245-255.e5.	2.9	110
129	The Ras Target AF-6 is a Substrate of the Fam Deubiquitinating Enzyme. Journal of Cell Biology, 1998, 142, 1053-1062.	2.3	109
130	Characterization of a five-cluster required for the biogenesis of type 4 fimbriae in Pseudomonas aeruginosa. Molecular Microbiology, 1995, 16, 497-508.	1.2	108
131	An RNA recognition motif in Wilms' tumour protein (WT1) revealed by structural modelling. Nature Genetics, 1996, 12, 329-332.	9.4	106
132	Large-Scale Appearance of Ultraconserved Elements in Tetrapod Genomes and Slowdown of the Molecular Clock. Molecular Biology and Evolution, 2008, 25, 402-408.	3.5	103
133	An analysis of the organization and evolution of type 4 fimbrial (MePhe) subunit proteins. Journal of Molecular Evolution, 1987, 25, 261-269.	0.8	102
134	Prediction of protein solvent accessibility using support vector machines. Proteins: Structure, Function and Bioinformatics, 2002, 48, 566-570.	1.5	102
135	Transposon-free regions in mammalian genomes. Genome Research, 2005, 16, 164-172.	2.4	102
136	Effects of a Novel Long Noncoding RNA, IncUSMycN, on N-Myc Expression and Neuroblastoma Progression. Journal of the National Cancer Institute, 2014, 106, .	3.0	98
137	Nucleosomes are preferentially positioned at exons in somatic and sperm cells. Cell Cycle, 2009, 8, 3420-3424.	1.3	95
138	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
139	Cloning and expression analysis of a novel mouse gene with sequence similarity to the Drosophila fat facets gene. Mechanisms of Development, 1997, 63, 29-38.	1.7	90
140	Evolution, biogenesis and function of promoter-associated RNAs. Cell Cycle, 2009, 8, 2332-2338.	1.3	89
141	Identification of two genes with prepilin-like leader sequences involved in type 4 fimbrial biogenesis in Pseudomonas aeruginosa. Journal of Bacteriology, 1996, 178, 3809-3817.	1.0	88
142	SVMtm: Support vector machines to predict transmembrane segments. Journal of Computational Chemistry, 2004, 25, 632-636.	1.5	87
143	Pseudomonas aeruginosa fimL regulates multiple virulence functions by intersecting with Vfr-modulated pathways. Molecular Microbiology, 2005, 55, 1357-1378.	1.2	85
144	MicroRNAs in the shoot apical meristem of soybean. Journal of Experimental Botany, 2011, 62, 2495-2506.	2.4	80

#	Article	IF	CITATIONS
145	MATHEMATICS/COMPUTATION: Accelerating Networks. Science, 2005, 307, 856-858.	6.0	79
146	Enhancers active in dopamine neurons are a primary link between genetic variation and neuropsychiatric disease. Nature Neuroscience, 2018, 21, 1482-1492.	7.1	79
147	Phosphorylation of the Pseudomonas aeruginosa Response Regulator AlgR Is Essential for Type IV Fimbria-Mediated Twitching Motility. Journal of Bacteriology, 2002, 184, 4544-4554.	1.0	77
148	Understanding the regulatory and transcriptional complexity of the genome through structure. Genome Research, 2013, 23, 1081-1088.	2.4	77
149	Regulated post-transcriptional RNA cleavage diversifies the eukaryotic transcriptome. Genome Research, 2010, 20, 1639-1650.	2.4	76
150	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
151	Deconstructing the Dogma. Annals of the New York Academy of Sciences, 2009, 1178, 29-46.	1.8	75
152	The evolution of RNAs with multiple functions. Biochimie, 2011, 93, 2013-2018.	1.3	75
153	The dark matter rises: the expanding world of regulatory RNAs. Essays in Biochemistry, 2013, 54, 1-16.	2.1	73
154	Construction of improved vectors for protein production in Pseudomonas aeruginosa. Gene, 1996, 172, 163-164.	1.0	72
155	Characterization of G3BPs: Tissue specific expression, chromosomal localisation andrasGAP120 binding studies. Journal of Cellular Biochemistry, 2002, 84, 173-187.	1.2	70
156	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
157	MicroRNAs-140-5p/140-3p Modulate Leydig Cell Numbers in the Developing Mouse Testis. Biology of Reproduction, 2013, 88, 143-143.	1.2	68
158	The State of Long Non-Coding RNA Biology. Non-coding RNA, 2018, 4, 17.	1.3	67
159	Cloning and expression in Escherichia coli of the gene encoding the structural subunit of Bacteroides nodosus fimbriae. Journal of Bacteriology, 1984, 160, 748-754.	1.0	67
160	Morphogenetic expression of Moraxella bovis fimbriae (pili) in Pseudomonas aeruginosa. Journal of Bacteriology, 1990, 172, 2601-2607.	1.0	65
161	Long noncoding RNAs in cell and developmental biology. Seminars in Cell and Developmental Biology, 2011, 22, 327.	2.3	65
162	RNA as the substrate for epigenomeâ€environment interactions. BioEssays, 2010, 32, 548-552.	1.2	64

#	Article	IF	CITATIONS
163	Transcriptome-wide identification of A > I RNA editing sites by inosine specific cleavage. Rna, 2013, 19, 257-270.	1.6	62
164	Organization of the fimbrial gene region of Bacteroides nodosus: class I and class II strains. Molecular Microbiology, 1991, 5, 543-560.	1.2	61
165	FAM deubiquitylating enzyme is essential for preimplantation mouse embryo development. Mechanisms of Development, 2001, 109, 151-160.	1.7	61
166	Identification of a novel gene, fimV, involved in twitching motility in Pseudomonas aeruginosa The GenBank accession number for the sequence determined in this work is U93274 Microbiology (United) Tj ETQ	ე0 <b>დ</b> ე rgB <sup>-</sup>	T /@wterlock 10
167	An interactive web-based Pseudomonas aeruginosa genome database: discovery of new genes, pathways and structures. Microbiology (United Kingdom), 2000, 146, 2351-2364.	0.7	59
168	Structural venomics reveals evolution of a complex venom by duplication and diversification of an ancient peptide-encoding gene. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 11399-11408.	3.3	59
169	Gene sequences and comparison of the fimbrial subunits representative of Bacteroides nodosus serotypes A to I: class I and class II strains. Molecular Microbiology, 1991, 5, 561-573.	1.2	57
170	Integrative analyses of the RNA modification machinery reveal tissue- and cancer-specific signatures. Genome Biology, 2020, 21, 97.	3.8	57
171	Functional expression of heterologous type 4 fimbriae in Pseudomonas aeruginosa. Gene, 1996, 175, 143-150.	1.0	56
172	Adar3 Is Involved in Learning and Memory in Mice. Frontiers in Neuroscience, 2018, 12, 243.	1.4	54
173	Q pili enhance the attachment of Moraxella bovis to bovine corneas in vitro. Molecular Microbiology, 1993, 7, 285-288.	1.2	50
174	Identification and Analysis of Chromodomain-Containing Proteins Encoded in the Mouse Transcriptome. Genome Research, 2003, 13, 1416-1429.	2.4	50
175	tonB3 Is Required for Normal Twitching Motility and Extracellular Assembly of Type IV Pili. Journal of Bacteriology, 2004, 186, 4387-4389.	1.0	49
176	Charting the unknown epitranscriptome. Nature Reviews Molecular Cell Biology, 2017, 18, 339-340.	16.1	49
177	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
178	Protection of sheep against footrot with a recombinant DNA-based fimbrial vaccine. Veterinary Microbiology, 1987, 14, 393-409.	0.8	47
179	Identification of novel non-coding RNAs using profiles of short sequence reads from next generation sequencing data. BMC Genomics, 2010, 11, 77.	1.2	46
180	Branchedâ€chain amino acid supplementation: impact on signaling and relevance to critical illness. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2013, 5, 449-460.	6.6	46

#	Article	IF	CITATIONS
181	Intergenic disease-associated regions are abundant in novel transcripts. Genome Biology, 2017, 18, 241.	3.8	45
182	The Isolation and Characterization of Fatty-Acid-Synthetase mRNA from Rat Mammary Gland. FEBS Journal, 1981, 114, 643-651.	0.2	44
183	The role of regulatory RNA in cognitive evolution. Trends in Cognitive Sciences, 2012, 16, 497-503.	4.0	44
184	Title is missing!. Genome Biology, 2003, 5, P1.	13.9	43
185	Isolation and characterization of Bacteroides nodosus fimbriae: structural subunit and basal protein antigens. Journal of Bacteriology, 1984, 160, 740-747.	1.0	40
186	Effects of substitution of aspartate-440 and tryptophan-487 in the thiamin diphosphate binding region of pyruvate decarboxylase fromZymomonas mobilis. FEBS Letters, 1992, 296, 95-98.	1.3	39
187	Identification of a gene, pilF, required for type 4 fimbrial biogenesis and twitching motility in Pseudomonas aeruginosa. Gene, 1996, 180, 49-56.	1.0	39
188	Response from Mattick and Alm: common architecture of type 4 fimbriae and complexes involved in macromolecular traffic. Trends in Microbiology, 1995, 3, 411-413.	3.5	38
189	The relationship between transcription initiation RNAs and CCCTC-binding factor (CTCF) localization. Epigenetics and Chromatin, 2011, 4, 13.	1.8	38
190	Shared antigenicity and immunogenicity of type 4 pilins expressed by Pseudomonas aeruginosa, Moraxella bovis, Neisseria gonorrhoaea, Dichelobacter nodosus, and Vibrio cholerae. Infection and Immunity, 1991, 59, 4674-4676.	1.0	38
191	UNCL, the mammalian homologue of UNC-50, is an inner nuclear membrane RNA-binding protein11Published on the World Wide Web on 10 August 2000 Brain Research, 2000, 877, 110-123.	1.1	37
192	Representing genetic variation with synthetic DNA standards. Nature Methods, 2016, 13, 784-791.	9.0	37
193	Escherichia coli contains a set of genes homologous to those involved in protein secretion, DNA uptake and the assembly of type-4 fimbriae in other bacteria. Gene, 1994, 150, 9-15.	1.0	36
194	Accelerating, hyperaccelerating, and decelerating networks. Physical Review E, 2005, 72, 016123.	0.8	36
195	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
196	Mapping of Mitochondrial RNA-Protein Interactions by Digital RNase Footprinting. Cell Reports, 2013, 5, 839-848.	2.9	36
197	Rocking the foundations of molecular genetics. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16400-16401.	3.3	35
198	Orthologous MicroRNA Genes Are Located in Cancer-Associated Genomic Regions in Human and Mouse. PLoS ONE, 2007, 2, e1133.	1.1	34

#	Article	IF	CITATIONS
199	The Long Noncoding RNA SPRIGHTLY Regulates Cell Proliferation in Primary Human Melanocytes. Journal of Investigative Dermatology, 2016, 136, 819-828.	0.3	34
200	Saccharopolyspora erythraea'sgenome is organised in high-order transcriptional regions mediated by targeted degradation at the metabolic switch. BMC Genomics, 2013, 14, 15.	1.2	33
201	Improved definition of the mouse transcriptome via targeted RNA sequencing. Genome Research, 2016, 26, 705-716.	2.4	33
202	Linc-ing Long Noncoding RNAs and Enhancer Function. Developmental Cell, 2010, 19, 485-486.	3.1	31
203	The impact of genomics on the future of medicine and health. Medical Journal of Australia, 2014, 201, 17-20.	0.8	30
204	Triplex-Inspector: an analysis tool for triplex-mediated targeting of genomic loci. Bioinformatics, 2013, 29, 1895-1897.	1.8	29
205	Maintenance of transposon-free regions throughout vertebrate evolution. BMC Genomics, 2007, 8, 470.	1.2	28
206	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
207	The extent of functionality in the human genome. The HUGO Journal, 2013, 7, .	4.1	28
208	Targeted, High-Resolution RNA Sequencing of Non-coding Genomic Regions Associated With Neuropsychiatric Functions. Frontiers in Genetics, 2019, 10, 309.	1.1	28
209	The potential of long noncoding RNA therapies. Trends in Pharmacological Sciences, 2022, 43, 269-280.	4.0	28
210	Co-localization of FAM and AF-6, the mammalian homologues of Drosophila faf and canoe, in mouse eye development. Mechanisms of Development, 2000, 91, 383-386.	1.7	27
211	Refining transcriptional programs in kidney development by integration of deep RNA-sequencing and array-based spatial profiling. BMC Genomics, 2011, 12, 441.	1.2	27
212	Comparative studies of the effects of acridines and other petite inducing drugs on the mitochondrial genome ofSaccharomyces cerevisiae. Molecular Genetics and Genomics, 1977, 152, 267-276.	2.4	26
213	Variation in the structural subunit and basal protein antigens of Bacteroides nodosus fimbriae. Journal of Bacteriology, 1986, 166, 453-460.	1.0	26
214	Construction of a gentamicin resistance gene probe for epidemiological studies. Antimicrobial Agents and Chemotherapy, 1985, 28, 96-102.	1.4	25
215	Biogenesis of mitochondria. Molecular Genetics and Genomics, 1975, 141, 291-304.	2.4	24
216	The first disulphide loop of the rabbit growth hormone receptor is required for binding to the hormone. Journal of Molecular Endocrinology, 1992, 9, 213-220.	1.1	24

#	Article	IF	CITATIONS
217	Isolation and characterization of a new nucleolar protein, Nrap, that is conserved from yeast to humans. Genes To Cells, 2002, 7, 115-132.	0.5	24
218	The Evx1/Evx1as gene locus regulates anterior-posterior patterning during gastrulation. Scientific Reports, 2016, 6, 26657.	1.6	24
219	Initiating an undiagnosed diseases program in the Western Australian public health system. Orphanet Journal of Rare Diseases, 2017, 12, 83.	1.2	24
220	Molecular Evolution of the HBII-52 snoRNA Cluster. Journal of Molecular Biology, 2008, 381, 810-815.	2.0	23
221	Structural and Functional Annotation of Long Noncoding RNAs. Methods in Molecular Biology, 2017, 1526, 65-85.	0.4	23
222	Nucleotide and predicted amino acid sequence of a cDNA clone encoding part of human transketolase. Biochemical and Biophysical Research Communications, 1992, 183, 1159-1166.	1.0	22
223	Molecular characterisation of Australian bovine enteroviruses. Veterinary Microbiology, 1999, 68, 71-81.	0.8	22
224	Is prokaryotic complexity limited by accelerated growth inregulatory overhead?. Genome Biology, 2003, 5, P2.	13.9	22
225	Effect of Site-Specific Mutations in Different Phosphotransfer Domains of the Chemosensory Protein ChpA on Pseudomonas aeruginosa Motility. Journal of Bacteriology, 2006, 188, 8479-8486.	1.0	22
226	Genome-wide methylated CpG island profiles of melanoma cells reveal a melanoma coregulation network. Scientific Reports, 2013, 3, 2962.	1.6	22
227	Prioritising the application of genomic medicine. Npj Genomic Medicine, 2017, 2, 35.	1.7	22
228	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
229	The central role of RNA in the genetic programming of complex organisms. Anais Da Academia Brasileira De Ciencias, 2010, 82, 933-939.	0.3	21
230	Transcription of the fimbrial subunit gene and an associated transfer RNA gene of Pseudomonas aeruginosa. Gene, 1988, 62, 219-227.	1.0	20
231	The human genome and the future of medicine. Medical Journal of Australia, 2003, 179, 212-216.	0.8	20
232	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
233	Type 4 Fimbriae. , 2020, , 127-146.		20
234	Fimbriae of Bacteroides nodosus: protein engineering of the structural subunit for the production of an exogenous peptide. Protein Engineering, Design and Selection, 1989, 2, 365-369.	1.0	19

#	Article	IF	CITATIONS
235	Retinoic acid-dependent upregulation of mouse folate receptor- $\hat{l}\pm$ expression in embryonic stem cells, and conservation of alternative splicing patterns. Gene, 1999, 230, 215-224.	1.0	19
236	Delineating Slowly and Rapidly Evolving Fractions of the Drosophila Genome. Journal of Computational Biology, 2008, 15, 407-430.	0.8	19
237	The Lethal Toxin from Australian Funnel-Web Spiders Is Encoded by an Intronless Gene. PLoS ONE, 2012, 7, e43699.	1.1	19
238	ADRAM is an experience-dependent long noncoding RNA that drives fear extinction through a direct interaction with the chaperone protein 14-3-3. Cell Reports, 2022, 38, 110546.	2.9	19
239	Nucleotide and amino acid sequence analysis of the thymidine kinase gene of a bovine encephalitis herpesvirus. Archives of Virology, 1991, 119, 199-210.	0.9	18
240	A Minimal Tiling Path Cosmid Library for Functional Analysis of the <i>Pseudomonas aeruginosa</i> PAO1 Genome. Microbial & Comparative Genomics, 2000, 5, 189-203.	0.6	18
241	Expression of Transposable Elements in Neural Tissues during Xenopus Development. PLoS ONE, 2011, 6, e22569.	1.1	18
242	Inherent size constraints on prokaryote gene networks due to ?accelerating? growth. Theory in Biosciences, 2005, 123, 381-411.	0.6	17
243	Has evolution learnt how to learn?. EMBO Reports, 2009, 10, 665-665.	2.0	17
244	Replicative Deoxyribonucleic Acid Synthesis in Isolated Mitochondria from <i>Saccharomyces cerevisiae</i> . Journal of Bacteriology, 1977, 130, 973-982.	1.0	17
245	Evidence for a functional association of DNA synthesis with the membrane in mitochondria of Saccharomyces cerevisiae. Molecular Biology Reports, 1975, 2, 101-106.	1.0	16
246	A â€~one tube reaction' for synthesis and amplification of total cDNA from small numbers of cells. Nucleic Acids Research, 1993, 21, 783-783.	6.5	16
247	Reactivation of a macropodid herpesvirus from the eastern grey kangaroo (Macropus giganteus) following corticosteroid treatment. Veterinary Microbiology, 1999, 68, 59-69.	0.8	16
248	Multiple Evolutionary Rate Classes in Animal Genome Evolution. Molecular Biology and Evolution, 2010, 27, 942-953.	3.5	15
249	Bioinformatics analysis of transcriptional regulation of circadian genes in rat liver. BMC Bioinformatics, 2014, 15, 83.	1.2	15
250	The characterisation of an esterase derived fromBabesia bovis and its use as a vaccine. Zeitschrift Für Parasitenkunde (Berlin, Germany), 1983, 69, 703-714.	0.8	14
251	GONOME: measuring correlations between GO terms and genomic positions. BMC Bioinformatics, 2006, 7, 94.	1.2	14
252	Topology and Dynamics of Signaling Networks: In Search of Transcriptional Control of the Inflammatory Response. Annual Review of Biomedical Engineering, 2013, 15, 1-28.	5.7	14

#	Article	IF	CITATIONS
253	Development and trial of a bovine herpesvirus 1 - thymidine kinase deletion virus as a vaccine. Australian Veterinary Journal, 1994, 71, 65-70.	0.5	13
254	Evidence for Control of Splicing by Alternative RNA Secondary Structures in Dipteran Homothorax Pre-mRNA. RNA Biology, 2006, 3, 36-39.	1.5	13
255	Extragenic suppressor mutations that restore twitching motility to <scp><i>fimL</i></scp> mutants of <i><scp>P</scp>seudomonas aeruginosa</i> are associated with elevated intracellular cyclic <scp>AMP</scp> levels. MicrobiologyOpen, 2012, 1, 490-501.	1.2	13
256	Dynamics of Hepatic Gene Expression Profile in a Rat Cecal Ligation and Puncture Model. Journal of Surgical Research, 2012, 176, 583-600.	0.8	13
257	The promise of personalised medicine. Lancet, The, 2016, 387, 433-434.	6.3	13
258	DotAligner: identification and clustering of RNA structure motifs. Genome Biology, 2017, 18, 244.	3.8	13
259	Cenetic Variations of Ultraconserved Elements in the Human Genome. OMICS A Journal of Integrative Biology, 2019, 23, 549-559.	1.0	13
260	Probing the phenomics of noncoding RNA. ELife, 2013, 2, e01968.	2.8	13
261	Mitochondrial DNA replication in petite mutants of yeast: Resistance to inhibition by ethidium bromide, berenil and euflavine. Molecular Genetics and Genomics, 1977, 152, 277-283.	2.4	12
262	Western blot (immunoblot) analysis of the fimbrial antigens of Bacteroides nodosus. Journal of Bacteriology, 1987, 169, 4018-4023.	1.0	12
263	Transpositional shuffling and quality control in male germ cells to enhance evolution of complex organisms. Annals of the New York Academy of Sciences, 2015, 1341, 156-163.	1.8	12
264	Impacts of genomics on the health and social costs of intellectual disability. Journal of Medical Genetics, 2020, 57, 479-486.	1.5	12
265	The location and nucleotide sequence of the thymidine kinase gene of bovine herpesvirus type 1.2. Journal of General Virology, 1990, 71, 2417-2424.	1.3	11
266	Expression of active yeast pyruvate decarboxylase in Escherichia coli. Journal of General Microbiology, 1991, 137, 2811-2815.	2.3	11
267	RNA driving the epigenetic bus. EMBO Journal, 2012, 31, 515-516.	3.5	11
268	CNS cell type–specific gene profiling of P301S tau transgenic mice identifies genes dysregulated by progressive tau accumulation. Journal of Biological Chemistry, 2019, 294, 14149-14162.	1.6	10
269	Identification of major antigenic proteins of bovine herpesvirus 1 and their correlation with virus neutralizing activity. Veterinary Microbiology, 1988, 16, 109-121.	0.8	9
270	Chromosomal location of the human transketolase gene. Cytogenetic and Genome Research, 1992, 61, 274-275.	0.6	9

#	Article	IF	CITATIONS
271	The double life of RNA. Biochimie, 2011, 93, viii-ix.	1.3	9
272	The Genomic Foundation Is Shifting. Science, 2011, 331, 874-874.	6.0	9
273	Subcellular relocalization and nuclear redistribution of the RNA methyltransferases TRMT1 and TRMT1L upon neuronal activation. RNA Biology, 2021, 18, 1905-1919.	1.5	9
274	Stoichiometry Based Steady-State Hepatic Flux Analysis: Computational and Experimental Aspects. Metabolites, 2012, 2, 268-291.	1.3	8
275	Splicing bypasses 3′ end formation signals to allow complex gene architectures. Gene, 2007, 403, 188-193.	1.0	7
276	Long-term gene expression profile dynamics following cecal ligation and puncture in the rat. Journal of Surgical Research, 2012, 178, 431-442.	0.8	7
277	Widespread formation of double-stranded RNAs in testis. Genome Research, 2021, 31, 1174-1186.	2.4	6
278	High frequency of intron retention and clustered H3K4me3-marked nucleosomes in short first introns of human long non-coding RNAs. Epigenetics and Chromatin, 2021, 14, 45.	1.8	6
279	Molecular Biology of the Fimbriae of Dichelobacter (Previously Bacteroides) nodosus. Brock/Springer Series in Contemporary Bioscience, 1993, , 517-545.	0.3	6
280	Seq and You Will Find. Current Gene Therapy, 2016, 16, 220-229.	0.9	6
281	The action of structural analogues of ethidium bromide on the mitochondrial genome of yeast. Molecular Biology Reports, 1977, 3, 443-449.	1.0	5
282	Bovine herpesvirus 1.1—an exotic disease agent?. Australian Veterinary Journal, 1993, 70, 272-273.	0.5	5
283	Stringent Programming of DNA Methylation in Humans. Twin Research and Human Genetics, 2010, 13, 405-411.	0.3	5
284	Homologous Mammalian Brain Cell Lysate System for the Initiation and Translation of Exogenous mRNAs. Journal of Neurochemistry, 1981, 37, 325-332.	2.1	4
285	Identification of conserved Drosophila-specific euchromatin-restricted non-coding sequence motifs. Genomics, 2010, 96, 154-166.	1.3	4
286	Macropodid herpesvirus 1 encodes genes for both thymidylate synthase and ICP34.5. Virus Genes, 2002, 24, 207-213.	0.7	3
287	Extracellular Vesicles from Neural Stem Cells Transfer IFN-Î <sup>3</sup> via Ifngr1 to Activate Stat1 Signaling in Target Cells. Molecular Cell, 2014, 56, 609.	4.5	3
288	The Non-Coding RNA Journal Club: Highlights on Recent Papers. Non-coding RNA, 2015, 1, 87-93.	1.3	3

#	Article	IF	CITATIONS
289	Sequencing and expression of the aroA gene from Dichelobacter nodosus. Gene, 1994, 145, 97-101.	1.0	2
290	RNA lights up. Nature Biotechnology, 2011, 29, 883-884.	9.4	2
291	Abstract 1598: LncRNA AK001796 as a therapeutic target in aggressive breast cancers. Cancer Research, 2016, 76, 1598-1598.	0.4	2
292	Extracellular vesicles from neural stem cells transfer the IFN-γ/IFNGR1 complex to activate Stat1-dependent signalling in target cells. Journal of Neuroimmunology, 2014, 275, 190-191.	1.1	1
293	Genome research. Nature, 1990, 346, 604-604.	13.7	0
294	There's more to a model than code. , 2005, , .		0
295	A NEW UNDERSTANDING OF THE HUMAN GENOME. , 2008, , .		0
296	In grateful recognition of our Editorial Board. BioEssays, 2012, 34, 1004-1005.	1.2	0
297	Response to A. M. Poole: Is all that junk really regulatory RNA?. Nature Reviews Genetics, 2004, 5, 324-324.	7.7	0
298	Abstract A039: The role of long noncoding RNAs in epithelial to mesenchymal transition and cancer stem cells. , 2013, , .		0
299	The Future of Molecular Pathology. , 2016, , 349-357.		0
300	Abstract A09: The long noncoding RNA SPRIGHTLY regulates cell proliferation in primary human melanocytes. , 2016, , .		0
301	Abstract 2453: Eradication of neuroblastoma by suppressing the expression of a single noncoding RNA. , 2018, , .		0
302	Cost effective, experimentally robust differential-expression analysis for human/mammalian, pathogen and dual-species transcriptomics. Microbial Genomics, 2020, 6, .	1.0	0