

# John S Mattick

## List of Publications by Year in descending order

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302  
papers

71,579  
citations

952

115  
h-index

632

257  
g-index

323  
all docs

323  
docs citations

323  
times ranked

69948  
citing authors

#	ARTICLE	IF	CITATIONS
1	The potential of long noncoding RNA therapies. <i>Trends in Pharmacological Sciences</i> , 2022, 43, 269-280.	8.7	28
2	ADRAM is an experience-dependent long noncoding RNA that drives fear extinction through a direct interaction with the chaperone protein 14-3-3. <i>Cell Reports</i> , 2022, 38, 110546.	6.4	19
3	Subcellular relocalization and nuclear redistribution of the RNA methyltransferases TRMT1 and TRMT1L upon neuronal activation. <i>RNA Biology</i> , 2021, 18, 1905-1919.	3.1	9
4	Quantitative profiling of pseudouridylation dynamics in native RNAs with nanopore sequencing. <i>Nature Biotechnology</i> , 2021, 39, 1278-1291.	17.5	144
5	Widespread formation of double-stranded RNAs in testis. <i>Genome Research</i> , 2021, 31, 1174-1186.	5.5	6
6	High frequency of intron retention and clustered H3K4me3-marked nucleosomes in short first introns of human long non-coding RNAs. <i>Epigenetics and Chromatin</i> , 2021, 14, 45.	3.9	6
7	Integrative analyses of the RNA modification machinery reveal tissue- and cancer-specific signatures. <i>Genome Biology</i> , 2020, 21, 97.	8.8	57
8	Structural venomics reveals evolution of a complex venom by duplication and diversification of an ancient peptide-encoding gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11399-11408.	7.1	59
9	Impacts of genomics on the health and social costs of intellectual disability. <i>Journal of Medical Genetics</i> , 2020, 57, 479-486.	3.2	12
10	Type 4 Fimbriae. , 2020, , 127-146.		20
11	Cost effective, experimentally robust differential-expression analysis for human/mammalian, pathogen and dual-species transcriptomics. <i>Microbial Genomics</i> , 2020, 6, .	2.0	0
12	CNS cell type-specific gene profiling of P301S tau transgenic mice identifies genes dysregulated by progressive tau accumulation. <i>Journal of Biological Chemistry</i> , 2019, 294, 14149-14162.	3.4	10
13	Genetic Variations of Ultraconserved Elements in the Human Genome. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 549-559.	2.0	13
14	Accurate detection of m6A RNA modifications in native RNA sequences. <i>Nature Communications</i> , 2019, 10, 4079.	12.8	322
15	Targeted, High-Resolution RNA Sequencing of Non-coding Genomic Regions Associated With Neuropsychiatric Functions. <i>Frontiers in Genetics</i> , 2019, 10, 309.	2.3	28
16	Universal Alternative Splicing of Noncoding Exons. <i>Cell Systems</i> , 2018, 6, 245-255.e5.	6.2	110
17	Enhancers active in dopamine neurons are a primary link between genetic variation and neuropsychiatric disease. <i>Nature Neuroscience</i> , 2018, 21, 1482-1492.	14.8	79
18	Whole genome sequencing provides better diagnostic yield and future value than whole exome sequencing. <i>Medical Journal of Australia</i> , 2018, 209, 197-199.	1.7	48

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19	Adar3 Is Involved in Learning and Memory in Mice. <i>Frontiers in Neuroscience</i> , 2018, 12, 243.	2.8	54
20	The State of Long Non-Coding RNA Biology. <i>Non-coding RNA</i> , 2018, 4, 17.	2.6	67
21	Abstract 2453: Eradication of neuroblastoma by suppressing the expression of a single noncoding RNA. , 2018, , .		0
22	The long non-coding RNA NEAT1 is responsive to neuronal activity and is associated with hyperexcitability states. <i>Scientific Reports</i> , 2017, 7, 40127.	3.3	92
23	Charting the unknown epitranscriptome. <i>Nature Reviews Molecular Cell Biology</i> , 2017, 18, 339-340.	37.0	49
24	Structural and Functional Annotation of Long Noncoding RNAs. <i>Methods in Molecular Biology</i> , 2017, 1526, 65-85.	0.9	23
25	Differential intron retention in <i>Jumonji</i> chromatin modifier genes is implicated in reptile temperature-dependent sex determination. <i>Science Advances</i> , 2017, 3, e1700731.	10.3	111
26	The Dimensions, Dynamics, and Relevance of the Mammalian Noncoding Transcriptome. <i>Trends in Genetics</i> , 2017, 33, 464-478.	6.7	181
27	The RNA modification landscape in human disease. <i>Rna</i> , 2017, 23, 1754-1769.	3.5	427
28	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.	1.6	20
29	Prioritising the application of genomic medicine. <i>Npj Genomic Medicine</i> , 2017, 2, 35.	3.8	22
30	Initiating an undiagnosed diseases program in the Western Australian public health system. <i>Orphanet Journal of Rare Diseases</i> , 2017, 12, 83.	2.7	24
31	Intergenic disease-associated regions are abundant in novel transcripts. <i>Genome Biology</i> , 2017, 18, 241.	8.8	45
32	DotAligner: identification and clustering of RNA structure motifs. <i>Genome Biology</i> , 2017, 18, 244.	8.8	13
33	The <i>Evx1/Evx1as</i> gene locus regulates anterior-posterior patterning during gastrulation. <i>Scientific Reports</i> , 2016, 6, 26657.	3.3	24
34	The Long Noncoding RNA SPRIGHTLY Regulates Cell Proliferation in Primary Human Melanocytes. <i>Journal of Investigative Dermatology</i> , 2016, 136, 819-828.	0.7	34
35	Improved definition of the mouse transcriptome via targeted RNA sequencing. <i>Genome Research</i> , 2016, 26, 705-716.	5.5	33
36	RNA Duplex Map in Living Cells Reveals Higher-Order Transcriptome Structure. <i>Cell</i> , 2016, 165, 1267-1279.	28.9	520

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37	Representing genetic variation with synthetic DNA standards. <i>Nature Methods</i> , 2016, 13, 784-791.	19.0	37
38	Spliced synthetic genes as internal controls in RNA sequencing experiments. <i>Nature Methods</i> , 2016, 13, 792-798.	19.0	123
39	The promise of personalised medicine. <i>Lancet, The</i> , 2016, 387, 433-434.	13.7	13
40	Seq and You Will Find. <i>Current Gene Therapy</i> , 2016, 16, 220-229.	2.0	6
41	The Future of Molecular Pathology. , 2016, , 349-357.		0
42	Abstract A09: The long noncoding RNA SPRIGHTLY regulates cell proliferation in primary human melanocytes. , 2016, , .		0
43	Abstract 1598: LncRNA AK001796 as a therapeutic target in aggressive breast cancers. <i>Cancer Research</i> , 2016, 76, 1598-1598.	0.9	2
44	The Non-Coding RNA Journal Club: Highlights on Recent Papers. <i>Non-coding RNA</i> , 2015, 1, 87-93.	2.6	3
45	Discovery and annotation of long noncoding RNAs. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 5-7.	8.2	581
46	Genome-wide discovery of human splicing branchpoints. <i>Genome Research</i> , 2015, 25, 290-303.	5.5	222
47	Long Noncoding RNA-Directed Epigenetic Regulation of Gene Expression Is Associated With Anxiety-like Behavior in Mice. <i>Biological Psychiatry</i> , 2015, 78, 848-859.	1.3	114
48	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	27.8	5,653
49	Quantitative gene profiling of long noncoding RNAs with targeted RNA sequencing. <i>Nature Methods</i> , 2015, 12, 339-342.	19.0	155
50	Analysis of 13 cell types reveals evidence for the expression of numerous novel primate- and tissue-specific microRNAs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1106-15.	7.1	376
51	Transpositional shuffling and quality control in male germ cells to enhance evolution of complex organisms. <i>Annals of the New York Academy of Sciences</i> , 2015, 1341, 156-163.	3.8	12
52	Mechanisms of Long Non-coding RNAs in Mammalian Nervous System Development, Plasticity, Disease, and Evolution. <i>Neuron</i> , 2015, 88, 861-877.	8.1	366
53	The impact of genomics on the future of medicine and health. <i>Medical Journal of Australia</i> , 2014, 201, 17-20.	1.7	30
54	The Functional Characterization of Long Noncoding RNA <i>SPRY4-IT1</i> in Human Melanoma Cells. <i>Oncotarget</i> , 2014, 5, 8959-8969.	1.8	142

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55	Extracellular Vesicles from Neural Stem Cells Transfer IFN- $\beta$ via Ifngr1 to Activate Stat1 Signaling in Target Cells. <i>Molecular Cell</i> , 2014, 56, 609.	9.7	3
56	Targeted sequencing for gene discovery and quantification using RNA CaptureSeq. <i>Nature Protocols</i> , 2014, 9, 989-1009.	12.0	171
57	The rise of regulatory RNA. <i>Nature Reviews Genetics</i> , 2014, 15, 423-437.	16.3	1,120
58	Extracellular vesicles from neural stem cells transfer the IFN- $\beta$ /IFNGR1 complex to activate Stat1-dependent signalling in target cells. <i>Journal of Neuroimmunology</i> , 2014, 275, 190-191.	2.3	1
59	Bioinformatics analysis of transcriptional regulation of circadian genes in rat liver. <i>BMC Bioinformatics</i> , 2014, 15, 83.	2.6	15
60	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, .	6.3	98
61	Extracellular Vesicles from Neural Stem Cells Transfer IFN- $\beta$ via Ifngr1 to Activate Stat1 Signaling in Target Cells. <i>Molecular Cell</i> , 2014, 56, 193-204.	9.7	258
62	The long non-coding RNA Gomafu is acutely regulated in response to neuronal activation and involved in schizophrenia-associated alternative splicing. <i>Molecular Psychiatry</i> , 2014, 19, 486-494.	7.9	356
63	Topology and Dynamics of Signaling Networks: In Search of Transcriptional Control of the Inflammatory Response. <i>Annual Review of Biomedical Engineering</i> , 2013, 15, 1-28.	12.3	14
64	<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.	2.8	33
65	Long noncoding RNAs and the genetics of cancer. <i>British Journal of Cancer</i> , 2013, 108, 2419-2425.	6.4	676
66	The extent of functionality in the human genome. <i>The HUGO Journal</i> , 2013, 7, .	4.1	28
67	Understanding the regulatory and transcriptional complexity of the genome through structure. <i>Genome Research</i> , 2013, 23, 1081-1088.	5.5	77
68	Transcriptome-wide identification of A > I RNA editing sites by inosine specific cleavage. <i>Rna</i> , 2013, 19, 257-270.	3.5	62
69	Mapping of Mitochondrial RNA-Protein Interactions by Digital RNase Footprinting. <i>Cell Reports</i> , 2013, 5, 839-848.	6.4	36
70	The dark matter rises: the expanding world of regulatory RNAs. <i>Essays in Biochemistry</i> , 2013, 54, 1-16.	4.7	73
71	DNase I-sensitive exons colocalize with promoters and distal regulatory elements. <i>Nature Genetics</i> , 2013, 45, 852-859.	21.4	112
72	Structure and function of long noncoding RNAs in epigenetic regulation. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 300-307.	8.2	1,325

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73	Triplex-Inspector: an analysis tool for triplex-mediated targeting of genomic loci. <i>Bioinformatics</i> , 2013, 29, 1895-1897.	4.1	29
74	Widespread purifying selection on RNA structure in mammals. <i>Nucleic Acids Research</i> , 2013, 41, 8220-8236.	14.5	144
75	MicroRNAs-140-5p/140-3p Modulate Leydig Cell Numbers in the Developing Mouse Testis. <i>Biology of Reproduction</i> , 2013, 88, 143-143.	2.7	68
76	A meta-analysis of the genomic and transcriptomic composition of complex life. <i>Cell Cycle</i> , 2013, 12, 2061-2072.	2.6	134
77	MicroRNAs Regulate Tumor Angiogenesis Modulated by Endothelial Progenitor Cells. <i>Cancer Research</i> , 2013, 73, 341-352.	0.9	122
78	Non-coding RNAs in homeostasis, disease and stress responses: an evolutionary perspective. <i>Briefings in Functional Genomics</i> , 2013, 12, 254-278.	2.7	111
79	Genome-wide methylated CpG island profiles of melanoma cells reveal a melanoma coregulation network. <i>Scientific Reports</i> , 2013, 3, 2962.	3.3	22
80	Branched-chain amino acid supplementation: impact on signaling and relevance to critical illness. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2013, 5, 449-460.	6.6	46
81	Probing the phenomics of noncoding RNA. <i>ELife</i> , 2013, 2, e01968.	6.0	13
82	Abstract A039: The role of long noncoding RNAs in epithelial to mesenchymal transition and cancer stem cells. , 2013, , .		0
83	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.	4.1	70
84	Long Noncoding RNAs in Cardiac Development and Pathophysiology. <i>Circulation Research</i> , 2012, 111, 1349-1362.	4.5	220
85	In grateful recognition of our Editorial Board. <i>BioEssays</i> , 2012, 34, 1004-1005.	2.5	0
86	Extragenic suppressor mutations that restore twitching motility to <i>Pseudomonas aeruginosa</i> mutants of <i>fimL</i> are associated with elevated intracellular cyclic AMP levels. <i>MicrobiologyOpen</i> , 2012, 1, 490-501.	3.0	13
87	Dynamics of Hepatic Gene Expression Profile in a Rat Cecal Ligation and Puncture Model. <i>Journal of Surgical Research</i> , 2012, 176, 583-600.	1.6	13
88	Long-term gene expression profile dynamics following cecal ligation and puncture in the rat. <i>Journal of Surgical Research</i> , 2012, 178, 431-442.	1.6	7
89	Stoichiometry Based Steady-State Hepatic Flux Analysis: Computational and Experimental Aspects. <i>Metabolites</i> , 2012, 2, 268-291.	2.9	8
90	Rocking the foundations of molecular genetics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16400-16401.	7.1	35

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91	RNA driving the epigenetic bus. <i>EMBO Journal</i> , 2012, 31, 515-516.	7.8	11
92	The Lethal Toxin from Australian Funnel-Web Spiders Is Encoded by an Intronless Gene. <i>PLoS ONE</i> , 2012, 7, e43699.	2.5	19
93	The role of regulatory RNA in cognitive evolution. <i>Trends in Cognitive Sciences</i> , 2012, 16, 497-503.	7.8	44
94	Genome-wide analysis of long noncoding RNA stability. <i>Genome Research</i> , 2012, 22, 885-898.	5.5	471
95	Triplexator: Detecting nucleic acid triple helices in genomic and transcriptomic data. <i>Genome Research</i> , 2012, 22, 1372-1381.	5.5	181
96	Targeted RNA sequencing reveals the deep complexity of the human transcriptome. <i>Nature Biotechnology</i> , 2012, 30, 99-104.	17.5	437
97	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.	2.5	22
98	lncRNAdb: a reference database for long noncoding RNAs. <i>Nucleic Acids Research</i> , 2011, 39, D146-D151.	14.5	508
99	The Melanoma-Upregulated Long Noncoding RNA <i>SPRY4-IT1</i> Modulates Apoptosis and Invasion. <i>Cancer Research</i> , 2011, 71, 3852-3862.	0.9	432
100	The Human Mitochondrial Transcriptome. <i>Cell</i> , 2011, 146, 645-658.	28.9	716
101	The evolution of RNAs with multiple functions. <i>Biochimie</i> , 2011, 93, 2013-2018.	2.6	75
102	MicroRNA regulation of neural plasticity and memory. <i>Neurobiology of Learning and Memory</i> , 2011, 96, 89-94.	1.9	158
103	Long noncoding RNAs in cell biology. <i>Seminars in Cell and Developmental Biology</i> , 2011, 22, 366-376.	5.0	301
104	Long noncoding RNAs in cell and developmental biology. <i>Seminars in Cell and Developmental Biology</i> , 2011, 22, 327.	5.0	65
105	Expression of distinct RNAs from 3' untranslated regions. <i>Nucleic Acids Research</i> , 2011, 39, 2393-2403.	14.5	185
106	The double life of RNA. <i>Biochimie</i> , 2011, 93, viii-ix.	2.6	9
107	Expression of Transposable Elements in Neural Tissues during <i>Xenopus</i> Development. <i>PLoS ONE</i> , 2011, 6, e22569.	2.5	18
108	The central role of RNA in human development and cognition. <i>FEBS Letters</i> , 2011, 585, 1600-1616.	2.8	212

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109	MicroRNAs in $\beta$ -Cell Biology, Insulin Resistance, Diabetes and Its Complications. <i>Diabetes</i> , 2011, 60, 1825-1831.	0.6	195
110	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.	3.5	321
111	RNA lights up. <i>Nature Biotechnology</i> , 2011, 29, 883-884.	17.5	2
112	Somatic retrotransposition alters the genetic landscape of the human brain. <i>Nature</i> , 2011, 479, 534-537.	27.8	621
113	The relationship between transcription initiation RNAs and CCCTC-binding factor (CTCF) localization. <i>Epigenetics and Chromatin</i> , 2011, 4, 13.	3.9	38
114	Refining transcriptional programs in kidney development by integration of deep RNA-sequencing and array-based spatial profiling. <i>BMC Genomics</i> , 2011, 12, 441.	2.8	27
115	RNA processing in human mitochondria. <i>Cell Cycle</i> , 2011, 10, 2904-2916.	2.6	226
116	Potential in vivo roles of nucleic acid triple-helices. <i>RNA Biology</i> , 2011, 8, 427-439.	3.1	166
117	Long noncoding RNAs are generated from the mitochondrial genome and regulated by nuclear-encoded proteins. <i>Rna</i> , 2011, 17, 2085-2093.	3.5	251
118	MicroRNAs in the shoot apical meristem of soybean. <i>Journal of Experimental Botany</i> , 2011, 62, 2495-2506.	4.8	80
119	The Genomic Foundation Is Shifting. <i>Science</i> , 2011, 331, 874-874.	12.6	9
120	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.	14.5	76
121	The Reality of Pervasive Transcription. <i>PLoS Biology</i> , 2011, 9, e1000625.	5.6	380
122	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.	2.1	28
123	A global view of genomic information "moving beyond the gene and the master regulator. <i>Trends in Genetics</i> , 2010, 26, 21-28.	6.7	208
124	Identification of novel non-coding RNAs using profiles of short sequence reads from next generation sequencing data. <i>BMC Genomics</i> , 2010, 11, 77.	2.8	46
125	Long noncoding RNAs in neuronal-glia fate specification and oligodendrocyte lineage maturation. <i>BMC Neuroscience</i> , 2010, 11, 14.	1.9	381
126	Long non-coding RNAs in nervous system function and disease. <i>Brain Research</i> , 2010, 1338, 20-35.	2.2	427



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127	RNA as the substrate for epigenomeâ€environment interactions. <i>BioEssays</i> , 2010, 32, 548-552.	2.5	64
128	Nonâ€coding RNAs: regulators of disease. <i>Journal of Pathology</i> , 2010, 220, 126-139.	4.5	906
129	Nuclear-localized tiny RNAs are associated with transcription initiation and splice sites in metazoans. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1030-1034.	8.2	146
130	The central role of RNA in the genetic programming of complex organisms. <i>Anais Da Academia Brasileira De Ciencias</i> , 2010, 82, 933-939.	0.8	21
131	A variant of the <i>KLK4</i> gene is expressed as a cis sense-antisense chimeric transcript in prostate cancer cells. <i>Rna</i> , 2010, 16, 1156-1166.	3.5	36
132	Stringent Programming of DNA Methylation in Humans. <i>Twin Research and Human Genetics</i> , 2010, 13, 405-411.	0.6	5
133	Dynamic isomiR regulation in <i>Drosophila</i> development. <i>Rna</i> , 2010, 16, 1881-1888.	3.5	184
134	Regulated post-transcriptional RNA cleavage diversifies the eukaryotic transcriptome. <i>Genome Research</i> , 2010, 20, 1639-1650.	5.5	76
135	Multiple Evolutionary Rate Classes in Animal Genome Evolution. <i>Molecular Biology and Evolution</i> , 2010, 27, 942-953.	8.9	15
136	Cross-mapping and the identification of editing sites in mature microRNAs in high-throughput sequencing libraries. <i>Genome Research</i> , 2010, 20, 257-264.	5.5	126
137	Linc-ing Long Noncoding RNAs and Enhancer Function. <i>Developmental Cell</i> , 2010, 19, 485-486.	7.0	31
138	Identification of conserved <i>Drosophila</i> -specific euchromatin-restricted non-coding sequence motifs. <i>Genomics</i> , 2010, 96, 154-166.	2.9	4
139	<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.	5.5	570
140	Genome-Wide Identification of Long Noncoding RNAs in CD8+ T Cells. <i>Journal of Immunology</i> , 2009, 182, 7738-7748.	0.8	221
141	NRED: a database of long noncoding RNA expression. <i>Nucleic Acids Research</i> , 2009, 37, D122-D126.	14.5	252
142	Evolution, biogenesis and function of promoter-associated RNAs. <i>Cell Cycle</i> , 2009, 8, 2332-2338.	2.6	89
143	The Genetic Signatures of Noncoding RNAs. <i>PLoS Genetics</i> , 2009, 5, e1000459.	3.5	639
144	Nucleosomes are preferentially positioned at exons in somatic and sperm cells. <i>Cell Cycle</i> , 2009, 8, 3420-3424.	2.6	95

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145	Complex architecture and regulated expression of the <i>Sox2ot</i> locus during vertebrate development. <i>Rna</i> , 2009, 15, 2013-2027.	3.5	200
146	A transcriptional sketch of a primary human breast cancer by 454 deep sequencing. <i>BMC Genomics</i> , 2009, 10, 163.	2.8	205
147	RNA regulation of epigenetic processes. <i>BioEssays</i> , 2009, 31, 51-59.	2.5	333
148	Has evolution learnt how to learn?. <i>EMBO Reports</i> , 2009, 10, 665-665.	4.5	17
149	Tiny RNAs associated with transcription start sites in animals. <i>Nature Genetics</i> , 2009, 41, 572-578.	21.4	327
150	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	21.4	408
151	Long non-coding RNAs: insights into functions. <i>Nature Reviews Genetics</i> , 2009, 10, 155-159.	16.3	5,105
152	Deconstructing the Dogma. <i>Annals of the New York Academy of Sciences</i> , 2009, 1178, 29-46.	3.8	75
153	Small RNAs derived from snoRNAs. <i>Rna</i> , 2009, 15, 1233-1240.	3.5	384
154	Regulation of Epidermal Growth Factor Receptor Signaling in Human Cancer Cells by MicroRNA-7. <i>Journal of Biological Chemistry</i> , 2009, 284, 5731-5741.	3.4	399
155	Pervasive transcription of the eukaryotic genome: functional indices and conceptual implications. <i>Briefings in Functional Genomics &amp; Proteomics</i> , 2009, 8, 407-423.	3.8	140
156	Noncoding RNA in development. <i>Mammalian Genome</i> , 2008, 19, 454-492.	2.2	423
157	Touchdown PCR for increased specificity and sensitivity in PCR amplification. <i>Nature Protocols</i> , 2008, 3, 1452-1456.	12.0	480
158	RNAs as extracellular signaling molecules. <i>Journal of Molecular Endocrinology</i> , 2008, 40, 151-159.	2.5	195
159	Noncoding RNAs in Long-Term Memory Formation. <i>Neuroscientist</i> , 2008, 14, 434-445.	3.5	116
160	Molecular Evolution of the HBII-52 snoRNA Cluster. <i>Journal of Molecular Biology</i> , 2008, 381, 810-815.	4.2	23
161	RNA editing, DNA recoding and the evolution of human cognition. <i>Trends in Neurosciences</i> , 2008, 31, 227-233.	8.6	144
162	The Eukaryotic Genome as an RNA Machine. <i>Science</i> , 2008, 319, 1787-1789.	12.6	579

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163	Long noncoding RNAs in mouse embryonic stem cell pluripotency and differentiation. <i>Genome Research</i> , 2008, 18, 1433-1445.	5.5	698
164	Differentiating Protein-Coding and Noncoding RNA: Challenges and Ambiguities. <i>PLoS Computational Biology</i> , 2008, 4, e1000176.	3.2	493
165	Large-Scale Appearance of Ultraconserved Elements in Tetrapod Genomes and Slowdown of the Molecular Clock. <i>Molecular Biology and Evolution</i> , 2008, 25, 402-408.	8.9	103
166	Delineating Slowly and Rapidly Evolving Fractions of the <i>Drosophila</i> Genome. <i>Journal of Computational Biology</i> , 2008, 15, 407-430.	1.6	19
167	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.	7.1	1,081
168	A NEW UNDERSTANDING OF THE HUMAN GENOME. , 2008, , .		0
169	RNAdb 2.0—an expanded database of mammalian non-coding RNAs. <i>Nucleic Acids Research</i> , 2007, 35, D178-D182.	14.5	149
170	Raising the estimate of functional human sequences: Figure 1.. <i>Genome Research</i> , 2007, 17, 1245-1253.	5.5	217
171	A new paradigm for developmental biology. <i>Journal of Experimental Biology</i> , 2007, 210, 1526-1547.	1.7	212
172	Splicing bypasses 3' end formation signals to allow complex gene architectures. <i>Gene</i> , 2007, 403, 188-193.	2.2	7
173	Noncoding RNAs and RNA Editing in Brain Development, Functional Diversification, and Neurological Disease. <i>Physiological Reviews</i> , 2007, 87, 799-823.	28.8	275
174	Orthologous MicroRNA Genes Are Located in Cancer-Associated Genomic Regions in Human and Mouse. <i>PLoS ONE</i> , 2007, 2, e1133.	2.5	34
175	The relationship between non-protein-coding DNA and eukaryotic complexity. <i>BioEssays</i> , 2007, 29, 288-299.	2.5	578
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