

Anton J Enright

List of Publications by Year in descending order

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Version: 2024-02-01

117
papers

39,482
citations

23879

60
h-index

23841

115
g-index

131
all docs

131
docs citations

131
times ranked

55002
citing authors

#	ARTICLE	IF	CITATIONS
1	miRBase: microRNA sequences, targets and gene nomenclature. <i>Nucleic Acids Research</i> , 2006, 34, D140-D144.	6.5	4,192
2	miRBase: tools for microRNA genomics. <i>Nucleic Acids Research</i> , 2007, 36, D154-D158.	6.5	3,854
3	The zebrafish reference genome sequence and its relationship to the human genome. <i>Nature</i> , 2013, 496, 498-503.	13.7	3,708
4	Human MicroRNA Targets. <i>PLoS Biology</i> , 2004, 2, e363.	2.6	3,253
5	An efficient algorithm for large-scale detection of protein families. <i>Nucleic Acids Research</i> , 2002, 30, 1575-1584.	6.5	3,173
6	MicroRNA targets in <i>Drosophila</i> . <i>Genome Biology</i> , 2003, 5, R1.	13.9	3,023
7	Requirement of <i>bic/microRNA-155</i> for Normal Immune Function. <i>Science</i> , 2007, 316, 608-611.	6.0	1,786
8	Identification of Virus-Encoded MicroRNAs. <i>Science</i> , 2004, 304, 734-736.	6.0	1,474
9	Zebrafish <i>MiR-430</i> Promotes Deadenylation and Clearance of Maternal mRNAs. <i>Science</i> , 2006, 312, 75-79.	6.0	1,405
10	MicroRNAs Regulate Brain Morphogenesis in Zebrafish. <i>Science</i> , 2005, 308, 833-838.	6.0	1,209
11	Protein interaction maps for complete genomes based on gene fusion events. <i>Nature</i> , 1999, 402, 86-90.	13.7	1,032
12	<i>microRNA-155</i> Regulates the Generation of Immunoglobulin Class-Switched Plasma Cells. <i>Immunity</i> , 2007, 27, 847-859.	6.6	724
13	Genomic analysis of human microRNA transcripts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17719-17724.	3.3	466
14	Network visualization and analysis of gene expression data using <i>BioLayout Express3D</i> . <i>Nature Protocols</i> , 2009, 4, 1535-1550.	5.5	443
15	Detection of functional modules from protein interaction networks. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 54, 49-57.	1.5	362
16	<i>Kraken</i> : A set of tools for quality control and analysis of high-throughput sequence data. <i>Methods</i> , 2013, 63, 41-49.	1.9	346
17	A <i>Slicer</i> -independent role for <i>Argonaute 2</i> in hematopoiesis and the microRNA pathway. <i>Genes and Development</i> , 2007, 21, 1999-2004.	2.7	313
18	RNA editing of human microRNAs. <i>Genome Biology</i> , 2006, 7, R27.	13.9	295

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19	The RNA m 6 A Reader YTHDF2 Is Essential for the Post-transcriptional Regulation of the Maternal Transcriptome and Oocyte Competence. <i>Molecular Cell</i> , 2017, 67, 1059-1067.e4.	4.5	287
20	The endonuclease activity of Mili fuels piRNA amplification that silences LINE1 elements. <i>Nature</i> , 2011, 480, 259-263.	13.7	285
21	An ENU-induced mutation of miR-96 associated with progressive hearing loss in mice. <i>Nature Genetics</i> , 2009, 41, 614-618.	9.4	281
22	The miR-144/451 locus is required for erythroid homeostasis. <i>Journal of Experimental Medicine</i> , 2010, 207, 1351-1358.	4.2	277
23	Prediction of microRNA targets. <i>Drug Discovery Today</i> , 2007, 12, 452-458.	3.2	262
24	Construction, Visualisation, and Clustering of Transcription Networks from Microarray Expression Data. <i>PLoS Computational Biology</i> , 2007, 3, e206.	1.5	261
25	Extracellular Vesicles from Neural Stem Cells Transfer IFN- β via Ifngr1 to Activate Stat1 Signaling in Target Cells. <i>Molecular Cell</i> , 2014, 56, 193-204.	4.5	258
26	A high-resolution mRNA expression time course of embryonic development in zebrafish. <i>ELife</i> , 2017, 6, .	2.8	257
27	Detecting microRNA binding and siRNA off-target effects from expression data. <i>Nature Methods</i> , 2008, 5, 1023-1025.	9.0	248
28	Malignant Germ Cell Tumors Display Common MicroRNA Profiles Resulting in Global Changes in Expression of Messenger RNA Targets. <i>Cancer Research</i> , 2010, 70, 2911-2923.	0.4	243
29	Computational Prediction of Protein-Protein Interactions. <i>Molecular Biotechnology</i> , 2008, 38, 1-17.	1.3	201
30	Efficient inhibition of miR-155 function in vivo by peptide nucleic acids. <i>Nucleic Acids Research</i> , 2010, 38, 4466-4475.	6.5	195
31	GeneRAGE: a robust algorithm for sequence clustering and domain detection. <i>Bioinformatics</i> , 2000, 16, 451-457.	1.8	186
32	MicroRNA-9 Inhibition of Cell Proliferation and Identification of Novel miR-9 Targets by Transcriptome Profiling in Breast Cancer Cells. <i>Journal of Biological Chemistry</i> , 2012, 287, 29516-29528.	1.6	170
33	Multiple Epigenetic Mechanisms and the piRNA Pathway Enforce LINE1 Silencing during Adult Spermatogenesis. <i>Molecular Cell</i> , 2013, 50, 601-608.	4.5	170
34	CAST: an iterative algorithm for the complexity analysis of sequence tracts. <i>Bioinformatics</i> , 2000, 16, 915-922.	1.8	165
35	RNA modifications detection by comparative Nanopore direct RNA sequencing. <i>Nature Communications</i> , 2021, 12, 7198.	5.8	163
36	Targeted Deletion of MicroRNA-22 Promotes Stress-Induced Cardiac Dilatation and Contractile Dysfunction. <i>Circulation</i> , 2012, 125, 2751-2761.	1.6	161

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37	Quantitative gene profiling of long noncoding RNAs with targeted RNA sequencing. <i>Nature Methods</i> , 2015, 12, 339-342.	9.0	155
38	BioLayout—an automatic graph layout algorithm for similarity visualization. <i>Bioinformatics</i> , 2001, 17, 853-854.	1.8	152
39	Zebrafish miR-1 and miR-133 shape muscle gene expression and regulate sarcomeric actin organization. <i>Genes and Development</i> , 2009, 23, 619-632.	2.7	149
40	MicroRNA degradation by a conserved target RNA regulates animal behavior. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 244-251.	3.6	149
41	mRNA 3' uridylation and poly(A) tail length sculpt the mammalian maternal transcriptome. <i>Nature</i> , 2017, 548, 347-351.	13.7	142
42	Integrated analysis of microRNA and mRNA expression and association with HIF binding reveals the complexity of microRNA expression regulation under hypoxia. <i>Molecular Cancer</i> , 2014, 13, 28.	7.9	135
43	Annotation of mammalian primary microRNAs. <i>BMC Genomics</i> , 2008, 9, 564.	1.2	121
44	Chimira: analysis of small RNA sequencing data and microRNA modifications. <i>Bioinformatics</i> , 2015, 31, 3365-3367.	1.8	118
45	Genomic positional conservation identifies topological anchor point RNAs linked to developmental loci. <i>Genome Biology</i> , 2018, 19, 32.	3.8	114
46	Protein families and TRIBES in genome sequence space. <i>Nucleic Acids Research</i> , 2003, 31, 4632-4638.	6.5	113
47	Functional associations of proteins in entire genomes by means of exhaustive detection of gene fusions. <i>Genome Biology</i> , 2001, 2, research0034.1.	13.9	108
48	Extracellular vesicles are independent metabolic units with asparaginase activity. <i>Nature Chemical Biology</i> , 2017, 13, 951-955.	3.9	107
49	Classification schemes for protein structure and function. <i>Nature Reviews Genetics</i> , 2003, 4, 508-519.	7.7	101
50	Combined agonist-antagonist genome-wide functional screening identifies broadly active antiviral microRNAs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 13830-13835.	3.3	96
51	spongeScan: A web for detecting microRNA binding elements in lncRNA sequences. <i>Nucleic Acids Research</i> , 2016, 44, W176-W180.	6.5	92
52	Visualizing genome and systems biology: technologies, tools, implementation techniques and trends, past, present and future. <i>GigaScience</i> , 2015, 4, 38.	3.3	84
53	MiR-221 Influences Effector Functions and Actin Cytoskeleton in Mast Cells. <i>PLoS ONE</i> , 2011, 6, e26133.	1.1	81
54	Terminal uridylyltransferases target RNA viruses as part of the innate immune system. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 778-786.	3.6	79

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55	Solid Tumors of Childhood Display Specific Serum microRNA Profiles. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 350-360.	1.1	74
56	The midbody interactome reveals unexpected roles for PP1 phosphatases in cytokinesis. <i>Nature Communications</i> , 2019, 10, 4513.	5.8	69
57	RNAcentral: A vision for an international database of RNA sequences. <i>Rna</i> , 2011, 17, 1941-1946.	1.6	67
58	Evaluation of annotation strategies using an entire genome sequence. <i>Bioinformatics</i> , 2003, 19, 717-726.	1.8	65
59	MiR-25 Regulates Wwp2 and Fbxw7 and Promotes Reprogramming of Mouse Fibroblast Cells to iPSCs. <i>PLoS ONE</i> , 2012, 7, e40938.	1.1	65
60	Estimation of Synteny Conservation and Genome Compaction Between Pufferfish (Fugu) and Human. <i>Yeast</i> , 2000, 1, 22-36.	0.8	64
61	<i>LIN28</i> Expression in Malignant Germ Cell Tumors Downregulates <i>let-7</i> and Increases Oncogene Levels. <i>Cancer Research</i> , 2013, 73, 4872-4884.	0.4	61
62	The two most common histological subtypes of malignant germ cell tumour are distinguished by global microRNA profiles, associated with differential transcription factor expression. <i>Molecular Cancer</i> , 2010, 9, 290.	7.9	60
63	MapMi: automated mapping of microRNA loci. <i>BMC Bioinformatics</i> , 2010, 11, 133.	1.2	58
64	A logic-based diagram of signalling pathways central to macrophage activation. <i>BMC Systems Biology</i> , 2008, 2, 36.	3.0	56
65	Myriads of protein families, and still counting. <i>Genome Biology</i> , 2003, 4, 401.	13.9	55
66	Mirnov: genome-free prediction of microRNAs from small RNA sequencing data and single-cells using decision forests. <i>Nucleic Acids Research</i> , 2017, 45, e177-e177.	6.5	54
67	Large-scale analysis of microRNA evolution. <i>BMC Genomics</i> , 2012, 13, 218.	1.2	52
68	BioLayoutJava. <i>Applied Bioinformatics</i> , 2005, 4, 71-74.	1.7	50
69	Extent, Causes, and Consequences of Small RNA Expression Variation in Human Adipose Tissue. <i>PLoS Genetics</i> , 2012, 8, e1002704.	1.5	48
70	A programmed wave of uridylation-primed mRNA degradation is essential for meiotic progression and mammalian spermatogenesis. <i>Cell Research</i> , 2019, 29, 221-232.	5.7	48
71	3' Uridylation controls mature microRNA turnover during CD4 T-cell activation. <i>Rna</i> , 2017, 23, 882-891.	1.6	47
72	Schwann cell reprogramming into repair cells increases exosome-loaded miRNA-21 promoting axonal growth. <i>Journal of Cell Science</i> , 2020, 133, .	1.2	46

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73	MiR-277/4989 regulate transcriptional landscape during juvenile to adult transition in the parasitic helminth <i>Schistosoma mansoni</i> . <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005559.	1.3	45
74	An Interferon Regulated MicroRNA Provides Broad Cell-Intrinsic Antiviral Immunity through Multihit Host-Directed Targeting of the Sterol Pathway. <i>PLoS Biology</i> , 2016, 14, e1002364.	2.6	45
75	Large-scale analysis of microRNA expression, epi-transcriptomic features and biogenesis. <i>Nucleic Acids Research</i> , 2017, 45, 1079-1090.	6.5	44
76	Non-coding RNA Expression, Function, and Variation during <i>Drosophila</i> Embryogenesis. <i>Current Biology</i> , 2018, 28, 3547-3561.e9.	1.8	44
77	miR-221 affects multiple cancer pathways by modulating the level of hundreds messenger RNAs. <i>Frontiers in Genetics</i> , 2013, 4, 64.	1.1	42
78	Systematic analysis of off-target effects in an RNAi screen reveals microRNAs affecting sensitivity to TRAIL-induced apoptosis. <i>BMC Genomics</i> , 2010, 11, 175.	1.2	41
79	COmplete GENome Tracking (COGENT): a flexible data environment for computational genomics. <i>Bioinformatics</i> , 2003, 19, 1451-1452.	1.8	40
80	Depletion of HPV16 early genes induces autophagy and senescence in a cervical carcinogenesis model, regardless of viral physical state. <i>Journal of Pathology</i> , 2013, 231, 354-366.	2.1	40
81	Serum levels of mature microRNAs in DICER1-mutated pleuropulmonary blastoma. <i>Oncogenesis</i> , 2014, 3, e87-e87.	2.1	40
82	High-density P300 enhancers control cell state transitions. <i>BMC Genomics</i> , 2015, 16, 903.	1.2	37
83	SylArray: a web server for automated detection of miRNA effects from expression data. <i>Bioinformatics</i> , 2010, 26, 2900-2901.	1.8	36
84	Enhanced Susceptibility to <i>Citrobacter rodentium</i> Infection in MicroRNA-155-Deficient Mice. <i>Infection and Immunity</i> , 2013, 81, 723-732.	1.0	35
85	Transposon-driven transcription is a conserved feature of vertebrate spermatogenesis and transcript evolution. <i>EMBO Reports</i> , 2017, 18, 1231-1247.	2.0	34
86	Activation of the TGF β 2 pathway impairs endothelial to haematopoietic transition. <i>Scientific Reports</i> , 2016, 6, 21518.	1.6	33
87	Improved definition of the mouse transcriptome via targeted RNA sequencing. <i>Genome Research</i> , 2016, 26, 705-716.	2.4	33
88	Reciprocal regulation of microRNA and mRNA profiles in neuronal development and synapse formation. <i>BMC Genomics</i> , 2009, 10, 419.	1.2	32
89	3D model of harlequin ichthyosis reveals inflammatory therapeutic targets. <i>Journal of Clinical Investigation</i> , 2020, 130, 4798-4810.	3.9	31
90	Transcription-associated protein families are primarily taxon-specific. <i>Bioinformatics</i> , 2001, 17, 95-97.	1.8	27

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91	Defective germline reprogramming rewires the spermatogonial transcriptome. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 394-404.	3.6	27
92	MicroRNA Targets in <i>Drosophila</i> . <i>Genome Biology</i> , 2003, 4, P8.	13.9	24
93	CoGenT++: an extensive and extensible data environment for computational genomics. <i>Bioinformatics</i> , 2005, 21, 3806-3810.	1.8	22
94	Fusion and Fission of Genes Define a Metric between Fungal Genomes. <i>PLoS Computational Biology</i> , 2008, 4, e1000200.	1.5	22
95	Detecting and Comparing Non-Coding RNAs in the High-Throughput Era. <i>International Journal of Molecular Sciences</i> , 2013, 14, 15423-15458.	1.8	22
96	MagicMatch--cross-referencing sequence identifiers across databases. <i>Bioinformatics</i> , 2005, 21, 3429-3430.	1.8	21
97	A MILI-independent piRNA biogenesis pathway empowers partial germline reprogramming. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 604-606.	3.6	18
98	Short- and long-range cis interactions between integrated HPV genomes and cellular chromatin dysregulate host gene expression in early cervical carcinogenesis. <i>PLoS Pathogens</i> , 2021, 17, e1009875.	2.1	18
99	Messenger RNA and microRNA profiling during early mouse EB formation. <i>Gene Expression Patterns</i> , 2011, 11, 334-344.	0.3	17
100	Denoising inferred functional association networks obtained by gene fusion analysis. <i>BMC Genomics</i> , 2007, 8, 460.	1.2	16
101	Lack of correlation between predicted and actual off-target effects of short-interfering RNAs targeting the human papillomavirus type 16 E7 oncogene. <i>British Journal of Cancer</i> , 2013, 108, 450-460.	2.9	16
102	Visualisation of BioPAX Networks using BioLayout Express3D. <i>F1000Research</i> , 2014, 3, 246.	0.8	16
103	A Neuronal Transcriptome Response Involving Stress Pathways is Buffered by Neuronal microRNAs. <i>Frontiers in Neuroscience</i> , 2012, 6, 156.	1.4	15
104	Exploring regulatory networks of miR-96 in the developing inner ear. <i>Scientific Reports</i> , 2016, 6, 23363.	1.6	14
105	iMotifs: an integrated sequence motif visualization and analysis environment. <i>Bioinformatics</i> , 2010, 26, 843-844.	1.8	11
106	In situ functional dissection of RNA cis-regulatory elements by multiplex CRISPR-Cas9 genome engineering. <i>Nature Communications</i> , 2017, 8, 2109.	5.8	11
107	Re-annotation of the physical map of <i>Glycine max</i> for polyploid-like regions by BAC end sequence driven whole genome shotgun read assembly. <i>BMC Genomics</i> , 2008, 9, 323.	1.2	10
108	Evolutionary and functional insights into <i>Leishmania META1</i> : evidence for lateral gene transfer and a role for META1 in secretion. <i>BMC Evolutionary Biology</i> , 2011, 11, 334.	3.2	9

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109	Large-Scale Identification of MicroRNA Targets in Murine Dgcr8-Deficient Embryonic Stem Cell Lines. PLoS ONE, 2012, 7, e41762.	1.1	8
110	Exploration of signals of positive selection derived from genotype-based human genome scans using re-sequencing data. Human Genetics, 2012, 131, 665-674.	1.8	8
111	Smallpox vaccination induces a substantial increase in commensal skin bacteria that promote pathology and influence the host response. PLoS Pathogens, 2022, 18, e1009854.	2.1	8
112	Mapping Functional Associations in the Entire Genome of <i>Drosophila melanogaster</i> Using Fusion Analysis. Comparative and Functional Genomics, 2003, 4, 337-341.	2.0	4
113	Visualization and analysis of RNA-Seq assembly graphs. Nucleic Acids Research, 2019, 47, 7262-7275.	6.5	4
114	miRBase: a database of microRNA sequences, targets and nomenclature. , 0, , 157-171.		2
115	Identification of Recurrent Mutations in the microRNA-Binding Sites of B-Cell Lymphoma-Associated Genes in Follicular Lymphoma. International Journal of Molecular Sciences, 2020, 21, 8795.	1.8	1
116	Deciphering the role of micrnas in early stages of haematopoiesis. Experimental Hematology, 2013, 41, S38.	0.2	0
117	mRNA 3' Uridylation and Poly(A) Tail Length Sculpt the Mammalian Maternal Transcriptome. Obstetrical and Gynecological Survey, 2017, 72, 656-656.	0.2	0