

# Anton J Enright

## List of Publications by Year in descending order

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117  
papers

39,482  
citations

20817

60  
h-index

20961

115  
g-index

131  
all docs

131  
docs citations

131  
times ranked

49615  
citing authors

#	ARTICLE	IF	CITATIONS
1	miRBase: microRNA sequences, targets and gene nomenclature. Nucleic Acids Research, 2006, 34, D140-D144.	14.5	4,192
2	miRBase: tools for microRNA genomics. Nucleic Acids Research, 2007, 36, D154-D158.	14.5	3,854
3	The zebrafish reference genome sequence and its relationship to the human genome. Nature, 2013, 496, 498-503.	27.8	3,708
4	Human MicroRNA Targets. PLoS Biology, 2004, 2, e363.	5.6	3,253
5	An efficient algorithm for large-scale detection of protein families. Nucleic Acids Research, 2002, 30, 1575-1584.	14.5	3,173
6	MicroRNA targets in Drosophila. Genome Biology, 2003, 5, R1.	9.6	3,023
7	Requirement of <i>bic/microRNA-155</i> for Normal Immune Function. Science, 2007, 316, 608-611.	12.6	1,786
8	Identification of Virus-Encoded MicroRNAs. Science, 2004, 304, 734-736.	12.6	1,474
9	Zebrafish MiR-430 Promotes Deadenylation and Clearance of Maternal mRNAs. Science, 2006, 312, 75-79.	12.6	1,405
10	MicroRNAs Regulate Brain Morphogenesis in Zebrafish. Science, 2005, 308, 833-838.	12.6	1,209
11	Protein interaction maps for complete genomes based on gene fusion events. Nature, 1999, 402, 86-90.	27.8	1,032
12	microRNA-155 Regulates the Generation of Immunoglobulin Class-Switched Plasma Cells. Immunity, 2007, 27, 847-859.	14.3	724
13	Genomic analysis of human microRNA transcripts. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 17719-17724.	7.1	466
14	Network visualization and analysis of gene expression data using BioLayout Express3D. Nature Protocols, 2009, 4, 1535-1550.	12.0	443
15	Detection of functional modules from protein interaction networks. Proteins: Structure, Function and Bioinformatics, 2003, 54, 49-57.	2.6	362
16	Kraken: A set of tools for quality control and analysis of high-throughput sequence data. Methods, 2013, 63, 41-49.	3.8	346
17	A Slicer-independent role for Argonaute 2 in hematopoiesis and the microRNA pathway. Genes and Development, 2007, 21, 1999-2004.	5.9	313
18	RNA editing of human microRNAs. Genome Biology, 2006, 7, R27.	9.6	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.	9.7	287
20	The endonuclease activity of Mili fuels piRNA amplification that silences LINE1 elements. <i>Nature</i> , 2011, 480, 259-263.	27.8	285
21	An ENU-induced mutation of miR-96 associated with progressive hearing loss in mice. <i>Nature Genetics</i> , 2009, 41, 614-618.	21.4	281
22	The miR-144/451 locus is required for erythroid homeostasis. <i>Journal of Experimental Medicine</i> , 2010, 207, 1351-1358.	8.5	277
23	Prediction of microRNA targets. <i>Drug Discovery Today</i> , 2007, 12, 452-458.	6.4	262
24	Construction, Visualisation, and Clustering of Transcription Networks from Microarray Expression Data. <i>PLoS Computational Biology</i> , 2007, 3, e206.	3.2	261
25	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
26	A high-resolution mRNA expression time course of embryonic development in zebrafish. <i>ELife</i> , 2017, 6, .	6.0	257
27	Detecting microRNA binding and siRNA off-target effects from expression data. <i>Nature Methods</i> , 2008, 5, 1023-1025.	19.0	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.	0.9	243
29	Computational Prediction of Protein-Protein Interactions. <i>Molecular Biotechnology</i> , 2008, 38, 1-17.	2.4	201
30	Efficient inhibition of miR-155 function in vivo by peptide nucleic acids. <i>Nucleic Acids Research</i> , 2010, 38, 4466-4475.	14.5	195
31	GeneRAGE: a robust algorithm for sequence clustering and domain detection. <i>Bioinformatics</i> , 2000, 16, 451-457.	4.1	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.	3.4	170
33	Multiple Epigenetic Mechanisms and the piRNA Pathway Enforce LINE1 Silencing during Adult Spermatogenesis. <i>Molecular Cell</i> , 2013, 50, 601-608.	9.7	170
34	CAST: an iterative algorithm for the complexity analysis of sequence tracts. <i>Bioinformatics</i> , 2000, 16, 915-922.	4.1	165
35	RNA modifications detection by comparative Nanopore direct RNA sequencing. <i>Nature Communications</i> , 2021, 12, 7198.	12.8	163
36	Targeted Deletion of MicroRNA-22 Promotes Stress-Induced Cardiac Dilation 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.	19.0	155
38	BioLayout—an automatic graph layout algorithm for similarity visualization. <i>Bioinformatics</i> , 2001, 17, 853-854.	4.1	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.	5.9	149
40	MicroRNA degradation by a conserved target RNA regulates animal behavior. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 244-251.	8.2	149
41	mRNA 3' uridylation and poly(A) tail length sculpt the mammalian maternal transcriptome. <i>Nature</i> , 2017, 548, 347-351.	27.8	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.	19.2	135
43	Annotation of mammalian primary microRNAs. <i>BMC Genomics</i> , 2008, 9, 564.	2.8	121
44	Chimira: analysis of small RNA sequencing data and microRNA modifications. <i>Bioinformatics</i> , 2015, 31, 3365-3367.	4.1	118
45	Genomic positional conservation identifies topological anchor point RNAs linked to developmental loci. <i>Genome Biology</i> , 2018, 19, 32.	8.8	114
46	Protein families and TRIBES in genome sequence space. <i>Nucleic Acids Research</i> , 2003, 31, 4632-4638.	14.5	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.	9.6	108
48	Extracellular vesicles are independent metabolic units with asparaginase activity. <i>Nature Chemical Biology</i> , 2017, 13, 951-955.	8.0	107
49	Classification schemes for protein structure and function. <i>Nature Reviews Genetics</i> , 2003, 4, 508-519.	16.3	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.	7.1	96
51	spongeScan: A web for detecting microRNA binding elements in lncRNA sequences. <i>Nucleic Acids Research</i> , 2016, 44, W176-W180.	14.5	92
52	Visualizing genome and systems biology: technologies, tools, implementation techniques and trends, past, present and future. <i>GigaScience</i> , 2015, 4, 38.	6.4	84
53	MIR-221 Influences Effector Functions and Actin Cytoskeleton in Mast Cells. <i>PLoS ONE</i> , 2011, 6, e26133.	2.5	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.	8.2	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.	2.5	74
56	The midbody interactome reveals unexpected roles for PP1 phosphatases in cytokinesis. <i>Nature Communications</i> , 2019, 10, 4513.	12.8	69
57	RNAcentral: A vision for an international database of RNA sequences. <i>Rna</i> , 2011, 17, 1941-1946.	3.5	67
58	Evaluation of annotation strategies using an entire genome sequence. <i>Bioinformatics</i> , 2003, 19, 717-726.	4.1	65
59	MiR-25 Regulates Wwp2 and Fbxw7 and Promotes Reprogramming of Mouse Fibroblast Cells to iPSCs. <i>PLoS ONE</i> , 2012, 7, e40938.	2.5	65
60	Estimation of Synteny Conservation and Genome Compaction Between Pufferfish (Fugu) and Human. <i>Yeast</i> , 2000, 1, 22-36.	1.7	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.	0.9	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.	19.2	60
63	MapMi: automated mapping of microRNA loci. <i>BMC Bioinformatics</i> , 2010, 11, 133.	2.6	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.	9.6	55
66	Mirnovor: 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.	14.5	54
67	Large-scale analysis of microRNA evolution. <i>BMC Genomics</i> , 2012, 13, 218.	2.8	52
68	BioLayoutJava. <i>Applied Bioinformatics</i> , 2005, 4, 71-74.	1.6	50
69	Extent, Causes, and Consequences of Small RNA Expression Variation in Human Adipose Tissue. <i>PLoS Genetics</i> , 2012, 8, e1002704.	3.5	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.	12.0	48
71	3' Uridylation controls mature microRNA turnover during CD4 T-cell activation. <i>Rna</i> , 2017, 23, 882-891.	3.5	47
72	Schwann cell reprogramming into repair cells increases exosome-loaded miRNA-21 promoting axonal growth. <i>Journal of Cell Science</i> , 2020, 133, .	2.0	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.	3.0	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.	5.6	45
75	Large-scale analysis of microRNA expression, epi-transcriptomic features and biogenesis. <i>Nucleic Acids Research</i> , 2017, 45, 1079-1090.	14.5	44
76	Non-coding RNA Expression, Function, and Variation during <i>Drosophila</i> Embryogenesis. <i>Current Biology</i> , 2018, 28, 3547-3561.e9.	3.9	44
77	miR-221 affects multiple cancer pathways by modulating the level of hundreds messenger RNAs. <i>Frontiers in Genetics</i> , 2013, 4, 64.	2.3	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.	2.8	41
79	COmplete GENome Tracking (COGENT): a flexible data environment for computational genomics. <i>Bioinformatics</i> , 2003, 19, 1451-1452.	4.1	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.	4.5	40
81	Serum levels of mature microRNAs in DICER1-mutated pleuropulmonary blastoma. <i>Oncogenesis</i> , 2014, 3, e87-e87.	4.9	40
82	High-density P300 enhancers control cell state transitions. <i>BMC Genomics</i> , 2015, 16, 903.	2.8	37
83	SylArray: a web server for automated detection of miRNA effects from expression data. <i>Bioinformatics</i> , 2010, 26, 2900-2901.	4.1	36
84	Enhanced Susceptibility to <i>Citrobacter rodentium</i> Infection in MicroRNA-155-Deficient Mice. <i>Infection and Immunity</i> , 2013, 81, 723-732.	2.2	35
85	Transposon-driven transcription is a conserved feature of vertebrate spermatogenesis and transcript evolution. <i>EMBO Reports</i> , 2017, 18, 1231-1247.	4.5	34
86	Activation of the TGF $\beta$ 2 pathway impairs endothelial to haematopoietic transition. <i>Scientific Reports</i> , 2016, 6, 21518.	3.3	33
87	Improved definition of the mouse transcriptome via targeted RNA sequencing. <i>Genome Research</i> , 2016, 26, 705-716.	5.5	33
88	Reciprocal regulation of microRNA and mRNA profiles in neuronal development and synapse formation. <i>BMC Genomics</i> , 2009, 10, 419.	2.8	32
89	3D model of harlequin ichthyosis reveals inflammatory therapeutic targets. <i>Journal of Clinical Investigation</i> , 2020, 130, 4798-4810.	8.2	31
90	Transcription-associated protein families are primarily taxon-specific. <i>Bioinformatics</i> , 2001, 17, 95-97.	4.1	27

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91	Defective germline reprogramming rewires the spermatogonial transcriptome. Nature Structural and Molecular Biology, 2018, 25, 394-404.	8.2	27
92	MicroRNA Targets in Drosophila. Genome Biology, 2003, 4, P8.	9.6	24
93	CoGenT++: an extensive and extensible data environment for computational genomics. Bioinformatics, 2005, 21, 3806-3810.	4.1	22
94	Fusion and Fission of Genes Define a Metric between Fungal Genomes. PLoS Computational Biology, 2008, 4, e1000200.	3.2	22
95	Detecting and Comparing Non-Coding RNAs in the High-Throughput Era. International Journal of Molecular Sciences, 2013, 14, 15423-15458.	4.1	22
96	MagicMatch-cross-referencing sequence identifiers across databases. Bioinformatics, 2005, 21, 3429-3430.	4.1	21
97	A MILI-independent piRNA biogenesis pathway empowers partial germline reprogramming. Nature Structural and Molecular Biology, 2017, 24, 604-606.	8.2	18
98	Short- and long-range cis interactions between integrated HPV genomes and cellular chromatin dysregulate host gene expression in early cervical carcinogenesis. PLoS Pathogens, 2021, 17, e1009875.	4.7	18
99	Messenger RNA and microRNA profiling during early mouse EB formation. Gene Expression Patterns, 2011, 11, 334-344.	0.8	17
100	Denoising inferred functional association networks obtained by gene fusion analysis. BMC Genomics, 2007, 8, 460.	2.8	16
101	Lack of correlation between predicted and actual off-target effects of short-interfering RNAs targeting the human papillomavirus type 16 E7 oncogene. British Journal of Cancer, 2013, 108, 450-460.	6.4	16
102	Visualisation of BioPAX Networks using BioLayout Express3D. F1000Research, 2014, 3, 246.	1.6	16
103	A Neuronal Transcriptome Response Involving Stress Pathways is Buffered by Neuronal microRNAs. Frontiers in Neuroscience, 2012, 6, 156.	2.8	15
104	Exploring regulatory networks of miR-96 in the developing inner ear. Scientific Reports, 2016, 6, 23363.	3.3	14
105	iMotifs: an integrated sequence motif visualization and analysis environment. Bioinformatics, 2010, 26, 843-844.	4.1	11
106	In situ functional dissection of RNA cis-regulatory elements by multiplex CRISPR-Cas9 genome engineering. Nature Communications, 2017, 8, 2109.	12.8	11
107	Re-annotation of the physical map of Glycine max for polyploid-like regions by BAC end sequence driven whole genome shotgun read assembly. BMC Genomics, 2008, 9, 323.	2.8	10
108	Evolutionary and functional insights into Leishmania META1: evidence for lateral gene transfer and a role for META1 in secretion. BMC Evolutionary Biology, 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.	2.5	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.	3.8	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.	4.7	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.	14.5	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.	4.1	1
116	Deciphering the role of micrornas in early stages of haematopoiesis. Experimental Hematology, 2013, 41, S38.	0.4	0
117	mRNA 3' Uridylation and Poly(A) Tail Length Sculpt the Mammalian Maternal Transcriptome. Obstetrical and Gynecological Survey, 2017, 72, 656-656.	0.4	0