

# 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	Smallpox vaccination induces a substantial increase in commensal skin bacteria that promote pathology and influence the host response. <i>PLoS Pathogens</i> , 2022, 18, e1009854.	2.1	8
2	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
3	RNA modifications detection by comparative Nanopore direct RNA sequencing. <i>Nature Communications</i> , 2021, 12, 7198.	5.8	163
4	Identification of Recurrent Mutations in the microRNA-Binding Sites of B-Cell Lymphoma-Associated Genes in Follicular Lymphoma. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8795.	1.8	1
5	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
6	3D model of harlequin ichthyosis reveals inflammatory therapeutic targets. <i>Journal of Clinical Investigation</i> , 2020, 130, 4798-4810.	3.9	31
7	Visualization and analysis of RNA-Seq assembly graphs. <i>Nucleic Acids Research</i> , 2019, 47, 7262-7275.	6.5	4
8	The midbody interactome reveals unexpected roles for PP1 phosphatases in cytokinesis. <i>Nature Communications</i> , 2019, 10, 4513.	5.8	69
9	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
10	MicroRNA degradation by a conserved target RNA regulates animal behavior. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 244-251.	3.6	149
11	Defective germline reprogramming rewires the spermatogonial transcriptome. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 394-404.	3.6	27
12	Non-coding RNA Expression, Function, and Variation during <i>Drosophila</i> Embryogenesis. <i>Current Biology</i> , 2018, 28, 3547-3561.e9.	1.8	44
13	Genomic positional conservation identifies topological anchor point RNAs linked to developmental loci. <i>Genome Biology</i> , 2018, 19, 32.	3.8	114
14	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
15	Transposon-driven transcription is a conserved feature of vertebrate spermatogenesis and transcript evolution. <i>EMBO Reports</i> , 2017, 18, 1231-1247.	2.0	34
16	Large-scale analysis of microRNA expression, epi-transcriptomic features and biogenesis. <i>Nucleic Acids Research</i> , 2017, 45, 1079-1090.	6.5	44
17	A MILI-independent piRNA biogenesis pathway empowers partial germline reprogramming. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 604-606.	3.6	18
18	Uridylation controls mature microRNA turnover during CD4 T-cell activation. <i>Rna</i> , 2017, 23, 882-891.	1.6	47

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19	Mirnova: 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
20	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
21	mRNA 3' uridylation and poly(A) tail length sculpt the mammalian maternal transcriptome. <i>Nature</i> , 2017, 548, 347-351.	13.7	142
22	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
23	Extracellular vesicles are independent metabolic units with asparaginase activity. <i>Nature Chemical Biology</i> , 2017, 13, 951-955.	3.9	107
24	mRNA 3' Uridylation and Poly(A) Tail Length Sculpt the Mammalian Maternal Transcriptome. <i>Obstetrical and Gynecological Survey</i> , 2017, 72, 656-656.	0.2	0
25	A high-resolution mRNA expression time course of embryonic development in zebrafish. <i>ELife</i> , 2017, 6, .	2.8	257
26	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
27	Exploring regulatory networks of miR-96 in the developing inner ear. <i>Scientific Reports</i> , 2016, 6, 23363.	1.6	14
28	Activation of the TGF $\beta$ 2 pathway impairs endothelial to haematopoietic transition. <i>Scientific Reports</i> , 2016, 6, 21518.	1.6	33
29	spongeScan: A web for detecting microRNA binding elements in lncRNA sequences. <i>Nucleic Acids Research</i> , 2016, 44, W176-W180.	6.5	92
30	Improved definition of the mouse transcriptome via targeted RNA sequencing. <i>Genome Research</i> , 2016, 26, 705-716.	2.4	33
31	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
32	High-density P300 enhancers control cell state transitions. <i>BMC Genomics</i> , 2015, 16, 903.	1.2	37
33	Quantitative gene profiling of long noncoding RNAs with targeted RNA sequencing. <i>Nature Methods</i> , 2015, 12, 339-342.	9.0	155
34	Chimira: analysis of small RNA sequencing data and microRNA modifications. <i>Bioinformatics</i> , 2015, 31, 3365-3367.	1.8	118
35	Visualizing genome and systems biology: technologies, tools, implementation techniques and trends, past, present and future. <i>GigaScience</i> , 2015, 4, 38.	3.3	84
36	Solid Tumors of Childhood Display Specific Serum microRNA Profiles. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 350-360.	1.1	74

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37	Serum levels of mature microRNAs in DICER1-mutated pleuropulmonary blastoma. <i>Oncogenesis</i> , 2014, 3, e87-e87.	2.1	40
38	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
39	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.	4.5	258
40	Visualisation of BioPAX Networks using BioLayout Express3D. <i>F1000Research</i> , 2014, 3, 246.	0.8	16
41	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
42	Kraken: A set of tools for quality control and analysis of high-throughput sequence data. <i>Methods</i> , 2013, 63, 41-49.	1.9	346
43	Deciphering the role of micrnas in early stages of haematopoiesis. <i>Experimental Hematology</i> , 2013, 41, S38.	0.2	0
44	The zebrafish reference genome sequence and its relationship to the human genome. <i>Nature</i> , 2013, 496, 498-503.	13.7	3,708
45	Multiple Epigenetic Mechanisms and the piRNA Pathway Enforce LINE1 Silencing during Adult Spermatogenesis. <i>Molecular Cell</i> , 2013, 50, 601-608.	4.5	170
46	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
47	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
48	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
49	<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
50	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
51	Extent, Causes, and Consequences of Small RNA Expression Variation in Human Adipose Tissue. <i>PLoS Genetics</i> , 2012, 8, e1002704.	1.5	48
52	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
53	MiR-25 Regulates <i>Wwp2</i> and <i>Fbxw7</i> and Promotes Reprogramming of Mouse Fibroblast Cells to iPSCs. <i>PLoS ONE</i> , 2012, 7, e40938.	1.1	65
54	Large-scale analysis of microRNA evolution. <i>BMC Genomics</i> , 2012, 13, 218.	1.2	52

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55	Large-Scale Identification of MicroRNA Targets in Murine Dgcr8-Deficient Embryonic Stem Cell Lines. PLoS ONE, 2012, 7, e41762.	1.1	8
56	A Neuronal Transcriptome Response Involving Stress Pathways is Buffered by Neuronal microRNAs. Frontiers in Neuroscience, 2012, 6, 156.	1.4	15
57	Targeted Deletion of MicroRNA-22 Promotes Stress-Induced Cardiac Dilation and Contractile Dysfunction. Circulation, 2012, 125, 2751-2761.	1.6	161
58	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
59	The endonuclease activity of Mili fuels piRNA amplification that silences LINE1 elements. Nature, 2011, 480, 259-263.	13.7	285
60	Messenger RNA and microRNA profiling during early mouse EB formation. Gene Expression Patterns, 2011, 11, 334-344.	0.3	17
61	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
62	RNAcentral: A vision for an international database of RNA sequences. Rna, 2011, 17, 1941-1946.	1.6	67
63	MiR-221 Influences Effector Functions and Actin Cytoskeleton in Mast Cells. PLoS ONE, 2011, 6, e26133.	1.1	81
64	MapMi: automated mapping of microRNA loci. BMC Bioinformatics, 2010, 11, 133.	1.2	58
65	Systematic analysis of off-target effects in an RNAi screen reveals microRNAs affecting sensitivity to TRAIL-induced apoptosis. BMC Genomics, 2010, 11, 175.	1.2	41
66	Malignant Germ Cell Tumors Display Common MicroRNA Profiles Resulting in Global Changes in Expression of Messenger RNA Targets. Cancer Research, 2010, 70, 2911-2923.	0.4	243
67	Efficient inhibition of miR-155 function in vivo by peptide nucleic acids. Nucleic Acids Research, 2010, 38, 4466-4475.	6.5	195
68	iMotifs: an integrated sequence motif visualization and analysis environment. Bioinformatics, 2010, 26, 843-844.	1.8	11
69	SylArray: a web server for automated detection of miRNA effects from expression data. Bioinformatics, 2010, 26, 2900-2901.	1.8	36
70	Combined agonist-antagonist genome-wide functional screening identifies broadly active antiviral microRNAs. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 13830-13835.	3.3	96
71	The miR-144/451 locus is required for erythroid homeostasis. Journal of Experimental Medicine, 2010, 207, 1351-1358.	4.2	277
72	The two most common histological subtypes of malignant germ cell tumour are distinguished by global microRNA profiles, associated with differential transcription factor expression. Molecular Cancer, 2010, 9, 290.	7.9	60

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73	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
74	Reciprocal regulation of microRNA and mRNA profiles in neuronal development and synapse formation. <i>BMC Genomics</i> , 2009, 10, 419.	1.2	32
75	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
76	Network visualization and analysis of gene expression data using BioLayout Express3D. <i>Nature Protocols</i> , 2009, 4, 1535-1550.	5.5	443
77	Computational Prediction of Protein-Protein Interactions. <i>Molecular Biotechnology</i> , 2008, 38, 1-17.	1.3	201
78	Detecting microRNA binding and siRNA off-target effects from expression data. <i>Nature Methods</i> , 2008, 5, 1023-1025.	9.0	248
79	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
80	Annotation of mammalian primary microRNAs. <i>BMC Genomics</i> , 2008, 9, 564.	1.2	121
81	A logic-based diagram of signalling pathways central to macrophage activation. <i>BMC Systems Biology</i> , 2008, 2, 36.	3.0	56
82	Fusion and Fission of Genes Define a Metric between Fungal Genomes. <i>PLoS Computational Biology</i> , 2008, 4, e1000200.	1.5	22
83	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
84	Construction, Visualisation, and Clustering of Transcription Networks from Microarray Expression Data. <i>PLoS Computational Biology</i> , 2007, 3, e206.	1.5	261
85	A Slicer-independent role for Argonaute 2 in hematopoiesis and the microRNA pathway. <i>Genes and Development</i> , 2007, 21, 1999-2004.	2.7	313
86	microRNA-155 Regulates the Generation of Immunoglobulin Class-Switched Plasma Cells. <i>Immunity</i> , 2007, 27, 847-859.	6.6	724
87	miRBase: tools for microRNA genomics. <i>Nucleic Acids Research</i> , 2007, 36, D154-D158.	6.5	3,854
88	Requirement of bic/microRNA-155 for Normal Immune Function. <i>Science</i> , 2007, 316, 608-611.	6.0	1,786
89	Denosing inferred functional association networks obtained by gene fusion analysis. <i>BMC Genomics</i> , 2007, 8, 460.	1.2	16
90	Prediction of microRNA targets. <i>Drug Discovery Today</i> , 2007, 12, 452-458.	3.2	262

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91	RNA editing of human microRNAs. <i>Genome Biology</i> , 2006, 7, R27.	13.9	295
92	miRBase: microRNA sequences, targets and gene nomenclature. <i>Nucleic Acids Research</i> , 2006, 34, D140-D144.	6.5	4,192
93	Zebrafish MiR-430 Promotes Deadenylation and Clearance of Maternal mRNAs. <i>Science</i> , 2006, 312, 75-79.	6.0	1,405
94	CoGenT++: an extensive and extensible data environment for computational genomics. <i>Bioinformatics</i> , 2005, 21, 3806-3810.	1.8	22
95	MagicMatch--cross-referencing sequence identifiers across databases. <i>Bioinformatics</i> , 2005, 21, 3429-3430.	1.8	21
96	MicroRNAs Regulate Brain Morphogenesis in Zebrafish. <i>Science</i> , 2005, 308, 833-838.	6.0	1,209
97	BioLayoutJava. <i>Applied Bioinformatics</i> , 2005, 4, 71-74.	1.7	50
98	Human MicroRNA Targets. <i>PLoS Biology</i> , 2004, 2, e363.	2.6	3,253
99	Identification of Virus-Encoded MicroRNAs. <i>Science</i> , 2004, 304, 734-736.	6.0	1,474
100	Mapping Functional Associations in the Entire Genome of <i>Drosophila melanogaster</i> Using Fusion Analysis. <i>Comparative and Functional Genomics</i> , 2003, 4, 337-341.	2.0	4
101	Detection of functional modules from protein interaction networks. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 54, 49-57.	1.5	362
102	Classification schemes for protein structure and function. <i>Nature Reviews Genetics</i> , 2003, 4, 508-519.	7.7	101
103	MicroRNA targets in <i>Drosophila</i> . <i>Genome Biology</i> , 2003, 5, R1.	13.9	3,023
104	Myriads of protein families, and still counting. <i>Genome Biology</i> , 2003, 4, 401.	13.9	55
105	Evaluation of annotation strategies using an entire genome sequence. <i>Bioinformatics</i> , 2003, 19, 717-726.	1.8	65
106	COmplete GENome Tracking (COGENT): a flexible data environment for computational genomics. <i>Bioinformatics</i> , 2003, 19, 1451-1452.	1.8	40
107	Protein families and TRIBES in genome sequence space. <i>Nucleic Acids Research</i> , 2003, 31, 4632-4638.	6.5	113
108	MicroRNA Targets in <i>Drosophila</i> . <i>Genome Biology</i> , 2003, 4, P8.	13.9	24

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109	An efficient algorithm for large-scale detection of protein families. <i>Nucleic Acids Research</i> , 2002, 30, 1575-1584.	6.5	3,173
110	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
111	Transcription-associated protein families are primarily taxon-specific. <i>Bioinformatics</i> , 2001, 17, 95-97.	1.8	27
112	BioLayout—an automatic graph layout algorithm for similarity visualization. <i>Bioinformatics</i> , 2001, 17, 853-854.	1.8	152
113	Estimation of Synteny Conservation and Genome Compaction Between Pufferfish ( <i>Fugu</i> ) and Human. <i>Yeast</i> , 2000, 1, 22-36.	0.8	64
114	GeneRAGE: a robust algorithm for sequence clustering and domain detection. <i>Bioinformatics</i> , 2000, 16, 451-457.	1.8	186
115	CAST: an iterative algorithm for the complexity analysis of sequence tracts. <i>Bioinformatics</i> , 2000, 16, 915-922.	1.8	165
116	Protein interaction maps for complete genomes based on gene fusion events. <i>Nature</i> , 1999, 402, 86-90.	13.7	1,032
117	miRBase: a database of microRNA sequences, targets and nomenclature. , 0, , 157-171.		2