

Anton J Enright

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

121
papers

31,583
citations

55
h-index

131
g-index

131
ext. papers

36,336
ext. citations

13
avg, IF

6.88
L-index

#	Paper	IF	Citations
121	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	7.6	1
120	RNA modifications detection by comparative Nanopore direct RNA sequencing. <i>Nature Communications</i> , 2021 , 12, 7198	17.4	18
119	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	7.6	5
118	Schwann cell reprogramming into repair cells increases miRNA-21 expression in exosomes promoting axonal growth. <i>Journal of Cell Science</i> , 2020 , 133,	5.3	18
117	3D model of harlequin ichthyosis reveals inflammatory therapeutic targets. <i>Journal of Clinical Investigation</i> , 2020 , 130, 4798-4810	15.9	15
116	The midbody interactome reveals unexpected roles for PP1 phosphatases in cytokinesis. <i>Nature Communications</i> , 2019 , 10, 4513	17.4	29
115	Visualization and analysis of RNA-Seq assembly graphs. <i>Nucleic Acids Research</i> , 2019 , 47, 7262-7275	20.1	1
114	A programmed wave of uridylation-primed mRNA degradation is essential for meiotic progression and mammalian spermatogenesis. <i>Cell Research</i> , 2019 , 29, 221-232	24.7	24
113	MicroRNA degradation by a conserved target RNA regulates animal behavior. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 244-251	17.6	81
112	Defective germline reprogramming rewires the spermatogonial transcriptome. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 394-404	17.6	16
111	Genomic positional conservation identifies topological anchor point RNAs linked to developmental loci. <i>Genome Biology</i> , 2018 , 19, 32	18.3	77
110	Terminal uridylyltransferases target RNA viruses as part of the innate immune system. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 778-786	17.6	44
109	Non-coding RNA Expression, Function, and Variation during Drosophila Embryogenesis. <i>Current Biology</i> , 2018 , 28, 3547-3561.e9	6.3	26
108	Transposon-driven transcription is a conserved feature of vertebrate spermatogenesis and transcript evolution. <i>EMBO Reports</i> , 2017 , 18, 1231-1247	6.5	26
107	Large-scale analysis of microRNA expression, epi-transcriptomic features and biogenesis. <i>Nucleic Acids Research</i> , 2017 , 45, 1079-1090	20.1	33
106	A MILI-independent piRNA biogenesis pathway empowers partial germline reprogramming. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 604-606	17.6	14
105	3S Uridylation controls mature microRNA turnover during CD4 T-cell activation. <i>Rna</i> , 2017 , 23, 882-891	5.8	30

104	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	20.1	35
103	A high-resolution mRNA expression time course of embryonic development in zebrafish. <i>ELife</i> , 2017 , 6,	8.9	111
102	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	4.8	21
101	The RNA mA 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	17.6	176
100	mRNA 3' uridylation and poly(A) tail length sculpt the mammalian maternal transcriptome. <i>Nature</i> , 2017 , 548, 347-351	50.4	82
99	In situ functional dissection of RNA cis-regulatory elements by multiplex CRISPR-Cas9 genome engineering. <i>Nature Communications</i> , 2017 , 8, 2109	17.4	7
98	Extracellular vesicles are independent metabolic units with asparaginase activity. <i>Nature Chemical Biology</i> , 2017 , 13, 951-955	11.7	70
97	Author response: A high-resolution mRNA expression time course of embryonic development in zebrafish 2017 ,		4
96	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	9.7	33
95	Exploring regulatory networks of miR-96 in the developing inner ear. <i>Scientific Reports</i> , 2016 , 6, 23363	4.9	11
94	Activation of the TGFβ pathway impairs endothelial to haematopoietic transition. <i>Scientific Reports</i> , 2016 , 6, 21518	4.9	23
93	spongeScan: A web for detecting microRNA binding elements in lncRNA sequences. <i>Nucleic Acids Research</i> , 2016 , 44, W176-80	20.1	59
92	Improved definition of the mouse transcriptome via targeted RNA sequencing. <i>Genome Research</i> , 2016 , 26, 705-16	9.7	23
91	Quantitative gene profiling of long noncoding RNAs with targeted RNA sequencing. <i>Nature Methods</i> , 2015 , 12, 339-42	21.6	119
90	Chimira: analysis of small RNA sequencing data and microRNA modifications. <i>Bioinformatics</i> , 2015 , 31, 3365-7	7.2	74
89	Visualizing genome and systems biology: technologies, tools, implementation techniques and trends, past, present and future. <i>GigaScience</i> , 2015 , 4, 38	7.6	60
88	Solid tumors of childhood display specific serum microRNA profiles. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 350-60	4	50
87	High-density P300 enhancers control cell state transitions. <i>BMC Genomics</i> , 2015 , 16, 903	4.5	27

86	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	42.1	104
85	Extracellular vesicles from neural stem cells transfer IFN- γ via Ifngr1 to activate Stat1 signaling in target cells. <i>Molecular Cell</i> , 2014 , 56, 193-204	17.6	195
84	Serum levels of mature microRNAs in DICER1-mutated pleuropulmonary blastoma. <i>Oncogenesis</i> , 2014 , 3, e87	6.6	36
83	Visualisation of BioPAX Networks using BioLayout Express (3D). <i>F1000Research</i> , 2014 , 3, 246	3.6	13
82	Detecting MicroRNA Signatures Using Gene Expression Analysis 2014 , 129-150		
81	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, 450-60	8.7	15
80	Kraken: a set of tools for quality control and analysis of high-throughput sequence data. <i>Methods</i> , 2013 , 63, 41-9	4.6	242
79	The zebrafish reference genome sequence and its relationship to the human genome. <i>Nature</i> , 2013 , 496, 498-503	50.4	2550
78	Multiple epigenetic mechanisms and the piRNA pathway enforce LINE1 silencing during adult spermatogenesis. <i>Molecular Cell</i> , 2013 , 50, 601-8	17.6	134
77	Enhanced susceptibility to <i>Citrobacter rodentium</i> infection in microRNA-155-deficient mice. <i>Infection and Immunity</i> , 2013 , 81, 723-32	3.7	34
76	Detecting and comparing non-coding RNAs in the high-throughput era. <i>International Journal of Molecular Sciences</i> , 2013 , 14, 15423-58	6.3	16
75	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, 354-66	9.4	28
74	LIN28 Expression in malignant germ cell tumors downregulates let-7 and increases oncogene levels. <i>Cancer Research</i> , 2013 , 73, 4872-84	10.1	50
73	miR-221 affects multiple cancer pathways by modulating the level of hundreds messenger RNAs. <i>Frontiers in Genetics</i> , 2013 , 4, 64	4.5	31
72	Large-scale analysis of microRNA evolution. <i>BMC Genomics</i> , 2012 , 13, 218	4.5	34
71	Large-scale identification of microRNA targets in murine Dgcr8-deficient embryonic stem cell lines. <i>PLoS ONE</i> , 2012 , 7, e41762	3.7	8
70	A Neuronal Transcriptome Response Involving Stress Pathways is Buffered by Neuronal microRNAs. <i>Frontiers in Neuroscience</i> , 2012 , 6, 156	5.1	13
69	Targeted deletion of microRNA-22 promotes stress-induced cardiac dilation and contractile dysfunction. <i>Circulation</i> , 2012 , 125, 2751-61	16.7	134

68	Exploration of signals of positive selection derived from genotype-based human genome scans using re-sequencing data. <i>Human Genetics</i> , 2012 , 131, 665-74	6.3	8
67	Extent, causes, and consequences of small RNA expression variation in human adipose tissue. <i>PLoS Genetics</i> , 2012 , 8, e1002704	6	43
66	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, 29516-28	5.4	146
65	MiR-25 regulates Wwp2 and Fbxw7 and promotes reprogramming of mouse fibroblast cells to iPSCs. <i>PLoS ONE</i> , 2012 , 7, e40938	3.7	58
64	The endonuclease activity of Mili fuels piRNA amplification that silences LINE1 elements. <i>Nature</i> , 2011 , 480, 259-63	50.4	225
63	Messenger RNA and microRNA profiling during early mouse EB formation. <i>Gene Expression Patterns</i> , 2011 , 11, 334-44	1.5	16
62	Evolutionary and functional insights into Leishmania META1: evidence for lateral gene transfer and a role for META1 in secretion. <i>BMC Evolutionary Biology</i> , 2011 , 11, 334	3	9
61	RNAcentral: A vision for an international database of RNA sequences. <i>Rna</i> , 2011 , 17, 1941-6	5.8	54
60	MiR-221 influences effector functions and actin cytoskeleton in mast cells. <i>PLoS ONE</i> , 2011 , 6, e26133	3.7	69
59	Malignant germ cell tumors display common microRNA profiles resulting in global changes in expression of messenger RNA targets. <i>Cancer Research</i> , 2010 , 70, 2911-23	10.1	201
58	Efficient inhibition of miR-155 function in vivo by peptide nucleic acids. <i>Nucleic Acids Research</i> , 2010 , 38, 4466-75	20.1	179
57	iMotifs: an integrated sequence motif visualization and analysis environment. <i>Bioinformatics</i> , 2010 , 26, 843-4	7.2	7
56	SylArray: a web server for automated detection of miRNA effects from expression data. <i>Bioinformatics</i> , 2010 , 26, 2900-1	7.2	34
55	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, 13830-5	11.5	85
54	The miR-144/451 locus is required for erythroid homeostasis. <i>Journal of Experimental Medicine</i> , 2010 , 207, 1351-8	16.6	233
53	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	42.1	48
52	MapMi: automated mapping of microRNA loci. <i>BMC Bioinformatics</i> , 2010 , 11, 133	3.6	52
51	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	4.5	36

50	Zebrafish miR-1 and miR-133 shape muscle gene expression and regulate sarcomeric actin organization. <i>Genes and Development</i> , 2009 , 23, 619-32	12.6	131
49	Reciprocal regulation of microRNA and mRNA profiles in neuronal development and synapse formation. <i>BMC Genomics</i> , 2009 , 10, 419	4.5	27
48	An ENU-induced mutation of miR-96 associated with progressive hearing loss in mice. <i>Nature Genetics</i> , 2009 , 41, 614-8	36.3	249
47	Network visualization and analysis of gene expression data using BioLayout Express(3D). <i>Nature Protocols</i> , 2009 , 4, 1535-50	18.8	305
46	Detecting microRNA binding and siRNA off-target effects from expression data. <i>Nature Methods</i> , 2008 , 5, 1023-5	21.6	220
45	Re-annotation of the physical map of Glycine max for polyploid-like regions by BAC end sequence driven whole genome shotgun read assembly. <i>BMC Genomics</i> , 2008 , 9, 323	4.5	10
44	Annotation of mammalian primary microRNAs. <i>BMC Genomics</i> , 2008 , 9, 564	4.5	110
43	A logic-based diagram of signalling pathways central to macrophage activation. <i>BMC Systems Biology</i> , 2008 , 2, 36	3.5	46
42	Fusion and fission of genes define a metric between fungal genomes. <i>PLoS Computational Biology</i> , 2008 , 4, e1000200	5	21
41	Computational prediction of protein-protein interactions. <i>Molecular Biotechnology</i> , 2008 , 38, 1-17	3	152
40	miRBase: tools for microRNA genomics. <i>Nucleic Acids Research</i> , 2008 , 36, D154-8	20.1	3326
39	Requirement of bic/microRNA-155 for normal immune function. <i>Science</i> , 2007 , 316, 608-11	33.3	1584
38	Denoising inferred functional association networks obtained by gene fusion analysis. <i>BMC Genomics</i> , 2007 , 8, 460	4.5	16
37	Prediction of microRNA targets. <i>Drug Discovery Today</i> , 2007 , 12, 452-8	8.8	229
36	Genomic analysis of human microRNA transcripts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 17719-24	11.5	402
35	Construction, visualisation, and clustering of transcription networks from microarray expression data. <i>PLoS Computational Biology</i> , 2007 , 3, 2032-42	5	190
34	A Slicer-independent role for Argonaute 2 in hematopoiesis and the microRNA pathway. <i>Genes and Development</i> , 2007 , 21, 1999-2004	12.6	277
33	microRNA-155 regulates the generation of immunoglobulin class-switched plasma cells. <i>Immunity</i> , 2007 , 27, 847-59	32.3	650

32	RNA editing of human microRNAs. <i>Genome Biology</i> , 2006 , 7, R27	18.3	270
31	miRBase: microRNA sequences, targets and gene nomenclature. <i>Nucleic Acids Research</i> , 2006 , 34, D140-40.1	40.1	3494
30	Zebrafish MiR-430 promotes deadenylation and clearance of maternal mRNAs. <i>Science</i> , 2006 , 312, 75-9	33.3	1222
29	MicroRNAs regulate brain morphogenesis in zebrafish. <i>Science</i> , 2005 , 308, 833-8	33.3	1080
28	BioLayout(Java): versatile network visualisation of structural and functional relationships. <i>Applied Bioinformatics</i> , 2005 , 4, 71-4		46
27	Computational Prediction of Protein-Protein Interactions 2005 , 629-652		1
26	CoGenT++: an extensive and extensible data environment for computational genomics. <i>Bioinformatics</i> , 2005 , 21, 3806-10	7.2	20
25	MagicMatch--cross-referencing sequence identifiers across databases. <i>Bioinformatics</i> , 2005 , 21, 3429-30	7.2	18
24	Human MicroRNA targets. <i>PLoS Biology</i> , 2004 , 2, e363	9.7	2746
23	Identification of virus-encoded microRNAs. <i>Science</i> , 2004 , 304, 734-6	33.3	1293
22	Detection of functional modules from protein interaction networks. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 54, 49-57	4.2	288
21	Evaluation of annotation strategies using an entire genome sequence. <i>Bioinformatics</i> , 2003 , 19, 717-26	7.2	58
20	Complete GENome Tracking (COGENT): a flexible data environment for computational genomics. <i>Bioinformatics</i> , 2003 , 19, 1451-2	7.2	35
19	Protein families and TRIBES in genome sequence space. <i>Nucleic Acids Research</i> , 2003 , 31, 4632-8	20.1	103
18	MicroRNA Targets in Drosophila 2003 , 4, P8		13
17	Mapping functional associations in the entire genome of Drosophila melanogaster using fusion analysis. <i>Comparative and Functional Genomics</i> , 2003 , 4, 337-41		3
16	Classification schemes for protein structure and function. <i>Nature Reviews Genetics</i> , 2003 , 4, 508-19	30.1	74
15	MicroRNA targets in Drosophila. <i>Genome Biology</i> , 2003 , 5, R1	18.3	2206

14	Myriads of protein families, and still counting. <i>Genome Biology</i> , 2003 , 4, 401	18.3	44
13	An efficient algorithm for large-scale detection of protein families. <i>Nucleic Acids Research</i> , 2002 , 30, 1575-84	18.4	2433
12	Transcription-associated protein families are primarily taxon-specific. <i>Bioinformatics</i> , 2001 , 17, 95-7	7.2	25
11	BioLayout--an automatic graph layout algorithm for similarity visualization. <i>Bioinformatics</i> , 2001 , 17, 853-4	7.2	130
10	Functional associations of proteins in entire genomes by means of exhaustive detection of gene fusions. <i>Genome Biology</i> , 2001 , 2, RESEARCH0034	18.3	79
9	Estimation of synteny conservation and genome compaction between pufferfish (<i>Fugu</i>) and human. <i>Yeast</i> , 2000 , 17, 22-36	3.4	50
8	GeneRAGE: a robust algorithm for sequence clustering and domain detection. <i>Bioinformatics</i> , 2000 , 16, 451-7	7.2	156
7	CAST: an iterative algorithm for the complexity analysis of sequence tracts. Complexity analysis of sequence tracts. <i>Bioinformatics</i> , 2000 , 16, 915-22	7.2	139
6	Protein interaction maps for complete genomes based on gene fusion events. <i>Nature</i> , 1999 , 402, 86-90	50.4	896
5	miRBase: a database of microRNA sequences, targets and nomenclature	157-171	
4	Genomic positional conservation identifies topological anchor point (tap)RNAs linked to developmental loci		7
3	Terminal uridylyltransferases target RNA viruses as part of the innate immune system in animals		1
2	RNA modifications detection by comparative Nanopore direct RNA sequencing		33
1	A high-resolution mRNA expression time course of embryonic development in zebrafish		2