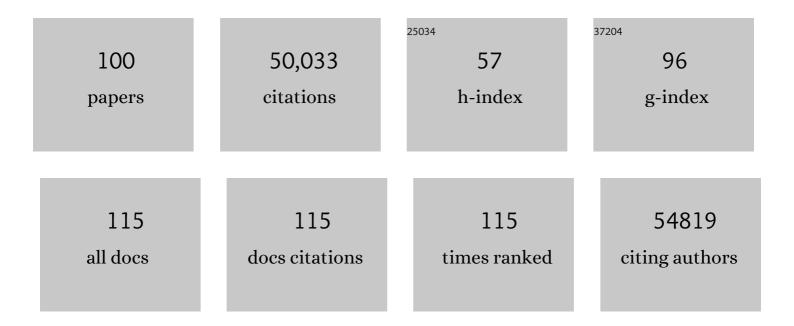
Sam Griffiths-Jones

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	miRBase: annotating high confidence microRNAs using deep sequencing data. Nucleic Acids Research, 2014, 42, D68-D73.	14.5	4,752
2	miRBase: microRNA sequences, targets and gene nomenclature. Nucleic Acids Research, 2006, 34, D140-D144.	14.5	4,192
3	miRBase: tools for microRNA genomics. Nucleic Acids Research, 2007, 36, D154-D158.	14.5	3,854
4	miRBase: integrating microRNA annotation and deep-sequencing data. Nucleic Acids Research, 2011, 39, D152-D157.	14.5	3,263
5	The Pfam protein families database. Nucleic Acids Research, 2004, 32, 138D-141.	14.5	3,084
6	miRBase: from microRNA sequences to function. Nucleic Acids Research, 2019, 47, D155-D162.	14.5	3,014
7	The Pfam Protein Families Database. Nucleic Acids Research, 2002, 30, 276-280.	14.5	2,067
8	Pfam: clans, web tools and services. Nucleic Acids Research, 2006, 34, D247-D251.	14.5	2,030
9	The microRNA Registry. Nucleic Acids Research, 2004, 32, 109D-111.	14.5	1,953
10	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	27.8	1,886
11	Identification of Mammalian microRNA Host Genes and Transcription Units. Genome Research, 2004, 14, 1902-1910.	5.5	1,704
12	A uniform system for microRNA annotation. Rna, 2003, 9, 277-279.	3.5	1,620
13	Rfam: an RNA family database. Nucleic Acids Research, 2003, 31, 439-441.	14.5	1,296
14	Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus fumigatus. Nature, 2005, 438, 1151-1156.	27.8	1,272
15	Rfam: annotating non-coding RNAs in complete genomes. Nucleic Acids Research, 2004, 33, D121-D124.	14.5	1,255
16	Sequencing of Aspergillus nidulans and comparative analysis with A. fumigatus and A. oryzae. Nature, 2005, 438, 1105-1115.	27.8	1,250
17	Criteria for Annotation of Plant MicroRNAs. Plant Cell, 2008, 20, 3186-3190.	6.6	1,158
18	Rfam: updates to the RNA families database. Nucleic Acids Research, 2009, 37, D136-D140.	14.5	820

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19	The Genome Sequence of Caenorhabditis briggsae: A Platform for Comparative Genomics. PLoS Biology, 2003, 1, e45.	5.6	812
20	The InterPro Database, 2003 brings increased coverage and new features. Nucleic Acids Research, 2003, 31, 315-318.	14.5	640
21	miRBase: The MicroRNA Sequence Database. , 2006, 342, 129-138.		531
22	Rfam 14: expanded coverage of metagenomic, viral and microRNA families. Nucleic Acids Research, 2021, 49, D192-D200.	14.5	475
23	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
24	Rfam: Wikipedia, clans and the "decimal" release. Nucleic Acids Research, 2011, 39, D141-D145.	14.5	355
25	DNA sequence and analysis of human chromosome 9. Nature, 2004, 429, 369-374.	27.8	314
26	The house spider genome reveals an ancient whole-genome duplication during arachnid evolution. BMC Biology, 2017, 15, 62.	3.8	286
27	Genome of the Host-Cell Transforming Parasite Theileria annulata Compared with T. parva. Science, 2005, 309, 131-133.	12.6	285
28	Small RNAs: Big Impact on Plant Development. Trends in Plant Science, 2017, 22, 1056-1068.	8.8	256
29	Structural relatedness of plant food allergens with specific reference to cross-reactive allergens: An in silico analysis. Journal of Allergy and Clinical Immunology, 2005, 115, 163-170.	2.9	245
30	The First Myriapod Genome Sequence Reveals Conservative Arthropod Gene Content and Genome Organisation in the Centipede Strigamia maritima. PLoS Biology, 2014, 12, e1002005.	5.6	221
31	The DNA sequence and biological annotation of human chromosome 1. Nature, 2006, 441, 315-321.	27.8	211
32	MicroRNA evolution by arm switching. EMBO Reports, 2011, 12, 172-177.	4.5	199
33	Reducing ligation bias of small RNAs in libraries for next generation sequencing. Silence: A Journal of RNA Regulation, 2012, 3, 4.	8.1	176
34	RNAcentral: a comprehensive database of non-coding RNA sequences. Nucleic Acids Research, 2017, 45, D128-D134.	14.5	174
35	miRBase: microRNA Sequences and Annotation. Current Protocols in Bioinformatics, 2010, 29, Unit 12.9.1-10.	25.8	171
36	Conservation of the H19 noncoding RNA and H19-IGF2 imprinting mechanism in therians. Nature Genetics, 2008, 40, 971-976.	21.4	169

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37	Dissecting the stability of a β-hairpin peptide that folds in water: NMR and molecular dynamics analysis of the β-turn and β-strand contributions to folding 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1999, 292, 1051-1069.	4.2	167
38	RNAcentral 2021: secondary structure integration, improved sequence search and new member databases. Nucleic Acids Research, 2021, 49, D212-D220.	14.5	160
39	RNAcentral: a hub of information for non-coding RNA sequences. Nucleic Acids Research, 2019, 47, D221-D229.	14.5	153
40	Functional Shifts in Insect microRNA Evolution. Genome Biology and Evolution, 2010, 2, 686-696.	2.5	131
41	Annotation of mammalian primary microRNAs. BMC Genomics, 2008, 9, 564.	2.8	121
42	Annotating Noncoding RNA Genes. Annual Review of Genomics and Human Genetics, 2007, 8, 279-298.	6.2	120
43	Structure, Folding, and Energetics of Cooperative Interactions between the β-Strands of a de Novo Designed Three-Stranded Antiparallel β-Sheet Peptide. Journal of the American Chemical Society, 2000, 122, 8350-8356.	13.7	115
44	Restoring the constitutional alignment with a restrictive kinematic protocol improves quantitative soft-tissue balance in total knee arthroplasty: a randomized controlled trial. Bone and Joint Journal, 2020, 102-B, 117-124.	4.4	115
45	Mutations in SNORD118 cause the cerebral microangiopathy leukoencephalopathy with calcifications and cysts. Nature Genetics, 2016, 48, 1185-1192.	21.4	114
46	RALEERNA ALignment Editor in Emacs. Bioinformatics, 2005, 21, 257-259.	4.1	109
47	RNAcentral: an international database of ncRNA sequences. Nucleic Acids Research, 2015, 43, D123-D129.	14.5	103
48	Bias in microRNA functional enrichment analysis. Bioinformatics, 2015, 31, 1592-1598.	4.1	100
49	The DNA sequence and analysis of human chromosome 13. Nature, 2004, 428, 522-528.	27.8	91
50	Clusters of microRNAs emerge by new hairpins in existing transcripts. Nucleic Acids Research, 2013, 41, 7745-7752.	14.5	84
51	Enhanced genome assembly and a new official gene set for Tribolium castaneum. BMC Genomics, 2020, 21, 47.	2.8	84
52	Plant protein families and their relationships to food allergy. Biochemical Society Transactions, 2002, 30, 906-910.	3.4	81
53	Genome-wide discovery and verification of novel structured RNAs in <i>Plasmodium falciparum</i> . Genome Research, 2008, 18, 281-292.	5.5	81
54	Transcriptome analysis for the chicken based on 19,626 finished cDNA sequences and 485,337 expressed sequence tags. Genome Research, 2005, 15, 174-183.	5.5	79

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55	Evolution and function of the extended miR-2 microRNA family. RNA Biology, 2012, 9, 242-248.	3.1	79
56	Energetics of Weak Interactions in a β-hairpin Peptide: Electrostatic and Hydrophobic Contributions to Stability from Lysine Salt Bridges. Journal of the American Chemical Society, 1999, 121, 11615-11620.	13.7	78
57	A guide to naming human non oding RNA genes. EMBO Journal, 2020, 39, e103777.	7.8	77
58	RNAcentral: A vision for an international database of RNA sequences. Rna, 2011, 17, 1941-1946.	3.5	67
59	The RNA WikiProject: Community annotation of RNA families. Rna, 2008, 14, 2462-2464.	3.5	66
60	Conserved RNA structures in the non-canonical Hac1/Xbp1 intron. RNA Biology, 2011, 8, 552-556.	3.1	66
61	Detection of microRNAs in color space. Bioinformatics, 2012, 28, 318-323.	4.1	63
62	Sex-Biased Expression of MicroRNAs in Schistosoma mansoni. PLoS Neglected Tropical Diseases, 2013, 7, e2402.	3.0	60
63	MicroRNAs from the same precursor have different targeting properties. Silence: A Journal of RNA Regulation, 2012, 3, 8.	8.1	57
64	Modulation of intrinsic φ,Ï^ propensities of amino acids by neighbouring residues in the coil regions of protein structures: NMR analysis and dissection of a β-hairpin peptide 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1998, 284, 1597-1609.	4.2	56
65	Intron Evolution in Saccharomycetaceae. Genome Biology and Evolution, 2014, 6, 2543-2556.	2.5	48
66	Song exposure regulates known and novel microRNAs in the zebra finch auditory forebrain. BMC Genomics, 2011, 12, 277.	2.8	45
67	Natural Antisense Transcripts and Long Non-Coding RNA in Neurospora crassa. PLoS ONE, 2014, 9, e91353.	2.5	42
68	MicroRNA evolution, expression, and function during short germband development in <i>Tribolium castaneum</i> . Genome Research, 2016, 26, 85-96.	5.5	42
69	tRNA anticodon shifts in eukaryotic genomes. Rna, 2014, 20, 269-281.	3.5	41
70	The Evolution of tRNA Genes in Drosophila. Genome Biology and Evolution, 2010, 2, 467-477.	2.5	40
71	Fast-evolving microRNAs are highly expressed in the early embryo of <i>Drosophila virilis</i> . Rna, 2014, 20, 360-372.	3.5	40
72	Effects of Amino Acid φ,Ï^ Propensities and Secondary Structure Interactions in Modulating Hα Chemical Shifts in Peptide and Protein β-Sheet. Journal of the American Chemical Society, 2001, 123, 12318-12324.	13.7	38

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73	Pervasive microRNA Duplication in Chelicerates: Insights from the Embryonic microRNA Repertoire of the Spider <i>Parasteatoda tepidariorum</i> . Genome Biology and Evolution, 2016, 8, 2133-2144.	2.5	38
74	C. elegans noncoding RNA genes. WormBook, 2005, , 1-7.	5.3	34
75	Mitochondrial Pseudogenes in the Nuclear Genomes of Drosophila. PLoS ONE, 2012, 7, e32593.	2.5	33
76	Target Repression Induced by Endogenous microRNAs: Large Differences, Small Effects. PLoS ONE, 2014, 9, e104286.	2.5	33
77	A selenocysteine tRNA and SECIS element in Plasmodium falciparum. Rna, 2005, 11, 119-122.	3.5	32
78	Structure, evolution and function of the bi-directionally transcribed iab-4/iab-8 microRNA locus in arthropods. Nucleic Acids Research, 2013, 41, 3352-3361.	14.5	32
79	Silencing miR-370-3p rescues funny current and sinus node function in heart failure. Scientific Reports, 2020, 10, 11279.	3.3	30
80	Novel Intronic RNA Structures Contribute to Maintenance of Phenotype in <i>Saccharomyces cerevisiae</i> . Genetics, 2016, 203, 1469-1481.	2.9	29
81	Large-scale profiling of noncoding RNA function in yeast. PLoS Genetics, 2018, 14, e1007253.	3.5	29
82	Folding of a β-hairpin peptide derived from the N-terminus of ubiquitin. FEBS Journal, 2000, 267, 3539-3548.	0.2	28
83	Multiple products from microRNA transcripts. Biochemical Society Transactions, 2013, 41, 850-854.	3.4	25
84	Annotating Non-Coding RNAs with Rfam. , 2005, Chapter 12, Unit 12.5.		24
85	Quo vadis microRNAs?. Trends in Genetics, 2020, 36, 461-463.	6.7	24
86	Conserved Temporal Patterns of MicroRNA Expression in Drosophila Support a Developmental Hourglass Model. Genome Biology and Evolution, 2014, 6, 2459-2467.	2.5	22
87	Identifying Protein Domains with the Pfam Database. Current Protocols in Bioinformatics, 2003, 1, 2.5.1-2.5.19.	25.8	20
88	The use of structure information to increase alignment accuracy does not aid homologue detection with profile HMMs. Bioinformatics, 2002, 18, 1243-1249.	4.1	19
89	Abundant expression of somatic transposon-derived piRNAs throughout Tribolium castaneum embryogenesis. Genome Biology, 2017, 18, 184.	8.8	19
90	Conservation and Losses of Non-Coding RNAs in Avian Genomes. PLoS ONE, 2015, 10, e0121797.	2.5	18

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91	Regulatory RNAs: A Universal Language for Inter-Domain Communication. International Journal of Molecular Sciences, 2020, 21, 8919.	4.1	18
92	Dynamical gene regulatory networks are tuned by transcriptional autoregulation with microRNA feedback. Scientific Reports, 2020, 10, 12960.	3.3	15
93	The Transcription Factor-microRNA Regulatory Network during hESC-chondrogenesis. Scientific Reports, 2020, 10, 4744.	3.3	11
94	An Analysis of Structural Influences on Selection in RNA Genes. Molecular Biology and Evolution, 2008, 26, 209-216.	8.9	8
95	Single-cell visualization of <i>mir-9a</i> and <i>Senseless</i> co-expression during <i>Drosophila melanogaster</i> embryonic and larval peripheral nervous system development. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	6
96	The embryonic transcriptome of Parhyale hawaiensis reveals different dynamics of microRNAs and mRNAs during the maternal-zygotic transition. Scientific Reports, 2022, 12, 174.	3.3	3
97	miRBase: a database of microRNA sequences, targets and nomenclature. , 0, , 157-171.		2
98	Editorial. Briefings in Functional Genomics & Proteomics, 2009, 8, 405-406.	3.8	2
99	Human microRNAs. , 2005, , .		Ο
100	<i>miR-9a</i> regulates levels of both <i>rhomboid</i> mRNA and protein in the early <i>Drosophila melanogaster</i> embryo. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	0