

Sam Griffiths-Jones

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.

100
papers

40,202
citations

54
h-index

115
g-index

115
ext. papers

45,962
ext. citations

13.6
avg, IF

7.85
L-index

#	Paper	IF	Citations
100	The embryonic transcriptome of <i>Parhyale hawaiiensis</i> reveals different dynamics of microRNAs and mRNAs during the maternal-zygotic transition.. <i>Scientific Reports</i> , 2022 , 12, 174	4.9	1
99	Single-cell visualization of mir-9a and Senseless co-expression during <i>Drosophila melanogaster</i> embryonic and larval peripheral nervous system development. <i>G3: Genes, Genomes, Genetics</i> , 2021 , 11,	3.2	1
98	RNAcentral 2021: secondary structure integration, improved sequence search and new member databases. <i>Nucleic Acids Research</i> , 2021 , 49, D212-D220	20.1	42
97	Rfam 14: expanded coverage of metagenomic, viral and microRNA families. <i>Nucleic Acids Research</i> , 2021 , 49, D192-D200	20.1	108
96	Restoring the constitutional alignment with a restrictive kinematic protocol improves quantitative soft-tissue balance in total knee arthroplasty: a randomized controlled trial. <i>Bone and Joint Journal</i> , 2020 , 102-B, 117-124	5.6	51
95	The Transcription Factor-microRNA Regulatory Network during hESC-chondrogenesis. <i>Scientific Reports</i> , 2020 , 10, 4744	4.9	7
94	A guide to naming human non-coding RNA genes. <i>EMBO Journal</i> , 2020 , 39, e103777	13	39
93	Enhanced genome assembly and a new official gene set for <i>Tribolium castaneum</i> . <i>BMC Genomics</i> , 2020 , 21, 47	4.5	35
92	Silencing miR-370-3p rescues funny current and sinus node function in heart failure. <i>Scientific Reports</i> , 2020 , 10, 11279	4.9	13
91	Regulatory RNAs: A Universal Language for Inter-Domain Communication. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	11
90	Dynamical gene regulatory networks are tuned by transcriptional autoregulation with microRNA feedback. <i>Scientific Reports</i> , 2020 , 10, 12960	4.9	5
89	Quo vadis microRNAs?. <i>Trends in Genetics</i> , 2020 , 36, 461-463	8.5	13
88	RNAcentral: a hub of information for non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2019 , 47, D221-D229	20.1	90
87	miRBase: from microRNA sequences to function. <i>Nucleic Acids Research</i> , 2019 , 47, D155-D162	20.1	1436
86	Large-scale profiling of noncoding RNA function in yeast. <i>PLoS Genetics</i> , 2018 , 14, e1007253	6	14
85	Small RNAs: Big Impact on Plant Development. <i>Trends in Plant Science</i> , 2017 , 22, 1056-1068	13.1	146
84	The house spider genome reveals an ancient whole-genome duplication during arachnid evolution. <i>BMC Biology</i> , 2017 , 15, 62	7.3	182

83	Abundant expression of somatic transposon-derived piRNAs throughout <i>Tribolium castaneum</i> embryogenesis. <i>Genome Biology</i> , 2017 , 18, 184	18.3	14
82	RNAcentral: a comprehensive database of non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2017 , 45, D128-D134	20.1	119
81	Mutations in SNORD118 cause the cerebral microangiopathy leukoencephalopathy with calcifications and cysts. <i>Nature Genetics</i> , 2016 , 48, 1185-92	36.3	74
80	Pervasive microRNA Duplication in Chelicerates: Insights from the Embryonic microRNA Repertoire of the Spider <i>Parasteatoda tepidariorum</i> . <i>Genome Biology and Evolution</i> , 2016 , 8, 2133-44	3.9	30
79	MicroRNA evolution, expression, and function during short germband development in <i>Tribolium castaneum</i> . <i>Genome Research</i> , 2016 , 26, 85-96	9.7	35
78	Novel Intronic RNA Structures Contribute to Maintenance of Phenotype in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2016 , 203, 1469-81	4	20
77	RNAcentral: an international database of ncRNA sequences. <i>Nucleic Acids Research</i> , 2015 , 43, D123-9	20.1	89
76	Conservation and losses of non-coding RNAs in avian genomes. <i>PLoS ONE</i> , 2015 , 10, e0121797	3.7	14
75	Bias in microRNA functional enrichment analysis. <i>Bioinformatics</i> , 2015 , 31, 1592-8	7.2	78
74	miRBase: annotating high confidence microRNAs using deep sequencing data. <i>Nucleic Acids Research</i> , 2014 , 42, D68-73	20.1	3795
73	Natural antisense transcripts and long non-coding RNA in <i>Neurospora crassa</i> . <i>PLoS ONE</i> , 2014 , 9, e91353	3.7	35
72	Target repression induced by endogenous microRNAs: large differences, small effects. <i>PLoS ONE</i> , 2014 , 9, e104286	3.7	24
71	Conserved temporal patterns of microRNA expression in <i>Drosophila</i> support a developmental hourglass model. <i>Genome Biology and Evolution</i> , 2014 , 6, 2459-67	3.9	15
70	The first myriapod genome sequence reveals conservative arthropod gene content and genome organisation in the centipede <i>Strigamia maritima</i> . <i>PLoS Biology</i> , 2014 , 12, e1002005	9.7	182
69	Fast-evolving microRNAs are highly expressed in the early embryo of <i>Drosophila virilis</i> . <i>Rna</i> , 2014 , 20, 360-72	5.8	27
68	tRNA anticodon shifts in eukaryotic genomes. <i>Rna</i> , 2014 , 20, 269-81	5.8	24
67	Intron evolution in <i>Saccharomycetaceae</i> . <i>Genome Biology and Evolution</i> , 2014 , 6, 2543-56	3.9	34
66	Multiple products from microRNA transcripts. <i>Biochemical Society Transactions</i> , 2013 , 41, 850-4	5.1	17

65	Sex-biased expression of microRNAs in <i>Schistosoma mansoni</i> . <i>PLoS Neglected Tropical Diseases</i> , 2013 , 7, e2402	4.8	47
64	Clusters of microRNAs emerge by new hairpins in existing transcripts. <i>Nucleic Acids Research</i> , 2013 , 41, 7745-52	20.1	65
63	Structure, evolution and function of the bi-directionally transcribed iab-4/iab-8 microRNA locus in arthropods. <i>Nucleic Acids Research</i> , 2013 , 41, 3352-61	20.1	26
62	Reducing ligation bias of small RNAs in libraries for next generation sequencing. <i>Silence: A Journal of RNA Regulation</i> , 2012 , 3, 4		140
61	MicroRNAs from the same precursor have different targeting properties. <i>Silence: A Journal of RNA Regulation</i> , 2012 , 3, 8		50
60	Mitochondrial pseudogenes in the nuclear genomes of <i>Drosophila</i> . <i>PLoS ONE</i> , 2012 , 7, e32593	3.7	27
59	Evolution and function of the extended miR-2 microRNA family. <i>RNA Biology</i> , 2012 , 9, 242-8	4.8	66
58	Detection of microRNAs in color space. <i>Bioinformatics</i> , 2012 , 28, 318-23	7.2	57
57	MicroRNA evolution by arm switching. <i>EMBO Reports</i> , 2011 , 12, 172-7	6.5	166
56	Song exposure regulates known and novel microRNAs in the zebra finch auditory forebrain. <i>BMC Genomics</i> , 2011 , 12, 277	4.5	39
55	miRBase: integrating microRNA annotation and deep-sequencing data. <i>Nucleic Acids Research</i> , 2011 , 39, D152-7	20.1	2830
54	Conserved RNA structures in the non-canonical Hac1/Xbp1 intron. <i>RNA Biology</i> , 2011 , 8, 552-6	4.8	49
53	Rfam: Wikipedia, clans and the "decimal" release. <i>Nucleic Acids Research</i> , 2011 , 39, D141-5	20.1	321
52	RNAcentral: A vision for an international database of RNA sequences. <i>Rna</i> , 2011 , 17, 1941-6	5.8	54
51	Functional shifts in insect microRNA evolution. <i>Genome Biology and Evolution</i> , 2010 , 2, 686-96	3.9	109
50	miRBase: microRNA sequences and annotation. <i>Current Protocols in Bioinformatics</i> , 2010 , Chapter 12, Unit 12.9.1-10	24.2	139
49	The evolution of tRNA genes in <i>Drosophila</i> . <i>Genome Biology and Evolution</i> , 2010 , 2, 467-77	3.9	34
48	Rfam: updates to the RNA families database. <i>Nucleic Acids Research</i> , 2009 , 37, D136-40	20.1	652

47	An analysis of structural influences on selection in RNA genes. <i>Molecular Biology and Evolution</i> , 2009 , 26, 209-16	8.3	8
46	Conservation of the H19 noncoding RNA and H19-IGF2 imprinting mechanism in therians. <i>Nature Genetics</i> , 2008 , 40, 971-6	36.3	141
45	Annotation of mammalian primary microRNAs. <i>BMC Genomics</i> , 2008 , 9, 564	4.5	110
44	Criteria for annotation of plant MicroRNAs. <i>Plant Cell</i> , 2008 , 20, 3186-90	11.6	992
43	Genome-wide discovery and verification of novel structured RNAs in Plasmodium falciparum. <i>Genome Research</i> , 2008 , 18, 281-92	9.7	72
42	The RNA WikiProject: community annotation of RNA families. <i>Rna</i> , 2008 , 14, 2462-4	5.8	50
41	miRBase: tools for microRNA genomics. <i>Nucleic Acids Research</i> , 2008 , 36, D154-8	20.1	3326
40	Annotating noncoding RNA genes. <i>Annual Review of Genomics and Human Genetics</i> , 2007 , 8, 279-98	9.7	110
39	Evolution of genes and genomes on the Drosophila phylogeny. <i>Nature</i> , 2007 , 450, 203-18	50.4	1586
38	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
37	Pfam: clans, web tools and services. <i>Nucleic Acids Research</i> , 2006 , 34, D247-51	20.1	1784
36	miRBase: the microRNA sequence database. <i>Methods in Molecular Biology</i> , 2006 , 342, 129-38	1.4	445
35	miRBase: microRNA sequences, targets and gene nomenclature. <i>Nucleic Acids Research</i> , 2006 , 34, D140-4	20.1	3494
34	The DNA sequence and biological annotation of human chromosome 1. <i>Nature</i> , 2006 , 441, 315-21	50.4	169
33	RALEE--RNA ALignment editor in Emacs. <i>Bioinformatics</i> , 2005 , 21, 257-9	7.2	98
32	Genome of the host-cell transforming parasite Theileria annulata compared with T. parva. <i>Science</i> , 2005 , 309, 131-3	33.3	235
31	Annotating non-coding RNAs with Rfam. <i>Current Protocols in Bioinformatics</i> , 2005 , Chapter 12, Unit 12.5	24.2	19
30	Structural relatedness of plant food allergens with specific reference to cross-reactive allergens: an in silico analysis. <i>Journal of Allergy and Clinical Immunology</i> , 2005 , 115, 163-70	11.5	212

29	Rfam: annotating non-coding RNAs in complete genomes. <i>Nucleic Acids Research</i> , 2005 , 33, D121-4	20.1	990
28	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005 , 438, 1151-6	50.4	1114
27	Sequencing of <i>Aspergillus nidulans</i> and comparative analysis with <i>A. fumigatus</i> and <i>A. oryzae</i> . <i>Nature</i> , 2005 , 438, 1105-15	50.4	1094
26	Transcriptome analysis for the chicken based on 19,626 finished cDNA sequences and 485,337 expressed sequence tags. <i>Genome Research</i> , 2005 , 15, 174-83	9.7	71
25	A selenocysteine tRNA and SECIS element in <i>Plasmodium falciparum</i> . <i>Rna</i> , 2005 , 11, 119-22	5.8	31
24	<i>C. elegans</i> noncoding RNA genes. <i>WormBook</i> , 2005 , 1-7		28
23	The DNA sequence and analysis of human chromosome 13. <i>Nature</i> , 2004 , 428, 522-8	50.4	71
22	DNA sequence and analysis of human chromosome 9. <i>Nature</i> , 2004 , 429, 369-74	50.4	102
21	The microRNA Registry. <i>Nucleic Acids Research</i> , 2004 , 32, D109-11	20.1	1664
20	Identification of mammalian microRNA host genes and transcription units. <i>Genome Research</i> , 2004 , 14, 1902-10	9.7	1451
19	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2004 , 32, D138-41	20.1	2720
18	Rfam 2004 ,		2
17	The genome sequence of <i>Caenorhabditis briggsae</i> : a platform for comparative genomics. <i>PLoS Biology</i> , 2003 , 1, E45	9.7	677
16	Identifying protein domains with the Pfam database. <i>Current Protocols in Bioinformatics</i> , 2003 , Chapter 2, Unit 2.5	24.2	13
15	A uniform system for microRNA annotation. <i>Rna</i> , 2003 , 9, 277-9	5.8	1332
14	Rfam: an RNA family database. <i>Nucleic Acids Research</i> , 2003 , 31, 439-41	20.1	970
13	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , 2003 , 31, 315-8	20.1	556
12	The use of structure information to increase alignment accuracy does not aid homologue detection with profile HMMs. <i>Bioinformatics</i> , 2002 , 18, 1243-9	7.2	19

11	Plant protein families and their relationships to food allergy. <i>Biochemical Society Transactions</i> , 2002 , 30, 906-10	5.1	60
10	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2002 , 30, 276-80	20.1	1839
9	Effects of amino acid phi,psi propensities and secondary structure interactions in modulating H alpha chemical shifts in peptide and protein beta-sheet. <i>Journal of the American Chemical Society</i> , 2001 , 123, 12318-24	16.4	38
8	Folding of a beta-hairpin peptide derived from the N-terminus of ubiquitin. Conformational preferences of beta-turn residues dictate non-native beta-strand interactions. <i>FEBS Journal</i> , 2000 , 267, 3539-48		25
7	Structure, Folding, and Energetics of Cooperative Interactions between the β Strands of a de Novo Designed Three-Stranded Antiparallel β Sheet Peptide. <i>Journal of the American Chemical Society</i> , 2000 , 122, 8350-8356	16.4	109
6	Energetics of Weak Interactions in a β hairpin Peptide: π Electrostatic and Hydrophobic Contributions to Stability from Lysine Salt Bridges. <i>Journal of the American Chemical Society</i> , 1999 , 121, 11615-11620	16.4	71
5	Dissecting the stability of a beta-hairpin peptide that folds in water: NMR and molecular dynamics analysis of the beta-turn and beta-strand contributions to folding. <i>Journal of Molecular Biology</i> , 1999 , 292, 1051-69	6.5	152
4	Modulation of intrinsic phi,psi propensities of amino acids by neighbouring residues in the coil regions of protein structures: NMR analysis and dissection of a beta-hairpin peptide. <i>Journal of Molecular Biology</i> , 1998 , 284, 1597-609	6.5	53
3	miRBase: a database of microRNA sequences, targets and nomenclature	157-171	
2	The house spider genome reveals an ancient whole-genome duplication during arachnid evolution		3
1	miR-9a regulates levels of both rhomboid mRNA and protein in the early <i>Drosophila melanogaster</i> embryo		1