

Sam Griffiths-Jones

List of Publications by Year in descending order

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100
papers

50,033
citations

24978

57
h-index

37111

96
g-index

115
all docs

115
docs citations

115
times ranked

54819
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	1.6	3
2	<i>miR-9a</i> regulates levels of both <i>rhomboid</i> mRNA and protein in the early <i>Drosophila melanogaster</i> embryo. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	0
3	RNAcentral 2021: secondary structure integration, improved sequence search and new member databases. <i>Nucleic Acids Research</i> , 2021, 49, D212-D220.	6.5	160
4	Rfam 14: expanded coverage of metagenomic, viral and microRNA families. <i>Nucleic Acids Research</i> , 2021, 49, D192-D200.	6.5	475
5	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. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	6
6	Silencing miR-370-3p rescues funny current and sinus node function in heart failure. <i>Scientific Reports</i> , 2020, 10, 11279.	1.6	30
7	Regulatory RNAs: A Universal Language for Inter-Domain Communication. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8919.	1.8	18
8	Dynamical gene regulatory networks are tuned by transcriptional autoregulation with microRNA feedback. <i>Scientific Reports</i> , 2020, 10, 12960.	1.6	15
9	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.	1.9	115
10	The Transcription Factor-microRNA Regulatory Network during hESC-chondrogenesis. <i>Scientific Reports</i> , 2020, 10, 4744.	1.6	11
11	A guide to naming human non-coding RNA genes. <i>EMBO Journal</i> , 2020, 39, e103777.	3.5	77
12	Enhanced genome assembly and a new official gene set for <i>Tribolium castaneum</i> . <i>BMC Genomics</i> , 2020, 21, 47.	1.2	84
13	Quo vadis microRNAs?. <i>Trends in Genetics</i> , 2020, 36, 461-463.	2.9	24
14	RNAcentral: a hub of information for non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2019, 47, D221-D229.	6.5	153
15	miRBase: from microRNA sequences to function. <i>Nucleic Acids Research</i> , 2019, 47, D155-D162.	6.5	3,014
16	Large-scale profiling of noncoding RNA function in yeast. <i>PLoS Genetics</i> , 2018, 14, e1007253.	1.5	29
17	Small RNAs: Big Impact on Plant Development. <i>Trends in Plant Science</i> , 2017, 22, 1056-1068.	4.3	256
18	RNAcentral: a comprehensive database of non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2017, 45, D128-D134.	6.5	174

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19	The house spider genome reveals an ancient whole-genome duplication during arachnid evolution. <i>BMC Biology</i> , 2017, 15, 62.	1.7	286
20	Abundant expression of somatic transposon-derived piRNAs throughout <i>Tribolium castaneum</i> embryogenesis. <i>Genome Biology</i> , 2017, 18, 184.	3.8	19
21	Novel Intronic RNA Structures Contribute to Maintenance of Phenotype in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2016, 203, 1469-1481.	1.2	29
22	Mutations in SNORD118 cause the cerebral microangiopathy leukoencephalopathy with calcifications and cysts. <i>Nature Genetics</i> , 2016, 48, 1185-1192.	9.4	114
23	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, 2133-2144.	1.1	38
24	MicroRNA evolution, expression, and function during short germband development in <i>Tribolium castaneum</i> . <i>Genome Research</i> , 2016, 26, 85-96.	2.4	42
25	Conservation and Losses of Non-Coding RNAs in Avian Genomes. <i>PLoS ONE</i> , 2015, 10, e0121797.	1.1	18
26	Bias in microRNA functional enrichment analysis. <i>Bioinformatics</i> , 2015, 31, 1592-1598.	1.8	100
27	RNAcentral: an international database of ncRNA sequences. <i>Nucleic Acids Research</i> , 2015, 43, D123-D129.	6.5	103
28	Natural Antisense Transcripts and Long Non-Coding RNA in <i>Neurospora crassa</i> . <i>PLoS ONE</i> , 2014, 9, e91353.	1.1	42
29	Target Repression Induced by Endogenous microRNAs: Large Differences, Small Effects. <i>PLoS ONE</i> , 2014, 9, e104286.	1.1	33
30	Conserved Temporal Patterns of MicroRNA Expression in <i>Drosophila</i> Support a Developmental Hourglass Model. <i>Genome Biology and Evolution</i> , 2014, 6, 2459-2467.	1.1	22
31	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.	2.6	221
32	Fast-evolving microRNAs are highly expressed in the early embryo of <i>Drosophila virilis</i> . <i>Rna</i> , 2014, 20, 360-372.	1.6	40
33	tRNA anticodon shifts in eukaryotic genomes. <i>Rna</i> , 2014, 20, 269-281.	1.6	41
34	Intron Evolution in <i>Saccharomycetaceae</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 2543-2556.	1.1	48
35	miRBase: annotating high confidence microRNAs using deep sequencing data. <i>Nucleic Acids Research</i> , 2014, 42, D68-D73.	6.5	4,752
36	Multiple products from microRNA transcripts. <i>Biochemical Society Transactions</i> , 2013, 41, 850-854.	1.6	25

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37	Sex-Biased Expression of MicroRNAs in <i>Schistosoma mansoni</i> . <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2402.	1.3	60
38	Clusters of microRNAs emerge by new hairpins in existing transcripts. <i>Nucleic Acids Research</i> , 2013, 41, 7745-7752.	6.5	84
39	Structure, evolution and function of the bi-directionally transcribed <i>iab-4/iab-8</i> microRNA locus in arthropods. <i>Nucleic Acids Research</i> , 2013, 41, 3352-3361.	6.5	32
40	Evolution and function of the extended miR-2 microRNA family. <i>RNA Biology</i> , 2012, 9, 242-248.	1.5	79
41	Detection of microRNAs in color space. <i>Bioinformatics</i> , 2012, 28, 318-323.	1.8	63
42	Reducing ligation bias of small RNAs in libraries for next generation sequencing. <i>Silence: A Journal of RNA Regulation</i> , 2012, 3, 4.	8.0	176
43	MicroRNAs from the same precursor have different targeting properties. <i>Silence: A Journal of RNA Regulation</i> , 2012, 3, 8.	8.0	57
44	Mitochondrial Pseudogenes in the Nuclear Genomes of <i>Drosophila</i> . <i>PLoS ONE</i> , 2012, 7, e32593.	1.1	33
45	miRBase: integrating microRNA annotation and deep-sequencing data. <i>Nucleic Acids Research</i> , 2011, 39, D152-D157.	6.5	3,263
46	MicroRNA evolution by arm switching. <i>EMBO Reports</i> , 2011, 12, 172-177.	2.0	199
47	Song exposure regulates known and novel microRNAs in the zebra finch auditory forebrain. <i>BMC Genomics</i> , 2011, 12, 277.	1.2	45
48	Conserved RNA structures in the non-canonical <i>Hac1/Xbp1</i> intron. <i>RNA Biology</i> , 2011, 8, 552-556.	1.5	66
49	Rfam: Wikipedia, clans and the "decimal" release. <i>Nucleic Acids Research</i> , 2011, 39, D141-D145.	6.5	355
50	RNAcentral: A vision for an international database of RNA sequences. <i>Rna</i> , 2011, 17, 1941-1946.	1.6	67
51	The Evolution of tRNA Genes in <i>Drosophila</i> . <i>Genome Biology and Evolution</i> , 2010, 2, 467-477.	1.1	40
52	Functional Shifts in Insect microRNA Evolution. <i>Genome Biology and Evolution</i> , 2010, 2, 686-696.	1.1	131
53	miRBase: microRNA Sequences and Annotation. <i>Current Protocols in Bioinformatics</i> , 2010, 29, Unit 12.9.1-10.	25.8	171
54	Editorial. <i>Briefings in Functional Genomics & Proteomics</i> , 2009, 8, 405-406.	3.8	2

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55	Rfam: updates to the RNA families database. <i>Nucleic Acids Research</i> , 2009, 37, D136-D140.	6.5	820
56	Conservation of the H19 noncoding RNA and H19-IGF2 imprinting mechanism in therians. <i>Nature Genetics</i> , 2008, 40, 971-976.	9.4	169
57	Annotation of mammalian primary microRNAs. <i>BMC Genomics</i> , 2008, 9, 564.	1.2	121
58	Criteria for Annotation of Plant MicroRNAs. <i>Plant Cell</i> , 2008, 20, 3186-3190.	3.1	1,158
59	Genome-wide discovery and verification of novel structured RNAs in <i>Plasmodium falciparum</i> . <i>Genome Research</i> , 2008, 18, 281-292.	2.4	81
60	An Analysis of Structural Influences on Selection in RNA Genes. <i>Molecular Biology and Evolution</i> , 2008, 26, 209-216.	3.5	8
61	The RNA WikiProject: Community annotation of RNA families. <i>Rna</i> , 2008, 14, 2462-2464.	1.6	66
62	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
63	miRBase: tools for microRNA genomics. <i>Nucleic Acids Research</i> , 2007, 36, D154-D158.	6.5	3,854
64	Annotating Noncoding RNA Genes. <i>Annual Review of Genomics and Human Genetics</i> , 2007, 8, 279-298.	2.5	120
65	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	13.7	1,886
66	miRBase: The MicroRNA Sequence Database. , 2006, 342, 129-138.		531
67	miRBase: microRNA sequences, targets and gene nomenclature. <i>Nucleic Acids Research</i> , 2006, 34, D140-D144.	6.5	4,192
68	The DNA sequence and biological annotation of human chromosome 1. <i>Nature</i> , 2006, 441, 315-321.	13.7	211
69	Pfam: clans, web tools and services. <i>Nucleic Acids Research</i> , 2006, 34, D247-D251.	6.5	2,030
70	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005, 438, 1151-1156.	13.7	1,272
71	Sequencing of <i>Aspergillus nidulans</i> and comparative analysis with <i>A. fumigatus</i> and <i>A. oryzae</i> . <i>Nature</i> , 2005, 438, 1105-1115.	13.7	1,250
72	Human microRNAs. , 2005, , .		0

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73	Transcriptome analysis for the chicken based on 19,626 finished cDNA sequences and 485,337 expressed sequence tags. <i>Genome Research</i> , 2005, 15, 174-183.	2.4	79
74	A selenocysteine tRNA and SECIS element in <i>Plasmodium falciparum</i> . <i>Rna</i> , 2005, 11, 119-122.	1.6	32
75	RALEE--RNA Alignment Editor in Emacs. <i>Bioinformatics</i> , 2005, 21, 257-259.	1.8	109
76	Genome of the Host-Cell Transforming Parasite <i>Theileria annulata</i> Compared with <i>T. parva</i> . <i>Science</i> , 2005, 309, 131-133.	6.0	285
77	Annotating Non-Coding RNAs with Rfam. , 2005, Chapter 12, Unit 12.5.		24
78	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, 163-170.	1.5	245
79	<i>C. elegans</i> noncoding RNA genes. <i>WormBook</i> , 2005, , 1-7.	5.3	34
80	The DNA sequence and analysis of human chromosome 13. <i>Nature</i> , 2004, 428, 522-528.	13.7	91
81	DNA sequence and analysis of human chromosome 9. <i>Nature</i> , 2004, 429, 369-374.	13.7	314
82	The microRNA Registry. <i>Nucleic Acids Research</i> , 2004, 32, 109D-111.	6.5	1,953
83	Identification of Mammalian microRNA Host Genes and Transcription Units. <i>Genome Research</i> , 2004, 14, 1902-1910.	2.4	1,704
84	Rfam: annotating non-coding RNAs in complete genomes. <i>Nucleic Acids Research</i> , 2004, 33, D121-D124.	6.5	1,255
85	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2004, 32, 138D-141.	6.5	3,084
86	Identifying Protein Domains with the Pfam Database. <i>Current Protocols in Bioinformatics</i> , 2003, 1, 2.5.1-2.5.19.	25.8	20
87	A uniform system for microRNA annotation. <i>Rna</i> , 2003, 9, 277-279.	1.6	1,620
88	Rfam: an RNA family database. <i>Nucleic Acids Research</i> , 2003, 31, 439-441.	6.5	1,296
89	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , 2003, 31, 315-318.	6.5	640
90	The Genome Sequence of <i>Caenorhabditis briggsae</i> : A Platform for Comparative Genomics. <i>PLoS Biology</i> , 2003, 1, e45.	2.6	812

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91	The use of structure information to increase alignment accuracy does not aid homologue detection with profile HMMs. <i>Bioinformatics</i> , 2002, 18, 1243-1249.	1.8	19
92	Plant protein families and their relationships to food allergy. <i>Biochemical Society Transactions</i> , 2002, 30, 906-910.	1.6	81
93	The Pfam Protein Families Database. <i>Nucleic Acids Research</i> , 2002, 30, 276-280.	6.5	2,067
94	Effects of Amino Acid β , γ Propensities and Secondary Structure Interactions in Modulating ^1H Chemical Shifts in Peptide and Protein β -Sheet. <i>Journal of the American Chemical Society</i> , 2001, 123, 12318-12324.	6.6	38
95	Folding of a β -hairpin peptide derived from the N-terminus of ubiquitin. <i>FEBS Journal</i> , 2000, 267, 3539-3548.	0.2	28
96	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.	6.6	115
97	Energetics of Weak Interactions in a β -hairpin Peptide: Electrostatic and Hydrophobic Contributions to Stability from Lysine Salt Bridges. <i>Journal of the American Chemical Society</i> , 1999, 121, 11615-11620.	6.6	78
98	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 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1999, 292, 1051-1069.	2.0	167
99	Modulation of intrinsic β , γ propensities of amino acids by neighbouring residues in the coil regions of protein structures: NMR analysis and dissection of a β -hairpin peptide 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1998, 284, 1597-1609.	2.0	56
100	miRBase: a database of microRNA sequences, targets and nomenclature. , 0, , 157-171.		2