

Simon Moxon

List of Publications by Citations

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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.

53
papers

9,372
citations

27
h-index

63
g-index

63
ext. papers

10,845
ext. citations

8.3
avg, IF

6.03
L-index

#	Paper	IF	Citations
53	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2004 , 32, D138-41	20.1	2720
52	Pfam: clans, web tools and services. <i>Nucleic Acids Research</i> , 2006 , 34, D247-51	20.1	1784
51	Rfam: annotating non-coding RNAs in complete genomes. <i>Nucleic Acids Research</i> , 2005 , 33, D121-4	20.1	990
50	Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. <i>Nature</i> , 2012 , 487, 94-8	50.4	859
49	Deep sequencing of tomato short RNAs identifies microRNAs targeting genes involved in fruit ripening. <i>Genome Research</i> , 2008 , 18, 1602-9	9.7	387
48	Identification of grapevine microRNAs and their targets using high-throughput sequencing and degradome analysis. <i>Plant Journal</i> , 2010 , 62, 960-76	6.9	278
47	A toolkit for analysing large-scale plant small RNA datasets. <i>Bioinformatics</i> , 2008 , 24, 2252-3	7.2	233
46	The UEA sRNA workbench: a suite of tools for analysing and visualizing next generation sequencing microRNA and small RNA datasets. <i>Bioinformatics</i> , 2012 , 28, 2059-61	7.2	232
45	High-throughput sequencing of <i>Medicago truncatula</i> short RNAs identifies eight new miRNA families. <i>BMC Genomics</i> , 2008 , 9, 593	4.5	227
44	Rapid transcriptional plasticity of duplicated gene clusters enables a clonally reproducing aphid to colonise diverse plant species. <i>Genome Biology</i> , 2017 , 18, 27	18.3	208
43	Profiling of short RNAs during fleshy fruit development reveals stage-specific sRNAome expression patterns. <i>Plant Journal</i> , 2011 , 67, 232-46	6.9	119
42	Deep sequencing of viroid-derived small RNAs from grapevine provides new insights on the role of RNA silencing in plant-viroid interaction. <i>PLoS ONE</i> , 2009 , 4, e7686	3.7	116
41	Structural and functional analysis of viral siRNAs. <i>PLoS Pathogens</i> , 2010 , 6, e1000838	7.6	113
40	Deep sequencing analysis of viral short RNAs from an infected Pinot Noir grapevine. <i>Virology</i> , 2010 , 408, 49-56	3.6	86
39	Identification of novel small RNAs in tomato (<i>Solanum lycopersicum</i>). <i>Planta</i> , 2007 , 226, 709-17	4.7	84
38	PAREsnip: a tool for rapid genome-wide discovery of small RNA/target interactions evidenced through degradome sequencing. <i>Nucleic Acids Research</i> , 2012 , 40, e103	20.1	78
37	Endogenous short RNAs generated by Dicer 2 and RNA-dependent RNA polymerase 1 regulate mRNAs in the basal fungus <i>Mucor circinelloides</i> . <i>Nucleic Acids Research</i> , 2010 , 38, 5535-41	20.1	77

36	Chromosomal-Level Assembly of the Asian Seabass Genome Using Long Sequence Reads and Multi-layered Scaffolding. <i>PLoS Genetics</i> , 2016 , 12, e1005954	6	77
35	DSYB catalyses the key step of dimethylsulfoniopropionate biosynthesis in many phytoplankton. <i>Nature Microbiology</i> , 2018 , 3, 430-439	26.6	61
34	RNAcentral: A vision for an international database of RNA sequences. <i>Rna</i> , 2011 , 17, 1941-6	5.8	54
33	A single argonaute gene participates in exogenous and endogenous RNAi and controls cellular functions in the basal fungus <i>Mucor circinelloides</i> . <i>PLoS ONE</i> , 2013 , 8, e69283	3.7	44
32	Distinct Effects of p19 RNA Silencing Suppressor on Small RNA Mediated Pathways in Plants. <i>PLoS Pathogens</i> , 2016 , 12, e1005935	7.6	43
31	A non-canonical RNA silencing pathway promotes mRNA degradation in basal Fungi. <i>PLoS Genetics</i> , 2015 , 11, e1005168	6	41
30	The RNAi machinery controls distinct responses to environmental signals in the basal fungus <i>Mucor circinelloides</i> . <i>BMC Genomics</i> , 2015 , 16, 237	4.5	35
29	Characterisation and expression of microRNAs in developing wings of the neotropical butterfly <i>Heliconius melpomene</i> . <i>BMC Genomics</i> , 2011 , 12, 62	4.5	35
28	miRCat2: accurate prediction of plant and animal microRNAs from next-generation sequencing datasets. <i>Bioinformatics</i> , 2017 , 33, 2446-2454	7.2	34
27	The UEA sRNA Workbench (version 4.4): a comprehensive suite of tools for analyzing miRNAs and sRNAs. <i>Bioinformatics</i> , 2018 , 34, 3382-3384	7.2	28
26	Deciphering the diversity of small RNAs in plants: the long and short of it. <i>Briefings in Functional Genomics & Proteomics</i> , 2009 , 8, 472-81		27
25	Identification of grapevine microRNAs and their targets using high-throughput sequencing and degradome analysis. <i>Plant Journal</i> , 2010 , 62, no-no	6.9	24
24	Heterarchy of transcription factors driving basal and luminal cell phenotypes in human urothelium. <i>Cell Death and Differentiation</i> , 2017 , 24, 809-818	12.7	21
23	Ago2-Dependent Processing Allows miR-451 to Evade the Global MicroRNA Turnover Elicited during Erythropoiesis. <i>Molecular Cell</i> , 2020 , 78, 317-328.e6	17.6	21
22	The cytoskeleton adaptor protein ankyrin-1 is upregulated by p53 following DNA damage and alters cell migration. <i>Cell Death and Disease</i> , 2016 , 7, e2184	9.8	21
21	A Database of microRNA Expression Patterns in <i>Xenopus laevis</i> . <i>PLoS ONE</i> , 2015 , 10, e0138313	3.7	18
20	Global discovery and characterization of small non-coding RNAs in marine microalgae. <i>BMC Genomics</i> , 2014 , 15, 697	4.5	17
19	Genome-wide microRNA screening in Nile tilapia reveals pervasive isomiRsXtranscription, sex-biased arm switching and increasing complexity of expression throughout development. <i>Scientific Reports</i> , 2018 , 8, 8248	4.9	17

18	MirPlex: a tool for identifying miRNAs in high-throughput sRNA datasets without a genome. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2013 , 320, 47-56	1.8	16
17	MicroRNA-10 modulates Hox genes expression during Nile tilapia embryonic development. <i>Mechanisms of Development</i> , 2016 , 140, 12-8	1.7	14
16	miR-133-mediated regulation of the Hedgehog pathway orchestrates embryo myogenesis. <i>Development (Cambridge)</i> , 2018 , 145,	6.6	14
15	An Improved microRNA Annotation of the Canine Genome. <i>PLoS ONE</i> , 2016 , 11, e0153453	3.7	13
14	A scoring matrix approach to detecting miRNA target sites. <i>Algorithms for Molecular Biology</i> , 2008 , 3, 3	1.8	11
13	Technical Note on the quality of DNA sequencing for the molecular characterisation of genetically modified plants. <i>EFSA Journal</i> , 2018 , 16, e05345	2.3	11
12	microRNAs associated with early neural crest development in <i>Xenopus laevis</i> . <i>BMC Genomics</i> , 2018 , 19, 59	4.5	11
11	The positive transcriptional elongation factor (P-TEFb) is required for neural crest specification. <i>Developmental Biology</i> , 2016 , 416, 361-72	3.1	10
10	Divergence in Transcriptional and Regulatory Responses to Mating in Male and Female Fruitflies. <i>Scientific Reports</i> , 2019 , 9, 16100	4.9	10
9	The evolutionary dynamics of microRNAs in domestic mammals. <i>Scientific Reports</i> , 2018 , 8, 17050	4.9	10
8	Metatranscriptomes from diverse microbial communities: assessment of data reduction techniques for rigorous annotation. <i>BMC Genomics</i> , 2014 , 15, 901	4.5	7
7	Assessment of the potential integration of the DNA plasmid vaccine CLYNAV into the salmon genome. <i>EFSA Journal</i> , 2017 , 15, e04689	2.3	6
6	Small RNA discovery and characterisation in eukaryotes using high-throughput approaches. <i>Advances in Experimental Medicine and Biology</i> , 2011 , 722, 239-54	3.6	6
5	An Assessment of the Next Generation of Animal miRNA Target Prediction Algorithms. <i>Methods in Molecular Biology</i> , 2017 , 1580, 175-191	1.4	2
4	FilTar: using RNA-Seq data to improve microRNA target prediction accuracy in animals. <i>Bioinformatics</i> , 2020 , 36, 2410-2416	7.2	1
3	FilTar: Using RNA-Seq data to improve microRNA target prediction accuracy in animals		1
2	Characterising open chromatin in chick embryos identifies cis-regulatory elements important for paraxial mesoderm formation and axis extension. <i>Nature Communications</i> , 2021 , 12, 1157	17.4	1
1	Mechanistic insights into non-coding Y RNA processing.. <i>RNA Biology</i> , 2022 , 19, 468-480	4.8	0

