Simon Moxon

List of Publications by Year
in descending order

56 papers	11,690 citations	159585 30 h-index	138484 58 g-index
63 all docs	63 docs citations	63 times ranked	17193 citing authors

#	Article	IF	Citations
1	The Pfam protein families database. Nucleic Acids Research, 2004, 32, 138D-141.	14.5	3,084
2	Pfam: clans, web tools and services. Nucleic Acids Research, 2006, 34, D247-D251.	14.5	2,030
3	Rfam: annotating non-coding RNAs in complete genomes. Nucleic Acids Research, 2004, 33, D121-D124.	14.5	1,255
4	Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. Nature, 2012, 487, 94-98.	27.8	1,086
5	Rapid transcriptional plasticity of duplicated gene clusters enables a clonally reproducing aphid to colonise diverse plant species. Genome Biology, 2017, 18, 27.	8.8	624
6	Deep sequencing of tomato short RNAs identifies microRNAs targeting genes involved in fruit ripening. Genome Research, 2008, 18, 1602-1609.	5.5	423
7	Identification of grapevine microRNAs and their targets using high throughput sequencing and degradome analysis. Plant Journal, 2010, 62, 960-76.	5.7	335
8	The UEA sRNA workbench: a suite of tools for analysing and visualizing next generation sequencing microRNA and small RNA datasets. Bioinformatics, 2012, 28, 2059-2061.	4.1	301
9	A toolkit for analysing large-scale plant small RNA datasets. Bioinformatics, 2008, 24, 2252-2253.	4.1	299
10	High-throughput sequencing of Medicago truncatula short RNAs identifies eight new miRNA families. BMC Genomics, 2008, 9, 593.	2.8	248
11	Profiling of short RNAs during fleshy fruit development reveals stage€specific sRNAome expression patterns. Plant Journal, 2011, 67, 232-246.	5.7	138
12	Deep Sequencing of Viroid-Derived Small RNAs from Grapevine Provides New Insights on the Role of RNA Silencing in Plant-Viroid Interaction. PLoS ONE, 2009, 4, e7686.	2.5	130
13	Structural and Functional Analysis of Viral siRNAs. PLoS Pathogens, 2010, 6, e1000838.	4.7	128
14	DSYB catalyses the key step of dimethylsulfoniopropionate biosynthesis in many phytoplankton. Nature Microbiology, 2018, 3, 430-439.	13.3	116
15	Deep sequencing analysis of viral short RNAs from an infected Pinot Noir grapevine. Virology, 2010, 408, 49-56.	2.4	109
16	Chromosomal-Level Assembly of the Asian Seabass Genome Using Long Sequence Reads and Multi-layered Scaffolding. PLoS Genetics, 2016, 12, e1005954.	3.5	105
17	Endogenous short RNAs generated by Dicer 2 and RNA-dependent RNA polymerase 1 regulate mRNAs in the basal fungus Mucor circinelloides. Nucleic Acids Research, 2010, 38, 5535-5541.	14.5	104
18	PAREsnip: a tool for rapid genome-wide discovery of small RNA/target interactions evidenced through degradome sequencing. Nucleic Acids Research, 2012, 40, e103-e103.	14.5	96

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19	Identification of novel small RNAs in tomato (Solanum lycopersicum). Planta, 2007, 226, 709-717.	3.2	90
20	RNAcentral: A vision for an international database of RNA sequences. Rna, 2011, 17, 1941-1946.	3.5	67
21	Distinct Effects of p19 RNA Silencing Suppressor on Small RNA Mediated Pathways in Plants. PLoS Pathogens, 2016, 12, e1005935.	4.7	67
22	A Non-canonical RNA Silencing Pathway Promotes mRNA Degradation in Basal Fungi. PLoS Genetics, 2015, 11, e1005168.	3.5	57
23	Identification of grapevine microRNAs and their targets using high-throughput sequencing and degradome analysis. Plant Journal, 2010, 62, no-no.	5.7	53
24	A Single Argonaute Gene Participates in Exogenous and Endogenous RNAi and Controls Cellular Functions in the Basal Fungus Mucor circinelloides. PLoS ONE, 2013, 8, e69283.	2.5	53
25	The UEA sRNA Workbench (version 4.4): a comprehensive suite of tools for analyzing miRNAs and sRNAs. Bioinformatics, 2018, 34, 3382-3384.	4.1	50
26	miRCat2: accurate prediction of plant and animal microRNAs from next-generation sequencing datasets. Bioinformatics, 2017, 33, 2446-2454.	4.1	49
27	Ago2-Dependent Processing Allows miR-451 to Evade the Global MicroRNA Turnover Elicited during Erythropoiesis. Molecular Cell, 2020, 78, 317-328.e6.	9.7	47
28	The RNAi machinery controls distinct responses to environmental signals in the basal fungus Mucor circinelloides. BMC Genomics, 2015, 16, 237.	2.8	45
29	Characterisation and expression of microRNAs in developing wings of the neotropical butterfly Heliconius melpomene. BMC Genomics, 2011, 12, 62.	2.8	44
30	Heterarchy of transcription factors driving basal and luminal cell phenotypes in human urothelium. Cell Death and Differentiation, 2017, 24, 809-818.	11.2	41
31	The cytoskeleton adaptor protein ankyrin-1 is upregulated by p53 following DNA damage and alters cell migration. Cell Death and Disease, 2016, 7, e2184-e2184.	6.3	29
32	Deciphering the diversity of small RNAs in plants: the long and short of it. Briefings in Functional Genomics & Proteomics, 2009, 8, 472-481.	3.8	28
33	miR-133 mediated regulation of the hedgehog pathway orchestrates embryo myogenesis. Development (Cambridge), 2018, 145, .	2.5	28
34	Genome-wide microRNA screening in Nile tilapia reveals pervasive isomiRsâ€™ transcription, sex-biased arm switching and increasing complexity of expression throughout development. Scientific Reports, 2018, 8, 8248.	3.3	25
35	Technical Note on the quality of DNA sequencing for the molecular characterisation of genetically modified plants. EFSA Journal, 2018, 16, e05345.	1.8	23
36	Divergence in Transcriptional and Regulatory Responses to Mating in Male and Female Fruitflies. Scientific Reports, 2019, 9, 16100.	3.3	23

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37	MirPlex: A Tool for Identifying miRNAs in High‑Throughput sRNA Datasets Without a Genome. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2013, 320, 47-56.	1.3	22
38	microRNAs associated with early neural crest development in Xenopus laevis. BMC Genomics, 2018, 19, 59.	2.8	22
39	Global discovery and characterization of small non-coding RNAs in marine microalgae. BMC Genomics, 2014, 15, 697.	2.8	21
40	A Database of microRNA Expression Patterns in Xenopus laevis. PLoS ONE, 2015, 10, e0138313.	2.5	21
41	An Improved microRNA Annotation of the Canine Genome. PLoS ONE, 2016, 11, e0153453.	2.5	20
42	MicroRNA-10 modulates Hox genes expression during Nile tilapia embryonic development. Mechanisms of Development, 2016, 140, 12-18.	1.7	20
43	The evolutionary dynamics of microRNAs in domestic mammals. Scientific Reports, 2018, 8, 17050.	3.3	17
44	A scoring matrix approach to detecting miRNA target sites. Algorithms for Molecular Biology, 2008, 3, 3.	1.2	16
45	The positive transcriptional elongation factor (P-TEFb) is required for neural crest specification. Developmental Biology, 2016, 416, 361-372.	2.0	12
46	Metatranscriptomes from diverse microbial communities: assessment of data reduction techniques for rigorous annotation. BMC Genomics, 2014, 15, 901.	2.8	11
47	Development of a Biotechnology Platform for the Fast-Growing Cyanobacterium Synechococcus sp. PCC 11901. Biomolecules, 2022, 12, 872.	4.0	9
48	Assessment of the potential integration of the DNA plasmid vaccine CLYNAV into the salmon genome. EFSA Journal, 2017, 15, e04689.	1.8	8
49	Characterising open chromatin in chick embryos identifies cis-regulatory elements important for paraxial mesoderm formation and axis extension. Nature Communications, 2021, 12, 1157.	12.8	8
50	Small RNA Discovery and Characterisation in Eukaryotes Using High-Throughput Approaches. Advances in Experimental Medicine and Biology, 2011, 722, 239-254.	1.6	6
51	Small-RNA Sequencing Reveals Altered Skeletal Muscle microRNAs and snoRNAs Signatures in Weanling Male Offspring from Mouse Dams Fed a Low Protein Diet during Lactation. Cells, 2021, 10, 1166.	4.1	4
52	Evolutionary history of sexual selection affects microRNA profiles in <i>Drosophila</i> sperm. Evolution; International Journal of Organic Evolution, 2022, 76, 310-319.	2.3	4
53	miRTil: An Extensive Repository for Nile Tilapia microRNA Next Generation Sequencing Data. Cells, 2020, 9, 1752.	4.1	3
54	FilTar: using RNA-Seq data to improve microRNA target prediction accuracy in animals. Bioinformatics, 2020, 36, 2410-2416.	4.1	3

#	ARTICLE	IF	CITATIONS
55	Mechanistic insights into non-coding Y RNA processing. RNA Biology, 2022, 19, 468-480.	3.1	3
56	An Assessment of the Next Generation of Animal miRNA Target Prediction Algorithms. Methods in Molecular Biology, 2017, 1580, 175-191.	0.9	2