

Simon Moxon

List of Publications by Year in descending order

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Version: 2024-02-01

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	Evolutionary history of sexual selection affects microRNA profiles in <i>Drosophila</i> sperm. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 310-319.	2.3	4
2	Mechanistic insights into non-coding Y RNA processing. <i>RNA Biology</i> , 2022, 19, 468-480.	3.1	3
3	Development of a Biotechnology Platform for the Fast-Growing Cyanobacterium <i>Synechococcus</i> sp. PCC 11901. <i>Biomolecules</i> , 2022, 12, 872.	4.0	9
4	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.	12.8	8
5	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. <i>Cells</i> , 2021, 10, 1166.	4.1	4
6	miRTil: An Extensive Repository for Nile Tilapia microRNA Next Generation Sequencing Data. <i>Cells</i> , 2020, 9, 1752.	4.1	3
7	Ago2-Dependent Processing Allows miR-451 to Evade the Global MicroRNA Turnover Elicited during Erythropoiesis. <i>Molecular Cell</i> , 2020, 78, 317-328.e6.	9.7	47
8	FilTar: using RNA-Seq data to improve microRNA target prediction accuracy in animals. <i>Bioinformatics</i> , 2020, 36, 2410-2416.	4.1	3
9	Divergence in Transcriptional and Regulatory Responses to Mating in Male and Female Fruitflies. <i>Scientific Reports</i> , 2019, 9, 16100.	3.3	23
10	DSYB catalyses the key step of dimethylsulfoniopropionate biosynthesis in many phytoplankton. <i>Nature Microbiology</i> , 2018, 3, 430-439.	13.3	116
11	The UEA sRNA Workbench (version 4.4): a comprehensive suite of tools for analyzing miRNAs and sRNAs. <i>Bioinformatics</i> , 2018, 34, 3382-3384.	4.1	50
12	Technical Note on the quality of DNA sequencing for the molecular characterisation of genetically modified plants. <i>EFSA Journal</i> , 2018, 16, e05345.	1.8	23
13	The evolutionary dynamics of microRNAs in domestic mammals. <i>Scientific Reports</i> , 2018, 8, 17050.	3.3	17
14	microRNAs associated with early neural crest development in <i>Xenopus laevis</i> . <i>BMC Genomics</i> , 2018, 19, 59.	2.8	22
15	miR-133 mediated regulation of the hedgehog pathway orchestrates embryo myogenesis. <i>Development (Cambridge)</i> , 2018, 145, .	2.5	28
16	Genome-wide microRNA screening in Nile tilapia reveals pervasive isomiRs™ transcription, sex-biased arm switching and increasing complexity of expression throughout development. <i>Scientific Reports</i> , 2018, 8, 8248.	3.3	25
17	Heterarchy of transcription factors driving basal and luminal cell phenotypes in human urothelium. <i>Cell Death and Differentiation</i> , 2017, 24, 809-818.	11.2	41
18	Rapid transcriptional plasticity of duplicated gene clusters enables a clonally reproducing aphid to colonise diverse plant species. <i>Genome Biology</i> , 2017, 18, 27.	8.8	624

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19	miRCat2: accurate prediction of plant and animal microRNAs from next-generation sequencing datasets. <i>Bioinformatics</i> , 2017, 33, 2446-2454.	4.1	49
20	An Assessment of the Next Generation of Animal miRNA Target Prediction Algorithms. <i>Methods in Molecular Biology</i> , 2017, 1580, 175-191.	0.9	2
21	Assessment of the potential integration of the DNA plasmid vaccine CLYNAV into the salmon genome. <i>EFSA Journal</i> , 2017, 15, e04689.	1.8	8
22	Chromosomal-Level Assembly of the Asian Seabass Genome Using Long Sequence Reads and Multi-layered Scaffolding. <i>PLoS Genetics</i> , 2016, 12, e1005954.	3.5	105
23	An Improved microRNA Annotation of the Canine Genome. <i>PLoS ONE</i> , 2016, 11, e0153453.	2.5	20
24	MicroRNA-10 modulates Hox genes expression during Nile tilapia embryonic development. <i>Mechanisms of Development</i> , 2016, 140, 12-18.	1.7	20
25	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-e2184.	6.3	29
26	The positive transcriptional elongation factor (P-TEFb) is required for neural crest specification. <i>Developmental Biology</i> , 2016, 416, 361-372.	2.0	12
27	Distinct Effects of p19 RNA Silencing Suppressor on Small RNA Mediated Pathways in Plants. <i>PLoS Pathogens</i> , 2016, 12, e1005935.	4.7	67
28	A Database of microRNA Expression Patterns in <i>Xenopus laevis</i> . <i>PLoS ONE</i> , 2015, 10, e0138313.	2.5	21
29	The RNAi machinery controls distinct responses to environmental signals in the basal fungus <i>Mucor circinelloides</i> . <i>BMC Genomics</i> , 2015, 16, 237.	2.8	45
30	A Non-canonical RNA Silencing Pathway Promotes mRNA Degradation in Basal Fungi. <i>PLoS Genetics</i> , 2015, 11, e1005168.	3.5	57
31	Metatranscriptomes from diverse microbial communities: assessment of data reduction techniques for rigorous annotation. <i>BMC Genomics</i> , 2014, 15, 901.	2.8	11
32	Global discovery and characterization of small non-coding RNAs in marine microalgae. <i>BMC Genomics</i> , 2014, 15, 697.	2.8	21
33	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.	1.3	22
34	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.	2.5	53
35	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-e103.	14.5	96
36	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, 2059-2061.	4.1	301

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37	Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. <i>Nature</i> , 2012, 487, 94-98.	27.8	1,086
38	Small RNA Discovery and Characterisation in Eukaryotes Using High-Throughput Approaches. <i>Advances in Experimental Medicine and Biology</i> , 2011, 722, 239-254.	1.6	6
39	Profiling of short RNAs during fleshy fruit development reveals stage-specific sRNAome expression patterns. <i>Plant Journal</i> , 2011, 67, 232-246.	5.7	138
40	Characterisation and expression of microRNAs in developing wings of the neotropical butterfly <i>Heliconius melpomene</i> . <i>BMC Genomics</i> , 2011, 12, 62.	2.8	44
41	RNAcentral: A vision for an international database of RNA sequences. <i>Rna</i> , 2011, 17, 1941-1946.	3.5	67
42	Deep sequencing analysis of viral short RNAs from an infected Pinot Noir grapevine. <i>Virology</i> , 2010, 408, 49-56.	2.4	109
43	Identification of grapevine microRNAs and their targets using high-throughput sequencing and degradome analysis. <i>Plant Journal</i> , 2010, 62, no-no.	5.7	53
44	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, 5535-5541.	14.5	104
45	Structural and Functional Analysis of Viral siRNAs. <i>PLoS Pathogens</i> , 2010, 6, e1000838.	4.7	128
46	Identification of grapevine microRNAs and their targets using high throughput sequencing and degradome analysis. <i>Plant Journal</i> , 2010, 62, 960-76.	5.7	335
47	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.	2.5	130
48	Deciphering the diversity of small RNAs in plants: the long and short of it. <i>Briefings in Functional Genomics & Proteomics</i> , 2009, 8, 472-481.	3.8	28
49	High-throughput sequencing of <i>Medicago truncatula</i> short RNAs identifies eight new miRNA families. <i>BMC Genomics</i> , 2008, 9, 593.	2.8	248
50	A scoring matrix approach to detecting miRNA target sites. <i>Algorithms for Molecular Biology</i> , 2008, 3, 3.	1.2	16
51	Deep sequencing of tomato short RNAs identifies microRNAs targeting genes involved in fruit ripening. <i>Genome Research</i> , 2008, 18, 1602-1609.	5.5	423
52	A toolkit for analysing large-scale plant small RNA datasets. <i>Bioinformatics</i> , 2008, 24, 2252-2253.	4.1	299
53	Identification of novel small RNAs in tomato (<i>Solanum lycopersicum</i>). <i>Planta</i> , 2007, 226, 709-717.	3.2	90
54	Pfam: clans, web tools and services. <i>Nucleic Acids Research</i> , 2006, 34, D247-D251.	14.5	2,030

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55	Rfam: annotating non-coding RNAs in complete genomes. Nucleic Acids Research, 2004, 33, D121-D124.	14.5	1,255
56	The Pfam protein families database. Nucleic Acids Research, 2004, 32, 138D-141.	14.5	3,084