

Andreas J Stroehlein

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

470
citations

687363

13
h-index

752698

20
g-index

28
all docs

28
docs citations

28
times ranked

682
citing authors

#	ARTICLE	IF	CITATIONS
1	Nuclear genome of <i>Bulinus truncatus</i> , an intermediate host of the carcinogenic human blood fluke <i>Schistosoma haematobium</i> . <i>Nature Communications</i> , 2022, 13, 977.	12.8	14
2	Chromosome-level genome of <i>Schistosoma haematobium</i> underpins genome-wide explorations of molecular variation. <i>PLoS Pathogens</i> , 2022, 18, e1010288.	4.7	13
3	<i>Bulinus truncatus</i> transcriptome – a resource to enable molecular studies of snail and schistosome biology. <i>Current Research in Parasitology and Vector-borne Diseases</i> , 2021, 1, 100015.	1.9	5
4	Nanopore Sequencing Resolves Elusive Long Tandem-Repeat Regions in Mitochondrial Genomes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1811.	4.1	18
5	High-quality reference genome for <i>Clonorchis sinensis</i> . <i>Genomics</i> , 2021, 113, 1605-1615.	2.9	19
6	Mitochondrial genome of <i>Bulinus truncatus</i> (Gastropoda: Lymnaeoidea): Implications for snail systematics and schistosome epidemiology. <i>Current Research in Parasitology and Vector-borne Diseases</i> , 2021, 1, 100017.	1.9	6
7	The developmental phosphoproteome of <i>Haemonchus contortus</i> . <i>Journal of Proteomics</i> , 2020, 213, 103615.	2.4	21
8	High-quality nuclear genome for <i>Sarcoptes scabiei</i> – A critical resource for a neglected parasite. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008720.	3.0	25
9	Major SCP/TAPS protein expansion in <i>Lucilia cuprina</i> is associated with novel tandem array organisation and domain architecture. <i>Parasites and Vectors</i> , 2020, 13, 598.	2.5	1
10	First record of a tandem-repeat region within the mitochondrial genome of <i>Clonorchis sinensis</i> using a long-read sequencing approach. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008552.	3.0	18
11	Expanded complement of Niemann-Pick type C2-like protein genes in <i>Clonorchis sinensis</i> suggests functions beyond sterol binding and transport. <i>Parasites and Vectors</i> , 2020, 13, 38.	2.5	3
12	High-quality <i>Schistosoma haematobium</i> genome achieved by single-molecule and long-range sequencing. <i>GigaScience</i> , 2019, 8, .	6.4	41
13	Dauer signalling pathway model for <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , 2019, 12, 187.	2.5	25
14	Comparative bioinformatic analysis suggests that specific dauer-like signalling pathway components regulate <i>Toxocara canis</i> development and migration in the mammalian host. <i>Parasites and Vectors</i> , 2019, 12, 32.	2.5	15
15	Advances in kinome research of parasitic worms - implications for fundamental research and applied biotechnological outcomes. <i>Biotechnology Advances</i> , 2018, 36, 915-934.	11.7	8
16	Interactive online application for the prediction, ranking and prioritisation of drug targets in <i>Schistosoma haematobium</i> . <i>Parasites and Vectors</i> , 2018, 11, 605.	2.5	0
17	Molecular alterations during larval development of <i>Haemonchus contortus</i> in vitro are under tight post-transcriptional control. <i>International Journal for Parasitology</i> , 2018, 48, 763-772.	3.1	30
18	Improved strategy for the curation and classification of kinases, with broad applicability to other eukaryotic protein groups. <i>Scientific Reports</i> , 2018, 8, 6808.	3.3	10

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19	The small RNA complement of adult <i>Schistosoma haematobium</i> . <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006535.	3.0	17
20	Whipworm kinomes reflect a unique biology and adaptation to the host animal. <i>International Journal for Parasitology</i> , 2017, 47, 857-866.	3.1	10
21	Screening of the "Stasis Box"™ identifies two kinase inhibitors under pharmaceutical development with activity against <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , 2017, 10, 323.	2.5	22
22	Analyses of Compact <i>Trichinella</i> Kinomes Reveal a MOS-Like Protein Kinase with a Unique N-Terminal Domain. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2847-2856.	1.8	6
23	CAP protein superfamily members in <i>Toxocara canis</i> . <i>Parasites and Vectors</i> , 2016, 9, 360.	2.5	6
24	Reconstruction of the insulin-like signalling pathway of <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , 2016, 9, 64.	2.5	12
25	Defining the <i>Schistosoma haematobium</i> kinome enables the prediction of essential kinases as anti-schistosome drug targets. <i>Scientific Reports</i> , 2015, 5, 17759.	3.3	37
26	The <i>Haemonchus contortus</i> kinome - a resource for fundamental molecular investigations and drug discovery. <i>Parasites and Vectors</i> , 2015, 8, 623.	2.5	14
27	<i>Lucilia cuprina</i> genome unlocks parasitic fly biology to underpin future interventions. <i>Nature Communications</i> , 2015, 6, 7344.	12.8	67
28	Flatworms have lost the right open reading frame kinase 3 gene during evolution. <i>Scientific Reports</i> , 2015, 5, 9417.	3.3	7