

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	Lucilia cuprina genome unlocks parasitic fly biology to underpin future interventions. Nature Communications, 2015, 6, 7344.	12.8	67
2	High-quality Schistosoma haematobium genome achieved by single-molecule and long-range sequencing. GigaScience, 2019, 8, .	6.4	41
3	Defining the Schistosoma haematobium kinome enables the prediction of essential kinases as anti-schistosome drug targets. Scientific Reports, 2015, 5, 17759.	3.3	37
4	Molecular alterations during larval development of Haemonchus contortus in vitro are under tight post-transcriptional control. International Journal for Parasitology, 2018, 48, 763-772.	3.1	30
5	Dauer signalling pathway model for Haemonchus contortus. Parasites and Vectors, 2019, 12, 187.	2.5	25
6	High-quality nuclear genome for Sarcoptes scabiei – A critical resource for a neglected parasite. PLoS Neglected Tropical Diseases, 2020, 14, e0008720.	3.0	25
7	Screening of the “Stasis Box”™ identifies two kinase inhibitors under pharmaceutical development with activity against Haemonchus contortus. Parasites and Vectors, 2017, 10, 323.	2.5	22
8	The developmental phosphoproteome of Haemonchus contortus. Journal of Proteomics, 2020, 213, 103615.	2.4	21
9	High-quality reference genome for Clonorchis sinensis. Genomics, 2021, 113, 1605-1615.	2.9	19
10	First record of a tandem-repeat region within the mitochondrial genome of Clonorchis sinensis using a long-read sequencing approach. PLoS Neglected Tropical Diseases, 2020, 14, e0008552.	3.0	18
11	Nanopore Sequencing Resolves Elusive Long Tandem-Repeat Regions in Mitochondrial Genomes. International Journal of Molecular Sciences, 2021, 22, 1811.	4.1	18
12	The small RNA complement of adult Schistosoma haematobium. PLoS Neglected Tropical Diseases, 2018, 12, e0006535.	3.0	17
13	Comparative bioinformatic analysis suggests that specific dauer-like signalling pathway components regulate Toxocara canis development and migration in the mammalian host. Parasites and Vectors, 2019, 12, 32.	2.5	15
14	The Haemonchus contortus kinome - a resource for fundamental molecular investigations and drug discovery. Parasites and Vectors, 2015, 8, 623.	2.5	14
15	Nuclear genome of Bulinus truncatus, an intermediate host of the carcinogenic human blood fluke Schistosoma haematobium. Nature Communications, 2022, 13, 977.	12.8	14
16	Chromosome-level genome of Schistosoma haematobium underpins genome-wide explorations of molecular variation. PLoS Pathogens, 2022, 18, e1010288.	4.7	13
17	Reconstruction of the insulin-like signalling pathway of Haemonchus contortus. Parasites and Vectors, 2016, 9, 64.	2.5	12
18	Whipworm kinomes reflect a unique biology and adaptation to the host animal. International Journal for Parasitology, 2017, 47, 857-866.	3.1	10

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	Flatworms have lost the right open reading frame kinase 3 gene during evolution. <i>Scientific Reports</i> , 2015, 5, 9417.	3.3	7
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	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
25	<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
26	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
27	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
28	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