

Pasi K. Korhonen

List of Publications by Year in descending order

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77
papers

2,117
citations

279701

23
h-index

289141

40
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all docs

77
docs citations

77
times ranked

2346
citing authors

#	ARTICLE	IF	CITATIONS
1	Harnessing model organism genomics to underpin the machine learning-based prediction of essential genes in eukaryotes – Biotechnological implications. <i>Biotechnology Advances</i> , 2022, 54, 107822.	6.0	9
2	An RNA Interference Tool to Silence Genes in <i>Sarcoptes scabiei</i> Eggs. <i>International Journal of Molecular Sciences</i> , 2022, 23, 873.	1.8	2
3	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.	5.8	14
4	Chromosome-level genome of <i>Schistosoma haematobium</i> underpins genome-wide explorations of molecular variation. <i>PLoS Pathogens</i> , 2022, 18, e1010288.	2.1	13
5	– Escalibur – A practical pipeline for the de novo analysis of nucleotide variation in nonmodel eukaryotes. <i>Molecular Ecology Resources</i> , 2022, , .	2.2	2
6	Chromosome-scale <i>Echinococcus granulosus</i> (genotype G1) genome reveals the Eg95 gene family and conservation of the EG95-vaccine molecule. <i>Communications Biology</i> , 2022, 5, 199.	2.0	7
7	<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.	0.7	5
8	Nanopore Sequencing Resolves Elusive Long Tandem-Repeat Regions in Mitochondrial Genomes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1811.	1.8	18
9	Molecular diagnosis of scabies using a novel probe-based polymerase chain reaction assay targeting high-copy number repetitive sequences in the <i>Sarcoptes scabiei</i> genome. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009149.	1.3	7
10	High-quality reference genome for <i>Clonorchis sinensis</i> . <i>Genomics</i> , 2021, 113, 1605-1615.	1.3	19
11	The mitogenome of <i>Halotydeus destructor</i> (Tucker) and its relationships with other trombidiform mites as inferred from nucleotide sequences and gene arrangements. <i>Ecology and Evolution</i> , 2021, 11, 14162-14174.	0.8	5
12	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.	0.7	6
13	The developmental phosphoproteome of <i>Haemonchus contortus</i> . <i>Journal of Proteomics</i> , 2020, 213, 103615.	1.2	21
14	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.	1.3	25
15	Toward integrative – omics of the barber – pole worm and related parasitic nematodes. <i>Infection, Genetics and Evolution</i> , 2020, 85, 104500.	1.0	11
16	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.	1.3	18
17	Marked mitochondrial genetic variation in individuals and populations of the carcinogenic liver fluke <i>Clonorchis sinensis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008480.	1.3	6
18	Elucidating the molecular and developmental biology of parasitic nematodes: Moving to a multiomics paradigm. <i>Advances in Parasitology</i> , 2020, 108, 175-229.	1.4	17

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19	An Evaluation of Machine Learning Approaches for the Prediction of Essential Genes in Eukaryotes Using Protein Sequence-Derived Features. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 785-796.	1.9	31
20	Dafachronic acid promotes larval development in <i>Haemonchus contortus</i> by modulating dauer signalling and lipid metabolism. <i>PLoS Pathogens</i> , 2019, 15, e1007960.	2.1	31
21	High-quality <i>Schistosoma haematobium</i> genome achieved by single-molecule and long-range sequencing. <i>GigaScience</i> , 2019, 8, .	3.3	41
22	Whole-genome sequence of the bovine blood fluke <i>Schistosoma bovis</i> supports interspecific hybridization with <i>S. haematobium</i> . <i>PLoS Pathogens</i> , 2019, 15, e1007513.	2.1	49
23	Long-read sequencing reveals a 4.4Åkb tandem repeat region in the mitogenome of <i>Echinococcus granulosus</i> (sensu stricto) genotype G1. <i>Parasites and Vectors</i> , 2019, 12, 238.	1.0	31
24	Comparative genome analysis indicates high evolutionary potential of pathogenicity genes in <i>Colletotrichum tanacetii</i> . <i>PLoS ONE</i> , 2019, 14, e0212248.	1.1	19
25	High throughput LC-MS/MS-based proteomic analysis of excretory-secretory products from short-term in vitro culture of <i>Haemonchus contortus</i> . <i>Journal of Proteomics</i> , 2019, 204, 103375.	1.2	44
26	Dauer signalling pathway model for <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , 2019, 12, 187.	1.0	25
27	Common workflow language (CWL)-based software pipeline for de novo genome assembly from long- and short-read data. <i>GigaScience</i> , 2019, 8, .	3.3	17
28	Molecular evidence for distinct modes of nutrient acquisition between visceral and neurotropic schistosomes of birds. <i>Scientific Reports</i> , 2019, 9, 1347.	1.6	17
29	Somatic proteome of <i>Haemonchus contortus</i> . <i>International Journal for Parasitology</i> , 2019, 49, 311-320.	1.3	38
30	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.	1.0	15
31	Improved genomic resources and new bioinformatic workflow for the carcinogenic parasite <i>Clonorchis sinensis</i> : Biotechnological implications. <i>Biotechnology Advances</i> , 2018, 36, 894-904.	6.0	20
32	A TGF- β type I receptor-like molecule with a key functional role in <i>Haemonchus contortus</i> development. <i>International Journal for Parasitology</i> , 2018, 48, 1023-1033.	1.3	16
33	The developmental lipidome of <i>Haemonchus contortus</i> . <i>International Journal for Parasitology</i> , 2018, 48, 887-895.	1.3	30
34	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.	1.3	30
35	Trehalose 6-phosphate phosphatases of <i>Pseudomonas aeruginosa</i> . <i>FASEB Journal</i> , 2018, 32, 5470-5482.	0.2	9
36	The small RNA complement of adult <i>Schistosoma haematobium</i> . <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006535.	1.3	17

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37	Clonorchis sinensis and Clonorchiasis: The Relevance of Exploring Genetic Variation. <i>Advances in Parasitology</i> , 2018, 100, 155-208.	1.4	18
38	Mitochondrial genomic comparison of <i>Clonorchis sinensis</i> from South Korea with other isolates of this species. <i>Infection, Genetics and Evolution</i> , 2017, 51, 160-166.	1.0	13
39	Mitochondrial genomes of two <i>Babesia</i> taxa from sheep in China as a foundation for population genetic and epidemiological investigations. <i>Infection, Genetics and Evolution</i> , 2017, 47, 51-55.	1.0	6
40	Whipworm kinomes reflect a unique biology and adaptation to the host animal. <i>International Journal for Parasitology</i> , 2017, 47, 857-866.	1.3	10
41	The apicoplast genomes of two taxonomic units of <i>Babesia</i> from sheep. <i>Veterinary Parasitology</i> , 2017, 233, 123-128.	0.7	10
42	Deguelin exerts potent nematocidal activity via the mitochondrial respiratory chain. <i>FASEB Journal</i> , 2017, 31, 4515-4532.	0.2	25
43	Comparative transcriptomic analyses of male and female adult <i>Toxocara canis</i> . <i>Gene</i> , 2017, 600, 85-89.	1.0	12
44	Use of a bioinformatic-assisted primer design strategy to establish a new nested PCR-based method for <i>Cryptosporidium</i> . <i>Parasites and Vectors</i> , 2017, 10, 509.	1.0	18
45	The Battle Against Flystrike – Past Research and New Prospects Through Genomics. <i>Advances in Parasitology</i> , 2017, 98, 227-281.	1.4	6
46	Best practice data life cycle approaches for the life sciences. <i>F1000Research</i> , 2017, 6, 1618.	0.8	23
47	Harnessing the <i>Toxocara</i> Genome to Underpin Toxocariasis Research and New Interventions. <i>Advances in Parasitology</i> , 2016, 91, 87-110.	1.4	23
48	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.	0.8	6
49	CAP protein superfamily members in <i>Toxocara canis</i> . <i>Parasites and Vectors</i> , 2016, 9, 360.	1.0	6
50	A blow to the fly – <i>Lucilia cuprina</i> draft genome and transcriptome to support advances in biology and biotechnology. <i>Biotechnology Advances</i> , 2016, 34, 605-620.	6.0	23
51	Divergent Transcriptional Responses to Physiological and Xenobiotic Stress in <i>Giardia duodenalis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 6034-6045.	1.4	33
52	Genomic resources for a unique, low-virulence <i>Babesia</i> taxon from China. <i>Parasites and Vectors</i> , 2016, 9, 564.	1.0	17
53	MicroRNAs of <i>Toxocara canis</i> and their predicted functional roles. <i>Parasites and Vectors</i> , 2016, 9, 229.	1.0	37
54	Molecular characterization of the <i>Haemonchus contortus</i> phosphoinositide-dependent protein kinase-1 gene (<i>Hc-pdk-1</i>). <i>Parasites and Vectors</i> , 2016, 9, 65.	1.0	13

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55	Pipeline for the identification and classification of ion channels in parasitic flatworms. <i>Parasites and Vectors</i> , 2016, 9, 155.	1.0	4
56	Phylogenomic and biogeographic reconstruction of the <i>Trichinella</i> complex. <i>Nature Communications</i> , 2016, 7, 10513.	5.8	107
57	Making sense of genomes of parasitic worms: Tackling bioinformatic challenges. <i>Biotechnology Advances</i> , 2016, 34, 663-686.	6.0	30
58	The complement of family M1 aminopeptidases of <i>Haemonchus contortus</i> – Biotechnological implications. <i>Biotechnology Advances</i> , 2016, 34, 65-76.	6.0	8
59	Comparative Transcriptomic Exploration Reveals Unique Molecular Adaptations of Neuropathogenic <i>Trichobilharzia</i> to Invade and Parasitize Its Avian Definitive Host. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004406.	1.3	25
60	Exploring molecular variation in <i>Schistosoma japonicum</i> in China. <i>Scientific Reports</i> , 2015, 5, 17345.	1.6	33
61	The <i>Haemonchus contortus</i> kinome - a resource for fundamental molecular investigations and drug discovery. <i>Parasites and Vectors</i> , 2015, 8, 623.	1.0	14
62	Time-Dependent Transcriptional Changes in Axenic <i>Giardia duodenalis</i> Trophozoites. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0004261.	1.3	16
63	Genetic blueprint of the zoonotic pathogen <i>Toxocara canis</i> . <i>Nature Communications</i> , 2015, 6, 6145.	5.8	103
64	The barber's pole worm CAP protein superfamily – A basis for fundamental discovery and biotechnology advances. <i>Biotechnology Advances</i> , 2015, 33, 1744-1754.	6.0	16
65	Low cost whole-organism screening of compounds for anthelmintic activity. <i>International Journal for Parasitology</i> , 2015, 45, 333-343.	1.3	106
66	<i>Lucilia cuprina</i> genome unlocks parasitic fly biology to underpin future interventions. <i>Nature Communications</i> , 2015, 6, 7344.	5.8	67
67	Exploring the role of two interacting phosphoinositide 3-kinases of <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , 2014, 7, 498.	1.0	13
68	Bioinformatic exploration of RIO protein kinases of parasitic and free-living nematodes. <i>International Journal for Parasitology</i> , 2014, 44, 827-836.	1.3	13
69	The <i>Opisthorchis viverrini</i> genome provides insights into life in the bile duct. <i>Nature Communications</i> , 2014, 5, 4378.	5.8	144
70	Analysis of the transcriptome of adult <i>Dictyocaulus filaria</i> and comparison with <i>Dictyocaulus viviparus</i> , with a focus on molecules involved in host-parasite interactions. <i>International Journal for Parasitology</i> , 2014, 44, 251-261.	1.3	6
71	Genome and transcriptome of the porcine whipworm <i>Trichuris suis</i> . <i>Nature Genetics</i> , 2014, 46, 701-706.	9.4	93
72	Mitochondrial genomes of <i>Trichinella</i> species and genotypes – a basis for diagnosis, and systematic and epidemiological explorations. <i>International Journal for Parasitology</i> , 2014, 44, 1073-1080.	1.3	40

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73	Identification of G protein-coupled receptors in <i>Schistosoma haematobium</i> and <i>S. mansoni</i> by comparative genomics. <i>Parasites and Vectors</i> , 2014, 7, 242.	1.0	37
74	Hc-daf-2 encodes an insulin-like receptor kinase in the barber's pole worm, <i>Haemonchus contortus</i> , and restores partial dauer regulation. <i>International Journal for Parasitology</i> , 2014, 44, 485-496.	1.3	25
75	Getting the most out of parasitic helminth transcriptomes using HelmDB: Implications for biology and biotechnology. <i>Biotechnology Advances</i> , 2013, 31, 1109-1119.	6.0	23
76	Insights into the immuno-molecular biology of <i>Angiostrongylus vasorum</i> through transcriptomics—Prospects for new interventions. <i>Biotechnology Advances</i> , 2013, 31, 1486-1500.	6.0	18
77	The genome and developmental transcriptome of the strongylid nematode <i>Haemonchus contortus</i> . <i>Genome Biology</i> , 2013, 14, R89.	13.9	192