

# Pasi K. Korhonen

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/7160790/pasi-k-korhonen-publications-by-citations.pdf>

**Version:** 2024-04-25

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

75  
papers

1,458  
citations

19  
h-index

35  
g-index

77  
ext. papers

1,862  
ext. citations

7.2  
avg. IF

4.37  
L-index

#	Paper	IF	Citations
75	The genome and developmental transcriptome of the strongylid nematode <i>Haemonchus contortus</i> . <i>Genome Biology</i> , <b>2013</b> , 14, R89	18.3	166
74	The <i>Opisthorchis viverrini</i> genome provides insights into life in the bile duct. <i>Nature Communications</i> , <b>2014</b> , 5, 4378	17.4	113
73	Low cost whole-organism screening of compounds for anthelmintic activity. <i>International Journal for Parasitology</i> , <b>2015</b> , 45, 333-43	4.3	81
72	Phylogenomic and biogeographic reconstruction of the <i>Trichinella</i> complex. <i>Nature Communications</i> , <b>2016</b> , 7, 10513	17.4	81
71	Genetic blueprint of the zoonotic pathogen <i>Toxocara canis</i> . <i>Nature Communications</i> , <b>2015</b> , 6, 6145	17.4	77
70	Genome and transcriptome of the porcine whipworm <i>Trichuris suis</i> . <i>Nature Genetics</i> , <b>2014</b> , 46, 701-6	36.3	77
69	<i>Lucilia cuprina</i> genome unlocks parasitic fly biology to underpin future interventions. <i>Nature Communications</i> , <b>2015</b> , 6, 7344	17.4	51
68	Mitochondrial genomes of <i>Trichinella</i> species and genotypes as a basis for diagnosis, and systematic and epidemiological explorations. <i>International Journal for Parasitology</i> , <b>2014</b> , 44, 1073-80	4.3	34
67	Whole-genome sequence of the bovine blood fluke <i>Schistosoma bovis</i> supports interspecific hybridization with <i>S. haematobium</i> . <i>PLoS Pathogens</i> , <b>2019</b> , 15, e1007513	7.6	27
66	Making sense of genomes of parasitic worms: Tackling bioinformatic challenges. <i>Biotechnology Advances</i> , <b>2016</b> , 34, 663-686	17.8	27
65	High-quality <i>Schistosoma haematobium</i> genome achieved by single-molecule and long-range sequencing. <i>GigaScience</i> , <b>2019</b> , 8,	7.6	26
64	Long-read sequencing reveals a 4.4kb tandem repeat region in the mitogenome of <i>Echinococcus granulosus</i> (sensu stricto) genotype G1. <i>Parasites and Vectors</i> , <b>2019</b> , 12, 238	4	25
63	Identification of G protein-coupled receptors in <i>Schistosoma haematobium</i> and <i>S. mansoni</i> by comparative genomics. <i>Parasites and Vectors</i> , <b>2014</b> , 7, 242	4	25
62	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> , <b>2014</b> , 44, 485-96	4.3	22
61	Getting the most out of parasitic helminth transcriptomes using HelmDB: implications for biology and biotechnology. <i>Biotechnology Advances</i> , <b>2013</b> , 31, 1109-19	17.8	22
60	MicroRNAs of <i>Toxocara canis</i> and their predicted functional roles. <i>Parasites and Vectors</i> , <b>2016</b> , 9, 229	4	20
59	A blow to the fly - <i>Lucilia cuprina</i> draft genome and transcriptome to support advances in biology and biotechnology. <i>Biotechnology Advances</i> , <b>2016</b> , 34, 605-620	17.8	20

58	Somatic proteome of <i>Haemonchus contortus</i> . <i>International Journal for Parasitology</i> , <b>2019</b> , 49, 311-320	4.3	20
57	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> , <b>2019</b> , 204, 103375	3.9	19
56	Dafachronic acid promotes larval development in <i>Haemonchus contortus</i> by modulating dauer signalling and lipid metabolism. <i>PLoS Pathogens</i> , <b>2019</b> , 15, e1007960	7.6	19
55	Exploring molecular variation in <i>Schistosoma japonicum</i> in China. <i>Scientific Reports</i> , <b>2015</b> , 5, 17345	4.9	19
54	Harnessing the <i>Toxocara</i> Genome to Underpin Toxocariasis Research and New Interventions. <i>Advances in Parasitology</i> , <b>2016</b> , 91, 87-110	3.2	19
53	Molecular alterations during larval development of <i>Haemonchus contortus</i> in vitro are under tight post-transcriptional control. <i>International Journal for Parasitology</i> , <b>2018</b> , 48, 763-772	4.3	19
52	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> , <b>2019</b> , 17, 785-796	6.8	18
51	Dauer signalling pathway model for <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , <b>2019</b> , 12, 187	4	16
50	Insights into the immuno-molecular biology of <i>Angiostrongylus vasorum</i> through transcriptomics--prospects for new interventions. <i>Biotechnology Advances</i> , <b>2013</b> , 31, 1486-500	17.8	16
49	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> , <b>2016</b> , 10, e0004406	4.8	16
48	The developmental lipidome of <i>Haemonchus contortus</i> . <i>International Journal for Parasitology</i> , <b>2018</b> , 48, 887-895	4.3	16
47	Deguelin exerts potent nematocidal activity the mitochondrial respiratory chain. <i>FASEB Journal</i> , <b>2017</b> , 31, 4515-4532	0.9	14
46	Best practice data life cycle approaches for the life sciences. <i>F1000Research</i> , <b>2017</b> , 6, 1618	3.6	14
45	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> , <b>2019</b> , 12, 32	4	14
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> , <b>2017</b> , 10, 509	4	13
43	Improved genomic resources and new bioinformatic workflow for the carcinogenic parasite <i>Clonorchis sinensis</i> : Biotechnological implications. <i>Biotechnology Advances</i> , <b>2018</b> , 36, 894-904	17.8	13
42	Divergent Transcriptional Responses to Physiological and Xenobiotic Stress in <i>Giardia duodenalis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , <b>2016</b> , 60, 6034-45	5.9	13
41	Comparative genome analysis indicates high evolutionary potential of pathogenicity genes in <i>Colletotrichum tanacetii</i> . <i>PLoS ONE</i> , <b>2019</b> , 14, e0212248	3.7	12

40	Common workflow language (CWL)-based software pipeline for de novo genome assembly from long- and short-read data. <i>GigaScience</i> , <b>2019</b> , 8,	7.6	12
39	The barber's pole worm CAP protein superfamily--A basis for fundamental discovery and biotechnology advances. <i>Biotechnology Advances</i> , <b>2015</b> , 33, 1744-54	17.8	12
38	Elucidating the molecular and developmental biology of parasitic nematodes: Moving to a multiomics paradigm. <i>Advances in Parasitology</i> , <b>2020</b> , 108, 175-229	3.2	12
37	Comparative transcriptomic analyses of male and female adult <i>Toxocara canis</i> . <i>Gene</i> , <b>2017</b> , 600, 85-89	3.8	12
36	The <i>Haemonchus contortus</i> kinome--a resource for fundamental molecular investigations and drug discovery. <i>Parasites and Vectors</i> , <b>2015</b> , 8, 623	4	12
35	Time-Dependent Transcriptional Changes in Axenic <i>Giardia duodenalis</i> Trophozoites. <i>PLoS Neglected Tropical Diseases</i> , <b>2015</b> , 9, e0004261	4.8	12
34	Exploring the role of two interacting phosphoinositide 3-kinases of <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , <b>2014</b> , 7, 498	4	12
33	<i>Clonorchis sinensis</i> and Clonorchiasis: The Relevance of Exploring Genetic Variation. <i>Advances in Parasitology</i> , <b>2018</b> , 100, 155-208	3.2	11
32	A TGF- $\beta$ type I receptor-like molecule with a key functional role in <i>Haemonchus contortus</i> development. <i>International Journal for Parasitology</i> , <b>2018</b> , 48, 1023-1033	4.3	11
31	Genomic resources for a unique, low-virulence <i>Babesia</i> taxon from China. <i>Parasites and Vectors</i> , <b>2016</b> , 9, 564	4	10
30	The small RNA complement of adult <i>Schistosoma haematobium</i> . <i>PLoS Neglected Tropical Diseases</i> , <b>2018</b> , 12, e0006535	4.8	10
29	Bioinformatic exploration of RIO protein kinases of parasitic and free-living nematodes. <i>International Journal for Parasitology</i> , <b>2014</b> , 44, 827-36	4.3	10
28	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> , <b>2020</b> , 14, e0008552	4.8	10
27	Mitochondrial genomic comparison of <i>Clonorchis sinensis</i> from South Korea with other isolates of this species. <i>Infection, Genetics and Evolution</i> , <b>2017</b> , 51, 160-166	4.5	9
26	Whipworm kinomes reflect a unique biology and adaptation to the host animal. <i>International Journal for Parasitology</i> , <b>2017</b> , 47, 857-866	4.3	9
25	Molecular characterization of the <i>Haemonchus contortus</i> phosphoinositide-dependent protein kinase-1 gene (Hc-pdk-1). <i>Parasites and Vectors</i> , <b>2016</b> , 9, 65	4	9
24	Trehalose 6-phosphate phosphatases of <i>Pseudomonas aeruginosa</i> . <i>FASEB Journal</i> , <b>2018</b> , 32, 5470-5482	0.9	9
23	The developmental phosphoproteome of <i>Haemonchus contortus</i> . <i>Journal of Proteomics</i> , <b>2020</b> , 213, 103615	3.5	9

22	Molecular evidence for distinct modes of nutrient acquisition between visceral and neurotropic schistosomes of birds. <i>Scientific Reports</i> , <b>2019</b> , 9, 1347	4.9	8
21	High-quality reference genome for <i>Clonorchis sinensis</i> . <i>Genomics</i> , <b>2021</b> , 113, 1605-1615	4.3	8
20	High-quality nuclear genome for <i>Sarcoptes scabiei</i> -A critical resource for a neglected parasite. <i>PLoS Neglected Tropical Diseases</i> , <b>2020</b> , 14, e0008720	4.8	7
19	Nanopore Sequencing Resolves Elusive Long Tandem-Repeat Regions in Mitochondrial Genomes. <i>International Journal of Molecular Sciences</i> , <b>2021</b> , 22,	6.3	7
18	The complement of family M1 aminopeptidases of <i>Haemonchus contortus</i> --Biotechnological implications. <i>Biotechnology Advances</i> , <b>2016</b> , 34, 65-76	17.8	6
17	Toward integrative genomics of the barber's pole worm and related parasitic nematodes. <i>Infection, Genetics and Evolution</i> , <b>2020</b> , 85, 104500	4.5	6
16	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> , <b>2017</b> , 47, 51-55	4.5	5
15	The apicoplast genomes of two taxonomic units of <i>Babesia</i> from sheep. <i>Veterinary Parasitology</i> , <b>2017</b> , 233, 123-128	2.8	5
14	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> , <b>2016</b> , 6, 2847-56	3.2	5
13	CAP protein superfamily members in <i>Toxocara canis</i> . <i>Parasites and Vectors</i> , <b>2016</b> , 9, 360	4	5
12	The Battle Against Flystrike - Past Research and New Prospects Through Genomics. <i>Advances in Parasitology</i> , <b>2017</b> , 98, 227-281	3.2	4
11	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> , <b>2014</b> , 44, 251-61	4.3	4
10	Marked mitochondrial genetic variation in individuals and populations of the carcinogenic liver fluke <i>Clonorchis sinensis</i> . <i>PLoS Neglected Tropical Diseases</i> , <b>2020</b> , 14, e0008480	4.8	4
9	Pipeline for the identification and classification of ion channels in parasitic flatworms. <i>Parasites and Vectors</i> , <b>2016</b> , 9, 155	4	3
8	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> , <b>2021</b> , 15, e0009149	4.8	2
7	transcriptome - a resource to enable molecular studies of snail and schistosome biology.. <i>Current Research in Parasitology and Vector-borne Diseases</i> , <b>2021</b> , 1, 100015		1
6	Mitochondrial genome of (Gastropoda: Lymnaeoidea): Implications for snail systematics and schistosome epidemiology.. <i>Current Research in Parasitology and Vector-borne Diseases</i> , <b>2021</b> , 1, 100017		1
5	Chromosome-level genome of <i>Schistosoma haematobium</i> underpins genome-wide explorations of molecular variation.. <i>PLoS Pathogens</i> , <b>2022</b> , 18, e1010288	7.6	1

4	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> , <b>2022</b> , 5, 199	6.7	1
3	Harnessing model organism genomics to underpin the machine learning-based prediction of essential genes in eukaryotes - Biotechnological implications. <i>Biotechnology Advances</i> , <b>2021</b> , 107822	17.8	0
2	The mitogenome of (Tucker) and its relationships with other trombidiform mites as inferred from nucleotide sequences and gene arrangements. <i>Ecology and Evolution</i> , <b>2021</b> , 11, 14162-14174	2.8	0
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> , <b>2022</b> , 13, 977	17.4	0