

# Pasi K. Korhonen

## List of Publications by Year in Descending Order

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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	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
74	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
73	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
72	High-quality reference genome for <i>Clonorchis sinensis</i> . <i>Genomics</i> , <b>2021</b> , 113, 1605-1615	4.3	8
71	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
70	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
69	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
68	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
67	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
66	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
65	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
64	The developmental phosphoproteome of <i>Haemonchus contortus</i> . <i>Journal of Proteomics</i> , <b>2020</b> , 213, 103615	3.5	9
63	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
62	Toward integrative omics of the barber's pole worm and related parasitic nematodes. <i>Infection, Genetics and Evolution</i> , <b>2020</b> , 85, 104500	4.5	6
61	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
60	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
59	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

58	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
57	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
56	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
55	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
54	Dauer signalling pathway model for <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , <b>2019</b> , 12, 187	4	16
53	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
52	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
51	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
50	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
49	Somatic proteome of <i>Haemonchus contortus</i> . <i>International Journal for Parasitology</i> , <b>2019</b> , 49, 311-320	4.3	20
48	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
47	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
46	Trehalose 6-phosphate phosphatases of <i>Pseudomonas aeruginosa</i> . <i>FASEB Journal</i> , <b>2018</b> , 32, 5470-5482	0.9	9
45	The small RNA complement of adult <i>Schistosoma haematobium</i> . <i>PLoS Neglected Tropical Diseases</i> , <b>2018</b> , 12, e0006535	4.8	10
44	<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
43	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
42	The developmental lipidome of <i>Haemonchus contortus</i> . <i>International Journal for Parasitology</i> , <b>2018</b> , 48, 887-895	4.3	16
41	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

40	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
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> , <b>2017</b> , 47, 51-55	4.5	5
38	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
37	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
36	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
35	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
34	Deguelin exerts potent nematocidal activity the mitochondrial respiratory chain. <i>FASEB Journal</i> , <b>2017</b> , 31, 4515-4532	0.9	14
33	Comparative transcriptomic analyses of male and female adult <i>Toxocara canis</i> . <i>Gene</i> , <b>2017</b> , 600, 85-89	3.8	12
32	Best practice data life cycle approaches for the life sciences. <i>F1000Research</i> , <b>2017</b> , 6, 1618	3.6	14
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	MicroRNAs of <i>Toxocara canis</i> and their predicted functional roles. <i>Parasites and Vectors</i> , <b>2016</b> , 9, 229	4	20
29	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
28	Pipeline for the identification and classification of ion channels in parasitic flatworms. <i>Parasites and Vectors</i> , <b>2016</b> , 9, 155	4	3
27	Phylogenomic and biogeographic reconstruction of the <i>Trichinella</i> complex. <i>Nature Communications</i> , <b>2016</b> , 7, 10513	17.4	81
26	Making sense of genomes of parasitic worms: Tackling bioinformatic challenges. <i>Biotechnology Advances</i> , <b>2016</b> , 34, 663-686	17.8	27
25	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
24	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
23	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

22	Analyses of Compact Trichinella 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
21	CAP protein superfamily members in <i>Toxocara canis</i> . <i>Parasites and Vectors</i> , <b>2016</b> , 9, 360	4	5
20	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
19	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
18	Genetic blueprint of the zoonotic pathogen <i>Toxocara canis</i> . <i>Nature Communications</i> , <b>2015</b> , 6, 6145	17.4	77
17	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
16	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
15	<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
14	Exploring molecular variation in <i>Schistosoma japonicum</i> in China. <i>Scientific Reports</i> , <b>2015</b> , 5, 17345	4.9	19
13	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
12	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
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	Genome and transcriptome of the porcine whipworm <i>Trichuris suis</i> . <i>Nature Genetics</i> , <b>2014</b> , 46, 701-6	36.3	77
9	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
8	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
7	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
6	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
5	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

4	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
3	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
2	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
1	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