

# Mark L Blaxter

## List of Publications by Year in descending order

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293  
papers

31,719  
citations

5896

81  
h-index

6300

158  
g-index

329  
all docs

329  
docs citations

329  
times ranked

29829  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide genetic marker discovery and genotyping using next-generation sequencing. <i>Nature Reviews Genetics</i> , 2011, 12, 499-510.	16.3	2,198
2	A molecular evolutionary framework for the phylum Nematoda. <i>Nature</i> , 1998, 392, 71-75.	27.8	1,697
3	Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. <i>Nature</i> , 2012, 487, 94-98.	27.8	1,086
4	Genome sequence of the metazoan plant-parasitic nematode <i>Meloidogyne incognita</i> . <i>Nature Biotechnology</i> , 2008, 26, 909-915.	17.5	1,012
5	BlobToolKit – Interactive Quality Assessment of Genome Assemblies. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1361-1374.	1.8	883
6	Defining operational taxonomic units using DNA barcode data. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2005, 360, 1935-1943.	4.0	729
7	Molecular barcodes for soil nematode identification. <i>Molecular Ecology</i> , 2002, 11, 839-850.	3.9	650
8	Exosomes secreted by nematode parasites transfer small RNAs to mammalian cells and modulate innate immunity. <i>Nature Communications</i> , 2014, 5, 5488.	12.8	640
9	How many biological replicates are needed in an RNA-seq experiment and which differential expression tool should you use?. <i>Rna</i> , 2016, 22, 839-851.	3.5	622
10	Genome-wide evidence for speciation with gene flow in <i>Heliconius</i> butterflies. <i>Genome Research</i> , 2013, 23, 1817-1828.	5.5	609
11	RADSeq: next-generation population genetics. <i>Briefings in Functional Genomics</i> , 2010, 9, 416-423.	2.7	600
12	BlobTools: Interrogation of genome assemblies. <i>F1000Research</i> , 0, 6, 1287.	1.6	600
13	Draft Genome of the Filarial Nematode Parasite <i>Brugia malayi</i> . <i>Science</i> , 2007, 317, 1756-1760.	12.6	571
14	Phylogeny of <i>Wolbachia</i> in filarial nematodes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1998, 265, 2407-2413.	2.6	493
15	The promise of a DNA taxonomy. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2004, 359, 669-679.	4.0	422
16	A supergene determines highly divergent male reproductive morphs in the ruff. <i>Nature Genetics</i> , 2016, 48, 79-83.	21.4	411
17	Genomic architecture and introgression shape a butterfly radiation. <i>Science</i> , 2019, 366, 594-599.	12.6	365
18	Analysis of the genome sequences of three <i>Drosophila melanogaster</i> spontaneous mutation accumulation lines. <i>Genome Research</i> , 2009, 19, 1195-1201.	5.5	343

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19	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015, 16, 76.	8.8	330
20	Second-generation environmental sequencing unmask marine metazoan biodiversity. <i>Nature Communications</i> , 2010, 1, 98.	12.8	321
21	Special features of <sc>RAD</sc> Sequencing data: implications for genotyping. <i>Molecular Ecology</i> , 2013, 22, 3151-3164.	3.9	318
22	Tetracycline therapy targets intracellular bacteria in the filarial nematode <i>Litomosoides sigmodontis</i> and results in filarial infertility. <i>Journal of Clinical Investigation</i> , 1999, 103, 11-18.	8.2	302
23	Genomic islands of divergence in hybridizing <i>Heliconius</i> butterflies identified by large-scale targeted sequencing. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 343-353.	4.0	294
24	An improved molecular phylogeny of the Nematoda with special emphasis on marine taxa. <i>Molecular Phylogenetics and Evolution</i> , 2007, 42, 622-636.	2.7	293
25	IL-4 dependent alternatively-activated macrophages have a distinctive in vivo gene expression phenotype. <i>BMC Immunology</i> , 2002, 3, 7.	2.2	290
26	Linkage Mapping and Comparative Genomics Using Next-Generation RAD Sequencing of a Non-Model Organism. <i>PLoS ONE</i> , 2011, 6, e19315.	2.5	270
27	<i>Caenorhabditis elegans</i> Is a Nematode. , 1998, 282, 2041-2046.		259
28	Blobology: exploring raw genome data for contaminants, symbionts and parasites using taxon-annotated GC-coverage plots. <i>Frontiers in Genetics</i> , 2013, 4, 237.	2.3	258
29	A transcriptomic analysis of the phylum Nematoda. <i>Nature Genetics</i> , 2004, 36, 1259-1267.	21.4	239
30	DESS: a versatile solution for preserving morphology and extractable DNA of nematodes. <i>Nematology</i> , 2006, 8, 367-376.	0.6	233
31	Comparing de novo assemblers for 454 transcriptome data. <i>BMC Genomics</i> , 2010, 11, 571.	2.8	217
32	No evidence for extensive horizontal gene transfer in the genome of the tardigrade <i>Hypsibius dujardini</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5053-5058.	7.1	214
33	Molecular phylogenetic analysis of the genus <i>Strongyloides</i> and related nematodes. <i>International Journal for Parasitology</i> , 2002, 32, 1507-1517.	3.1	208
34	The evolution of parasitism in Nematoda. <i>Parasitology</i> , 2015, 142, S26-S39.	1.5	199
35	Counting angels with DNA. <i>Nature</i> , 2003, 421, 122-123.	27.8	195
36	jMOTU and Taxonator: Turning DNA Barcode Sequences into Annotated Operational Taxonomic Units. <i>PLoS ONE</i> , 2011, 6, e19259.	2.5	180

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37	Ancient Origin of Glycosyl Hydrolase Family 9 Cellulase Genes. <i>Molecular Biology and Evolution</i> , 2005, 22, 1273-1284.	8.9	171
38	Comparative genomics of the tardigrades <i>Hypsibius dujardini</i> and <i>Ramazzottius varieornatus</i> . <i>PLoS Biology</i> , 2017, 15, e2002266.	5.6	170
39	Nematode surface coats: Actively evading immunity. <i>Parasitology Today</i> , 1992, 8, 243-247.	3.0	169
40	Genome-wide patterns of divergence and gene flow across a butterfly radiation. <i>Molecular Ecology</i> , 2013, 22, 814-826.	3.9	160
41	Molecular Analysis of Nematode Diversity and the Evolution of Parasitism. <i>Parasitology Today</i> , 1999, 15, 188-193.	3.0	158
42	<i>Caenorhabditis elegans</i> as a model for parasitic nematodes. <i>International Journal for Parasitology</i> , 1998, 28, 395-411.	3.1	156
43	The genome of the yellow potato cyst nematode, <i>Globodera rostochiensis</i> , reveals insights into the basis of parasitism and virulence. <i>Genome Biology</i> , 2016, 17, 124.	8.8	156
44	Analysis of gene expression from the <i>Wolbachia</i> genome of a filarial nematode supports both metabolic and defensive roles within the symbiosis. <i>Genome Research</i> , 2012, 22, 2467-2477.	5.5	155
45	Globins in nonvertebrate species: dispersal by horizontal gene transfer and evolution of the structure-function relationships. <i>Molecular Biology and Evolution</i> , 1996, 13, 324-333.	8.9	154
46	Ecdysozoan Mitogenomics: Evidence for a Common Origin of the Legged Invertebrates, the Panarthropoda. <i>Genome Biology and Evolution</i> , 2010, 2, 425-440.	2.5	154
47	Use of RNA interference to investigate gene function in the human filarial nematode parasite <i>Brugia malayi</i> . <i>Molecular and Biochemical Parasitology</i> , 2003, 129, 41-51.	1.1	145
48	Hox Gene Loss during Dynamic Evolution of the Nematode Cluster. <i>Current Biology</i> , 2003, 13, 37-40.	3.9	142
49	Comparative genomics of nematodes. <i>Trends in Genetics</i> , 2005, 21, 573-581.	6.7	141
50	Linking Genomics and Ecology to Investigate the Complex Evolution of an Invasive <i>Drosophila</i> Pest. <i>Genome Biology and Evolution</i> , 2013, 5, 745-757.	2.5	138
51	<i>Drosophila suzukii</i> . <i>Current Biology</i> , 2013, 23, R8-R9.	3.9	137
52	Systematic Position and Phylogeny. , 2002, , 1-30.		136
53	Proteomic analysis of secretory products from the model gastrointestinal nematode <i>Heligmosomoides polygyrus</i> reveals dominance of Venom Allergen-Like (VAL) proteins. <i>Journal of Proteomics</i> , 2011, 74, 1573-1594.	2.4	136
54	Formin Is Associated with Left-Right Asymmetry in the Pond Snail and the Frog. <i>Current Biology</i> , 2016, 26, 654-660.	3.9	135

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55	A molecular palaeobiological exploration of arthropod terrestrialization. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150133.	4.0	131
56	PartiGene--constructing partial genomes. <i>Bioinformatics</i> , 2004, 20, 1398-1404.	4.1	129
57	Phylogenetic Relationships of the Wolbachia of Nematodes and Arthropods. <i>PLoS Pathogens</i> , 2006, 2, e94.	4.7	127
58	The genome of the heartworm, <i>Dirofilaria immitis</i> , reveals drug and vaccine targets. <i>FASEB Journal</i> , 2012, 26, 4650-4661.	0.5	124
59	The Earth BioGenome Project 2020: Starting the clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	124
60	Genes expressed in <i>Brugia malayi</i> infective third stage larvae. <i>Molecular and Biochemical Parasitology</i> , 1996, 77, 77-93.	1.1	120
61	Wolbachia genomes: revealing the biology of parasitism and mutualism. <i>Trends in Parasitology</i> , 2006, 22, 60-65.	3.3	120
62	Characterisation of QTL-linked and genome-wide restriction site-associated DNA (RAD) markers in farmed Atlantic salmon. <i>BMC Genomics</i> , 2012, 13, 244.	2.8	120
63	Sequence locally, think globally: The Darwin Tree of Life Project. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	120
64	prot4EST: translating expressed sequence tags from neglected genomes. <i>BMC Bioinformatics</i> , 2004, 5, 187.	2.6	118
65	Ancient and Novel Small RNA Pathways Compensate for the Loss of piRNAs in Multiple Independent Nematode Lineages. <i>PLoS Biology</i> , 2015, 13, e1002061.	5.6	118
66	Identification and characterisation of a <i>Leishmania donovani</i> antigen belonging to the 70-kDa heat-shock protein family. <i>FEBS Journal</i> , 1990, 190, 377-384.	0.2	117
67	Both Free-Living and Parasitic Nematodes Induce a Characteristic Th2 Response That Is Dependent on the Presence of Intact Glycans. <i>Infection and Immunity</i> , 2004, 72, 398-407.	2.2	110
68	Nematodes: The Worm and Its Relatives. <i>PLoS Biology</i> , 2011, 9, e1001050.	5.6	110
69	Identification of the major soluble cuticular glycoprotein of lymphatic filarial nematode parasites (gp29) as a secretory homolog of glutathione peroxidase.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1992, 89, 5837-5841.	7.1	108
70	Comparative genomics of 10 new <i>Caenorhabditis</i> species. <i>Evolution Letters</i> , 2019, 3, 217-236.	3.3	106
71	A survey of genes expressed in adults of the human hookworm, <i>Necator americanus</i> . <i>Parasitology</i> , 2000, 120, 171-184.	1.5	105
72	Comparative Genome Analysis Provides Insights into the Evolution and Adaptation of <i>Pseudomonas syringae</i> pv. <i>aesculi</i> on <i>Aesculus hippocastanum</i> . <i>PLoS ONE</i> , 2010, 5, e10224.	2.5	104

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73	A chromosome-level genome assembly of <i>Cydia pomonella</i> provides insights into chemical ecology and insecticide resistance. <i>Nature Communications</i> , 2019, 10, 4237.	12.8	102
74	Silencing of Germline-Expressed Genes by DNA Elimination in Somatic Cells. <i>Developmental Cell</i> , 2012, 23, 1072-1080.	7.0	101
75	Molecular Genealogy of Some Nematode Taxa as Based on Cytochrome c and Globin Amino Acid Sequences. <i>Molecular Phylogenetics and Evolution</i> , 1994, 3, 92-101.	2.7	99
76	The complex hybrid origins of the root knot nematodes revealed through comparative genomics. <i>PeerJ</i> , 2014, 2, e356.	2.0	99
77	Immunological genomics of <i>Brugia malayi</i> : filarial genes implicated in immune evasion and protective immunity. <i>Parasite Immunology</i> , 2001, 23, 327-344.	1.5	98
78	Extracellular <i>Onchocerca</i> -derived small RNAs in host nodules and blood. <i>Parasites and Vectors</i> , 2015, 8, 58.	2.5	98
79	Comparative Genomics of Apomictic Root-Knot Nematodes: Hybridization, Ploidy, and Dynamic Genome Change. <i>Genome Biology and Evolution</i> , 2017, 9, 2844-2861.	2.5	98
80	The filarial genome project: analysis of the nuclear, mitochondrial and endosymbiont genomes of <i>Brugia malayi</i> . <i>International Journal for Parasitology</i> , 2000, 30, 411-419.	3.1	94
81	A gene family of cathepsin L-like proteases of filarial nematodes are associated with larval molting and cuticle and eggshell remodeling. <i>Molecular and Biochemical Parasitology</i> , 2004, 136, 227-242.	1.1	94
82	Transcriptome profiling of developmental and xenobiotic responses in a keystone soil animal, the oligochaete annelid <i>Lumbricus rubellus</i> . <i>BMC Genomics</i> , 2008, 9, 266.	2.8	93
83	The components of the <i>Daphnia pulex</i> immune system as revealed by complete genome sequencing. <i>BMC Genomics</i> , 2009, 10, 175.	2.8	93
84	Phylogeny and DNA barcoding of inquiline oak gallwasps (Hymenoptera: Cynipidae) of the Western Palearctic. <i>Molecular Phylogenetics and Evolution</i> , 2010, 55, 210-225.	2.7	92
85	Nematode Spliced Leaders – Ubiquity, Evolution and Utility. <i>International Journal for Parasitology</i> , 1996, 26, 1025-1033.	3.1	92
86	Hox gene evolution in nematodes: novelty conserved. <i>Current Opinion in Genetics and Development</i> , 2003, 13, 593-598.	3.3	90
87	ButterflyBase: a platform for lepidopteran genomics. <i>Nucleic Acids Research</i> , 2007, 36, D582-D587.	14.5	90
88	An Abundant, trans-spliced mRNA from <i>Toxocara canis</i> Infective Larvae Encodes a 26-kDa Protein with Homology to Phosphatidylethanolamine-binding Proteins. <i>Journal of Biological Chemistry</i> , 1995, 270, 18517-18522.	3.4	88
89	annot8r: GO, EC and KEGG annotation of EST datasets. <i>BMC Bioinformatics</i> , 2008, 9, 180.	2.6	87
90	Making sense of EST sequences by CLOBBing them. <i>BMC Bioinformatics</i> , 2002, 3, 31.	2.6	86

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91	Expressed Sequence Tags: An Overview. <i>Methods in Molecular Biology</i> , 2009, 533, 1-12.	0.9	86
92	Forms and Functions of Nematode Surfaces. <i>Experimental Parasitology</i> , 1993, 77, 380-384.	1.2	85
93	poRe: an R package for the visualization and analysis of nanopore sequencing data. <i>Bioinformatics</i> , 2015, 31, 114-115.	4.1	85
94	The Evolution of Biased Codon and Amino Acid Usage in Nematode Genomes. <i>Molecular Biology and Evolution</i> , 2006, 23, 2303-2315.	8.9	84
95	Nematoda: Genes, Genomes and the Evolution of Parasitism. <i>Advances in Parasitology</i> , 2003, 54, 101-195.	3.2	83
96	DNA taxonomy of a neglected animal phylum: an unexpected diversity of tardigrades. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2004, 271, S189-92.	2.6	83
97	The ash dieback invasion of Europe was founded by two genetically divergent individuals. <i>Nature Ecology and Evolution</i> , 2018, 2, 1000-1008.	7.8	82
98	Differentially expressed, abundant trans-spliced cDNAs from larval <i>Brugia malayi</i> 1Note: Nucleotide sequence data reported in this paper are available in the EMBL, GenBank, and DDJB databases under the accession numbers U57547, U80971-U80980, U81008 and U84736.1. <i>Molecular and Biochemical Parasitology</i> , 1997, 87, 85-95.	1.1	78
99	Nemoglobins: Divergent nematode globins. <i>Parasitology Today</i> , 1993, 9, 353-360.	3.0	77
100	Are filarial nematode <i>Wolbachia</i> obligate mutualist symbionts?. <i>Trends in Ecology and Evolution</i> , 2004, 19, 163-166.	8.7	77
101	Statistical models for RNA-seq data derived from a two-condition 48-replicate experiment. <i>Bioinformatics</i> , 2015, 31, 3625-3630.	4.1	76
102	Molecular taxonomics for biodiversity surveys: already a reality. <i>Trends in Ecology and Evolution</i> , 2003, 18, 268-269.	8.7	75
103	Quality control of next-generation sequencing data without a reference. <i>Frontiers in Genetics</i> , 2014, 5, 111.	2.3	75
104	Secretion of an Argonaute protein by a parasitic nematode and the evolution of its siRNA guides. <i>Nucleic Acids Research</i> , 2019, 47, 3594-3606.	14.5	75
105	Experimental evolution, genetic analysis and genome re-sequencing reveal the mutation conferring artemisinin resistance in an isogenic lineage of malaria parasites. <i>BMC Genomics</i> , 2010, 11, 499.	2.8	74
106	<i>Toxocara canis</i> : A labile antigenic surface coat overlying the epicuticle of infective larvae. <i>Experimental Parasitology</i> , 1992, 75, 72-86.	1.2	73
107	A Transcriptomic Analysis of <i>Echinococcus granulosus</i> Larval Stages: Implications for Parasite Biology and Host Adaptation. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1897.	3.0	72
108	RAD-seq derived markers flank the shell colour and banding loci of the <i>Cepaea nemoralis</i> supergene. <i>Molecular Ecology</i> , 2013, 22, 3077-3089.	3.9	72

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109	KinFin: Software for Taxon-Aware Analysis of Clustered Protein Sequences. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3349-3357.	1.8	72
110	Operon Conservation and the Evolution of trans-Splicing in the Phylum Nematoda. <i>PLoS Genetics</i> , 2006, 2, e198.	3.5	71
111	Globin and Globin Gene Structure of the Nerve Myoglobin of <i>Aphrodite aculeata</i> . <i>Journal of Biological Chemistry</i> , 1996, 271, 19865-19870.	3.4	69
112	On the Extent and Origins of Genic Novelty in the Phylum Nematoda. <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e258.	3.0	68
113	Genomics and the biology of parasites. <i>BioEssays</i> , 1999, 21, 131-147.	2.5	67
114	The <i>Brugia malayi</i> genome project: expressed sequence tags and gene discovery. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2002, 96, 7-17.	1.8	67
115	Characterization of a Novel Filarial Serine Protease Inhibitor, Ov-SPI-1, from <i>Onchocerca volvulus</i> , with Potential Multifunctional Roles during Development of the Parasite. <i>Journal of Biological Chemistry</i> , 2005, 280, 40845-40856.	3.4	66
116	NEMBASE: a resource for parasitic nematode ESTs. <i>Nucleic Acids Research</i> , 2004, 32, 427D-430.	14.5	65
117	A single chromosome assembly of <i>Bacteroides fragilis</i> strain BE1 from Illumina and MinION nanopore sequencing data. <i>GigaScience</i> , 2015, 4, 60.	6.4	64
118	Expressed Sequence Tags: Medium-Throughput Protocols<1>. , 2004, 270, 075-092.		63
119	Polyphenism in social insects: insights from a transcriptome-wide analysis of gene expression in the life stages of the key pollinator, <i>Bombus terrestris</i> . <i>BMC Genomics</i> , 2011, 12, 623.	2.8	63
120	Nematode spliced leaders—ubiquity, evolution and utility. <i>International Journal for Parasitology</i> , 1996, 26, 1025-33.	3.1	63
121	SimiTri—visualizing similarity relationships for groups of sequences. <i>Bioinformatics</i> , 2003, 19, 390-395.	4.1	62
122	Gene structure, activity and localization of a catalase from intracellular bacteria in <i>Onchocerca volvulus</i> 1Note: Nucleotide sequence data reported in this paper are available in the EMBL, GenBank and DDJB databases under the accession numbers X82176, AF069070 and AF069069.1. <i>Molecular and Biochemical Parasitology</i> , 1998, 96, 69-81.	1.1	61
123	400,000 nematode ESTs on the Net. <i>Trends in Parasitology</i> , 2003, 19, 283-286.	3.3	61
124	NEMBASE4: The nematode transcriptome resource. <i>International Journal for Parasitology</i> , 2011, 41, 881-894.	3.1	60
125	Signal sequence analysis of expressed sequence tags from the nematode <i>Nippostrongylus brasiliensis</i> and the evolution of secreted proteins in parasites. <i>Genome Biology</i> , 2004, 5, R39.	9.6	59
126	Genetic Drift, Not Life History or RNAi, Determine Long-Term Evolution of Transposable Elements. <i>Genome Biology and Evolution</i> , 2016, 8, 2964-2978.	2.5	58



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127	The phylogenetics of Anguillicolidae (Nematoda: Anguilliculoidea), swimbladder parasites of eels. <i>BMC Evolutionary Biology</i> , 2012, 12, 60.	3.2	56
128	Analysis of Genes Expressed at the Infective Larval Stage Validates Utility of <i>Litomosoides sigmodontis</i> as a Murine Model for Filarial Vaccine Development. <i>Infection and Immunity</i> , 2000, 68, 5454-5458.	2.2	55
129	A Cryptoendolithic Community in Volcanic Glass. <i>Astrobiology</i> , 2009, 9, 369-381.	3.0	55
130	A high-coverage draft genome of the mycalesine butterfly <i>Bicyclus anynana</i> . <i>GigaScience</i> , 2017, 6, 1-7.	6.4	55
131	Symbiont Genes in Host Genomes: Fragments with a Future?. <i>Cell Host and Microbe</i> , 2007, 2, 211-213.	11.0	54
132	Revealing the Dark Matter of the Genome. <i>Science</i> , 2010, 330, 1758-1759.	12.6	52
133	Deep resequencing of serial sputum isolates of <i>Mycobacterium tuberculosis</i> during therapeutic failure due to poor compliance reveals stepwise mutation of key resistance genes on an otherwise stable genetic background. <i>Journal of Infection</i> , 2011, 62, 212-217.	3.3	52
134	The biology of nematode- and IL4R1-dependent murine macrophage polarization in vivo as defined by RNA-Seq and targeted lipidomics. <i>Blood</i> , 2012, 120, e93-e104.	1.4	52
135	Systematic Position and Phylogeny. , 0, , .		52
136	Toward 959 nematode genomes. <i>Worm</i> , 2012, 1, 42-50.	1.0	51
137	Characterisation of the British honey bee metagenome. <i>Nature Communications</i> , 2018, 9, 4995.	12.8	51
138	Why sequence all eukaryotes?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	51
139	Characterisation of an immunodominant glycoprotein antigen of <i>Onchocerca volvulus</i> with homologues in other filarial nematodes and <i>Caenorhabditis elegans</i> . <i>Molecular and Biochemical Parasitology</i> , 1995, 69, 185-195.	1.1	49
140	Quantification of <i>Wolbachia</i> bacteria in <i>Brugia malayi</i> through the nematode lifecycle. <i>Molecular and Biochemical Parasitology</i> , 2004, 137, 361-364.	1.1	49
141	Bacterial Colonization and Weathering of Terrestrial Obsidian in Iceland. <i>Geomicrobiology Journal</i> , 2008, 25, 25-37.	2.0	49
142	Phylogenomics and Analysis of Shared Genes Suggest a Single Transition to Mutualism in <i>Wolbachia</i> of Nematodes. <i>Genome Biology and Evolution</i> , 2013, 5, 1668-1674.	2.5	49
143	Palaeosymbiosis Revealed by Genomic Fossils of <i>Wolbachia</i> in a Strongyloidean Nematode. <i>PLoS Genetics</i> , 2014, 10, e1004397.	3.5	49
144	Genome comparisons indicate recent transfer of <i>Wolbachia</i> like <i>Wolbachia</i> between sister species <i>Drosophila suzukii</i> and <i>D. Åsubpulchrella</i> . <i>Ecology and Evolution</i> , 2017, 7, 9391-9404.	1.9	49

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145	A Hemoglobin with an Optical Function. <i>Journal of Biological Chemistry</i> , 2000, 275, 4810-4815.	3.4	48
146	Functional diversification of Argonautes in nematodes: an expanding universe. <i>Biochemical Society Transactions</i> , 2013, 41, 881-886.	3.4	47
147	Medical significance of <i>Caenorhabditis elegans</i> . <i>Annals of Medicine</i> , 2000, 32, 23-30.	3.8	46
148	Linking toxicant physiological mode of action with induced gene expression changes in <i>Caenorhabditis elegans</i> . <i>BMC Systems Biology</i> , 2010, 4, 32.	3.0	46
149	Characterization of the mantle transcriptome in bivalves: <i>Pecten maximus</i> , <i>Mytilus edulis</i> and <i>Crassostrea gigas</i> . <i>Marine Genomics</i> , 2016, 27, 9-15.	1.1	46
150	A telomere-to-telomere assembly of <i>Oscheius tipulae</i> and the evolution of rhabditid nematode chromosomes. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	45
151	<i>Caenorhabditis elegans</i> has a circadian clock. <i>Current Biology</i> , 2002, 12, R47-R49.	3.9	44
152	A P2X receptor from the tardigrade species <i>Hypsibius dujardini</i> with fast kinetics and sensitivity to zinc and copper. <i>BMC Evolutionary Biology</i> , 2009, 9, 17.	3.2	44
153	959 Nematode Genomes: a semantic wiki for coordinating sequencing projects. <i>Nucleic Acids Research</i> , 2012, 40, D1295-D1300.	14.5	44
154	Genomic dissection of an extended phenotype: Oak galling by a cynipid gall wasp. <i>PLoS Genetics</i> , 2019, 15, e1008398.	3.5	44
155	Structural, Functional, and Genetic Characterization of <i>Gastrophilus</i> Hemoglobin. <i>Journal of Biological Chemistry</i> , 1998, 273, 32467-32474.	3.4	43
156	The genome of <i>Romanomermis culicivorax</i> : revealing fundamental changes in the core developmental genetic toolkit in Nematoda. <i>BMC Genomics</i> , 2013, 14, 923.	2.8	43
157	A molecular analysis of desiccation tolerance mechanisms in the anhydrobiotic nematode <i>Panagrolaimus superbus</i> using expressed sequenced tags. <i>BMC Research Notes</i> , 2012, 5, 68.	1.4	41
158	Quantitative genome re-sequencing defines multiple mutations conferring chloroquine resistance in rodent malaria. <i>BMC Genomics</i> , 2012, 13, 106.	2.8	40
159	Chromosome-Wide Evolution and Sex Determination in the Three-Sexed Nematode <i>Auanema rhodensis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1211-1230.	1.8	39
160	Supergroup C <i>Wolbachia</i> , mutualist symbionts of filarial nematodes, have a distinct genome structure. <i>Open Biology</i> , 2015, 5, 150099.	3.6	38
161	Genomic tools and cDNA derived markers for butterflies. <i>Molecular Ecology</i> , 2005, 14, 2883-2897.	3.9	37
162	The effect of model choice on phylogenetic inference using mitochondrial sequence data: Lessons from the scorpions. <i>Molecular Phylogenetics and Evolution</i> , 2007, 43, 583-595.	2.7	37

#	ARTICLE	IF	CITATIONS
163	Comparative Transcriptomic Responses to Chronic Cadmium, Fluoranthene, and Atrazine Exposure in <i>Lumbricus rubellus</i> . <i>Environmental Science &amp; Technology</i> , 2008, 42, 4208-4214.	10.0	37
164	Simultaneous genome sequencing of symbionts and their hosts. <i>Symbiosis</i> , 2011, 55, 119-126.	2.3	37
165	Comparative Epigenomics Reveals that RNA Polymerase II Pausing and Chromatin Domain Organization Control Nematode piRNA Biogenesis. <i>Developmental Cell</i> , 2019, 48, 793-810.e6.	7.0	37
166	Genome sequence of the root-knot nematode <i>Meloidogyne luci</i> . <i>Journal of Nematology</i> , 2020, 52, 1-5.	0.9	37
167	200,000 nematode expressed sequence tags on the Net. <i>Trends in Parasitology</i> , 2001, 17, 394-396.	3.3	36
168	Expressed sequence tag survey of gene expression in the scab mite <i>Psoroptes ovis</i> allergens, proteases and free-radical scavengers. <i>Parasitology</i> , 2003, 126, 451-460.	1.5	36
169	The genome of the emerging barley pathogen <i>Ramularia collo-cygni</i> . <i>BMC Genomics</i> , 2016, 17, 584.	2.8	36
170	Genes and genomes of <i>Necator americanus</i> and related hookworms. <i>International Journal for Parasitology</i> , 2000, 30, 347-355.	3.1	35
171	Abundant larval transcript-1 and -2 genes from <i>Brugia malayi</i> : diversity of genomic environments but conservation of 5' promoter sequences functional in <i>Caenorhabditis elegans</i> . <i>Molecular and Biochemical Parasitology</i> , 2002, 125, 59-71.	1.1	35
172	The Genome of <i>Caenorhabditis bovis</i> . <i>Current Biology</i> , 2020, 30, 1023-1031.e4.	3.9	35
173	<i>Caenorhabditis monodelphis</i> sp. n.: defining the stem morphology and genomics of the genus <i>Caenorhabditis</i> . <i>BMC Zoology</i> , 2017, 2, .	1.0	33
174	Standards recommendations for the Earth BioGenome Project. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	33
175	The earthworm Expressed Sequence Tag projectThe 7th international symposium on earthworm ecology - Cardiff - Wales - 2002. <i>Pedobiologia</i> , 2003, 47, 447-451.	1.2	32
176	Comparative Analysis of the Secretome from a Model Filarial Nematode ( <i>Litomosoides sigmodontis</i> ) Reveals Maximal Diversity in Gravid Female Parasites. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2527-2544.	3.8	32
177	Field cricket genome reveals the footprint of recent, abrupt adaptation in the wild. <i>Evolution Letters</i> , 2020, 4, 19-33.	3.3	32
178	Nematode spliced leaders ubiquity, evolution and utility. <i>International Journal for Parasitology</i> , 1996, 26, 1025-1033.	3.1	31
179	A unified nomenclature for filarial genes. <i>Parasitology Today</i> , 1997, 13, 416-417.	3.0	31
180	Imagining Sisyphus happy: DNA barcoding and the unnamed majority. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150329.	4.0	30

#	ARTICLE	IF	CITATIONS
181	Patterns and processes in the evolution of animal parasitic nematodes. <i>Nematology</i> , 2000, 2, 43-55.	0.6	29
182	Denaturing gradient gel electrophoresis (DGGE) as a tool for identification of marine nematodes. <i>Marine Ecology - Progress Series</i> , 2005, 291, 103-113.	1.9	29
183	Sequence, expression and evolution of the globins of the parasitic nematode <i>Nippostrongylus brasiliensis</i> . <i>Molecular and Biochemical Parasitology</i> , 1994, 68, 1-14.	1.1	28
184	A conserved set of maternal genes? Insights from a molluscan transcriptome. <i>International Journal of Developmental Biology</i> , 2014, 58, 501-511.	0.6	28
185	Alimentary Fibropapilloma in Cattle: A Spontaneous Tumor, Nonpermissive for Papillomavirus Replication. <i>Journal of the National Cancer Institute</i> , 1984, 73, 499-504.	6.3	27
186	A genome sequence survey of the filarial nematode <i>Brugia malayi</i> : repeats, gene discovery, and comparative genomics. <i>Molecular and Biochemical Parasitology</i> , 2004, 137, 215-227.	1.1	27
187	Signatures of the Evolution of Parthenogenesis and Cryptobiosis in the Genomes of Panagrolaimid Nematodes. <i>IScience</i> , 2019, 21, 587-602.	4.1	27
188	A Bivalve Biomineralization Toolbox. <i>Molecular Biology and Evolution</i> , 2021, 38, 4043-4055.	8.9	27
189	The 5S ribosomal RNA intergenic region of parasitic nematodes: variation in size and presence of SL1 RNA. <i>Molecular and Biochemical Parasitology</i> , 1996, 83, 235-239.	1.1	26
190	Most of the Response Elicited against <i>Wolbachia</i> Surface Protein in Filarial Nematode Infection Is Due to the Infective Larval Stage. <i>Journal of Infectious Diseases</i> , 2004, 189, 120-127.	4.0	26
191	Functional genomics for parasitic nematodes and platyhelminths. <i>Trends in Parasitology</i> , 2004, 20, 178-184.	3.3	26
192	Fine Mapping of the Pond Snail Left-Right Asymmetry (Chirality) Locus Using RAD-Seq and Fibre-FISH. <i>PLoS ONE</i> , 2013, 8, e71067.	2.5	26
193	Rapid parallel adaptation despite gene flow in silent crickets. <i>Nature Communications</i> , 2021, 12, 50.	12.8	26
194	Specific serodiagnosis of visceral leishmaniasis using a <i>Leishmania donovani</i> antigen identified by expression cloning. <i>Molecular and Biochemical Parasitology</i> , 1988, 30, 259-270.	1.1	25
195	Characterisation of the two most abundant genes in the <i>Haemonchus contortus</i> expressed sequence tag dataset. <i>International Journal for Parasitology</i> , 2005, 35, 513-522.	3.1	25
196	Para-allopatry in hybridizing fire-bellied toads ( <i>Bombina orientalis</i> and <i>B. variegata</i> ): Inference from transcriptome-wide coalescence analyses. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1803-1818.	2.3	25
197	Molecular palaeontology illuminates the evolution of ecdysozoan vision. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, .	2.6	25
198	Tardigrades. <i>Current Biology</i> , 2002, 12, R475.	3.9	24

#	ARTICLE	IF	CITATIONS
199	Animal roots and shoots. <i>Nature</i> , 2005, 434, 1076-1077.	27.8	24
200	Reminder to deposit DNA sequences. <i>Science</i> , 2016, 352, 780-780.	12.6	24
201	Males as somatic investment in a parthenogenetic nematode. <i>Science</i> , 2019, 363, 1210-1213.	12.6	24
202	Stage-specific Proteomes from <i>Onchocerca ochengi</i> , Sister Species of the Human River Blindness Parasite, Uncover Adaptations to a Nodular Lifestyle. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2554-2575.	3.8	23
203	Transcriptional host-virus interaction of <i>Emiliana huxleyi</i> (Haptophyceae) and EhV-86 deduced from combined analysis of expressed sequence tags and microarrays. <i>European Journal of Phycology</i> , 2010, 45, 1-12.	2.0	22
204	Genomics and transcriptomics across the diversity of the Nematoda. <i>Parasite Immunology</i> , 2012, 34, 108-120.	1.5	22
205	A metagenetic approach to determine the diversity and distribution of cyst nematodes at the level of the country, the field and the individual. <i>Molecular Ecology</i> , 2015, 24, 5842-5851.	3.9	22
206	Sex- and Gamete-Specific Patterns of X Chromosome Segregation in a Trioecious Nematode. <i>Current Biology</i> , 2018, 28, 93-99.e3.	3.9	22
207	High genetic diversity in the <i>Dirofilaria repens</i> species complex revealed by mitochondrial genomes of feline microfilaria samples from Narathiwat, Thailand. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 389-399.	3.0	22
208	The filarial genome network. <i>Parasitology Today</i> , 1995, 11, 441-442.	3.0	21
209	The earthworm Expressed Sequence Tag project. <i>Pedobiologia</i> , 2003, 47, 447-451.	1.2	21
210	<i>Daphnia magna</i> microRNAs respond to nutritional stress and ageing but are not transgenerational. <i>Molecular Ecology</i> , 2018, 27, 1402-1412.	3.9	21
211	Genome-wide methylation is modified by caloric restriction in <i>Daphnia magna</i> . <i>BMC Genomics</i> , 2019, 20, 197.	2.8	21
212	Dissection of Ramularia Leaf Spot Disease by Integrated Analysis of Barley and Ramularia collo-cygni Transcriptome Responses. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 176-193.	2.6	21
213	The Transcriptomic Basis of Oviposition Behaviour in the Parasitoid Wasp <i>Nasonia vitripennis</i> . <i>PLoS ONE</i> , 2013, 8, e68608.	2.5	21
214	Phylogeny of <i>Bursaphelenchus</i> species derived from analysis of ribosomal internal transcribed spacer DNA sequences. <i>Nematology</i> , 1999, 1, 539-548.	0.6	20
215	An expressed sequence tag survey of gene expression in the pond snail <i>Lymnaea stagnalis</i> , an intermediate vector of <i>Fasciola hepatica</i> . <i>Parasitology</i> , 2005, 130, 539-552.	1.5	20
216	The CCAP KnowledgeBase: linking protistan and cyanobacterial biological resources with taxonomic and molecular data. <i>Systematics and Biodiversity</i> , 2013, 11, 407-413.	1.2	20

#	ARTICLE	IF	CITATIONS
217	The small subunit ribosomal RNA sequence of <i>Strongyloides stercoralis</i> . <i>International Journal for Parasitology</i> , 2000, 30, 939-941.	3.1	19
218	The New Subfamily of Cathepsin-Z-like Protease Genes Includes Tc-cpz-1, a Cysteine Protease Gene Expressed in <i>Toxocara canis</i> Adults and Infective Stage Larvae. <i>Experimental Parasitology</i> , 2000, 94, 201-207.	1.2	19
219	Construction of bacterial artificial chromosome libraries from the parasitic nematode <i>Brugia malayi</i> and physical mapping of the genome of its <i>Wolbachia</i> endosymbiont. <i>International Journal for Parasitology</i> , 2004, 34, 733-746.	3.1	19
220	The Aquatic Symbiosis Genomics Project: probing the evolution of symbiosis across the tree of life. <i>Wellcome Open Research</i> , 0, 6, 254.	1.8	19
221	Africa: sequence 100,000 species to safeguard biodiversity. <i>Nature</i> , 2022, 603, 388-392.	27.8	19
222	Differential display of genes expressed in the filarial nematode <i>Litomosoides sigmodontis</i> reveals a putative phosphate permease up-regulated after depletion of <i>Wolbachia</i> endobacteria. <i>International Journal of Medical Microbiology</i> , 2006, 296, 287-299.	3.6	18
223	Toward Universal Forward Genetics: Using a Draft Genome Sequence of the Nematode <i>Oscheius tipulae</i> To Identify Mutations Affecting Vulva Development. <i>Genetics</i> , 2017, 206, 1747-1761.	2.9	18
224	Improving the annotation of the <i>Heterorhabditis bacteriophora</i> genome. <i>GigaScience</i> , 2018, 7, .	6.4	18
225	Developing EPIC markers for chalcidoid Hymenoptera from EST and genomic data. <i>Molecular Ecology Resources</i> , 2011, 11, 521-529.	4.8	17
226	MolluscDB: a genome and transcriptome database for molluscs. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200157.	4.0	17
227	Cuticular proteins of <i>Brugia</i> filarial parasites. <i>Acta Tropica</i> , 1990, 47, 373-380.	2.0	16
228	The genome sequence of the Norway rat, <i>Rattus norvegicus</i> Berkenhout 1769. <i>Wellcome Open Research</i> , 2021, 6, 118.	1.8	16
229	ReproPhylo: An Environment for Reproducible Phylogenomics. <i>PLoS Computational Biology</i> , 2015, 11, e1004447.	3.2	16
230	Isolation, characterization and immunolocalization of a globin-like antigen from <i>Ostertagia ostertagi</i> adults. <i>Parasitology</i> , 1996, 113, 63-69.	1.5	15
231	Internet resources for the parasite genome projects. <i>Trends in Genetics</i> , 1997, 13, 40-41.	6.7	15
232	Two worms are better than one. <i>Nature</i> , 2003, 426, 395-396.	27.8	15
233	The genome sequence of the brown trout, <i>Salmo trutta</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 2021, 6, 108.	1.8	15
234	Chemiluminescent Detection of Sequential DNA Hybridizations to High-Density, Filter-Arrayed cDNA Libraries: A Subtraction Method for Novel Gene Discovery. <i>BioTechniques</i> , 1999, 27, 146-152.	1.8	14

#	ARTICLE	IF	CITATIONS
235	Sum of the arthropod parts. <i>Nature</i> , 2001, 413, 121-122.	27.8	14
236	The Nematode Story: Hox Gene Loss and Rapid Evolution. <i>Advances in Experimental Medicine and Biology</i> , 2010, 689, 101-110.	1.6	14
237	The worm in the world and the world in the worm. <i>BMC Biology</i> , 2012, 10, 57.	3.8	14
238	Annotated mitochondrial genome with Nanopore R9 signal for <i>Nippostrongylus brasiliensis</i> . <i>F1000Research</i> , 2017, 6, 56.	1.6	14
239	GenomeHubs: simple containerized setup of a custom Ensembl database and web server for any species. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	13
240	Launching the Tree of Life Gateway. <i>Wellcome Open Research</i> , 2021, 6, 125.	1.8	13
241	Sequencing and analysis of a 63 kb bacterial artificial chromosome insert from the <i>Wolbachia</i> endosymbiont of the human filarial parasite <i>Brugia malayi</i> . <i>International Journal for Parasitology</i> , 2002, 32, 159-166.	3.1	12
242	RADSeq: next-generation population genetics. <i>Briefings in Functional Genomics</i> , 2011, 10, 108-108.	2.7	12
243	Genome-enabled discovery of candidate virulence loci in <i>Striga hermonthica</i> , a devastating parasite of African cereal crops. <i>New Phytologist</i> , 2022, 236, 622-638.	7.3	12
244	Protein motifs in filarial chitinases. <i>Parasitology Today</i> , 1996, 12, 42.	3.0	11
245	Reports from the Cutting Edge of Parasitic Genome Analysis. <i>Parasitology Today</i> , 1999, 15, 430-431.	3.0	11
246	Expressed Sequence Tags: Analysis and Annotation. <i>Nature</i> , 2004, 270, 093-126.		11
247	Oviposition but Not Sex Allocation Is Associated with Transcriptomic Changes in Females of the Parasitoid Wasp <i>Nasonia vitripennis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2885-2892.	1.8	11
248	iPhy: an integrated phylogenetic workbench for supermatrix analyses. <i>BMC Bioinformatics</i> , 2011, 12, 30.	2.6	10
249	Building genomic infrastructure: Sequencing platinum-standard reference-quality genomes of all cetacean species. <i>Marine Mammal Science</i> , 2020, 36, 1356-1366.	1.8	10
250	Hybridization to High-Density Filter Arrays of a <i>Brugia malayi</i> BAC Library with Biotinylated Oligonucleotides and PCR Products. <i>BioTechniques</i> , 2001, 30, 1216-1224.	1.8	8
251	Velvet worms. <i>Current Biology</i> , 2011, 21, R238-R240.	3.9	8
252	afterParty: turning raw transcriptomes into permanent resources. <i>BMC Bioinformatics</i> , 2013, 14, 301.	2.6	8

#	ARTICLE	IF	CITATIONS
253	Badgerâ€™an accessible genome exploration environment. <i>Bioinformatics</i> , 2013, 29, 2788-2789.	4.1	8
254	The transcriptome of the invasive eel swimbladder nematode parasite <i>Anguillicola crassus</i> . <i>BMC Genomics</i> , 2013, 14, 87.	2.8	8
255	The genome sequence of the bootlace worm, <i>Lineus longissimus</i> (Gunnerus, 1770). <i>Wellcome Open Research</i> , 2021, 6, 272.	1.8	8
256	Transcriptome analyses of <i>Anguillicola crassus</i> from native and novel hosts. <i>PeerJ</i> , 2014, 2, e684.	2.0	7
257	A white paper on nematode comparative genomics. <i>Journal of Nematology</i> , 2005, 37, 408-16.	0.9	7
258	Genome sequencing: time to widen our horizons. <i>Briefings in Functional Genomics &amp; Proteomics</i> , 2002, 1, 7-9.	3.8	6
259	The Evolution of Tyrosine-Recombinase Elements in Nematoda. <i>PLoS ONE</i> , 2014, 9, e106630.	2.5	6
260	The genome sequence of the Eurasian river otter, <i>Lutra lutra</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 2020, 5, 33.	1.8	6
261	Regulated use of an alternative spliced leader exon in the plant parasitic nematode <i>Meloidogyne javanica</i> 1Note: Nucleotide sequences reported in this paper have been deposited in Genbank with accession numbers U78985â€™U79007.1. <i>Molecular and Biochemical Parasitology</i> , 1997, 86, 107-110.	1.1	5
262	TaxMan: a taxonomic database manager. <i>BMC Bioinformatics</i> , 2006, 7, 536.	2.6	5
263	Coexist, Cooperate and Thrive: <i>Wolbachia</i> as Long-Term Symbionts of Filarial Nematodes. , 2007, 5, 66-76.		5
264	Association of the Matrix Attachment Region Recognition Signature with coding regions in <i>Caenorhabditis elegans</i> . <i>BMC Genomics</i> , 2007, 8, 418.	2.8	5
265	Horizontal Gene Transfer in Metazoa: Examples and Methods. , 2019, , 203-226.		5
266	Formin, an opinion. <i>Development (Cambridge)</i> , 2020, 147, .	2.5	5
267	Obtaining Accurate Translations from Expressed Sequence Tags. <i>Methods in Molecular Biology</i> , 2009, 533, 221-239.	0.9	5
268	Characterization of a <i>Leishmania donovani</i> antigen similar to heat shock protein 70. <i>Biochemical Society Transactions</i> , 1989, 17, 168-169.	3.4	4
269	Molecular Helminthology Moves Forward. <i>Parasitology Today</i> , 2000, 16, 5-6.	3.0	4
270	The bacterial catalase from filarial DNA preparations derives from common pseudomonad contaminants and not from <i>Wolbachia</i> endosymbionts. <i>Parasitology Research</i> , 2004, 94, 141-6.	1.6	4



#	ARTICLE	IF	CITATIONS
271	The genome sequence of the ringlet, <i>Aphantopus hyperantus</i> Linnaeus 1758. Wellcome Open Research, 0, 6, 165.	1.8	4
272	The genome sequence of the European turtle dove, <i>Streptopelia turtur</i> Linnaeus 1758. Wellcome Open Research, 0, 6, 191.	1.8	4
273	The genome sequence of the eastern grey squirrel, <i>Sciurus carolinensis</i> Gmelin, 1788. Wellcome Open Research, 2020, 5, 27.	1.8	4
274	Development: The Maternalâ€“Zygotic Transition Revisited. <i>Current Biology</i> , 2014, 24, R72-R75.	3.9	3
275	The genome sequence of the European golden eagle, <i>Aquila chrysaetos chrysaetos</i> Linnaeus 1758. Wellcome Open Research, 2021, 6, 112.	1.8	3
276	EST Processing: From Trace to Sequence. <i>Methods in Molecular Biology</i> , 2009, 533, 189-220.	0.9	3
277	The genome sequence of the Eurasian red squirrel, <i>Sciurus vulgaris</i> Linnaeus 1758. Wellcome Open Research, 2020, 5, 18.	1.8	3
278	Rapid characterization of recombinant $\lambda$ gt11 clones expressing parasite antigens. <i>Parasitology Today</i> , 1987, 3, 315-317.	3.0	2
279	The genome sequence of the common pipistrelle, <i>Pipistrellus pipistrellus</i> Schreber 1774. Wellcome Open Research, 0, 6, 117.	1.8	2
280	The genome sequence of the European robin, <i>Erithacus rubecula</i> Linnaeus 1758. Wellcome Open Research, 0, 6, 172.	1.8	2
281	A dense linkage map for a large repetitive genome: discovery of the sex-determining region in hybridizing fire-bellied toads ( <i>Bombina bombina</i> and <i>Bombina variegata</i> ). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	2
282	Patenting of genes. <i>Nature</i> , 1992, 355, 104-104.	27.8	1
283	The genome sequence of the European water vole, <i>Arvicola amphibius</i> Linnaeus 1758. Wellcome Open Research, 0, 6, 162.	1.8	1
284	Look! The worm wiggles and the mouse sniffs. <i>Trends in Genetics</i> , 1998, 14, 125.	6.7	0
285	Bioinformatics for Geneticists. Edited by M. R. Barnes and I. C. Grey. John Wiley and Sons, Chichester, UK. 2003. 350 pages. ISBN 0 470 84394 2. Price Â£45.00 (paperback). ISBN 0 470 84393 4. Price Â£90.00 (hardback).. <i>Genetical Research</i> , 2003, 82, 223-224.	0.9	0
286	Parasite genomics. , 2003, , 3-l.		0
287	Exploring Parasite Gene Space. <i>BMC Bioinformatics</i> , 2005, 6, P27.	2.6	0
288	Molecular helminthology in the Rockies. Keystone Symposium on Molecular Helminthology, Copper Mountain, Colorado, USA, 9-13 April 2005. <i>Genome Biology</i> , 2005, 6, 329.	9.6	0

#	ARTICLE	IF	CITATIONS
289	Phylogenomics: A Primer. By Rob DeSalle and Jeffrey A. Rosenfeld. New York: Garland Science (Taylor & Johnson) 2013, 88, 352-352.	1.0784314	14
290	Data Analysis in Molecular Biology and Evolution. Xuhua Xia. Quarterly Review of Biology, 2001, 76, 344-344.	0.1	0
291	Genomic dissection of an extended phenotype: Oak galling by a cynipid gall wasp. , 2019, 15, e1008398.		0
292	Genomic dissection of an extended phenotype: Oak galling by a cynipid gall wasp. , 2019, 15, e1008398.		0
293	Genomic dissection of an extended phenotype: Oak galling by a cynipid gall wasp. , 2019, 15, e1008398.		0