

Neil Hall

List of Publications by Year in descending order

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Version: 2024-02-01

152
papers

25,103
citations

20817

60
h-index

7518

151
g-index

158
all docs

158
docs citations

158
times ranked

28752
citing authors

#	ARTICLE	IF	CITATIONS
1	COVID-19 adaptive evolution during the pandemic – Implications of new SARS-CoV-2 variants on public health policies. <i>Virulence</i> , 2021, 12, 2013-2016.	4.4	7
2	Inter-kingdom relationships in Crohn’s disease explored using a multi-omics approach. <i>Gut Microbes</i> , 2021, 13, 1930871.	9.8	16
3	COVID-19 evolution during the pandemic – Implications of new SARS-CoV-2 variants on disease control and public health policies. <i>Virulence</i> , 2021, 12, 507-508.	4.4	142
4	The <i>Mastigamoeba balamuthi</i> Genome and the Nature of the Free-Living Ancestor of <i>Entamoeba</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 2240-2259.	8.9	14
5	Taxon-Specific Proteins of the Pathogenic <i>Entamoeba</i> Species <i>E. histolytica</i> and <i>E. nuttalli</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 641472.	3.9	9
6	Dissecting the molecular diversity and commonality of bovine and human treponemes identifies key survival and adhesion mechanisms. <i>PLoS Pathogens</i> , 2021, 17, e1009464.	4.7	7
7	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. <i>PeerJ</i> , 2021, 9, e10941.	2.0	79
8	Expanded genome-wide comparisons give novel insights into population structure and genetic heterogeneity of <i>Leishmania tropica</i> complex. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008684.	3.0	14
9	Netazepide Inhibits Expression of Pappalysin 2 in Type 1 Gastric Neuroendocrine Tumors. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2020, 10, 113-132.	4.5	8
10	Evolution of <i>Salmonella enterica</i> serotype Typhimurium driven by anthropogenic selection and niche adaptation. <i>PLoS Genetics</i> , 2020, 16, e1008850.	3.5	48
11	Increasing prevalence of a fluoroquinolone resistance mutation amongst <i>Campylobacter jejuni</i> isolates from four human infectious intestinal disease studies in the United Kingdom. <i>PLoS ONE</i> , 2020, 15, e0227535.	2.5	9
12	<i>Salmonella</i> identified in pigs in Kenya and Malawi reveals the potential for zoonotic transmission in emerging pork markets. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008796.	3.0	17
13	The diversity, evolution and ecology of <i>Salmonella</i> in venomous snakes. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007169.	3.0	16
14	DNA extraction and amplicon production strategies deeply influence the outcome of gut microbiome studies. <i>Scientific Reports</i> , 2019, 9, 9328.	3.3	51
15	Single cell ecology. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20190076.	4.0	11
16	Molecular evolution of cytochrome C oxidase-I protein of insects living in Saudi Arabia. <i>PLoS ONE</i> , 2019, 14, e0224336.	2.5	9
17	Multilocus Analysis Resolves the European Finch Epidemic Strain of <i>Trichomonas gallinae</i> and Suggests Introgression from Divergent <i>Trichomonads</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 2391-2402.	2.5	17
18	Genetic Diversity and Gene Family Expansions in Members of the Genus <i>Entamoeba</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 688-705.	2.5	22

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19	Analysis of the recombination landscape of hexaploid bread wheat reveals genes controlling recombination and gene conversion frequency. <i>Genome Biology</i> , 2019, 20, 69.	8.8	79
20	Gene expression profiling to elucidate the pharmacological and toxicological effects of <i>Ricinus communis</i> L. leaf extract in mammalian cells. <i>Biotechnology and Biotechnological Equipment</i> , 2019, 33, 397-407.	1.3	6
21	A New PCR-Based Species Genotyping Differentiation Approach in <i>Entamoeba</i> . <i>Biosciences, Biotechnology Research Asia</i> , 2019, 16, 491-508.	0.5	0
22	Genomics of habitat choice and adaptive evolution in a deep-sea fish. <i>Nature Ecology and Evolution</i> , 2018, 2, 680-687.	7.8	41
23	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
24	A modified sequence capture approach allowing standard and methylation analyses of the same enriched genomic DNA sample. <i>BMC Genomics</i> , 2018, 19, 250.	2.8	5
25	Comparative genomic analysis of the "pseudofungus" <i>Hyphochytrium catenoides</i> . <i>Open Biology</i> , 2018, 8, 170184.	3.6	31
26	The Structure of a Conserved Telomeric Region Associated with Variant Antigen Loci in the Blood Parasite <i>Trypanosoma congolense</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 2458-2473.	2.5	19
27	Hidden variation in polyploid wheat drives local adaptation. <i>Genome Research</i> , 2018, 28, 1319-1332.	5.5	41
28	Towards better models and mechanistic biomarkers for drug-induced gastrointestinal injury. , 2017, 172, 181-194.		19
29	Transcriptomic and metabolic responses of <i>Calotropis procera</i> to salt and drought stress. <i>BMC Plant Biology</i> , 2017, 17, 231.	3.6	30
30	Identification of candidate protective variants for common diseases and evaluation of their protective potential. <i>BMC Genomics</i> , 2017, 18, 575.	2.8	15
31	Transcriptomic analysis of salt stress responsive genes in <i>Rhazya stricta</i> . <i>PLoS ONE</i> , 2017, 12, e0177589.	2.5	27
32	SMRT Gate: A method for validation of synthetic constructs on Pacific Biosciences sequencing platforms. <i>BioTechniques</i> , 2017, 63, 13-20.	1.8	6
33	Comparison of the human gastric microbiota in hypochlorhydric states arising as a result of <i>Helicobacter pylori</i> -induced atrophic gastritis, autoimmune atrophic gastritis and proton pump inhibitor use. <i>PLoS Pathogens</i> , 2017, 13, e1006653.	4.7	156
34	Bacterial sensing underlies artificial sweetener-induced growth of gut <i>actobacillus</i> . <i>Environmental Microbiology</i> , 2016, 18, 2159-2171.	3.8	27
35	Analysis of transcriptional response to heat stress in <i>Rhazya stricta</i> . <i>BMC Plant Biology</i> , 2016, 16, 252.	3.6	39
36	GeneMill: A 21st century platform for innovation. <i>Biochemical Society Transactions</i> , 2016, 44, 681-683.	3.4	7

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37	Mapping by sequencing in complex polyploid genomes using genic sequence capture: a case study to map yellow rust resistance in hexaploid wheat. <i>Plant Journal</i> , 2016, 87, 403-419.	5.7	47
38	Revised Genome Sequence of the Purple Photosynthetic Bacterium <i>Blastochloris viridis</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	7
39	The industrial melanism mutation in British peppered moths is a transposable element. <i>Nature</i> , 2016, 534, 102-105.	27.8	386
40	Transcriptome sequencing of human breast cancer reveals aberrant intronic transcription in amplicons and dysregulation of alternative splicing with major therapeutic implications. <i>International Journal of Oncology</i> , 2016, 48, 130-144.	3.3	7
41	Illumina error profiles: resolving fine-scale variation in metagenomic sequencing data. <i>BMC Bioinformatics</i> , 2016, 17, 125.	2.6	303
42	A comprehensive benchmarking study of protocols and sequencing platforms for 16S rRNA community profiling. <i>BMC Genomics</i> , 2016, 17, 55.	2.8	387
43	Characterising the Canine Oral Microbiome by Direct Sequencing of Reverse-Transcribed rRNA Molecules. <i>PLoS ONE</i> , 2016, 11, e0157046.	2.5	38
44	High Throughput Sequencing of <i>Entamoeba</i> 27nt Small RNA Population Reveals Role in Permanent Gene Silencing But No Effect on Regulating Gene Expression Changes during Stage Conversion, Oxidative, or Heat Shock Stress. <i>PLoS ONE</i> , 2015, 10, e0134481.	2.5	12
45	Insight into biases and sequencing errors for amplicon sequencing with the Illumina MiSeq platform. <i>Nucleic Acids Research</i> , 2015, 43, e37-e37.	14.5	626
46	A genome-wide survey of DNA methylation in hexaploid wheat. <i>Genome Biology</i> , 2015, 16, 273.	8.8	77
47	Draft Genome Sequence of <i>Bacillus</i> Species from the Rhizosphere of the Desert Plant <i>Rhazya stricta</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	7
48	Environmental metabarcoding reveals heterogeneous drivers of microbial eukaryote diversity in contrasting estuarine ecosystems. <i>ISME Journal</i> , 2015, 9, 1208-1221.	9.8	120
49	Editorial overview: Genomics: The era of genomically-enabled microbiology. <i>Current Opinion in Microbiology</i> , 2015, 23, ix-x.	5.1	0
50	Sexual reproduction and genetic exchange in parasitic protists. <i>Parasitology</i> , 2015, 142, S120-S127.	1.5	61
51	Complete Genome Sequence of <i>Leptospira interrogans</i> Serovar Bratislava, Strain PigK151. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
52	A haplotype map of allohexaploid wheat reveals distinct patterns of selection on homoeologous genomes. <i>Genome Biology</i> , 2015, 16, 48.	8.8	216
53	A simple procedure for directly obtaining haplotype sequences of diploid genomes. <i>BMC Genomics</i> , 2015, 16, 642.	2.8	2
54	Genomic changes during evolution of animal parasitism in eukaryotes. <i>Current Opinion in Genetics and Development</i> , 2015, 35, 86-92.	3.3	6

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55	Novel Host-Related Virulence Factors Are Encoded by Squirrelpox Virus, the Main Causative Agent of Epidemic Disease in Red Squirrels in the UK. PLoS ONE, 2014, 9, e96439.	2.5	24
56	Using genic sequence capture in combination with a syntenic pseudo genome to map a deletion mutant in a wheat species. Plant Journal, 2014, 80, 895-904.	5.7	30
57	Dietary supplementation with lactose or artificial sweetener enhances swine gut <i>Lactobacillus</i> population abundance. British Journal of Nutrition, 2014, 111, S30-S35.	2.3	77
58	The evolutionary dynamics of variant antigen genes in Babesia reveal a history of genomic innovation underlying host-parasite interaction. Nucleic Acids Research, 2014, 42, 7113-7131.	14.5	90
59	Population genomics of the killer whale indicates ecotype evolution in sympatry involving both selection and drift. Molecular Ecology, 2014, 23, 5179-5192.	3.9	48
60	Colonic mucosa-associated diffusely adherent <i>afaC+</i> Escherichia coli expressing <i>lpfA</i> and <i>pks</i> are increased in inflammatory bowel disease and colon cancer. Gut, 2014, 63, 761-770.	12.1	203
61	Elucidating variations in the nucleotide sequence of Ebola virus associated with increasing pathogenicity. Genome Biology, 2014, 15, 540.	8.8	44
62	Genome Sequence of the Tsetse Fly (<i>Glossina morsitans</i>): Vector of African Trypanosomiasis. Science, 2014, 344, 380-386.	12.6	254
63	It's only human. Genome Biology, 2014, 15, 104.	9.6	4
64	The revolution of whole genome sequencing to study parasites. Molecular and Biochemical Parasitology, 2014, 195, 77-81.	1.1	19
65	The Kardashian index: a measure of discrepant social media profile for scientists. Genome Biology, 2014, 15, 424.	8.8	145
66	Long non-coding RNAs and enhancer RNAs regulate the lipopolysaccharide-induced inflammatory response in human monocytes. Nature Communications, 2014, 5, 3979.	12.8	281
67	Small RNA pyrosequencing in the protozoan parasite Entamoeba histolytica reveals strain-specific small RNAs that target virulence genes. BMC Genomics, 2013, 14, 53.	2.8	27
68	The genome and transcriptome of the enteric parasite Entamoeba invadens, a model for encystation. Genome Biology, 2013, 14, R77.	9.6	111
69	After the gold rush. Genome Biology, 2013, 14, 115.	9.6	26
70	Whole-Genome Sequencing of Trypanosoma brucei Reveals Introgression between Subspecies That Is Associated with Virulence. MBio, 2013, 4, .	4.1	42
71	Genomic Characterisation of Invasive Non-Typhoidal Salmonella enterica Subspecies enterica Serovar Bovismorbificans Isolates from Malawi. PLoS Neglected Tropical Diseases, 2013, 7, e2557.	3.0	24
72	Exploring the Diversity of Arcobacter butzleri from Cattle in the UK Using MLST and Whole Genome Sequencing. PLoS ONE, 2013, 8, e55240.	2.5	43

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73	The Genome of the Obligate Intracellular Parasite <i>Trachipleistophora hominis</i> : New Insights into Microsporidian Genome Dynamics and Reductive Evolution. <i>PLoS Pathogens</i> , 2012, 8, e1002979.	4.7	127
74	Genomic diversity of the human intestinal parasite <i>Entamoeba histolytica</i> . <i>Genome Biology</i> , 2012, 13, R38.	9.6	39
75	Why science and synchronized swimming should not be Olympic sports. <i>Genome Biology</i> , 2012, 13, 171.	8.8	1
76	Analysis of the bread wheat genome using whole-genome shotgun sequencing. <i>Nature</i> , 2012, 491, 705-710.	27.8	983
77	Application of next-generation sequencing technologies in virology. <i>Journal of General Virology</i> , 2012, 93, 1853-1868.	2.9	241
78	From a Single Whole Exome Read to Notions of Clinical Screening: Primary Ciliary Dyskinesia and <i>RSPH9</i> p.Lys268del in the Arabian Peninsula. <i>Annals of Human Genetics</i> , 2012, 76, 211-220.	0.8	24
79	A Multilocus Sequence Typing System (MLST) reveals a high level of diversity and a genetic component to <i>Entamoeba histolytica</i> virulence. <i>BMC Microbiology</i> , 2012, 12, 151.	3.3	47
80	Genomic insights into the other malaria. <i>Nature Genetics</i> , 2012, 44, 962-963.	21.4	10
81	Host-Parasite interactions in <i>Entamoeba histolytica</i> and <i>Entamoeba dispar</i> : what have we learned from their genomes?. <i>Parasite Immunology</i> , 2012, 34, 90-99.	1.5	56
82	Targeted resequencing of the allohexaploid wheat exome. <i>Plant Biotechnology Journal</i> , 2012, 10, 733-742.	8.3	133
83	Full genome re-sequencing reveals a novel circadian clock mutation in <i>Arabidopsis</i> . <i>Genome Biology</i> , 2011, 12, R28.	9.6	69
84	Evolutionary genomics of <i>Entamoeba</i> . <i>Research in Microbiology</i> , 2011, 162, 637-645.	2.1	33
85	Towards the Human Colorectal Cancer Microbiome. <i>PLoS ONE</i> , 2011, 6, e20447.	2.5	470
86	Genomic variations define divergence of water/wildlife-associated <i>Campylobacter jejuni</i> niche specialists from common clonal complexes. <i>Environmental Microbiology</i> , 2011, 13, 1549-1560.	3.8	52
87	Transcript-specific, single-nucleotide polymorphism discovery and linkage analysis in hexaploid bread wheat (<i>Triticum aestivum</i> L.). <i>Plant Biotechnology Journal</i> , 2011, 9, 1086-1099.	8.3	220
88	Horizontal gene transfer facilitated the evolution of plant parasitic mechanisms in the oomycetes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15258-15263.	7.1	225
89	Genetic Characterization Indicates that a Specific Subpopulation of <i>Pseudomonas aeruginosa</i> Is Associated with Keratitis Infections. <i>Journal of Clinical Microbiology</i> , 2011, 49, 993-1003.	3.9	81
90	Identification of a Mutation Associated with Fatal Foal Immunodeficiency Syndrome in the Fell and Dales Pony. <i>PLoS Genetics</i> , 2011, 7, e1002133.	3.5	34

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91	Evidence of Gene Conversion in Genes Encoding the Gal/GalNac Lectin Complex of <i>Entamoeba</i> . <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1209.	3.0	27
92	A De Novo Expression Profiling of <i>Anopheles funestus</i> , Malaria Vector in Africa, Using 454 Pyrosequencing. <i>PLoS ONE</i> , 2011, 6, e17418.	2.5	47
93	<i>Arabidopsis thaliana</i> Leaf Form Evolved via Loss of KNOX Expression in Leaves in Association with a Selective Sweep. <i>Current Biology</i> , 2010, 20, 2223-2228.	3.9	88
94	Antagonistic coevolution accelerates molecular evolution. <i>Nature</i> , 2010, 464, 275-278.	27.8	492
95	GeMInA, Genomic Metadata for Infectious Agents, a geospatial surveillance pathogen database. <i>Nucleic Acids Research</i> , 2010, 38, D754-D764.	14.5	25
96	Comparative Genomics and Transduction Potential of <i>Enterococcus faecalis</i> Temperate Bacteriophages. <i>Journal of Bacteriology</i> , 2010, 192, 1122-1130.	2.2	71
97	New Assembly, Reannotation and Analysis of the <i>Entamoeba histolytica</i> Genome Reveal New Genomic Features and Protein Content Information. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e716.	3.0	97
98	A Comprehensive Genetic Analysis of Candidate Genes Regulating Response to <i>Trypanosoma congolense</i> Infection in Mice. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e880.	3.0	14
99	Accurate determination of microbial diversity from 454 pyrosequencing data. <i>Nature Methods</i> , 2009, 6, 639-641.	19.0	895
100	Whole genome sequencing of a natural recombinant <i>Toxoplasma gondii</i> strain reveals chromosome sorting and local allelic variants. <i>Genome Biology</i> , 2009, 10, R53.	9.6	51
101	The genome of the simian and human malaria parasite <i>Plasmodium knowlesi</i> . <i>Nature</i> , 2008, 455, 799-803.	27.8	338
102	Fast forward genetics. <i>Nature Biotechnology</i> , 2008, 26, 1248-1249.	17.5	11
103	Genome wide survey, discovery and evolution of repetitive elements in three <i>Entamoeba</i> species. <i>BMC Genomics</i> , 2008, 9, 595.	2.8	53
104	Patterns of Evolution in the Unique tRNA Gene Arrays of the Genus <i>Entamoeba</i> . <i>Molecular Biology and Evolution</i> , 2007, 25, 187-198.	8.9	62
105	Structure and Content of the <i>Entamoeba histolytica</i> Genome. <i>Advances in Parasitology</i> , 2007, 65, 51-190.	3.2	188
106	Advanced sequencing technologies and their wider impact in microbiology. <i>Journal of Experimental Biology</i> , 2007, 210, 1518-1525.	1.7	309
107	Regulation of Sexual Development of <i>Plasmodium</i> by Translational Repression. <i>Science</i> , 2006, 313, 667-669.	12.6	407
108	Unique organisation of tRNA genes in <i>Entamoeba histolytica</i> . <i>Molecular and Biochemical Parasitology</i> , 2006, 146, 24-29.	1.1	54

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109	Common inheritance of chromosome Ia associated with clonal expansion of <i>Toxoplasma gondii</i> . <i>Genome Research</i> , 2006, 16, 1119-1125.	5.5	51
110	Eukaryotic parasite genome projects. , 2005, , .		0
111	The genome of the protist parasite <i>Entamoeba histolytica</i> . <i>Nature</i> , 2005, 433, 865-868.	27.8	783
112	The genome of the social amoeba <i>Dictyostelium discoideum</i> . <i>Nature</i> , 2005, 435, 43-57.	27.8	1,179
113	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005, 438, 1151-1156.	27.8	1,272
114	The diversity of Rab GTPases in <i>Entamoeba histolytica</i> . <i>Experimental Parasitology</i> , 2005, 110, 244-252.	1.2	120
115	Insights into the <i>P. y. yoelii</i> hepatic stage transcriptome reveal complex transcriptional patterns. <i>Molecular and Biochemical Parasitology</i> , 2005, 142, 184-192.	1.1	14
116	A case for a <i>Glossina</i> genome project. <i>Trends in Parasitology</i> , 2005, 21, 107-111.	3.3	31
117	<i>Entamoeba</i> : still more to be learned from the genome. <i>Trends in Parasitology</i> , 2005, 21, 453.	3.3	12
118	Gene Arrays at <i>Pneumocystis carinii</i> Telomeres. <i>Genetics</i> , 2005, 170, 1589-1600.	2.9	66
119	<i>Plasmodium falciparum</i> Variant Surface Antigen Expression Patterns during Malaria. <i>PLoS Pathogens</i> , 2005, 1, e26.	4.7	158
120	A <i>Plasmodium</i> Whole-Genome Synteny Map: Indels and Synteny Breakpoints as Foci for Species-Specific Genes. <i>PLoS Pathogens</i> , 2005, 1, e44.	4.7	131
121	An ancestral oomycete locus contains late blight avirulence gene <i>Avr3a</i> , encoding a protein that is recognized in the host cytoplasm. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7766-7771.	7.1	414
122	The genetic map and comparative analysis with the physical map of <i>Trypanosoma brucei</i> . <i>Nucleic Acids Research</i> , 2005, 33, 6688-6693.	14.5	56
123	Comparative Genomics of Trypanosomatid Parasitic Protozoa. <i>Science</i> , 2005, 309, 404-409.	12.6	713
124	Genome of the Host-Cell Transforming Parasite <i>Theileria annulata</i> Compared with <i>T. parva</i> . <i>Science</i> , 2005, 309, 131-133.	12.6	285
125	Genome Sequence of <i>Theileria parva</i> , a Bovine Pathogen That Transforms Lymphocytes. <i>Science</i> , 2005, 309, 134-137.	12.6	309
126	Comparative genomics of malaria parasites. <i>Current Opinion in Genetics and Development</i> , 2005, 15, 609-613.	3.3	27

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127	The Genome of the African Trypanosome <i>Trypanosoma brucei</i> . <i>Science</i> , 2005, 309, 416-422.	12.6	1,496
128	A Comprehensive Survey of the Plasmodium Life Cycle by Genomic, Transcriptomic, and Proteomic Analyses. <i>Science</i> , 2005, 307, 82-86.	12.6	743
129	The genome of model malaria parasites, and comparative genomics. <i>Current Issues in Molecular Biology</i> , 2005, 7, 23-37.	2.4	53
130	Comparative Genomics of Transcriptional Control in the Human Malaria Parasite <i>Plasmodium falciparum</i> . <i>Genome Research</i> , 2004, 14, 1548-1554.	5.5	221
131	Evolutionary Pressures on Apicoplast Transit Peptides. <i>Molecular Biology and Evolution</i> , 2004, 21, 2183-2194.	8.9	75
132	A transcriptomic analysis of the phylum Nematoda. <i>Nature Genetics</i> , 2004, 36, 1259-1267.	21.4	239
133	Gene synteny and evolution of genome architecture in trypanosomatids. <i>Molecular and Biochemical Parasitology</i> , 2004, 134, 183-191.	1.1	92
134	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
135	GeneDB: a resource for prokaryotic and eukaryotic organisms. <i>Nucleic Acids Research</i> , 2004, 32, 339D-343.	14.5	199
136	Insight into the genome of <i>Aspergillus fumigatus</i> : analysis of a 922kb region encompassing the nitrate assimilation gene cluster. <i>Fungal Genetics and Biology</i> , 2004, 41, 443-453.	2.1	55
137	Parasite Genome Databases and Web-Based Resources. , 2004, 270, 045-074.		6
138	400,000 nematode ESTs on the Net. <i>Trends in Parasitology</i> , 2003, 19, 283-286.	3.3	61
139	Gene discovery in the <i>Entamoeba invadens</i> genome. <i>Molecular and Biochemical Parasitology</i> , 2003, 129, 23-31.	1.1	54
140	Pilot survey of expressed sequence tags (ESTs) from the asexual blood stages of <i>Plasmodium vivax</i> in human patients. <i>Malaria Journal</i> , 2003, 2, 21.	2.3	7
141	The DNA sequence of chromosome I of an African trypanosome: gene content, chromosome organisation, recombination and polymorphism. <i>Nucleic Acids Research</i> , 2003, 31, 4864-4873.	14.5	56
142	The Intestinal Protozoan Parasite <i>Entamoeba histolytica</i> Contains 20 Cysteine Protease Genes, of Which Only a Small Subset Is Expressed during In Vitro Cultivation. <i>Eukaryotic Cell</i> , 2003, 2, 501-509.	3.4	157
143	The <i>ingi</i> and RIME non-LTR Retrotransposons Are Not Randomly Distributed in the Genome of <i>Trypanosoma brucei</i> . <i>Molecular Biology and Evolution</i> , 2003, 21, 520-528.	8.9	30
144	A New, Expressed Multigene Family Containing a Hot Spot for Insertion of Retroelements Is Associated with Polymorphic Subtelomeric Regions of <i>Trypanosoma brucei</i> . <i>Eukaryotic Cell</i> , 2002, 1, 137-151.	3.4	82

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145	The architecture of variant surface glycoprotein gene expression sites in <i>Trypanosoma brucei</i> . <i>Molecular and Biochemical Parasitology</i> , 2002, 122, 131-140.	1.1	98
146	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
147	Sequence of <i>Plasmodium falciparum</i> chromosomes 1, 3 and 13. <i>Nature</i> , 2002, 419, 527-531.	27.8	156
148	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	27.8	3,881
149	Analysis of the <i>Plasmodium falciparum</i> proteome by high-accuracy mass spectrometry. <i>Nature</i> , 2002, 419, 537-542.	27.8	596
150	Royal Society Discussion Meeting: Utilising the Genome Sequence of Parasitic Protozoa. <i>Comparative and Functional Genomics</i> , 2001, 2, 257-262.	2.0	1
151	Detailed Structure of <i>Pneumocystis carinii</i> Chromosome Ends. <i>Journal of Eukaryotic Microbiology</i> , 2001, 48, 118s-120s.	1.7	5
152	Structure-function analysis of NADPH:nitrate reductase from <i>Aspergillus nidulans</i> : analysis of altered pyridine nucleotide specificity in vivo. <i>Microbiology (United Kingdom)</i> , 2000, 146, 1399-1406.	1.8	11