

Neil Hall

List of Publications by Year in descending order

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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	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	27.8	3,881
2	The Genome of the African Trypanosome <i>Trypanosoma brucei</i> . <i>Science</i> , 2005, 309, 416-422.	12.6	1,496
3	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005, 438, 1151-1156.	27.8	1,272
4	The genome of the social amoeba <i>Dictyostelium discoideum</i> . <i>Nature</i> , 2005, 435, 43-57.	27.8	1,179
5	Analysis of the bread wheat genome using whole-genome shotgun sequencing. <i>Nature</i> , 2012, 491, 705-710.	27.8	983
6	Accurate determination of microbial diversity from 454 pyrosequencing data. <i>Nature Methods</i> , 2009, 6, 639-641.	19.0	895
7	The genome of the protist parasite <i>Entamoeba histolytica</i> . <i>Nature</i> , 2005, 433, 865-868.	27.8	783
8	A Comprehensive Survey of the <i>Plasmodium</i> Life Cycle by Genomic, Transcriptomic, and Proteomic Analyses. <i>Science</i> , 2005, 307, 82-86.	12.6	743
9	Comparative Genomics of Trypanosomatid Parasitic Protozoa. <i>Science</i> , 2005, 309, 404-409.	12.6	713
10	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
11	Analysis of the <i>Plasmodium falciparum</i> proteome by high-accuracy mass spectrometry. <i>Nature</i> , 2002, 419, 537-542.	27.8	596
12	Antagonistic coevolution accelerates molecular evolution. <i>Nature</i> , 2010, 464, 275-278.	27.8	492
13	Towards the Human Colorectal Cancer Microbiome. <i>PLoS ONE</i> , 2011, 6, e20447.	2.5	470
14	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
15	Regulation of Sexual Development of <i>Plasmodium</i> by Translational Repression. <i>Science</i> , 2006, 313, 667-669.	12.6	407
16	A comprehensive benchmarking study of protocols and sequencing platforms for 16S rRNA community profiling. <i>BMC Genomics</i> , 2016, 17, 55.	2.8	387
17	The industrial melanism mutation in British peppered moths is a transposable element. <i>Nature</i> , 2016, 534, 102-105.	27.8	386
18	The genome of the simian and human malaria parasite <i>Plasmodium knowlesi</i> . <i>Nature</i> , 2008, 455, 799-803.	27.8	338

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19	Genome Sequence of <i>Theileria parva</i> , a Bovine Pathogen That Transforms Lymphocytes. <i>Science</i> , 2005, 309, 134-137.	12.6	309
20	Advanced sequencing technologies and their wider impact in microbiology. <i>Journal of Experimental Biology</i> , 2007, 210, 1518-1525.	1.7	309
21	Illumina error profiles: resolving fine-scale variation in metagenomic sequencing data. <i>BMC Bioinformatics</i> , 2016, 17, 125.	2.6	303
22	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
23	Long non-coding RNAs and enhancer RNAs regulate the lipopolysaccharide-induced inflammatory response in human monocytes. <i>Nature Communications</i> , 2014, 5, 3979.	12.8	281
24	Genome Sequence of the Tsetse Fly (<i>Glossina morsitans</i>): Vector of African Trypanosomiasis. <i>Science</i> , 2014, 344, 380-386.	12.6	254
25	Application of next-generation sequencing technologies in virology. <i>Journal of General Virology</i> , 2012, 93, 1853-1868.	2.9	241
26	A transcriptomic analysis of the phylum Nematoda. <i>Nature Genetics</i> , 2004, 36, 1259-1267.	21.4	239
27	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
28	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
29	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
30	A haplotype map of allohexaploid wheat reveals distinct patterns of selection on homoeologous genomes. <i>Genome Biology</i> , 2015, 16, 48.	8.8	216
31	Colonic mucosa-associated diffusely adherent <i>afaC+</i> <i>Escherichia coli</i> expressing <i>lpfA</i> and <i>pks</i> are increased in inflammatory bowel disease and colon cancer. <i>Gut</i> , 2014, 63, 761-770.	12.1	203
32	GeneDB: a resource for prokaryotic and eukaryotic organisms. <i>Nucleic Acids Research</i> , 2004, 32, 339D-343.	14.5	199
33	Structure and Content of the <i>Entamoeba histolytica</i> Genome. <i>Advances in Parasitology</i> , 2007, 65, 51-190.	3.2	188
34	<i>Plasmodium falciparum</i> Variant Surface Antigen Expression Patterns during Malaria. <i>PLoS Pathogens</i> , 2005, 1, e26.	4.7	158
35	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
36	Sequence of <i>Plasmodium falciparum</i> chromosomes 1, 3 and 13. <i>Nature</i> , 2002, 419, 527-531.	27.8	156

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37	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
38	The Kardashian index: a measure of discrepant social media profile for scientists. <i>Genome Biology</i> , 2014, 15, 424.	8.8	145
39	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
40	Targeted resequencing of the allohexaploid wheat exome. <i>Plant Biotechnology Journal</i> , 2012, 10, 733-742.	8.3	133
41	A Plasmodium Whole-Genome Synteny Map: Indels and Synteny Breakpoints as Foci for Species-Specific Genes. <i>PLoS Pathogens</i> , 2005, 1, e44.	4.7	131
42	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
43	The diversity of Rab GTPases in <i>Entamoeba histolytica</i> . <i>Experimental Parasitology</i> , 2005, 110, 244-252.	1.2	120
44	Environmental metabarcoding reveals heterogeneous drivers of microbial eukaryote diversity in contrasting estuarine ecosystems. <i>ISME Journal</i> , 2015, 9, 1208-1221.	9.8	120
45	The genome and transcriptome of the enteric parasite <i>Entamoeba invadens</i> , a model for encystation. <i>Genome Biology</i> , 2013, 14, R77.	9.6	111
46	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
47	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
48	Gene synteny and evolution of genome architecture in trypanosomatids. <i>Molecular and Biochemical Parasitology</i> , 2004, 134, 183-191.	1.1	92
49	The evolutionary dynamics of variant antigen genes in <i>Babesia</i> reveal a history of genomic innovation underlying host-parasite interaction. <i>Nucleic Acids Research</i> , 2014, 42, 7113-7131.	14.5	90
50	<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
51	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
52	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
53	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
54	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

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55	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. <i>PeerJ</i> , 2021, 9, e10941.	2.0	79
56	Dietary supplementation with lactose or artificial sweetener enhances swine gut <i>Lactobacillus</i> population abundance. <i>British Journal of Nutrition</i> , 2014, 111, S30-S35.	2.3	77
57	A genome-wide survey of DNA methylation in hexaploid wheat. <i>Genome Biology</i> , 2015, 16, 273.	8.8	77
58	Evolutionary Pressures on Apicoplast Transit Peptides. <i>Molecular Biology and Evolution</i> , 2004, 21, 2183-2194.	8.9	75
59	Comparative Genomics and Transduction Potential of <i>Enterococcus faecalis</i> Temperate Bacteriophages. <i>Journal of Bacteriology</i> , 2010, 192, 1122-1130.	2.2	71
60	Full genome re-sequencing reveals a novel circadian clock mutation in <i>Arabidopsis</i> . <i>Genome Biology</i> , 2011, 12, R28.	9.6	69
61	Gene Arrays at <i>Pneumocystis carinii</i> Telomeres. <i>Genetics</i> , 2005, 170, 1589-1600.	2.9	66
62	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
63	400,000 nematode ESTs on the Net. <i>Trends in Parasitology</i> , 2003, 19, 283-286.	3.3	61
64	Sexual reproduction and genetic exchange in parasitic protists. <i>Parasitology</i> , 2015, 142, S120-S127.	1.5	61
65	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
66	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
67	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
68	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
69	Gene discovery in the <i>Entamoeba invadens</i> genome. <i>Molecular and Biochemical Parasitology</i> , 2003, 129, 23-31.	1.1	54
70	Unique organisation of tRNA genes in <i>Entamoeba histolytica</i> . <i>Molecular and Biochemical Parasitology</i> , 2006, 146, 24-29.	1.1	54
71	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
72	The genome of model malaria parasites, and comparative genomics. <i>Current Issues in Molecular Biology</i> , 2005, 7, 23-37.	2.4	53

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73	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
74	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
75	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
76	DNA extraction and amplicon production strategies deeply influence the outcome of gut microbiome studies. <i>Scientific Reports</i> , 2019, 9, 9328.	3.3	51
77	Population genomics of the killer whale indicates ecotype evolution in sympatry involving both selection and drift. <i>Molecular Ecology</i> , 2014, 23, 5179-5192.	3.9	48
78	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
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	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
81	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
82	Elucidating variations in the nucleotide sequence of Ebola virus associated with increasing pathogenicity. <i>Genome Biology</i> , 2014, 15, 540.	8.8	44
83	Exploring the Diversity of <i>Arcobacter butzleri</i> from Cattle in the UK Using MLST and Whole Genome Sequencing. <i>PLoS ONE</i> , 2013, 8, e55240.	2.5	43
84	Whole-Genome Sequencing of <i>Trypanosoma brucei</i> Reveals Introgression between Subspecies That Is Associated with Virulence. <i>MBio</i> , 2013, 4, .	4.1	42
85	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
86	Hidden variation in polyploid wheat drives local adaptation. <i>Genome Research</i> , 2018, 28, 1319-1332.	5.5	41
87	Genomic diversity of the human intestinal parasite <i>Entamoeba histolytica</i> . <i>Genome Biology</i> , 2012, 13, R38.	9.6	39
88	Analysis of transcriptional response to heat stress in <i>Rhazya stricta</i> . <i>BMC Plant Biology</i> , 2016, 16, 252.	3.6	39
89	Characterising the Canine Oral Microbiome by Direct Sequencing of Reverse-Transcribed rRNA Molecules. <i>PLoS ONE</i> , 2016, 11, e0157046.	2.5	38
90	Abundant larval transcript-1 and -2 genes from <i>Brugia malayi</i> : diversity of genomic environments but conservation of 5â€² promoter sequences functional in <i>Caenorhabditis elegans</i> . <i>Molecular and Biochemical Parasitology</i> , 2002, 125, 59-71.	1.1	35

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91	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
92	Evolutionary genomics of <i>Entamoeba</i> . <i>Research in Microbiology</i> , 2011, 162, 637-645.	2.1	33
93	A case for a <i>Glossina</i> genome project. <i>Trends in Parasitology</i> , 2005, 21, 107-111.	3.3	31
94	Comparative genomic analysis of the "pseudofungus" <i>Hyphochytrium catenoides</i> . <i>Open Biology</i> , 2018, 8, 170184.	3.6	31
95	The ingi 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
96	Using genic sequence capture in combination with a syntenic pseudo genome to map a deletion mutant in a wheat species. <i>Plant Journal</i> , 2014, 80, 895-904.	5.7	30
97	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
98	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
99	Comparative genomics of malaria parasites. <i>Current Opinion in Genetics and Development</i> , 2005, 15, 609-613.	3.3	27
100	Small RNA pyrosequencing in the protozoan parasite <i>Entamoeba histolytica</i> reveals strain-specific small RNAs that target virulence genes. <i>BMC Genomics</i> , 2013, 14, 53.	2.8	27
101	Bacterial sensing underlies artificial sweetener-induced growth of gut <i>actobacillus</i> . <i>Environmental Microbiology</i> , 2016, 18, 2159-2171.	3.8	27
102	Transcriptomic analysis of salt stress responsive genes in <i>Rhazya stricta</i> . <i>PLoS ONE</i> , 2017, 12, e0177589.	2.5	27
103	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
104	After the gold rush. <i>Genome Biology</i> , 2013, 14, 115.	9.6	26
105	GeMInA, Genomic Metadata for Infectious Agents, a geospatial surveillance pathogen database. <i>Nucleic Acids Research</i> , 2010, 38, D754-D764.	14.5	25
106	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
107	Genomic Characterisation of Invasive Non-Typhoidal <i>Salmonella enterica</i> Subspecies <i>enterica</i> Serovar <i>Bovismorbificans</i> Isolates from Malawi. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2557.	3.0	24
108	Novel Host-Related Virulence Factors Are Encoded by Squirrelpox Virus, the Main Causative Agent of Epidemic Disease in Red Squirrels in the UK. <i>PLoS ONE</i> , 2014, 9, e96439.	2.5	24

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109	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
110	The revolution of whole genome sequencing to study parasites. <i>Molecular and Biochemical Parasitology</i> , 2014, 195, 77-81.	1.1	19
111	Towards better models and mechanistic biomarkers for drug-induced gastrointestinal injury. , 2017, 172, 181-194.		19
112	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
113	Multilocus Analysis Resolves the European Finch Epidemic Strain of <i>Trichomonas gallinae</i> and Suggests Introgression from Divergent Trichomonads. <i>Genome Biology and Evolution</i> , 2019, 11, 2391-2402.	2.5	17
114	Salmonella 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
115	The diversity, evolution and ecology of Salmonella in venomous snakes. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007169.	3.0	16
116	Inter-kingdom relationships in Crohn's disease explored using a multi-omics approach. <i>Gut Microbes</i> , 2021, 13, 1930871.	9.8	16
117	Identification of candidate protective variants for common diseases and evaluation of their protective potential. <i>BMC Genomics</i> , 2017, 18, 575.	2.8	15
118	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
119	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
120	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
121	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
122	<i>Entamoeba</i> : still more to be learned from the genome. <i>Trends in Parasitology</i> , 2005, 21, 453.	3.3	12
123	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
124	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
125	Fast forward genetics. <i>Nature Biotechnology</i> , 2008, 26, 1248-1249.	17.5	11
126	Single cell ecology. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20190076.	4.0	11

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127	Genomic insights into the other malaria. <i>Nature Genetics</i> , 2012, 44, 962-963.	21.4	10
128	Molecular evolution of cytochrome C oxidase-I protein of insects living in Saudi Arabia. <i>PLoS ONE</i> , 2019, 14, e0224336.	2.5	9
129	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
130	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
131	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
132	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
133	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
134	GeneMill: A 21st century platform for innovation. <i>Biochemical Society Transactions</i> , 2016, 44, 681-683.	3.4	7
135	Revised Genome Sequence of the Purple Photosynthetic Bacterium <i>Blastochloris viridis</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	7
136	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
137	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
138	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
139	Parasite Genome Databases and Web-Based Resources. , 2004, 270, 045-074.		6
140	Genomic changes during evolution of animal parasitism in eukaryotes. <i>Current Opinion in Genetics and Development</i> , 2015, 35, 86-92.	3.3	6
141	SMRT Gate: A method for validation of synthetic constructs on Pacific Biosciences sequencing platforms. <i>BioTechniques</i> , 2017, 63, 13-20.	1.8	6
142	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
143	Detailed Structure of <i>Pneumocystis carinii</i> Chromosome Ends. <i>Journal of Eukaryotic Microbiology</i> , 2001, 48, 118s-120s.	1.7	5
144	Complete Genome Sequence of <i>Leptospira interrogans</i> Serovar Bratislava, Strain PigK151. <i>Genome Announcements</i> , 2015, 3, .	0.8	5

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145	A modified sequence capture approach allowing standard and methylation analyses of the same enriched genomic DNA sample. BMC Genomics, 2018, 19, 250.	2.8	5
146	Itâ€™s only human. Genome Biology, 2014, 15, 104.	9.6	4
147	A simple procedure for directly obtaining haplotype sequences of diploid genomes. BMC Genomics, 2015, 16, 642.	2.8	2
148	Royal Society Discussion Meeting: Utilising the Genome Sequence of Parasitic Protozoa. Comparative and Functional Genomics, 2001, 2, 257-262.	2.0	1
149	Why science and synchronized swimming should not be Olympic sports. Genome Biology, 2012, 13, 171.	8.8	1
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