

James A Cotton

List of Publications by Year in descending order

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109
papers

7,879
citations

50244

46
h-index

56687

83
g-index

137
all docs

137
docs citations

137
times ranked

9289
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole genome sequencing of multiple <i>Leishmania donovani</i> clinical isolates provides insights into population structure and mechanisms of drug resistance. <i>Genome Research</i> , 2011, 21, 2143-2156.	2.4	381
2	Genomic Insights into the Origin of Parasitism in the Emerging Plant Pathogen <i>Bursaphelenchus xylophilus</i> . <i>PLoS Pathogens</i> , 2011, 7, e1002219.	2.1	351
3	Genome-wide signatures of convergent evolution in echolocating mammals. <i>Nature</i> , 2013, 502, 228-231.	13.7	321
4	The genome and transcriptome of <i>Haemonchus contortus</i> , a key model parasite for drug and vaccine discovery. <i>Genome Biology</i> , 2013, 14, R88.	13.9	293
5	The Ediacaran emergence of bilaterians: congruence between the genetic and the geological fossil records. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 1435-1443.	1.8	286
6	New approaches for unravelling reassortment pathways. <i>BMC Evolutionary Biology</i> , 2013, 13, 1.	3.2	278
7	Genetic Analysis of the Cytoplasmic Dynein Subunit Families. <i>PLoS Genetics</i> , 2006, 2, e1.	1.5	276
8	Genome Sequence of the Tsetse Fly (<i>Glossina morsitans</i>): Vector of African Trypanosomiasis. <i>Science</i> , 2014, 344, 380-386.	6.0	254
9	The genomic basis of parasitism in the Strongyloides clade of nematodes. <i>Nature Genetics</i> , 2016, 48, 299-307.	9.4	226
10	The genome and life-stage specific transcriptomes of <i>Globodera pallida</i> elucidate key aspects of plant parasitism by a cyst nematode. <i>Genome Biology</i> , 2014, 15, R43.	13.9	212
11	Comparative Genomics of the Apicomplexan Parasites <i>Toxoplasma gondii</i> and <i>Neospora caninum</i> : Coccidia Differing in Host Range and Transmission Strategy. <i>PLoS Pathogens</i> , 2012, 8, e1002567.	2.1	206
12	The evolution of color vision in nocturnal mammals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 8980-8985.	3.3	202
13	Convergent sequence evolution between echolocating bats and dolphins. <i>Current Biology</i> , 2010, 20, R53-R54.	1.8	202
14	Supertrees Disentangle the Chimerical Origin of Eukaryotic Genomes. <i>Molecular Biology and Evolution</i> , 2007, 24, 1752-1760.	3.5	157
15	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.	3.8	156
16	Reduced Efficacy of Praziquantel Against <i>Schistosoma mansoni</i> Is Associated With Multiple Rounds of Mass Drug Administration. <i>Clinical Infectious Diseases</i> , 2016, 63, ciw506.	2.9	150
17	<i>Plasmodium malariae</i> and <i>P. ovale</i> genomes provide insights into malaria parasite evolution. <i>Nature</i> , 2017, 542, 101-104.	13.7	150
18	Evolutionary genomics of epidemic visceral leishmaniasis in the Indian subcontinent. <i>ELife</i> , 2016, 5, .	2.8	147

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19	Genomic Confirmation of Hybridisation and Recent Inbreeding in a Vector-Isolated <i>Leishmania</i> Population. <i>PLoS Genetics</i> , 2014, 10, e1004092.	1.5	142
20	Phylogenomic Analyses Elucidate the Evolutionary Relationships of Bats. <i>Current Biology</i> , 2013, 23, 2262-2267.	1.8	139
21	Whipworm genome and dual-species transcriptome analyses provide molecular insights into an intimate host-parasite interaction. <i>Nature Genetics</i> , 2014, 46, 693-700.	9.4	139
22	The Peculiar Epidemiology of Dracunculiasis in Chad. <i>American Journal of Tropical Medicine and Hygiene</i> , 2014, 90, 61-70.	0.6	131
23	The hearing gene <i>Prestin</i> reunites echolocating bats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 13959-13964.	3.3	116
24	Gene Expression in <i>Leishmania</i> Is Regulated Predominantly by Gene Dosage. <i>MBio</i> , 2017, 8, .	1.8	108
25	The genome of <i>Onchocerca volvulus</i> , agent of river blindness. <i>Nature Microbiology</i> , 2017, 2, 16216.	5.9	107
26	Genomic and transcriptomic variation defines the chromosome-scale assembly of <i>Haemonchus contortus</i> , a model gastrointestinal worm. <i>Communications Biology</i> , 2020, 3, 656.	2.0	91
27	Global genome diversity of the <i>Leishmania donovani</i> complex. <i>ELife</i> , 2020, 9, .	2.8	90
28	The Shape of Supertrees to Come: Tree Shape Related Properties of Fourteen Supertree Methods. <i>Systematic Biology</i> , 2005, 54, 419-431.	2.7	88
29	Parallel signatures of sequence evolution among hearing genes in echolocating mammals: an emerging model of genetic convergence. <i>Heredity</i> , 2012, 108, 480-489.	1.2	86
30	The prokaryotic tree of life: past, present and future?. <i>Trends in Ecology and Evolution</i> , 2008, 23, 276-281.	4.2	82
31	Genomic and Molecular Characterization of Miltefosine Resistance in <i>Leishmania infantum</i> Strains with Either Natural or Acquired Resistance through Experimental Selection of Intracellular Amastigotes. <i>PLoS ONE</i> , 2016, 11, e0154101.	1.1	80
32	Tempo and Mode of Diversification of Lake Tanganyika Cichlid Fishes. <i>PLoS ONE</i> , 2008, 3, e1730.	1.1	78
33	Complete avian malaria parasite genomes reveal features associated with lineage-specific evolution in birds and mammals. <i>Genome Research</i> , 2018, 28, 547-560.	2.4	78
34	Going nuclear: gene family evolution and vertebrate phylogeny reconciled. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2002, 269, 1555-1561.	1.2	76
35	Eukaryotic genes of archaeobacterial origin are more important than the more numerous eubacterial genes, irrespective of function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17252-17255.	3.3	74
36	Whole genome resequencing of the human parasite <i>Schistosoma mansoni</i> reveals population history and effects of selection. <i>Scientific Reports</i> , 2016, 6, 20954.	1.6	72

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37	Measuring Support and Finding Unsupported Relationships in Supertrees. <i>Systematic Biology</i> , 2005, 54, 823-831.	2.7	70
38	Whole genome sequencing of experimental hybrids supports meiosis-like sexual recombination in <i>Leishmania</i> . <i>PLoS Genetics</i> , 2019, 15, e1008042.	1.5	70
39	Majority-Rule Supertrees. <i>Systematic Biology</i> , 2007, 56, 445-452.	2.7	68
40	Population genomic and evolutionary modelling analyses reveal a single major QTL for ivermectin drug resistance in the pathogenic nematode, <i>Haemonchus contortus</i> . <i>BMC Genomics</i> , 2019, 20, 218.	1.2	68
41	<i>In vitro</i> selection of miltefosine resistance in promastigotes of <i>Leishmania donovani</i> from Nepal: genomic and metabolomic characterization. <i>Molecular Microbiology</i> , 2016, 99, 1134-1148.	1.2	67
42	Comparative genomics of canine-isolated <i>Leishmania (Leishmania) amazonensis</i> from an endemic focus of visceral leishmaniasis in Governador Valadares, southeastern Brazil. <i>Scientific Reports</i> , 2017, 7, 40804.	1.6	65
43	Genome-wide Approaches to Investigate Anthelmintic Resistance. <i>Trends in Parasitology</i> , 2019, 35, 289-301.	1.5	61
44	Ecological divergence and hybridization of Neotropical <i>Leishmania</i> parasites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25159-25168.	3.3	60
45	Relative time scales reveal multiple origins of parallel disjunct distributions of African caecilian amphibians. <i>Biology Letters</i> , 2007, 3, 505-508.	1.0	59
46	A Genome Resequencing-Based Genetic Map Reveals the Recombination Landscape of an Outbred Parasitic Nematode in the Presence of Polyploidy and Polyandry. <i>Genome Biology and Evolution</i> , 2018, 10, 396-409.	1.1	58
47	Rates and patterns of gene duplication and loss in the human genome. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2005, 272, 277-283.	1.2	57
48	Cetaceans on a Molecular Fast Track to Ultrasonic Hearing. <i>Current Biology</i> , 2010, 20, 1834-1839.	1.8	56
49	Characterization and comparative analysis of the complete <i>Haemonchus contortus</i> β -tubulin gene family and implications for benzimidazole resistance in strongylid nematodes. <i>International Journal for Parasitology</i> , 2013, 43, 465-475.	1.3	53
50	Genomes of <i>Leishmania</i> parasites directly sequenced from patients with visceral leishmaniasis in the Indian subcontinent. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007900.	1.3	48
51	Population genetic analysis of Chadian Guinea worms reveals that human and non-human hosts share common parasite populations. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006747.	1.3	46
52	Stage-Specific Transcriptome and Proteome Analyses of the Filarial Parasite <i>Onchocerca volvulus</i> and Its <i>Wolbachia</i> Endosymbiont. <i>MBio</i> , 2016, 7, .	1.8	45
53	Properties of Supertree Methods in the Consensus Setting. <i>Systematic Biology</i> , 2007, 56, 330-337.	2.7	41
54	Genome wide comparison of Ethiopian <i>Leishmania donovani</i> strains reveals differences potentially related to parasite survival. <i>PLoS Genetics</i> , 2018, 14, e1007133.	1.5	40

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55	The Evolution of Bat Vestibular Systems in the Face of Potential Antagonistic Selection Pressures for Flight and Echolocation. PLoS ONE, 2013, 8, e61998.	1.1	38
56	Sex chromosome evolution in parasitic nematodes of humans. Nature Communications, 2020, 11, 1964.	5.8	38
57	The genome of <i>Leishmania adleri</i> from a mammalian host highlights chromosome fission in <i>Sauroleishmania</i> . Scientific Reports, 2017, 7, 43747.	1.6	34
58	Integrated genomic and metabolomic profiling of ISC1, an emerging <i>Leishmania donovani</i> population in the Indian subcontinent. Infection, Genetics and Evolution, 2018, 62, 170-178.	1.0	32
59	Evaluation of DNA Extraction Methods on Individual Helminth Egg and Larval Stages for Whole-Genome Sequencing. Frontiers in Genetics, 2019, 10, 826.	1.1	30
60	Whole-genome sequencing of <i>Schistosoma mansoni</i> reveals extensive diversity with limited selection despite mass drug administration. Nature Communications, 2021, 12, 4776.	5.8	28
61	Experimental Design in Caecilian Systematics: Phylogenetic Information of Mitochondrial Genomes and Nuclear rag1. Systematic Biology, 2009, 58, 425-438.	2.7	27
62	The Expanding World of Human Leishmaniasis. Trends in Parasitology, 2017, 33, 341-344.	1.5	27
63	Long-read assembly and comparative evidence-based reanalysis of <i>Cryptosporidium</i> genome sequences reveal expanded transporter repertoire and duplication of entire chromosome ends including subtelomeric regions. Genome Research, 2022, 32, 203-213.	2.4	26
64	Tangled Tales from Multiple Markers. Computational Biology, 2004, , 107-125.	0.1	23
65	The Information Content of Trees and Their Matrix Representations. Systematic Biology, 2004, 53, 989-1001.	2.7	22
66	Supertrees join the mainstream of phylogenetics. Trends in Ecology and Evolution, 2009, 24, 1-3.	4.2	22
67	<i>Leishmania naiffi</i> and <i>Leishmania guyanensis</i> reference genomes highlight genome structure and gene evolution in the <i>Viannia</i> subgenus. Royal Society Open Science, 2018, 5, 172212.	1.1	22
68	Transcriptomic profiling of nematode parasites surviving vaccine exposure. International Journal for Parasitology, 2018, 48, 395-402.	1.3	20
69	Evaluation of whole genome amplification and bioinformatic methods for the characterization of <i>Leishmania</i> genomes at a single cell level. Scientific Reports, 2020, 10, 15043.	1.6	20
70	<i>Haemonchus contortus</i> . Advances in Parasitology, 2016, 93, 569-598.	1.4	19
71	Transcriptomic analyses implicate neuronal plasticity and chloride homeostasis in ivermectin resistance and response to treatment in a parasitic nematode. PLoS Pathogens, 2022, 18, e1010545.	2.1	19
72	Gene tree parsimony vs. uninode coding for phylogenetic reconstruction. Molecular Phylogenetics and Evolution, 2003, 29, 298-308.	1.2	18

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73	Mosaic aneuploidy in Leishmania: the perspective of whole genome sequencing. Trends in Parasitology, 2014, 30, 554-555.	1.5	18
74	Eradication genomics—lessons for parasite control. Science, 2018, 361, 130-131.	6.0	18
75	Population genomic evidence that human and animal infections in Africa come from the same populations of Dracunculus medinensis. PLoS Neglected Tropical Diseases, 2020, 14, e0008623.	1.3	18
76	Discriminating Supported and Unsupported Relationships in Supertrees Using Triplets. Systematic Biology, 2006, 55, 345-350.	2.7	17
77	Genomic analysis of natural intra-specific hybrids among Ethiopian isolates of Leishmania donovani. PLoS Neglected Tropical Diseases, 2020, 14, e0007143.	1.3	17
78	The role of Notch signalling and numb function in mechanosensory organ formation in the spider Cupiennius salei. Developmental Biology, 2009, 327, 121-131.	0.9	14
79	Experimental Design in Phylogenetics: Testing Predictions from Expected Information. Systematic Biology, 2012, 61, 661-674.	2.7	14
80	Analytical Methods for Detecting Paralogy in Molecular Datasets. Methods in Enzymology, 2005, 395, 700-724.	0.4	12
81	The tree of genomes: An empirical comparison of genome-phylogeny reconstruction methods. BMC Evolutionary Biology, 2008, 8, 312.	3.2	12
82	Transcriptional and genomic parallels between the monoxenous parasite Herpetomonas muscarum and Leishmania. PLoS Genetics, 2019, 15, e1008452.	1.5	12
83	Genetree: A Tool for Exploring Gene Family Evolution. Computational Biology, 2000, , 525-536.	0.1	12
84	Speciation processes in putative island endemic sister bat species: false impressions from mitochondrial <sc>DNA</sc> and microsatellite data. Molecular Ecology, 2015, 24, 5910-5926.	2.0	11
85	An expressed, endogenous Nodavirus-like element captured by a retrotransposon in the genome of the plant parasitic nematode Bursaphelenchus xylophilus. Scientific Reports, 2016, 6, 39749.	1.6	11
86	A method for single pair mating in an obligate parasitic nematode. International Journal for Parasitology, 2018, 48, 159-165.	1.3	11
87	Stops making sense: translational trade-offs and stop codon reassignment. BMC Evolutionary Biology, 2011, 11, 227.	3.2	10
88	The confounding effects of high genetic diversity on the determination and interpretation of differential gene expression analysis in the parasitic nematode Haemonchus contortus. International Journal for Parasitology, 2019, 49, 847-858.	1.3	10
89	Diversity and Within-Host Evolution of Leishmania donovani from Visceral Leishmaniasis Patients with and without HIV Coinfection in Northern Ethiopia. MBio, 2021, 12, e0097121.	1.8	9
90	Modelling the Effects of Mass Drug Administration on the Molecular Epidemiology of Schistosomes. Advances in Parasitology, 2015, 87, 293-327.	1.4	8

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91	The <i>Phlebotomus papatasi</i> systemic transcriptional response to trypanosomatid-contaminated blood does not differ from the non-infected blood meal. <i>Parasites and Vectors</i> , 2021, 14, 15.	1.0	7
92	Retroviruses from retrotransposons. <i>Genome Biology</i> , 2001, 2, 1.	3.8	6
93	A new profusion of planktonic eukaryotes. <i>Genome Biology</i> , 2001, 2, 1.	3.8	6
94	The shape of human gene family phylogenies. <i>BMC Evolutionary Biology</i> , 2006, 6, 66.	3.2	5
95	Genomic and Phenotypic Characterization of Experimentally Selected Resistant <i>Leishmania donovani</i> Reveals a Role for Dynamin-1-Like Protein in the Mechanism of Resistance to a Novel Antileishmanial Compound. <i>MBio</i> , 2022, 13, e0326421.	1.8	5
96	A genetic TRP down the channel to praziquantel resistance. <i>Trends in Parasitology</i> , 2022, 38, 351-352.	1.5	5
97	Molecular Evolution and Phylogeny of <i>Leishmania</i> . , 2018, , 19-57.		4
98	Linked surveillance and genetic data uncovers programmatically relevant geographic scale of Guinea worm transmission in Chad. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009609.	1.3	4
99	Homologous recombination in animal mitochondria. <i>Genome Biology</i> , 2001, 2, 1.	3.8	3
100	Geographic Origin and Vertical Transmission of <i>Leishmania infantum</i> Parasites in Hunting Hounds, United States. <i>Emerging Infectious Diseases</i> , 2022, 28, .	2.0	3
101	Endosymbiont Capture, a Repeated Process of Endosymbiont Transfer with Replacement in Trypanosomatids <i>Angomonas</i> spp.. <i>Pathogens</i> , 2021, 10, 702.	1.2	2
102	Systematic identification of genes encoding cell surface and secreted proteins that are essential for in vitro growth and infection in <i>Leishmania donovani</i> . <i>PLoS Pathogens</i> , 2022, 18, e1010364.	2.1	2
103	From sequence reads to evolutionary inferences. , 0, , 305-335.		0
104	A Way Straight-Forward for <i>Leishmania</i> Genetics. <i>Trends in Parasitology</i> , 2020, 36, 719-721.	1.5	0
105	The Ediacaran emergence of bilaterians: congruence between the genetic and the geological fossil records. , 2009, , 15-23.		0
106	Title is missing!. , 2019, 15, e1008452.		0
107	Title is missing!. , 2019, 15, e1008452.		0
108	Title is missing!. , 2019, 15, e1008452.		0

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109	Replacement of Leishmania (Leishmania) infantum Populations in an Endemic Focus of Visceral Leishmaniasis in Brazil. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	0