

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	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. <i>Genome Research</i> , 2022, 32, 203-213.	2.4	26
2	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
3	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
4	A genetic TRP down the channel to praziquantel resistance. <i>Trends in Parasitology</i> , 2022, 38, 351-352.	1.5	5
5	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
6	Transcriptomic analyses implicate neuronal plasticity and chloride homeostasis in ivermectin resistance and response to treatment in a parasitic nematode. <i>PLoS Pathogens</i> , 2022, 18, e1010545.	2.1	19
7	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
8	Diversity and Within-Host Evolution of <i>Leishmania donovani</i> from Visceral Leishmaniasis Patients with and without HIV Coinfection in Northern Ethiopia. <i>MBio</i> , 2021, 12, e0097121.	1.8	9
9	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
10	Whole-genome sequencing of <i>Schistosoma mansoni</i> reveals extensive diversity with limited selection despite mass drug administration. <i>Nature Communications</i> , 2021, 12, 4776.	5.8	28
11	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
12	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
13	A Way Straight-Forward for <i>Leishmania</i> Genetics. <i>Trends in Parasitology</i> , 2020, 36, 719-721.	1.5	0
14	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
15	Evaluation of whole genome amplification and bioinformatic methods for the characterization of <i>Leishmania</i> genomes at a single cell level. <i>Scientific Reports</i> , 2020, 10, 15043.	1.6	20
16	Sex chromosome evolution in parasitic nematodes of humans. <i>Nature Communications</i> , 2020, 11, 1964.	5.8	38
17	Genomic analysis of natural intra-specific hybrids among Ethiopian isolates of <i>Leishmania donovani</i> . <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0007143.	1.3	17
18	Population genomic evidence that human and animal infections in Africa come from the same populations of <i>Dracunculus medinensis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008623.	1.3	18

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19	Global genome diversity of the <i>Leishmania donovani</i> complex. <i>ELife</i> , 2020, 9, .	2.8	90
20	Transcriptional and genomic parallels between the monoxenous parasite <i>Herpetomonas muscarum</i> and <i>Leishmania</i> . <i>PLoS Genetics</i> , 2019, 15, e1008452.	1.5	12
21	The confounding effects of high genetic diversity on the determination and interpretation of differential gene expression analysis in the parasitic nematode <i>Haemonchus contortus</i> . <i>International Journal for Parasitology</i> , 2019, 49, 847-858.	1.3	10
22	Evaluation of DNA Extraction Methods on Individual Helminth Egg and Larval Stages for Whole-Genome Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 826.	1.1	30
23	Genome-wide Approaches to Investigate Anthelmintic Resistance. <i>Trends in Parasitology</i> , 2019, 35, 289-301.	1.5	61
24	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
25	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
26	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
27	Title is missing!. , 2019, 15, e1008452.		0
28	Title is missing!. , 2019, 15, e1008452.		0
29	Title is missing!. , 2019, 15, e1008452.		0
30	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
31	<i>Leishmania naiffi</i> and <i>Leishmania guyanensis</i> reference genomes highlight genome structure and gene evolution in the <i>Viannia</i> subgenus. <i>Royal Society Open Science</i> , 2018, 5, 172212.	1.1	22
32	Integrated genomic and metabolomic profiling of ISC1, an emerging <i>Leishmania donovani</i> population in the Indian subcontinent. <i>Infection, Genetics and Evolution</i> , 2018, 62, 170-178.	1.0	32
33	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
34	Transcriptomic profiling of nematode parasites surviving vaccine exposure. <i>International Journal for Parasitology</i> , 2018, 48, 395-402.	1.3	20
35	A method for single pair mating in an obligate parasitic nematode. <i>International Journal for Parasitology</i> , 2018, 48, 159-165.	1.3	11
36	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

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37	Molecular Evolution and Phylogeny of Leishmania. , 2018, , 19-57.		4
38	Eradication genomicsâ€™ lessons for parasite control. Science, 2018, 361, 130-131.	6.0	18
39	Genome wide comparison of Ethiopian Leishmania donovani strains reveals differences potentially related to parasite survival. PLoS Genetics, 2018, 14, e1007133.	1.5	40
40	Comparative genomics of canine-isolated Leishmania (Leishmania) amazonensis from an endemic focus of visceral leishmaniasis in Governador Valadares, southeastern Brazil. Scientific Reports, 2017, 7, 40804.	1.6	65
41	Plasmodium malariae and P. ovale genomes provide insights into malaria parasite evolution. Nature, 2017, 542, 101-104.	13.7	150
42	The genome of Leishmania adleri from a mammalian host highlights chromosome fission in Saurouleishmania. Scientific Reports, 2017, 7, 43747.	1.6	34
43	The Expanding World of Human Leishmaniasis. Trends in Parasitology, 2017, 33, 341-344.	1.5	27
44	Gene Expression in <i>Leishmania</i> Is Regulated Predominantly by Gene Dosage. MBio, 2017, 8, .	1.8	108
45	The genome of Onchocerca volvulus, agent of river blindness. Nature Microbiology, 2017, 2, 16216.	5.9	107
46	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
47	Whole genome resequencing of the human parasite Schistosoma mansoni reveals population history and effects of selection. Scientific Reports, 2016, 6, 20954.	1.6	72
48	<i>In vitro</i> selection of miltefosine resistance in promastigotes of <i>Leishmania donovani</i> from Nepal: genomic and metabolomic characterization. Molecular Microbiology, 2016, 99, 1134-1148.	1.2	67
49	Haemonchus contortus. Advances in Parasitology, 2016, 93, 569-598.	1.4	19
50	Reduced Efficacy of Praziquantel Against <i>Schistosoma mansoni</i> Is Associated With Multiple Rounds of Mass Drug Administration. Clinical Infectious Diseases, 2016, 63, ciw506.	2.9	150
51	Stage-Specific Transcriptome and Proteome Analyses of the Filarial Parasite Onchocerca volvulus and Its <i>Wolbachia</i> Endosymbiont. MBio, 2016, 7, .	1.8	45
52	The genome of the yellow potato cyst nematode, Globodera rostochiensis, reveals insights into the basis of parasitism and virulence. Genome Biology, 2016, 17, 124.	3.8	156
53	The genomic basis of parasitism in the Strongyloides clade of nematodes. Nature Genetics, 2016, 48, 299-307.	9.4	226
54	Genomic and Molecular Characterization of Miltefosine Resistance in Leishmania infantum Strains with Either Natural or Acquired Resistance through Experimental Selection of Intracellular Amastigotes. PLoS ONE, 2016, 11, e0154101.	1.1	80

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55	Evolutionary genomics of epidemic visceral leishmaniasis in the Indian subcontinent. <i>ELife</i> , 2016, 5, .	2.8	147
56	Speciation processes in putative island endemic sister bat species: false impressions from mitochondrial <sc>DNA</sc> and microsatellite data. <i>Molecular Ecology</i> , 2015, 24, 5910-5926.	2.0	11
57	Modelling the Effects of Mass Drug Administration on the Molecular Epidemiology of Schistosomes. <i>Advances in Parasitology</i> , 2015, 87, 293-327.	1.4	8
58	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
59	Genome Sequence of the Tsetse Fly (<i>Glossina morsitans</i>): Vector of African Trypanosomiasis. <i>Science</i> , 2014, 344, 380-386.	6.0	254
60	Mosaic aneuploidy in <i>Leishmania</i> : the perspective of whole genome sequencing. <i>Trends in Parasitology</i> , 2014, 30, 554-555.	1.5	18
61	The Peculiar Epidemiology of Dracunculiasis in Chad. <i>American Journal of Tropical Medicine and Hygiene</i> , 2014, 90, 61-70.	0.6	131
62	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
63	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
64	Genome-wide signatures of convergent evolution in echolocating mammals. <i>Nature</i> , 2013, 502, 228-231.	13.7	321
65	Phylogenomic Analyses Elucidate the Evolutionary Relationships of Bats. <i>Current Biology</i> , 2013, 23, 2262-2267.	1.8	139
66	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
67	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
68	New approaches for unravelling reassortment pathways. <i>BMC Evolutionary Biology</i> , 2013, 13, 1.	3.2	278
69	The Evolution of Bat Vestibular Systems in the Face of Potential Antagonistic Selection Pressures for Flight and Echolocation. <i>PLoS ONE</i> , 2013, 8, e61998.	1.1	38
70	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
71	Experimental Design in Phylogenetics: Testing Predictions from Expected Information. <i>Systematic Biology</i> , 2012, 61, 661-674.	2.7	14
72	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

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73	Stops making sense: translational trade-offs and stop codon reassignment. <i>BMC Evolutionary Biology</i> , 2011, 11, 227.	3.2	10
74	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
75	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
76	Convergent sequence evolution between echolocating bats and dolphins. <i>Current Biology</i> , 2010, 20, R53-R54.	1.8	202
77	Cetaceans on a Molecular Fast Track to Ultrasonic Hearing. <i>Current Biology</i> , 2010, 20, 1834-1839.	1.8	56
78	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
79	Supertrees join the mainstream of phylogenetics. <i>Trends in Ecology and Evolution</i> , 2009, 24, 1-3.	4.2	22
80	The role of Notch signalling and numb function in mechanosensory organ formation in the spider <i>Cupiennius salei</i> . <i>Developmental Biology</i> , 2009, 327, 121-131.	0.9	14
81	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
82	Experimental Design in Caecilian Systematics: Phylogenetic Information of Mitochondrial Genomes and Nuclear rag1. <i>Systematic Biology</i> , 2009, 58, 425-438.	2.7	27
83	The Ediacaran emergence of bilaterians: congruence between the genetic and the geological fossil records. , 2009, , 15-23.		0
84	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
85	The tree of genomes: An empirical comparison of genome-phylogeny reconstruction methods. <i>BMC Evolutionary Biology</i> , 2008, 8, 312.	3.2	12
86	The prokaryotic tree of life: past, present and future?. <i>Trends in Ecology and Evolution</i> , 2008, 23, 276-281.	4.2	82
87	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
88	Tempo and Mode of Diversification of Lake Tanganyika Cichlid Fishes. <i>PLoS ONE</i> , 2008, 3, e1730.	1.1	78
89	Properties of Supertree Methods in the Consensus Setting. <i>Systematic Biology</i> , 2007, 56, 330-337.	2.7	41
90	Majority-Rule Supertrees. <i>Systematic Biology</i> , 2007, 56, 445-452.	2.7	68

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91	Supertrees Disentangle the Chimerical Origin of Eukaryotic Genomes. <i>Molecular Biology and Evolution</i> , 2007, 24, 1752-1760.	3.5	157
92	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
93	The shape of human gene family phylogenies. <i>BMC Evolutionary Biology</i> , 2006, 6, 66.	3.2	5
94	Genetic Analysis of the Cytoplasmic Dynein Subunit Families. <i>PLoS Genetics</i> , 2006, 2, e1.	1.5	276
95	Discriminating Supported and Unsupported Relationships in Supertrees Using Triplets. <i>Systematic Biology</i> , 2006, 55, 345-350.	2.7	17
96	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
97	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
98	Measuring Support and Finding Unsupported Relationships in Supertrees. <i>Systematic Biology</i> , 2005, 54, 823-831.	2.7	70
99	Analytical Methods for Detecting Paralogy in Molecular Datasets. <i>Methods in Enzymology</i> , 2005, 395, 700-724.	0.4	12
100	The Information Content of Trees and Their Matrix Representations. <i>Systematic Biology</i> , 2004, 53, 989-1001.	2.7	22
101	Tangled Tales from Multiple Markers. <i>Computational Biology</i> , 2004, , 107-125.	0.1	23
102	Gene tree parsimony vs. uninode coding for phylogenetic reconstruction. <i>Molecular Phylogenetics and Evolution</i> , 2003, 29, 298-308.	1.2	18
103	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
104	Homologous recombination in animal mitochondria. <i>Genome Biology</i> , 2001, 2, 1.	3.8	3
105	Retroviruses from retrotransposons. <i>Genome Biology</i> , 2001, 2, 1.	3.8	6
106	A new profusion of planktonic eukaryotes. <i>Genome Biology</i> , 2001, 2, 1.	3.8	6
107	Genetree: A Tool for Exploring Gene Family Evolution. <i>Computational Biology</i> , 2000, , 525-536.	0.1	12
108	From sequence reads to evolutionary inferences. , 0, , 305-335.		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