

Alistair C Darby

List of Publications by Year in descending order

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116
papers

7,264
citations

81900

39
h-index

66911

78
g-index

131
all docs

131
docs citations

131
times ranked

10153
citing authors

#	ARTICLE	IF	CITATIONS
1	Functional and Evolutionary Insights from the Genomes of Three Parasitoid <i>Nasonia</i> Species. <i>Science</i> , 2010, 327, 343-348.	12.6	808
2	Improved reference genome of <i>Aedes aegypti</i> informs arbovirus vector control. <i>Nature</i> , 2018, 563, 501-507.	27.8	426
3	A comprehensive benchmarking study of protocols and sequencing platforms for 16S rRNA community profiling. <i>BMC Genomics</i> , 2016, 17, 55.	2.8	387
4	The industrial melanism mutation in British peppered moths is a transposable element. <i>Nature</i> , 2016, 534, 102-105.	27.8	386
5	Genome Sequence of the Tsetse Fly (<i>Glossina morsitans</i>): Vector of African Trypanosomiasis. <i>Science</i> , 2014, 344, 380-386.	12.6	254
6	Application of next-generation sequencing technologies in virology. <i>Journal of General Virology</i> , 2012, 93, 1853-1868.	2.9	241
7	The mosaic genome structure of the <i>Wolbachia w</i> Ri strain infecting <i>Drosophila simulans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5725-5730.	7.1	236
8	Linking the bacterial community in pea aphids with host-plant use and natural enemy resistance. <i>Ecological Entomology</i> , 2004, 29, 60-65.	2.2	227
9	The <i>Orientia tsutsugamushi</i> genome reveals massive proliferation of conjugative type IV secretion system and host cell interaction genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7981-7986.	7.1	219
10	Intracellular pathogens go extreme: genome evolution in the Rickettsiales. <i>Trends in Genetics</i> , 2007, 23, 511-520.	6.7	211
11	Genomic Analysis of Highly Virulent Georgia 2007/1 Isolate of African Swine Fever Virus. <i>Emerging Infectious Diseases</i> , 2011, 17, 599-605.	4.3	186
12	Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. <i>Cell</i> , 2021, 184, 5179-5188.e8.	28.9	182
13	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
14	Diversity of Bacteria Associated with Natural Aphid Populations. <i>Applied and Environmental Microbiology</i> , 2003, 69, 7216-7223.	3.1	129
15	Acetogenesis from H ₂ plus CO ₂ and nitrogen fixation by an endosymbiotic spirochete of a termite-gut cellulolytic protist. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10224-10230.	7.1	108
16	Antioxidants promote establishment of trypanosome infections in tsetse. <i>Parasitology</i> , 2007, 134, 827-831.	1.5	105
17	Comparative genomics of Shiga toxin encoding bacteriophages. <i>BMC Genomics</i> , 2012, 13, 311.	2.8	98
18	Characteristics of the genome of <i>Arsenophonus nasoniae</i> , sonâ€killer bacterium of the wasp <i>Nasonia</i> . <i>Insect Molecular Biology</i> , 2010, 19, 75-89.	2.0	94

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19	Endosymbiont gene functions impaired and rescued by polymerase infidelity at poly(A) tracts. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 14934-14939.	7.1	92
20	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
21	Elucidation of the Transmission Patterns of an Insect-Borne Bacterium. Applied and Environmental Microbiology, 2003, 69, 4403-4407.	3.1	88
22	An aphid-borne bacterium allied to the secondary symbionts of whitefly. FEMS Microbiology Ecology, 2001, 36, 43-50.	2.7	86
23	Aphid-Symbiotic Bacteria Cultured in Insect Cell Lines. Applied and Environmental Microbiology, 2005, 71, 4833-4839.	3.1	81
24	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
25	Comparative Genomics and Transduction Potential of <i>Enterococcus faecalis</i> Temperate Bacteriophages. Journal of Bacteriology, 2010, 192, 1122-1130.	2.2	71
26	Taking the pseudo out of pseudogenes. Current Opinion in Microbiology, 2015, 23, 102-109.	5.1	67
27	Evaluation of Lysis Methods for the Extraction of Bacterial DNA for Analysis of the Vaginal Microbiota. PLoS ONE, 2016, 11, e0163148.	2.5	67
28	The genomic and metabolic diversity of Rickettsia. Research in Microbiology, 2007, 158, 745-753.	2.1	64
29	Investigation of the Bacterial Communities Associated with Females of Lutzomyia Sand Fly Species from South America. PLoS ONE, 2012, 7, e42531.	2.5	58
30	Intraguild predators and the spatial distribution of a parasitoid. Oecologia, 2000, 124, 367-372.	2.0	57
31	Identification of Three Novel Superantigen-Encoding Genes in <i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> , <i>szef</i> , <i>szen</i> , and <i>szep</i> . Infection and Immunity, 2010, 78, 4817-4827.	2.2	56
32	Challenging the Wigglesworthia, Sodalis, Wolbachia symbiosis dogma in tsetse flies: Spiroplasma is present in both laboratory and natural populations. Scientific Reports, 2017, 7, 4699.	3.3	53
33	Impact of oral metronidazole treatment on the vaginal microbiota and correlates of treatment failure. American Journal of Obstetrics and Gynecology, 2020, 222, 157.e1-157.e13.	1.3	53
34	Iron Necessity: The Secret of Wolbachia's Success?. PLoS Neglected Tropical Diseases, 2014, 8, e3224.	3.0	51
35	Characterisation of the faecal metabolome and microbiome of Thoroughbred racehorses. Equine Veterinary Journal, 2015, 47, 580-586.	1.7	51
36	DNA extraction and amplicon production strategies deeply influence the outcome of gut mycobiome studies. Scientific Reports, 2019, 9, 9328.	3.3	51

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37	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
38	Phylogeny and prevalence of kobuviruses in dogs and cats in the UK. <i>Veterinary Microbiology</i> , 2013, 164, 246-252.	1.9	48
39	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
40	The draft genome sequence of <i>Arsenophonus nasoniae</i> , sonâ€killer bacterium of <i>Nasonia vitripennis</i> , reveals genes associated with virulence and symbiosis. <i>Insect Molecular Biology</i> , 2010, 19, 59-73.	2.0	46
41	Genome sequence of <i>Candidatus Arsenophonus lipopteni</i> , the exclusive symbiont of a blood sucking fly <i>Lipoptena cervi</i> (Diptera: Hippoboscidae). <i>Standards in Genomic Sciences</i> , 2016, 11, 72.	1.5	46
42	Intermittent Lactobacilli-containing Vaginal Probiotic or Metronidazole Use to Prevent Bacterial Vaginosis Recurrence: A Pilot Study Incorporating Microscopy and Sequencing. <i>Scientific Reports</i> , 2020, 10, 3884.	3.3	40
43	Draft genome of the honey bee ectoparasitic mite, <i>Tropilaelaps mercedesae</i> , is shaped by the parasitic life history. <i>GigaScience</i> , 2017, 6, 1-17.	6.4	39
44	The Tick Cell Biobank: A global resource for in vitro research on ticks, other arthropods and the pathogens they transmit. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 1364-1371.	2.7	39
45	Comparative genomics of <i>Brachyspira pilosicoli</i> strains: genome rearrangements, reductions and correlation of genetic compliment with phenotypic diversity. <i>BMC Genomics</i> , 2012, 13, 454.	2.8	38
46	Integrated transcriptomic and proteomic analysis of the global response of <i>Wolbachia</i> to doxycycline-induced stress. <i>ISME Journal</i> , 2014, 8, 925-937.	9.8	38
47	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
48	Characterization of Pneumonia Due to <i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> in Dogs. <i>Vaccine Journal</i> , 2010, 17, 1790-1796.	3.1	36
49	Factors Affecting Trypanosome Maturation in Tsetse Flies. <i>PLoS ONE</i> , 2007, 2, e239.	2.5	36
50	The rapid isolation and growth dynamics of the tsetse symbiont <i>Sodalis glossinidius</i> . <i>FEMS Microbiology Letters</i> , 2005, 248, 69-74.	1.8	35
51	The effect of gut microbiota elimination in <i>Drosophila melanogaster</i> : A howâ€to guide for hostâ€microbiota studies. <i>Ecology and Evolution</i> , 2018, 8, 4150-4161.	1.9	35
52	Visualization of pseudogenes in intracellular bacteria reveals the different tracks to gene destruction. <i>Genome Biology</i> , 2008, 9, R42.	9.6	32
53	Genomes of trombidid mites reveal novel predicted allergens and laterally transferred genes associated with secondary metabolism. <i>GigaScience</i> , 2018, 7, .	6.4	32
54	Extrachromosomal DNA of the Symbiont <i>Sodalis glossinidius</i> . <i>Journal of Bacteriology</i> , 2005, 187, 5003-5007.	2.2	31

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55	Draft Genome Sequence of the <i>Bactrocera oleae</i> Symbiont <i>Candidatus</i> Erwinia dacicola. Genome Announcements, 2016, 4, .	0.8	30
56	Low calorie sweeteners and gut microbiota. Physiology and Behavior, 2016, 164, 494-500.	2.1	30
57	Trypanosomatid parasite dynamically changes the transcriptome during infection and modifies honey bee physiology. Communications Biology, 2020, 3, 51.	4.4	28
58	Characterisation of the genomes of four putative vesiculoviruses: tench rhabdovirus, grass carp rhabdovirus, perch rhabdovirus and eel rhabdovirus European X. Archives of Virology, 2013, 158, 2371-2377.	2.1	27
59	Bacterial sensing underlies artificial sweetener-induced growth of gut <i>Lactobacillus</i> . Environmental Microbiology, 2016, 18, 2159-2171.	3.8	27
60	Optimised conditions for handling and transport of male <i>Acanthopheles arabiensis</i> : effects of low temperature, compaction, and ventilation on male quality. Entomologia Experimentalis Et Applicata, 2017, 164, 276-283.	1.4	26
61	Impact of maternal antibodies and microbiota development on the immunogenicity of oral rotavirus vaccine in African, Indian, and European infants. Nature Communications, 2021, 12, 7288.	12.8	26
62	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
63	Diminutive, degraded but dissimilar: Wolbachia genomes from filarial nematodes do not conform to a single paradigm. Microbial Genomics, 2020, 6, .	2.0	24
64	A Tale of Three Species: Adaptation of <i>Sodalis glossinidius</i> to Tsetse Biology, <i>Wigglesworthia</i> Metabolism, and Host Diet. MBio, 2019, 10, .	4.1	23
65	The significance of a facultative bacterium to natural populations of the pea aphid <i>Acyrtosiphon pisum</i> . Ecological Entomology, 2003, 28, 145-150.	2.2	22
66	Comparative Genomics of <i>Staphylococcus</i> Reveals Determinants of Speciation and Diversification of Antimicrobial Defense. Frontiers in Microbiology, 2018, 9, 2753.	3.5	22
67	Multi-locus sequence typing of <i>Ixodes ricinus</i> and its symbiont <i>Candidatus</i> Midichloria mitochondrii across Europe reveals evidence of local co-cladogenesis in Scotland. Ticks and Tick-borne Diseases, 2019, 10, 52-62.	2.7	22
68	Cryptic Diversity within the Major Trypanosomiasis Vector <i>Glossina fuscipes</i> Revealed by Molecular Markers. PLoS Neglected Tropical Diseases, 2011, 5, e1266.	3.0	22
69	Genomic diversity across the <i>Rickettsia</i> and <i>Candidatus</i> <i>Megaira</i> ™ genera and proposal of genus status for the <i>Torix</i> group. Nature Communications, 2022, 13, 2630.	12.8	22
70	Complete Genome Sequence of <i>Mycoplasma haemofelis</i> , a Hemotropic Mycoplasma. Journal of Bacteriology, 2011, 193, 2060-2061.	2.2	21
71	Impact of maternal antibodies and infant gut microbiota on the immunogenicity of rotavirus vaccines in African, Indian and European infants: protocol for a prospective cohort study. BMJ Open, 2017, 7, e016577.	1.9	21
72	Ecological and microbiological diversity of chigger mites, including vectors of scrub typhus, on small mammals across stratified habitats in Thailand. Animal Microbiome, 2019, 1, 18.	3.8	21

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73	<i>Rickettsia buchneri</i> , symbiont of the deer tick <i>Ixodes scapularis</i> , can colonise the salivary glands of its host. <i>Ticks and Tick-borne Diseases</i> , 2020, 11, 101299.	2.7	21
74	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
75	Characterization of Circulating <i>Clostridium difficile</i> Strains, Host Response and Intestinal Microbiome in Hospitalized Children With Diarrhea. <i>Pediatric Infectious Disease Journal</i> , 2020, 39, 221-228.	2.0	19
76	The olfactory responses of coccinellids to aphids on plants. <i>Entomologia Experimentalis Et Applicata</i> , 2000, 95, 113-117.	1.4	18
77	Exploration of the Fecal Microbiota and Biomarker Discovery in Equine Grass Sickness. <i>Journal of Proteome Research</i> , 2018, 17, 1120-1128.	3.7	18
78	Functional Genomics of a Symbiotic Community: Shared Traits in the Olive Fruit Fly Gut Microbiota. <i>Genome Biology and Evolution</i> , 2020, 12, 3778-3791.	2.5	16
79	Inter-kingdom relationships in Crohn's disease explored using a multi-omics approach. <i>Gut Microbes</i> , 2021, 13, 1930871.	9.8	16
80	Molecular characterization of the uncultivable hemotropic bacterium <i>Mycoplasma haemofelis</i> . <i>Veterinary Research</i> , 2011, 42, 83.	3.0	15
81	Divergence of a strain of <i>Pseudomonas aeruginosa</i> during an outbreak of ovine mastitis. <i>Veterinary Microbiology</i> , 2015, 175, 105-113.	1.9	15
82	Isolation and Propagation of Laboratory Strains and a Novel Flea-Derived Field Strain of <i>Wolbachia</i> in Tick Cell Lines. <i>Microorganisms</i> , 2020, 8, 988.	3.6	15
83	Insect Symbiont Gene Expression in the Midgut Bacteriocytes of a Blood-Sucking Parasite. <i>Genome Biology and Evolution</i> , 2020, 12, 429-442.	2.5	15
84	<i>Mycoplasma tullyi</i> sp. nov., isolated from penguins of the genus <i>Spheniscus</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 3692-3698.	1.7	15
85	Human papillomavirus infection and cervical dysplasia in HIV-positive women. <i>Aids</i> , 2020, 34, 115-125.	2.2	14
86	The Hypercomplex Genome of an Insect Reproductive Parasite Highlights the Importance of Lateral Gene Transfer in Symbiont Biology. <i>MBio</i> , 2020, 11, .	4.1	14
87	Genome Sequence for <i>Candidatus Mycoplasma haemominutum</i> , a Low-Pathogenicity Hemoplasma Species. <i>Journal of Bacteriology</i> , 2012, 194, 905-906.	2.2	13
88	Amplicon and Metagenomic Analysis of Middle East Respiratory Syndrome (MERS) Coronavirus and the Microbiome in Patients with Severe MERS. <i>MSphere</i> , 2021, 6, e0021921.	2.9	12
89	Large-scale and significant expression from pseudogenes in <i>Sodalis glossinidius</i> a facultative bacterial endosymbiont. <i>Microbial Genomics</i> , 2020, 6, .	2.0	12
90	Fast forward genetics. <i>Nature Biotechnology</i> , 2008, 26, 1248-1249.	17.5	11

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91	Isolation in Natural Host Cell Lines of Wolbachia Strains wPip from the Mosquito <i>Culex pipiens</i> and wPap from the Sand Fly <i>Phlebotomus papatasi</i> . <i>Insects</i> , 2021, 12, 871.	2.2	11
92	The inherited microbiota of arthropods, and their importance in understanding resistance and immunity. , 2009, , 119-136.		11
93	The draft genome of strain cCpun from biting midges confirms insect Cardinium are not a monophyletic group and reveals a novel gene family expansion in a symbiont. <i>PeerJ</i> , 2019, 7, e6448.	2.0	10
94	Draft Genome Sequence of <i>Stenotrophomonas maltophilia</i> SBo1 Isolated from <i>Bactrocera oleae</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	9
95	Amplified fragment length polymorphism (AFLP) analysis of closely related wild and captive tsetse fly (<i>Glossina morsitans morsitans</i>) populations. <i>Parasites and Vectors</i> , 2010, 3, 47.	2.5	8
96	Analysis of SARS-CoV-2 known and novel subgenomic mRNAs in cell culture, animal model, and clinical samples using LeTRS, a bioinformatic tool to identify unique sequence identifiers. <i>GigaScience</i> , 2022, 11, .	6.4	8
97	Revised Genome Sequence of the Purple Photosynthetic Bacterium <i>Blastochloris viridis</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	7
98	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
99	Proof of Concept of a Three-Stage, In Vitro Fermentation Model of the Equine Large Intestine. <i>Applied and Environmental Microbiology</i> , 2019, 86, .	3.1	7
100	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
101	An aphid-borne bacterium allied to the secondary symbionts of whitefly. <i>FEMS Microbiology Ecology</i> , 2001, 36, 43-50.	2.7	7
102	The sequence of a male-specific genome region containing the sex determination switch in <i>Aedes aegypti</i> . <i>Parasites and Vectors</i> , 2018, 11, 549.	2.5	6
103	High-Quality Draft Genome Sequence and Annotation of the Basidiomycete Yeast <i>Sporisorium graminicola</i> CBS10092, a Producer of Mannosylerythritol Lipids. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	6
104	COPD Causation and Workplace Exposures: An Assessment of Agreement among Expert Clinical Raters. <i>COPD: Journal of Chronic Obstructive Pulmonary Disease</i> , 2013, 10, 172-179.	1.6	5
105	Complete Genome Sequence of <i>Leptospira interrogans</i> Serovar Bratislava, Strain PigK151. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
106	Draft Genome of <i>Busseola fusca</i> , the Maize Stalk Borer, a Major Crop Pest in Sub-Saharan Africa. <i>Genome Biology and Evolution</i> , 2019, 11, 2203-2207.	2.5	5
107	Isolation of <i>Candidatus Rickettsia vini</i> from Belgian <i>Ixodes arboricola</i> ticks and propagation in tick cell lines. <i>Ticks and Tick-borne Diseases</i> , 2020, 11, 101511.	2.7	5
108	Draft Genome Sequence of <i>Cytophaga fermentans</i> JCM 21142 ^T , a Facultative Anaerobe Isolated from Marine Mud. <i>Genome Announcements</i> , 2014, 2, .	0.8	4

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109	Draft Genome Sequence of <i>Chryseobacterium</i> Strain CBo1 Isolated from <i>Bactrocera oleae</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	4
110	AcGI1, a novel genomic island carrying antibiotic resistance integron In687 in multidrug resistant <i>Achromobacter xylosoxidans</i> in a teaching hospital in Thailand. <i>FEMS Microbiology Letters</i> , 2020, 367, .	1.8	4
111	Symbiosis Research as a Novel Strategy for Insect Pest Control. , 2009, , 207-231.		2
112	Aquatic Hemiptera in Southwest Cameroon: Biodiversity of Potential Reservoirs of <i>Mycobacterium ulcerans</i> and Multiple <i>Wolbachia</i> Sequence Types Revealed by Metagenomics. <i>Diversity</i> , 2019, 11, 225.	1.7	2
113	A gene expression panel for estimating age in males and females of the sleeping sickness vector <i>Glossina morsitans</i> . <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009797.	3.0	1
114	OWE-010â€¦Bacterial and fungal communities in faeces and biopsies in IBD. , 2018, , .		0
115	Complete genome characterization of human noroviruses allows comparison of minor alleles during acute and chronic infections. <i>Access Microbiology</i> , 2021, 3, 000203.	0.5	0
116	The Tick Cell Biobank: new arthropod cell lines for arbovirus research. <i>Access Microbiology</i> , 2019, 1, .	0.5	0