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	Genomic diversity across the Rickettsia and â€˜Candidatus Megairaâ€™ genera and proposal of genus status for the Torix group. Nature Communications, 2022, 13, 2630.	12.8	22
2	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. GigaScience, 2022, 11, .	6.4	8
3	Inter-kingdom relationships in Crohnâ€™s disease explored using a multi-omics approach. Gut Microbes, 2021, 13, 1930871.	9.8	16
4	Complete genome characterization of human noroviruses allows comparison of minor alleles during acute and chronic infections. Access Microbiology, 2021, 3, 000203.	0.5	0
5	Dissecting the molecular diversity and commonality of bovine and human treponemes identifies key survival and adhesion mechanisms. PLoS Pathogens, 2021, 17, e1009464.	4.7	7
6	Amplicon and Metagenomic Analysis of Middle East Respiratory Syndrome (MERS) Coronavirus and the Microbiome in Patients with Severe MERS. MSphere, 2021, 6, e0021921.	2.9	12
7	Isolation in Natural Host Cell Lines of Wolbachia Strains wPip from the Mosquito Culex pipiens and wPap from the Sand Fly Phlebotomus papatasi. Insects, 2021, 12, 871.	2.2	11
8	Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. Cell, 2021, 184, 5179-5188.e8.	28.9	182
9	A gene expression panel for estimating age in males and females of the sleeping sickness vector Glossina morsitans. PLoS Neglected Tropical Diseases, 2021, 15, e0009797.	3.0	1
10	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
11	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
12	Rickettsia buchneri, symbiont of the deer tick Ixodes scapularis, can colonise the salivary glands of its host. Ticks and Tick-borne Diseases, 2020, 11, 101299.	2.7	21
13	Human papillomavirus infection and cervical dysplasia in HIV-positive women. Aids, 2020, 34, 115-125.	2.2	14
14	Functional Genomics of a Symbiotic Community: Shared Traits in the Olive Fruit Fly Gut Microbiota. Genome Biology and Evolution, 2020, 12, 3778-3791.	2.5	16
15	Characterization of Circulating Clostridium difficile Strains, Host Response and Intestinal Microbiome in Hospitalized Children With Diarrhea. Pediatric Infectious Disease Journal, 2020, 39, 221-228.	2.0	19
16	AcGI1, a novel genomic island carrying antibiotic resistance integron In687 in multidrug resistant Achromobacter xylosoxidans in a teaching hospital in Thailand. FEMS Microbiology Letters, 2020, 367, .	1.8	4
17	Intermittent Lactobacilli-containing Vaginal Probiotic or Metronidazole Use to Prevent Bacterial Vaginosis Recurrence: A Pilot Study Incorporating Microscopy and Sequencing. Scientific Reports, 2020, 10, 3884.	3.3	40
18	Isolation and Propagation of Laboratory Strains and a Novel Flea-Derived Field Strain of Wolbachia in Tick Cell Lines. Microorganisms, 2020, 8, 988.	3.6	15

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19	Isolation of Candidatus Rickettsia vini from Belgian Ixodes arboricola ticks and propagation in tick cell lines. Ticks and Tick-borne Diseases, 2020, 11, 101511.	2.7	5
20	Insectâ€"Symbiont Gene Expression in the Midgut Bacteriocytes of a Blood-Sucking Parasite. Genome Biology and Evolution, 2020, 12, 429-442.	2.5	15
21	Trypanosomatid parasite dynamically changes the transcriptome during infection and modifies honey bee physiology. Communications Biology, 2020, 3, 51.	4.4	28
22	The Hypercomplex Genome of an Insect Reproductive Parasite Highlights the Importance of Lateral Gene Transfer in Symbiont Biology. MBio, 2020, 11, .	4.1	14
23	Large-scale and significant expression from pseudogenes in Sodalis glossinidius â€“ a facultative bacterial endosymbiont. Microbial Genomics, 2020, 6, .	2.0	12
24	Diminutive, degraded but dissimilar: Wolbachia genomes from filarial nematodes do not conform to a single paradigm. Microbial Genomics, 2020, 6, .	2.0	24
25	DNA extraction and amplicon production strategies deeply infâ€Šluence the outcome of gut mycobiome studies. Scientific Reports, 2019, 9, 9328.	3.3	51
26	â€œBowel on the Benchâ€: Proof of Concept of a Three-Stage, In Vitro Fermentation Model of the Equine Large Intestine. Applied and Environmental Microbiology, 2019, 86, .	3.1	7
27	A Tale of Three Species: Adaptation of Sodalis glossinidius to Tsetse Biology, Wigglesworthia Metabolism, and Host Diet. MBio, 2019, 10, .	4.1	23
28	Draft Genome of Busseola fusca, the Maize Stalk Borer, a Major Crop Pest in Sub-Saharan Africa. Genome Biology and Evolution, 2019, 11, 2203-2207.	2.5	5
29	Aquatic Hemiptera in Southwest Cameroon: Biodiversity of Potential Reservoirs of Mycobacterium ulcerans and Multiple Wolbachia Sequence Types Revealed by Metagenomics. Diversity, 2019, 11, 225.	1.7	2
30	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
31	Multi-locus sequence typing of Ixodes ricinus and its symbiont Candidatus Midichloria mitochondrii across Europe reveals evidence of local co-cladogenesis in Scotland. Ticks and Tick-borne Diseases, 2019, 10, 52-62.	2.7	22
32	High-Quality Draft Genome Sequence and Annotation of the Basidiomycete Yeast Sporisorium graminicola CBS10092, a Producer of Mannosylerythritol Lipids. Microbiology Resource Announcements, 2019, 8, .	0.6	6
33	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. PeerJ, 2019, 7, e6448.	2.0	10
34	The Tick Cell Biobank: new arthropod cell lines for arbovirus research. Access Microbiology, 2019, 1, .	0.5	0
35	The effect of gut microbiota elimination in Drosophila melanogaster: A howâ€to guide for hostâ€“microbiota studies. Ecology and Evolution, 2018, 8, 4150-4161.	1.9	35
36	Exploration of the Fecal Microbiota and Biomarker Discovery in Equine Grass Sickness. Journal of Proteome Research, 2018, 17, 1120-1128.	3.7	18

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37	OWE-010â€...Bacterial and fungal communities in faeces and biopsies in IBD. , 2018, , .		0
38	Genomes of trombidid mites reveal novel predicted allergens and laterally transferred genes associated with secondary metabolism. GigaScience, 2018, 7, .	6.4	32
39	Improved reference genome of Aedes aegypti informs arbovirus vector control. Nature, 2018, 563, 501-507.	27.8	426
40	Comparative Genomics of Staphylococcus Reveals Determinants of Speciation and Diversification of Antimicrobial Defense. Frontiers in Microbiology, 2018, 9, 2753.	3.5	22
41	The sequence of a male-specific genome region containing the sex determination switch in Aedes aegypti. Parasites and Vectors, 2018, 11, 549.	2.5	6
42	The Structure of a Conserved Telomeric Region Associated with Variant Antigen Loci in the Blood Parasite Trypanosoma congolense. Genome Biology and Evolution, 2018, 10, 2458-2473.	2.5	19
43	The Tick Cell Biobank: A global resource for in vitro research on ticks, other arthropods and the pathogens they transmit. Ticks and Tick-borne Diseases, 2018, 9, 1364-1371.	2.7	39
44	Draft Genome Sequence of Chryseobacterium Strain CBo1 Isolated from Bactrocera oleae. Genome Announcements, 2017, 5, .	0.8	4
45	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
46	Optimised conditions for handling and transport of male <scp>A</scp>nopheles arabiensis: effects of low temperature, compaction, and ventilation on male quality. Entomologia Experimentalis Et Applicata, 2017, 164, 276-283.	1.4	26
47	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
48	Draft genome of the honey bee ectoparasitic mite, Tropilaelaps mercedesae, is shaped by the parasitic life history. GigaScience, 2017, 6, 1-17.	6.4	39
49	Mycoplasma tullyi sp. nov., isolated from penguins of the genus Spheniscus. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3692-3698.	1.7	15
50	Evaluation of Lysis Methods for the Extraction of Bacterial DNA for Analysis of the Vaginal Microbiota. PLoS ONE, 2016, 11, e0163148.	2.5	67
51	Bacterial sensing underlies artificial sweetenerâ€induced growth of gut <scp>L</scp>actobacillus. Environmental Microbiology, 2016, 18, 2159-2171.	3.8	27
52	Draft Genome Sequence of the Bactrocera oleae Symbiont â€œ Candidatus Erwinia dacicolaâ€• Genome Announcements, 2016, 4, .	0.8	30
53	Draft Genome Sequence of Stenotrophomonas maltophilia SBo1 Isolated from Bactrocera oleae. Genome Announcements, 2016, 4, .	0.8	9
54	Genome sequence of Candidatus Arsenophonus lipopteni, the exclusive symbiont of a blood sucking fly Lipoptena cervi (Diptera: Hippoboscidae). Standards in Genomic Sciences, 2016, 11, 72.	1.5	46

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55	Revised Genome Sequence of the Purple Photosynthetic Bacterium Blastochloris viridis. Genome Announcements, 2016, 4, .	0.8	7
56	The industrial melanism mutation in British peppered moths is a transposable element. Nature, 2016, 534, 102-105.	27.8	386
57	Transcriptome sequencing of human breast cancer reveals aberrant intronic transcription in amplicons and dysregulation of alternative splicing with major therapeutic implications. International Journal of Oncology, 2016, 48, 130-144.	3.3	7
58	Low calorie sweeteners and gut microbiota. Physiology and Behavior, 2016, 164, 494-500.	2.1	30
59	A comprehensive benchmarking study of protocols and sequencing platforms for 16S rRNA community profiling. BMC Genomics, 2016, 17, 55.	2.8	387
60	Supergroup C Wolbachia , mutualist symbionts of filarial nematodes, have a distinct genome structure. Open Biology, 2015, 5, 150099.	3.6	38
61	Characterisation of the faecal metabolome and microbiome of Thoroughbred racehorses. Equine Veterinary Journal, 2015, 47, 580-586.	1.7	51
62	Complete Genome Sequence of Leptospira interrogans Serovar Bratislava, Strain PigK151. Genome Announcements, 2015, 3, .	0.8	5
63	Acetogenesis from H ₂ plus CO ₂ and nitrogen fixation by an endosymbiotic spirochete of a termite-gut cellulolytic protist. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10224-10230.	7.1	108
64	Divergence of a strain of Pseudomonas aeruginosa during an outbreak of ovine mastitis. Veterinary Microbiology, 2015, 175, 105-113.	1.9	15
65	Taking the pseudo out of pseudogenes. Current Opinion in Microbiology, 2015, 23, 102-109.	5.1	67
66	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
67	Dietary supplementation with lactose or artificial sweetener enhances swine gutLactobacilluspopulation abundance. British Journal of Nutrition, 2014, 111, S30-S35.	2.3	77
68	Integrated transcriptomic and proteomic analysis of the global response of Wolbachia to doxycycline-induced stress. ISME Journal, 2014, 8, 925-937.	9.8	38
69	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
70	Iron Necessity: The Secret of Wolbachia's Success?. PLoS Neglected Tropical Diseases, 2014, 8, e3224.	3.0	51
71	Draft Genome Sequence of Cytophaga fermentans JCM 21142 ^T , a Facultative Anaerobe Isolated from Marine Mud. Genome Announcements, 2014, 2, .	0.8	4
72	Genome Sequence of the Tsetse Fly (Glossina morsitans): Vector of African Trypanosomiasis. Science, 2014, 344, 380-386.	12.6	254

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73	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
74	Phylogeny and prevalence of kobuviruses in dogs and cats in the UK. Veterinary Microbiology, 2013, 164, 246-252.	1.9	48
75	Phylogenomics and Analysis of Shared Genes Suggest a Single Transition to Mutualism in Wolbachia of Nematodes. Genome Biology and Evolution, 2013, 5, 1668-1674.	2.5	49
76	COPD Causation and Workplace Exposures: An Assessment of Agreement among Expert Clinical Raters. COPD: Journal of Chronic Obstructive Pulmonary Disease, 2013, 10, 172-179.	1.6	5
77	Genome Sequence for â€œCandidatus Mycoplasma haemominutum,â€•a Low-Pathogenicity Hemoplasma Species. Journal of Bacteriology, 2012, 194, 905-906.	2.2	13
78	Application of next-generation sequencing technologies in virology. Journal of General Virology, 2012, 93, 1853-1868.	2.9	241
79	Analysis of gene expression from the Wolbachia genome of a filarial nematode supports both metabolic and defensive roles within the symbiosis. Genome Research, 2012, 22, 2467-2477.	5.5	155
80	Comparative genomics of Shiga toxin encoding bacteriophages. BMC Genomics, 2012, 13, 311.	2.8	98
81	Comparative genomics of Brachyspira pilosicoli strains: genome rearrangements, reductions and correlation of genetic compliment with phenotypic diversity. BMC Genomics, 2012, 13, 454.	2.8	38
82	Investigation of the Bacterial Communities Associated with Females of Lutzomyia Sand Fly Species from South America. PLoS ONE, 2012, 7, e42531.	2.5	58
83	Molecular characterization of the uncultivatable hemotropic bacterium Mycoplasma haemofelis. Veterinary Research, 2011, 42, 83.	3.0	15
84	Genomic Analysis of Highly Virulent Georgia 2007/1 Isolate of African Swine Fever Virus. Emerging Infectious Diseases, 2011, 17, 599-605.	4.3	186
85	Complete Genome Sequence of Mycoplasma haemofelis, a Hemotropic Mycoplasma. Journal of Bacteriology, 2011, 193, 2060-2061.	2.2	21
86	Cryptic Diversity within the Major Trypanosomiasis Vector Glossina fuscipes Revealed by Molecular Markers. PLoS Neglected Tropical Diseases, 2011, 5, e1266.	3.0	22
87	A De Novo Expression Profiling of Anopheles funestus, Malaria Vector in Africa, Using 454 Pyrosequencing. PLoS ONE, 2011, 6, e17418.	2.5	47
88	Characteristics of the genome of Arsenophonus nasoniae, sonâ€killer bacterium of the wasp Nasonia. Insect Molecular Biology, 2010, 19, 75-89.	2.0	94
89	The draft genome sequence of Arsenophonus nasoniae, sonâ€killer bacterium of Nasonia vitripennis, reveals genes associated with virulence and symbiosis. Insect Molecular Biology, 2010, 19, 59-73.	2.0	46
90	Characterization of Pneumonia Due to Streptococcus equi subsp. zooepidemicus in Dogs. Vaccine Journal, 2010, 17, 1790-1796.	3.1	36

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91	Identification of Three Novel Superantigen-Encoding Genes in Streptococcus equi subsp. zooepidemicus , szeF , szeN , and szeP. Infection and Immunity, 2010, 78, 4817-4827.	2.2	56
92	Comparative Genomics and Transduction Potential of Enterococcus faecalis Temperate Bacteriophages. Journal of Bacteriology, 2010, 192, 1122-1130.	2.2	71
93	Amplified fragment length polymorphism (AFLP) analysis of closely related wild and captive tsetse fly (Glossina morsitans morsitans) populations. Parasites and Vectors, 2010, 3, 47.	2.5	8
94	Functional and Evolutionary Insights from the Genomes of Three Parasitoid Nasonia Species. Science, 2010, 327, 343-348.	12.6	808
95	The mosaic genome structure of the Wolbachia w Ri strain infecting Drosophila simulans. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5725-5730.	7.1	236
96	Symbiosis Research as a Novel Strategy for Insect Pest Control. , 2009, , 207-231.		2
97	The inherited microbiota of arthropods, and their importance in understanding resistance and immunity. , 2009, , 119-136.		11
98	Fast forward genetics. Nature Biotechnology, 2008, 26, 1248-1249.	17.5	11
99	Visualization of pseudogenes in intracellular bacteria reveals the different tracks to gene destruction. Genome Biology, 2008, 9, R42.	9.6	32
100	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
101	The Orientia tsutsugamushi genome reveals massive proliferation of conjugative type IV secretion system and host cell interaction genes. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7981-7986.	7.1	219
102	Antioxidants promote establishment of trypanosome infections in tsetse. Parasitology, 2007, 134, 827-831.	1.5	105
103	The genomic and metabolic diversity of Rickettsia. Research in Microbiology, 2007, 158, 745-753.	2.1	64
104	Intracellular pathogens go extreme: genome evolution in the Rickettsiales. Trends in Genetics, 2007, 23, 511-520.	6.7	211
105	Factors Affecting Trypanosome Maturation in Tsetse Flies. PLoS ONE, 2007, 2, e239.	2.5	36
106	The rapid isolation and growth dynamics of the tsetse symbiontSodalis glossinidius. FEMS Microbiology Letters, 2005, 248, 69-74.	1.8	35
107	Extrachromosomal DNA of the Symbiont Sodalis glossinidius. Journal of Bacteriology, 2005, 187, 5003-5007.	2.2	31
108	Aphid-Symbiotic Bacteria Cultured in Insect Cell Lines. Applied and Environmental Microbiology, 2005, 71, 4833-4839.	3.1	81

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109	Linking the bacterial community in pea aphids with host-plant use and natural enemy resistance. Ecological Entomology, 2004, 29, 60-65.	2.2	227
110	Diversity of Bacteria Associated with Natural AphidPopulations. Applied and Environmental Microbiology, 2003, 69, 7216-7223.	3.1	129
111	Elucidation of the Transmission Patterns of an Insect-Borne Bacterium. Applied and Environmental Microbiology, 2003, 69, 4403-4407.	3.1	88
112	The significance of a facultative bacterium to natural populations of the pea aphid Acyrthosiphon pisum. Ecological Entomology, 2003, 28, 145-150.	2.2	22
113	An aphid-borne bacterium allied to the secondary symbionts of whitefly. FEMS Microbiology Ecology, 2001, 36, 43-50.	2.7	86
114	An aphid-borne bacterium allied to the secondary symbionts of whitefly. FEMS Microbiology Ecology, 2001, 36, 43-50.	2.7	7
115	The olfactory responses of coccinellids to aphids on plants. Entomologia Experimentalis Et Applicata, 2000, 95, 113-117.	1.4	18
116	Intraguild predators and the spatial distribution of a parasitoid. Oecologia, 2000, 124, 367-372.	2.0	57