

Alasdair C Ivens

List of Publications by Year in descending order

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115
papers

10,549
citations

41344

49
h-index

33894

99
g-index

117
all docs

117
docs citations

117
times ranked

12388
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genome of the Kinetoplastid Parasite, <i>Leishmania major</i> . <i>Science</i> , 2005, 309, 436-442.	12.6	1,237
2	The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , 2009, 460, 352-358.	27.8	945
3	Comparative Genomics of Trypanosomatid Parasitic Protozoa. <i>Science</i> , 2005, 309, 404-409.	12.6	713
4	Comparative genomic analysis of three <i>Leishmania</i> species that cause diverse human disease. <i>Nature Genetics</i> , 2007, 39, 839-847.	21.4	648
5	Exosomes secreted by nematode parasites transfer small RNAs to mammalian cells and modulate innate immunity. <i>Nature Communications</i> , 2014, 5, 5488.	12.8	640
6	Genome sequence of a proteolytic (Group I) <i>Clostridium botulinum</i> strain Hall A and comparative analysis of the clostridial genomes. <i>Genome Research</i> , 2007, 17, 1082-1092.	5.5	228
7	Sir2 Paralogues Cooperate to Regulate Virulence Genes and Antigenic Variation in <i>Plasmodium falciparum</i> . <i>PLoS Biology</i> , 2009, 7, e1000084.	5.6	211
8	GeneDB: a resource for prokaryotic and eukaryotic organisms. <i>Nucleic Acids Research</i> , 2004, 32, 339D-343.	14.5	199
9	A gene expression atlas of the domestic pig. <i>BMC Biology</i> , 2012, 10, 90.	3.8	199
10	Genome-wide dissection of the quorum sensing signalling pathway in <i>Trypanosoma brucei</i> . <i>Nature</i> , 2014, 505, 681-685.	27.8	186
11	Genomic analysis of the causative agents of coccidiosis in domestic chickens. <i>Genome Research</i> , 2014, 24, 1676-1685.	5.5	176
12	Combinatorial quorum sensing allows bacteria to resolve their social and physical environment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4280-4284.	7.1	163
13	A structurally distinct TGF- β mimic from an intestinal helminth parasite potently induces regulatory T cells. <i>Nature Communications</i> , 2017, 8, 1741.	12.8	159
14	Parasite-Derived MicroRNAs in Host Serum As Novel Biomarkers of Helminth Infection. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2701.	3.0	143
15	Protein and small non-coding RNA-enriched extracellular vesicles are released by the pathogenic blood fluke <i>Schistosoma mansoni</i> . <i>Journal of Extracellular Vesicles</i> , 2015, 4, 28665.	12.2	140
16	The lung environment controls alveolar macrophage metabolism and responsiveness in type 2 inflammation. <i>Nature Immunology</i> , 2019, 20, 571-580.	14.5	140
17	HpARI Protein Secreted by a Helminth Parasite Suppresses Interleukin-33. <i>Immunity</i> , 2017, 47, 739-751.e5.	14.3	130
18	Epigenetic Silencing of <i>Plasmodium falciparum</i> Genes Linked to Erythrocyte Invasion. <i>PLoS Pathogens</i> , 2007, 3, e107.	4.7	129

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19	Genome and Phylogenetic Analyses of <i>Trypanosoma evansi</i> Reveal Extensive Similarity to <i>T. brucei</i> and Multiple Independent Origins for Dyskinetoplasty. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e3404.	3.0	124
20	Altered retinal microRNA expression profile in a mouse model of retinitis pigmentosa. <i>Genome Biology</i> , 2007, 8, R248.	9.6	120
21	Anti-schistosomal Intervention Targets Identified by Lifecycle Transcriptomic Analyses. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e543.	3.0	116
22	Linkage of an X-chromosome cleft palate gene. <i>Nature</i> , 1987, 326, 91-92.	27.8	115
23	Small RNA Profiling in Dengue Virus 2-Infected <i>Aedes</i> Mosquito Cells Reveals Viral piRNAs and Novel Host miRNAs. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004452.	3.0	113
24	Identification of a human neonatal immune-metabolic network associated with bacterial infection. <i>Nature Communications</i> , 2014, 5, 4649.	12.8	112
25	Dynamics of Colon Monocyte and Macrophage Activation During Colitis. <i>Frontiers in Immunology</i> , 2018, 9, 2764.	4.8	111
26	Sex Determination in the Social Amoeba <i>Dictyostelium discoideum</i> . <i>Science</i> , 2010, 330, 1533-1536.	12.6	100
27	Gene Expression Patterns in Larval <i>Schistosoma mansoni</i> Associated with Infection of the Mammalian Host. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1274.	3.0	98
28	Extracellular <i>Onchocerca</i> -derived small RNAs in host nodules and blood. <i>Parasites and Vectors</i> , 2015, 8, 58.	2.5	98
29	Differences in the Faecal Microbiome in <i>Schistosoma haematobium</i> Infected Children vs. Uninfected Children. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003861.	3.0	94
30	Gene synteny and evolution of genome architecture in trypanosomatids. <i>Molecular and Biochemical Parasitology</i> , 2004, 134, 183-191.	1.1	92
31	A dominant role for the methyl-CpG-binding protein Mbd2 in controlling Th2 induction by dendritic cells. <i>Nature Communications</i> , 2015, 6, 6920.	12.8	87
32	Protein variation in blood-dwelling schistosome worms generated by differential splicing of micro-exon gene transcripts. <i>Genome Research</i> , 2010, 20, 1112-1121.	5.5	86
33	Comparative Expression Profiling of <i>Leishmania</i> : Modulation in Gene Expression between Species and in Different Host Genetic Backgrounds. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e476.	3.0	86
34	Genetic nomenclature for <i>Trypanosoma</i> and <i>Leishmania</i> . <i>Molecular and Biochemical Parasitology</i> , 1998, 97, 221-224.	1.1	83
35	Genome-wide discovery and verification of novel structured RNAs in <i>Plasmodium falciparum</i> . <i>Genome Research</i> , 2008, 18, 281-292.	5.5	81
36	A Physical Map of the <i>Leishmania major</i> Genome. <i>Genome Research</i> , 1998, 8, 135-145.	5.5	78

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37	Expression profiling of the Leishmania life cycle: cDNA arrays identify developmentally regulated genes present but not annotated in the genome. <i>Molecular and Biochemical Parasitology</i> , 2004, 136, 87-100.	1.1	76
38	Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of <i>Schistosoma mansoni</i> . <i>International Journal for Parasitology</i> , 2006, 36, 1-8.	3.1	74
39	Clinically Relevant Mutant DNA Gyrase Alters Supercoiling, Changes the Transcriptome, and Confers Multidrug Resistance. <i>MBio</i> , 2013, 4, .	4.1	73
40	The human homeobox gene HOX7 maps to chromosome 4p16.1 and may be implicated in Wolf-Hirschhorn syndrome. <i>Human Genetics</i> , 1990, 84, 473-6.	3.8	70
41	Genome-wide transcriptional changes induced by phagocytosis or growth on bacteria in <i>Dictyostelium</i> . <i>BMC Genomics</i> , 2008, 9, 291.	2.8	68
42	Genomics and the biology of parasites. <i>BioEssays</i> , 1999, 21, 131-147.	2.5	67
43	Widespread duplications in the genomes of laboratory stocks of <i>Dictyostelium discoideum</i> . <i>Genome Biology</i> , 2008, 9, R75.	9.6	67
44	Structure and sequence of the human homeobox gene HOX7. <i>Genomics</i> , 1991, 11, 670-678.	2.9	66
45	<i>Leishmania major</i> chromosome 3 contains two long convergent polycistronic gene clusters separated by a tRNA gene. <i>Nucleic Acids Research</i> , 2003, 31, 4201-4210.	14.5	65
46	Advances in schistosome genomics. <i>Trends in Parasitology</i> , 2004, 20, 154-157.	3.3	61
47	Prophage Sequences Defining Hot Spots of Genome Variation in <i>Salmonella enterica</i> Serovar Typhimurium Can Be Used To Discriminate between Field Isolates. <i>Journal of Clinical Microbiology</i> , 2007, 45, 2590-2598.	3.9	59
48	Differentially expressed <i>Leishmania major</i> gp63 genes encode cell surface leishmanolysin with distinct signals for glycosylphosphatidylinositol attachment1Note: Nucleotide sequence data reported in this paper are available in the GenBank database under the accession number AF039721.1. <i>Molecular and Biochemical Parasitology</i> , 1998, 93, 31-41.	1.1	58
49	Coming in on schistosomes: prospects and limitations for post-genomics. <i>Trends in Parasitology</i> , 2007, 23, 14-20.	3.3	53
50	Microarray-based comparative genomic analyses of the human malaria parasite <i>Plasmodium falciparum</i> using Affymetrix arrays. <i>Molecular and Biochemical Parasitology</i> , 2005, 144, 177-186.	1.1	52
51	Characterization of the Genomes of a Diverse Collection of <i>Salmonella enterica</i> Serovar Typhimurium Definitive Phage Type 104. <i>Journal of Bacteriology</i> , 2008, 190, 8155-8162.	2.2	51
52	From genomes to vaccines: <i>Leishmania</i> as a model. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2002, 357, 5-11.	4.0	49
53	Sequencing and analysis of chromosome 1 of <i>Eimeria tenella</i> reveals a unique segmental organization. <i>Genome Research</i> , 2007, 17, 311-319.	5.5	49
54	<i>Salmonella</i> Typhi sense host neuroendocrine stress hormones and release the toxin haemolysin E. <i>EMBO Reports</i> , 2011, 12, 252-258.	4.5	47

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55	Dictyostelium transcriptional responses to Pseudomonas aeruginosa: common and specific effects from PAO1 and PA14 strains. BMC Microbiology, 2008, 8, 109.	3.3	46
56	A gene expression comparison of Trypanosoma brucei and Trypanosoma congolense in the bloodstream of the mammalian host reveals species-specific adaptations to density-dependent development. PLoS Neglected Tropical Diseases, 2018, 12, e0006863.	3.0	46
57	Ectopic Recombination of a Malaria var Gene during Mitosis Associated with an Altered var Switch Rate. Journal of Molecular Biology, 2009, 389, 453-469.	4.2	45
58	Boudicca , a Retrovirus-Like Long Terminal Repeat Retrotransposon from the Genome of the Human Blood Fluke Schistosoma mansoni. Journal of Virology, 2003, 77, 6153-6166.	3.4	44
59	Inducible mechanisms of disease tolerance provide an alternative strategy of acquired immunity to malaria. ELife, 2021, 10, .	6.0	43
60	Genomic and phenotypic variation in epidemic-spanning Salmonella enterica serovar Enteritidis isolates. BMC Microbiology, 2009, 9, 237.	3.3	42
61	Assembly and annotation of the mitochondrial minicircle genome of a differentiation-competent strain of Trypanosoma brucei. Nucleic Acids Research, 2019, 47, 11304-11325.	14.5	42
62	Interspecies quorum sensing in co-infections can manipulate trypanosome transmission potential. Nature Microbiology, 2017, 2, 1471-1479.	13.3	40
63	The Complete Chromosomal Organization of the Reference Strain of the Leishmania Genome Project, L. major 'Friedlin'. Parasitology Today, 1998, 14, 301-303.	3.0	39
64	A draft genome for the African crocodylian trypanosome Trypanosoma grayi. Scientific Data, 2014, 1, 140024.	5.3	39
65	TGF- β 2 mimic proteins form an extended gene family in the murine parasite Heligmosomoides polygyrus. International Journal for Parasitology, 2018, 48, 379-385.	3.1	39
66	Gene copy number variation throughout the Plasmodium falciparum genome. BMC Genomics, 2009, 10, 353.	2.8	38
67	Regulation of Trypanosoma brucei Total and Polysomal mRNA during Development within Its Mammalian Host. PLoS ONE, 2013, 8, e67069.	2.5	38
68	The Leishmania genome project: new insights into gene organization and function. Medical Microbiology and Immunology, 2001, 190, 9-12.	4.8	36
69	Non-linear hierarchy of the quorum sensing signalling pathway in bloodstream form African trypanosomes. PLoS Pathogens, 2018, 14, e1007145.	4.7	36
70	The Amoebal MAP Kinase Response to Legionella pneumophila Is Regulated by DupA. Cell Host and Microbe, 2009, 6, 253-267.	11.0	35
71	The gut microbiome but not the resistome is associated with urogenital schistosomiasis in preschool-aged children. Communications Biology, 2020, 3, 155.	4.4	33
72	Whole blood gene expression profiling of neonates with confirmed bacterial sepsis. Genomics Data, 2015, 3, 41-48.	1.3	32

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73	Genome-wide RNAi selection identifies a regulator of transmission stage-enriched gene families and cell-type differentiation in <i>Trypanosoma brucei</i> . <i>PLoS Pathogens</i> , 2017, 13, e1006279.	4.7	30
74	An Alternative Strategy for Trypanosome Survival in the Mammalian Bloodstream Revealed through Genome and Transcriptome Analysis of the Ubiquitous Bovine Parasite <i>Trypanosoma (Megatrypanum) theileri</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 2093-2109.	2.5	29
75	Unravelling the <i>Leishmania</i> genome. <i>Current Opinion in Genetics and Development</i> , 1996, 6, 704-710.	3.3	28
76	<i>Leishmania</i> RAB7: characterisation of terminal endocytic stages in an intracellular parasite. <i>Molecular and Biochemical Parasitology</i> , 2002, 123, 105-113.	1.1	27
77	Macrophage Migration Inhibitory Factor (MIF) Is Essential for Type 2 Effector Cell Immunity to an Intestinal Helminth Parasite. <i>Frontiers in Immunology</i> , 2019, 10, 2375.	4.8	26
78	NMD3 regulates both mRNA and rRNA nuclear export in African trypanosomes via an XPO1-linked pathway. <i>Nucleic Acids Research</i> , 2015, 43, 4491-4504.	14.5	25
79	A new <i>Dictyostelium</i> prestalk cell sub-type. <i>Developmental Biology</i> , 2010, 339, 390-397.	2.0	23
80	Mapping immune variation and var gene switching in naive hosts infected with <i>Plasmodium falciparum</i> . <i>ELife</i> , 2021, 10, .	6.0	22
81	Helminth-induced Th2 cell dysfunction is distinct from exhaustion and is maintained in the absence of antigen. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007908.	3.0	21
82	A global map of the <i>Leishmania</i> major genome: prelude to genomic sequencing. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 1997, 91, 111-115.	1.8	20
83	Altered Patterns of Gene Expression Underlying the Enhanced Immunogenicity of Radiation-Attenuated Schistosomes. <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e240.	3.0	20
84	Heterogeneity of Phenotype and Function Reflects the Multistage Development of T Follicular Helper Cells. <i>Frontiers in Immunology</i> , 2017, 8, 489.	4.8	19
85	Comparative analysis of small RNAs released by the filarial nematode <i>Litomosoides sigmodontis</i> in vitro and in vivo. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007811.	3.0	19
86	Secondary DNA structure analysis of the coding strand switch regions of five <i>Leishmania</i> major Friedlin chromosomes. <i>Current Genetics</i> , 2001, 40, 186-194.	1.7	18
87	<i>Leishmania</i> major: Histone H1 Gene Expression from the sw3Locus. <i>Experimental Parasitology</i> , 1999, 91, 151-160.	1.2	17
88	Combinatorial Communication in Bacteria: Implications for the Origins of Linguistic Generativity. <i>PLoS ONE</i> , 2014, 9, e95929.	2.5	17
89	The generation of ordered sets of cosmid DNA clones from human chromosome region 11p. <i>Genomics</i> , 1992, 13, 89-94.	2.9	16
90	Identification and cloning of Lmairk, a member of the Aurora/Ipl1p protein kinase family, from the human protozoan parasite <i>Leishmania</i> . <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2001, 1519, 241-245.	2.4	16

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91	Molecular cloning and characterization of two new isoforms of the protein kinase A catalytic subunit from the human parasite <i>Leishmania</i> . <i>Gene</i> , 2002, 288, 65-75.	2.2	16
92	The TCA cycle is not required for selection or survival of multidrug-resistant <i>Salmonella</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 589-599.	3.0	14
93	Inhibition of Microprocessor Function during the Activation of the Type I Interferon Response. <i>Cell Reports</i> , 2018, 23, 3275-3285.	6.4	14
94	Comparison of two DNA microarrays for detection of plasmid-mediated antimicrobial resistance and virulence factor genes in clinical isolates of Enterobacteriaceae and non-Enterobacteriaceae. <i>International Journal of Antimicrobial Agents</i> , 2010, 35, 593-598.	2.5	13
95	The Methyl-CpG-Binding Protein Mbd2 Regulates Susceptibility to Experimental Colitis via Control of CD11c+ Cells and Colonic Epithelium. <i>Frontiers in Immunology</i> , 2020, 11, 183.	4.8	11
96	Two Novel Src Homology 2 Domain Proteins Interact to Regulate <i>Dictyostelium</i> Gene Expression during Growth and Early Development. <i>Journal of Biological Chemistry</i> , 2010, 285, 22927-22935.	3.4	9
97	High-Throughput Chemical Screening for Antivirulence Developmental Phenotypes in <i>Trypanosoma brucei</i> . <i>Eukaryotic Cell</i> , 2014, 13, 412-426.	3.4	9
98	Identification of a Functional Small Noncoding RNA of African Swine Fever Virus. <i>Journal of Virology</i> , 2020, 94, .	3.4	9
99	Site-specific and substrate-specific control of accurate mRNA editing by a helicase complex in trypanosomes. <i>Rna</i> , 2020, 26, 1862-1881.	3.5	9
100	X Chromosome Genes Involved in the Regulation of Facial Clefting and Spina Bifida. <i>The Cleft Palate Journal</i> , 1990, 27, 131-135.	0.6	8
101	Integration of tools and resources for display and analysis of genomic data for protozoan parasites. <i>International Journal for Parasitology</i> , 2005, 35, 481-493.	3.1	8
102	Modulation of dendritic cell alternative activation and function by the vitamin A metabolite retinoic acid. <i>International Immunology</i> , 2015, 27, 589-596.	4.0	8
103	Developmental competence and antigen switch frequency can be uncoupled in <i>Trypanosoma brucei</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 22774-22782.	7.1	7
104	Quantitative Analysis of MicroRNAs in <i>Vaccinia</i> virus Infection Reveals Diversity in Their Susceptibility to Modification and Suppression. <i>PLoS ONE</i> , 2015, 10, e0131787.	2.5	6
105	Targets downstream of Cdk8 in <i>Dictyostelium</i> development. <i>BMC Developmental Biology</i> , 2011, 11, 2.	2.1	4
106	Harnessing the genome: development of a hierarchical typing scheme for methicillin-resistant <i>Staphylococcus aureus</i> . <i>Journal of Medical Microbiology</i> , 2013, 62, 36-45.	1.8	4
107	A <i>Dictyostelium</i> SH2 adaptor protein required for correct DIF-1 signaling and pattern formation. <i>Developmental Biology</i> , 2011, 353, 290-301.	2.0	3
108	A global analysis of low-complexity regions in the <i>Trypanosoma brucei</i> proteome reveals enrichment in the C-terminus of nucleic acid binding proteins providing potential targets of phosphorylation. <i>Wellcome Open Research</i> , 0, 5, 219.	1.8	2

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109	A software framework for microarray and gene expression object model (MAGE-OM) array design annotation. BMC Genomics, 2008, 9, 133.	2.8	1
110	Leishmania major chromosome 3 contains two long convergent polycistronic gene clusters separated by a tRNA gene. Nucleic Acids Research, 2004, 32, 6716-6716.	14.5	0
111	O14â€œ..Whole blood profiling of T-cell derived miRNA allows the development of prognostic models in IBD. , 2021, , .		0
112	A global analysis of low-complexity regions in the Trypanosoma brucei proteome reveals enrichment in the C-terminus of nucleic acid binding proteins providing potential targets of phosphorylation. Wellcome Open Research, 2020, 5, 219.	1.8	0
113	Title is missing!. , 2019, 13, e0007908.		0
114	Title is missing!. , 2019, 13, e0007908.		0
115	Title is missing!. , 2019, 13, e0007908.		0