Jenefer Blackwell

List of Publications by Year in descending order

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213 papers 18,118 citations

18436 62 h-index 126 g-index

219 all docs

219 docs citations

times ranked

219

21655 citing authors

#	Article	IF	CITATIONS
1	Anti–Interleukin-10 Unleashes Transcriptional Response to Leishmanial Antigens in Visceral Leishmaniasis Patients. Journal of Infectious Diseases, 2021, 223, 517-521.	1.9	5
2	Zika Virus Changes Methylation of Genes Involved in Immune Response and Neural Development in Brazilian Babies Born With Congenital Microcephaly. Journal of Infectious Diseases, 2021, 223, 435-440.	1.9	16
3	A Genome-wide Association Study Identifies <i>SERPINB10, CRLF3, STX7</i> , <i>LAMP3, IFNG-AS1</i> , and <i>KRT80</i> As Risk Loci Contributing to Cutaneous Leishmaniasis in Brazil. Clinical Infectious Diseases, 2021, 72, e515-e525.	2.9	16
4	Common and Rare Genetic Variants That Could Contribute to Severe Otitis Media in an Australian Aboriginal Population. Clinical Infectious Diseases, 2021, 73, 1860-1870.	2.9	4
5	Reference exome data for Australian Aboriginal populations to support health-based research. Scientific Data, 2020, 7, 129.	2.4	0
6	Reference exome data for a Northern Brazilian population. Scientific Data, 2020, 7, 360.	2.4	0
7	Genetics, Transcriptomics and Meta-Taxonomics in Visceral Leishmaniasis. Frontiers in Cellular and Infection Microbiology, 2020, 10, 590888.	1.8	6
8	A flexible computational pipeline for research analyses of unsolved clinical exome cases. Npj Genomic Medicine, 2020, 5, 54.	1.7	4
9	Human genetics of leishmania infections. Human Genetics, 2020, 139, 813-819.	1.8	25
10	Transketolase and vitamin B1 influence on ROS-dependent neutrophil extracellular traps (NETs) formation. PLoS ONE, 2019, 14, e0221016.	1.1	16
11	Transcriptional blood signatures for active and amphotericin B treated visceral leishmaniasis in India. PLoS Neglected Tropical Diseases, 2019, 13, e0007673.	1.3	16
12	Meta-taxonomic analysis of prokaryotic and eukaryotic gut flora in stool samples from visceral leishmaniasis cases and endemic controls in Bihar State India. PLoS Neglected Tropical Diseases, 2019, 13, e0007444.	1.3	37
13	Determinants for progression from asymptomatic infection to symptomatic visceral leishmaniasis: A cohort study. PLoS Neglected Tropical Diseases, 2019, 13, e0007216.	1.3	36
14	Personalised analytics for rare disease diagnostics. Nature Communications, 2019, 10, 5274.	5.8	15
15	Genetic Susceptibility to Visceral Leishmaniasis. , 2019, , 71-85.		3
16	<scp>HLA</scp> â€≺scp>DR Class <scp>II</scp> expression on myeloid and lymphoid cells in relation to <scp>HLA</scp> â€≺scp>DRB1 as a genetic risk factor for visceral leishmaniasis. Immunology, 2019, 156, 174-186.	2.0	4
17	Epitope-Binding Characteristics for Risk versus Protective DRB1 Alleles for Visceral Leishmaniasis. Journal of Immunology, 2018, 200, 2727-2737.	0.4	15
18	An in silico pipeline to filter the Toxoplasma gondii proteome for proteins that could traffic to the host cell nucleus and influence host cell epigenetic regulation. Memorias Do Instituto Oswaldo Cruz, 2018, 113, e170471.	0.8	4

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19	Arylsulphatase A Pseudodeficiency (ARSA-PD), hypertension and chronic renal disease in Aboriginal Australians. Scientific Reports, 2018, 8, 10912.	1.6	5
20	Epigenetic dysregulation of host gene expression in Toxoplasma infection with specific reference to dopamine and amyloid pathways. Infection, Genetics and Evolution, 2018, 65, 159-162.	1.0	17
21	Comprehensive candidate gene analysis for symptomatic or asymptomatic outcomes of <i>Leishmania infantum</i> infection in Brazil. Annals of Human Genetics, 2017, 81, 41-48.	0.3	8
22	Analysis of expression of FLI1 and MMP1 in American cutaneous leishmaniasis caused by Leishmania braziliensis infection. Infection, Genetics and Evolution, 2017, 49, 212-220.	1.0	9
23	Comparative analyses of whole genome sequences of Leishmania infantum isolates from humans and dogs in northeastern Brazil. International Journal for Parasitology, 2017, 47, 655-665.	1.3	32
24	Expression profiling of Sudanese visceral leishmaniasis patients pre―and postâ€ŧreatment with sodium stibogluconate. Parasite Immunology, 2017, 39, e12431.	0.7	16
25	Genome-Wide Analysis of Genetic Risk Factors for Rheumatic Heart Disease in Aboriginal Australians Provides Support for Pathogenic Molecular Mimicry. Journal of Infectious Diseases, 2017, 216, 1460-1470.	1.9	60
26	Toxoplasma Modulates Signature Pathways of Human Epilepsy, Neurodegeneration & Emp; Cancer. Scientific Reports, 2017, 7, 11496.	1.6	97
27	Burkholderia pseudomallei Evades Nramp1 (Slc11a1)- and NADPH Oxidase-Mediated Killing in Macrophages and Exhibits Nramp1-Dependent Virulence Gene Expression. Frontiers in Cellular and Infection Microbiology, 2017, 7, 350.	1.8	5
28	Toxoplasma gondii Infection Is Associated with Mitochondrial Dysfunction in-Vitro. Frontiers in Cellular and Infection Microbiology, 2017, 7, 512.	1.8	38
29	The rare and undiagnosed diseases diagnostic service $\hat{a}\in$ application of massively parallel sequencing in a state-wide clinical service. Orphanet Journal of Rare Diseases, 2016, 11, 77.	1.2	48
30	Fine mapping under linkage peaks for symptomatic or asymptomatic outcomes of Leishmania infantum infection in Brazil. Infection, Genetics and Evolution, 2016, 43, 1-5.	1.0	6
31	Reference genotype and exome data from an Australian Aboriginal population for health-based research. Scientific Data, 2016, 3, 160023.	2.4	19
32	Polymorphism in a lincRNA Associates with a Doubled Risk of Pneumococcal Bacteremia in Kenyan Children. American Journal of Human Genetics, 2016, 98, 1092-1100.	2.6	39
33	The â^' 308 bp TNF gene polymorphism influences tumor necrosis factor expression in leprosy patients in Bahia State, Brazil. Infection, Genetics and Evolution, 2016, 39, 147-154.	1.0	8
34	Immunogenetics of Parasitic and Bacterial Disease. , 2016, , 7-15.		0
35	Candidate gene analysis supports a role for polymorphisms at TCF7L2 as risk factors for type 2 diabetes in Sudan. Journal of Diabetes and Metabolic Disorders, 2015, 15, 4.	0.8	10
36	Wound healing genes and susceptibility to cutaneous leishmaniasis in Brazil: Role of COL1A1. Infection, Genetics and Evolution, 2015, 30, 225-229.	1.0	13

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37	Genome-wide association study of IgG1 responses to the choline-binding protein PspC of Streptococcus pneumoniae. Genes and Immunity, 2015, 16, 289-296.	2.2	3
38	First Genome-Wide Association Study in an Australian Aboriginal Population Provides Insights into Genetic Risk Factors for Body Mass Index and Type 2 Diabetes. PLoS ONE, 2015, 10, e0119333.	1.1	35
39	Immunogenetics of Host Response to Parasites in Humans. , 2014, , 483-490.		1
40	Genome-wide association study of vitamin D levels in children: replication in the Western Australian Pregnancy Cohort (Raine) study. Genes and Immunity, 2014, 15, 578-583.	2.2	47
41	Comparison of Methods to Account for Relatedness in Genome-Wide Association Studies with Family-Based Data. PLoS Genetics, 2014, 10, e1004445.	1.5	122
42	Insights into the possible role of IFNG and IFNGR1 in Kala-azar and Post Kala-azar Dermal Leishmaniasis in Sudanese patients. BMC Infectious Diseases, 2014, 14, 662.	1.3	4
43	The correlation between reading and mathematics ability at age twelve has a substantial genetic component. Nature Communications, 2014, 5, 4204.	5.8	72
44	A Genomeâ€Wide Search for Type 2 Diabetes Susceptibility Genes in an Extended Arab Family. Annals of Human Genetics, 2013, 77, 488-503.	0.3	28
45	Genetic and functional evidence for a role for SLC11A1 in susceptibility to otitis media in early childhood in a Western Australian population. Infection, Genetics and Evolution, 2013, 16, 411-418.	1.0	7
46	Common variants in the HLA-DRB1–HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. Nature Genetics, 2013, 45, 208-213.	9.4	86
47	Genome-wide association study of intraocular pressure identifies the GLCCI1/ICA1 region as a glaucoma susceptibility locus. Human Molecular Genetics, 2013, 22, 4653-4660.	1.4	29
48	Cytokine Responses to Novel Antigens in an Indian Population Living in an Area Endemic for Visceral Leishmaniasis. PLoS Neglected Tropical Diseases, 2012, 6, e1874.	1.3	56
49	Common variants at the MHC locus and at chromosome 16q24.1 predispose to Barrett's esophagus. Nature Genetics, 2012, 44, 1131-1136.	9.4	162
50	Cytokine Responses to Novel Antigens in a Peri-Urban Population in Brazil Exposed to Leishmania infantum chagasi. American Journal of Tropical Medicine and Hygiene, 2012, 87, 663-670.	0.6	20
51	Genome-wide association study identifies a variant in HDAC9 associated with large vessel ischemic stroke. Nature Genetics, 2012, 44, 328-333.	9.4	375
52	Genetic Research and Aboriginal and Torres Strait Islander Australians. Journal of Bioethical Inquiry, 2012, 9, 419-432.	0.9	28
53	Genome-Wide Association Study to Identify the Genetic Determinants of Otitis Media Susceptibility in Childhood. PLoS ONE, 2012, 7, e48215.	1.1	57
54	Genetic susceptibility to otitis media in childhood. Laryngoscope, 2012, 122, 665-675.	1.1	40

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55	Wound healing genes and susceptibility to cutaneous leishmaniasis in Brazil. Infection, Genetics and Evolution, 2012, 12, 1102-1110.	1.0	31
56	Genetic and functional evaluation of the role of DLL1 in susceptibility to visceral leishmaniasis in India. Infection, Genetics and Evolution, 2012, 12, 1195-1201.	1.0	18
57	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	13.7	2,400
58	FLI1 polymorphism affects susceptibility to cutaneous leishmaniasis in Brazil. Genes and Immunity, 2011, 12, 589-594.	2.2	27
59	Common variants near ATM are associated with glycemic response to metformin in type 2 diabetes. Nature Genetics, 2011, 43, 117-120.	9.4	390
60	FBXO11, a regulator of the TGF \hat{l}^2 pathway, is associated with severe otitis media in Western Australian children. Genes and Immunity, 2011, 12, 352-359.	2.2	63
61	Interaction between ERAP1 and HLA-B27 in ankylosing spondylitis implicates peptide handling in the mechanism for HLA-B27 in disease susceptibility. Nature Genetics, 2011, 43, 761-767.	9.4	778
62	Unraveling the genetics of otitis media: from mouse to human and back again. Mammalian Genome, 2011, 22, 66-82.	1.0	58
63	Genetic and functional evaluation of the role of CXCR1 and CXCR2 in susceptibility to visceral leishmaniasis in north-east India. BMC Medical Genetics, 2011, 12, 162.	2.1	19
64	Genetic and Functional Evidence Implicating DLL1 as the Gene That Influences Susceptibility to Visceral Leishmaniasis at Chromosome 6q27. Journal of Infectious Diseases, 2011, 204, 467-477.	1.9	15
65	TLR1/2 Activation during Heterologous Prime-Boost Vaccination (DNA-MVA) Enhances CD8+ T Cell Responses Providing Protection against Leishmania (Viannia). PLoS Neglected Tropical Diseases, 2011, 5, e1204.	1.3	52
66	The â^2518bp promoter polymorphism at CCL2/MCP1 influences susceptibility to mucosal but not localized cutaneous leishmaniasis in Brazil. Infection, Genetics and Evolution, 2010, 10, 607-613.	1.0	34
67	CXCR1 and SLC11A1polymorphisms affect susceptibility to cutaneous leishmaniasis in Brazil: a case-control and family-based study. BMC Medical Genetics, 2010, 11, 10.	2.1	48
68	Evidence for associations between the purinergic receptor P2X7 (P2RX7) and toxoplasmosis. Genes and Immunity, 2010, 11, 374-383.	2.2	95
69	A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. Nature Genetics, 2010, 42, 985-990.	9.4	918
70	Geographic Information Systems and Applied Spatial Statistics Are Efficient Tools to Study Hansen's Disease (Leprosy) and to Determine Areas of Greater Risk of Disease. American Journal of Tropical Medicine and Hygiene, 2010, 82, 306-314.	0.6	48
71	P2X7 Receptor-Mediated Killing of an Intracellular Parasite, <i>Toxoplasma gondii </i> , by Human and Murine Macrophages. Journal of Immunology, 2010, 184, 7040-7046.	0.4	124
72	Classification and Regression Tree and Spatial Analyses Reveal Geographic Heterogeneity in Genome Wide Linkage Study of Indian Visceral Leishmaniasis. PLoS ONE, 2010, 5, e15807.	1.1	29

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73	Candidate gene analysis of ocular toxoplasmosis in Brazil: evidence for a role for toll-like receptor 9 (TLR9). Memorias Do Instituto Oswaldo Cruz, 2009, 104, 1187-1190.	0.8	45
74	Host genetic and epigenetic factors in toxoplasmosis. Memorias Do Instituto Oswaldo Cruz, 2009, 104, 162-169.	0.8	29
75	HLA and Infectious Diseases. Clinical Microbiology Reviews, 2009, 22, 370-385.	5.7	305
76	Influence of <i> Slc11a1 < /i > (formerly <i> Nramp1 < /i >) on DSS-induced colitis in mice. Journal of Leukocyte Biology, 2009, 85, 703-710.</i></i>	1.5	11
77	Genetics and visceral leishmaniasis: of mice and man. Parasite Immunology, 2009, 31, 254-266.	0.7	94
78	Genome-wide association study of ulcerative colitis identifies three new susceptibility loci, including the HNF4A region. Nature Genetics, 2009, 41, 1330-1334.	9.4	483
79	Genetic Admixture in Brazilians Exposed to Infection with <i>Leishmania chagasi</i> . Annals of Human Genetics, 2009, 73, 304-313.	0.3	21
80	Genetic association between a chemokine gene CXCL-10 (IP-10, interferon gamma inducible protein 10) and susceptibility to tuberculosis. Clinica Chimica Acta, 2009, 406, 98-102.	0.5	51
81	Influence of macrophage resistance gene Lsh/lty/Bcg (candidate Nramp) on Toxoplasma gondii infection in mice. Clinical and Experimental Immunology, 2008, 97, 107-112.	1.1	25
82	Postgenomic research on leishmaniasis: a critical self-appraisal. Trends in Parasitology, 2008, 24, 401-405.	1.5	1
83	Genetic and Epigenetic Factors at COL2A1 and ABCA4 Influence Clinical Outcome in Congenital Toxoplasmosis. PLoS ONE, 2008, 3, e2285.	1.1	102
84	Heterologous Priming-Boosting with DNA and Modified Vaccinia Virus Ankara Expressing Tryparedoxin Peroxidase Promotes Long-Term Memory against Leishmania major in Susceptible BALB/c Mice. Infection and Immunity, 2007, 75, 852-860.	1.0	27
85	Y Chromosome Lineage- and Village-Specific Genes on Chromosomes 1p22 and 6q27 Control Visceral Leishmaniasis in Sudan. PLoS Genetics, 2007, 3, e71.	1.5	64
86	Genetic Predisposition to Selfâ€Curing Infection with the Protozoan <i>Leishmania chagasi:</i> A Genomewide Scan. Journal of Infectious Diseases, 2007, 196, 1261-1269.	1.9	52
87	Slc11a1, Formerly Nramp1, Is Expressed in Dendritic Cells and Influences Major Histocompatibility Complex Class II Expression and Antigen-Presenting Cell Function. Infection and Immunity, 2007, 75, 5059-5067.	1.0	57
88	Evolution of Differences in Transport Function in Slc11a Family Members. Journal of Biological Chemistry, 2007, 282, 35646-35656.	1.6	38
89	IFNG and IFNGR1 gene polymorphisms and susceptibility to post-kala-azar dermal leishmaniasis in Sudan. Genes and Immunity, 2007, 8, 75-78.	2.2	45
90	Genome-wide scan for visceral leishmaniasis susceptibility genes in Brazil. Genes and Immunity, 2007, 8, 84-90.	2.2	42

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91	Genes at human chromosome 5q31.1 regulate delayed-type hypersensitivity responses associated with Leishmania chagasi infection. Genes and Immunity, 2007, 8, 539-551.	2.2	47
92	Analysis of the BTNL2 truncating splice site mutation in tuberculosis, leprosy and Crohn's disease. Tissue Antigens, 2007, 69, 236-241.	1.0	30
93	Genetic susceptibility to infectious diseases: big is beautiful, but will bigger be even better?. Lancet Infectious Diseases, The, 2006, 6, 653-663.	4.6	195
94	From genome to vaccines for leishmaniasis: Screening 100 novel vaccine candidates against murine Leishmania major infection. Vaccine, 2006, 24, 2602-2616.	1.7	76
95	Genome-Wide Scan for Loci Influencing Quantitative Immune Response Traits in the Belem Family Study: Comparison of Methods and Summary of Results. Annals of Human Genetics, 2006, 70, 78-97.	0.3	11
96	IL6â^'174 G/C Promoter Polymorphism Influences Susceptibility to Mucosal but Not Localized Cutaneous Leishmaniasis in Brazil. Journal of Infectious Diseases, 2006, 194, 519-527.	1.9	87
97	Sudanese mucosal leishmaniasis: isolation of a parasite within the Leishmania donovani complex that differs genotypically from L. donovani causing classical visceral leishmaniasis. Infection, Genetics and Evolution, 2005, 5, 29-33.	1.0	26
98	Association between SLC11A1 (formerly NRAMP1) and the risk of sarcoidosis in Poland. European Journal of Human Genetics, 2005, 13, 829-834.	1.4	62
99	IL-10 from Regulatory T Cells Determines Vaccine Efficacy in Murine <i>Leishmania major</i> Infection. Journal of Immunology, 2005, 175, 2517-2524.	0.4	143
100	Interleukin-4 (IL-4) and IL-10 Collude in Vaccine Failure for Novel Exacerbatory Antigens in Murine Leishmania major Infection. Infection and Immunity, 2005, 73, 7620-7628.	1.0	42
101	Slc11a1-mediated resistance toSalmonella entericaserovar Typhimurium andLeishmania donovaniinfections does not require functional inducible nitric oxide synthase or phagocyte oxidase activity. Journal of Leukocyte Biology, 2005, 77, 311-320.	1.5	47
102	The Genome of the Kinetoplastid Parasite, Leishmania major. Science, 2005, 309, 436-442.	6.0	1,237
103	Candidate gene association study of solute carrier family 11a members 1 (SLC11A1) and 2 (SLC11A2) genes in Alzheimer's disease. Neuroscience Letters, 2005, 374, 124-128.	1.0	32
104	Mycobacterial Purified Protein Derivatives Stimulate Innate Immunity: Malawians Show Enhanced Tumor Necrosis Factor Alpha, Interleukin- $\hat{1}^2$ (IL- $\hat{1}^2$), and IL-10 Responses Compared to Those of Adolescents in the United Kingdom. Infection and Immunity, 2004, 72, 1807-1811.	1.0	20
105	No association between interferon-Â receptor-1 gene polymorphism and pulmonary tuberculosis in a Gambian population sample. Thorax, 2004, 59, 291-294.	2.7	38
106	DNA- Salmonella enterica Serovar Typhimurium Primer-Booster Vaccination Biases towards T Helper 1 Responses and Enhances Protection against Leishmania major Infection in Mice. Infection and Immunity, 2004, 72, 4924-4928.	1.0	36
107	Evidence for a cluster of genes on chromosome $17q11\hat{a}\in q21$ controlling susceptibility to tuberculosis and leprosy in Brazilians. Genes and Immunity, 2004, 5, 46-57.	2.2	135
108	Genome-wide scans for leprosy and tuberculosis susceptibility genes in Brazilians. Genes and Immunity, 2004, 5, 63-67.	2.2	94

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109	Expression profiling of the Leishmania life cycle: cDNA arrays identify developmentally regulated genes present but not annotated in the genome. Molecular and Biochemical Parasitology, 2004, 136, 87-100.	0.5	76
110	Genetics and visceral leishmaniasis in the Sudan: seeking a link. Trends in Parasitology, 2004, 20, 268-274.	1.5	36
111	SLC11A1 (NRAMP1) but not SLC11A2 (NRAMP2) polymorphisms are associated with susceptibility to tuberculosis in a high-incidence community in South Africa. International Journal of Tuberculosis and Lung Disease, 2004, 8, 1464-71.	0.6	55
112	Allele frequency and genotype distribution of polymorphisms within disease-related genes is influenced by ethnic population sub-structuring in Sudan. Genetica, 2003, 119, 57-63.	0.5	16
113	Divalent cation transport and susceptibility to infectious and autoimmune disease: continuation of the lty/Lsh/Bcg/Nramp1/Slc11a1 gene story. Immunology Letters, 2003, 85, 197-203.	1.1	132
114	Polymorphism in the Interferon-gamma Receptor-1 Gene and Susceptibility to Pulmonary Tuberculosis in The Gambia. Scandinavian Journal of Immunology, 2003, 58, 383-385.	1.3	27
115	Genetic susceptibility to visceral leishmaniasis in The Sudan: linkage and association with IL4 and IFNGR1. Genes and Immunity, 2003, 4, 351-355.	2.2	79
116	Solute carrier 11a1 (Slc11a1; formerly Nramp1) regulates metabolism and release of iron acquired by phagocytic, but not transferrin-receptor-mediated, iron uptake. Biochemical Journal, 2002, 363, 89-94.	1.7	60
117	From genomes to vaccines:Leishmaniaas a model. Philosophical Transactions of the Royal Society B: Biological Sciences, 2002, 357, 5-11.	1.8	49
118	BCG-induced increase in interferon-gamma response to mycobacterial antigens and efficacy of BCG vaccination in Malawi and the UK: two randomised controlled studies. Lancet, The, 2002, 359, 1393-1401.	6.3	279
119	Genetics and genomics in infectious disease. International Journal of Infectious Diseases, 2002, 6, S8-S9.	1.5	3
120	Atopy in children in relation to BCG vaccination and genetic polymorphisms at SLC11A1 (formerly) Tj ETQq0 0 0	rgBT_/Ove	rlock 10 Tf 50
121	Genetic analysis of multicase families of visceral leishmaniasis in northeastern Brazil: no major role for class II or class III regions of HLA. Genes and Immunity, 2002, 3, 350-358.	2.2	26
122	Nramp1 is expressed in neurons and is associated with behavioural and immune responses to stress. Neurogenetics, 2001, 3, 69-78.	0.7	47
123	SLC11A1 (formerly NRAMP1) and disease resistance. Microreview. Cellular Microbiology, 2001, 3, 773-784.	1.1	231
124	Genetic epidemiology of visceral leishmaniasis in northeastern Brazil. Genetic Epidemiology, 2001, 20, 383-396.	0.6	47
125	Association and linkage of leprosy phenotypes with HLA class II and tumour necrosis factor genes. Genes and Immunity, 2001, 2, 196-204.	2.2	92
126	Modern genetics and leprosy susceptibility. Leprosy Review, 2001, 72, 352-6.	0.1	11

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127	Relationship between IFN-gamma and skin test responsiveness to Mycobacterium tuberculosis PPD in healthy, non-BCG-vaccinated young adults in Northern Malawi. International Journal of Tuberculosis and Lung Disease, 2001, 5, 664-72.	0.6	56
128	Understanding the multiple functions of Nramp1. Microbes and Infection, 2000, 2, 317-321.	1.0	128
129	Corrigendum to "Intra and inter-specific microsatellite variation in the Leishmania subgenus Viannia― Molecular and Biochemical Parasitology, 2000, 107, 331.	0.5	1
130	IL-13 Is a Susceptibility Factor for <i>Leishmania major</i> Infection. Journal of Immunology, 2000, 164, 1458-1462.	0.4	138
131	Roles of Nramp1, HLA, and a gene(s) in allelic association with IL-4, in determining T helper subset differentiation. Microbes and Infection, 1999, 1, 95-102.	1.0	14
132	Genetic regulation of macrophage activation: understanding the function of Nramp1 (=Ity/Lsh/Bcg). Immunology Letters, 1999, 65, 73-80.	1.1	103
133	Multiple causes of size variation in the diploid megabase chromosomes of African tyrpanosomes. Chromosome Research, 1999, 7, 191-203.	1.0	38
134	Intra and inter-specific microsatellite variation in the Leishmania subgenus Viannia. Molecular and Biochemical Parasitology, 1999, 103, 71-77.	0.5	46
135	Tumour Necrosis Factor alpha and Mucocutaneous Leishmaniasis. Parasitology Today, 1999, 15, 73-75.	3.1	43
136	Status of protozoan genome analysis: trypanosomatids. Parasitology, 1999, 118, 11-14.	0.7	13
137	Immunostimulatory DNA as an Adjuvant in Vaccination against <i>Leishmania major</i> Immunity, 1999, 67, 3719-3726.	1.0	134
138	Evidence for a functional repeat polymorphism in the promoter of the human NRAMP1 gene that correlates with autoimmune versus infectious disease susceptibility. Journal of Medical Genetics, 1999, 36, 295-9.	1.5	144
139	Myasthenia Gravis with Thymic Hyperplasia Is Associated with Polymorphisms in the Tumor Necrosis Factor Region. Annals of the New York Academy of Sciences, 1998, 841, 368-370.	1.8	11
140	The molecular karyotype of the megabase chromosomes of Trypanosoma brucei and the assignment of chromosome markers. Molecular and Biochemical Parasitology, 1998, 94, 155-173.	0.5	109
141	Genetic nomenclature for Trypanosoma and Leishmania. Molecular and Biochemical Parasitology, 1998, 97, 221-224.	0.5	83
142	Identification and characterisation of a functional peroxidoxin from Leishmania major1Note: Nucleotide sequence data reported in this paper are available in the EMBL, GenBankâ,,¢ and DDJB databases under the accession number AF069386.1. Molecular and Biochemical Parasitology, 1998, 96, 125-137.	0.5	105
143	T cell responses to crude and defined leishmanial antigens in patients from the Lower Amazon region of Brazil infected with different species of Leishmania of the subgenera Leishmania and Viannia. Parasite Immunology, 1998, 20, 19-26.	0.7	31
144	Polymorphism in tumor necrosis factor genes associated with myasthenia gravis. Journal of Neuroimmunology, 1998, 88, 137-143.	1.1	33

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145	Genetics of host resistance and susceptibility to intramacrophage pathogens: a study of multicase families of tuberculosis, leprosy and leishmaniasis in north-eastern Brazil. International Journal for Parasitology, 1998, 28, 21-28.	1.3	55
146	T cell responses to crude and defined leishmanial antigens in patients from the Lower Amazon region of Brazil infected with different species of Leishmania of the subgenera Leishmania and Viannia., 1998, 20, 19.		16
147	Genetic Control of Immune Response to Recombinant Antigens Carried by an Attenuated <i>Salmonella typhimurium </i> Vaccine Strain: <i>Nramp1 </i> Influences T-Helper Subset Responses and Protection against Leishmanial Challenge. Infection and Immunity, 1998, 66, 1910-1917.	1.0	64
148	Immunogenetics of leishmanial and mycobacterial infections: the Belem Family Study. Philosophical Transactions of the Royal Society B: Biological Sciences, 1997, 352, 1331-1345.	1.8	88
149	Evidence that genetic susceptibility to Mycobacterium tuberculosis in a brazilian population is under oligogenic control: Linkage study of the candidate genes NRAMP1 and TBFA. Tubercle and Lung Disease, 1997, 78, 35-45.	2.1	128
150	Nramp1 transfection transfers lty/Lsh/Bcg-related pleiotropic effects on macrophage activation: influence on antigen processing and presentation. Infection and Immunity, 1997, 65, 380-386.	1.0	71
151	Analysis of the candidate gene NRAMP1 in the first 61 ARC National Repository families for rheumatoid arthritis. Journal of Rheumatology, 1997, 24, 212-4.	1.0	9
152	Unravelling the Leishmania genome. Current Opinion in Genetics and Development, 1996, 6, 704-710.	1.5	28
153	Genetic susceptibility to leishmanial infections: studies in mice and man. Parasitology, 1996, 112, S67-S74.	0.7	129
154	Toxoplasma gondii expressed sequence tags: insight into tachyzoite gene expression. Molecular and Biochemical Parasitology, 1996, 75, 179-186.	0.5	58
155	An expressed sequence tag analysis of a full-length, spliced-leader cDNA library from Leishmania major promastigotes. Molecular and Biochemical Parasitology, 1996, 76, 345-348.	0.5	46
156	Structure and function of the natural-resistance-associated macrophage protein (Nramp1), a candidate protein for infectious and autoimmune disease susceptibility. Trends in Molecular Medicine, 1996, 2, 205-211.	2.6	93
157	Identification of C to T mutation at position â^'236 bp in the humanNRAMP1 gene promoter. Immunogenetics, 1996, 44, 309-311.	1.2	17
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159	Identification of C to T mutation at position ?236 bp in the human NRAMP1 gene promoter. Immunogenetics, 1996, 44, 309-311.	1.2	4
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