

Pascal Rihet

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

2,400
citations

218677

26
h-index

214800

47
g-index

61
all docs

61
docs citations

61
times ranked

3094
citing authors

#	ARTICLE	IF	CITATIONS
1	Alternatively spliced NKp30 isoforms affect the prognosis of gastrointestinal stromal tumors. <i>Nature Medicine</i> , 2011, 17, 700-707.	30.7	282
2	Evidence for an association between human resistance to <i>Schistosoma mansoni</i> and high anti- <i>S. mansoni</i> IgE levels. <i>European Journal of Immunology</i> , 1991, 21, 2679-2686.	2.9	262
3	Resistance to <i>Schistosoma mansoni</i> in Humans: Influence of the IgE/IgG4 Balance and IgG2 in Immunity to Reinfection after Chemotherapy. <i>Journal of Infectious Diseases</i> , 1993, 168, 1000-1008.	4.0	185
4	High Immunoglobulin G2 (IgG2) and Low IgG4 Levels Are Associated with Human Resistance to <i>Plasmodium falciparum</i> Malaria. <i>Infection and Immunity</i> , 2000, 68, 1252-1258.	2.2	145
5	Malaria in Humans: <i>Plasmodium falciparum</i> Blood Infection Levels Are Linked to Chromosome 5q31-q33. <i>American Journal of Human Genetics</i> , 1998, 63, 498-505.	6.2	136
6	Strong serum inhibition of specific IgE correlated to competing IgG4, revealed by a new methodology in subjects from <i>S. mansoni</i> endemic area. <i>European Journal of Immunology</i> , 1992, 22, 2063-2070.	2.9	96
7	Genome-Wide Expression Profiling Deciphers Host Responses Altered during Dengue Shock Syndrome and Reveals the Role of Innate Immunity in Severe Dengue. <i>PLoS ONE</i> , 2010, 5, e11671.	2.5	66
8	Environmental, Genetic and Immunological Factors in Human Resistance to <i>Schistosoma Mansoni</i> . <i>Immunological Investigations</i> , 1992, 21, 423-453.	2.0	65
9	Hemoglobin C is associated with reduced <i>Plasmodium falciparum</i> parasitemia and low risk of mild malaria attack. <i>Human Molecular Genetics</i> , 2003, 13, 1-6.	2.9	57
10	TNF as a malaria candidate gene: polymorphism-screening and family-based association analysis of mild malaria attack and parasitemia in Burkina Faso. <i>Genes and Immunity</i> , 2005, 6, 472-480.	4.1	56
11	Linkage and association between <i>Plasmodium falciparum</i> blood infection levels and chromosome 5q31-q33. <i>Genes and Immunity</i> , 2003, 4, 265-268.	4.1	54
12	Gene expression analysis reveals early changes in several molecular pathways in cerebral malaria-susceptible mice versus cerebral malaria-resistant mice. <i>BMC Genomics</i> , 2007, 8, 452.	2.8	51
13	Gene Expression Profiling Discriminates between Cerebral Malaria (CM) Susceptible Mice and CM Resistant Mice. <i>Journal of Infectious Diseases</i> , 2006, 193, 312-321.	4.0	50
14	Early Gene Expression Analysis in 9L Orthotopic Tumor-Bearing Rats Identifies Immune Modulation in Molecular Response to Synchrotron Microbeam Radiation Therapy. <i>PLoS ONE</i> , 2013, 8, e81874.	2.5	50
15	Confirmation and dissection of QTL controlling resistance to malaria in mice. <i>Mammalian Genome</i> , 2004, 15, 390-398.	2.2	48
16	Linkage of mild malaria to the major histocompatibility complex in families living in Burkina Faso. <i>Human Molecular Genetics</i> , 2003, 12, 375-378.	2.9	47
17	Mapping of a new quantitative trait locus for resistance to malaria in mice by a comparative mapping approach with human Chromosome 5q31-q33. <i>Immunogenetics</i> , 2004, 56, 115-117.	2.4	42
18	Sperm mRNAs and microRNAs as candidate markers for the impact of toxicants on human spermatogenesis: an application to tobacco smoking. <i>Systems Biology in Reproductive Medicine</i> , 2015, 61, 139-149.	2.1	41

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19	Modification of P-selectin glycoprotein ligand-1 with a natural killer cell-restricted sulfated lactosamine creates an alternate ligand for L-selectin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 3400-3405.	7.1	41
20	IL-12R β 2 Is Essential for the Development of Experimental Cerebral Malaria. <i>Journal of Immunology</i> , 2012, 188, 1905-1914.	0.8	38
21	Functional Polymorphisms in the Regulatory Regions of the VNN1 Gene Are Associated with Susceptibility to Inflammatory Bowel Diseases. <i>Inflammatory Bowel Diseases</i> , 2013, 19, 2315-2325.	1.9	38
22	Deletion of Nkx2-5 in trabecular myocardium reveals the developmental origins of pathological heterogeneity associated with ventricular non-compaction cardiomyopathy. <i>PLoS Genetics</i> , 2018, 14, e1007502.	3.5	37
23	Familial Correlation of Immunoglobulin G Subclass Responses to Plasmodium falciparum Antigens in Burkina Faso. <i>Infection and Immunity</i> , 2001, 69, 996-1001.	2.2	34
24	Platelets Alter Gene Expression Profile in Human Brain Endothelial Cells in an In Vitro Model of Cerebral Malaria. <i>PLoS ONE</i> , 2011, 6, e19651.	2.5	32
25	Influence of Carriage of Hemoglobin AS and the Fc γ 3 Receptor Ila ϵ R131 Allele on Levels of Immunoglobulin G2 Antibodies to Plasmodium falciparum Merozoite Antigens in Gabonese Children. <i>Journal of Infectious Diseases</i> , 2005, 192, 1975-1980.	4.0	31
26	Natural Killer Cells Modulation in Hematological Malignancies. <i>Frontiers in Immunology</i> , 2013, 4, 459.	4.8	29
27	Identification of AREG and PLK1 pathway modulation as a potential key of the response of intracranial 9L tumor to microbeam radiation therapy. <i>International Journal of Cancer</i> , 2015, 136, 2705-2716.	5.1	26
28	Malaria resistance genes are associated with the levels of IgG subclasses directed against Plasmodium falciparum blood-stage antigens in Burkina Faso. <i>Malaria Journal</i> , 2012, 11, 308.	2.3	24
29	The transcriptional signatures of Sodalid glossinidius in the Glossina palpalis gambiense flies negative for Trypanosoma brucei gambiense contrast with those of this symbiont in tsetse flies positive for the parasite: Possible involvement of a Sodalid-hosted prophage in fly Trypanosoma refractoriness?. <i>Infection, Genetics and Evolution</i> , 2014, 24, 41-56.	2.3	24
30	Pathology of Tnf-deficient mice infected with Plasmodium chabaudi adami 408XZ. <i>Experimental Parasitology</i> , 2006, 114, 271-278.	1.2	21
31	Association analyses of NCR3 polymorphisms with P. falciparum mild malaria. <i>Microbes and Infection</i> , 2007, 9, 160-166.	1.9	20
32	A genome scan for Plasmodium falciparum malaria identifies quantitative trait loci on chromosomes 5q31, 6p21.3, 17p12, and 19p13. <i>Malaria Journal</i> , 2014, 13, 198.	2.3	19
33	Striatal Molecular Signature of Subchronic Subthalamic Nucleus High Frequency Stimulation in Parkinsonian Rat. <i>PLoS ONE</i> , 2013, 8, e60447.	2.5	18
34	Peripheral T α cell lymphoma gene expression profiling and potential therapeutic exploitations. <i>British Journal of Haematology</i> , 2010, 150, 21-27.	2.5	17
35	Association of a functional TNF variant with Plasmodium falciparum parasitaemia in a congolese population. <i>Genes and Immunity</i> , 2017, 18, 152-157.	4.1	15
36	Gene expression profiling in blood from cerebral malaria patients and mild malaria patients living in Senegal. <i>BMC Medical Genomics</i> , 2019, 12, 148.	1.5	15

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37	Family-based association of a low producing lymphotoxin- β allele with reduced Plasmodium falciparum parasitemia. <i>Microbes and Infection</i> , 2008, 10, 673-679.	1.9	14
38	Genetic variations in genes involved in heparan sulphate biosynthesis are associated with Plasmodium falciparum parasitaemia: a familial study in Burkina Faso. <i>Malaria Journal</i> , 2012, 11, 108.	2.3	14
39	Serum Pantetheinase/ Vanin Levels Regulate Erythrocyte Homeostasis and Severity of Malaria. <i>American Journal of Pathology</i> , 2015, 185, 3039-3052.	3.8	14
40	Natural killer cells in acute myeloid leukemia patients: from phenotype to transcriptomic analysis. <i>Immunologic Research</i> , 2016, 64, 1225-1236.	2.9	14
41	IL12B polymorphisms are linked but not associated with Plasmodium falciparum parasitemia: a familial study in Burkina Faso. <i>Genes and Immunity</i> , 2008, 9, 405-411.	4.1	13
42	Host susceptibility to malaria in human and mice: compatible approaches to identify potential resistant genes. <i>Physiological Genomics</i> , 2014, 46, 1-16.	2.3	13
43	Evidence for epistasis between hemoglobin C and immune genes in human P. falciparum malaria: a family study in Burkina Faso. <i>Genes and Immunity</i> , 2011, 12, 481-489.	4.1	11
44	Genetic Predisposition to the Mortality in Septic Shock Patients: From GWAS to the Identification of a Regulatory Variant Modulating the Activity of a CISH Enhancer. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5852.	4.1	11
45	Comparison of pathology in susceptible A/J and resistant C57BL/6J mice after infection with different sub-strains of Plasmodium chabaudi. <i>Experimental Parasitology</i> , 2004, 108, 134-141.	1.2	9
46	Identification of ATP2B4 Regulatory Element Containing Functional Genetic Variants Associated with Severe Malaria. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4849.	4.1	9
47	Transcriptional Response in a Sepsis Mouse Model Reflects Transcriptional Response in Sepsis Patients. <i>International Journal of Molecular Sciences</i> , 2022, 23, 821.	4.1	8
48	Beyond genome-wide scan: Association of a cis-regulatory NCR3 variant with mild malaria in a population living in the Republic of Congo. <i>PLoS ONE</i> , 2017, 12, e0187818.	2.5	7
49	Interplay between trauma and Pseudomonas entomophila infection in flies: a central role of the JNK pathway and of CrebA. <i>Scientific Reports</i> , 2017, 7, 16222.	3.3	7
50	<i>NCR3</i> polymorphism, haematological parameters, and severe malaria in Senegalese patients. <i>PeerJ</i> , 2018, 6, e6048.	2.0	7
51	Identification of overexpressed genes in Sodalís glossinidius inhabiting trypanosome-infected self-cured tsetse flies. <i>Frontiers in Microbiology</i> , 2014, 5, 255.	3.5	6
52	Vorinostat and Mithramycin A in combination therapy as an interesting strategy for the treatment of SÅ@zary T lymphoma: a transcriptomic approach. <i>Archives of Dermatological Research</i> , 2017, 309, 611-623.	1.9	6
53	Genetic and enzymatic characterization of 3-O-sulfotransferase SNPs associated with Plasmodium falciparum parasitaemia. <i>Glycobiology</i> , 2018, 28, 534-541.	2.5	5
54	A transcriptomic signature predicting septic outcome in patients undergoing autologous stem cell transplantation. <i>Experimental Hematology</i> , 2018, 65, 49-56.	0.4	5

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55	Genome-wide significant linkage to IgG subclass responses against Plasmodium falciparum antigens on chromosomes 8p22-p21, 9q34 and 20q13. <i>Genes and Immunity</i> , 2015, 16, 187-192.	4.1	4
56	Natural killer cells in patients with polycythemia vera. <i>Human Immunology</i> , 2015, 76, 644-650.	2.4	3
57	TAGOOS: genome-wide supervised learning of non-coding loci associated to complex phenotypes. <i>Nucleic Acids Research</i> , 2019, 47, e79-e79.	14.5	3
58	Technical data of the transcriptomic analysis performed on tsetse fly symbionts, <i>Sodalis glossinidius</i> and <i>Wigglesworthia glossinidia</i> , harbored, respectively by non-infected, <i>Trypanosoma brucei</i> gambiense infected and self-cured <i>Glossina palpalis gambiensis</i> tsetse flies. <i>Genomics Data</i> , 2015, 4, 133-136.	1.3	1
59	Facteurs g�n�tiques et immunologiques d�terminant la r�sistance � la bilharziose en r�gion d'end�mie. <i>Medecine/Sciences</i> , 1992, 8, 108.	0.2	1