

Bart Ferwerda

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

2,875
citations

331670

21
h-index

330143

37
g-index

41
all docs

41
docs citations

41
times ranked

4779
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole genome sequencing identifies variants associated with sarcoidosis in a family with a high prevalence of sarcoidosis. <i>Clinical Rheumatology</i> , 2021, 40, 3735-3743.	2.2	8
2	Evaluation of the Khorana, PROTECHT, and 5â€¢SNP scores for prediction of venous thromboembolism in patients with cancer. <i>Journal of Thrombosis and Haemostasis</i> , 2021, 19, 2974-2983.	3.8	14
3	Genetic Variation in <i>Neisseria meningitidis</i> Does Not Influence Disease Severity in Meningococcal Meningitis. <i>Frontiers in Medicine</i> , 2020, 7, 594769.	2.6	8
4	Diversification in immunogenicity genes caused by selective pressures in invasive meningococci. <i>Microbial Genomics</i> , 2020, 6, .	2.0	6
5	Joint sequencing of human and pathogen genomes reveals the genetics of pneumococcal meningitis. <i>Nature Communications</i> , 2019, 10, 2176.	12.8	83
6	Residual Variation Intolerance Score Detects Loci Under Selection in Neuroinvasive <i>Listeria monocytogenes</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2702.	3.5	1
7	Mannose-binding lectin-associated serine protease 2 (MASP-2) contributes to poor disease outcome in humans and mice with pneumococcal meningitis. <i>Journal of Neuroinflammation</i> , 2017, 14, 2.	7.2	24
8	Sequencing of the variable region of <i>rpsB</i> to discriminate between <i>Streptococcus pneumoniae</i> and other streptococcal species. <i>Open Biology</i> , 2017, 7, 170074.	3.6	23
9	Large scale genomic analysis shows no evidence for pathogen adaptation between the blood and cerebrospinal fluid niches during bacterial meningitis. <i>Microbial Genomics</i> , 2017, 3, e000103.	2.0	53
10	Differences in Inflammation Patterns Induced by African and Asian <i>Burkholderia pseudomallei</i> Isolates in Mice. <i>American Journal of Tropical Medicine and Hygiene</i> , 2017, 96, 1365-1369.	1.4	2
11	Functional polymorphisms of macrophage migration inhibitory factor as predictors of morbidity and mortality of pneumococcal meningitis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3597-3602.	7.1	55
12	Variation of 46 Innate Immune Genes Evaluated for their Contribution in Pneumococcal Meningitis Susceptibility and Outcome. <i>EBioMedicine</i> , 2016, 10, 77-84.	6.1	11
13	Exome Array Analysis of Susceptibility to Pneumococcal Meningitis. <i>Scientific Reports</i> , 2016, 6, 29351.	3.3	7
14	V-akt murine thymoma viral oncogene homolog 3 (AKT3) contributes to poor disease outcome in humans and mice with pneumococcal meningitis. <i>Acta Neuropathologica Communications</i> , 2016, 4, 50.	5.2	4
15	Patterns of Ancestry, Signatures of Natural Selection, and Genetic Association with Stature in Western African Pygmies. <i>PLoS Genetics</i> , 2012, 8, e1002641.	3.5	118
16	Different Patterns of Toll-Like Receptor 2 Polymorphisms in Populations of Various Ethnic and Geographic Origins. <i>Infection and Immunity</i> , 2012, 80, 1917-1922.	2.2	36
17	High variability of TLR4 gene in different ethnic groups in Iran. <i>Innate Immunity</i> , 2012, 18, 492-502.	2.4	12
18	Evolutionary History and Adaptation from High-Coverage Whole-Genome Sequences of Diverse African Hunter-Gatherers. <i>Cell</i> , 2012, 150, 457-469.	28.9	289

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19	Association of Mal/TIRAP S180L variant polymorphism with decreased infection risk in patients with advanced HIV-1 infection. <i>Cytokine</i> , 2012, 60, 104-107.	3.2	5
20	The Loss of Functional Caspase-12 in Europe Is a Pre-Neolithic Event. <i>PLoS ONE</i> , 2012, 7, e37022.	2.5	10
21	Gene-Centric Meta-Analysis of Lipid Traits in African, East Asian and Hispanic Populations. <i>PLoS ONE</i> , 2012, 7, e50198.	2.5	40
22	Toll-Like Receptor 4 Polymorphisms in Dengue Virus-Infected Children. <i>American Journal of Tropical Medicine and Hygiene</i> , 2011, 85, 352-354.	1.4	8
23	Genetic Variation of Innate Immune Genes in HIV-Infected African Patients With or Without Oropharyngeal Candidiasis. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2010, 55, 87-94.	2.1	48
24	Evolutionary and Functional Analysis of Celiac Risk Loci Reveals SH2B3 as a Protective Factor against Bacterial Infection. <i>American Journal of Human Genetics</i> , 2010, 86, 970-977.	6.2	168
25	Association of Toll-Like Receptor 4 Asp299Gly and Thr399Ile Polymorphisms with Increased Infection Risk in Patients with Advanced HIV-1 Infection. <i>Clinical Infectious Diseases</i> , 2010, 51, 242-247.	5.8	29
26	Influence of genetic variations in TLR4 and TIRAP/Mal on the course of sepsis and pneumonia and cytokine release: an observational study in three cohorts. <i>Critical Care</i> , 2010, 14, R103.	5.8	72
27	Persistence of full-length caspase-12 and its relation to malaria in West and Central African populations. <i>European Cytokine Network</i> , 2010, 21, 77-83.	2.0	9
28	Functional and genetic evidence that the Mal/TIRAP allele variant 180L has been selected by providing protection against septic shock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 10272-10277.	7.1	87
29	Early Stop Polymorphism in Human DECTIN-1 Is Associated with Increased <i>Candida</i> Colonization in Hematopoietic Stem Cell Transplant Recipients. <i>Clinical Infectious Diseases</i> , 2009, 49, 724-732.	5.8	226
30	Human Dectin-1 Deficiency and Mucocutaneous Fungal Infections. <i>New England Journal of Medicine</i> , 2009, 361, 1760-1767.	27.0	671
31	Caspase-12 and the Inflammatory Response to <i>Yersinia pestis</i> . <i>PLoS ONE</i> , 2009, 4, e6870.	2.5	26
32	ADAMTS13 Deficiency with Elevated Levels of Ultra-Large and Active von Willebrand Factor in <i>P. falciparum</i> and <i>P. vivax</i> Malaria. <i>American Journal of Tropical Medicine and Hygiene</i> , 2009, 80, 492-498.	1.4	74
33	ADAMTS13 deficiency with elevated levels of ultra-large and active von Willebrand factor in <i>P. falciparum</i> and <i>P. vivax</i> malaria. <i>American Journal of Tropical Medicine and Hygiene</i> , 2009, 80, 492-8.	1.4	42
34	Functional Consequences of Toll-like Receptor 4 Polymorphisms. <i>Molecular Medicine</i> , 2008, 14, 346-352.	4.4	245
35	TLR4 polymorphisms, infectious diseases, and evolutionary pressure during migration of modern humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 16645-16650.	7.1	293
36	The toll-like receptor 4 Asp299Gly variant and tuberculosis susceptibility in HIV-infected patients in Tanzania. <i>Aids</i> , 2007, 21, 1375-1377.	2.2	66

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37	Joint Sequencing of Human and Pathogen Genomes Reveals the Genetics of Pneumococcal Meningitis. SSRN Electronic Journal, 0, , .	0.4	1