

Kurt R Wollenberg

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

617
citations

687363

13
h-index

794594

19
g-index

24
all docs

24
docs citations

24
times ranked

1137
citing authors

#	ARTICLE	IF	CITATIONS
1	Patterns of genomic interrelatedness of publicly available samples in the TB portals database. <i>Tuberculosis</i> , 2022, 133, 102171.	1.9	1
2	Malaria parasites use a soluble RhopH complex for erythrocyte invasion and an integral form for nutrient uptake. <i>ELife</i> , 2021, 10, .	6.0	35
3	Patterns of Coevolutionary Adaptations across Time and Space in Mouse Gammaretroviruses and Three Restrictive Host Factors. <i>Viruses</i> , 2021, 13, 1864.	3.3	5
4	A retrospective genomic analysis of drug-resistant strains of <i>M. tuberculosis</i> in a high-burden setting, with an emphasis on comparative diagnostics and reactivation and reinfection status. <i>BMC Infectious Diseases</i> , 2020, 20, 17.	2.9	16
5	Comparative analysis of genomic variability for drug-resistant strains of <i>Mycobacterium tuberculosis</i> : The special case of Belarus. <i>Infection, Genetics and Evolution</i> , 2020, 78, 104137.	2.3	6
6	TB DEPOT (Data Exploration Portal): A multi-domain tuberculosis data analysis resource. <i>PLoS ONE</i> , 2019, 14, e0217410.	2.5	13
7	The phylogeny of 48 alleles, experimentally verified at 21Åkb, and its application to clinical allele detection. <i>Journal of Translational Medicine</i> , 2019, 17, 43.	4.4	2
8	Role of humoral immunity against hepatitis B virus core antigen in the pathogenesis of acute liver failure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11369-E11378.	7.1	59
9	Whole-Genome Sequencing of <i>Mycobacterium tuberculosis</i> Provides Insight into the Evolution and Genetic Composition of Drug-Resistant Tuberculosis in Belarus. <i>Journal of Clinical Microbiology</i> , 2017, 55, 457-469.	3.9	47
10	The TB Portals: an Open-Access, Web-Based Platform for Global Drug-Resistant-Tuberculosis Data Sharing and Analysis. <i>Journal of Clinical Microbiology</i> , 2017, 55, 3267-3282.	3.9	89
11	Diminished viral replication and compartmentalization of hepatitis C virus in hepatocellular carcinoma tissue. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 1375-1380.	7.1	50
12	The Avian XPR1 Gammaretrovirus Receptor Is under Positive Selection and Is Disabled in Bird Species in Contact with Virus-Infected Wild Mice. <i>Journal of Virology</i> , 2013, 87, 10094-10104.	3.4	17
13	Molecular Epidemiology of <i>Neisseria meningitidis</i> Serogroup B in Brazil. <i>PLoS ONE</i> , 2012, 7, e33016.	2.5	37
14	Adaptive Evolution of <i>Mus</i> Apobec3 Includes Retroviral Insertion and Positive Selection at Two Clusters of Residues Flanking the Substrate Groove. <i>PLoS Pathogens</i> , 2010, 6, e1000974.	4.7	49
15	Molecular Evolution of Immune Genes in the Malaria Mosquito <i>Anopheles gambiae</i> . <i>PLoS ONE</i> , 2009, 4, e4549.	2.5	41
16	Origin, antiviral function and evidence for positive selection of the gammaretrovirus restriction gene Fv1 in the genus <i>Mus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3259-3263.	7.1	75
17	A complex of three related membrane proteins is conserved on malarial merozoites. <i>Molecular and Biochemical Parasitology</i> , 2009, 167, 135-143.	1.1	14
18	Adaptive evolution of the virus resistance gene Apobec in the genus <i>Mus</i> . <i>Retrovirology</i> , 2009, 6, O7.	2.0	0

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19	Speed-mapping quantitative trait loci using microarrays. <i>Nature Methods</i> , 2007, 4, 839-841.	19.0	41
20	cpDNA Inheritance in Interspecific Crosses and Evolutionary Inference in Louisiana Irises. <i>American Journal of Botany</i> , 1993, 80, 344.	1.7	18