

Kristof Theys

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

1,365
citations

471061

17
h-index

377514

34
g-index

46
all docs

46
docs citations

46
times ranked

2577
citing authors

#	ARTICLE	IF	CITATIONS
1	Global epidemiology of drug resistance after failure of WHO recommended first-line regimens for adult HIV-1 infection: a multicentre retrospective cohort study. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 565-575.	4.6	217
2	HIV-1 subtype distribution and its demographic determinants in newly diagnosed patients in Europe suggest highly compartmentalized epidemics. <i>Retrovirology</i> , 2013, 10, 7.	0.9	129
3	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. <i>Briefings in Bioinformatics</i> , 2021, 22, 642-663.	3.2	110
4	An integrated map of HIV genome-wide variation from a population perspective. <i>Retrovirology</i> , 2015, 12, 18.	0.9	90
5	A new ensemble coevolution system for detecting HIV-1 protein coevolution. <i>Biology Direct</i> , 2015, 10, 1.	1.9	78
6	Genetic Diversity and Selective Pressure in Hepatitis C Virus Genotypes 1–6: Significance for Direct-Acting Antiviral Treatment and Drug Resistance. <i>Viruses</i> , 2015, 7, 5018-5039.	1.5	59
7	VIRULIGN: fast codon-correct alignment and annotation of viral genomes. <i>Bioinformatics</i> , 2019, 35, 1763-1765.	1.8	59
8	CRF19_cpx is an Evolutionary fit HIV-1 Variant Strongly Associated With Rapid Progression to AIDS in Cuba. <i>EBioMedicine</i> , 2015, 2, 244-254.	2.7	56
9	The impact of HIV-1 within-host evolution on transmission dynamics. <i>Current Opinion in Virology</i> , 2018, 28, 92-101.	2.6	47
10	A computational method for the identification of Dengue, Zika and Chikungunya virus species and genotypes. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007231.	1.3	44
11	HIV-1 genotypic drug resistance testing: digging deep, reaching wide?. <i>Current Opinion in Virology</i> , 2015, 14, 16-23.	2.6	36
12	Within-patient mutation frequencies reveal fitness costs of CpG dinucleotides and drastic amino acid changes in HIV. <i>PLoS Genetics</i> , 2018, 14, e1007420.	1.5	35
13	RegaDB: community-driven data management and analysis for infectious diseases. <i>Bioinformatics</i> , 2013, 29, 1477-1480.	1.8	29
14	SANTA-SIM: simulating viral sequence evolution dynamics under selection and recombination. <i>Virus Evolution</i> , 2019, 5, vez003.	2.2	26
15	HIV-1 Infection in Cyprus, the Eastern Mediterranean European Frontier: A Densely Sampled Transmission Dynamics Analysis from 1986 to 2012. <i>Scientific Reports</i> , 2018, 8, 1702.	1.6	24
16	Treatment-associated polymorphisms in protease are significantly associated with higher viral load and lower CD4 count in newly diagnosed drug-naive HIV-1 infected patients. <i>Retrovirology</i> , 2012, 9, 81.	0.9	23
17	Assessing transmissibility of HIV-1 drug resistance mutations from treated and from drug-naive individuals. <i>Aids</i> , 2015, 29, 2045-2052.	1.0	21
18	Sub-Epidemics Explain Localized High Prevalence of Reduced Susceptibility to Rilpivirine in Treatment-Naive HIV-1-Infected Patients: Subtype and Geographic Compartmentalization of Baseline Resistance Mutations. <i>AIDS Research and Human Retroviruses</i> , 2016, 32, 427-433.	0.5	19

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19	Mapping the genomic diversity of HCV subtypes 1a and 1b: Implications of structural and immunological constraints for vaccine and drug development. <i>Virus Evolution</i> , 2016, 2, vew024.	2.2	17
20	Epidemic dispersion of HIV and HCV in a population of co-infected Romanian injecting drug users. <i>PLoS ONE</i> , 2017, 12, e0185866.	1.1	17
21	A genetic IFN/STAT1/FAS axis determines CD4 T stem cell memory levels and apoptosis in healthy controls and Adult T-cell Leukemia patients. <i>Oncolmmunology</i> , 2018, 7, e1426423.	2.1	17
22	Modelled <i>in vivo</i> HIV Fitness under drug Selective Pressure and Estimated Genetic Barrier Towards Resistance are Predictive for Virological Response. <i>Antiviral Therapy</i> , 2008, 13, 399-408.	0.6	17
23	PhyloGeoTool: interactively exploring large phylogenies in an epidemiological context. <i>Bioinformatics</i> , 2017, 33, 3993-3995.	1.8	16
24	Advances in Visualization Tools for Phylogenomic and Phylodynamic Studies of Viral Diseases. <i>Frontiers in Public Health</i> , 2019, 7, 208.	1.3	15
25	Exploring resistance pathways for first-generation NS3/4A protease inhibitors boceprevir and telaprevir using Bayesian network learning. <i>Infection, Genetics and Evolution</i> , 2017, 53, 15-23.	1.0	14
26	Time to Harmonize Dengue Nomenclature and Classification. <i>Viruses</i> , 2018, 10, 569.	1.5	14
27	Estimating the individualized HIV-1 genetic barrier to resistance using a nelfinavir fitness landscape. <i>BMC Bioinformatics</i> , 2010, 11, 409.	1.2	12
28	Drivers of HIV-1 transmission: The Portuguese case. <i>PLoS ONE</i> , 2019, 14, e0218226.	1.1	12
29	HIV-1 drug resistance: where do polymorphisms fit in?. <i>Future Microbiology</i> , 2013, 8, 303-306.	1.0	11
30	On the contribution of Angola to the initial spread of HIV-1. <i>Infection, Genetics and Evolution</i> , 2016, 46, 219-222.	1.0	11
31	Zika genomics urgently need standardized and curated reference sequences. <i>PLoS Pathogens</i> , 2017, 13, e1006528.	2.1	10
32	An Evolutionary Model-Based Approach To Quantify the Genetic Barrier to Drug Resistance in Fast-Evolving Viruses and Its Application to HIV-1 Subtypes and Integrase Inhibitors. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	10
33	The rise and fall of K65R in a Portuguese HIV-1 Drug Resistance database, despite continuously increasing use of tenofovir [†] . <i>Infection, Genetics and Evolution</i> , 2009, 9, 683-688.	1.0	8
34	Increasing Prevalence of HIV-1 Transmitted Drug Resistance in Portugal: Implications for First Line Treatment Recommendations. <i>Viruses</i> , 2020, 12, 1238.	1.5	7
35	Modelled <i>in vivo</i> HIV fitness under drug selective pressure and estimated genetic barrier towards resistance are predictive for virological response. <i>Antiviral Therapy</i> , 2008, 13, 399-407.	0.6	7
36	Discordant predictions of residual activity could impact dolutegravir prescription upon raltegravir failure. <i>Journal of Clinical Virology</i> , 2015, 70, 120-127.	1.6	6

#	ARTICLE	IF	CITATIONS
37	Bayesian Best-Arm Identification for Selecting Influenza Mitigation Strategies. Lecture Notes in Computer Science, 2019, , 456-471.	1.0	5
38	Genome-wide diversity of Zika virus: Exploring spatio-temporal dynamics to guide a new nomenclature proposal. Virus Evolution, 2022, 8, veac029.	2.2	5
39	Characterization of Nucleoside Reverse Transcriptase Inhibitor-Associated Mutations in the RNase H Region of HIV-1 Subtype C Infected Individuals. Viruses, 2017, 9, 330.	1.5	4
40	Efficient Evaluation of Influenza Mitigation Strategies Using Preventive Bandits. Lecture Notes in Computer Science, 2017, , 67-85.	1.0	3