Kristof Theys

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7296758/publications.pdf

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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	Genome-wide diversity of Zika virus: Exploring spatio-temporal dynamics to guide a new nomenclature proposal. Virus Evolution, 2022, 8, veac029.	2.2	5
2	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. Briefings in Bioinformatics, 2021, 22, 642-663.	3.2	110
3	Increasing Prevalence of HIV-1 Transmitted Drug Resistance in Portugal: Implications for First Line Treatment Recommendations. Viruses, 2020, 12, 1238.	1.5	7
4	Advances in Visualization Tools for Phylogenomic and Phylodynamic Studies of Viral Diseases. Frontiers in Public Health, 2019, 7, 208.	1.3	15
5	Drivers of HIV-1 transmission: The Portuguese case. PLoS ONE, 2019, 14, e0218226.	1.1	12
6	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. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	10
7	A computational method for the identification of Dengue, Zika and Chikungunya virus species and genotypes. PLoS Neglected Tropical Diseases, 2019, 13, e0007231.	1.3	44
8	SANTA-SIM: simulating viral sequence evolution dynamics under selection and recombination. Virus Evolution, 2019, 5, vez003.	2.2	26
9	VIRULIGN: fast codon-correct alignment and annotation of viral genomes. Bioinformatics, 2019, 35, 1763-1765.	1.8	59
10	Bayesian Best-Arm Identification for Selecting Influenza Mitigation Strategies. Lecture Notes in Computer Science, 2019, , 456-471.	1.0	5
11	A genetic IFN/STAT1/FAS axis determines CD4 T stem cell memory levels and apoptosis in healthy controls and Adult T-cell Leukemia patients. OncoImmunology, 2018, 7, e1426423.	2.1	17
12	HIV-1 Infection in Cyprus, the Eastern Mediterranean European Frontier: A Densely Sampled Transmission Dynamics Analysis from 1986 to 2012. Scientific Reports, 2018, 8, 1702.	1.6	24
13	The impact of HIV-1 within-host evolution on transmission dynamics. Current Opinion in Virology, 2018, 28, 92-101.	2.6	47
14	Within-patient mutation frequencies reveal fitness costs of CpG dinucleotides and drastic amino acid changes in HIV. PLoS Genetics, 2018, 14, e1007420.	1.5	35
15	Time to Harmonize Dengue Nomenclature and Classification. Viruses, 2018, 10, 569.	1.5	14
16	Exploring resistance pathways for first-generation NS3/4A protease inhibitors boceprevir and telaprevir using Bayesian network learning. Infection, Genetics and Evolution, 2017, 53, 15-23.	1.0	14
17	Efficient Evaluation of Influenza Mitigation Strategies Using Preventive Bandits. Lecture Notes in Computer Science, 2017, , 67-85.	1.0	3
18	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

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19	PhyloGeoTool: interactively exploring large phylogenies in an epidemiological context. Bioinformatics, 2017, 33, 3993-3995.	1.8	16
20	Epidemic dispersion of HIV and HCV in a population of co-infected Romanian injecting drug users. PLoS ONE, 2017, 12, e0185866.	1.1	17
21	Zika genomics urgently need standardized and curated reference sequences. PLoS Pathogens, 2017, 13, e1006528.	2.1	10
22	On the contribution of Angola to the initial spread of HIV-1. Infection, Genetics and Evolution, 2016, 46, 219-222.	1.0	11
23	Mapping the genomic diversity of HCV subtypes 1a and 1b: Implications of structural and immunological constraints for vaccine and drug development. Virus Evolution, 2016, 2, vew024.	2.2	17
24	Global epidemiology of drug resistance after failure of WHO recommended first-line regimens for adult HIV-1 infection: a multicentre retrospective cohort study. Lancet Infectious Diseases, The, 2016, 16, 565-575.	4.6	217
25	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. AIDS Research and Human Retroviruses, 2016, 32, 427-433.	0.5	19
26	Assessing transmissibility of HIV-1 drug resistance mutations from treated and from drug-naive individuals. Aids, 2015, 29, 2045-2052.	1.0	21
27	Genetic Diversity and Selective Pressure in Hepatitis C Virus Genotypes 1â€“6: Significance for Direct-Acting Antiviral Treatment and Drug Resistance. Viruses, 2015, 7, 5018-5039.	1.5	59
28	HIV-1 genotypic drug resistance testing: digging deep, reaching wide?. Current Opinion in Virology, 2015, 14, 16-23.	2.6	36
29	An integrated map of HIV genome-wide variation from a population perspective. Retrovirology, 2015, 12, 18.	0.9	90
30	A new ensemble coevolution system for detecting HIV-1 protein coevolution. Biology Direct, 2015, 10, 1.	1.9	78
31	CRF19_cpx is an Evolutionary fit HIV-1 Variant Strongly Associated With Rapid Progression to AIDS in Cuba. EBioMedicine, 2015, 2, 244-254.	2.7	56
32	Discordant predictions of residual activity could impact dolutegravir prescription upon raltegravir failure. Journal of Clinical Virology, 2015, 70, 120-127.	1.6	6
33	HIV-1 subtype distribution and its demographic determinants in newly diagnosed patients in Europe suggest highly compartmentalized epidemics. Retrovirology, 2013, 10, 7.	0.9	129
34	HIV-1 drug resistance: where do polymorphisms fit in?. Future Microbiology, 2013, 8, 303-306.	1.0	11
35	RegaDB: community-driven data management and analysis for infectious diseases. Bioinformatics, 2013, 29, 1477-1480.	1.8	29
36	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. Retrovirology, 2012, 9, 81.	0.9	23

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37	Estimating the individualized HIV-1 genetic barrier to resistance using a nelfinavir fitness landscape. BMC Bioinformatics, 2010, 11, 409.	1.2	12
38	The rise and fall of K65R in a Portuguese HIV-1 Drug Resistance database, despite continuously increasing use of tenofovirâ˜†. Infection, Genetics and Evolution, 2009, 9, 683-688.	1.0	8
39	Modelled in vivo HIV fitness under drug selective pressure and estimated genetic barrier towards resistance are predictive for virological response. Antiviral Therapy, 2008, 13, 399-407.	0.6	7
40	Modelled<i>in vivo</i>HIV Fitness under drug Selective Pressure and Estimated Genetic Barrier Towards Resistance are Predictive for Virological Response. Antiviral Therapy, 2008, 13, 399-408.	0.6	17