Wasfi Fares

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2610986/publications.pdf

Version: 2024-02-01

713013 758635 24 500 12 21 citations h-index g-index papers 27 27 27 1152 citing authors all docs docs citations times ranked

#	Article	IF	CITATIONS
1	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. Science, 2021, 374, 423-431.	6.0	144
2	An integrated overview of the midgut bacterial flora composition of Phlebotomus perniciosus, a vector of zoonotic visceral leishmaniasis in the Western Mediterranean Basin. PLoS Neglected Tropical Diseases, 2017, 11, e0005484.	1.3	38
3	Changes of Sand Fly Populations and Leishmania infantum Infection Rates in an Irrigated Village Located in Arid Central Tunisia. International Journal of Environmental Research and Public Health, 2016, 13, 329.	1.2	34
4	Sero-epidemiological survey of Crimean-Congo hemorrhagic fever virus in Tunisia. Parasite, 2016, 23, 10.	0.8	28
5	Tick-borne encephalitis virus in Ixodes ricinus (Acari: Ixodidae) ticks, Tunisia. Ticks and Tick-borne Diseases, 2021, 12, 101606.	1.1	23
6	Infection of sand flies collected from different bio-geographical areas of Tunisia with phleboviruses. Acta Tropica, 2015, 141, 1-6.	0.9	20
7	Serologic evidence of exposure to Rift Valley fever virus detected in Tunisia. New Microbes and New Infections, 2016, 9, 1-7.	0.8	20
8	Ixodes inopinatus and Ixodes ricinus (Acari: Ixodidae) Are Sympatric Ticks in North Africa. Journal of Medical Entomology, 2020, 57, 952-956.	0.9	19
9	Isolation, full genomic characterization and neutralization-based human seroprevalence of Medjerda Valley virus, a novel sandfly-borne phlebovirus belonging to the Salehabad virus complex in northern Tunisia. Journal of General Virology, 2016, 97, 602-610.	1.3	19
10	Presence of sandfly-borne phleboviruses of two antigenic complexes (Sandfly fever Naples virus and) Tj ETQq0 C microneutralisation-based seroprevalence study in dogs. Parasites and Vectors, 2014, 7, 476.	0 0 rgBT /C 1.0	verlock 10 Tf 5
11	Multiplexed Magnetofluorescent Bioplatform for the Sensitive Detection of SARS-CoV-2 Viral RNA without Nucleic Acid Amplification. Analytical Chemistry, 2021, 93, 11225-11232.	3.2	17
12	Phylogenetic analysis of complete VP1 sequences of echoviruses 11 and 6: high genetic diversity and circulation of genotypes with a wide geographical and temporal range. Journal of Medical Microbiology, 2011, 60, 1017-1025.	0.7	15
13	SARS-CoV2 RT-PCR assays: In vitroï»; comparison of 4 WHO approved protocols on clinical specimens and its implications for real laboratory practice through variant emergence. Virology Journal, 2022, 19, 54.	1.4	15
14	The Impact of Illegal Waste Sites on the Transmission of Zoonotic Cutaneous Leishmaniasis in Central Tunisia. International Journal of Environmental Research and Public Health, 2021, 18, 66.	1.2	13
15	Molecular Epidemiology of SARS-CoV-2 in Tunisia (North Africa) through Several Successive Waves of COVID-19. Viruses, 2022, 14, 624.	1.5	13
16	Update on molecular characterization of coxsackievirus B5 strains. Journal of Medical Virology, 2011, 83, 1247-1254.	2.5	12
17	Co-circulation of Toscana virus and Leishmania infantum in a focus of zoonotic visceral leishmaniasis from Central Tunisia. Acta Tropica, 2020, 204, 105342.	0.9	11
18	Phleboviruses associated with sand flies in arid bio-geographical areas of Central Tunisia. Acta Tropica, 2016, 158, 13-19.	0.9	10

#	Article	IF	CITATION
19	Genetic characterization of West Nile Virus strains during neuroinvasives infection outbreak in Tunisia, 2018. Transboundary and Emerging Diseases, 2021, 68, 2414-2421.	1.3	7
20	Sequencing Using a Two-Step Strategy Reveals High Genetic Diversity in the S Gene of SARS-CoV-2 after a High-Transmission Period in Tunis, Tunisia. Microbiology Spectrum, 2021, 9, e0063921.	1.2	7
21	Absence of Crimean-Congo haemorrhagic fever virus in the tick Hyalomma aegyptium parasitizing the spur-thighed tortoise (Testudo graeca) in Tunisia. Parasite, 2019, 26, 35.	0.8	6
22	The value of West Nile virus RNA detection by real-time RT-PCR in urine samples from patients with neuroinvasive forms. Archives of Microbiology, 2022, 204, 238.	1.0	4
23	Whole genome sequencing and phylogenetic analysis of six SARS-CoV-2 strains isolated during COVID-19 pandemic in Tunisia, North Africa. BMC Genomics, 2021, 22, 540.	1.2	3
24	Risk Assessment of the Role of the Ecotones in the Transmission of Zoonotic Cutaneous Leishmaniasis in Central Tunisia. International Journal of Environmental Research and Public Health, 2021, 18, 9274.	1.2	3