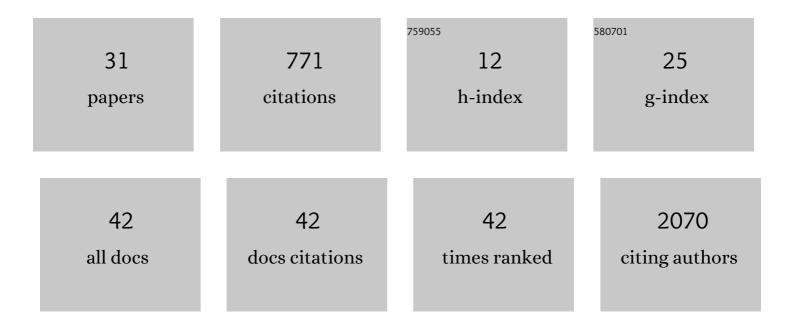
Francesco Messina

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1474091/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. Scientific Data, 2020, 7, 136.	2.4	99
2	Molecular characterization of SARS-CoV-2 from the first case of COVID-19 in Italy. Clinical Microbiology and Infection, 2020, 26, 954-956.	2.8	91
3	COVID-19: viral–host interactome analyzed by network based-approach model to study pathogenesis of SARS-CoV-2 infection. Journal of Translational Medicine, 2020, 18, 233.	1.8	80
4	Gut Microbiota Has a Widespread and Modifiable Effect on Host Gene Regulation. MSystems, 2019, 4, .	1.7	74
5	COVID19 Disease Map, a computational knowledge repository of virus–host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	3.2	53
6	Compartmentalized Replication of SARS-Cov-2 in Upper vs. Lower Respiratory Tract Assessed by Whole Genome Quasispecies Analysis. Microorganisms, 2020, 8, 1302.	1.6	40
7	Molecular analysis of clinical isolates of ceftazidime-avibactam-resistant Klebsiella pneumoniae. Clinical Microbiology and Infection, 2021, 27, 1040.e1-1040.e6.	2.8	38
8	SARS-CoV-2 Phylogenetic Analysis, Lazio Region, Italy, February–March 2020. Emerging Infectious Diseases, 2020, 26, 1842-1845.	2.0	33
9	Expanding Usutu virus circulation in Italy: detection in the Lazio region, central Italy, 2017 to 2018. Eurosurveillance, 2019, 24, .	3.9	29
10	Risk and predictive factors of prolonged viral RNA shedding in upper respiratory specimens in a large cohort of COVID-19 patients admitted to an Italian reference hospital. International Journal of Infectious Diseases, 2021, 105, 532-539.	1.5	20
11	Multi-omics approach to COVID-19: a domain-based literature review. Journal of Translational Medicine, 2021, 19, 501.	1.8	18
12	Virological Characterization of the First 2 COVID-19 Patients Diagnosed in Italy: Phylogenetic Analysis, Virus Shedding Profile From Different Body Sites, and Antibody Response Kinetics. Open Forum Infectious Diseases, 2020, 7, ofaa403.	0.4	17
13	Chikungunya Outbreak in the Republic of the Congo, 2019—Epidemiological, Virological and Entomological Findings of a South-North Multidisciplinary Taskforce Investigation. Viruses, 2020, 12, 1020.	1.5	15
14	Looking for pathways related to COVID-19: confirmation of pathogenic mechanisms by SARS-CoV-2–host interactome. Cell Death and Disease, 2021, 12, 788.	2.7	13
15	Spatially Explicit Models to Investigate Geographic Patterns in the Distribution of Forensic STRs: Application to the North-Eastern Mediterranean. PLoS ONE, 2016, 11, e0167065.	1.1	12
16	Mitochondrial DNA variation in an isolated area of Central Italy. Annals of Human Biology, 2010, 37, 385-402.	0.4	11
17	Traces of forgotten historical events in mountain communities in <scp>C</scp> entral <scp>I</scp> taly: A genetic insight. American Journal of Human Biology, 2015, 27, 508-519.	0.8	9
18	A finely resolved phylogeny of Y chromosome Hg J illuminates the processes of Phoenician and Greek colonizations in the Mediterranean. Scientific Reports, 2018, 8, 7465.	1.6	9

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#	Article	IF	CITATIONS
19	Linking between genetic structure and geographical distance: Study of the maternal gene pool in the Ethiopian population. Annals of Human Biology, 2017, 44, 53-69.	0.4	8
20	Signs of continental ancestry in urban populations of Peru through autosomal STR loci and mitochondrial DNA typing. PLoS ONE, 2018, 13, e0200796.	1.1	8
21	Virological and Serological Characterisation of SARS-CoV-2 Infections Diagnosed After mRNA BNT162b2 Vaccination Between December 2020 and March 2021. Frontiers in Medicine, 2021, 8, 815870.	1.2	8
22	Reduced Susceptibility to Carbapenems in a Klebsiella pneumoniae Clinical Isolate Producing SCO-1 and CTX-M-15 β-Lactamases Together with OmpK35 and OmpK36 Porin Deficiency. Antimicrobial Agents and Chemotherapy, 2020, 64, .	1.4	7
23	About the origin of the first two Sarsâ€CoVâ€2 infections in Italy: Inference not supported by appropriate sequence analysis. Journal of Medical Virology, 2020, 92, 1404-1405.	2.5	7
24	Enlarging the gene-geography of Europe and the Mediterranean area to STR loci of common forensic use: longitudinal and latitudinal frequency gradients. Annals of Human Biology, 2018, 45, 77-85.	0.4	5
25	Origin of HAV strains responsible for 2016–2017 outbreak among MSM: Viral phylodynamics in Lazio region. PLoS ONE, 2020, 15, e0234010.	1.1	5
26	The Easy-to-Use SARS-CoV-2 Assembler for Genome Sequencing: Development Study. JMIR Bioinformatics and Biotechnology, 2022, 3, e31536.	0.4	5
27	Importance of Surveillance of New Delhi Metallo-Beta-Lactamase Klebsiella pneumoniae: Molecular Characterization and Clonality of Strains Isolated in the Lazio Region, Italy. Infection and Drug Resistance, 2021, Volume 14, 3659-3665.	1.1	4
28	A genetic portrait of the Southâ€Eastern Carpathians based on autosomal short tandem repeats loci used in forensics. American Journal of Human Biology, 2018, 30, e23139.	0.8	3
29	Rationale and Criteria for a COVID-19 Model Framework. Viruses, 2021, 13, 1309.	1.5	3
30	An historical approach to the genetic distribution of KIR and HLA ligands in Eastern Sicilians compared to modern descendants of their invaders. Human Immunology, 2018, 79, 5-12.	1.2	2
31	SARS-CoV-2 Early Screening at the Point of Entry: Travelers From Bangladesh to Italy–July 2020. Frontiers in Genetics, 2021, 12, 625607.	1.1	1