

MOLECULAR EPIDEMIOLOGY

NEW	Primo Autore	Titolo	Rivista	DOI
	--	The COVID-19 Host Genetics Initiative, a global initiative to elucidate the role of host genetic factors in susceptibility and severity of the SARS-CoV-2 virus pandemic	Eur J Hum Genet	https://dx.doi.org/10.1038/s41431-020-0636-6
	A. Abdellaoui	Regional differences in reported Covid-19 cases show genetic correlations with higher socio-economic status and better health, potentially confounding studies on the genetics of disease susceptibility	medRxiv	https://dx.doi.org/10.1101/2020.04.24.20075333
	A. Abou Tayoun, et al.	Whole genome and phylogenetic analysis of SARS-CoV-2 strains from the index and early patients with COVID-19 in Dubai, United Arab Emirates, 29 January to 18 March 2020	bioRxiv	https://dx.doi.org/10.1101/2020.05.06.080606
	A. Aledo-Serrano, et al.	Genetic epilepsies and COVID-19 pandemic: Lessons from the caregiver perspective	Epilepsia	https://dx.doi.org/10.1111/epi.16537
	A. B. Franklin, et al.	Spillover of SARS-CoV-2 into novel wild hosts in North America: A conceptual model for perpetuation of the pathogen	Sci Total Environ	https://dx.doi.org/10.1016/j.scitotenv.2020.139358
	A. Bajaj, et al.	Understanding SARS-CoV-2: Genetic Diversity, Transmission and Cure in Human	Indian J Microbiol	https://dx.doi.org/10.1007/s12088-020-00869-4
	A. Banerjee, et al.	The novel Coronavirus enigma: Phylogeny and mutation analyses of SARS-CoV-2 viruses circulating in India during early 2020	bioRxiv	https://dx.doi.org/10.1101/2020.05.25.114199
	A. Baum, et al.	Antibody cocktail to SARS-CoV-2 spike protein prevents rapid mutational escape seen with individual antibodies	Science	https://dx.doi.org/10.1126/science.abd0831
	A. Danchin, et al.	SARS-CoV-2 variants: Relevance for symptom granularity, epidemiology, immunity (herd, vaccines), virus origin and containment?	Environ Microbiol	https://dx.doi.org/10.1111/1462-2920.15053
	A. E. Castillo, et al.	Phylogenetic analysis of the first four SARS-CoV-2 cases in Chile	J Med Virol	https://dx.doi.org/10.1002/jmv.25797
NEW	A. F. Barakat, et al.	Timeline from receipt to online publication of COVID-19 original research articles	medRxiv	https://dx.doi.org/10.1101/2020.06.22.20137653
	A. Goren, et al.	What does androgenetic alopecia have to do with COVID-19? An insight into a potential new therapy	Dermatologic therapy	https://dx.doi.org/10.1111/dth.13365
NEW	A. Graudenzi, et al.	Mutational Signatures and Heterogeneous Host Response Revealed Via Large-Scale Characterization of SARS-COV-2 Genomic Diversity	bioRxiv	https://dx.doi.org/10.1101/2020.07.06.189944
	A. H. Rad SM, et al.	Implications of SARS-CoV-2 mutations for genomic RNA structure and host microRNA targeting	bioRxiv	https://dx.doi.org/10.1101/2020.05.15.098947
	A. H. Sawalha, et al.	Epigenetic dysregulation of ACE2 and interferon-regulated genes might suggest increased COVID-19 susceptibility and severity in lupus patients	Clin Immunol	--

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NEW	A. Hosseini Rad Sm, et al.	Implications of SARS-CoV-2 Mutations for Genomic RNA Structure and Host microRNA Targeting	International journal of molecular sciences	https://dx.doi.org/10.3390/ijms21134807
	A. J. Brown, et al.	Broad spectrum antiviral remdesivir inhibits human endemic and zoonotic deltacoronaviruses with a highly divergent RNA dependent RNA polymerase	Antiviral research	https://dx.doi.org/10.1016/j.antiviral.2019.104541
	A. J. Rodriguez-Morales, et al.	History is repeating itself: Probable zoonotic spillover as the cause of the 2019 novel Coronavirus Epidemic	Le infezioni in medicina	http://ovidsp.ovid.com/ovidweb.cgi?T=JS&PAGE=reference&D=prem&NEWS=N&AN=32009128
	A. K. Sharma, et al.	Deep phylogenetic analysis of Orthocoronavirinae genomes traces the origin, evolution and transmission route of 2019 novel coronavirus	bioRxiv	https://dx.doi.org/10.1101/2020.05.12.091199
	A. Kanteh, et al.	Origin of imported SARS-CoV-2 strains in The Gambia identified from Whole Genome Sequences	bioRxiv	https://dx.doi.org/10.1101/2020.04.30.070771
NEW	A. Khan, et al.	Phylogenetic Analysis and Structural Perspectives of RNA-Dependent RNA-Polymerase Inhibition from SARS-CoV-2 with Natural Products	Interdiscip Sci	https://dx.doi.org/10.1007/s12539-020-00381-9
	A. L. Phelan, et al.	The Novel Coronavirus Originating in Wuhan, China: Challenges for Global Health Governance	JAMA - Journal of the American Medical Association	http://dx.doi.org/10.1001/jama.2020.1097
	A. Lai, et al.	Early phylogenetic estimate of the effective reproduction number of SARS-CoV-2	Journal of medical virology	https://dx.doi.org/10.1002/jmv.25723
	A. Lopez-Rincon, et al.	A Missense Mutation in SARS-CoV-2 Potentially Differentiates Between Asymptomatic and Symptomatic Cases	Bulletin of the World Health Organization	http://www.who.int/bulletin/online_first/20-258889.pdf
	A. M. Rice, et al.	Evidence for strong mutation bias towards, and selection against, T/U content in SARS-CoV2: implications for attenuated vaccine design	bioRxiv	https://dx.doi.org/10.1101/2020.05.11.088112
NEW	A. M. Rice, et al.	Evidence for strong mutation bias towards, and selection against, U content in SARS-CoV-2: implications for vaccine design	Mol Biol Evol	https://dx.doi.org/10.1093/molbev/msaa188
	A. Maitra, et al.	Mutations in SARS-CoV-2 viral RNA identified in Eastern India: Possible implications for the ongoing outbreak in India and impact on viral structure and host susceptibility	J Biosci	=
	A. Nemudryi, et al.	Temporal detection and phylogenetic assessment of SARS-CoV-2 in municipal wastewater	medRxiv : the preprint server for health sciences	https://dx.doi.org/10.1101/2020.04.15.20066746
	A. O. Obajuluwa, et al.	In-silico nucleotide and protein analyses of S-gene region in selected zoonotic coronaviruses reveal conserved domains and evolutionary emergence with trajectory course of viral entry from SARS-CoV2 genomic data	Arxiv	http://arxiv.org/abs/2005.02809

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NEW	Primo Autore	Titolo	Rivista	DOI
NEW	A. Sharma, et al.	Computational search for potential COVID-19 drugs from FDA approved drugs and small molecules of natural origin identifies several anti-virals and plant products	J Biosci	--
	A. Tabibzadeh, et al.	SARS-CoV-2 molecular and phylogenetic analysis in COVID-19 patients: A preliminary report from Iran	Infect Genet Evol	https://dx.doi.org/10.1016/j.meegid.2020.104387
	A. Ul Alam, et al.	Understanding the possible origin and genotyping of first Bangladeshi SARS-CoV-2 strain	J Med Virol	https://dx.doi.org/10.1002/jmv.26115
	A. Walker, et al.	Genetic structure of SARS-CoV-2 in Western Germany reflects clonal superspreading and multiple independent introduction events	medRxiv	https://dx.doi.org/10.1101/2020.04.25.20079517
	A. Walker, et al.	Genetic structure of SARS-CoV-2 reflects clonal superspreading and multiple independent introduction events, North-Rhine Westphalia, Germany, February and March 2020	Eurosurveillance	http://dx.doi.org/10.2807/1560-7917.ES.2020.25.22.2000746
	A. Wu, et al.	Mutations, Recombination and Insertion in the Evolution of 2019-nCoV	bioRxiv : the preprint server for biology	https://dx.doi.org/10.1101/2020.02.29.971101
NEW	A. Y. Elgendy, et al.	The Landscape of Medical Literature in the Era of COVID-19: Original Research Versus Opinion Pieces	Journal of general internal medicine	https://dx.doi.org/10.1007/s11606-020-06021-8
	Anonymous	Department of Error: Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study (The Lancet (2020) 395(10225) (689-697), (S0140673620302609), (10.1016/S014	The Lancet	http://dx.doi.org/10.1016/S0140-6736%2820%2930302-0
	B. Bartolini, et al.	SARS-CoV-2 Phylogenetic Analysis, Lazio Region, Italy, February-March 2020	Emerg Infect Dis	https://dx.doi.org/10.3201/eid2608.201525
	B. M. Kuehn	Genetic Analysis Tracks SARS-CoV-2 Mutations in Human Hosts	Jama	https://dx.doi.org/10.1001/jama.2020.9825
	B. Robson	COVID-19 Coronavirus spike protein analysis for synthetic vaccines, a peptidomimetic antagonist, and therapeutic drugs, and analysis of a proposed achilles' heel conserved region to minimize probability of escape mutations and drug resistance	Comput Biol Med	https://dx.doi.org/10.1016/j.combiomed.2020.103749
NEW	C. A. Schmitt, et al.	ACE2 and TMPRSS2 variation in savanna monkeys (<i>Chlorocebus</i> spp.): Potential risk for zoonotic/anthroponotic transmission of SARS-CoV-2 and a potential model for functional studies	PLoS One	https://dx.doi.org/10.1371/journal.pone.0235106
	C. Bhattacharyya, et al.	Global Spread of SARS-CoV-2 Subtype with Spike Protein Mutation D614G is Shaped by Human Genomic Variations that Regulate Expression of TMPRSS2 and MX1 Genes	bioRxiv	https://dx.doi.org/10.1101/2020.05.04.075911

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	C. Contini, et al.	The novel zoonotic COVID-19 pandemic: An expected global health concern	J Infect Dev Ctries	https://dx.doi.org/10.3855/jidc.12671
	C. Farkas, et al.	Insights on early mutational events in SARS-CoV-2 virus reveal founder effects across geographical regions	PeerJ	https://dx.doi.org/10.7717/peerj.9255
NEW	C. I. van der Made, et al.	Presence of Genetic Variants Among Young Men With Severe COVID-19	Jama	https://dx.doi.org/10.1001/jama.2020.13719
NEW	C. Lu, et al.	Genetic risk factors for death with SARS-CoV-2 from the UK Biobank	medRxiv	https://dx.doi.org/10.1101/2020.07.01.20144592
	C. Mavian, et al.	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable	Proceedings of the National Academy of Sciences of the United States of America	http://dx.doi.org/10.1073/pnas.2007295117
NEW	C. P. Sjaarda, et al.	Chasing the origin of SARS-CoV-2 in Canada's COVID-19 cases: A genomics study	bioRxiv	https://dx.doi.org/10.1101/2020.06.25.171744
NEW	C. Strafella, et al.	Analysis of ACE2 Genetic Variability among Populations Highlights a Possible Link with COVID-19-Related Neurological Complications	Genes (Basel)	https://dx.doi.org/10.3390/genes11070741
NEW	C. Toh, et al.	Evaluation of a genetic risk score for severity of COVID-19 using human chromosomal-scale length variation	medRxiv	https://dx.doi.org/10.1101/2020.07.06.20147637
NEW	C. Wylezich, et al.	Next-generation diagnostics: virus capture facilitates a sensitive viral diagnosis for epizootic and zoonotic pathogens including SARS-CoV-2	bioRxiv	https://dx.doi.org/10.1101/2020.06.30.181446
NEW	C.-H. G. Initiative	The COVID-19 Host Genetics Initiative, a global initiative to elucidate the role of host genetic factors in susceptibility and severity of the SARS-CoV-2 virus pandemic	European journal of human genetics : EJHG	https://dx.doi.org/10.1038/s41431-020-0636-6
	D. A. Alvarez-Diaz, et al.	Molecular analysis of several in-house rRT-PCR protocols for SARS-CoV-2 detection in the context of genetic variability of the virus in Colombia	Infection, Genetics and Evolution	http://dx.doi.org/10.1016/j.meegid.2020.104390
	D. A. Kolin, et al.	Clinical and Genetic Characteristics of Covid-19 Patients from UK Biobank	medRxiv	https://dx.doi.org/10.1101/2020.05.05.20075507
	D. Benvenuto, et al.	Evidence for mutations in SARS-CoV-2 Italian isolates potentially affecting virus transmission	J Med Virol	https://dx.doi.org/10.1002/jmv.26104
	D. Benvenuto, et al.	Evolutionary analysis of SARS-CoV-2: how mutation of Non-Structural Protein 6 (NSP6) could affect viral autophagy	J Infect	https://dx.doi.org/10.1016/j.jinf.2020.03.058
NEW	D. Bushman, et al.	Detection and Genetic Characterization of Community Based SARS-CoV-2 Infections - New York City, March 2020	MMWR Morb Mortal Wkly Rep	https://dx.doi.org/10.15585/mmwr.mm6928a5
	D. Eskier, et al.	Mutation density changes in SARS-CoV-2 are related to the pandemic stage but to a lesser extent in the dominant strain with mutations in spike and RdRp	bioRxiv	https://dx.doi.org/10.1101/2020.06.15.153239
	D. Eskier, et al.	RdRp mutations are associated with SARS-CoV-2 genome evolution	bioRxiv	https://dx.doi.org/10.1101/2020.05.20.104885

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	D. Gemmati, et al.	COVID-19 and Individual Genetic Susceptibility/Receptivity: Role of ACE1/ACE2 Genes, Immunity, Inflammation and Coagulation. Might the Double X-chromosome in Females Be Protective against SARS-CoV-2 Compared to the Single X-Chromosome in Males?	International journal of molecular sciences	https://dx.doi.org/10.3390/ijms21103474
NEW	D. H. Katz, et al.	Proteomic Profiling in Biracial Cohorts Implicates DC-SIGN as a Mediator of Genetic Risk in COVID-19	medRxiv	https://dx.doi.org/10.1101/2020.06.09.20125690
NEW	D. Howard	Genetic Programming visitation scheduling solution can deliver a less austere COVID-19 pandemic population lockdown	Arxiv	http://arxiv.org/abs/2006.10748
NEW	D. M. Morens, et al.	The Origin of COVID-19 and Why It Matters	Am J Trop Med Hyg	https://dx.doi.org/10.4269/ajtmh.20-0849
	D. Ramazzotti, et al.	Characterization of intra-host SARS-CoV-2 variants improves phylogenomic reconstruction and may reveal functionally convergent mutations	bioRxiv	https://dx.doi.org/10.1101/2020.04.22.044404
NEW	E. A. Lopera Maya, et al.	Lack of Association Between Genetic Variants at ACE2 and TMPRSS2 Genes Involved in SARS-CoV-2 Infection and Human Quantitative Phenotypes	Front Genet	https://dx.doi.org/10.3389/fgene.2020.00613
	E. Bontempi	Commercial exchanges instead of air pollution as possible origin of COVID-19 initial diffusion phase in Italy: More efforts are necessary to address interdisciplinary research	Environmental research	https://dx.doi.org/10.1016/j.envres.2020.109775
NEW	E. G. Stafford	Highlighting the role of veterinary pharmacists in zoonotic diseases including COVID-19	J Am Pharm Assoc (2003)	https://dx.doi.org/10.1016/j.japh.2020.06.021
	E. Lopera, et al.	Lack of association between genetic variants at ACE2 and TMPRSS2 genes involved in SARS-CoV-2 infection and human quantitative phenotypes	medRxiv	https://dx.doi.org/10.1101/2020.04.22.20074963
NEW	E. M. Snyder, et al.	ACE2 and COVID-19: using antihypertensive medications and pharmacogenetic considerations	Pharmacogenomics	https://dx.doi.org/10.2217/pgs-2020-0048
	E. M. Snyder, et al.	Angiotensin converting enzyme 2 (ACE2) and COVID-19: using antihypertensive medications, pharmacogenetic considerations	Pharmacogenomics	https://dx.doi.org/10.2217/pgs-2020-0048
	E. Volz, et al.	Report 5 - Phylogenetic analysis of SARS-CoV-2 Faculty of Medicine Imperial College London	--	https://www.imperial.ac.uk/mrc-global-infectious-disease-analysis/covid-19/report-5-phylogenetics-of-sars-cov-2/
NEW	E. W. Fakhouri, et al.	Genetic Polymorphisms Complicate COVID-19 Therapy: Pivotal Role of HO-1 in Cytokine Storm	Antioxidants (Basel)	https://dx.doi.org/10.3390/antiox9070636
	F. A. Khan	The role of selectivity of the SARS-CoV-2 virus for human genetic profiles in susceptibility and resistance to COVID-19	New Microbes New Infect	https://dx.doi.org/10.1016/j.nmni.2020.100697

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	F. Carletti, et al.	About the origin of the first two Sars-CoV-2 infections in Italy: inference not supported by appropriate sequence analysis	J Med Virol	https://dx.doi.org/10.1002/jmv.25833
	F. Coppee, et al.	Severe acute respiratory syndrome coronavirus 2: virus mutations in specific European populations	New Microbes New Infect	https://dx.doi.org/10.1016/j.nmni.2020.100696
	F. Li, et al.	MERS Coronavirus: An Emerging Zoonotic Virus	Viruses	https://dx.doi.org/10.3390/v11070663
	G. B. Chand, et al.	Identification of novel mutations in RNA-dependent RNA polymerases of SARS-CoV-2 and their implications	bioRxiv	https://dx.doi.org/10.1101/2020.05.05.079939
NEW	G. B. Chand, et al.	Identification of novel mutations in RNA-dependent RNA polymerases of SARS-CoV-2 and their implications on its protein structure	PeerJ	https://dx.doi.org/10.7717/peerj.9492
	G. D. Vavougiou	A data-driven hypothesis on the epigenetic dysregulation of host metabolism by SARS coronaviral infection: Potential implications for the SARS-CoV-2 modus operandi	Med Hypotheses	https://dx.doi.org/10.1016/j.mehy.2020.109759
NEW	G. Hahn, et al.	Unsupervised cluster analysis of SARS-CoV-2 genomes indicates that recent (June 2020) cases in Beijing are from a genetic subgroup that consists of mostly European and South(east) Asian samples, of which the latter are the most recent	bioRxiv	https://dx.doi.org/10.1101/2020.06.22.165936
	G. K. M, et al.	Prediction of number of cases expected and estimation of the final size of coronavirus epidemic in India using the logistic model and genetic algorithm	Arxiv	http://arxiv.org/abs/2003.12017
NEW	G. Lippi, et al.	Do genetic polymorphisms in angiotensin converting enzyme 2 (ACE2) gene play a role in coronavirus disease 2019 (COVID-19)?	Clin Chem Lab Med	https://dx.doi.org/10.1515/cclm-2020-0727
	G. Wong, et al.	Zoonotic origins of human coronavirus 2019 (HCoV-19 / SARS-CoV-2): why is this work important?	Zoological research	https://dx.doi.org/10.24272/j.issn.2095-8137.2020.031
	G. Zehender, et al.	GENOMIC CHARACTERISATION AND PHYLOGENETIC ANALYSIS OF SARS-COV-2 IN ITALY	Journal of medical virology	http://dx.doi.org/10.1002/jmv.25794
NEW	H. Guo, et al.	Evolutionary arms race between virus and host drives genetic diversity in bat SARS related coronavirus spike genes	J Virol	https://dx.doi.org/10.1128/jvi.00902-20
	H. Guohu, et al.	Spread dynamics of SARS-CoV-2 epidemic in China: a phylogenetic analysis	medRxiv	https://dx.doi.org/10.1101/2020.05.20.20107854
	H. Ikitimur, et al.	"Determining Host Factors Contributing to Disease Severity in a Family Cluster of 29 Hospitalized SARS-CoV-2 Patients: Could Genetic Factors Be Relevant in the Clinical Course of COVID-19?"	J Med Virol	https://dx.doi.org/10.1002/jmv.26106

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	H. J. He, et al.	Etiology and genetic evolution of canine coronavirus circulating in five provinces of China, during 2018-2019	Microb Pathog	https://dx.doi.org/10.1016/j.micpath.2020.104209
NEW	H. K. H. Luk, et al.	Molecular epidemiology, evolution and phylogeny of SARS coronavirus	Infection, genetics and evolution : journal of molecular epidemiology and evolutionary genetics in infectious diseases	https://dx.doi.org/10.1016/j.meegid.2019.03.001
	H. Li, et al.	Human-animal interactions and bat coronavirus spillover potential among rural residents in Southern China	Biosaf Health	https://dx.doi.org/10.1016/j.bsheal.2019.10.004
NEW	H. Mou, et al.	Mutations from bat ACE2 orthologs markedly enhance ACE2-Fc neutralization of SARS-CoV-2	bioRxiv	https://dx.doi.org/10.1101/2020.06.29.178459
	H. S. Yoo, et al.	COVID-19 and veterinarians for one health, zoonotic and reverse-zoonotic transmissions	J Vet Sci	https://dx.doi.org/10.4142/jvs.2020.21.e51
	H. Singh, et al.	Mapping the genomic landscape & diversity of COVID-19 based on >3950 clinical isolates of SARS-CoV-2: Likely origin & transmission dynamics of isolates sequenced in India	Indian J Med Res	https://dx.doi.org/10.4103/ijmr.IJMR_1253_20
	H. Wang, et al.	The genetic sequence, origin, and diagnosis of SARS-CoV-2	European journal of clinical microbiology & infectious diseases : official publication of the European Society of Clinical Microbiology	https://dx.doi.org/10.1007/s10096-020-03899-4
NEW	H. Zeberg, et al.	The major genetic risk factor for severe COVID-19 is inherited from Neandertals	bioRxiv	https://dx.doi.org/10.1101/2020.07.03.186296
	I. Karacan, et al.	The origin of SARS-CoV-2 in Istanbul: Sequencing findings from the epicenter of the pandemic in Turkey	North Clin Istanb	https://dx.doi.org/10.14744/nci.2020.90532
NEW	I. O. Adebale, et al.	Phylogenetic analysis of SARS-CoV-2 genomes in Turkey	Turk J Biol	https://dx.doi.org/10.3906/biy-2005-35
NEW	I. Saha, et al.	Genome-wide analysis of Indian SARS-CoV-2 genomes for the identification of genetic mutation and SNP	Infection, genetics and evolution : journal of molecular epidemiology and evolutionary genetics in infectious diseases	https://dx.doi.org/10.1016/j.meegid.2020.104457
	J. A. Jaimes, et al.	Phylogenetic Analysis and Structural Modeling of SARS-CoV-2 Spike Protein Reveals an Evolutionary Distinct and Proteolytically-Sensitive Activation Loop	J Mol Biol	https://dx.doi.org/10.1016/j.jmb.2020.04.009
	J. A. Patino-Galindo, et al.	Recombination and lineage-specific mutations led to the emergence of SARS-CoV-2	bioRxiv : the preprint server for biology	https://dx.doi.org/10.1101/2020.02.10.942748
	J. A. Poterico, et al.	Genetic variants and source of introduction of SARS-CoV-2 in South America	J Med Virol	https://dx.doi.org/10.1002/jmv.26001
	J. A. Sheikh, et al.	Emerging genetic diversity among clinical isolates of SARS-CoV-2: Lessons for today	Infect Genet Evol	https://dx.doi.org/10.1016/j.meegid.2020.104330
NEW	J. Chen, et al.	Mutations Strengthened SARS-CoV-2 Infectivity	J Mol Biol	https://dx.doi.org/10.1016/j.jmb.2020.07.009
	J. Chen, et al.	Mutations strengthened SARS-CoV-2 infectivity	Arxiv	http://arxiv.org/abs/2005.14669
	J. Cui, et al.	Origin and evolution of pathogenic coronaviruses	Nature reviews. Microbiology	https://dx.doi.org/10.1038/s41579-018-0118-9

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	J. D. Jensen, et al.	Considering mutational meltdown as a potential SARS-CoV-2 treatment strategy	Heredity (Edinb)	https://dx.doi.org/10.1038/s41437-020-0314-z
NEW	J. D. Ram�rez, et al.	Genetic Diversity Among SARS-CoV2 Strains in South America may Impact Performance of Molecular Detection	Pathogens	https://dx.doi.org/10.3390/pathogens9070580
	J. Giandhari, et al.	Early transmission of SARS-CoV-2 in South Africa: An epidemiological and phylogenetic report	medRxiv : the preprint server for health sciences	https://dx.doi.org/10.1101/2020.05.29.20116376
NEW	J. Malaiyan, et al.	An update on origin of SARS-CoV-2: Despite closest identity, bat (RaTG13) and Pangolin derived Coronaviruses varied in the critical binding site and O-linked glycan residues	J Med Virol	https://dx.doi.org/10.1002/jmv.26261
	J. McCoy, et al.	Racial Variations in COVID-19 Deaths May Be Due to Androgen Receptor Genetic Variants Associated with Prostate Cancer and Androgenetic Alopecia. Are Anti-Androgens a Potential Treatment for COVID-19?	Journal of cosmetic dermatology	https://dx.doi.org/10.1111/jocd.13455
	J. O. Wertheim	A glimpse into the origins of genetic diversity in SARS-CoV-2	Clinical infectious diseases : an official publication of the Infectious Diseases Society of America	http://dx.doi.org/10.1093/cid/ciaa213
	J. R. Delanghe, et al.	ACE Ins/Del genetic polymorphism and epidemiological findings in COVID-19	Clinical chemistry and laboratory medicine	https://dx.doi.org/10.1515/cclm-2020-0605
NEW	J. R. Giudicessi, et al.	Genetic Susceptibility for COVID-19-Associated Sudden Cardiac Death in African Americans	Heart Rhythm	https://dx.doi.org/10.1016/j.hrthm.2020.04.045
	J. S. Kim, et al.	Genome-Wide Identification and Characterization of Point Mutations in the SARS-CoV-2 Genome	Osong Public Health Res Perspect	https://dx.doi.org/10.24171/j.phrp.2020.11.3.05
	J. S. Mackenzie, et al.	COVID-19-A Novel Zoonotic Disease: A Review of the Disease, the Virus, and Public Health Measures	Asia Pac J Public Health	https://dx.doi.org/10.1177/1010539520931326
	J. T. Wu, et al.	Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study	Lancet	https://dx.doi.org/10.1016/s0140-6736(20)30260-9
	J. Torres-Lopez	[What is the origin of SARS-CoV-2?]	Cual es el origen del SARS-CoV-2?	http://ovidsp.ovid.com/ovidweb.cgi?T=JS&PAGE=reference&D=prem&NEWS=N&AN=32412715
NEW	J. Zhao, et al.	Snapshot of the evolution and mutation patterns of SARS-CoV-2	bioRxiv	https://dx.doi.org/10.1101/2020.07.04.187435
	J. von der Thusen, et al.	Histopathology and genetic susceptibility in COVID-19 pneumonia	Eur J Clin Invest	https://dx.doi.org/10.1111/eci.13259
NEW	K. Fujikura, et al.	Genetic variations in the human severe acute respiratory syndrome coronavirus receptor ACE2 and serine protease TMPRSS2	J Clin Pathol	https://dx.doi.org/10.1136/jclinpath-2020-206867
	K. J. Godri Pollitt, et al.	COVID-19 vulnerability: the potential impact of genetic susceptibility and airborne transmission	Hum Genomics	https://dx.doi.org/10.1186/s40246-020-00267-3

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NEW	K. Kadkhoda	Severe acute respiratory syndrome coronavirus 2, original antigenic sin, and antibody-dependent enhancement: menage a trois	Current opinion in rheumatology	https://dx.doi.org/10.1097/BOR.0000000000000728
NEW	K. Rimfeld, et al.	Genetic correlates of psychological responses to the COVID-19 crisis in young adult twins in Great Britain	Res Sq	https://dx.doi.org/10.21203/rs.3.rs-31853/v1
	K. Shirato, et al.	Development of Genetic Diagnostic Methods for Novel Coronavirus 2019 (nCoV-2019) in Japan	Jpn J Infect Dis	https://dx.doi.org/10.7883/yoken.JJID.2020.061
	K. Somasundaram, et al.	Genomics of Indian SARS-CoV-2: Implications in genetic diversity, possible origin and spread of virus	medRxiv	https://dx.doi.org/10.1101/2020.04.25.20079475
	K. Taylor, et al.	Analysis of Genetic Host Response Risk Factors in Severe COVID-19 Patients	medRxiv	https://dx.doi.org/10.1101/2020.06.17.20134015
	K. Wada, et al.	Time-series analyses of directional sequence changes in SARS-CoV-2 genomes and an efficient search method for advantageous mutations for growth in human cells	bioRxiv	https://dx.doi.org/10.1101/2020.06.16.151282
NEW	L. A. McKay, et al.	Prevalence and mutation analysis of the spike protein in feline enteric coronavirus and feline infectious peritonitis detected in household and shelter cats in western Canada	Canadian journal of veterinary research = Revue canadienne de recherche veterinaire	--
	L. Kachuri, et al.	The landscape of host genetic factors involved in infection to common viruses and SARS-CoV-2	medRxiv : the preprint server for health sciences	https://dx.doi.org/10.1101/2020.05.01.20088054
NEW	L. M. Irham, et al.	Genetic variants that influence SARS-CoV-2 receptor TMPRSS2 expression among population cohorts from multiple continents	Biochem Biophys Res Commun	https://dx.doi.org/10.1016/j.bbrc.2020.05.179
	L. Miralles-Pechuñin, et al.	A Deep Q-learning/genetic Algorithms Based Novel Methodology For Optimizing Covid-19 Pandemic Government Actions	Arxiv	http://arxiv.org/abs/2005.07656
NEW	L. R. Lopes, et al.	Molecular evolution and phylogenetic analysis of SARS-CoV-2 and hosts ACE2 protein suggest Malayan pangolin as intermediary host	Braz J Microbiol	https://dx.doi.org/10.1007/s42770-020-00321-1
	L. Sangl, et al.	Detection of feline coronavirus RNA, spike gene mutations, and feline coronavirus antigen in macrophages in aqueous humor of cats in the diagnosis of feline infectious peritonitis	J Vet Diagn Invest	https://dx.doi.org/10.1177/1040638720927362
	L. Shen, et al.	Children's Hospital Los Angeles COVID-19 Analysis Research Database (CARD) - A Resource for Rapid SARS-CoV-2 Genome Identification Using Interactive Online Phylogenetic Tools	bioRxiv	https://dx.doi.org/10.1101/2020.05.11.089763
	L. Valenti, et al.	Lack of genetic evidence that fatty liver disease predisposes to COVID-19	Journal of hepatology	http://dx.doi.org/10.1016/j.jhep.2020.05.015
	L. Zhang, et al.	Origin and evolution of the 2019 novel coronavirus	Clinical infectious diseases : an official publication of the Infectious Diseases Society of America	http://dx.doi.org/10.1093/cid/ciaa112

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NEW	Primo Autore	Titolo	Rivista	DOI
NEW	L. Zhang, et al.	The D614G mutation in the SARS-CoV-2 spike protein reduces S1 shedding and increases infectivity	bioRxiv : the preprint server for biology20200627	https://dx.doi.org/10.1101/2020.06.12.148726
	L. van Dorp, et al.	Emergence of genomic diversity and recurrent mutations in SARS-CoV-2	Infection, genetics and evolution : journal of molecular epidemiology and evolutionary genetics in infectious diseases	https://dx.doi.org/10.1016/j.meegid.2020.104351
NEW	M. A. AlBalwi, et al.	Evolving sequence mutations in the Middle East Respiratory Syndrome Coronavirus (MERS-CoV)	Journal of infection and public health	https://dx.doi.org/10.1016/j.jiph.2020.06.030
	M. A. Shereen, et al.	COVID-19 infection: Origin, transmission, and characteristics of human coronaviruses	J Adv Res	https://dx.doi.org/10.1016/j.jare.2020.03.005
	M. Abouelhoda, et al.	SARS-CoV-2 receptor mutation in Egyptian population	medRxiv	https://dx.doi.org/10.1101/2020.04.27.20082206
NEW	M. B. Uddin, et al.	Ancestral origin, antigenic resemblance and epidemiological insights of novel coronavirus (SARS-CoV-2): Global burden and Bangladesh perspective	Infect Genet Evol	https://dx.doi.org/10.1016/j.meegid.2020.104440
NEW	M. Barry, et al.	Nosocomial outbreak of the Middle East Respiratory Syndrome coronavirus: A phylogenetic, epidemiological, clinical and infection control analysis	Travel Med Infect Dis	https://dx.doi.org/10.1016/j.tmaid.2020.101807
	M. C. Wong, et al.	Evidence of recombination in coronaviruses implicating pangolin origins of nCoV-2019	bioRxiv : the preprint server for biology	https://dx.doi.org/10.1101/2020.02.07.939207
	M. Debnath, et al.	Genetic gateways to COVID-19 infection: Implications for risk, severity, and outcomes	FASEB journal : official publication of the Federation of American Societies for Experimental Biology	https://dx.doi.org/10.1096/fj.202001115R
NEW	M. Fidahic, et al.	Research methodology and characteristics of journal articles with original data, preprint articles and registered clinical trial protocols about COVID-19	BMC Med Res Methodol	https://dx.doi.org/10.1186/s12874-020-01047-2
	M. Kloc, et al.	The Role of Genetic Sex and Mitochondria in Response to COVID-19 Infection	International archives of allergy and immunology	https://dx.doi.org/10.1159/000508560
	M. LAAMARTI, et al.	Large scale genomic analysis of 3067 SARS-CoV-2 genomes reveals a clonal geodistribution and a rich genetic variations of hotspots mutations	bioRxiv	https://dx.doi.org/10.1101/2020.05.03.074567
NEW	M. Laamarti, et al.	Genetic analysis of SARS-CoV-2 strains collected from North Africa: viral origins and mutational spectrum	bioRxiv	https://dx.doi.org/10.1101/2020.06.30.181123
	M. LoPresti, et al.	The Role of Host Genetic Factors in Coronavirus Susceptibility: Review of Animal and Systematic Review of Human Literature	medRxiv : the preprint server for health sciences	https://dx.doi.org/10.1101/2020.05.30.20117788
	M. Mori, et al.	A deadly spillover: SARS-CoV-2 outbreak	Expert Opin Ther Pat	https://dx.doi.org/10.1080/13543776.2020.1760838
NEW	M. Pietzner, et al.	Genetic architecture of host proteins interacting with SARS-CoV-2	bioRxiv : the preprint server for biology	https://dx.doi.org/10.1101/2020.07.01.182709
	M. S. Nadeem, et al.	Origin, Potential Therapeutic Targets and Treatment for Coronavirus Disease (COVID-19)	Pathogens (Basel, Switzerland)	https://dx.doi.org/10.3390/pathogens9040307

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NEW	Primo Autore	Titolo	Rivista	DOI
	M. Saadat	No significant correlation between ACE Ins/Del genetic polymorphism and COVID-19 infection	Clinical chemistry and laboratory medicine	https://dx.doi.org/10.1515/cclm-2020-0577
	M. Thakur, et al.	How did SARS-CoV-19 spread in India from Italy, Iran and China? Genetic surveillance of early cases and virus demography	bioRxiv	https://dx.doi.org/10.1101/2020.04.26.062406
	M. Tiwari, et al.	Investigating the genomic landscape of novel coronavirus (2019-nCoV) to identify non-synonymous mutations for use in diagnosis and drug design	Journal of clinical virology : the official publication of the Pan American Society for Clinical Virology	https://dx.doi.org/10.1016/j.jcv.2020.104441
NEW	M. Vinciguerra, et al.	Atherosclerosis as Pathogenetic Substrate for Sars-Cov2 Cytokine Storm	J Clin Med	https://dx.doi.org/10.3390/jcm9072095
	M. Wells	Ideas and the origin of evidence during the COVID-19 pandemic	Emerg Med J	https://dx.doi.org/10.1136/emermed-2020-210000
NEW	N. D. Grubaugh, et al.	Making Sense of Mutation: What D614G Means for the COVID-19 Pandemic Remains Unclear	Cell	https://dx.doi.org/10.1016/j.cell.2020.06.040
NEW	N. Kaushal, et al.	Mutational Frequencies of SARS-CoV-2 Genome during the Beginning Months of the Outbreak in USA	Pathogens	https://dx.doi.org/10.3390/pathogens9070565
	N. M. Fountain-Jones, et al.	Emerging phylogenetic structure of the SARS-CoV-2 pandemic	bioRxiv	https://dx.doi.org/10.1101/2020.05.19.103846
	N. Zhao, et al.	Tracking the origin of early COVID-19 cases in Canada	International journal of infectious diseases : IJID : official publication of the International Society for Infectious Diseases	https://dx.doi.org/10.1016/j.ijid.2020.05.046
	P. Forster, et al.	Phylogenetic network analysis of SARS-CoV-2 genomes	Proc Natl Acad Sci U S A	https://dx.doi.org/10.1073/pnas.2004999117
	P. Hao, et al.	Is SARS-CoV-2 originated from laboratory? A rebuttal to the claim of formation via laboratory recombination	Emerging Microbes and Infections	http://dx.doi.org/10.1080/22221751.2020.1738279
	P. I. Lee, et al.	Emerging threats from zoonotic coronaviruses-from SARS and MERS to 2019-nCoV	J Microbiol Immunol Infect	https://dx.doi.org/10.1016/j.jmii.2020.02.001
NEW	P. S. X. Yap, et al.	An overview of the genetic variations of the SARS-CoV-2 genomes isolated in Southeast Asian countries	J Microbiol Biotechnol	https://dx.doi.org/10.4014/jmb.2006.06009
	P. Saha, et al.	A virus that has gone viral: Amino-acid mutation in S protein of Indian-isolate of Coronavirus COVID-19 might impact receptor-binding, thus infectivity	Bioscience reports	https://dx.doi.org/10.1042/BSR20201312
NEW	P. Saha, et al.	A virus that has gone viral: amino acid mutation in S protein of Indian isolate of Coronavirus COVID-19 might impact receptor binding, and thus, infectivity	Bioscience reports	https://dx.doi.org/10.1042/BSR20201312
	P. Simmonds	Rampant C->U hypermutation in the genomes of SARS-CoV-2 and other coronaviruses â€” causes and consequences for their short and long evolutionary trajectories	bioRxiv	https://dx.doi.org/10.1101/2020.05.01.072330

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NEW	Primo Autore	Titolo	Rivista	DOI
NEW	P. Simmonds	Rampant C→U Hypermethylation in the Genomes of SARS-CoV-2 and Other Coronaviruses: Causes and Consequences for Their Short- and Long-Term Evolutionary Trajectories	mSphere	https://dx.doi.org/10.1128/mSphere.00408-20
	P. Stefanelli, et al.	Whole genome and phylogenetic analysis of two SARS-CoV-2 strains isolated in Italy in January and February 2020: additional clues on multiple introductions and further circulation in Europe	Euro Surveill	https://dx.doi.org/10.2807/1560-7917.es.2020.25.13.2000305
NEW	Q. Nie, et al.	Phylogenetic and phylodynamic analyses of SARS-CoV-2	Virus Res	https://dx.doi.org/10.1016/j.virusres.2020.198098
	R. D. S. Bezerra, et al.	The Novel Coronavirus SARS-CoV-2: From a Zoonotic Infection to Coronavirus Disease-19 (COVID19)	J Med Virol	https://dx.doi.org/10.1002/jmv.26072
	R. H. Arnold	COVID-19 - Does This Disease Kill Due to Imbalance of the Renin Angiotensin System (RAS) Caused by Genetic and Gender Differences in the Response to Viral ACE 2 Attack?	Heart Lung Circ	https://dx.doi.org/10.1016/j.hlc.2020.05.004
	R. K. Pathan, et al.	Time series prediction of COVID-19 by mutation rate analysis using recurrent neural network-based LSTM model	Chaos Solitons Fractals	https://dx.doi.org/10.1016/j.chaos.2020.110018
	R. Kaden	Early Phylogenetic Diversification of SARS-CoV-2: Determination of Variants and the Effect on Epidemiology, Immunology, and Diagnostics	J Clin Med	https://dx.doi.org/10.3390/jcm9061615
	R. Lu, et al.	Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding	Lancet (London, England)	https://dx.doi.org/10.1016/S0140-6736(20)30251-8
NEW	R. Matyasek, et al.	Mutation Patterns of Human SARS-CoV-2 and Bat RaTG13 Coronavirus Genomes Are Strongly Biased Towards C>U Transitions, Indicating Rapid Evolution in Their Hosts	Genes	https://dx.doi.org/10.3390/genes11070761
	R. Ozturk	COVID-19: Pathogenesis, Genetic Polymorphism, Clinical Features and Laboratory Findings	Turk J Med Sci	https://dx.doi.org/10.3906/sag-2005-287
	R. P. Rajkumar	Contamination and infection: What the coronavirus pandemic could reveal about the evolutionary origins of obsessive-compulsive disorder	Psychiatry research	https://dx.doi.org/10.1016/j.psychres.2020.113062
	R. Salgotra, et al.	Time Series Analysis and Forecast of the COVID-19 Pandemic in India using Genetic Programming	Chaos Solitons Fractals	https://dx.doi.org/10.1016/j.chaos.2020.109945
	R. Sheervalilou, et al.	COVID-19 under spotlight: A close look at the origin, transmission, diagnosis, and treatment of the 2019-nCoV disease	J Cell Physiol	https://dx.doi.org/10.1002/jcp.29735
	R. Tiwari, et al.	COVID-19: animals, veterinary and zoonotic links	The veterinary quarterly	https://dx.doi.org/10.1080/01652176.2020.1766725
	R. Wang, et al.	Mutations on COVID-19 diagnostic targets	Arxiv	http://arxiv.org/abs/2005.02188

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NEW	Primo Autore	Titolo	Rivista	DOI
	S. A. MacGowan, et al.	Missense variants in ACE2 are predicted to encourage and inhibit interaction with SARS-CoV-2 Spike and contribute to genetic risk in COVID-19	bioRxiv	https://dx.doi.org/10.1101/2020.05.03.074781
	S. A. Nadeau, et al.	The origin and early spread of SARS-CoV-2 in Europe	medRxiv	https://dx.doi.org/10.1101/2020.06.10.20127738
	S. Ahmad, et al.	Design of a Novel Multi Epitope-Based Vaccine for Pandemic Coronavirus Disease (COVID-19) by Vaccinomics and Probable Prevention Strategy against Avenging Zoonotics	Eur J Pharm Sci	https://dx.doi.org/10.1016/j.ejps.2020.105387
NEW	S. Alagu Lakshmi, et al.	Ethnomedicines of Indian origin for combating COVID-19 infection by hampering the viral replication: using structure-based drug discovery approach	J Biomol Struct Dyn	https://dx.doi.org/10.1080/07391102.2020.1778537
	S. Alberti, et al.	Genetic drift and environmental spreading dynamics of COVID-19	medRxiv	https://dx.doi.org/10.1101/2020.05.08.20095448
	S. Banerjee, et al.	Mutational spectra of SARS-CoV-2 orf1ab polyprotein and Signature mutations in the United States of America	bioRxiv	https://dx.doi.org/10.1101/2020.05.01.071654
	S. Chirumbolo	Might the many positive COVID19 subjects in Italy have been caused by resident bat-derived zoonotic beta-coronaviruses instead of the Wuhan (China) outbreak?	Journal of Medical Virology	http://dx.doi.org/10.1002/jmv.25777
NEW	S. Chlamydas, et al.	Epigenetic mechanisms regulating COVID-19 infection	Epigenetics	https://dx.doi.org/10.1080/15592294.2020.1796896
NEW	S. Farah, et al.	Phylogenomics and phylodynamics of SARS-CoV-2 retrieved genomes from India	medRxiv	https://dx.doi.org/10.1101/2020.06.23.20138222
	S. J. Sanchez-Pacheco, et al.	Median-joining network analysis of SARS-CoV-2 genomes is neither phylogenetic nor evolutionary	Proceedings of the National Academy of Sciences of the United States of America	http://dx.doi.org/10.1073/pnas.2007062117
	S. Johri, et al.	Integrated analysis of bulk multi omic and single-cell sequencing data confirms the molecular origin of hemodynamic changes in Covid-19 infection explaining coagulopathy and higher geriatric mortality	medRxiv	https://dx.doi.org/10.1101/2020.04.26.20081182
	S. K. P. Lau, et al.	Possible Bat Origin of Severe Acute Respiratory Syndrome Coronavirus 2	Emerg Infect Dis	https://dx.doi.org/10.3201/eid2607.200092
	S. Kavukcu, et al.	Could MEFV mutation carriage status have a protective role for COVID-19 pandemic?	Medical Hypotheses	http://dx.doi.org/10.1016/j.mehy.2020.109889
NEW	S. Laha, et al.	Characterizations of SARS-CoV-2 mutational profile, spike protein stability and viral transmission	Infect Genet Evol	https://dx.doi.org/10.1016/j.meegid.2020.104445
	S. Liu, et al.	Distinct genetic spectrums and evolution patterns of SARS-CoV-2	medRxiv	https://dx.doi.org/10.1101/2020.06.16.20132902
	S. M. Chaw, et al.	The origin and underlying driving forces of the SARS-CoV-2 outbreak	J Biomed Sci	https://dx.doi.org/10.1186/s12929-020-00665-8

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NEW	Primo Autore	Titolo	Rivista	DOI
	S. M. Kasibhatla, et al.	Understanding evolution of SARS-CoV-2: a perspective from analysis of genetic diversity of RdRp gene	J Med Virol	https://dx.doi.org/10.1002/jmv.25909
NEW	S. Minhas	Could India be the origin of next COVID-19 like epidemic?	Sci Total Environ	https://dx.doi.org/10.1016/j.scitotenv.2020.138918
	S. Mohammadpour, et al.	An updated review of the association of host genetic factors with susceptibility and resistance to COVID-19	J Cell Physiol	https://dx.doi.org/10.1002/jcp.29868
	S. Nelson-Sathi, et al.	Structural and Functional Implications of Non-synonymous Mutations in the Spike protein of 2,954 SARS-CoV-2 Genomes	bioRxiv	https://dx.doi.org/10.1101/2020.05.02.071811
	S. Piplani, et al.	In silico comparison of spike protein-ACE2 binding affinities across species:significance for the possible origin of the SARS-CoV-2 virus	Arxiv	http://arxiv.org/abs/2005.06199
	S. S. Hassan, et al.	Molecular conservation and differential mutation on ORF3a gene in Indian SARS-CoV2 genomes	Genomics	https://dx.doi.org/10.1016/j.ygeno.2020.06.016
NEW	S. S. Hassan, et al.	SARS-CoV2 envelope protein: Non-synonymous mutations and its consequences	Genomics	https://dx.doi.org/10.1016/j.ygeno.2020.07.001
	S. Sen, et al.	Coronaviruses: origin and evolution	Med J Armed Forces India	https://dx.doi.org/10.1016/j.mjafi.2020.04.008
	S. W. K. Wong	Assessing the impacts of mutations to the structure of COVID-19 spike protein via sequential Monte Carlo	Arxiv	http://arxiv.org/abs/2005.07550
	S.-J. Kim, et al.	A Novel Synonymous Mutation of SARS-CoV-2: Is This Possible to Affect Their Antigenicity and Immunogenicity?	Vaccines	https://dx.doi.org/10.3390/vaccines8020220
NEW	T. H. Mallhi, et al.	Risks of Zoonotic Transmission of COVID-19 during Eid-UI-Adha in Pakistan	Disaster Med Public Health Prep	https://dx.doi.org/10.1017/dmp.2020.278
	T. Khan, et al.	COVID-19: A Worldwide, Zoonotic, Pandemic Outbreak	Alternative therapies in health and medicine	http://ovidsp.ovid.com/ovidweb.cgi?T=JS&PAGE=reference&D=medp&NEWS=N&AN=32412918
	T. M. Wassenaar, et al.	2019_nCoV/SARS-CoV-2: rapid classification of betacoronaviruses and identification of Traditional Chinese Medicine as potential origin of zoonotic coronaviruses	Letters in applied microbiology	https://dx.doi.org/10.1111/lam.13285
	T. Matsuda, et al.	Phylogenetic analyses of the severe acute respiratory syndrome coronavirus 2 reflected the several routes of introduction to Taiwan, the United States, and Japan	Arxiv	http://arxiv.org/abs/2002.08802
NEW	T. N. Starr, et al.	Deep mutational scanning of SARS-CoV-2 receptor binding domain reveals constraints on folding and ACE2 binding	bioRxiv : the preprint server for biology20200627	https://dx.doi.org/10.1101/2020.06.17.157982
	T. Phan	Genetic diversity and evolution of SARS-CoV-2	Infection, genetics and evolution : journal of molecular epidemiology and evolutionary genetics in infectious diseases	https://dx.doi.org/10.1016/i.meegid.2020.104260

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NEW	Primo Autore	Titolo	Rivista	DOI
	T. T. Nguyen, et al.	Origin of Novel Coronavirus (COVID-19): A Computational Biology Study using Artificial Intelligence	bioRxiv	https://dx.doi.org/10.1101/2020.05.12.091397
	T. Zhang, et al.	Probable Pangolin Origin of SARS-CoV-2 Associated with the COVID-19 Outbreak	Curr Biol	https://dx.doi.org/10.1016/j.cub.2020.03.022
	T.-Y. Yeh, et al.	Faster <i>de novo</i> mutation of SARS-CoV-2 in shipboard quarantine	Bulletin of the World Health Organization	http://www.who.int/bulletin/online_first/20-255752.pdf
NEW	V. D. Menachery, et al.	Trypsin Treatment Unlocks Barrier for Zoonotic Bat Coronavirus Infection	J Virol	https://dx.doi.org/10.1128/jvi.01774-19
	V. Harypursat, et al.	Six weeks into the 2019 coronavirus disease (COVID-19) outbreak- it is time to consider strategies to impede the emergence of new zoonotic infections	Chinese medical journal	https://dx.doi.org/10.1097/CM9.0000000000000760
NEW	V. Singh	Can Vitamins, as Epigenetic Modifiers, Enhance Immunity in COVID-19 Patients with Non-communicable Disease?	Current nutrition reports	https://dx.doi.org/10.1007/s13668-020-00330-4
	V. Thomas, et al.	The genetic landscape of COVID-19: A South Asian perspective	J Pak Med Assoc	https://dx.doi.org/10.5455/jpma.09
	V. V. Khurstalev, et al.	Translation-associated mutational U-pressure in the first ORF of SARS-CoV-2 and other coronaviruses	bioRxiv	https://dx.doi.org/10.1101/2020.05.05.078238
NEW	W. Zaman, et al.	COVID-19: Phylogenetic approaches may help in finding resources for natural cure	Phytotherapy research : PTR	https://dx.doi.org/10.1002/ptr.6787
	X. Li, et al.	Bat origin of a new human coronavirus: there and back again	Science China. Life sciences	http://dx.doi.org/10.1007/s11427-020-1645-7
	X. Yang, et al.	Genetic cluster analysis of SARS-CoV-2 and the identification of those responsible for the major outbreaks in various countries	Emerg Microbes Infect	https://dx.doi.org/10.1080/22221751.2020.1773745
	Y. Cao, et al.	Comparative genetic analysis of the novel coronavirus (2019-nCoV/SARS-CoV-2) receptor ACE2 in different populations	Cell Discov	https://dx.doi.org/10.1038/s41421-020-0147-1
	Y. Gao, et al.	Phylogenetic study of 2019-nCoV by using alignment-free method	Arxiv	http://arxiv.org/abs/2003.01324
NEW	Y. Hou, et al.	New insights into genetic susceptibility of COVID-19: an ACE2 and TMPRSS2 polymorphism analysis	BMC Med	https://dx.doi.org/10.1186/s12916-020-01673-z
	Y. Junejo, et al.	Novel SARS-CoV-2/COVID-19: Origin, pathogenesis, genes and genetic variations, immune responses and phylogenetic analysis	Gene Rep	https://dx.doi.org/10.1016/j.genrep.2020.100752
	Y. M. Zhang, et al.	Genetic Roadmap for Kidney Involvement of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Infection	Clin J Am Soc Nephrol	https://dx.doi.org/10.2215/cjn.04370420
	Y. P. Wu, et al.	CT manifestations of the coronavirus disease 2019 of imported infection versus second-generation infection in patients outside the original district (Wuhan, China) of this disease: An observational study	Medicine (Baltimore)	https://dx.doi.org/10.1097/md.00000000000020370

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NEW	Primo Autore	Titolo	Rivista	DOI
	Y. S. Jeong	2019 novel coronavirus disease outbreak and molecular genetic characteristics of severe acute respiratory syndrome-coronavirus-2	Journal of Bacteriology and Virology	http://dx.doi.org/10.4167/jbv.2020.50.1.001
NEW	Y. Xing, et al.	MicroGMT: A Mutation Tracker for SARS-CoV-2 and Other Microbial Genome Sequences	Front Microbiol	https://dx.doi.org/10.3389/fmicb.2020.01502
	Y. Xu	Unveiling the Origin and Transmission of 2019-nCoV	Trends Microbiol	https://dx.doi.org/10.1016/j.tim.2020.02.001
	Y. Z. Zhang, et al.	A Genomic Perspective on the Origin and Emergence of SARS-CoV-2	Cell	https://dx.doi.org/10.1016/j.cell.2020.03.035
NEW	Y. Zhang, et al.	Interferon-Induced Transmembrane Protein 3 Genetic Variant rs12252-C Associated With Disease Severity in Coronavirus Disease 2019	J Infect Dis	https://dx.doi.org/10.1093/infdis/jiaa224
	Y.-R. Guo, et al.	The origin, transmission and clinical therapies on coronavirus disease 2019 (COVID-19) outbreak - an update on the status	Military Medical Research	https://dx.doi.org/10.1186/s40779-020-00240-0
NEW	Z. Daniloski, et al.	The D614G mutation in SARS-CoV-2 Spike increases transduction of multiple human cell types	bioRxiv : the preprint server for biology20200627	https://dx.doi.org/10.1101/2020.06.14.151357
NEW	Z. Ma, et al.	Reverse genetic systems: Rational design of coronavirus live attenuated vaccines with immune sequelae	Adv Virus Res	https://dx.doi.org/10.1016/bs.aivir.2020.06.003
	Z.-w. Chen, et al.	Global genetic diversity patterns and transmissions of SARS-CoV-2	medRxiv	https://dx.doi.org/10.1101/2020.05.05.20091413
NEW	P. J. Azurmendi	[Are there genetic variants that can modify the course of the COVID-19 pandemic?]	Hay variantes geneticas que puedan modificar el curso de la pandemia por COVID-19?	--