

# COVID- 19 Pandemic: A Biosocial Approach of Understanding

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## ABSTRACT

The outbreak covid pandemic has become exponentially high across the globe ever since the advent of the latest coronaviral epidemic COVID-19 triggered by the SARS-CoV-2 virus. The centre or the core of this pandemic is believed to be the city of Wuhan, China, as the first four cases of an acute respiratory syndrome of unknown etiology were detected among people with a contact link to a local seafood market (“wet market”) in Wuhan City China on 29 December 2019. It is anticipated that the spread of this disease is based on a large number of infected people who had exposure to the wet animal market in Wuhan City where live animals are sold and purchased. Researches and investigations were done to look for a host reservoir or intermediate carriers from which the infection could spread to the human population. Eventually, two snake species were identified which were believed to be the possible COVID-19 reservoirs although, there is still a lack of proper evidence. The complex nature of the interaction between human and animal health has dragged the attention of recent cross-disciplinary interest to come together under the banner of a holistic approach that explicitly recognises the multiple disciplines required to address such complicated health issues.

**Key Words :** Covid pandemic, Epidemiology, Biosocial research, Holistic approach

## INTRODUCTION

Since December 2019, health scenario around the world is struggling with an increasing number of cases of a viral respiratory syndrome that emerged in China. The cause is a new strain in the coronavirus family, provisionally named 2019 novel coronavirus (2019-nCoV)1, SARS-CoV-2 or COVID-19.2.

This 2019 coronavirus disease (COVID-19) epidemic is a public health emergency of international concern and poses a challenge to biological as well as socio-cultural resilience. Coronavirus disease 2019 (COVID-19) is profoundly affecting lives around the globe. Isolation, contact restrictions and economic shutdown are creating a huge transformation to the psychosocial environment of every community.

With more than 188,693,726 COVID positive cases and over 4,067,180 cases of fatalities, the coronavirus pandemic is growing day by day to hit massively across

the world. In addition to instilling a sense of fear and panic, COVID-19 is changing the very definition of ‘normalcy’ and the systems of the daily lives of every community. As the strongest weapon to contain the spread of the highly infectious novel coronavirus, the majority of the countries, including India have closed borders and initiated strict nationwide lockdowns.

Coronaviruses (CoVs) belong to the genus Coronavirus in Coronaviridae family. CoVs are enveloped, positive-stranded RNA viruses with a nucleocapsid (capsid with nucleic acid) reported size of 300–400 nm under the electron microscope (Woo *et al.*, 2010). All varieties of this genus are pleomorphic viruses which generally display 80–160 nm and 27–32 kb positive polarity of crown-shaped peplomers (Woo *et al.*, 2010). CoV recombinations are very large as RNA-dependent RNA polymerase (RdRP) jumps, and transcription errors are growing day by day, which has enough potentiality to lead to genetic drifting within the same strain (Din and

Boppana, 2020; Drexler *et al.*, 2010 and Fan *et al.*, 2020). CoVs are zoonotic viruses with a high mutation rate and are found in humans as well as other animal species, with numerical clinical symptoms from asymptomatic to the hospitalization with an intensive-care intervention (Cascella *et al.*, 2020). CoVs were not detected as highly pathogenic in humans until they were identified in Guangdong in 2002 and 2003 among the patients of the severe acute respiratory syndrome (SARS).

The outbreak of this pandemic has become exponentially high across the globe ever since the advent of the latest coronaviral epidemic COVID-19 triggered by the SARS-CoV-2 virus (Ahn *et al.*, 2020 and Fan *et al.*, 2020). In consideration of the possibility of a pandemic, scientists and physicians have been trying to grasp this emerging virus and its pathophysiology to recognize potential therapeutic protocols and to find therapeutic agents and vaccinations that are successful in (Cascella *et al.*, 2020) the disease management. On 12 December 2019, the first case of COVID-19 was identified with common pneumonia and some other basic symptoms, while within the end of December 2019, around 27 cases of extreme viral pneumonia were registered (WHO. Novel coronavirus (2019-ncov)). Consequently, numerous pneumonia cases that were localized in Wuhan in December 2019 were identified, and sources were noticed. Etiological studies of people that came to the hospital due to specific viruses have been conducted. The medical history of these patients has increased the likelihood of a virus outbreak. Novel SARS-COV-2 from wild bats and group 2  $\beta$ -CoVs, along with severe acute respiratory syndrome-related coronavirus (SARS-COV), was officially reported and registered on 22 January 2020.

Since there were several new SARS-CoV-2 cases in association with the Huanan market in Wuhan (Woo *et al.*, 2010 and Peng *et al.*, 2020). An animal host was suspected to be a source of virus transmission. As SARS-CoV-2 is identical to previous bat SARS-CoV (Wrapp *et al.*, 2020 and Woo *et al.*, 2010). bats were identified as a possible host for their progenitor.

SARS-CoV-2 infection was initially thought to transmit from human-to-human through direct contact and droplets (Fan *et al.*, 2020). Again, it has been reported that people are known to be more infectious when they are most (sickest) symptomatic. Besides, an individual may get SARS-CoV-2 by contacting a surface or entity contaminated with the virus by rubbing ears, nose and

maybe eyes after direct contact. The SARS-CoV-2 virus in some of the infected populations where 'community spread' has taken place is more prone to be circulated quickly and sustainably among humans.

### **Clinical Symptoms:**

It has been known from public care bodies, reviews and guidelines provided for identifying the clinical cases according to the seriousness of the clinical conditions, the SARS-CoV-2 might be mild, moderate or severe based on the strength of the immune system of the infected individual. Acute influenza with sepsis and septic shock and ARDS are the major severe health symptoms. A definite pattern in the bulk of cases has been noticed in the scientific development of the disease. It has been reported that, after around a week from the onset of the infection, infected individual's health outcomes have unexpectedly worsened, as a respiratory function has declined rapidly. The extreme respiratory failure conditions along with sepsis and septic shock therefore should be considered as a crucial symptom in this infection (Cascella *et al.*, 2020).

Affected individuals with less complicated (mild to moderate) symptoms usually have signs that include mild to moderate fever, dry cough, sore throat, respiratory irritation, fatigue, stomach aches and malaise, whereas reported dyspnea or laboured breathing in patients were quite common (WHO. Novel coronavirus (2019-ncov)). Moderate pneumonia along with some other sings of respiratory distress associated with cough and shortness of breath (or children's tachypnoea, etc.) were reported for patients with some case (Din and Boppana, 2020 and Drexler *et al.*, 2010). Extreme pneumonia fever, caused by heavy illnesses associated with respiratory depression or hypoxia (SpO<sub>2</sub> <90% in the room) were found to be some striking manifestations of this infection in many cases. Fever is consistent with extreme pneumonia (Al Johani and Hajeer, 2016). Nevertheless, the degree of fever is reportedly mild or sometimes missing in many cases, even in extreme cases of the disease. Cyanosis can occur among children due to insufficient oxygen in the blood. This situation indicates some severe new respiratory problems and an overall deterioration of respiratory feature that has already been established. The intensity of hypoxia in various types of acute respiratory distress syndrome (ARDS) is found to be distinct and varied among patients (WHO. Novel coronavirus (2019-ncov)).

Besides, sepsis is a life-threatening organ dysfunction due to dysregulated host responses to suspected or proven organ dysfunctions (Liu *et al.*, 2020) is another major risk factor for this disease. The clinical descriptions of patients with SARS-CoV-2 and sepsis are particularly severe, with a wide variety of signs, symptoms like cardiac disorders, extreme dyspnoea and hypoxemia, abnormal vomiting, acidosis, altered mental state and functional organ changes and many more with the possible association of signs of multi-organ shock presented as hyperbilirubinemia laboratory results (WHO. Novel coronavirus (2019-ncov)

The symptoms of COVID-19 infection start to be expressed physically after an incubation period of 5-6 days (Imai *et al.*, 2020). That may vary from 6 to 41 days with a median of 14<sup>th</sup> day (Wang *et al.*, 2020; Wang *et al.*, 2020; Wan *et al.*, 2020 and WHO. Novel coronavirus, 2019-ncov). This length of the incubation period may vary from one to another depending on the patient's immune system and age and other biological as well as environmental factors. The length of this incubation period is shorter among patients with more than 70 years of age relative to those who belong to the age below 70 years (Drexler *et al.*, 2010). The most common symptoms at the onset of infection are found to be fatigue in association with cough and fever while the other important symptoms include lymphopenia, haemoptysis, headache, sputum production and mild to severe diarrhoea (Din and Boppana, 2020). The clinical features like acute cardiac injury, acute respiratory distress syndrome with moderate to severe Pneumonia can potentially lead to death. In certain cases, several peripheral ground-glass opacities (GGO) can be identified through CT scan in subpleural regions of both lungs which likely induce both localized and systemic immune response leading to increased inflammation (Liu *et al.*, 2020).

### **Epidemiology :**

The centre or the core of this pandemic is believed to be the city of Wuhan, China, as the first four cases of an acute respiratory syndrome of unknown etiology were detected among people with a contact link to a local seafood market ("wet market") in Wuhan City China on 29 December 2019 (Liu *et al.*, 2020). It has been noticed that early detected cases had some kind of history of interaction with the seafood market (Chen *et al.*, 2020). In the next phase transmission from human to human through close contact was found as a secondary cause

of COVID-19 infection. There has been a sharp increase in the frequency of infected individuals with no history of wildlife exposure or visiting Wuhan and several cases of infection have been identified among medical professionals as well (Hoffmann *et al.*, 2020). Eventually, it has become apparent that COVID-19 infection spreads with exposure to the virus and both normal and immunosuppressed individuals are susceptible to this infection. Majority of the affected populations belonged to the age group of 35 -55 years with fewer cases found among children and infants (Chen *et al.*, 2020 and Ziebuhr *et al.*, 2000). In a recent study on the dynamics of early transmission of the virus, it has been reported that the median age of patients was 59 years ranging from 15 - 89 years with the majority being males (59%)(Imai *et al.*, 2020). Individuals with low immune function system mostly from old age group and those with renal and hepatic dysfunction were considered to have a high risk of fatality (Imai *et al.*, 2020).

Regarding the probable zoonotic origin of COVID19, it is anticipated that the spread of this disease is based on a large number of infected people who had exposure to the wet animal market in Wuhan City where live animals are sold and purchased. Researches and investigations were done to look for a host reservoir or intermediate carriers from which the infection could spread to the human population. Eventually, two snake species were identified which were believed to be the possible COVID-19 reservoirs although, there is still a lack of proper evidence. The genomic sequence analysis of COVID - 19 showed its 88 % identity with two bat-derived severe acute respiratory syndromes (SARS)-like coronaviruses suggesting that bats are the most likely link between COVID-19 and humans (Kim *et al.*, 2016).

Several studies have told that transmission from person to person is a possible way for COVID-19 infection to spread because it was noticed that this COVID-19 infection affected many individuals who did not even visit Wuhan's wet animal market (Rebecca Irons, 2020; Liu *et al.*, 2020 and Shirato *et al.*, 2014) later the same situation was evident worldwide among many populations. Now it is apparent that transmission of this infection from person to person took place mainly through direct contact or by droplets released by an infected person through coughing or sneezing. The lung epithelial cells are the primary target of the virus. It has been stated that human-to-human transmissions of SARS-CoV occur through binding between cellular receptor known as the

angiotensin-converting enzyme 2 (ACE2) receptor and receptor-binding domain of virus spikes (Kim *et al.*, 2016). It is important to mention here that the receptor-binding domain sequence of COVID-19 is similar to that of SARS-CoV. From these findings, it is apparent that the most likely entry into the host cells is through the ACE2 receptor (Shirato *et al.*, 2014).

### **Future perspectives and the Bio-Social domain:**

This crisis of the Covid-19 pandemic is unquestionably a biosocial phenomenon. It demands multi-dimensional intervention that can take account and more productively align biological and social understandings of the pandemic to understand and explain multiple aspects of human life and their complex interactions with this pandemic situation. In this frame, a holistic Anthropological approach has much to contribute to the growing quest for understandings of coronavirus and its socio-ecological effects on human health and wellbeing, as well its social, economic, and cultural impacts.

The basic components of the biosocial framework here are simple but it has a profound depth as space, ecology, society, culture and the human body are procreative of one and another. Human health and wellbeing can then be seen as interwoven biological and social constructs that exist at the nexus of such a relationship. Space and the network of human relationship here takes a major role in the rapid spread of the disease. Pandemics like COVID 19 is a broad historical issue and offers both a warning on the past failures of this relationship and a scope to think through future structures of the city as well as the framework of this interaction between space and human relationship. It is very much relevant to notice that, the current pandemic affords the chance to question the comfort of the dense urban network as a construct that improves well-being in terms efficiency of a well accessed urban life and throws challenges to the well-being of urban life by creating potential conditions for the spread of illness. It challenges the economic structure of the nation as well as the class hierarchy concept and allows rethinking about the nature of the urban 'commute'. "The 'commute', the metaphorical bloodstream of the city, brings life and labour into the centre, promoting economy and even creativity (Einstein claimed to be inspired by commuter trains in thinking through theories of time-dilation and relativity). However, the commute reflects urban sprawl, informing the conditions that lead to chronic illnesses. If a biosocial

"Anthropology of the Body" can ask how cities and bodies shape each other, the challenges of a pandemic give us the ethnographic moment to explore this aspect of health in ways we might not witness otherwise" (Rebecca Irons, 2020).

Combating the current outbreak demands prompt and rigorous actions to control the transmission of COVID-19 infection from person to person. Special attention and interventions are needed to be applied to protecting or reducing transmission in vulnerable groups and health care providers. For medical personnel, health care professionals, public health individuals and researchers involved in the 2019-nCoV guidelines to follow are published (Wang *et al.*, 2020). The cases of early deaths in COVID-19 outbreak occurred mainly among the elderly possibly due to a disrupted immune system that allows the rapid progression of viral respiratory infection (Imai *et al.*, 2020). Therefore, the decontaminating regents should be provided by public services and facilities regularly. The physical contact with contaminated things particularly urine, blood and sputum samples should be handled with proper precautions as these can potentially serve as an alternative route of transmission (WHO. Novel coronavirus (2019-ncov). Most of the countries around the world particularly US, China, India, UAE etc. have implemented major control and prevention measures like implementing state-wise or country wise lockdown and travel screenings to control virus spread. The epidemiological changes occurring in COVID-19 infection should be monitored keenly taking into account potential transmission routes and subclinical infections, as well as the adaptative response, evolutionary changes of possible intermediate animals and reservoir and spread of the virus among humans. A large number of factors remain to be noticed in this regard.

While the full epidemiological data about the affected cases by the new coronavirus is still incomplete it has become clear that some groups are more at risk than others. Age is one of the major risk factors that has delineated a vulnerable population. But several demographic dimensions of the global picture are now emerging from the Covid-19 epidemic concerning sex/gender differences and also indicating the population-specific affinity of this disease. This demographic overview can disclose the complex interaction between the spread of the infection and the major sociocultural components which vary from community to community. These still partially understood demographics of the

pandemic reflect particular forms of biosocial difference in which the interdependence and reciprocity between the biological and social are complexly entangled and where social inequalities also potential enough to shape several embodied biological risk factors, morbidity and mortality.

Coronavirus is not that new to human society. COVID-19 is caused by the novel coronavirus but coronaviruses have been among us for years. This is a large family of viruses along with its different strains (genetic variants) choose different species as their hosts. It was after the SARS outbreak that researchers have noticed that coronaviruses originate among some species of bats. Subsequently, scientists have reported diverse SARS-like coronaviruses found in bats in China and other countries. It was clear from many studies that several coronaviruses have not the ability to infect humans. Then, what was the cause of the spill over? Viruses can only replicate inside living organisms. Hence, the more living organisms it can infect the better it can replicate and pass on its genes. Places which consume different kinds of animals in great quantities, therefore, act as perfect hotspots for viruses to replicate and potentially evolve further to go strong and to infect more than one species.

It has been noticed that organisms like novel coronavirus have different generation times and those with a shorter generation time evolve faster. That is the reason why we are in an arms race with many pathogens, such as the ones that cause malaria or AIDS because they evolve to become more resistant to the drugs, we apply to control them. Therefore, multidirectional approaches of evolution biology, epidemiology, health and disease are of vital importance in tracking the past and the future of the pathogens. By careful understanding of phylogenetic trees, the origin, growth, evolution and adaptation, the growth of this disease could be traced and analysed. From the viewpoint of adaptation and adaptability, it is advantageous for a virus to stay away from killing its host since it needs living organisms to multiply in number and spread. But when there are enough hosts available around or the situation when there is not the adequate practice of physical distancing (like soldiers staying so closely together in the trenches during the World War 1, which triggered the 1918 influenza pandemic), the virus may evolve to be more virulent (the degree of potentiality to damage the host organism) as it can spread easily, even if its current host does not stay alive for long. For that reason, the chances of the novel

coronavirus mutating to a strain with higher or lower virulence, depending on the fact that how easily it can spread among hosts. So, it is clear that as long as it is being transmitted easily among its new host- humans, the chance of the virus to disappear is minimum.

By the progress of the efforts on breaking contacts between the affected and normal, it is very much important to acknowledge the role played by the hidden journeys of animal-human interactions. Very recently an article published by the Royal Society suggested that zoonotic disease (those capable of animal-human movement) will progressively grow to be an increasing threat to human life due to the ever-closer interactions of environments and ecologies with new hosts (Ferretti *et al.*, 2020). The complex nature of the interaction between human and animal health has dragged the attention of recent cross-disciplinary interest to come together under the banner of a holistic approach that explicitly recognises the multiple disciplines required to address such complicated health issues. Amongst other benefits, the One Health approach provides an intellectual space and pragmatic structure to respond to rapid and emerging threats such as C-19 (Wu *et al.*, 2020). Biosocial researchers have a key role to play in this approach by providing necessary insights into how social and biological frameworks can drive human biocultural landscapes with this kind of emerging diseases. To combat a health crisis like COVID 19 and any other Pandemic, a holistic Anthropological approach needs to play a central role in reshaping our perceptions about the relationships between species and ecologies across the globe.

## REFERENCES

- Ahn, D.G., Shin, H.J., Kim, M.H. *et al.* (2020). Current Status of Epidemiology, Diagnosis, Therapeutics, and Vaccines for Novel Coronavirus Disease 2019 (COVID-19). *J. Microbiol. Biotechnol.*, **30**(3) : 313–324 [PubMed] [Google Scholar]
- Al Johani, S. and Hajeer, A.H. (2016). MERS-CoV diagnosis: an update. *J. Infect. Public Health*, **9**(3) : 216–219 (2016). [PMC free article] [PubMed] [Google Scholar]
- Cascella, M., Rajnik, M., Cuomo, A., Dulebohn, S.C. and Di Napoli, R. (2020). Features, evaluation and treatment coronavirus (COVID-19). StatPearls, Treasure Island (FL) (2020). [Google Scholar]
- Chen, W.H., Strych, U., Hotez, P.J. and Bottazzi, M.E. (2020). The SARS-CoV-2 vaccine pipeline: an overview. *Curr. Trop. Med. Rep.*, 1–4 (2020). [PMC free article] [PubMed]

- [Google Scholar]
- Chen, Z., Zhang, W., Lu, Y. *et al.* (2020). From SARS-CoV to Wuhan 2019-nCoV Outbreak: Similarity of Early Epidemic and Prediction of Future Trends. *Cell-Host-Microbe-D-20-00063*. 10.2139/ssrn.3528722 [CrossRef] [Google Scholar]
- Din, Mau and Boppana, L.K.T. (2020). An update on the 2019-nCoV outbreak. *Am. J. Infect. Control*, (Epub ahead of print). [PMC free article] [PubMed] [Google Scholar]
- Drexler, J.F., Gloza-Rausch, F., Glende, J. *et al.* (2010). Genomic characterization of severe acute respiratory syndrome-related coronavirus in European bats and classification of coronaviruses based on partial RNA-dependent RNA polymerase gene sequences. *J. Virol.*, **84**(21) : 11336–11349 (2010). [PMC free article] [PubMed] [Google Scholar]
- Fan, J., Liu, X., Pan, W., Douglas, M. and Bao, S. (2020). Epidemiology of 2019 Novel Coronavirus Disease-19 in Gansu Province, China, 2020. *Emerg. Infect. Dis.*, **26**(6), (2020). [Google Scholar]
- Ferretti, L., Wymant, C., Kendall, M. *et al.* (2020). Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing. *Science*. [PMC free article] [PubMed] [Google Scholar]
- Hoffmann, M., Kleine-Weber, H., Schroeder, S. *et al.* (2020). SARS-CoV-2 cell entry depends on ACE2 and TMPRSS2 and is blocked by a clinically proven protease inhibitor. *Cell*, **181**(2) : 271–280.e8. [PMC free article] [PubMed] [Google Scholar]
- Imai, N., Dorigatti, I., Cori, A., Donnelly, C., Riley, S. and Ferguson, N.M. (2020). Report 2: Estimating the potential total number of novel Coronavirus cases in Wuhan City, China. Imperial College London; [Google Scholar].
- Kim, M.N., Ko, Y.J., Seong, M.W., Kim, J.S., Shin, B.M. and Sung, H. (2016). Analytical and clinical validation of six commercial Middle East Respiratory Syndrome coronavirus RNA detection kits based on real-time reverse-transcription PCR. *Ann. Lab. Med.*, **36**(5) : 450–456. [PMC free article] [PubMed] [Google Scholar]
- Liu, C., Zhou, Q., Li, Y. *et al.* (2020). Research and Development on Therapeutic Agents and Vaccines for COVID-19 and Related Human Coronavirus Diseases. *ACS Central Science*, **6**(3), 315–331. [PMC free article] [PubMed] [Google Scholar]
- Liu, F., Xu, A., Zhang, Y. *et al.* (2020). Patients of COVID-19 may benefit from sustained lopinavir-combined regimen and the increase of eosinophil may predict the outcome of COVID-19 progression. *Int. J. Infect. Dis.* [PMC free article] [PubMed] [Google Scholar]
- Peng, Z., Xing-Lou, Y. and Xian-Guang, W. (2020). A pneumonia outbreak associated with a new coronavirus of probable bat origin. [J/OL]. *Nature*, **579** : 270–273 (2020). [PMC free article] [PubMed] [Google Scholar]
- Rebecca Irons (2020). Biosocial Medical Anthropology in the time of Covid -19. New challenges and opportunities. Medical Anthropology at UCL. <http://medanthucl.com>
- Shirato, K., Yano, T., Senba, S. *et al.* (2014). Detection of Middle East respiratory syndrome coronavirus using reverse transcription loop-mediated isothermal amplification (RT-LAMP). *Virol. J.*, **11**(1) : 139. [PMC free article] [PubMed] [Google Scholar]
- Wang, C., Pan, R., Wan, X., Tan, Y., Xu, L., Ho, C.S. *et al.* (2020). Immediate psychological responses and associated factors during the initial stage of the 2019 coronavirus disease (COVID-19) epidemic among the general population in China. *Int J Environ Res Public Health*, **17**(5):1729.
- Wang, D., Hu, B., Hu, C. *et al.* (2020). Clinical characteristics of 138 hospitalized patients with 2019 novel coronavirus – infected pneumonia in Wuhan, China. *JAMA*, **323**(11) : 1061–1069. [PMC free article] [PubMed] [Google Scholar]
- Wan, Y., Shang, J., Graham, R., Baric, R.S. and Li, F. (2020). Receptor recognition by the novel coronavirus from Wuhan: an analysis based on decade-long structural studies of SARS coronavirus. *J. Virol.*, **94**(7). [PMC free article] [PubMed] [Google Scholar]• Fundamental research on viral structure and genome arrangement and important aspect in developing suitable therapeutics.
- WHO. Novel coronavirus (2019-ncov) technical guidance: laboratory testing for 2019-ncov in humans (2020). [www.who.int/emergencies/diseases/novel-coronavirus-2019/technical-guidance/laboratory-guidance](http://www.who.int/emergencies/diseases/novel-coronavirus-2019/technical-guidance/laboratory-guidance)
- Woo, P.C., Huang, Y., Lau, S.K. and Yuen, K.Y. (2010). Coronavirus genomics and bioinformatics analysis. *Viruses*, **2**(8) : 1804–1820. [PMC free article] [PubMed] [Google Scholar]
- Wrapp, D., Wang, N., Corbett, K.S. *et al.* (2020). Cryo-EM structure of the 2019-nCoV spike in the prefusion conformation. *Science*, **367**(6483) : 1260–1263. [PMC free article] [PubMed] [Google Scholar]
- Wu, F., Zhao, S. and Yu, B. (2020). A new coronavirus associated with human respiratory disease in China. *Nature*, **579**(7798) : 265–269. [PMC free article] [PubMed] [Google Scholar]
- Ziebuhr, J., Snijder, E.J. and Gorbalenya, A.E. (2000). Virus-encoded proteinases and proteolytic processing in the Nidovirales. *J. Gen. Virol.*, **81**(4) : 853–879. [PubMed] [Google Scholar]

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