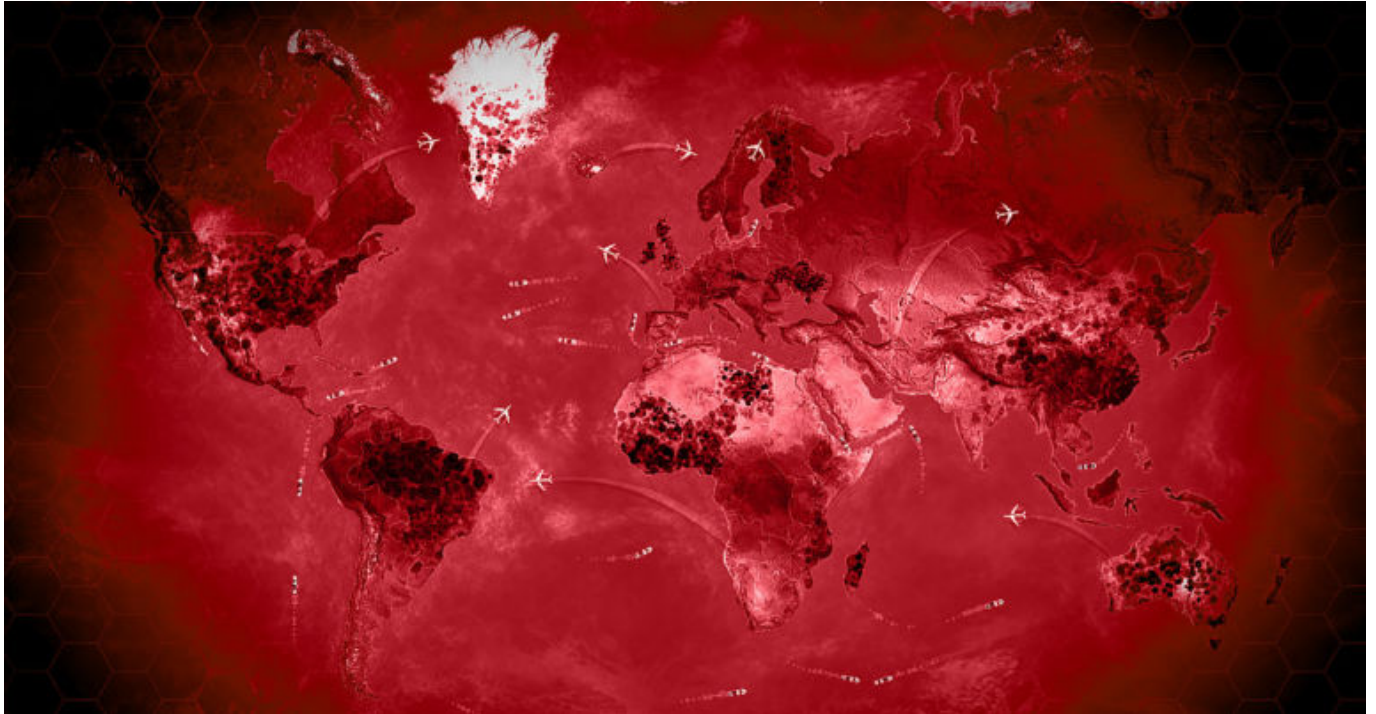


**Web Scrapping science papers from site:
PubMed on the topic - "Coronavirus 2019-nCoV".**



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[Diagnosis and clinical management of 2019 novel coronavirus infection: an operational recommendation of Peking Union Medical College Hospital (V2.0)].

<https://www.ncbi.nlm.nih.gov/pubmed/32023681>

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Pathogenicity and Transmissibility of 2019-nCoV-A Quick Overview and Comparison with Other Emerging Viruses.

<https://www.ncbi.nlm.nih.gov/pubmed/32032682>

A zoonotic coronavirus, labeled as 2019-nCoV by The World Health Organization (WHO), has been identified as the causative agent of the viral pneumonia outbreak in Wuhan, China, at the end of 2019. Although 2019-nCoV can cause a severe respiratory illness like SARS and MERS, evidence from clinics suggested that 2019-nCoV is generally less pathogenic than SARS-CoV, and much less

than MERS-CoV. The transmissibility of 2019-nCoV is still debated and needs to be further assessed. To avoid the 2019-nCoV outbreak turning into an epidemic or even a pandemic and to minimize the mortality rate, China activated emergency response procedures, but much remains to be learned about the features of the virus to refine the risk assessment and response. Here, the current knowledge in 2019-nCoV pathogenicity and transmissibility is summarized in comparison with several commonly known emerging viruses, and information urgently needed for a better control of the disease is highlighted.

Return of the Coronavirus: 2019-nCoV.

<https://www.ncbi.nlm.nih.gov/pubmed/31991541>

The emergence of a novel coronavirus (2019-nCoV) has awakened the echoes of SARS-CoV from nearly two decades ago. Yet, with technological advances and important lessons gained from previous outbreaks, perhaps the world is better equipped to deal with the most recent emergent group 2B coronavirus.

[2019-nCoV: new challenges from coronavirus].

<https://www.ncbi.nlm.nih.gov/pubmed/32023682>

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Recent advances in the detection of respiratory virus infection in humans.

<https://www.ncbi.nlm.nih.gov/pubmed/31944312>

Respiratory tract viral infection caused by viruses or bacteria is one of the most common diseases in human worldwide, while those caused by emerging viruses, such as the novel coronavirus, 2019-nCoV that caused the pneumonia outbreak in Wuhan, China most recently, have posed great threats to global public health. Identification of the causative viral pathogens of respiratory tract viral infections is important to select an appropriate treatment, save people's lives, stop the epidemics, and avoid unnecessary use of antibiotics. Conventional diagnostic tests, such as the assays for rapid detection of antiviral antibodies or viral antigens, are widely used in many clinical laboratories. With the development of modern technologies, new diagnostic strategies, including multiplex nucleic acid amplification and microarray-based assays, are emerging. This review summarizes currently available and novel emerging diagnostic methods for the detection of common respiratory viruses, such as influenza virus, human respiratory syncytial virus, coronavirus, human adenovirus, and human rhinovirus. Multiplex assays for simultaneous detection of multiple respiratory viruses are also described. It is anticipated that such data will assist researchers and clinicians to develop appropriate diagnostic strategies for timely and effective detection of respiratory virus infections.

Full-genome evolutionary analysis of the novel corona virus (2019-nCoV) rejects the hypothesis of emergence as a result of a recent recombination event.

<https://www.ncbi.nlm.nih.gov/pubmed/32004758>

A novel coronavirus (2019-nCoV) associated with human to human transmission and severe human infection has been recently reported from the city of Wuhan in China. Our objectives were to characterize the genetic relationships of the 2019-nCoV and to search for putative recombination within the subgenus of sarbecovirus.

Molecular Diagnosis of a Novel Coronavirus (2019-nCoV) Causing an Outbreak of Pneumonia.

<https://www.ncbi.nlm.nih.gov/pubmed/32031583>

A novel coronavirus of zoonotic origin (2019-nCoV) has recently been identified in patients with acute respiratory disease. This virus is genetically similar to SARS coronavirus and bat SARS-like coronaviruses. The outbreak was initially detected in Wuhan, a major city of China, but has subsequently been detected in other provinces of China. Travel-associated cases have also been reported in a few other countries. Outbreaks in health care workers indicate human-to-human

transmission. Molecular tests for rapid detection of this virus are urgently needed for early identification of infected patients.

The First Case of 2019 Novel Coronavirus Pneumonia Imported into Korea from Wuhan, China: Implication for Infection Prevention and Control Measures.

<https://www.ncbi.nlm.nih.gov/pubmed/32030925>

In December 2019, a viral pneumonia outbreak caused by a novel betacoronavirus, the 2019 novel coronavirus (2019-nCoV), began in Wuhan, China. We report the epidemiological and clinical features of the first patient with 2019-nCoV pneumonia imported into Korea from Wuhan. This report suggests that in the early phase of 2019-nCoV pneumonia, chest radiography would miss patients with pneumonia and highlights taking travel history is of paramount importance for early detection and isolation of 2019-nCoV cases.

[Suggestions for prevention of 2019 novel coronavirus infection in otolaryngology head and neck surgery medical staff].

<https://www.ncbi.nlm.nih.gov/pubmed/32023680>

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The Novel Coronavirus: A Bird's Eye View.

<https://www.ncbi.nlm.nih.gov/pubmed/32020915>

The novel coronavirus (2019-nCoV) outbreak, which initially began in China, has spread to many countries around the globe, with the number of confirmed cases increasing every day. With a death toll exceeding that of the SARS-CoV outbreak back in 2002 and 2003 in China, 2019-nCoV has led to a public health emergency of international concern, putting all health organizations on high alert.

Herein, we present on an overview of the currently available information on the pathogenesis, epidemiology, clinical presentation, diagnosis, and treatment of this virus.

Genomic variance of the 2019-nCoV coronavirus.

<https://www.ncbi.nlm.nih.gov/pubmed/32027036>

There is rising global concern for the recently emerged novel Coronavirus (2019-nCoV). Full genomic sequences have been released by the worldwide scientific community in the last few weeks in order to understand the evolutionary origin and molecular characteristics of this virus. Taking advantage of all the genomic information currently available, we constructed a phylogenetic tree including also representatives of other coronaviridae, such as Bat coronavirus (BCoV) and SARS. We confirm high sequence similarity (>99%) between all sequenced 2019-nCoVs genomes available, with the closest BCoV sequence sharing 96.2% sequence identity, confirming the notion of a zoonotic origin of 2019-nCoV. Despite the low heterogeneity of the 2019-nCoV genomes, we could identify at least two hyper-variable genomic hotspots, one of which is responsible for a Serine/Leucine variation in the viral ORF8-encoded protein. Finally, we perform a full proteomic comparison with other coronaviridae, identifying key aminoacidic differences to be considered for antiviral strategies deriving from previous anti-coronavirus approaches. This article is protected by copyright. All rights reserved.

RNA based mNGS approach identifies a novel human coronavirus from two individual pneumonia cases in 2019 Wuhan outbreak.

<https://www.ncbi.nlm.nih.gov/pubmed/32020836>

From December 2019, an outbreak of unusual pneumonia was reported in Wuhan with many cases linked to Huanan Seafood Market that sells seafood as well as live exotic animals. We investigated two patients who developed acute respiratory syndromes after independent contact history with this market. The two patients shared common clinical features including fever, cough, and multiple ground-glass opacities in the bilateral lung field with patchy infiltration. Here, we highlight the use of a low-input metagenomic next-generation sequencing (mNGS) approach on RNA extracted from bronchoalveolar lavage fluid (BALF). It rapidly identified a novel coronavirus (named 2019-nCoV according to World Health Organization announcement) which was the sole pathogens in the sample with very high abundance level (1.5% and 0.62% of total RNA sequenced). The entire viral genome is 29,881â€¦nt in length (GenBank MN988668 and MN988669, Sequence Read Archive

database Bioproject accession PRJNA601736) and is classified into β -coronavirus genus. Phylogenetic analysis indicates that 2019-nCoV is close to coronaviruses (CoVs) circulating in Rhinolophus (Horseshoe bats), such as 98.7% nucleotide identity to partial RdRp gene of bat coronavirus strain BtCoV/4991 (GenBank KP876546, 370â€¦nt sequence of RdRp and lack of other genome sequence) and 87.9% nucleotide identity to bat coronavirus strain bat-SL-CoVZC45 and bat-SL-CoVZXC21. Evolutionary analysis based on ORF1a/1b, S, and N genes also suggests 2019-nCoV is more likely a novel CoV independently introduced from animals to humans.

Estimating the Unreported Number of Novel Coronavirus (2019-nCoV) Cases in China in the First Half of January 2020: A Data-Driven Modelling Analysis of the Early Outbreak.

<https://www.ncbi.nlm.nih.gov/pubmed/32024089>

In December 2019, an outbreak of respiratory illness caused by a novel coronavirus (2019-nCoV) emerged in Wuhan, China and has swiftly spread to other parts of China and a number of foreign countries. The 2019-nCoV cases might have been under-reported roughly from 1 to 15 January 2020, and thus we estimated the number of unreported cases and the basic reproduction number, R_0 , of 2019-nCoV.

CT Imaging Features of 2019 Novel Coronavirus (2019-nCoV).

<https://www.ncbi.nlm.nih.gov/pubmed/32017661>

In this retrospective case series, chest CT scans of 21 symptomatic patients from China infected with the 2019 Novel Coronavirus (2019-nCoV) were reviewed with emphasis on identifying and characterizing the most common findings. Typical CT findings included bilateral pulmonary parenchymal ground-glass and consolidative pulmonary opacities, sometimes with a rounded morphology and a peripheral lung distribution. Notably, lung cavitation, discrete pulmonary nodules, pleural effusions, and lymphadenopathy were absent. Follow-up imaging in a subset of patients during the study time window often demonstrated mild or moderate progression of disease as manifested by increasing extent and density of lung opacities.

Epidemiological and clinical characteristics of 99 cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study.

<https://www.ncbi.nlm.nih.gov/pubmed/32007143>

In December, 2019, a pneumonia associated with the 2019 novel coronavirus (2019-nCoV) emerged in Wuhan, China. We aimed to further clarify the epidemiological and clinical characteristics of 2019-nCoV pneumonia.

Emerging Coronavirus 2019-nCoV Pneumonia.

<https://www.ncbi.nlm.nih.gov/pubmed/32027573>

Background The chest CT findings of patients with coronavirus 2019-nCoV pneumonia have not previously been described in detail. **Purpose** To investigate the clinical, laboratory, and imaging findings of emerging coronavirus 2019-nCoV pneumonia in humans. **Materials and Methods** Fifty-one patients (25 men and 26 women, 16-76 years old) with 2019-nCoV pneumonia confirmed with the positive new coronavirus nucleic acid antibody underwent thin-section CT. The imaging findings, clinical and laboratory data were evaluated. **Results** Fifty of 51 patients (98%) had a history of the endemic center Wuhan contact. Fever (49/51, 96%) and cough (24/51, 47%) were the most common symptoms. Most patients had a normal white blood cell count (37/51, 73%), neutrophil count (44/51, 86.3%) and normal (17/51, 35.3%) or reduced (33/51, 64.7%) lymphocyte count. CT images showed pure ground glass opacity (GGO) in 39/51 (77%) patients, GGO with reticular and/or interlobular septal thickening in 38/51 (75%) patients. GGO with consolidation was present in 30/51 (59%) and pure consolidation in 28/51 (55%) patients. 44/51 (86%) patients had bilateral lung involvement, while 41/51 (80%) involved the posterior part of the lungs and 44/51 (86%) were peripheral. There were more consolidated lung lesions in patients 5 or more days from disease onset to CT scan versus 4 or fewer days (431/712 lesions vs. 129/612 lesions, $p < 0.001$). Patients more than 50 years old had more consolidated lung lesions than those 50 years or younger (212/470 vs. 198/854, $p < 0.001$). Follow up CT in 13 patients showed improvement in 7 (54%) patients and progression in 4 (31%) patients. **Conclusions** Patients with fever and/or cough and with conspicuous ground glass opacity lesions in the peripheral and posterior lungs on CT images combined with normal or decreased white blood cells and a history of epidemic exposure are highly suspected of 2019-nCoV pneumonia.

Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding.

<https://www.ncbi.nlm.nih.gov/pubmed/32007145>

In late December, 2019, patients presenting with viral pneumonia due to an unidentified microbial

agent were reported in Wuhan, China. A novel coronavirus was subsequently identified as the causative pathogen, provisionally named 2019 novel coronavirus (2019-nCoV). As of Jan 26, 2020, more than 2000 cases of 2019-nCoV infection have been confirmed, most of which involved people living in or visiting Wuhan, and human-to-human transmission has been confirmed.

Pattern of early human-to-human transmission of Wuhan 2019 novel coronavirus (2019-nCoV), December 2019 to January 2020.

<https://www.ncbi.nlm.nih.gov/pubmed/32019669>

Since December 2019, China has been experiencing a large outbreak of a novel coronavirus (2019-nCoV) which can cause respiratory disease and severe pneumonia. We estimated the basic reproduction number R_0 of 2019-nCoV to be around 2.2 (90% high density interval: 1.4-3.8), indicating the potential for sustained human-to-human transmission. Transmission characteristics appear to be of similar magnitude to severe acute respiratory syndrome-related coronavirus (SARS-CoV) and pandemic influenza, indicating a risk of global spread.

A pneumonia outbreak associated with a new coronavirus of probable bat origin.

<https://www.ncbi.nlm.nih.gov/pubmed/32015507>

Since the SARS outbreak 18 years ago, a large number of severe acute respiratory syndrome-related coronaviruses (SARSr-CoV) have been discovered in their natural reservoir host, bats¹⁻⁴. Previous studies indicated that some of those bat SARSr-CoVs have the potential to infect humans⁵⁻⁷. Here we report the identification and characterization of a novel coronavirus (2019-nCoV) which caused an epidemic of acute respiratory syndrome in humans in Wuhan, China. The epidemic, which started from 12 December 2019, has caused 2,050 laboratory-confirmed infections with 56 fatal cases by 26 January 2020. Full-length genome sequences were obtained from five patients at the early stage of the outbreak. They are almost identical to each other and share 79.5% sequence identity to SARS-CoV. Furthermore, it was found that 2019-nCoV is 96% identical at the whole-genome level to a bat coronavirus. The pairwise protein sequence analysis of seven conserved non-structural proteins show that this virus belongs to the species of SARSr-CoV. The 2019-nCoV virus was then isolated from the bronchoalveolar lavage fluid of a critically ill patient, which can be neutralized by sera from several patients. Importantly, we have confirmed that this novel CoV uses the same cell entry receptor, ACE2, as SARS-CoV.

Epidemiological characteristics of 2019 novel coronavirus: an interim review.

<https://www.ncbi.nlm.nih.gov/pubmed/32023775>

The 2019-nCoV from Wuhan, China is now recognized as a public health emergency of global concern.

Receptor recognition by novel coronavirus from Wuhan: An analysis based on decade-long structural studies of SARS.

<https://www.ncbi.nlm.nih.gov/pubmed/31996437>

Recently a novel coronavirus (2019-nCoV) has emerged from Wuhan, China, causing symptoms in humans similar to those caused by SARS coronavirus (SARS-CoV). Since SARS-CoV outbreak in 2002, extensive structural analyses have revealed key atomic-level interactions between SARS-CoV spike protein receptor-binding domain (RBD) and its host receptor angiotensin-converting enzyme 2 (ACE2), which regulate both the cross-species and human-to-human transmissions of SARS-CoV. Here we analyzed the potential receptor usage by 2019-nCoV, based on the rich knowledge about SARS-CoV and the newly released sequence of 2019-nCoV. First, the sequence of 2019-nCoV RBD, including its receptor-binding motif (RBM) that directly contacts ACE2, is similar to that of SARS-CoV, strongly suggesting that 2019-nCoV uses ACE2 as its receptor. Second, several critical residues in 2019-nCoV RBM (particularly Gln493) provide favorable interactions with human ACE2, consistent with 2019-nCoV's capacity for human cell infection. Third, several other critical residues in 2019-nCoV RBM (particularly Asn501) are compatible with, but not ideal for, binding human ACE2, suggesting that 2019-nCoV has acquired some capacity for human-to-human transmission. Last, while phylogenetic analysis indicates a bat origin of 2019-nCoV, 2019-nCoV also potentially recognizes ACE2 from a diversity of animal species (except mice and rats), implicating these animal species as possible intermediate hosts or animal models for 2019-nCoV infections. These analyses provide insights into the receptor usage, cell entry, host cell infectivity and animal origin of 2019-nCoV, and may help epidemic surveillance and preventive measures against 2019-nCoV.

Significance The recent emergence of Wuhan coronavirus (2019-nCoV) puts the world on alert. 2019-nCoV is reminiscent of the SARS-CoV outbreak in 2002-2003. Our decade-long structural studies on the receptor recognition by SARS-CoV have identified key interactions between SARS-CoV spike protein and its host receptor angiotensin-converting enzyme 2 (ACE2), which regulate both the cross-species and human-to-human transmissions of SARS-CoV. One of the goals of SARS-CoV research was to build an atomic-level iterative framework of virus-receptor

interactions to facilitate epidemic surveillance, predict species-specific receptor usage, and identify potential animal hosts and animal models of viruses. Based on the sequence of 2019-nCoV spike protein, we apply this predictive framework to provide novel insights into the receptor usage and likely host range of 2019-nCoV. This study provides a robust test of this reiterative framework, providing the basic, translational and public health research communities with predictive insights that may help study and battle this novel 2019-nCoV.

A Novel Coronavirus from Patients with Pneumonia in China, 2019.

<https://www.ncbi.nlm.nih.gov/pubmed/31978945>

In December 2019, a cluster of patients with pneumonia of unknown cause was linked to a seafood wholesale market in Wuhan, China. A previously unknown betacoronavirus was discovered through the use of unbiased sequencing in samples from patients with pneumonia. Human airway epithelial cells were used to isolate a novel coronavirus, named 2019-nCoV, which formed another clade within the subgenus sarbecovirus, Orthocoronavirinae subfamily. Different from both MERS-CoV and SARS-CoV, 2019-nCoV is the seventh member of the family of coronaviruses that infect humans. Enhanced surveillance and further investigation are ongoing. (Funded by the National Key Research and Development Program of China and the National Major Project for Control and Prevention of Infectious Disease in China.).

Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study.

<https://www.ncbi.nlm.nih.gov/pubmed/32014114>

Since Dec 31, 2019, the Chinese city of Wuhan has reported an outbreak of atypical pneumonia caused by the 2019 novel coronavirus (2019-nCoV). Cases have been exported to other Chinese cities, as well as internationally, threatening to trigger a global outbreak. Here, we provide an estimate of the size of the epidemic in Wuhan on the basis of the number of cases exported from Wuhan to cities outside mainland China and forecast the extent of the domestic and global public health risks of epidemics, accounting for social and non-pharmaceutical prevention interventions.

2019-nCoV acute respiratory disease, Australia: Epidemiology Report 1 (Reporting week 26 January - 1 February 2020).

<https://www.ncbi.nlm.nih.gov/pubmed/32027812>

This is the first epidemiological report of novel coronavirus (2019-nCoV) acute respiratory disease infections reported in Australia at 19:00 Australian Eastern Daylight Time [AEDT] 1 February 2020. It includes data on Australian cases notified during the week 26 January to 1 February 2020 and in the previous week (19 to 25 January 2020), the international situation and current information on the severity, transmission and spread of the 2019-nCoV infection.

Immunoinformatics-aided identification of T cell and B cell epitopes in the surface glycoprotein of 2019-nCoV.

<https://www.ncbi.nlm.nih.gov/pubmed/32022276>

The 2019 novel coronavirus (2019-nCoV) outbreak has caused a large number of deaths with thousands of confirmed cases worldwide, especially in East Asia. This study took an immunoinformatics approach to identify significant cytotoxic T lymphocyte (CTL) and B cell epitopes in the 2019-nCoV surface glycoprotein. Also, interactions between identified CTL epitopes and their corresponding MHC class I supertype representatives prevalent in China were studied by molecular dynamics simulations. We identified five CTL epitopes, three sequential B cell epitopes and five discontinuous B cell epitopes in the viral surface glycoprotein. Also, during simulations, the CTL epitopes were observed to be binding MHC class I peptide-binding grooves via multiple contacts, with continuous hydrogen bonds and salt bridge anchors, indicating their potential in generating immune responses. Some of these identified epitopes can be potential candidates for development of 2019-nCoV vaccines. This article is protected by copyright. All rights reserved.

Updates on Wuhan 2019 Novel Coronavirus Epidemic.

<https://www.ncbi.nlm.nih.gov/pubmed/32017153>

What emerged in December 2019 as a cluster of respiratory ailments with inexplicable etiological findings in Wuhan has now claimed roughly 259 lives, sickened nearly 12 thousand more, and spread to at least 26 more nations including Hong Kong, Taiwan and Macao. This article is protected by copyright. All rights reserved.

[Potential antiviral therapeutics for 2019 Novel Coronavirus].

<https://www.ncbi.nlm.nih.gov/pubmed/32023685>

Since December 2019, a total of 41 cases of pneumonia of unknown etiology have been confirmed in Wuhan city, Hubei Province, China. Wuhan city is a major transportation hub with a population of more than 11 million people. Most of the patients visited a local fish and wild animal market last month. At a national press conference held today, Dr. Jianquo Xu, an academician of the Chinese

Academy of Engineering, who led a scientific team announced that a new-type coronavirus, tentatively named by World Health Organization as the 2019-new coronavirus (2019-nCoV), had caused this outbreak (1).

Clinical Characteristics of 138 Hospitalized Patients With 2019 Novel Coronavirus-Infected Pneumonia in Wuhan, China.

<https://www.ncbi.nlm.nih.gov/pubmed/32031570>

In December 2019, novel coronavirus (2019-nCoV)-infected pneumonia (NCIP) occurred in Wuhan, China. The number of cases has increased rapidly but information on the clinical characteristics of affected patients is limited.

Emerging coronaviruses: Genome structure, replication, and pathogenesis.

<https://www.ncbi.nlm.nih.gov/pubmed/31967327>

The recent emergence of a novel coronavirus (2019-nCoV), which is causing an outbreak of unusual viral pneumonia in patients in Wuhan, a central city in China, is another warning of the risk of CoVs posed to public health. In this minireview, we provide a brief introduction of the general features of CoVs and describe diseases caused by different CoVs in humans and animals. This review will help understand the biology and potential risk of CoVs that exist in richness in wildlife such as bats.

[Efficient management of novel coronavirus pneumonia by efficient prevention and control in scientific manner].

<https://www.ncbi.nlm.nih.gov/pubmed/32023684>

2019年12月，中国湖北省武汉市发生新型冠状病毒感染的肺炎病例，引起全球关注。新型冠状病毒（2019-nCoV）是一种新型冠状病毒，其基因组为单链RNA，长约30 kb。该病毒主要通过呼吸道传播，潜伏期通常为2-14天。目前，全球已有数千例确诊病例，且病例数仍在增加。世界卫生组织（WHO）已将此次疫情列为全球公共卫生紧急事件。目前，尚无特效药物，治疗主要以对症支持为主。预防方面，建议佩戴口罩、勤洗手、避免聚集等。未来，应加强病毒监测和疫苗研发，以应对类似疫情的再次发生。

<https://www.ncbi.nlm.nih.gov/pubmed/32007627>

Novel coronavirus (2019-nCoV) early-stage importation risk to Europe, January 2020.

<https://www.ncbi.nlm.nih.gov/pubmed/32019667>

Early Transmission Dynamics in Wuhan, China, of Novel Coronavirus-Infected Pneumonia.

<https://www.ncbi.nlm.nih.gov/pubmed/31995857>

[Pulmonary rehabilitation guidelines in the principle of 4S for patients infected with 2019 novel coronavirus (2019-nCoV)].

<https://www.ncbi.nlm.nih.gov/pubmed/32023687>

The first two cases of 2019-nCoV in Italy: where they come from?

<https://www.ncbi.nlm.nih.gov/pubmed/32022275>

A novel Coronavirus, 2019-nCoV, has been identified as the causal pathogen of an ongoing epidemic, with the first cases reported in Wuhan, China, last December 2019, and has since spread to other countries worldwide, included Europe and very recently Italy. In this short report, phylogenetic reconstruction was used to better understand the transmission dynamic of the virus from its first introduction in China focusing on the more recent evidence of infection in a couple of Chinese tourists arrived in Italy on 23rd January 2020 and labeled as Coronavirus Italian cases. A Maximum Clade Credibility tree has been built using a dataset of 54 genome sequences of 2019-nCoV plus 2 closely related bat strains (SARS-like CoV) available in GeneBank. Bayesian time-scaled phylogenetic analysis was implemented in BEAST 1.10.4. The Bayesian phylogenetic reconstruction showed that the 2019-2020 nCoV firstly introduced in Wuhan on the 25th November 2019, started epidemic transmission reaching many countries worldwide, including Europe and Italy where the two strains isolated dated back 19th January 2020, the same that the Chinese tourists arrived in Italy. Strains isolated outside China were intermixed with strains isolated in China as evidence of likely imported cases in Rome, Italy and Europe, as well. In conclusion, this report suggests that further spread of 2019-nCoV epidemic was supported by human mobility and that quarantine of suspected or diagnosed cases is useful to prevent further transmission. Viral genome phylogenetic analysis represents a useful tool for evaluation of transmission dynamics and preventive action. This article is protected by copyright. All rights reserved.

Drug treatment options for the 2019-new coronavirus (2019-nCoV).

<https://www.ncbi.nlm.nih.gov/pubmed/31996494>

As of January 22, 2020, a total of 571 cases of the 2019-new coronavirus (2019-nCoV) have been reported in 25 provinces (districts and cities) in China. At present, there is no vaccine or antiviral treatment for human and animal coronavirus, so that identifying the drug treatment options as soon as possible is critical for the response to the 2019-nCoV outbreak. Three general methods, which include existing broad-spectrum antiviral drugs using standard assays, screening of a chemical library containing many existing compounds or databases, and the redevelopment of new specific drugs based on the genome and biophysical understanding of individual coronaviruses, are used to discover the potential antiviral treatment of human pathogen coronavirus. Lopinavir /Ritonavir, Nucleoside analogues, Neuraminidase inhibitors, Remdesivir, peptide (EK1), arbidol, RNA synthesis inhibitors (such as TDF, 3TC), anti-inflammatory drugs (such as hormones and other molecules), Chinese traditional medicine, such ShuFengJieDu Capsules and Lianhuaqingwen Capsule, could be

the drug treatment options for 2019-nCoV. However, the efficacy and safety of these drugs for 2019-nCoV still need to be further confirmed by clinical experiments.

Genomic characterization of the 2019 novel human-pathogenic coronavirus isolated from a patient with atypical pneumonia after visiting Wuhan.

<https://www.ncbi.nlm.nih.gov/pubmed/31987001>

A mysterious outbreak of atypical pneumonia in late 2019 was traced to a seafood wholesale market in Wuhan of China. Within a few weeks, a novel coronavirus tentatively named as 2019 novel coronavirus (2019-nCoV) was announced by the World Health Organization. We performed bioinformatics analysis on a virus genome from a patient with 2019-nCoV infection and compared it with other related coronavirus genomes. Overall, the genome of 2019-nCoV has 89% nucleotide identity with bat SARS-like-CoVZXC21 and 82% with that of human SARS-CoV. The phylogenetic trees of their orf1a/b, Spike, Envelope, Membrane and Nucleoprotein also clustered closely with those of the bat, civet and human SARS coronaviruses. However, the external subdomain of Spike's receptor binding domain of 2019-nCoV shares only 40% amino acid identity with other SARS-related coronaviruses. Remarkably, its orf3b encodes a completely novel short protein. Furthermore, its new orf8 likely encodes a secreted protein with an alpha-helix, following with a beta-sheet(s) containing six strands. Learning from the roles of civet in SARS and camel in MERS, hunting for the animal source of 2019-nCoV and its more ancestral virus would be important for understanding the origin and evolution of this novel lineage B betacoronavirus. These findings provide the basis for starting further studies on the pathogenesis, and optimizing the design of diagnostic, antiviral and vaccination strategies for this emerging infection.

Initial Public Health Response and Interim Clinical Guidance for the 2019 Novel Coronavirus Outbreak - United States, December 31, 2019-February 4, 2020.

<https://www.ncbi.nlm.nih.gov/pubmed/32027631>

On December 31, 2019, Chinese health officials reported a cluster of cases of acute respiratory illness in persons associated with the Hunan seafood and animal market in the city of Wuhan, Hubei Province, in central China. On January 7, 2020, Chinese health officials confirmed that a novel coronavirus (2019-nCoV) was associated with this initial cluster (1). As of February 4, 2020, a total of 20,471 confirmed cases, including 2,788 (13.6%) with severe illness,* and 425 deaths (2.1%) had been reported by the National Health Commission of China (2). Cases have also been reported in

26 locations outside of mainland China, including documentation of some person-to-person transmission and one death (2). As of February 4, 11 cases had been reported in the United States. On January 30, the World Health Organization (WHO) Director-General declared that the 2019-nCoV outbreak constitutes a Public Health Emergency of International Concern. On January 31, the U.S. Department of Health and Human Services (HHS) Secretary declared a U.S. public health emergency to respond to 2019-nCoV. Also on January 31, the president of the United States signed a "Proclamation on Suspension of Entry as Immigrants and Nonimmigrants of Persons who Pose a Risk of Transmitting 2019 Novel Coronavirus," which limits entry into the United States of persons who traveled to mainland China to U.S. citizens and lawful permanent residents and their families (3). CDC, multiple other federal agencies, state and local health departments, and other partners are implementing aggressive measures to slow transmission of 2019-nCoV in the United States (4,5). These measures require the identification of cases and their contacts in the United States and the appropriate assessment and care of travelers arriving from mainland China to the United States. These measures are being implemented in anticipation of additional 2019-nCoV cases in the United States. Although these measures might not prevent the eventual establishment of ongoing, widespread transmission of the virus in the United States, they are being implemented to 1) slow the spread of illness; 2) provide time to better prepare health care systems and the general public to be ready if widespread transmission with substantial associated illness occurs; and 3) better characterize 2019-nCoV infection to guide public health recommendations and the development of medical countermeasures including diagnostics, therapeutics, and vaccines. Public health authorities are monitoring the situation closely. As more is learned about this novel virus and this outbreak, CDC will rapidly incorporate new knowledge into guidance for action by CDC and state and local health departments.

Detection of 2019 novel coronavirus (2019-nCoV) by real-time RT-PCR.

<https://www.ncbi.nlm.nih.gov/pubmed/31992387>

BackgroundThe ongoing outbreak of the recently emerged novel coronavirus (2019-nCoV) poses a challenge for public health laboratories as virus isolates are unavailable while there is growing evidence that the outbreak is more widespread than initially thought, and international spread through travellers does already occur.**Aim**We aimed to develop and deploy robust diagnostic methodology for use in public health laboratory settings without having virus material available.**Methods**Here we present a validated diagnostic workflow for 2019-nCoV, its design relying

on close genetic relatedness of 2019-nCoV with SARS coronavirus, making use of synthetic nucleic acid technology. Results The workflow reliably detects 2019-nCoV, and further discriminates 2019-nCoV from SARS-CoV. Through coordination between academic and public laboratories, we confirmed assay exclusivity based on 297 original clinical specimens containing a full spectrum of human respiratory viruses. Control material is made available through European Virus Archive - Global (EVAg), a European Union infrastructure project. Conclusion The present study demonstrates the enormous response capacity achieved through coordination of academic and public laboratories in national and European research networks.

A rapid advice guideline for the diagnosis and treatment of 2019 novel coronavirus (2019-nCoV) infected pneumonia (standard version).

<https://www.ncbi.nlm.nih.gov/pubmed/32029004>

In December 2019, a new type viral pneumonia cases occurred in Wuhan, Hubei Province; and then named "2019 novel coronavirus (2019-nCoV)" by the World Health Organization (WHO) on 12 January 2020. For it is a never been experienced respiratory disease before and with infection ability widely and quickly, it attracted the world's attention but without treatment and control manual. For the request from frontline clinicians and public health professionals of 2019-nCoV infected pneumonia management, an evidence-based guideline urgently needs to be developed. Therefore, we drafted this guideline according to the rapid advice guidelines methodology and general rules of WHO guideline development; we also added the first-hand management data of Zhongnan Hospital of Wuhan University. This guideline includes the guideline methodology, epidemiological characteristics, disease screening and population prevention, diagnosis, treatment and control (including traditional Chinese Medicine), nosocomial infection prevention and control, and disease nursing of the 2019-nCoV. Moreover, we also provide a whole process of a successful treatment case of the severe 2019-nCoV infected pneumonia and experience and lessons of hospital rescue for 2019-nCoV infections. This rapid advice guideline is suitable for the first frontline doctors and nurses, managers of hospitals and healthcare sections, community residents, public health persons, relevant researchers, and all person who are interested in the 2019-nCoV.

Real-time tentative assessment of the epidemiological characteristics of novel coronavirus infections in Wuhan, China, as at 22 January 2020.

<https://www.ncbi.nlm.nih.gov/pubmed/31992388>

A novel coronavirus (2019-nCoV) causing severe acute respiratory disease emerged recently in Wuhan, China. Information on reported cases strongly indicates human-to-human spread, and the most recent information is increasingly indicative of sustained human-to-human transmission. While the overall severity profile among cases may change as more mild cases are identified, we estimate a risk of fatality among hospitalised cases at 14% (95% confidence interval: 3.9-32%).

Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China.

<https://www.ncbi.nlm.nih.gov/pubmed/31986264>

A recent cluster of pneumonia cases in Wuhan, China, was caused by a novel betacoronavirus, the 2019 novel coronavirus (2019-nCoV). We report the epidemiological, clinical, laboratory, and radiological characteristics and treatment and clinical outcomes of these patients.

Measures for diagnosing and treating infections by a novel coronavirus responsible for a pneumonia outbreak originating in Wuhan, China.

<https://www.ncbi.nlm.nih.gov/pubmed/32017984>

On 10 January 2020, a new coronavirus causing a pneumonia outbreak in Wuhan City in central China was denoted as 2019-nCoV by the World Health Organization (WHO). As of 24 January 2020, there were 887 confirmed cases of 2019-nCoV infection, including 26 deaths, reported in China and other countries. Therefore, combating this new virus and stopping the epidemic is a matter of urgency. Here, we focus on advances in research and development of fast diagnosis methods, as well as potential prophylactics and therapeutics to prevent or treat 2019-nCoV infection.

Preliminary estimation of the basic reproduction number of novel coronavirus (2019-nCoV) in China, from 2019 to 2020: A data-driven analysis in the early phase of the outbreak.

<https://www.ncbi.nlm.nih.gov/pubmed/32007643>

An ongoing outbreak of a novel coronavirus (2019-nCoV) pneumonia hit a major city of China, Wuhan, December 2019 and subsequently reached other provinces/regions of China and countries. We present estimates of the basic reproduction number, R_0 , of 2019-nCoV in the early phase of the outbreak.

First Case of 2019 Novel Coronavirus in the United States.

<https://www.ncbi.nlm.nih.gov/pubmed/32004427>

An outbreak of novel coronavirus (2019-nCoV) that began in Wuhan, China, has spread rapidly, with cases now confirmed in multiple countries. We report the first case of 2019-nCoV infection confirmed in the United States and describe the identification, diagnosis, clinical course, and management of the case, including the patient's initial mild symptoms at presentation with progression to pneumonia on day 9 of illness. This case highlights the importance of close coordination between clinicians and public health authorities at the local, state, and federal levels, as well as the need for rapid dissemination of clinical information related to the care of patients with this emerging infection.

Homologous recombination within the spike glycoprotein of the newly identified coronavirus may boost cross-species transmission from snake to human.

<https://www.ncbi.nlm.nih.gov/pubmed/31967321>

The current outbreak of viral pneumonia in the city of Wuhan, China, was caused by a novel coronavirus designated 2019-nCoV by the World Health Organization, as determined by sequencing the viral RNA genome. Many patients were potentially exposed to wildlife animals at the Huanan seafood wholesale market, where poultry, snake, bats, and other farm animals were also sold. To determine the possible virus reservoir, we have carried out comprehensive sequence analysis and comparison in conjunction with relative synonymous codon usage (RSCU) bias among different animal species based on existing sequences of the newly identified coronavirus 2019-nCoV. Results obtained from our analyses suggest that the 2019-nCoV appears to be a recombinant virus between the bat coronavirus and an origin-unknown coronavirus. The recombination occurred within the viral spike glycoprotein, which recognizes cell surface receptor. Additionally, our findings suggest that snake is the most probable wildlife animal reservoir for the 2019-nCoV based on its RSCU bias resembling snake compared to other animals. Taken together, our results suggest that homologous recombination within the spike glycoprotein may contribute to cross-species transmission from snake to humans. This article is protected by copyright. All rights reserved.

The Extent of Transmission of Novel Coronavirus in Wuhan, China, 2020.

<https://www.ncbi.nlm.nih.gov/pubmed/31991628>

A cluster of pneumonia cases linked to a novel coronavirus (2019-nCoV) was reported by China in

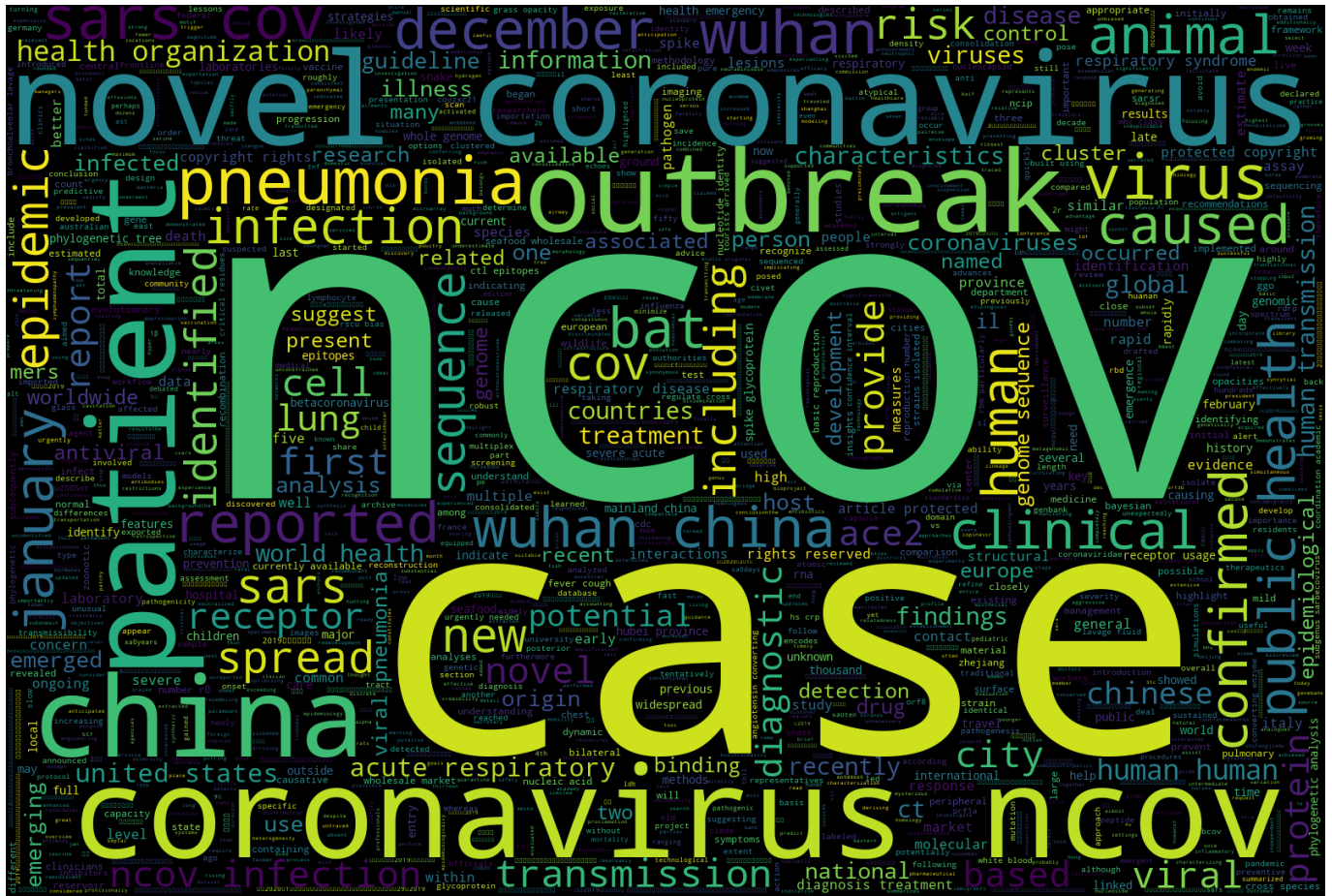
late December 2019. Reported case incidence has now reached the hundreds, but this is likely an underestimate. As of 24 January 2020, with reports of thirteen exportation events, we estimate the cumulative incidence in China at 5502 cases (95% confidence interval: 3027, 9057). The most plausible number of infections is in the order of thousands, rather than hundreds, and there is a strong indication that untraced exposures other than the one in the epidemiologically linked seafood market in Wuhan have occurred.

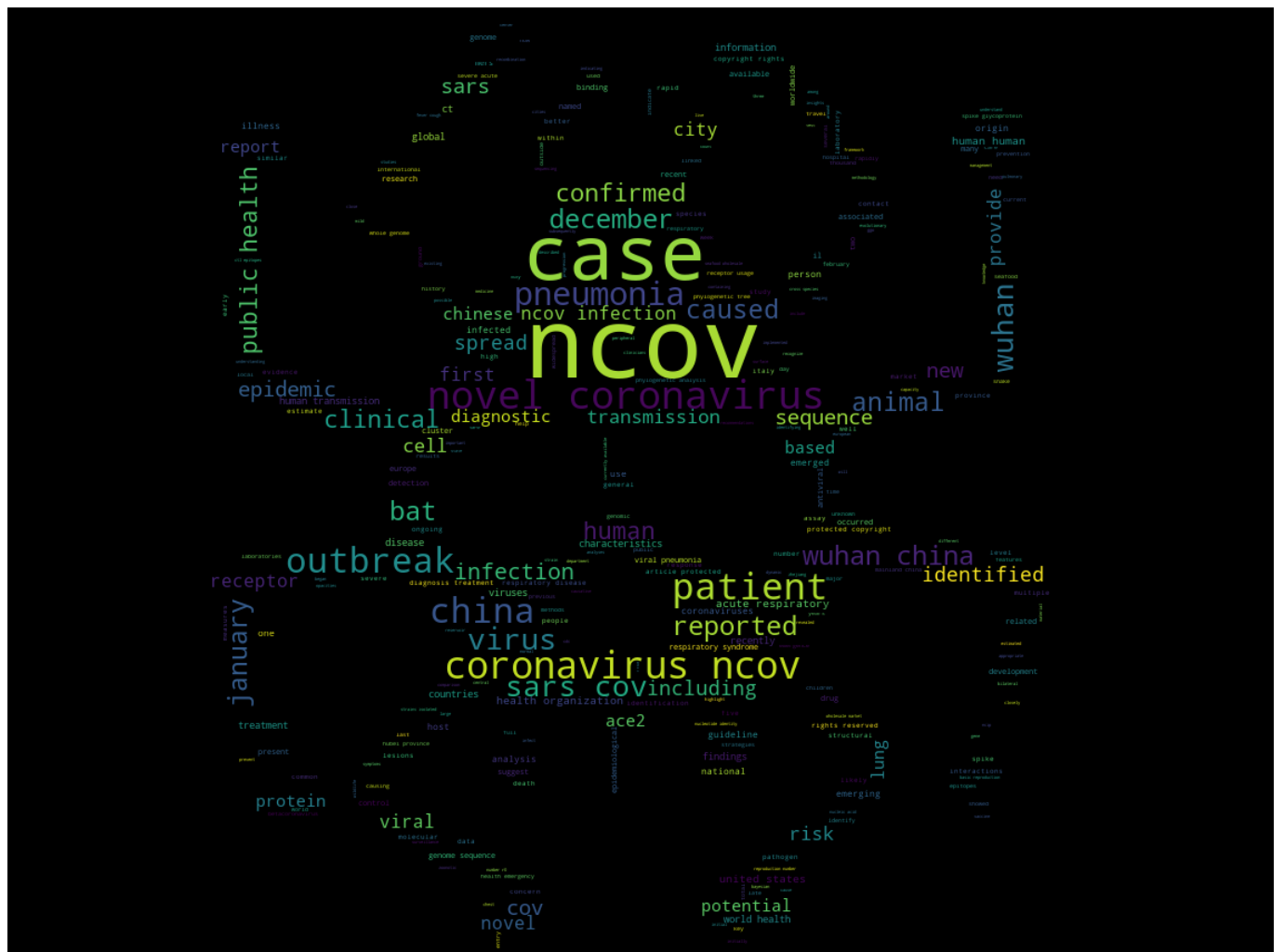
Updated understanding of the outbreak of 2019 novel coronavirus (2019-nCoV) in Wuhan, China.

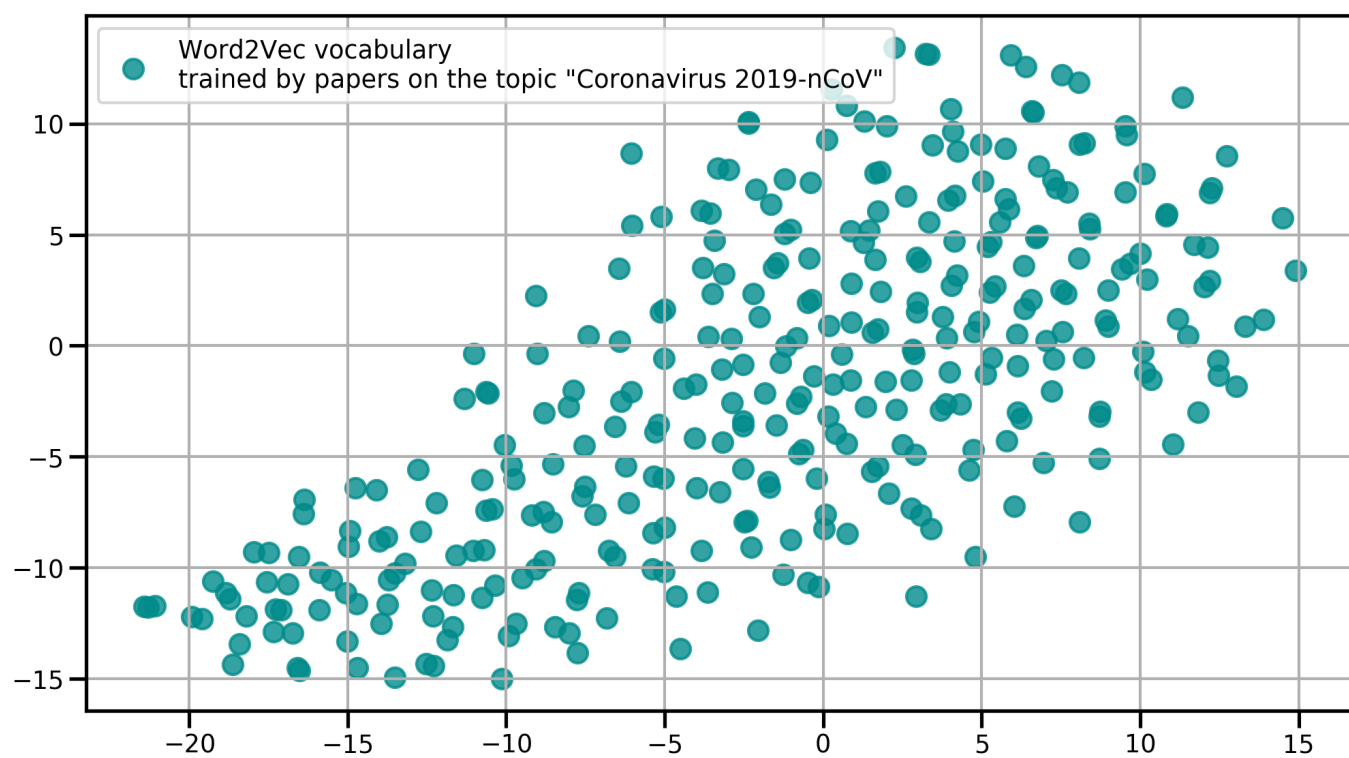
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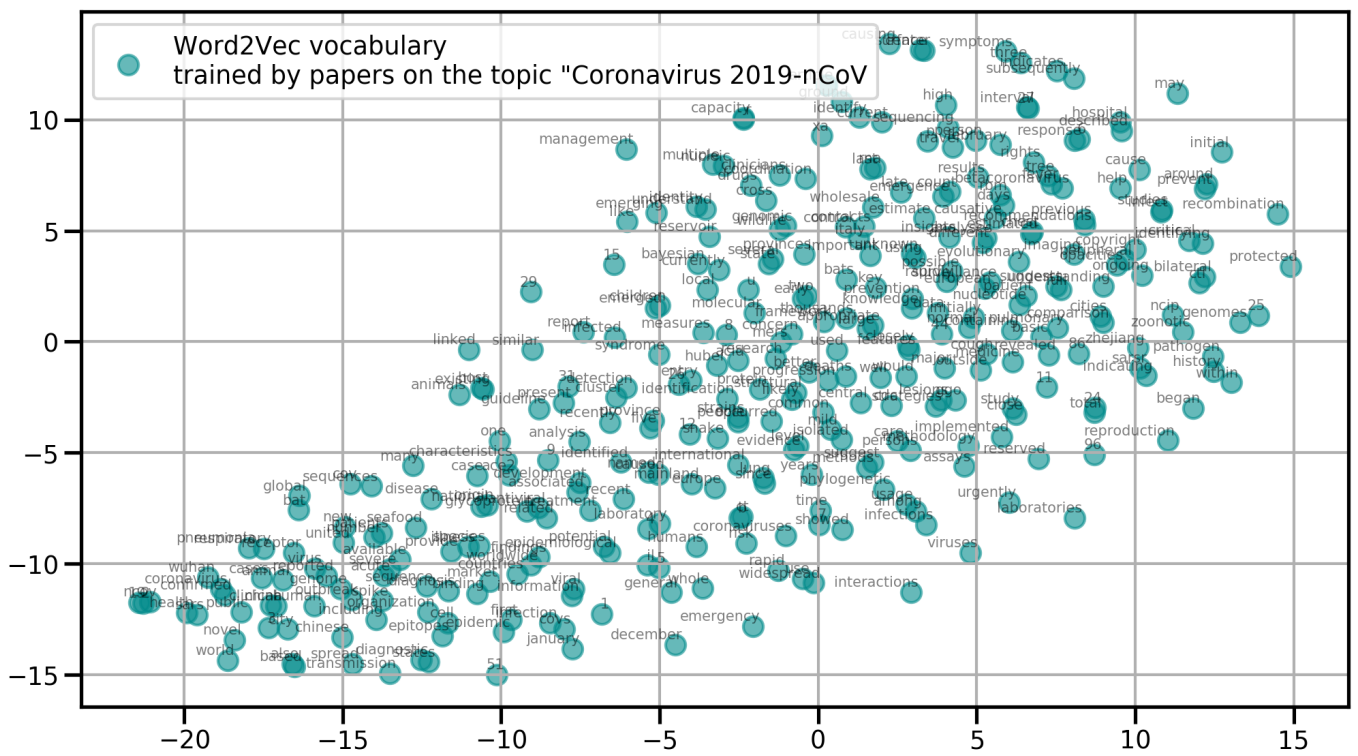
To help health workers and the public recognize and deal with the 2019 novel coronavirus (2019-nCoV) quickly, effectively and calmly with an updated understanding.

Top Words Cloud

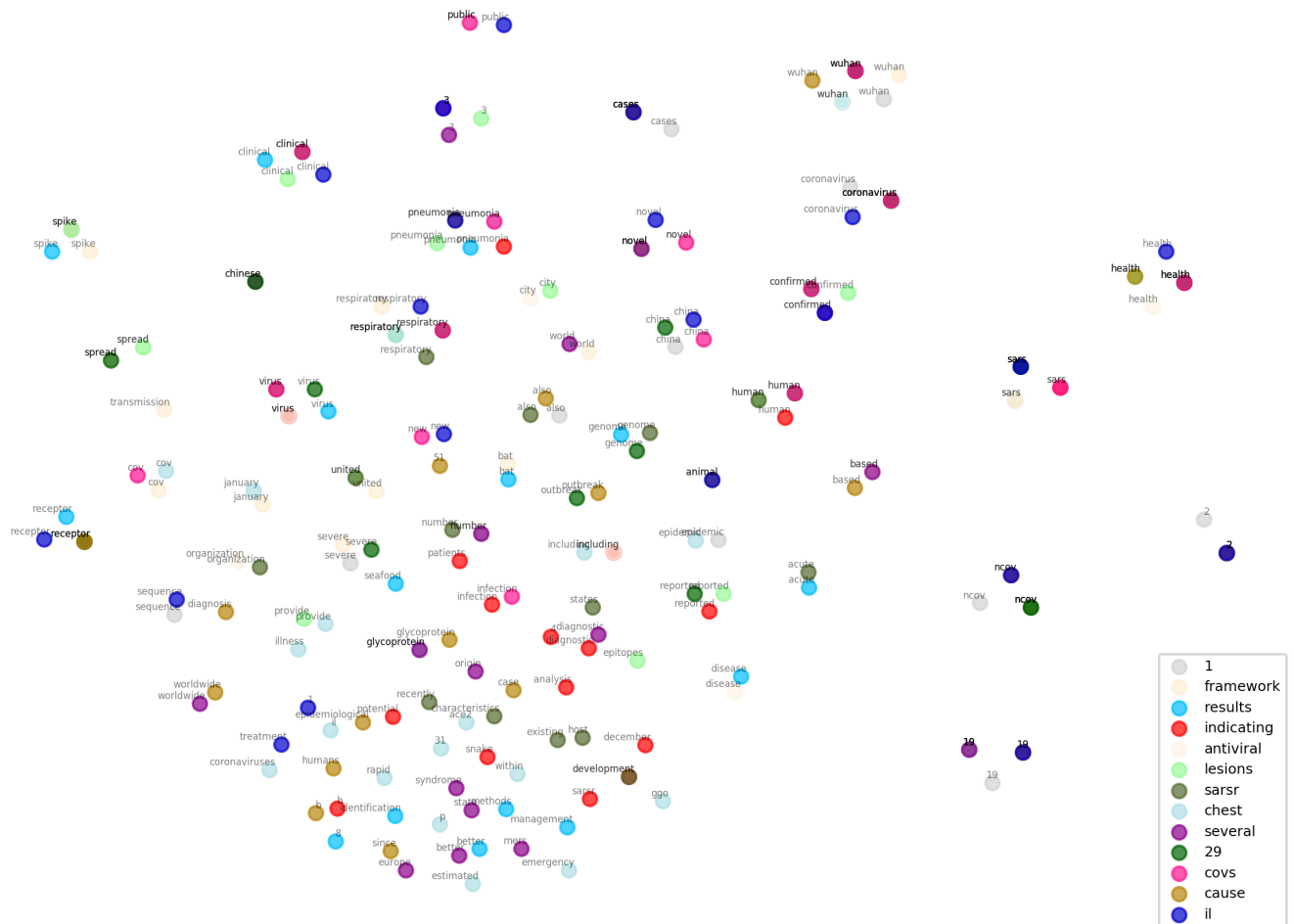




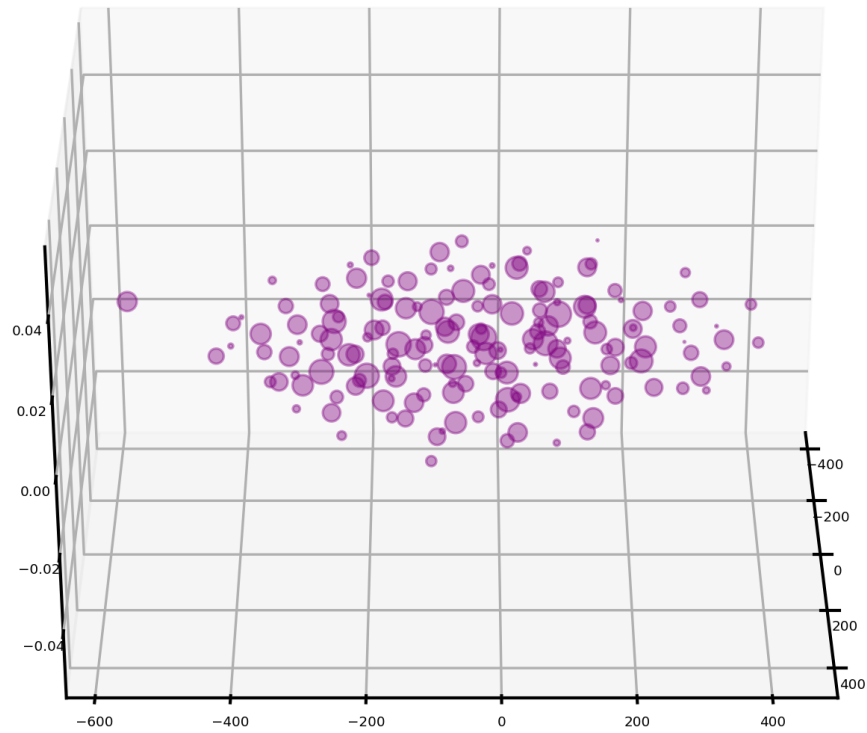




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