

(b)(3):50 USC 3024(i)

(b)(3):10 USC 424; (b)(3):50 USC 3024(i); (b)(6)

(b)(3):50 USC
3024(i)

SARS-CoV-2 highly
adaptable to
humans early in the
outbreak early in the
outbreak

The SARS-CoV-2
COVID-19 virus has a
combination of
multiple unique
structures that have
not been observed in
its most closely
related coronaviruses,
nor has the ancestral
virus been identified in
animal hosts,
according to a 2020
journal article.

(b)(3):50 USC 3024(i)

Zhang et al., 2020

Andersen et al., 2020

(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(e)

(b)(3):50 USC 3024(i)

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(b)(3):50 USC 3024(i)

(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(e)

This is the first time scientists have seen this combination of multiple these unique structures in the genus same-Betacoronavirus, s-to which SARS-CoV-2 belongs genus

(b)(3):50 USC 3024(i)

Andersen et al., 2020

According to reputable scientists, the multiple structures individually have been observed in other coronaviruses in nature

(b)(3):50 USC 3024(i)

Andersen et al., 2020

(b)(3):50 USC 3024(i)

Coronavirus genetic engineering capabilities have significantly matured worldwide since 2005

(b)(3):50 USC 3024(i)

(b)(3):50 USC 3024(i)

Zeng et al., 2016; Hu et al., 2017; Menachery et al., 2015; Roberts et al., 2015; Belouzard et al., 2009; Follis et al., 2006; Almazan et al., 2014

(b)(3):10 USC 424; (b)(3):50 USC 3024(i)
(b)(6)

(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(e)

The WIV conducts research on novel coronaviruses and uses genetic engineering to understand pathogenicity.

(b)(3):50 USC 3024(i)

Zeng et al., 2016; Hu et al., 2017; Ren et al., 2008; Ge et al., 2013; Menachery et al., 2015, 2016; Yang et al., 2015; Wang et al., 2019

First direct in vitro manipulation of full-length coronavirus cDNA at Huazhong University. Will simplify the construction of mutant infectious

(b)(3):50 USC 3024(i)

Wang et al., 2019

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(b)(3):50 USC 3024(i)

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(b)(3):50 USC 3024(i)

clones and help
accelerate progress in
coronavirus research

(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(e); (b)(6)

Coronavirus reverse
genetics system at
WIV

(b)(3):50 USC 3024(i)

Zeng et al., 2016; Hu et al.,
2017

NIH grant funded
EcoHealth Alliance and
NIH grant to WIV up to
2021 to conduct gain
of function (GOF)
studies on chimeric
bat coronaviruses.

Assumes SARS-CoV-2 is a
chimeric virus

NIH 2R01AI110964-06

(b)(3):50 USC 3024(i)

Demonstrated GOF
studies in several
coronaviruses
including SARS, MERS,
IBV, and PEDV that
adds Furin cleavage
site

(b)(3):50 USC 3024(i)

Cheng et al., 2019; Wan et
al., 2019; Shen et al., 2019;
Wang et al., 2019;
Menachery et al., 2019;
Zhou et al., 2018; Letko et
al., 2018

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(b)(3):50 USC 3024(i)

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(b)(3):50 USC 3024(i)

(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(e); (b)(6)

Trained scientists in
coronavirus research

(b)(3):50 USC 3024(i)

Zeng et al., 2016; Hu et
2017; Ren et al., 2008;
et al., 2013; Ge et al., 2016

(b)(3):10 USC 424; (b)(3):50 USC
3024(i); (b)(6)

(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(d); Sec. 1.4(e); (b)(6)

RATG13

ZC45 and ZXC 21
homology to SARS-
COV-2

(b)(3):50 USC 3024(i)

Lin et al., 2020; Segreto
2020; Monali et al., 2020

Wu, 2020

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(b)(3):50 USC 3024(i)

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(b)(3):50 USC 3024(i)

(b)(3):50 USC
3024(i)

(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(e); (b)(6)

WIV Modified COV
spike genes with spike
genes from different
COV? constructs

(b)(3):50 USC 3024(i)

Hu et al., 2017

COV sSpike gene
swapping using WIV
reverse genetics
system

Zeng et al., 2016; Hu et al.,
2017

(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(e); (b)(6)

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(b)(3):50 USC 3024(i)

(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(e); (b)(6)

Furin cleavage sequence of SARS-COV-2 published by Shi in 2017	(b)(3):50 USC 3024(i)	Ge et al., 2017
Codon optimized spike gene constructed at WIV using restriction fragment length polymorphism		Shang et al., 2020; Zeng et al., 2016
With the furin cleavage site on the S protein, 2019-nCoV gains ability to infect organs or tissues insensitive to other COVs	(b)(3):50 USC 3024(i)	Wang et al., 2020

(b)(3):10 USC 424; (b)(3):50 USC 3024(i)
(b)(6)

(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(b); Sec. 1.4(c); Sec. 1.4(d); Sec. 1.4(e); (b)(6)

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(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(e)

No natural reservoir or intermediate host linked to the pandemic has been identified

(b)(3):50 USC 3024(i)

Andersen et al., 2020

(b)(1); (b)(3):10 USC 424; (b)(3):50 USC 3024(i); Sec. 1.4(b); Sec. 1.4(c); Sec. 1.4(d); Sec. 1.4(e)

(b)(3):50 USC 3024(i)

Xiao et al., 2020

(b)(3):10 USC 424; (b)(3):50 USC 3024(i); (b)(6)

(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(b); Sec. 1.4(c); Sec. 1.4(d); Sec. 1.4(e)

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The following page is withheld in full citing (b)(1), (b)(3) 10 USC 424 + 50 USC 3024(i), and (b)(6), and is not provided.

(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(e)

(b)(3):50 USC 3024(i)		
(b)(3):50 USC 3024(i)	(b)(3):50 USC 3024(i)	Zhang et al., 2020
SARS-CoV-2 highly [redacted] to humans early in the outbreak		Andersen et al., 2020
The COVID-19 virus has multiple unique structures that have not been observed in its most closely related coronaviruses, nor has the ancestral virus been		

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(b)(3):50 USC 3024(i)

identified in animal hosts, according to a 2020 journal article.						
This is the first time scientists have seen the combination of these unique structures in the same Coronavirus genus	(b)(3):50 USC 3024(i)				Andersen et al., 2020	
The WIV conducts research on novel coronaviruses and uses genetic engineering to understand pathogenicity.	(b)(3):50 USC 3024(i)				Zeng et al., 2016; Hu et al., 2017; Ren et al., 2008; Ge et al., 2013; Menachery et al., 2015, 2016; Yang et al., 2015; Wang et al., 2019	
(b)(3):50 USC 3024(i)						
(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(e)						
to WIV up to 2021 to conduct GOF studies on chimeric bat coronaviruses.	(b)(3):50 USC 3024(i)				NIH 2R01AI110964-06	
Demonstrated GOF studies in SARS, MERS, JRV, and PEDV. Furin cleavage site	(b)(3):50 USC 3024(i)				Cheng et al., 2019; Wan et al., 2019; Shen et al., 2019; Wang et al., 2019; Menachery et al., 2019; Zhou et al., 2018; Letko et al., 2018	
(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(e)						
RATG13	(b)(3):50 USC 3024(i)	(b)(3):50 USC 3024(i)			Lin et al., 2020; Segrete 2020; Monali et al., 2020	
ZC45 and ZXC 21 homology to SARS-CoV-2	(b)(3):50 USC 3024(i)			Wu, 2020		
(b)(3):50 USC 3024(i)				Hu et al., 2017		
				Zeng et al., 2016; Hu et al., 2017		
(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(e); (b)(6)						

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(b)(3):50 USC 3024(i)

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(b)(3):50 USC 3024(i)

(b)(1); (b)(3):10 USC 424; (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(e); (b)(6)

Furin cleavage sequence of SARS-CoV-2 published by Shi in 2017

(b)(3):50 USC 3024(i)

(b)(3):50 USC 3024(i)

Ge et al., 2017

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Shang et al., 2020; Zeng et al., 2016

With the furin cleavage site on the S protein, 2019-nCoV gains ability to infect organs or tissues insensitive to other CoVs

Wang et al., 2020

No natural reservoir or intermediate host has been identified

Andersen et al., 2020

(b)(1); (b)(3):10 USC 424; (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(e)

(b)(1); (b)(3):10 USC 424; (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(e)

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(b)(3):50 USC 3024(i)

~~TOP SECRET~~ (b)(3):50 USC 3024(i)

(b)(1); (b)(3):10 USC 424; (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(e)					
According to reputable scientists, all of the novel features individually have been observed in other coronaviruses in nature.	(b)(3):50 USC 3024(i)				Andersen et al., 2020
(b)(3):50 USC 3024(i)					
(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(e)					

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