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

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

SARS-CoV-2 highly

to humans ~~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)

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

Zhang et al., 2020

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)

This is the first time
scientists have seen

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

Andersen et al., 2020

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

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these combination of multiple these unique structures in the genus same-Betacoronavirus, s-to which SARS-CoV-2 belongs genus						
According to reputable scientists, the multiple structures individually have been observed in other coronaviruses in nature.	(b)(3):50 USC 3024(i)					
(b)(3):50 USC 3024(i)	(b)(3):50 USC 3024(i)					Andersen et al., 2020
	(b)(3):50 USC 3024(i)					
Coronavirus engineering capabilities have significantly matured worldwide since 2005	(b)(3):50 USC 3024(i)					Zeng et al., 2016; Hu et al., 2017; Menachery et al., 2015; Roberts et al., 2009; Belouzard et al., 2009; Follis et al., 2006; Almaz et al., 2014
(b)(1); (b)(3):10 USC 424; (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(e); (b)(6)						
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)					
First direct in vitro manipulation of full-length coronavirus cDNA at Huazhong University. Will simplify the construction of mutant infectious clones and help accelerate progress in coronavirus research	(b)(3):50 USC 3024(i)					Wang et al., 2019
						(b)(3):10 USC 424; (b)(3):50 USC 3024(i); (b)(6)

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

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

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(b)(1); (b)(3):10 USC 424; (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	(b)(3):10 USC 424; (b)(3):50 USC 3024(i); (b)(6)
NIH grant funded EcoHealth Alliance and NIH grant to WIV up to 2021 to conduct gain of function (GOF) studies on chimeric bat coronaviruses.						
	(b)(3):50 USC 3024(i)				NIH 2R01AI110964-06	
		(b)(3):50 USC 3024(i)				
Demonstrated GOF studies in <u>several</u> 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	

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

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

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

(b)(3):10 USC 424; (b)(3):50 USC 3024(i); (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)(1); (b)(3):10 USC 424; (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

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

WIV Modified <u>COV</u> spike genes with spike genes from different <u>(COV?)</u> constructs	(b)(3):50 USC 3024(i)	Hu et al., 2017
<u>COV</u> <u>s</u> Spike 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)

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

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

(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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(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)

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

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

SARS-CoV-2 highly exposed to
humans early in the outbreak.

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
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.

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

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

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

Zhang et al., 2020

Andersen et al., 2020

Andersen et al., 2020

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

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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)

to WIV up to 2021 to conduct
GOF studies on chimeric bat
coronaviruses;

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

NH12R01AH10964-06

Demonstrated GOF studies in
SARS, MERS, IBV, 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); (b)(6)

RATG13

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

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

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

ZC45 and ZXC-21 homology to SARS-CoV-2

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)

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

Ge et al., 2017

Codon optimized spike gene constructed at WIV using restriction fragment length polymorphism

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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):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)

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

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

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