

(b)(3):50 USC 3024(i)	(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)
	SARS-CoV-2 highly [redacted] 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.	
	Zhang et al., 2020 Andersen et al., 2020	(b)(3):50 USC 3024(i)

(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)(3):50 USC 3024(i)			(b)(3):50 USC 3024(i)	
(b)(3):50 USC 3024(i) According to reputable scientists, individually have been observed in other coronaviruses in nature, (b)(3):50 USC 3024(i) Coronavirus synthetic engineering capabilities have significantly matured worldwide since 2005	(b)(3):50 USC 3024(i)		Andersen et al., 2020	(b)(3):50 USC 3024(i)
	(b)(3):50 USC 3024(i)		Andersen et al., 2020	
	(b)(3):50 USC 3024(i)		Zeng et al., 2016; Hu et al., 2017; Menachery et al., 2015; Roberts et al., 2007; Belouzard et	

							al., 2009; Follis et al., 2006; Almazan et al., 2014	
(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	
	(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)(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	Assumes SARS-CoV-2 is chimeric
grant to WIV up to 2021 to conduct GOF studies on chimeric bat coronaviruses,	(b)(3):50 USC 3024(i)			NIH 2RO1AI110964-06	

[illegible]

(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(d); Sec. 1.4(e); (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
			Wu, 2020
ZC45 and ZXC 21 homology to SARS-COV- 2			

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

WIV Modified spike genes with spike genes from different constructs	(b)(3):50 USC 3024(i)	Hu et al., 2017	
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)

(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

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

Codon optimized spike gene constructed at WIV using restriction fragment length polymorphism	(b)(3):50 USC 3024(i)	Shang et al., 2020; Zeng et al., 2016	
With the furin cleavage site on the S protein, 2019-nCoV probably gains ability to infect organs or tissues insensitive to other COV's	(b)(3):50 USC 3024(i)	Wang et al., 2020	
(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(b); Sec. 1.4(c); Sec. 1.4(d); Sec. 1.4(e)			

[illegible]

(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(c); Sec. 1.4(e)	
(b)(3):50 USC 3024(i)	Xiao et al., 2020
(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(b); Sec. 1.4(c); Sec. 1.4(d); Sec. 1.4(e)	

The following 2 pages are withheld in full citing (b)(1) and (b)(3) 50 USC 3024(i) and are 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)	SARS-CoV-2 highly [redacted] to humans early in the outbreak	(b)(3):50 USC 3024(i)	Zhang et al., 2020
	The COVID-19 virus has multiple unique structures that have not been observed in its most closely related coronaviruses, nor has		Andersen et al., 2020

studies on chimeric bat coronaviruses.					
(b)(3):50 USC 3024(i)					
Demonstrated GOF studies in SARS, MERS, IBV, and PEDV [redacted] Furin cleavage site					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 [redacted]					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)

(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)		

(b)(1); (b)(3):50 USC 3024(i); Sec. 1.4(c)			
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,	(b)(3):50 USC 3024(i)	Wang et al., 2020	

(b)(3):50 USC 3024(i)	2019-nCoV gains ability to infect organs or tissues insensitive to other COVs								
	No natural reservoir or intermediate host has been identified	(b)(3):50 USC 3024(i)						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)				
		(b)(3):50 USC 3024(i)	Andersen et al., 2020	

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

individually have been observed in other coronaviruses in nature, (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)