

Number	BetaCoV Spike Protein Domain (20 AA segment at S1/S2 junction)	GenBank Protein Accession (Representative)	Betacoronavirus (InterPro/UniProt description)	FCS (RXR)	NLS (pat7)	O-Glycosite Pair ([S/T]XXPXXX[S/T])
1	672 ASYQTQ TNS FR RR RSVASQS 691 * ^ ^ **	YP_009724390.1	Severe acute respiratory syndrome coronavirus 2 (2019-nCoV) ^a	+	+	+
2	672 ASYQ TH TNSFR RR RSVASQS 691 * ^ ^ **	QZ238148.1	Severe acute respiratory syndrome coronavirus 2 (2019-nCoV)	+	+	+
3	672 ASYHTQ TNS FR RR RSVASQS 691 * ^ ^ **	QZ236053.1	Severe acute respiratory syndrome coronavirus 2 (2019-nCoV)	+	+	+
4	672 ASYQ TH TNSFR RR RSVASQS 691 * ^ ^ **	QZ231638.1	Severe acute respiratory syndrome coronavirus 2 (2019-nCoV)	+	+	+
5	672 ASYQTQ TNS FR RR RSVASQS 691 * ^ ^ **	QZ230997.1	Severe acute respiratory syndrome coronavirus 2 (2019-nCoV)	+	+	+
6	672 ASYQTQ TNS FR RR RSVASQS 691 * ^ ^ **	QZ230487.1	Severe acute respiratory syndrome coronavirus 2 (2019-nCoV)	+	+	+
7	672 ASYQTQ TNS FR RR RSVASQS 691 * ^ ^ **	QZ254696.1	Severe acute respiratory syndrome coronavirus 2 (2019-nCoV)	+	+	+
8	672 ASYQTQ TNS FR RR RSVASQS 691 * ^ ^ **	QZ250798.1	Severe acute respiratory syndrome coronavirus 2 (2019-nCoV)	+	+	+
9	672 ASYQTQ TNS FR RR RSVAIQS 691 * ^ ^ **	QZ236833.1	Severe acute respiratory syndrome coronavirus 2 (2019-nCoV)	+	+	+
10	672 ASYQTQ TNS FR RR RSVASQS 691 * ^ ^ **	QZ253778.1	Severe acute respiratory syndrome coronavirus 2 (2019-nCoV)	+	+	+
11	672 ASYHTQ TNS FR RR RSVASQS 691 * ^ ^ **	QZ236641.1	Severe acute respiratory syndrome coronavirus 2 (2019-nCoV)	+	+	+
12	667 GAGICASY S FR RR RSVASQS 686 * ^ ^ **	QSS76529.1	Severe acute respiratory syndrome coronavirus 2 (2019-nCoV)	+	+	+
13	672 ASYQTQ TNS FR RR RSVASQS 691 * ^ ^ **	QZ242759.1	Severe acute respiratory syndrome coronavirus 2 (2019-nCoV)	+	+	+
14	672 ASYQTQ TNS FR RR RSVASQS 691 * ^ ^ **	QZ250798.1	Severe acute respiratory syndrome coronavirus 2 (2019-nCoV)	+	+	+
15	671 ASYQTQ TNS FR RR RSVASQS 690 * ^ ^ **	QHS34546.1	Severe acute respiratory syndrome coronavirus 2 (2019-nCoV)	+	+	+
16	672 ASYQ TH TNSFR RR RSVASQS 691 * ^ ^ **	QZ232672.1	Severe acute respiratory syndrome coronavirus 2 (2019-nCoV)	+	+	+
17	672 ASYQTQ TNS FR RR RSVASQS 691 * ^ ^ **	QKX37093.1	Severe acute respiratory syndrome coronavirus 2 (2019-nCoV) ^b	+	+	+
18	672 ASYQTQ TNS FR RR RSVPSQS 691 * ^ ^ **	QOQ53336.1	Severe acute respiratory syndrome coronavirus 2 (2019-nCoV) ^c	+	+	+
19	738 L PD T P S T L T FR RR RSV P GEM 757 * ^ ^ **	QKX95939.1	Middle East respiratory syndrome-related coronavirus (MERS-CoV) ^d	+	+	+
20	738 L PD T P S T L T FR RR RSV P GEM 757 * ^ ^ **	AFS88936.1	Middle East respiratory syndrome-related coronavirus (MERS-CoV) ^e	+	-	+
21	740 SG F C I D Y A L P S S R R K R R G I S 759 * ^ ^	Q0ZJ11	Human coronavirus HKU1 (HCoV-HKU1) ^f	+	+	-
22	672 ASYQTQ TNS ----RSVASQS 687	QHR63300.2	Bat coronavirus RaTG13 ^g	-	-	-

a) SARS-CoV-2 reference genome (first isolate Wuhan-Hu-1); origin: China: Hubei; collection date: December 2019

b) Earliest SARS-CoV-2 A684V variant with pat7 in S1/S2 domain identical to MERS-MA30 (number 19); origin: Saudi Arabia: Jeddah; collection date: 15 March 2020

c) Earliest SARS-CoV-2 A684V/A688P variant with closest S1/S2 domain sequence to MERS-MA30 (number 19); origin: Iran; collection date: March 2020

d) Murine adapted (MA30), synthetic MERS CoV clone from 2017 after serial (30) passage in genetically humanized (transgenic human dipeptidyl peptidase 4 receptor knockin) laboratory mice; origin: USA: Iowa

e) Earliest MERS CoV (isolate Human betacoronavirus 2c EMC/2012); origin: Saudi Arabia: Jeddah; collection date: 13 June 2013

f) Genotype B HKU1 strain 25 betacoronavirus; origin: China: Hongkong; collection date: January 2005

g) Closest evolutionary betacoronavirus relative of SARS-CoV-2 by full genomic sequence (as of 2024; identical data for bat betacoronavirus BANAL-20-52); origin: China; collection date: 24 July 2013

AA: Amino Acid; FCS: Furin Cleavage Site; NLS: Nuclear Localization Signal