## Aligned using an external algorithm

## Consensus

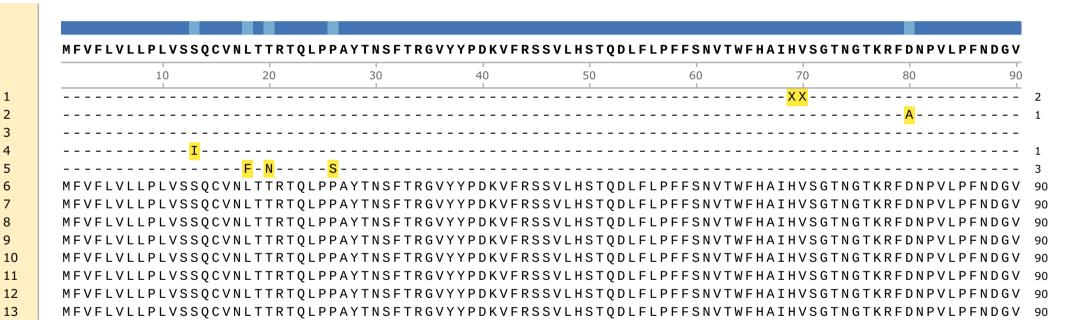
- **1.** B.1.1.7
- 2. B.1.351
- 3. B.1.427
- **4.** B.1.429
- **5.** P.1

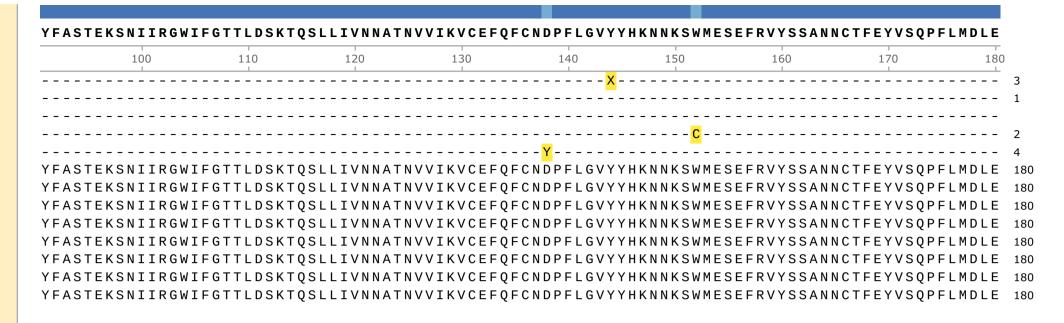
1 2

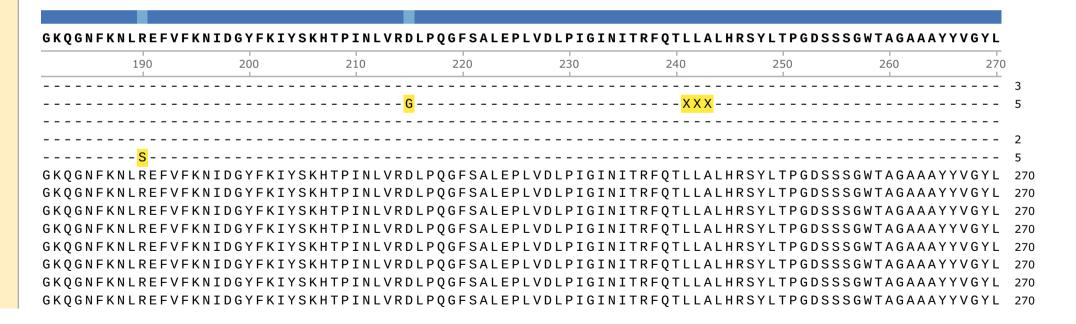
10

11

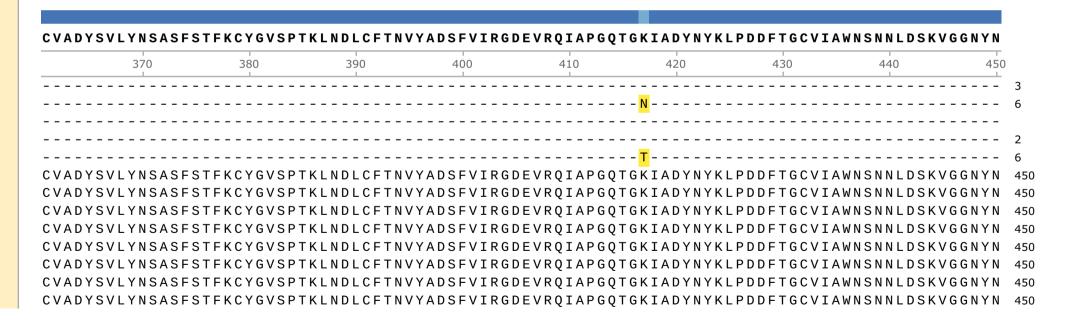
- **6.** Ref YP 009724390.1 surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]
- 7. Ref OHD43416.1 surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]
- 8. mRNA-1273 vaccine translated
- 9. BNT-162b2 vaccine translated
- 0. Ad26.COV2-S vaccine translated
- 1. NVX-CoV2373 vaccine translated
- 2. Sputnik V alleged unmodified YP 009724390.1
- 3. AZD1222 alleged unmodified YP 009724390.1

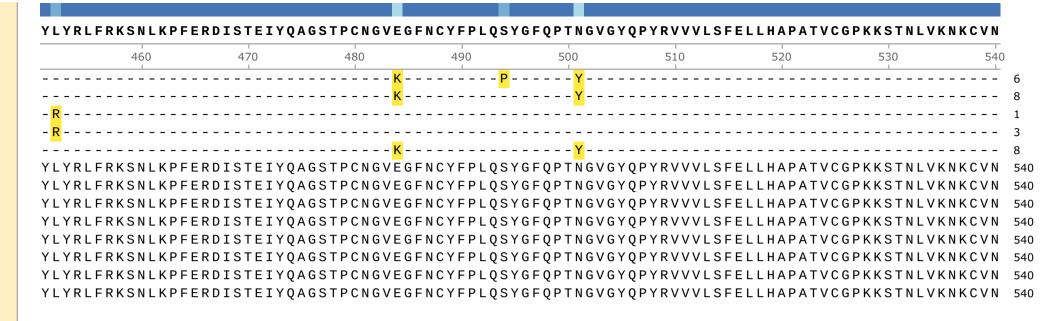


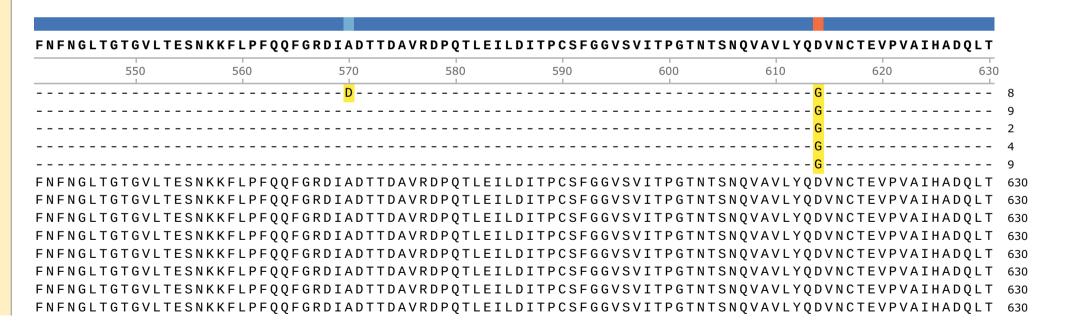




280	290	300	310	320	330	340	350	36
TFLLKYNENGT	ITDAVDCALDP	LSETKCTLKS	SFTVEKGIYQT	SNFRVQPTES	SIVRFPNITNL	CPFGEVFNAT	RFASVYAWNR	KRISN
TFLLKYNENGT	ITDAVDCALDP	LSETKCTLKS	SFTVEKGIYQT	SNFRVQPTES	SIVRFPNITNL	CPFGEVFNAT	RFASVYAWNR	KRISN
TFLLKYNENGT	ITDAVDCALDP	LSETKCTLKS	SFTVEKGIYQT	SNFRVQPTES	SIVRFPNITNL	CPFGEVFNAT	RFASVYAWNR	KRISN
TFLLKYNENGT	ITDAVDCALDP	LSETKCTLKS	SFTVEKGIYQT	SNFRVQPTES	SIVRFPNITNL	CPFGEVFNAT	RFASVYAWNR	KRISI
TFLLKYNENGT	ITDAVDCALDP	LSETKCTLKS	SFTVEKGIYQT	SNFRVQPTES	SIVRFPNITNL	CPFGEVFNAT	RFASVYAWNR	KRISI
TFLLKYNENGT	ITDAVDCALDP	LSETKCTLKS	SFTVEKGIYQT	SNFRVQPTES	SIVRFPNITNL	CPFGEVFNAT	RFASVYAWNR	KRISI
TELLKYNENOT	TTDAVDCALDP	LSETKCTLKS	SETVEKGIYOT	SNFRVOPTES	SIVRFPNITNL	CPFGEVFNAT	RFASVYAWNR	KRIS
(I F L L K Y N E N G I	TIDATOREDI							

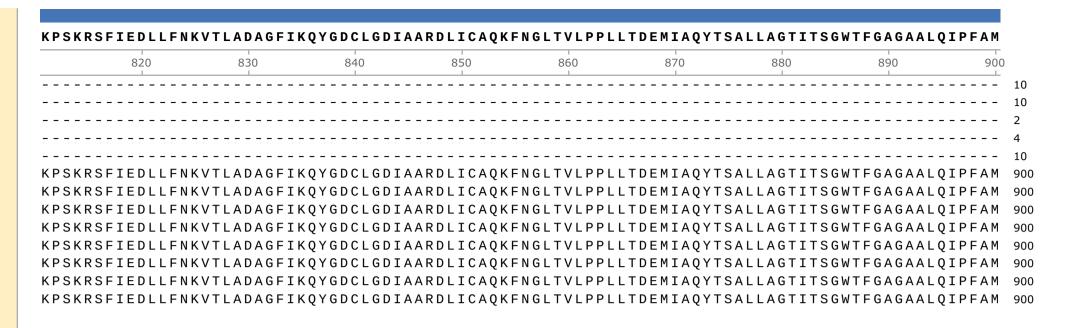


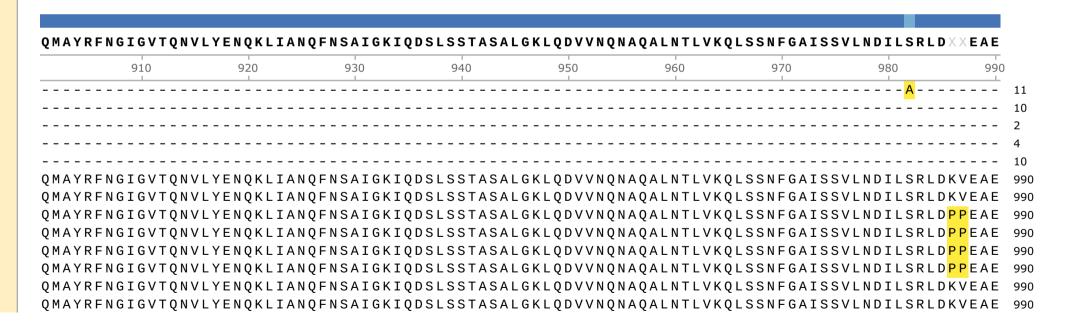






81	800	790	780	770	760	750	740	730
					·			
							SVDCTMVTCG	TEILPVSMTKTS
-				=	= =			TEILPVSMTKTS
-				-				TEILPVSMTKTS
-				-				TEILPVSMTKTS
QILPDPS	FGGFNFS	YKTPPIKD	KNTQEVFAQV	RALTGIAVEQ	YGSFCTQLNF	OSTECSNLLL	VDCTMYICGI	TEILPVSMTKTS
	EGGENES	YKTPPTKD	KNTOFVFAOV	RALTGTAVEO	YGSECTOLNE	OSTECSNILLO	V D C T M Y T C G I	TEILPVSMTKTS





1000	1010	1020	1030	1040	1050	1060	1070	108
			- I					
DRLITGRLQSLO	QTYVTQQLIRA	AAEIRASANLA	ATKMSECVL(	GQSKRVDFCGk	KGYHLMSFPQ:	SAPHGVVFLHV	TYVPAQEKN	<del>-</del> TTAPA
DRLITGRLQSLO	QTYVTQQLIRA	AAEIRASANLA	ATKMSECVLO	GQSKRVDFCGk	KGYHLMSFPQ:	SAPHGVVFLHV	TYVPAQEKN	<del>-</del> TTAPA
DRLITGRLQSLO	QTYVTQQLIRA	AAEIRASANLA	ATKMSECVLO	GQSKRVDFCGk	KGYHLMSFPQ:	SAPHGVVFLHV	TYVPAQEKN	<del>-</del> TTAPA
DRLITGRLQSLO	QTYVTQQLIRA	AAEIRASANLA	ATKMSECVLO	GQSKRVDFCGk	KGYHLMSFPQ:	SAPHGVVFLHV	TYVPAQEKN	<del>-</del> TTAPA
DRLITGRLQSLO	QTYVTQQLIRA	AAEIRASANLA	ATKMSECVLO	GQSKRVDFCGK	KGYHLMSFPQ:	SAPHGVVFLHV	TYVPAQEKN	TTAPA
DRLITGRLQSLO	QTYVTQQLIRA	AAEIRASANLA	ATKMSECVLO	GQSKRVDFCGk	KGYHLMSFPQ:	SAPHGVVFLHV	TYVPAQEKN	<del>-</del> T T A P A
							T)///D A O E I/ N	
DRLITGRLQSLO	QTYVTQQLIR <i>A</i>	AAEIRASANLA	ATKMSECVLO	3 Q S K R V D F C G F	KGYHLMSFPQ:	SAPHGVVFLHV	TYVPAQEKN	-IIAPA

1090	1100	1110	1120	1130	1140	1150	1160	117
			<mark>H</mark>					
DGKAHFPREGVI								
DGKAHFPREGVI		•			•			
DGKAHFPREGVI	- V S N G T H W F V T	QRNFYEPQII	TTDNTFVSGN	ICDVVIGIVNN	TVYDPLQPEL	DSFKEELDKY	FKNHTSPDVD	LGDIS
DGKAHFPREGVI	- V S N G T H W F V T	QRNFYEPQII	TTDNTFVSGN	NCDVVIGIVNN	TVYDPLQPEL	DSFKEELDKY	FKNHTSPDVD	LGDIS
DGKAHFPREGVI	- V S N G T H W F V T	QRNFYEPQII	TTDNTFVSGN	NCDVVIGIVNN	TVYDPLQPEL	DSFKEELDKY	FKNHTSPDVD	LGDIS
DGKAHFPREGVI	- VSNGTHWFVT	QRNFYEPQII	TTDNTFVSGN	ICDVVIGIVNN	TVYDPLQPEL	DSFKEELDKY	FKNHTSPDVD	LGDIS
DGKAHFPREGVI	- V S N G T H W F V T	ORNEYEPOTT	TTDNTFVSGN	ICDVVIGIVNN	TVYDPLOPEI	DSEKEELDKY	FKNHTSPDVD	LGDIS

1180	1190	1200	1210	1220	1230	1240	1250	126
	<mark>N</mark>							
	<del>-</del>							
ASVVNIQKEIDF	RLNEVAKNLNE	ESLIDLQELGI	KYEQYIKWPWY	/IWLGFIAGL]	CAIVMVTIMLO	CCMTSCCSCLK	GCCSCGSCCK	FDEDD
ASVVNIQKEIDF	RLNEVAKNLNE	SLIDLQELGI	(YEQYIKWPW)	/IWLGFIAGL	CAIVMVTIMLO	CCMTSCCSCLK	GCCSCGSCCK	FDEDD
ASVVNIQKEIDE	RLNEVAKNLNE	ESLIDLQELGI	KYEQYIKWPWY	/IWLGFIAGL]	CAIVMVTIMLO	CCMTSCCSCLK	GCCSCGSCCK	FDEDD
ASVVNIQKEIDE	RLNEVAKNLNE	SLIDLQELGI	KYEQYIKWPWY	/IWLGFIAGL]	CAIVMVTIMLO	CCMTSCCSCLK	GCCSCGSCCK	FDEDD
ASVVNIQKEIDE	RLNEVAKNLNE	SLIDLQELGI	(YEQYIKWPW)	/IWLGFIAGL]	CAIVMVTIMLO	CCMTSCCSCLK	GCCSCGSCCK	FDEDD
ASVVNIQKEIDF	RLNEVAKNLNE	SLIDLQELGI	(YEQYIKWPW)	/IWLGFIAGL]	CAIVMVTIMLO	CCMTSCCSCLK	GCCSCGSCCK	FDEDD
ASVVNIQKEIDE	RLNEVAKNLNE	ESLIDLQELGI	(YEQYIKWPW)	/IWLGFIAGL]	CAIVMVTIMLO	CCMTSCCSCLK	GCCSCGSCCK	FDEDD
IASVVNIQKEIDF		-	-					

SEPVLKGVKLHYT	
1270	
	13
	10
	2
	4
	11
SEPVLKGVKLHYT	1273

**Consensus Threshold:** >50%

**Compare to:** Ref QHD43416.1 surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]

Amino acids that don't match the reference are marked with yellow highlighting.

**Created:** 11 Jun 2021

Last Modified: 11 Jun 2021

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