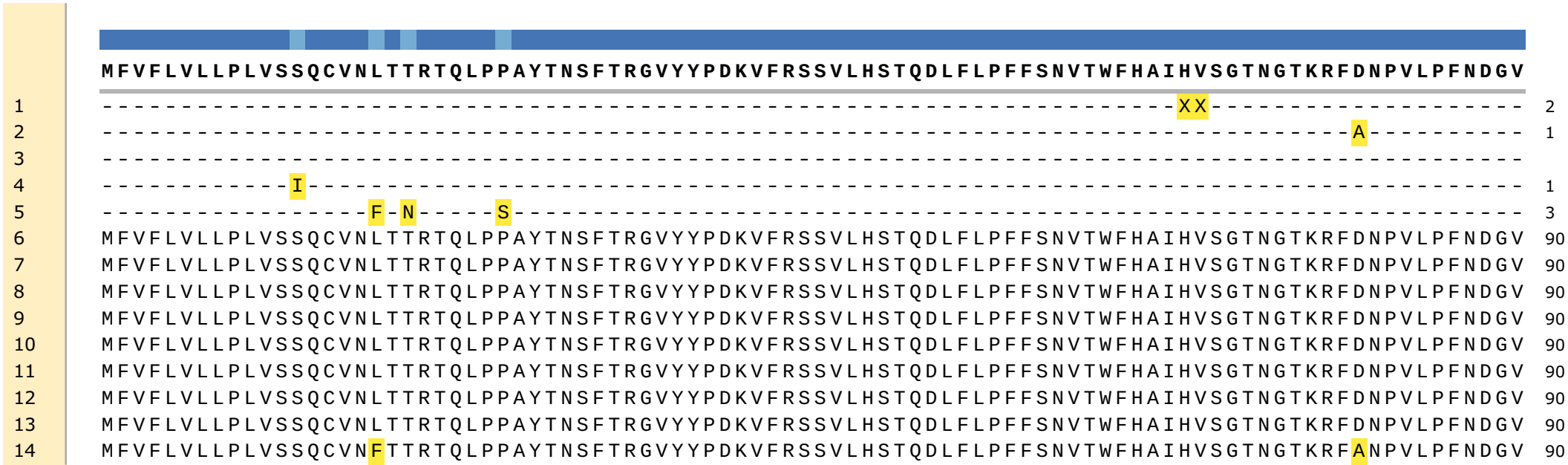


Consensus

- 1. B.1.1.7
- 2. B.1.351
- 3. B.1.427
- 4. B.1.429
- 5. P.1
- 6. Ref YP_009724390.1 surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]
- 7. Ref QHD43416.1 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
- 4. AZD2816 modified YP_009724390.1 variants from B.1.351



YFASTKSNIIRGWIFGTTLDSKIQSLIIVNNATNVVIKVCFEQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVVSQPFLMDLE

1	-----X-----	3
2	-----	1
3	-----	
4	-----C-----	2
5	-----Y-----	4
6	YFASTEKSNIIRGWIFGTTLD SKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESSEFRVYSSANNCTFEYVSQPFLMDLE	180
7	YFASTEKSNIIRGWIFGTTLD SKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESSEFRVYSSANNCTFEYVSQPFLMDLE	180
8	YFASTEKSNIIRGWIFGTTLD SKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESSEFRVYSSANNCTFEYVSQPFLMDLE	180
9	YFASTEKSNIIRGWIFGTTLD SKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESSEFRVYSSANNCTFEYVSQPFLMDLE	180
10	YFASTEKSNIIRGWIFGTTLD SKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESSEFRVYSSANNCTFEYVSQPFLMDLE	180
11	YFASTEKSNIIRGWIFGTTLD SKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESSEFRVYSSANNCTFEYVSQPFLMDLE	180
12	YFASTEKSNIIRGWIFGTTLD SKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESSEFRVYSSANNCTFEYVSQPFLMDLE	180
13	YFASTEKSNIIRGWIFGTTLD SKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESSEFRVYSSANNCTFEYVSQPFLMDLE	180
14	YFASTEKSNIIRGWIFGTTLD SKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESSEFRVYSSANNCTFEYVSQPFLMDLE	180

GKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLALHRSYLTTPGDSSSGWTAGAAAYYVGYL

1	-----		3
2	-----G-----XXX-----		5
3	-----		
4	-----		2
5	-----S-----		5
6	GKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLALHRSYLT	PGDSSSGWTAGAAAYYVGYL	270
7	GKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLALHRSYLT	PGDSSSGWTAGAAAYYVGYL	270
8	GKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLALHRSYLT	PGDSSSGWTAGAAAYYVGYL	270
9	GKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLALHRSYLT	PGDSSSGWTAGAAAYYVGYL	270
10	GKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLALHRSYLT	PGDSSSGWTAGAAAYYVGYL	270
11	GKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLALHRSYLT	PGDSSSGWTAGAAAYYVGYL	270
12	GKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLALHRSYLT	PGDSSSGWTAGAAAYYVGYL	270
13	GKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLALHRSYLT	PGDSSSGWTAGAAAYYVGYL	270
14	GKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRGLPQGFSALEPLVDLPIGINITRFQTL - - LHRSYLT	PGDSSSGWTAGAAAYYVGYL	268

QPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISN													
1	-	-	-	-	-	-	-	-	-	-	-	-	3
2	-	-	-	-	-	-	-	-	-	-	-	-	5
3	-	-	-	-	-	-	-	-	-	-	-	-	
4	-	-	-	-	-	-	-	-	-	-	-	-	2
5	-	-	-	-	-	-	-	-	-	-	-	-	5
6	Q	P	R	T	F	L	L	K	Y	N	E	N	360
7	Q	P	R	T	F	L	L	K	Y	N	E	N	360
8	Q	P	R	T	F	L	L	K	Y	N	E	N	360
9	Q	P	R	T	F	L	L	K	Y	N	E	N	360
10	Q	P	R	T	F	L	L	K	Y	N	E	N	360
11	Q	P	R	T	F	L	L	K	Y	N	E	N	360
12	Q	P	R	T	F	L	L	K	Y	N	E	N	360
13	Q	P	R	T	F	L	L	K	Y	N	E	N	360
14	Q	P	R	T	F	L	L	K	Y	N	E	N	358
CVADYSVLVNSASFSTFKCYGVSP TKLNDLCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYN													
1	-	-	-	-	-	-	-	-	-	-	-	-	3
2	-	-	-	-	-	-	-	-	-	N	-	-	6
3	-	-	-	-	-	-	-	-	-	-	-	-	
4	-	-	-	-	-	-	-	-	-	-	-	-	2
5	-	-	-	-	-	-	-	-	-	T	-	-	6
6	C	V	A	D	Y	S	V	L	V	N	S	A	450
7	C	V	A	D	Y	S	V	L	V	N	S	A	450
8	C	V	A	D	Y	S	V	L	V	N	S	A	450
9	C	V	A	D	Y	S	V	L	V	N	S	A	450
10	C	V	A	D	Y	S	V	L	V	N	S	A	450
11	C	V	A	D	Y	S	V	L	V	N	S	A	450
12	C	V	A	D	Y	S	V	L	V	N	S	A	450
13	C	V	A	D	Y	S	V	L	V	N	S	A	450
14	C	V	A	D	Y	S	V	L	V	N	S	A	448

[illegible]

	FNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLT																																
1	-----D-----G-----																															8	
2	-----G-----																															9	
3	-----G-----																															2	
4	-----G-----																															4	
5	-----G-----																															9	
6	FNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLT																																630
7	FNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLT																																630
8	FNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLT																																630
9	FNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLT																																630
10	FNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLT																																630
11	FNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLT																																630
12	FNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLT																																630
13	FNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLT																																630
14	FNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQGVNCTEVPVAIHADQLT																																628

	PTWRVYSTGSNVFQTRAGCLIGA	EHVNNSYEC	DIPIGAGICASYQTQTNSP	XRA	XSVASQSIIAYTMSLGA	ENSVAYSNN	NSIAIPTNFTI	
1	-----H-----I-----							10
2	-----V-----							10
3	-----							2
4	-----							4
5	-----Y-----							10
6	PTWRVYSTGSNVFQTRAGCLIGA	EHVNNSYEC	DIPIGAGICASYQTQTNSP	RRAR	SVASQSIIAYTMSLGA	ENSVAYSNN	NSIAIPTNFTI	720
7	PTWRVYSTGSNVFQTRAGCLIGA	EHVNNSYEC	DIPIGAGICASYQTQTNSP	RRAR	SVASQSIIAYTMSLGA	ENSVAYSNN	NSIAIPTNFTI	720
8	PTWRVYSTGSNVFQTRAGCLIGA	EHVNNSYEC	DIPIGAGICASYQTQTNSP	RRAR	SVASQSIIAYTMSLGA	ENSVAYSNN	NSIAIPTNFTI	720
9	PTWRVYSTGSNVFQTRAGCLIGA	EHVNNSYEC	DIPIGAGICASYQTQTNSP	RRAR	SVASQSIIAYTMSLGA	ENSVAYSNN	NSIAIPTNFTI	720
10	PTWRVYSTGSNVFQTRAGCLIGA	EHVNNSYEC	DIPIGAGICASYQTQTNSP	SRAG	SVASQSIIAYTMSLGA	ENSVAYSNN	NSIAIPTNFTI	720
11	PTWRVYSTGSNVFQTRAGCLIGA	EHVNNSYEC	DIPIGAGICASYQTQTNSP	GGAG	SVASQSIIAYTMSLGA	ENSVAYSNN	NSIAIPTNFTI	720
12	PTWRVYSTGSNVFQTRAGCLIGA	EHVNNSYEC	DIPIGAGICASYQTQTNSP	RRAR	SVASQSIIAYTMSLGA	ENSVAYSNN	NSIAIPTNFTI	720
13	PTWRVYSTGSNVFQTRAGCLIGA	EHVNNSYEC	DIPIGAGICASYQTQTNSP	RRAR	SVASQSIIAYTMSLGA	ENSVAYSNN	NSIAIPTNFTI	720
14	PTWRVYSTGSNVFQTRAGCLIGA	EHVNNSYEC	DIPIGAGICASYQTQTNSP	RRAR	SVASQSIIAYTMSLG	VENS	VAYSNNNSIAIPTNFTI	718

	SVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPS	
1	-----	10
2	-----	10
3	-----	2
4	-----	4
5	-----	10
6	SVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPS	810
7	SVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPS	810
8	SVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPS	810
9	SVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPS	810
10	SVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPS	810
11	SVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPS	810
12	SVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPS	810
13	SVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPS	810
14	SVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPS	808

	KPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDemiaQYTSALLAGTITSGWTFGAGAALQIPFAM	
1	-----	10
2	-----	10
3	-----	2
4	-----	4
5	-----	10
6	KPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDemiaQYTSALLAGTITSGWTFGAGAALQIPFAM	900
7	KPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDemiaQYTSALLAGTITSGWTFGAGAALQIPFAM	900
8	KPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDemiaQYTSALLAGTITSGWTFGAGAALQIPFAM	900
9	KPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDemiaQYTSALLAGTITSGWTFGAGAALQIPFAM	900
10	KPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDemiaQYTSALLAGTITSGWTFGAGAALQIPFAM	900
11	KPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDemiaQYTSALLAGTITSGWTFGAGAALQIPFAM	900
12	KPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDemiaQYTSALLAGTITSGWTFGAGAALQIPFAM	900
13	KPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDemiaQYTSALLAGTITSGWTFGAGAALQIPFAM	900
14	KPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDemiaQYTSALLAGTITSGWTFGAGAALQIPFAM	898

[illegible]

VQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPA													
1	-	-	-	-	-	-	-	-	-	-	-	-	11
2	-	-	-	-	-	-	-	-	-	-	-	-	10
3	-	-	-	-	-	-	-	-	-	-	-	-	2
4	-	-	-	-	-	-	-	-	-	-	-	-	4
5	-	-	-	-	-	-	I	-	-	-	-	-	11
6	V	Q	I	D	R	L	I	T	G	R	L	Q	1080
7	V	Q	I	D	R	L	I	T	G	R	L	Q	1080
8	V	Q	I	D	R	L	I	T	G	R	L	Q	1080
9	V	Q	I	D	R	L	I	T	G	R	L	Q	1080
10	V	Q	I	D	R	L	I	T	G	R	L	Q	1080
11	V	Q	I	D	R	L	I	T	G	R	L	Q	1080
12	V	Q	I	D	R	L	I	T	G	R	L	Q	1080
13	V	Q	I	D	R	L	I	T	G	R	L	Q	1080
14	V	Q	I	D	R	L	I	T	G	R	L	Q	1078
ICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDIS													
1	-	-	-	-	-	-	H	-	-	-	-	-	12
2	-	-	-	-	-	-	-	-	-	-	-	-	10
3	-	-	-	-	-	-	-	-	-	-	-	-	2
4	-	-	-	-	-	-	-	-	-	-	-	-	4
5	-	-	-	-	-	-	-	-	-	-	-	-	11
6	I	C	H	D	G	K	A	H	F	P	R	E	1170
7	I	C	H	D	G	K	A	H	F	P	R	E	1170
8	I	C	H	D	G	K	A	H	F	P	R	E	1170
9	I	C	H	D	G	K	A	H	F	P	R	E	1170
10	I	C	H	D	G	K	A	H	F	P	R	E	1170
11	I	C	H	D	G	K	A	H	F	P	R	E	1170
12	I	C	H	D	G	K	A	H	F	P	R	E	1170
13	I	C	H	D	G	K	A	H	F	P	R	E	1170
14	I	C	H	D	G	K	A	H	F	P	R	E	1168

[illegible][illegible]

Consensus Threshold: >50%

Compare to: the consensus

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

Created: 28 Jun 2021

Last Modified: 28 Jun 2021