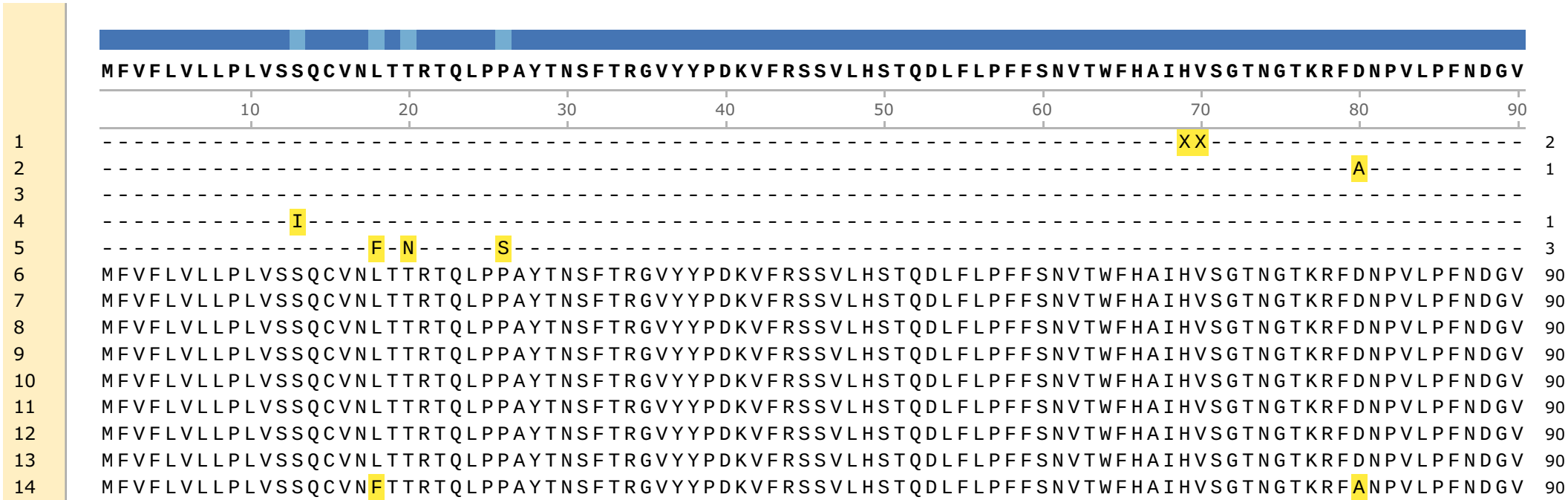
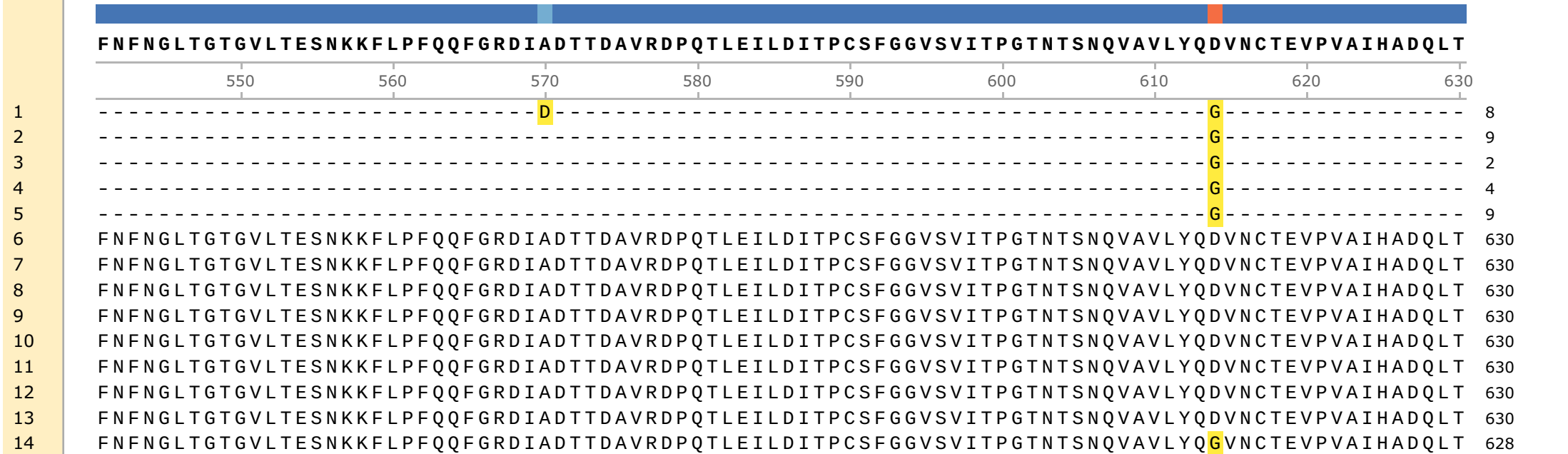
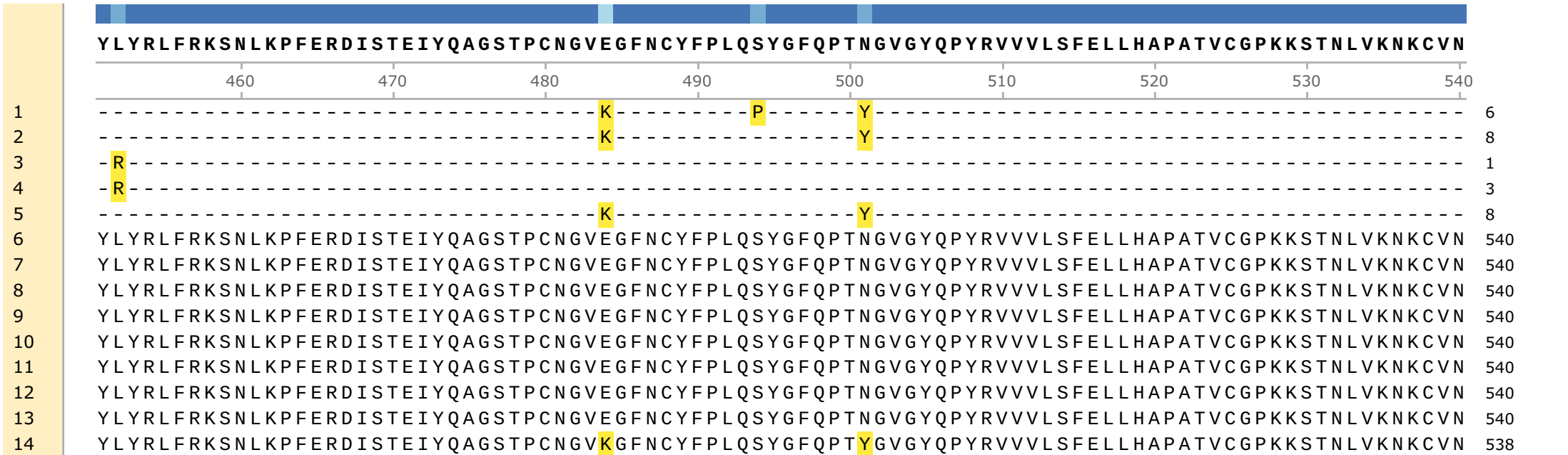


Consensus

- 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



[illegible][illegible]



PTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPXRAXSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNFTI														
640650660670680690700710720														
1	-----H-----I-----													10
2	-----V-----													10
3	-----													2
4	-----													4
5	-----Y-----													10
6	PTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNFTI													720
7	PTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNFTI													720
8	PTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNFTI													720
9	PTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNFTI													720
10	PTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNFTI													720
11	PTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPGGAGSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNFTI													720
12	PTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNFTI													720
13	PTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNFTI													720
14	PTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGVENSVAYSNNSIAIPTNFTI													718

SVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPS													
	730	740	750	760	770	780	790	800	810				
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			

KPSKR SFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDemiaQYTSALLAGTITSGWTFGAGAALQIPFAM													
	820	830	840	850	860	870	880	890	900				
1	-----	-----	-----	-----	-----	-----	-----	-----	-----				10
2	-----	-----	-----	-----	-----	-----	-----	-----	-----				10
3	-----	-----	-----	-----	-----	-----	-----	-----	-----				2
4	-----	-----	-----	-----	-----	-----	-----	-----	-----				4
5	-----	-----	-----	-----	-----	-----	-----	-----	-----				10
6	KPSKR	SFIED	LLFNK	VTLAD	AGFIK	QYGDCL	GDIAARD	LICAQK	FNGLTV	LPPLL	TDemia	QYTSALL	AGTITSGWTFGAGAALQIPFAM 900
7	KPSKR	SFIED	LLFNK	VTLAD	AGFIK	QYGDCL	GDIAARD	LICAQK	FNGLTV	LPPLL	TDemia	QYTSALL	AGTITSGWTFGAGAALQIPFAM 900
8	KPSKR	SFIED	LLFNK	VTLAD	AGFIK	QYGDCL	GDIAARD	LICAQK	FNGLTV	LPPLL	TDemia	QYTSALL	AGTITSGWTFGAGAALQIPFAM 900
9	KPSKR	SFIED	LLFNK	VTLAD	AGFIK	QYGDCL	GDIAARD	LICAQK	FNGLTV	LPPLL	TDemia	QYTSALL	AGTITSGWTFGAGAALQIPFAM 900
10	KPSKR	SFIED	LLFNK	VTLAD	AGFIK	QYGDCL	GDIAARD	LICAQK	FNGLTV	LPPLL	TDemia	QYTSALL	AGTITSGWTFGAGAALQIPFAM 900
11	KPSKR	SFIED	LLFNK	VTLAD	AGFIK	QYGDCL	GDIAARD	LICAQK	FNGLTV	LPPLL	TDemia	QYTSALL	AGTITSGWTFGAGAALQIPFAM 900
12	KPSKR	SFIED	LLFNK	VTLAD	AGFIK	QYGDCL	GDIAARD	LICAQK	FNGLTV	LPPLL	TDemia	QYTSALL	AGTITSGWTFGAGAALQIPFAM 900
13	KPSKR	SFIED	LLFNK	VTLAD	AGFIK	QYGDCL	GDIAARD	LICAQK	FNGLTV	LPPLL	TDemia	QYTSALL	AGTITSGWTFGAGAALQIPFAM 900
14	KPSKR	SFIED	LLFNK	VTLAD	AGFIK	QYGDCL	GDIAARD	LICAQK	FNGLTV	LPPLL	TDemia	QYTSALL	AGTITSGWTFGAGAALQIPFAM 898

QMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDXXEAE													
	910	920	930	940	950	960	970	980	990				
1	-----	-----	-----	-----	-----	-----	-----	A-----	-----				11
2	-----	-----	-----	-----	-----	-----	-----	-----	-----				10
3	-----	-----	-----	-----	-----	-----	-----	-----	-----				2
4	-----	-----	-----	-----	-----	-----	-----	-----	-----				4
5	-----	-----	-----	-----	-----	-----	-----	-----	-----				10
6	QMAYR	FNGIG	VTQNV	LYENQ	KLIANQ	FNSAIG	KIQDSL	SSTASAL	GKLQDV	VNQNAQ	ALNTLV	KQLSSN	FGAISSVLNDILSRD KVEAE 990
7	QMAYR	FNGIG	VTQNV	LYENQ	KLIANQ	FNSAIG	KIQDSL	SSTASAL	GKLQDV	VNQNAQ	ALNTLV	KQLSSN	FGAISSVLNDILSRD KVEAE 990
8	QMAYR	FNGIG	VTQNV	LYENQ	KLIANQ	FNSAIG	KIQDSL	SSTASAL	GKLQDV	VNQNAQ	ALNTLV	KQLSSN	FGAISSVLNDILSRD PPEAE 990
9	QMAYR	FNGIG	VTQNV	LYENQ	KLIANQ	FNSAIG	KIQDSL	SSTASAL	GKLQDV	VNQNAQ	ALNTLV	KQLSSN	FGAISSVLNDILSRD PPEAE 990
10	QMAYR	FNGIG	VTQNV	LYENQ	KLIANQ	FNSAIG	KIQDSL	SSTASAL	GKLQDV	VNQNAQ	ALNTLV	KQLSSN	FGAISSVLNDILSRD PPEAE 990
11	QMAYR	FNGIG	VTQNV	LYENQ	KLIANQ	FNSAIG	KIQDSL	SSTASAL	GKLQDV	VNQNAQ	ALNTLV	KQLSSN	FGAISSVLNDILSRD PPEAE 990
12	QMAYR	FNGIG	VTQNV	LYENQ	KLIANQ	FNSAIG	KIQDSL	SSTASAL	GKLQDV	VNQNAQ	ALNTLV	KQLSSN	FGAISSVLNDILSRD KVEAE 990
13	QMAYR	FNGIG	VTQNV	LYENQ	KLIANQ	FNSAIG	KIQDSL	SSTASAL	GKLQDV	VNQNAQ	ALNTLV	KQLSSN	FGAISSVLNDILSRD KVEAE 990
14	QMAYR	FNGIG	VTQNV	LYENQ	KLIANQ	FNSAIG	KIQDSL	SSTASAL	GKLQDV	VNQNAQ	ALNTLV	KQLSSN	FGAISSVLNDILSRD KVEAE 988

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13
14



VQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPA



1	-----	11
2	-----	10
3	-----	2
4	-----	4
5	-----	11
6	VQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPA	1080
7	VQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPA	1080
8	VQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPA	1080
9	VQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPA	1080
10	VQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPA	1080
11	VQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPA	1080
12	VQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPA	1080
13	VQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPA	1080
14	VQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPA	1078



ICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDIS



1	-----	12
2	-----	10
3	-----	2
4	-----	4
5	-----	11
6	ICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDIS	1170
7	ICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDIS	1170
8	ICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDIS	1170
9	ICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDIS	1170
10	ICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDIS	1170
11	ICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDIS	1170
12	ICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDIS	1170
13	ICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDIS	1170
14	ICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDIS	1168

	GINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCCLKGCCSCGSCCKFDEDD									
	1180	1190	1200	1210	1220	1230	1240	1250	1260	
1	-----	N-----	-----	-----	-----	-----	-----	-----	-----	13
2	-----	-----	-----	-----	-----	-----	-----	-----	-----	10
3	-----	-----	-----	-----	-----	-----	-----	-----	-----	2
4	-----	-----	-----	-----	-----	-----	-----	-----	-----	4
5	-----	-----	-----	-----	-----	-----	-----	-----	-----	11
6	GINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCCLKGCCSCGSCCKFDEDD									1260
7	GINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCCLKGCCSCGSCCKFDEDD									1260
8	GINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCCLKGCCSCGSCCKFDEDD									1260
9	GINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCCLKGCCSCGSCCKFDEDD									1260
10	GINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCCLKGCCSCGSCCKFDEDD									1260
11	GINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCCLKGCCSCGSCCKFDEDD									1260
12	GINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCCLKGCCSCGSCCKFDEDD									1260
13	GINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCCLKGCCSCGSCCKFDEDD									1260
14	GINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCCLKGCCSCGSCCKFDEDD									1258

	SEPVLKGVKLHYT---									
	1270									
1	-----									13
2	-----									10
3	-----									2
4	-----									4
5	-----									11
6	SEPVLKGVKLHYT---									1273
7	SEPVLKGVKLHYT---									1273
8	SEPVLKGVKLHYT---									1273
9	SEPVLKGVKLHYT---									1273
10	SEPVLKGVKLHYT---									1273
11	SEPVLKGVKLHYT---									1273
12	SEPVLKGVKLHYT---									1273
13	SEPVLKGVKLHYT---									1273
14	SEPVLKGVKLHYT---									1271

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