

In Silico Analysis of SARS-CoV2 Spike Proteins of Different Field Variants

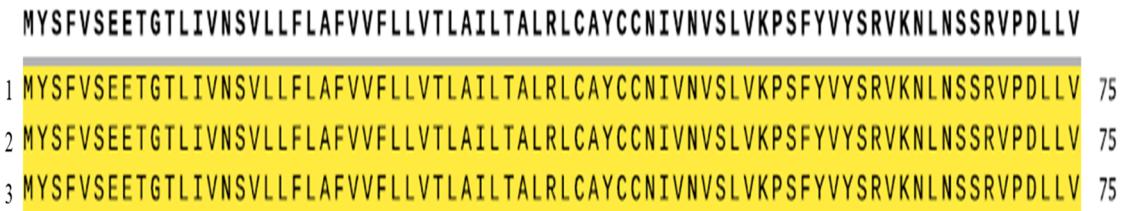
Muhammad Haseeb *, Afreenish Amir and Aamer Ikram

Department of Microbiology National Institute of Health, Islamabad 45500, Pakistan

* Correspondence: muhammadhaseebtariq19@gmail.com

Supplementary Figures

1. Envelope Protein



MYSFVSEETGTLIVNSVLLFLAFVVFLVTLAILTALRLCAYCCNIVNVSLVKPSFYVYSRVKNLNSSRVPDLLV
1 MYSFVSEETGTLIVNSVLLFLAFVVFLVTLAILTALRLCAYCCNIVNVSLVKPSFYVYSRVKNLNSSRVPDLLV 75
2 MYSFVSEETGTLIVNSVLLFLAFVVFLVTLAILTALRLCAYCCNIVNVSLVKPSFYVYSRVKNLNSSRVPDLLV 75
3 MYSFVSEETGTLIVNSVLLFLAFVVFLVTLAILTALRLCAYCCNIVNVSLVKPSFYVYSRVKNLNSSRVPDLLV 75

Figure S1. Schematic view of contigs of the envelope protein of 1. Alpha variant (B.1.1.7) (UDQ41840.1) and 2. Delta variant (B.1.617.21) (UDU36748.1) of SARS-CoV-2 with 3. reference strain (Wuhan) (YP_009724392.1).

2. Membrane Protein

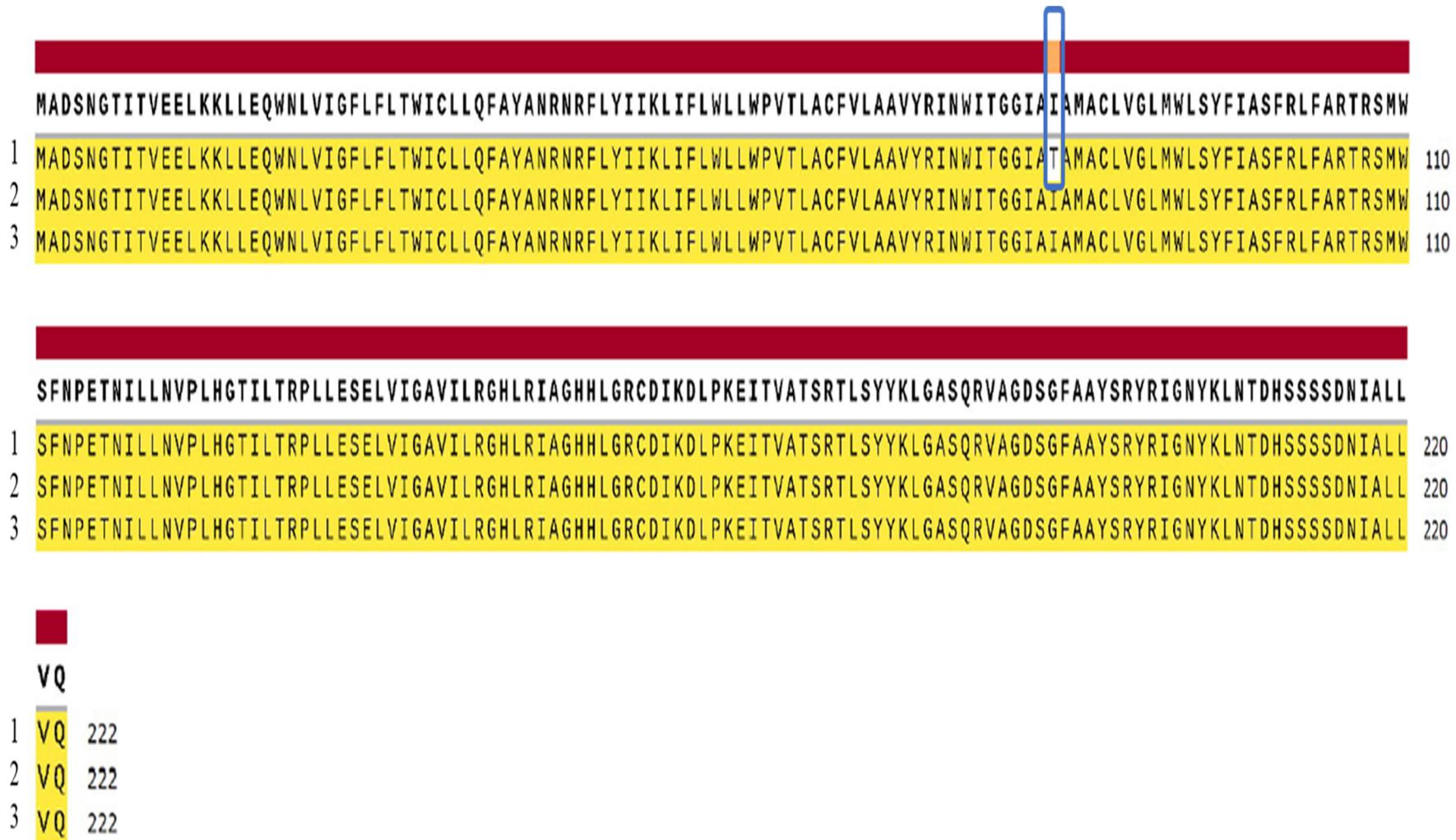


Figure S2. Schematic view of contigs of the membrane glycoprotein of 1. Alpha Variant (B.1.1.7) (UDQ41841.1) and 2. Delta Variant (B.1.617.21) (UDU36749.1) of SARs-CoV-2 with 3. reference strain (Wuhan) (YP_009724393.1).

3. Nucleocapsid Phosphoprotein

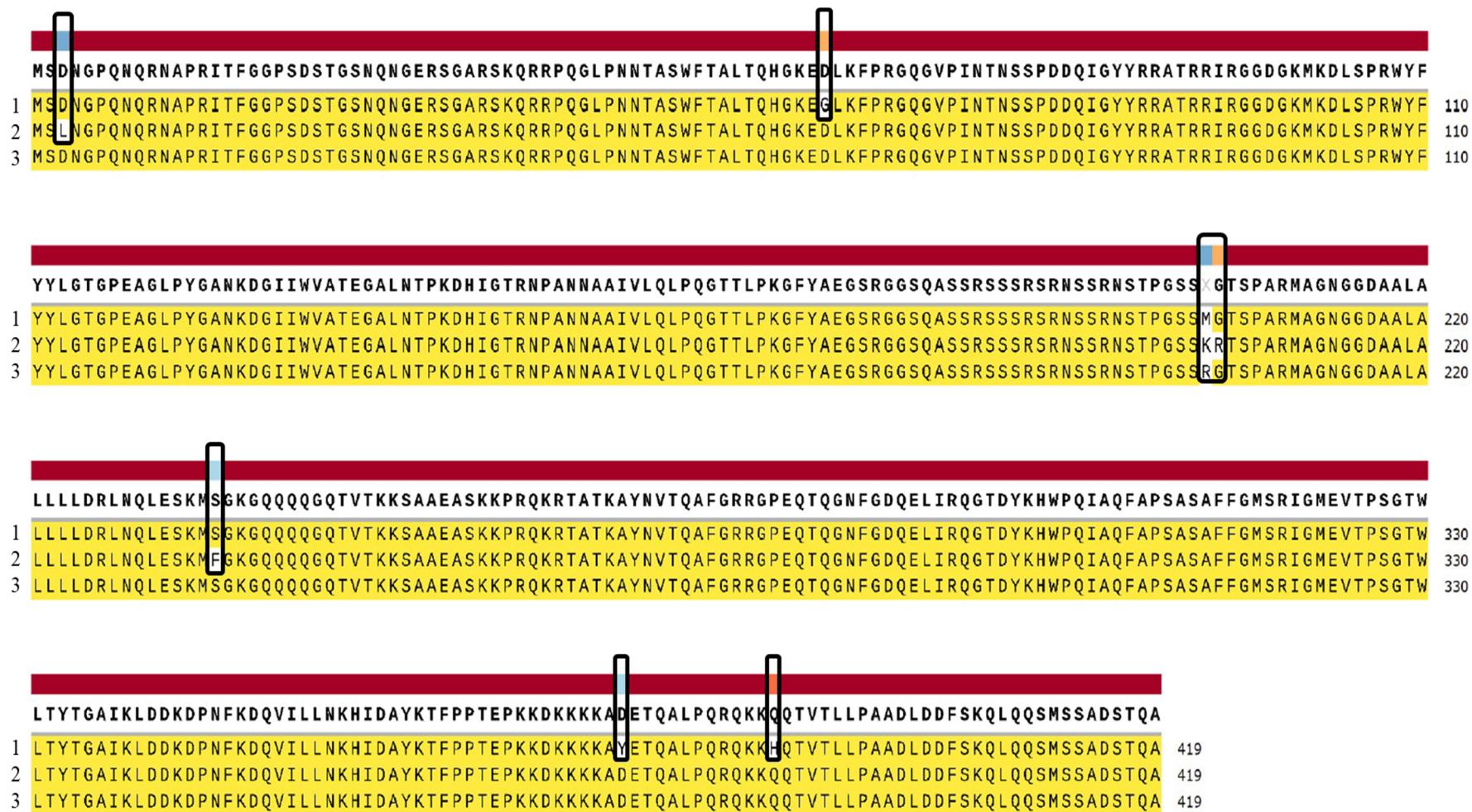


Figure S3. Schematic view of contigs of the Nucleocapsid phosphoprotein of 1. Alpha Variant (B.1.1.7) (UDQ41846.1) and 2. Delta Variant (B.1.617.21) (UDU36754.1) of SARs-CoV-2 with 3. reference strain (Wuhan) (YP_009724397.2).

4. ORF10 protein

	MGYINVFAFPFTIYSLLLCRMNSRNYIAQVDVVNFNLT	
1	MGYINVFAFPFTIYSLLLCRMNSRNYIAQVDVVNFNLT	38
2	MGYINVFAFPFTIYSLLLCRMNSRNYIAQVDVVNFNLT	38
3	MGYINVFAFPFTIYSLLLCRMNSRNYIAQVDVVNFNLT	38

Figure S4. Schematic view of contigs of the ORF10 protein of 1. Alpha Variant (B.1.1.7) (UDQ41847.1) and 2. Delta Variant (B.1.617.21) (UDU36755.1) of SARs-CoV-2 with 3. reference Strain (Wuhan) (YP_009725255.1).

5. ORF1a polyprotein

MESLVPGFNEKTHVQLSLPVLQVRDVLRGFGDSVEEVLSLEARQHLKDGTGCLVEVEKGVLPLQEQPYVFIKRSDARTAPHGHVMVELVAELEGIQYGRSGETLGVLVPH

1 MESLVPGFNEKTHVQLSLPVLQVRDVLRGFGDSVEEVLSLEARQHLKDGTGCLVEVEKGVLPLQEQPYVFIKRSDARTAPHGHVMVELVAELEGIQYGRSGETLGVLVPH 110

2 MESLVPGFNEKTHVQLSLPVLQVRDVLRGFGDSVEEVLSLEARQHLKDGTGCLVEVEKGVLPLQEQPYVFIKRSDARTAPHGHVMVELVAELEGIQYGRSGETLGVLVPH 110

3 MESLVPGFNEKTHVQLSLPVLQVRDVLRGFGDSVEEVLSLEARQHLKDGTGCLVEVEKGVLPLQEQPYVFIKRSDARTAPHGHVMVELVAELEGIQYGRSGETLGVLVPH 110

VGEIPVAYRKVLLRKNGNKGAGGHSYGADLKSFDLGDELGTDPYEDFQENWNTKHSSGVTRELMRELNGGAYTRYVDNNFCGPDGYPLECIKDLLARAGKASCTLSEQLD

1 VGEIPVAYRKVLLRKNGNKGAGGHSYGADLKSFDLGDELGTDPYEDFQENWNTKHSSGVTRELMRELNGGAYTRYVDNNFCGPDGYPLECIKDLLARAGKASCTLSEQLD 220

2 VGEIPVAYRKVLLRKNGNKGAGGHSYGADLKSFDLGDELGTDPYEDFQENWNTKHSSGVTRELMRELNGGAYTRYVDNNFCGPDGYPLECIKDLLVRAKGASCTLSEQLD 220

3 VGEIPVAYRKVLLRKNGNKGAGGHSYGADLKSFDLGDELGTDPYEDFQENWNTKHSSGVTRELMRELNGGAYTRYVDNNFCGPDGYPLECIKDLLARAGKASCTLSEQLD 220

FIDTKRGVYCCREHEHEIAWYTERSEKSYELQTPFEIKLAKKFDTFNGECPNFVPLNSIIKTIQPRVEKKLDGMGRIRSVYPVASPNECNQMCLSTLMKCDHCGETS

1 FIDTKRGVYCCREHEHEIAWYTERSEKSYELQTPFEIKLAKKFDTFNGECPNFVPLNSIIKTIQPRVEKKLDGMGRIRSVYPVASPNECNQMCLSTLMKCDHCGETS 330

2 FIDTKRGVYCCREHEHEIAWYTERSEKSYELQTPFEIKLAKKFDTFNGECPNFVPLNSIIKTIQPRVEKKLDGMGRIRSVYPVASPNECNQMCLSTLMKCDHCGETS 330

3 FIDTKRGVYCCREHEHEIAWYTERSEKSYELQTPFEIKLAKKFDTFNGECPNFVPLNSIIKTIQPRVEKKLDGMGRIRSVYPVASPNECNQMCLSTLMKCDHCGETS 330

WQTGDFVKATCEFCGTENLTKEGATTGYLPQNAVVKIYCPACHNSEVGPEHSLAEYHNESGLKTILRKGGRTIAFGGCVF SYVGCHNK CAYWVPRASANIGCNHTGVVG

1 WQTGDFVKATCEFCGTENLTKEGATTGYLPQNAVVKIYCPACHNSEVGPEHSLAEYHNESGLKTILRKGGRTIAFGGCVF SYVGCHNK CAYWVPRASANIGCNHTGVVG 440

2 WQTGDFVKATCEFCGTENLTKEGATTGYLPQNAVVKIYCPACHNSEVGPEHSLAEYHNESGLKTILRKGGRTIAFGGCVF SYVGCHNK CAYWVPRASANIGCNHTGVVG 440

3 WQTGDFVKATCEFCGTENLTKEGATTGYLPQNAVVKIYCPACHNSEVGPEHSLAEYHNESGLKTILRKGGRTIAFGGCVF SYVGCHNK CAYWVPRASANIGCNHTGVVG 440

EGSEGLNDNLLEILQKEKVNIIVGDFKLNEEIAILASFASATSAFVETVKGLDYKAFKQIVESCGNFVTKGAKKGAWNIGEQKSILSPLYAFASEAARVRSIFSR

1 EGSEGLNDNLLEILQKEKVNIIVGDFKLNEEIAILASFASATSAFVETVKGLDYKAFKQIVESCGNFVTKGAKKGAWNIGEQKSILSPLYAFASEAARVRSIFSR 550

2 EGSEGLNDNLLEILQKEKVNIIVGDFKLNEEIAILASFASATSAFVETVKGLDYKAFKQIVESCGNFVTKGAKKGAWNIGEQKSILSPLYAFASEAARVRSIFSR 550

3 EGSEGLNDNLLEILQKEKVNIIVGDFKLNEEIAILASFASATSAFVETVKGLDYKAFKQIVESCGNFVTKGAKKGAWNIGEQKSILSPLYAFASEAARVRSIFSR 550

TLETAQNSVRVLQKAITILDGISQYSLRLIDAMMFTSDLATNNLVVMAYITGGVVQLTSQWLTLNIFGTVYEKLKPVLWLEEKFKEGVEFLRDGWEIVKFISTCACEIV

1 TLETAQNSVRVLQKAITILDGISQYSLRLIDAMMFTSDLATNNLVVMAYITGGVVQLTSQWLTLNIFGTVYEKLKPVLWLEEKFKEGVEFLRDGWEIVKFISTCACEIV 660

2 TLETAQNSVRVLQKAITILDGISQYSLRLIDAMMFTSDLATNNLVVMAYITGGVVQLTSQWLTLNIFGTVYEKLKPVLWLEEKFKEGVEFLRDGWEIVKFISTCACEIV 660

3 TLETAQNSVRVLQKAITILDGISQYSLRLIDAMMFTSDLATNNLVVMAYITGGVVQLTSQWLTLNIFGTVYEKLKPVLWLEEKFKEGVEFLRDGWEIVKFISTCACEIV 660

GGQIVTCAKEIKEVQTFFKLVNKFLALCADSIIIGGAKLKALNLGETFVTHSKGLYRKCVKSREETGLLMPKAPKEIIFLEGETLPTEVLTEEVVLKTGDLQPLEQPT

1 GGQIVTCAKEIKEVQTFFKLVNKFLALCADSIIIGGAKLKALNLGETFVTHSKGLYRKCVKSREETGLLMPKAPKEIIFLEGETLPTEVLTEEVVLKTGDLQPLEQPT 770

2 GGQIVTCAKEIKEVQTFFKLVNKFLALCADSIIIGGAKLKALNLGETFVTHSKGLYRKCVKSREETGLLMPKAPKEIIFLEGETLPTEVLTEEVVLKTGDLQPLEQPT 770

3 GGQIVTCAKEIKEVQTFFKLVNKFLALCADSIIIGGAKLKALNLGETFVTHSKGLYRKCVKSREETGLLMPKAPKEIIFLEGETLPTEVLTEEVVLKTGDLQPLEQPT 770

SEAVEAPLVGTPVCINGMLLEIKDTEKYCALAPNMVTNNFTLKGGA
PTKVTFGDDTVIEVQGYKSVNITFELDERIDKVLNEKCSAYTVELGTEVNEFACVVADAVI

1 SEAVEAPLVGTPVCINGMLLEIKDTEKYCALAPNMVTNNFTLKGGA
PTKVTFGDDTVIEVQGYKSVNITFELDERIDKVLNEKCSAYTVELGTEVNEFACVVADAVI 880

2 SEAVEAPLVGTPVCINGMLLEIKDTEKYCALAPNMVTNNFTLKGGA
PTKVTFGDDTVIEVQGYKSVNITFELDERIDKVLNEKCSAYTVELGTEVNEFACVVADAVI 880

3 SEAVEAPLVGTPVCINGMLLEIKDTEKYCALAPNMVTNNFTLKGGA
PTKVTFGDDTVIEVQGYKSVNITFELDERIDKVLNEKCSAYTVELGTEVNEFACVVADAVI 880

KTLPVSELLTPLGIDLDEWSMATYYLFDESGEFLASHMYCSFYPPDEDEEEGDCEEEEFPSTQYEYGTEDDYQGKPLEFGATSAALQPEEEQEEWLDDDSQQTVGQ

1 KTLQPSELLTPLGIDLDEWSMATYYLFDESGEFLASHMYCSFYPPDEDEEEGDCEEEEFPSTQYEYGTEDDYQGKPLEFGATSAALQPEEEQEEWLDDDSQQTVGQ 990

2 KTLQPSELLTPLGIDLDEWSMATYYLFDESGEFLASHMYCSFYPPDEDEEEGDCEEEEFPSTQYEYGTEDDYQGKPLEFGATSAALQPEEEQEEWLDDDSQQTVGQ 990

3 KTLQPSELLTPLGIDLDEWSMATYYLFDESGEFLASHMYCSFYPPDEDEEEGDCEEEEFPSTQYEYGTEDDYQGKPLEFGATSAALQPEEEQEEWLDDDSQQTVGQ 990

QDGSEDNQTTTIIQTIVEVQPQLEMEITPVVQTIIEVNSFSGYLKLTNDVYIKNADIVEEAKVKPTVVVNAANVYLKHGGGVAGALNKATNNAMQVESDDYIATNGPLKVG

1 QDGSEDNQTTTIIQTIVEVQPQLEMEITPVVQTIIEVNSFSGYLKLTNDVYIKNADIVEEAKVKPTVVVNAANVYLKHGGGVAGALNKATNNAMQVESDDYIATNGPLKVG 1100

2 QDGSEDNQTTTIIQTIVEVQPQLEMEITPVVQTIIEVNSFSGYLKLTNDVYIKNADIVEEAKVKPTVVVNAANVYLKHGGGVAGALNKATNNAMQVESDDYIATNGPLKVG 1100

3 QDGSEDNQTTTIIQTIVEVQPQLEMEITPVVQTIIEVNSFSGYLKLTNDVYIKNADIVEEAKVKPTVVVNAANVYLKHGGGVAGALNKATNNAMQVESDDYIATNGPLKVG 1100

GSCVLSGHNLAKHCLHVVGPNVNKGEDIQLLKSAYENFNQHEVLLAPLLSAGIFGADPIHSRVCVDTVRTNVYLAVFDFKNLYDKLVSSFLEMKSEKQVEQKIAEIPKEE

1 GSCVLSGHNLAKHCLHVVGPNVNKGEDIQLLKSAYENFNQHEVLLAPLLSAGIFGADPIHSRVCVDTVRTNVYLAVFDFKNLYDKLVSSFLEMKSEKQVEQKIAEIPKEE 1210

2 GSCVLSGHNLAKHCLHVVGPNVNKGEDIQLLKSAYENFNQHEVLLAPLLSAGIFGADPIHSRVCVDTVRTNVYLAVFDFKNLYDKLVSSFLEMKSEKQVEQKIAEIPKEE 1210

3 GSCVLSGHNLAKHCLHVVGPNVNKGEDIQLLKSAYENFNQHEVLLAPLLSAGIFGADPIHSRVCVDTVRTNVYLAVFDFKNLYDKLVSSFLEMKSEKQVEQKIAEIPKEE 1210

VKPFITESKPSVEQRKQDDKKIKACVEEVTTLEETKFLTENLLYIDINGNLHPDSATLVDIDITFLKKDAPYIVGDVVQEGVLTAVVVIPTKKAGGTTEMLAKALRKV

1 VKPFITESKPSVEQRKQDDKKIKACVEEVTTLEETKFLTENLLYIDINGNLHPDSATLVDIDITFLKKDAPYIVGDVVQEGVLTAVVVIPTKKAGGTTEMLAKALRKV 1320

2 VKPFITESKPSVEQRKQDDKKIKACVEEVTTLEETKFLTENLLYIDINGNLHPDSATLVDIDITFLKKDAPYIVGDVVQEGVLTAVVVIPTKKAGGTTEMLAKALRKV 1320

3 VKPFITESKPSVEQRKQDDKKIKACVEEVTTLEETKFLTENLLYIDINGNLHPDSATLVDIDITFLKKDAPYIVGDVVQEGVLTAVVVIPTKKAGGTTEMLAKALRKV 1320

PTDNYITTYPGQGLNGYTVVEAKTVLKCKSAFYILPSIISNEKQEILGTVSWNLREMLAHAEETRKLMPVCVETKAIVSTIQRKYKGIKIQEGVVVDYGARFYFYSKTT
1 PTDNYITTYPGQGLNGYTVVEAKTVLKCKSAFYILPSIISNEKQEILGTVSWNLREMLAHAEETRKLMPVCVETKAIVSIIQRKYKGIKIQEGVVVDYGARFYFYSKTT 1430
2 PTDNYITTYPGQGLNGYTVVEAKTVLKCKSAFYILPSIISNEKQEILGTVSWNLREMLAHAEETRKLMPVCVETKAIVSTIQRKYKGIKIQEGVVVDYGARFYFYSKTT 1430
3 PTDNYITTYPGQGLNGYTVVEAKTVLKCKSAFYILPSIISNEKQEILGTVSWNLREMLAHAEETRKLMPVCVETKAIVSTIQRKYKGIKIQEGVVVDYGARFYFYSKTT 1430

VASLINTLNDLNETLVTMPLGYVTHGLNLEEAARYMRSLKVPATVSSPDAVTAYNGYLSSKTPEEHFIETISLAGSYKDWSYSQSTQLGIEFLKRGDKSVYYTSN
1 VASLINTLNDLNETLVTMPLGYVTHGLNLEEAARYMRSLKVPATVSSPDAVTAYNGYLSSKTPEEHFIETISLAGSYKDWSYSQSTQLGIEFLKRGDKSVYYTSN 1540
2 VASLINTLNDLNETLVTMPLGYVTHGLNLEEAARYMRSLKVPATVSSPDAVTAYNGYLSSKTPEEHFIETISLAGSYKDWSYSQSTQLGIEFLKRGDKSVYYTSN 1540
3 VASLINTLNDLNETLVTMPLGYVTHGLNLEEAARYMRSLKVPATVSSPDAVTAYNGYLSSKTPEEHFIETISLAGSYKDWSYSQSTQLGIEFLKRGDKSVYYTSN 1540

PTTFHLDGEVITFDNLKTLLSLREVRTIKVFTTVDNINLHTQVVDMSMTYQQFGPTYLDGADVTKIKPHNSHEGKTFYVLPNDTLRVEAFEYYHTTDPFLGRYMSAL
1 PTTFHLDGEVITFDNLKTLLSLREVRTIKVFTTVDNINLHTQVVDMSMTYQQFGPTYLDGADVTKIKPHNSHEGKTFYVLPNDTLRVEAFEYYHTTDPFLGRYMSAL 1650
2 PTTFHLDGEVITFDNLKTLLSLREVRTIKVFTTVDNINLHTQVVDMSMTYQQFGPTYLDGADVTKIKPHNSHEGKTFYVLPNDTLRVEAFEYYHTTDPFLGRYMSAL 1650
3 PTTFHLDGEVITFDNLKTLLSLREVRTIKVFTTVDNINLHTQVVDMSMTYQQFGPTYLDGADVTKIKPHNSHEGKTFYVLPNDTLRVEAFEYYHTTDPFLGRYMSAL 1650

NHTKKWKPQVNGLTSIKWADNNCYLATALLLQQIELKFNPALQDAYYRARAGEAANFCALILAYCNKTVGELGDVRETMYSYLFQHANLDSCKRVLNVVCKTCGQQQT
1 NHTKKWKPQVNGLTSIKWADNNCYLATALLLQQIELKFNPALQDAYYRARAGEAANFCALILAYCNKTVGELGDVRETMYSYLFQHANLDSCKRVLNVVCKTCGQQQT 1760
2 NHTKKWKPQVNGLTSIKWADNNCYLATALLLQQIELKFNPALQDAYYRARAGEAANFCALILAYCNKTVGELGDVRETMYSYLFQHANLDSCKRVLNVVCKTCGQQQT 1760
3 NHTKKWKPQVNGLTSIKWADNNCYLATALLLQQIELKFNPALQDAYYRARAGEAANFCALILAYCNKTVGELGDVRETMYSYLFQHANLDSCKRVLNVVCKTCGQQQT 1760

TLKGVEAVMYMGTLSYEQFKKGVQIPCTCGKQATKYLVQQESPFVMMSSAPPAQYELKHGFTCASEYTGNYQCGHYKHITSKETLYCIDGALLTKSSEYKGPITDVFYKE
1 TLKGVEAVMYMGTLSYEQFKKGVQIPCTCGKQATKYLVQQESPFVMMSSAPPAQYELKHGFTCASEYTGNYQCGHYKHITSKETLYCIDGALLTKSSEYKGPITDVFYKE 1870
2 TLKGVEAVMYMGTLSYEQFKKGVQIPCTCGKQATKYLVQQESPFVMMSSAPPAQYELKHGFTCASEYTGNYQCGHYKHITSKETLYCIDGALLTKSSEYKGPITDVFYKE 1870
3 TLKGVEAVMYMGTLSYEQFKKGVQIPCTCGKQATKYLVQQESPFVMMSSAPPAQYELKHGFTCASEYTGNYQCGHYKHITSKETLYCIDGALLTKSSEYKGPITDVFYKE 1870

NS~~TTT~~IKPVTVYKLDGVVCTEIDPKLDNYYKKDNSYFTEQPIDLVPNQPY~~P~~NASFDNFKFVCDNIKFADDLNQLTGYKKPASRELKVTFPDNGDVAIDYKHYTPSFK
1 NS~~TTT~~IKPVTVYKLDGVVCTEIDPKLDNYYKKDNSYFTEQPIDLVPNQPY~~Q~~NASFDNFKFVCDNIKFADDLNQLTGYKKPASRELKVTFPDNGDVAIDYKHYTPSFK 1980
2 NS~~T~~TTT~~I~~IKPVTVYKLDGVVCTEIDPKLDNYYKKDNSYFTEQPIDLVPNQPY~~P~~NASFDNFKFVCDNIKFADDLNQLTGYKKPASRELKVTFPDNGDVAIDYKHYTPSFK 1980
3 NS~~TTT~~IKPVTVYKLDGVVCTEIDPKLDNYYKKDNSYFTEQPIDLVPNQPY~~P~~NASFDNFKFVCDNIKFADDLNQLTGYKKPASRELKVTFPDNGDVAIDYKHYTPSFK 1980

KGAKLLHKPIVWHVNNATNKATYKPNTWCIRCLWSTKPVETSNSFDVLKSEDAQGMDNLACEDLKPVSEEVENPTI~~Q~~KDVLECNVKTTEVVGDIILKPANNSLKITEEV
1 KGAKLLHKPIVWHVNNATNKATYKPNTWCIRCLWSTKPVETSNSFDVLKSEDAQGMDNLACEDLKPVSEEVENPTI~~Q~~KDVLECNVKTTEVVGDIILKPANNSLKITEEV 2090
2 KGAKLLHKPIVWHVNNATNKATYKPNTWCIRCLWSTKPVETSNSFDVLKSEDAQGMDNLACEDLKPVSEEVENPTI~~Q~~KDVLECNVKTTEVVGDIILKPANNSLKITEEV 2090
3 KGAKLLHKPIVWHVNNATNKATYKPNTWCIRCLWSTKPVETSNSFDVLKSEDAQGMDNLACEDLKPVSEEVENPTI~~Q~~KDVLECNVKTTEVVGDIILKPANNSLKITEEV 2090

GHTDLMAAYVDNSSLT~~I~~KKPNELSRLV~~L~~GLKT~~L~~A~~H~~GLAAVNSVPWDTIAN~~Y~~AKPFLNKVV~~S~~TTTNIVTRCLNRVCTNYMPYFFT~~L~~LLQLCTFTRSTNSRIKASMPTTI~~A~~K
1 GHTDLMAAYVDNSSLT~~I~~KKPNELSRLV~~L~~GLKT~~L~~A~~H~~GLAAVNSVPWDTIAN~~Y~~AKPFLNKVV~~S~~TTTNIVTRCLNRVCTNYMPYFFT~~L~~LLQLCTFTRSTNSRIKASMPTTI~~A~~K 2200
2 GHTDLMAAYVDNSSLT~~I~~KKPNELSRLV~~L~~GLKT~~L~~A~~H~~GLAAVNSVPWDTIAN~~Y~~AKPFLNKVV~~S~~TTTNIVTRCLNRVCTNYMPYFFT~~L~~LLQLCTFTRSTNSRIKASMPTTI~~A~~K 2200
3 GHTDLMAAYVDNSSLT~~I~~KKPNELSRLV~~L~~GLKT~~L~~A~~H~~GLAAVNSVPWDTIAN~~Y~~AKPFLNKVV~~S~~TTTNIVTRCLNRVCTNYMPYFFT~~L~~LLQLCTFTRSTNSRIKASMPTTI~~A~~K 2200

NTVKSGKFCLEASFNYLKSPNFSKLINIIWFLLLSVCLGSLIYSTAALGVLMNLGMPSYCTGYREGYNSTNVTIATYCTGSIPCSVCLSGLDSDLTYPSETIQIT

1 NTVKSGKFCLEASFNYLKSPNFSKLINIIWFLLLSVCLGSLIYSTAALGVLMNLGMPSYCTGYREGYNSTNVTIATYCTGSIPCSVCLSGLDSDLTYPSETIQIT 2310

2 NTVKSGKFCLEASFNYLKSPNFSKLINIIWFLLLSVCLGSLIYSTAALGVLMNLGMPSYCTGYREGYNSTNVTIATYCTGSIPCSVCLSGLDSDLTYPSETIQIT 2310

3 NTVKSGKFCLEASFNYLKSPNFSKLINIIWFLLLSVCLGSLIYSTAALGVLMNLGMPSYCTGYREGYNSTNVTIATYCTGSIPCSVCLSGLDSDLTYPSETIQIT 2310

ISSFKWDLTAFGLVAEWFLAYILFTRFFYVLGLAAIMQLFFSYFAVHFISNSWLMWLIIINLVQMAPISAMVRMYIFFASFYVVWKSYVHVDGCNSSTCMMCYKRNRATR

1 ISSFKWDLTAFGLVAEWFLAYILFTRFFYVLGLAAIMQLFFSYFAVHFISNSWLMWLIIINLVQMAPISAMVRMYIFFASFYVVWKSYVHVDGCNSSTCMMCYKRNRATR 2420

2 ISSFKWDLTAFGLVAEWFLAYILFTRFFYVLGLAVIMQLFFSYFAVHFISNSWLMWLIIINLVQMAPISAMVRMYIFFASFYVVWKSYVHVDGCNSSTCMMCYKRNRATR 2420

3 ISSFKWDLTAFGLVAEWFLAYILFTRFFYVLGLAAIMQLFFSYFAVHFISNSWLMWLIIINLVQMAPISAMVRMYIFFASFYVVWKSYVHVDGCNSSTCMMCYKRNRATR 2420

VECTTIVNGVRRSFYVYANGGKGFCKLHNWNCSVNCDFCAGSTFISDEVARDSLQFKRPINPTDQSSYIVDSVTVKNGSIHLYFDKAGQKTYERHSLSHFVNLDNLRA

1 VECTTIVNGVRRSFYVYANGGKGFCKLHNWNCSVNCDFCAGSTFISDEVARDSLQFKRPINPTDQSSYIVDSVTVKNGSIHLYFDKAGQKTYERHSLSHFVNLDNLRA 2530

2 VECTTIVNGVRRSFYVYANGGKGFCKLHNWNCSVNCDFCAGSTFISDEVARDSLQFKRPINPTDQSSYIVDSVTVKNGSIHLYFDKAGQKTYERHSLSHFVNLDNLRA 2530

3 VECTTIVNGVRRSFYVYANGGKGFCKLHNWNCSVNCDFCAGSTFISDEVARDSLQFKRPINPTDQSSYIVDSVTVKNGSIHLYFDKAGQKTYERHSLSHFVNLDNLRA 2530

NTKGSLPINVIVFDGSKCEESSAKSASVYYSQLMCQPILLLDQALVSDVGDSAEAVKMFDAYVNTFSSTFNVPMEKLKTLVATAEELAKNVSLDNVLSTFISAARQG

1 NTKGSLPINVIVFDGSKCEESSAKSASVYYSQLMCQPILLLDQALVSDVGDSAEAVKMFDAYVNTFSSTFNVPMEKLKTLVATAEELAKNVSLDNVLSTFISAARQG 2640

2 NTKGSLPINVIVFDGSKCEESSAKSASVYYSQLMCQPILLLDQALVSDVGDSAEAVKMFDAYVNTFSSTFNVPMEKLKTLVATAEELAKNVSLDNVLSTFISAARQG 2640

3 NTKGSLPINVIVFDGSKCEESSAKSASVYYSQLMCQPILLLDQALVSDVGDSAEAVKMFDAYVNTFSSTFNVPMEKLKTLVATAEELAKNVSLDNVLSTFISAARQG 2640

FVDSDVETKDVVECLKLHQSDIEVTGDSNNYMLTYNKVENMTPRDLGACIDCSARHINAQVAKSHNIALIWNVKDFMSLSEQLRKQIRSAAKNNLPFKLTCAATTRQV

1 FVDSDVETKDVVECLKLHQSDIEVTGDSNNYMLTYNKVENMTPRDLGACIDCSARHINAQVAKSHNIALIWNVKDFMSLSEQLRKQIRSAAKNNLPFKLTCAATTRQV 2750
2 FVDSDVETKDVVECLKLHQSDIEVTGDSNNYMLTYNKVENMTPRDLGACIDCSARHINAQVAKSHNIALIWNVKDFMSLSEQLRKQIRSAAKNNLPFKLTCAATTRQV 2750
3 FVDSDVETKDVVECLKLHQSDIEVTGDSNNYMLTYNKVENMTPRDLGACIDCSARHINAQVAKSHNIALIWNVKDFMSLSEQLRKQIRSAAKNNLPFKLTCAATTRQV 2750

VNVVTTKIALKGGKIVNNWLQQLIKVTLVFLVAAIFYLITPVHVM SKHTDFSSEIIIGYKAIDGGVTRDIASTDTCFANKHADFDTWFSQRGGSYTNDKACPLIAAVITR

1 VNVVTTKIALKGGKIVNNWLQQLIKVTLVFLVAAIFYLITPVHVM SKHTDFSSEIIIGYKAIDGGVTRDIASTDTCFANKHADFDTWFSQRGGSYTNDKACPLIAAVITR 2860
2 VNVVTTKIALKGGKIVNNWLQQLIKVTLVFLVAAIFYLITPVHVM SKHTDFSSEIIIGYKAIDGGVTRDIASTDTCFANKHADFDTWFSQRGGSYTNDKACPLIAAVITR 2860
3 VNVVTTKIALKGGKIVNNWLQQLIKVTLVFLVAAIFYLITPVHVM SKHTDFSSEIIIGYKAIDGGVTRDIASTDTCFANKHADFDTWFSQRGGSYTNDKACPLIAAVITR 2860

EVGFVVPGPGTILRTTNGDFLHFLPRVFSAVGNICYTPSKLIEYTDATSACVLAAECTIFKDASGKPVPYCYDTNVLEGSVAYESLRPDTRYVLMGDGSIIQFPNTYLE

1 EVGFVVPGPGTILRTTNGDFLHFLPRVFSAVGNICYTPSKLIEYTDATSACVLAAECTIFKDASGKPVPYCYDTNVLEGSVAYESLRPDTRYVLMGDGSIIQFPNTYLE 2970
2 EVGFVVPGPGTILRTTNGDFLHFLPRVFSAVGNICYTPSKLIEYTDATSACVLAAECTIFKDASGKPVPYCYDTNVLEGSVAYESLRPDTRYVLMGDGSIIQFPNTYLE 2970
3 EVGFVVPGPGTILRTTNGDFLHFLPRVFSAVGNICYTPSKLIEYTDATSACVLAAECTIFKDASGKPVPYCYDTNVLEGSVAYESLRPDTRYVLMGDGSIIQFPNTYLE 2970

GSVRVVTTFDSEYCRHGT CERSEAGCVSTSGRWVLNNNDYYRS LPGVFCGVDAVNLLTNMFTPLI QPI GALDISASIVAGGIVAI VVTCLAYYFMRFRRAFGEYSHVVAF

1 GSVRVVTTFDSEYCRHGT CERSEAGCVSTSGRWVLNNNDYYRS LPGVFCGVDAVNLLTNMFTPLI QPI GALDISASIVAGGIVAI VVTCLAYYFMRFRRAFGEYSHVVAF 3080
2 GSVRVVTTFDSEYCRHGT CERSEAGCVSTSGRWVLNNNDYYRS LPGVFCGVDAVNLLTNMFTPLI QPI GALDISASIVAGGIVAI VVTCLAYYFMRFRRAFGEYSHVVAF 3080
3 GSVRVVTTFDSEYCRHGT CERSEAGCVSTSGRWVLNNNDYYRS LPGVFCGVDAVNLLTNMFTPLI QPI GALDISASIVAGGIVAI VVTCLAYYFMRFRRAFGEYSHVVAF 3080

NTLLFLMSFTVLCLTPVYSFLPGVYSVIYLYLTFLNDVSFLAHIQWMVMFTPLVPFWITIAYIICISTKHFYWFFSNYLKRRVVNGVSFSTFEEAALCTFLNKEMY
1 NTLLFLMSFTVLCLTPVYSFLPGVYSVIYLYLTFLNDVSFLAHIQWMVMFTPLVPFWITIAYIICISTKHFYWFFSNYLKRRVVNGVSFSTFEEAALCTFLNKEMY 3190
2 NTLLFLMSFTVLCLTPVYSFLPGVYSVIYLYLTFLNDVSFLAHIQWMVMFTPLVPFWITIAYIICISTKHFYWFFSNYLKRRVVNGVSFSTFEEAALCTFLNKEMY 3190
3 NTLLFLMSFTVLCLTPVYSFLPGVYSVIYLYLTFLNDVSFLAHIQWMVMFTPLVPFWITIAYIICISTKHFYWFFSNYLKRRVVNGVSFSTFEEAALCTFLNKEMY 3190

LKLRSDVLLPLTQYNRYLALYNKYKYFSGAMDTSYREAACCHLAKALNDFNSNSGDVLYQPPQTSITSAVLQSGFRKMAFPSGKVEGCMVQVTCGTTLNGWLDDVYY
1 LKLRSDVLLPLTQYNRYLALYNKYKYFSGAMDTSYREAACCHLAKALNDFNSNSGDVLYQPPQTSITSAVLQSGFRKMAFPSGKVEGCMVQVTCGTTLNGWLDDVYY 3300
2 LKLRSDVLLPLTQYNRYLALYNKYKYFSGAMDTSYREAACCHLAKALNDFNSNSGDVLYQPPQTSITSAVLQSGFRKMAFPSGKVEGCMVQVTCGTTLNGWLDDVYY 3300
3 LKLRSDVLLPLTQYNRYLALYNKYKYFSGAMDTSYREAACCHLAKALNDFNSNSGDVLYQPPQTSITSAVLQSGFRKMAFPSGKVEGCMVQVTCGTTLNGWLDDVYY 3300

CPRHVICTSEDMLNPNEYEDLLIRKSNNHFLVQAGNVQLRVIGHSMQNCVLKLKVDTANPKTPKYKFVRIQPGQTFSVLACYNGSPSGVYQCAMRPNFTIKGSFLNGSCGS
1 CPRHVICTSEDMLNPNEYEDLLIRKSNNHFLVQAGNVQLRVIGHSMQNCVLKLKVDTANPKTPKYKFVRIQPGQTFSVLACYNGSPSGVYQCAMRPNFTIKGSFLNGSCGS 3410
2 CPRHVICTSEDMLNPNEYEDLLIRKSNNHFLVQAGNVQLRVIGHSMQNCVLKLKVDTANPKTPKYKFVRIQPGQTFSVLACYNGSPSGVYQCAMRPNFTIKGSFLNGSCGS 3410
3 CPRHVICTSEDMLNPNEYEDLLIRKSNNHFLVQAGNVQLRVIGHSMQNCVLKLKVDTANPKTPKYKFVRIQPGQTFSVLACYNGSPSGVYQCAMRPNFTIKGSFLNGSCGS 3410

VGFNIDYDCVSFCYMHHMELPTGVHAGTDLEGNFYGPFDRQTAQAAGTDTTITVNVLAWLYAAVINGDRWFLNRFTTLNDFNLVAMKNYEPLTQDHVDILGPLSAQT
1 VGFNIDYDCVSFCYMHHMELPTGVHAGTDLEGNFYGPFDRQTAQAAGTDTTITVNVLAWLYAAVINGDRWFLNRFTTLNDFNLVAMKNYEPLTQDHVDILGPLSAQT 3520
2 VGFNIDYDCVSFCYMHHMELPTGVHAGTDLEGNFYGPFDRQTAQAAGTDTTITVNVLAWLYAAVINGDRWFLNRFTTLNDFNLVAMKNYEPLTQDHVDILGPLSAQT 3520
3 VGFNIDYDCVSFCYMHHMELPTGVHAGTDLEGNFYGPFDRQTAQAAGTDTTITVNVLAWLYAAVINGDRWFLNRFTTLNDFNLVAMKNYEPLTQDHVDILGPLSAQT 3520

GIAVLDMCASLKE^LQNGMNGRTILGSALLEDEFTPFDVVRQCSGVTFQSAVKRTIKGT^HHWLLLTI^TTSLLVLVQSTQWSLFFF^YENAF^LPFAMGIIAMSAFAMMFVK
1 GIAVLDMCASLKE^LQNGMNGRTILGSALLEDEFTPFDVVRQCSGVT^FQSAVKRTIKGT^HWLLLTI^TTSLLVLVQSTQWSLFFF^YENAF^LPFAMGIIAMSAFAMMFVK 3630
2 GIAVLDMCASLKE^LQNGMNGRTILGSALLEDEFTPFDVVRQCSGVT^FQSAVKRTIKGT^HWLLLTI^TTSLLVLVQSTQWSLFFF^YENAF^LPFAMGIIAMSAFAMMFVK 3630
3 GIAVLDMCASLKE^LQNGMNGRTILGSALLEDEFTPFDVVRQCSGVT^FQSAVKRTIKGT^HWLLLTI^TTSLLVLVQSTQWSLFFF^YENAF^LPFAMGIIAMSAFAMMFVK 3630

HKHAF^LCLFLLP^SLATVAYFNMVYMPASWVMRIMT^TWLDMDVDT^LSGF^KLKDCV^MYASAV^VL^LILMTARTVYDDGARRV^WTLMN^VLT^LVYKVYYGNALDQAISMWALIISV
1 HKHAF^LCLFLLP^SLATVAYFNMVYMPASWVMRIMT^TWLDMDVDT^LSGF^KLKDCV^MYASAV^VL^LILMTARTVYDDGARRV^WTLMN^VLT^LVYKVYYGNALDQAISMWALIISV 3740
2 HKHAF^LCLFLLP^SLATVAYFNMVYMPASWVMRIMT^TWLDMDVDT^LSGF^KLKDCV^MYASAV^VL^LILMTARTVYDDGARRV^WTLMN^VLT^LVYKVYYGNALDQAISMWALIISV 3737
3 HKHAF^LCLFLLP^SLATVAYFNMVYMPASWVMRIMT^TWLDMDVDT^LSGF^KLKDCV^MYASAV^VL^LILMTARTVYDDGARRV^WTLMN^VLT^LVYKVYYGNALDQAISMWALIISV 3740

TSNYSGVVTTVMFLARGIVFM^CVEYCP^IFFITGNTLQCIMLV^CFLGY^FCTCYFGLF^CLLNRY^RFRL^TLG^VDYL^VSTQE^FRYMNSQ^GLLPPKNSIDAF^KLNI^KLLGVGGK
1 TSNYSGVVTTVMFLARGIVFM^CVEYCP^IFFITGNTLQCIMLV^CFLGY^FCTCYFGLF^CLLNRY^RFRL^TLG^VDYL^VSTQE^FRYMNSQ^GLLPPKNSIDAF^KLNI^KLLGVGGK 3850
2 TSNYSGVVTTVMFLARGIVFM^CVEYCP^IFFITGNTLQCIMLV^CFLGY^FCTCYFGLF^CLLNRY^RFRL^TLG^VDYL^VSTQE^FRYMNSQ^GLLPPKNSIDAF^KLNI^KLLGVGGK 3847
3 TSNYSGVVTTVMFLARGIVFM^CVEYCP^IFFITGNTLQCIMLV^CFLGY^FCTCYFGLF^CLLNRY^RFRL^TLG^VDYL^VSTQE^FRYMNSQ^GLLPPKNSIDAF^KLNI^KLLGVGGK 3850

PCIKVATVQSKMSDV^KCTSVVLLS^LV^LQQLRVESSSKLWAQCVQLHNDILLAKDTTEAF^EKMVS^LS^LV^LSMQGA^VDINKLCEEMLDNRATLQAIASEFSSLPSYAAFATA
1 PCIKVATVQSKMSDV^KCTSVVLLS^LV^LQQLRVESSSKLWAQCVQLHNDILLAKDTTEAF^EKMVS^LS^LV^LSMQGA^VDINKLCEEMLDNRATLQAIASEFSSLPSYAAFATA 3960
2 PCIKVATVQSKMSDV^KCTSVVLLS^LV^LQQLRVESSSKLWAQCVQLHNDILLAKDTTEAF^EKMVS^LS^LV^LSMQGA^VDINKLCEEMLDNRATLQAIASEFSSLPSYAAFATA 3957
3 PCIKVATVQSKMSDV^KCTSVVLLS^LV^LQQLRVESSSKLWAQCVQLHNDILLAKDTTEAF^EKMVS^LS^LV^LSMQGA^VDINKLCEEMLDNRATLQAIASEFSSLPSYAAFATA 3960

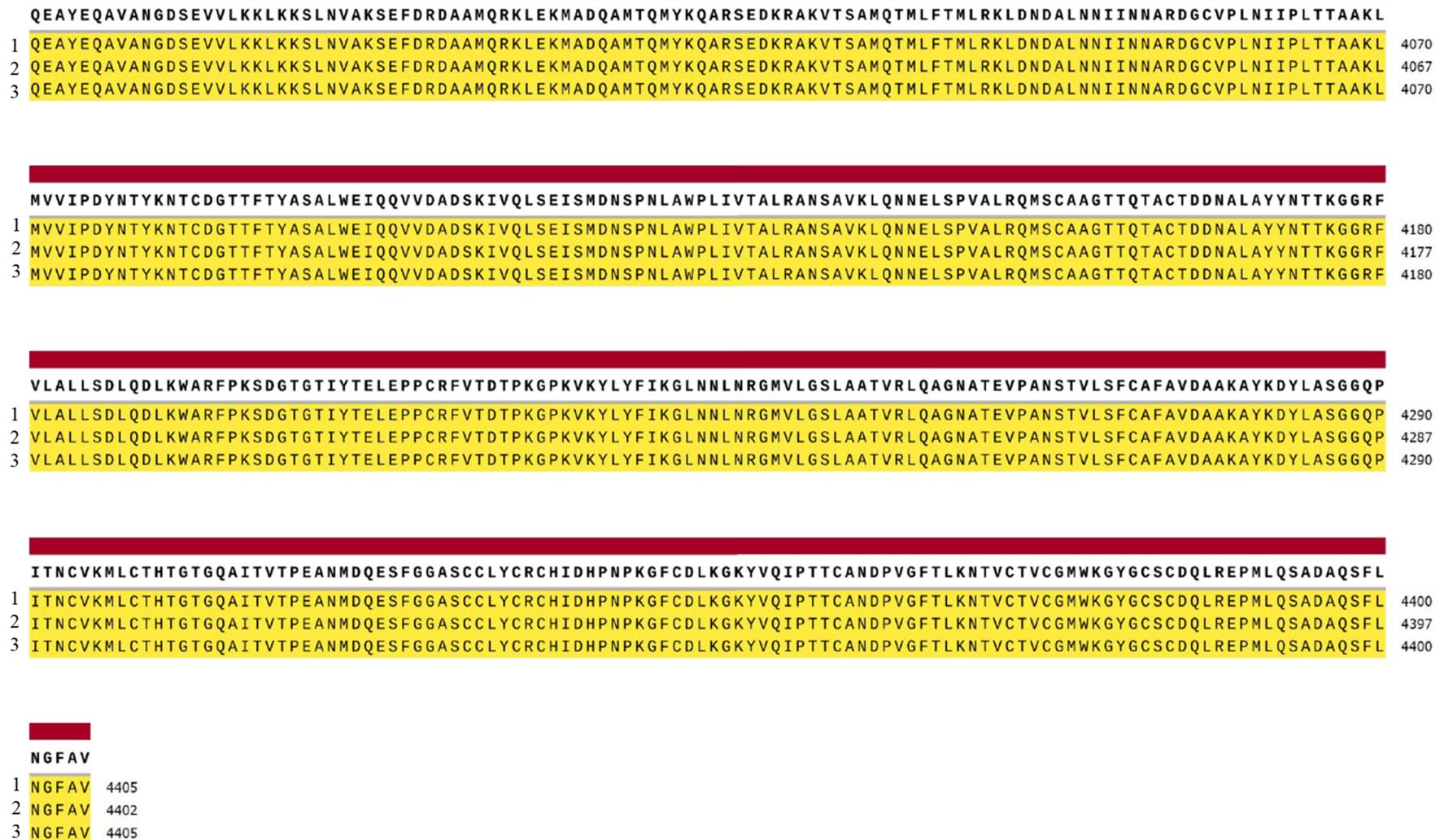


Figure S5. Schematic view of contigs of the ORF1a polyprotein of 1. Alpha Variant (B.1.1.7) (UDQ41837.1) and 2. Delta Variant (B.1.617.21) (UDU36745.1) of SARs-CoV-2 with 3. reference Strain (Wuhan) (YP_009725295.1).

6. ORF1ab polyprotein

MESLVPGFNEKTHVQLSLPVLQVRDVLRGFGDSVEEVLSearQHLKDGTGLVEVEKGVLQLEQPYVFIKRSDARTAPHGHVMVELVAELEGIQYGRSGETLGVLVPH
1 MESLVPGFNEKTHVQLSLPVLQVRDVLRGFGDSVEEVLSearQHLKDGTGLVEVEKGVLQLEQPYVFIKRSDARTAPHGHVMVELVAELEGIQYGRSGETLGVLVPH 110
2 MESLVPGFNEKTHVQLSLPVLQVRDVLRGFGDSVEEVLSearQHLKDGTGLVEVEKGVLQLEQPYVFIKRSDARTAPHGHVMVELVAELEGIQYGRSGETLGVLVPH 110
3 MESLVPGFNEKTHVQLSLPVLQVRDVLRGFGDSVEEVLSearQHLKDGTGLVEVEKGVLQLEQPYVFIKRSDARTAPHGHVMVELVAELEGIQYGRSGETLGVLVPH 110

VGEIPVAYRKVLLRKNGNKGAGGHSYGADLKSFDLGDELGTDPYEDFQENWNTKHSSGVTRLEMRELNGGAYTRYVDNNFCGPDPGYPLECIKDLLARAGKASCTLSEQLD
1 VGEIPVAYRKVLLRKNGNKGAGGHSYGADLKSFDLGDELGTDPYEDFQENWNTKHSSGVTRLEMRELNGGAYTRYVDNNFCGPDPGYPLECIKDLLARAGKASCTLSEQLD 220
2 VGEIPVAYRKVLLRKNGNKGAGGHSYGADLKSFDLGDELGTDPYEDFQENWNTKHSSGVTRLEMRELNGGAYTRYVDNNFCGPDPGYPLECIKDLLVRAGKASCTLSEQLD 220
3 VGEIPVAYRKVLLRKNGNKGAGGHSYGADLKSFDLGDELGTDPYEDFQENWNTKHSSGVTRLEMRELNGGAYTRYVDNNFCGPDPGYPLECIKDLLARAGKASCTLSEQLD 220

FIDTKRGVYCCREHEHEIAWYTERSEKSYELQTPFEIKLAKKFDTFNGECPNFVPLNSIIKTIQPRVEKKLDGFMRIRSVYPVASPNECNQMCLSTLMKCDHCGETS
1 FIDTKRGVYCCREHEHEIAWYTERSEKSYELQTPFEIKLAKKFDTFNGECPNFVPLNSIIKTIQPRVEKKLDGFMRIRSVYPVASPNECNQMCLSTLMKCDHCGETS 330
2 FIDTKRGVYCCREHEHEIAWYTERSEKSYELQTPFEIKLAKKFDTFNGECPNFVPLNSIIKTIQPRVEKKLDGFMRIRSVYPVASPNECNQMCLSTLMKCDHCGETS 330
3 FIDTKRGVYCCREHEHEIAWYTERSEKSYELQTPFEIKLAKKFDTFNGECPNFVPLNSIIKTIQPRVEKKLDGFMRIRSVYPVASPNECNQMCLSTLMKCDHCGETS 330

WQTGDFVKATCEFCGTENLTKEGATTGYLQPNAVVKIYCPACHNSEVGPEHSLAEYHNESGLKTLRKGGRTIAFGGCVF SYVGCHNK CAYWVPRASANIGC NHTGVVG
1 WQTGDFVKATCEFCGTENLTKEGATTGYLQPNAVVKIYCPACHNSEVGPEHSLAEYHNESGLKTLRKGGRTIAFGGCVF SYVGCHNK CAYWVPRASANIGC NHTGVVG 440
2 WQTGDFVKATCEFCGTENLTKEGATTGYLQPNAVVKIYCPACHNSEVGPEHSLAEYHNESGLKTLRKGGRTIAFGGCVF SYVGCHNK CAYWVPRASANIGC NHTGVVG 440
3 WQTGDFVKATCEFCGTENLTKEGATTGYLQPNAVVKIYCPACHNSEVGPEHSLAEYHNESGLKTLRKGGRTIAFGGCVF SYVGCHNK CAYWVPRASANIGC NHTGVVG 440

EGSEGLNDNLLEILQKEKVNIIVGDFKLNEEIAILASFASASTSAFVETVKGLDYKAFKQIVESCGNFVTKGKAKKGAWNIGEQKSILSPLYAFASEARVRSIFSR
1 EGSEGLNDNLLEILQKEKVNIIVGDFKLNEEIAILASFASASTSAFVETVKGLDYKAFKQIVESCGNFVTKGKAKKGAWNIGEQKSILSPLYAFASEARVRSIFSR 550
2 EGSEGLNDNLLEILQKEKVNIIVGDFKLNEEIAILASFASASTSAFVETVKGLDYKAFKQIVESCGNFVTKGKAKKGAWNIGEQKSILSPLYAFASEARVRSIFSR 550
3 EGSEGLNDNLLEILQKEKVNIIVGDFKLNEEIAILASFASASTSAFVETVKGLDYKAFKQIVESCGNFVTKGKAKKGAWNIGEQKSILSPLYAFASEARVRSIFSR 550

TLETAQNSVRVLQKAAITILDGISQYSLRLIDAMMFSDLATNNLVVMAYITGGVVQLTSQWLTNIFGTVYEKLKPVLDWLEEKFKEGVEFLRDGWEI/KFISTCACEIV
1 TLETAQNSVRVLQKAAITILDGISQYSLRLIDAMMFSDLATNNLVVMAYITGGVVQLTSQWLTNIFGTVYEKLKPVLDWLEEKFKEGVEFLRDGWEI/KFISTCACEIV 660
2 TLETAQNSVRVLQKAAITILDGISQYSLRLIDAMMFSDLATNNLVVMAYITGGVVQLTSQWLTNIFGTVYEKLKPVLDWLEEKFKEGVEFLRDGWEI/KFISTCACEIV 660
3 TLETAQNSVRVLQKAAITILDGISQYSLRLIDAMMFSDLATNNLVVMAYITGGVVQLTSQWLTNIFGTVYEKLKPVLDWLEEKFKEGVEFLRDGWEI/KFISTCACEIV 660

GGQIVTCAKEIKESVQTFFKLVNKFLALCADSIIIGGAKLKALNLGETFVTHSKGLYRKCVKSREETGLLMPLKAPKEIIFLEGETLPTEVLTEEVVLKTGDLQPLEQPT
1 GGQIVTCAKEIKESVQTFFKLVNKFLALCADSIIIGGAKLKALNLGETFVTHSKGLYRKCVKSREETGLLMPLKAPKEIIFLEGETLPTEVLTEEVVLKTGDLQPLEQPT 770
2 GGQIVTCAKEIKESVQTFFKLVNKFLALCADSIIIGGAKLKALNLGETFVTHSKGLYRKCVKSREETGLLMPLKAPKEIIFLEGETLPTEVLTEEVVLKTGDLQPLEQPT 770
3 GGQIVTCAKEIKESVQTFFKLVNKFLALCADSIIIGGAKLKALNLGETFVTHSKGLYRKCVKSREETGLLMPLKAPKEIIFLEGETLPTEVLTEEVVLKTGDLQPLEQPT 770

SEAVERPLVGTPVCINGMLLEIKDTEKYCALAPNMVTNNFTLKGGAAPTAKVTFGDDTVIEVQGYKSVNITFELDERIDKVLNEKCSAYTVELGTEVNEFACVVADAVI
1 SEAVERPLVGTPVCINGMLLEIKDTEKYCALAPNMVTNNFTLKGGAAPTAKVTFGDDTVIEVQGYKSVNITFELDERIDKVLNEKCSAYTVELGTEVNEFACVVADAVI 880
2 SEAVERPLVGTPVCINGMLLEIKDTEKYCALAPNMVTNNFTLKGGAAPTAKVTFGDDTVIEVQGYKSVNITFELDERIDKVLNEKCSAYTVELGTEVNEFACVVADAVI 880
3 SEAVERPLVGTPVCINGMLLEIKDTEKYCALAPNMVTNNFTLKGGAAPTAKVTFGDDTVIEVQGYKSVNITFELDERIDKVLNEKCSAYTVELGTEVNEFACVVADAVI 880

KTLQPVSELLTPLGIDLDEWSMATYYLFDESGEFKLASHMYCSFYPPDEDEEEGDCEEEEFPSTQYEYGTEDDYQGKPLEFGATSAALQPEEEQEEDWLDDDSQQTVGQ
1 KTLQPVSELLTPLGIDLDEWSMATYYLFDESGEFKLASHMYCSFYPPDEDEEEGDCEEEEFPSTQYEYGTEDDYQGKPLEFGATSAALQPEEEQEEDWLDDDSQQTVGQ 990
2 KTLQPVSELLTPLGIDLDEWSMATYYLFDESGEFKLASHMYCSFYPPDEDEEEGDCEEEEFPSTQYEYGTEDDYQGKPLEFGATSAALQPEEEQEEDWLDDDSQQTVGQ 990
3 KTLQPVSELLTPLGIDLDEWSMATYYLFDESGEFKLASHMYCSFYPPDEDEEEGDCEEEEFPSTQYEYGTEDDYQGKPLEFGATSAALQPEEEQEEDWLDDDSQQTVGQ 990

QDGSEDNQTTEIQTIVEVQPQLEMEITPVVQTIEVNSFSGYLKLTNDVYIKNADIVEEAKVKPTVVNAANVYLKHGGGVAGALNKATNNAMQVESDDYIATNGPLKVG
1 QDGSEDNQTTEIQTIVEVQPQLEMEITPVVQTIEVNSFSGYLKLTNDVYIKNADIVEEAKVKPTVVNAANVYLKHGGGVAGALNKATNNAMQVESDDYIATNGPLKVG 1100
2 QDGSEDNQTTEIQTIVEVQPQLEMEITPVVQTIEVNSFSGYLKLTNDVYIKNADIVEEAKVKPTVVNAANVYLKHGGGVAGALNKATNNAMQVESDDYIATNGPLKVG 1100
3 QDGSEDNQTTEIQTIVEVQPQLEMEITPVVQTIEVNSFSGYLKLTNDVYIKNADIVEEAKVKPTVVNAANVYLKHGGGVAGALNKATNNAMQVESDDYIATNGPLKVG 1100

GSCVLSGHNLAKHCLHVVGPNVNKGEDIQLLKSAYENFNQHEVLLAPLLSAGIFGADPIHSLRVCVDTVRTNVYLAVFDFKNLYDKLVSSFLEMKSEKQVEQKIAEIPKEE
1 GSCVLSGHNLAKHCLHVVGPNVNKGEDIQLLKSAYENFNQHEVLLAPLLSAGIFGADPIHSLRVCVDTVRTNVYLAVFDFKNLYDKLVSSFLEMKSEKQVEQKIAEIPKEE 1210
2 GSCVLSGHNLAKHCLHVVGPNVNKGEDIQLLKSAYENFNQHEVLLAPLLSAGIFGADPIHSLRVCVDTVRTNVYLAVFDFKNLYDKLVSSFLEMKSEKQVEQKIAEIPKEE 1210
3 GSCVLSGHNLAKHCLHVVGPNVNKGEDIQLLKSAYENFNQHEVLLAPLLSAGIFGADPIHSLRVCVDTVRTNVYLAVFDFKNLYDKLVSSFLEMKSEKQVEQKIAEIPKEE 1210

VKPFITESKPSVEQRKQDDKKIKACVEEVTTLEETKFLTENLLYIDINGNLHPDSATLVDIDITFLKKDAPYIVGDVVQEGVLTAVVVIPTKKAGGTTEMLAKALRKV
1 VKPFITESKPSVEQRKQDDKKIKACVEEVTTLEETKFLTENLLYIDINGNLHPDSATLVDIDITFLKKDAPYIVGDVVQEGVLTAVVVIPTKKAGGTTEMLAKALRKV 1320
2 VKPFITESKPSVEQRKQDDKKIKACVEEVTTLEETKFLTENLLYIDINGNLHPDSATLVDIDITFLKKDAPYIVGDVVQEGVLTAVVVIPTKKAGGTTEMLAKALRKV 1320
3 VKPFITESKPSVEQRKQDDKKIKACVEEVTTLEETKFLTENLLYIDINGNLHPDSATLVDIDITFLKKDAPYIVGDVVQEGVLTAVVVIPTKKAGGTTEMLAKALRKV 1320

PTDNYITTPGQGLNGYTVEEAKTVLKKCKSAFYILPSIISNEKQEILGTVSWNLREMLAHAEETRKLMPVCVETKAIVSTIQRKYKGIKIQEGVVVDYGARFYFYTSKTT

1 PTDNYITTPGQGLNGYTVEEAKTVLKKCKSAFYILPSIISNEKQEILGTVSWNLREMLAHAEETRKLMPVCVETKAIVSTIQRKYKGIKIQEGVVVDYGARFYFYTSKTT 1430

2 PTDNYITTPGQGLNGYTVEEAKTVLKKCKSAFYILPSIISNEKQEILGTVSWNLREMLAHAEETRKLMPVCVETKAIVSTIQRKYKGIKIQEGVVVDYGARFYFYTSKTT 1430

3 PTDNYITTPGQGLNGYTVEEAKTVLKKCKSAFYILPSIISNEKQEILGTVSWNLREMLAHAEETRKLMPVCVETKAIVSTIQRKYKGIKIQEGVVVDYGARFYFYTSKTT 1430

VASLINTLNDLNETLVTMPLGYVTHGLNLEEAARYMRSLKVPATSVSSPDAVTAYNGYLTSSSKTPEEHFIELTISLAGSYKDWSYSQSTQLGIEFLKRGDKSVYYTSN

1 VASLINTLNDLNETLVTMPLGYVTHGLNLEEAARYMRSLKVPATSVSSPDAVTAYNGYLTSSSKTPEEHFIELTISLAGSYKDWSYSQSTQLGIEFLKRGDKSVYYTSN 1540

2 VASLINTLNDLNETLVTMPLGYVTHGLNLEEAARYMRSLKVPATSVSSPDAVTAYNGYLTSSSKTPEEHFIELTISLAGSYKDWSYSQSTQLGIEFLKRGDKSVYYTSN 1540

3 VASLINTLNDLNETLVTMPLGYVTHGLNLEEAARYMRSLKVPATSVSSPDAVTAYNGYLTSSSKTPEEHFIELTISLAGSYKDWSYSQSTQLGIEFLKRGDKSVYYTSN 1540

PTTFHLDGEVITFDNLKTLLSLREVRTIKVFTTVDNINLHTQVVDMSMTYQQQFGPTYLDGADVTKIKPHNSHEGKTFYVLPNDDTLRVEAFYYHTTDPFLGRYMSAL

1 PTTFHLDGEVITFDNLKTLLSLREVRTIKVFTTVDNINLHTQVVDMSMTYQQQFGPTYLDGADVTKIKPHNSHEGKTFYVLPNDDTLRVEAFYYHTTDPFLGRYMSAL 1650

2 PTTFHLDGEVITFDNLKTLLSLREVRTIKVFTTVDNINLHTQVVDMSMTYQQQFGPTYLDGADVTKIKPHNSHEGKTFYVLPNDDTLRVEAFYYHTTDPFLGRYMSAL 1650

3 PTTFHLDGEVITFDNLKTLLSLREVRTIKVFTTVDNINLHTQVVDMSMTYQQQFGPTYLDGADVTKIKPHNSHEGKTFYVLPNDDTLRVEAFYYHTTDPFLGRYMSAL 1650

NHTKKWKPQVNGLTSIKWADNNCYLATALLLQQIELKFNPALQDAYYRARAGEAANFCALILAYCNKTVGELGDVRETMSPYLQFQHANLDSCKRVLNVVCKTCGQQQT

1 NHTKKWKPQVNGLTSIKWADNNCYLATALLLQQIELKFNPALQDAYYRARAGEAANFCALILAYCNKTVGELGDVRETMSPYLQFQHANLDSCKRVLNVVCKTCGQQQT 1760

2 NHTKKWKPQVNGLTSIKWADNNCYLATALLLQQIELKFNPALQDAYYRARAGEADNFCAALILAYCNKTVGELGDVRETMSPYLQFQHANLDSCKRVLNVVCKTCGQQQT 1760

3 NHTKKWKPQVNGLTSIKWADNNCYLATALLLQQIELKFNPALQDAYYRARAGEAANFCALILAYCNKTVGELGDVRETMSPYLQFQHANLDSCKRVLNVVCKTCGQQQT 1760

TLKGVEAVMYMGTLSYEQFKKGVQIPCTCGKQATKYLVQQESPFVMMSSAPPAQYELKHGHTCASEYTGNYQCGHYKHITSKETLYCIDGALLTKSSEYKGPITDVFYKE

1 TLKGVEAVMYMGTLSYEQFKKGVQIPCTCGKQATKYLVQQESPFVMMSSAPPAQYELKHGHTCASEYTGNYQCGHYKHITSKETLYCIDGALLTKSSEYKGPITDVFYKE 1870

2 TLKGVEAVMYMGTLSYEQFKKGVQIPCTCGKQATKYLVQQESPFVMMSSAPPAQYELKHGHTCASEYTGNYQCGHYKHITSKETLYCIDGALLTKSSEYKGPITDVFYKE 1870

3 TLKGVEAVMYMGTLSYEQFKKGVQIPCTCGKQATKYLVQQESPFVMMSSAPPAQYELKHGHTCASEYTGNYQCGHYKHITSKETLYCIDGALLTKSSEYKGPITDVFYKE 1870

NSYTTTIKPVTYKLDGVVCTEIDPKLDNYYKKDNSYFTEQPIDLVPNQPYPNASFDNFKFVCDNIKFADDLNQLTYKKPASRELKVTFPDNGDVAIDYKHYTPSFK

1 NSYTTTIKPVTYKLDGVVCTEIDPKLDNYYKKDNSYFTEQPIDLVPNQPYPNASFDNFKFVCDNIKFADDLNQLTYKKPASRELKVTFPDNGDVAIDYKHYTPSFK 1980

2 NSYTTTIKPVTYKLDGVVCTEIDPKLDNYYKKDNSYFTEQPIDLVPNQPYPNASFDNFKFVCDNIKFADDLNQLTYKKPASRELKVTFPDNGDVAIDYKHYTPSFK 1980

3 NSYTTTIKPVTYKLDGVVCTEIDPKLDNYYKKDNSYFTEQPIDLVPNQPYPNASFDNFKFVCDNIKFADDLNQLTYKKPASRELKVTFPDNGDVAIDYKHYTPSFK 1980

KGAKLLHKPIVWHVNNATNKATYKPNTWCIRCLWSTKPVETSNSFDVLKSEDAQGMNDLACEDLKPVSEEVVENPTIQKDVLNVKTTEVVGDIILKPANNSLKITEEV

1 KGAKLLHKPIVWHVNNATNKATYKPNTWCIRCLWSTKPVETSNSFDVLKSEDAQGMNDLACEDLKPVSEEVVENPTIQKDVLNVKTTEVVGDIILKPANNSLKITEEV 2090

2 KGAKLLHKPIVWHVNNATNKATYKPNTWCIRCLWSTKPVETSNSFDVLKSEDAQGMNDLACEDLKPVSEEVVENPTIQKDVLNVKTTEVVGDIILKPANNSLKITEEV 2090

3 KGAKLLHKPIVWHVNNATNKATYKPNTWCIRCLWSTKPVETSNSFDVLKSEDAQGMNDLACEDLKPVSEEVVENPTIQKDVLNVKTTEVVGDIILKPANNSLKITEEV 2090

GHTDLMAAYVDNSSLTICKPNELSRLVGLKLTLATHGLAAVNSVPWDTIANYAKPFLNKKVVSTTNTIVTRCLNRVCTNYMPYFTLLLQLCTFTRSTSRIKASMPTTIAK

1 GHTDLMAAYVDNSSLTICKPNELSRLVGLKLTLATHGLAAVNSVPWDTIANYAKPFLNKKVVSTTNTIVTRCLNRVCTNYMPYFTLLLQLCTFTRSTSRIKASMPTTIAK 2200

2 GHTDLMAAYVDNSSLTICKPNELSRLVGLKLTLATHGLAAVNSVPWDTIANYAKPFLNKKVVSTTNTIVTRCLNRVCTNYMPYFTLLLQLCTFTRSTSRIKASMPTTIAK 2200

3 GHTDLMAAYVDNSSLTICKPNELSRLVGLKLTLATHGLAAVNSVPWDTIANYAKPFLNKKVVSTTNTIVTRCLNRVCTNYMPYFTLLLQLCTFTRSTSRIKASMPTTIAK 2200

NTVKSGKFCLEASFNYLKSPNFSKLINIIIWFLLLSVCLGSLIYSTAALGVLMNLGMPSYCTGYREGYNSTNVTIATYCTGSIPCSVCLSGLDSDLTYPSETIQIT
1 NTVKSGKFCLEASFNYLKSPNFSKLINIIIWFLLLSVCLGSLIYSTAALGVLMNLGMPSYCTGYREGYNSTNVTIATYCTGSIPCSVCLSGLDSDLTYPSETIQIT 2310
2 NTVKSGKFCLEASFNYLKSPNFSKLINIIIWFLLLSVCLGSLIYSTAALGVLMNLGMPSYCTGYREGYNSTNVTIATYCTGSIPCSVCLSGLDSDLTYPSETIQIT 2310
3 NTVKSGKFCLEASFNYLKSPNFSKLINIIIWFLLLSVCLGSLIYSTAALGVLMNLGMPSYCTGYREGYNSTNVTIATYCTGSIPCSVCLSGLDSDLTYPSETIQIT 2310

ISSFKWDLTAFGLVAEWFLAYILFTRFFYVLGLAAIMQLFFSYFAVHFISNSWLMWLIIINLVQMAPISAMVRMYIFFASFYVVWKSYVHVDGCNSSTCMMCYKRNRATR
1 ISSFKWDLTAFGLVAEWFLAYILFTRFFYVLGLAAIMQLFFSYFAVHFISNSWLMWLIIINLVQMAPISAMVRMYIFFASFYVVWKSYVHVDGCNSSTCMMCYKRNRATR 2420
2 ISSFKWDLTAFGLVAEWFLAYILFTRFFYVLGLAAIMQLFFSYFAVHFISNSWLMWLIIINLVQMAPISAMVRMYIFFASFYVVWKSYVHVDGCNSSTCMMCYKRNRATR 2420
3 ISSFKWDLTAFGLVAEWFLAYILFTRFFYVLGLAAIMQLFFSYFAVHFISNSWLMWLIIINLVQMAPISAMVRMYIFFASFYVVWKSYVHVDGCNSSTCMMCYKRNRATR 2420

VECTTIVNGRRSFYVYANGGKGFCKLHNWNCVNCDFCAGSTFISDEVARDSLQFKRPINPTDQSSYIVDSVTVKNGSIHLYFDKAGQKTYERHSLSHFVNLDNLRA
1 VECTTIVNGRRSFYVYANGGKGFCKLHNWNCVNCDFCAGSTFISDEVARDSLQFKRPINPTDQSSYIVDSVTVKNGSIHLYFDKAGQKTYERHSLSHFVNLDNLRA 2530
2 VECTTIVNGRRSFYVYANGGKGFCKLHNWNCVNCDFCAGSTFISDEVARDSLQFKRPINPTDQSSYIVDSVTVKNGSIHLYFDKAGQKTYERHSLSHFVNLDNLRA 2530
3 VECTTIVNGRRSFYVYANGGKGFCKLHNWNCVNCDFCAGSTFISDEVARDSLQFKRPINPTDQSSYIVDSVTVKNGSIHLYFDKAGQKTYERHSLSHFVNLDNLRA 2530

NTKGSLPINVIVFDGSKCEESSAKSASVYYSQLMCQPILLLDQALVSDVGDSAEVAVKMFADYVNTFSSTFNVPMEKLKTLVATAEELAKNVLDNVLSTFISAARQG
1 NTKGSLPINVIVFDGSKCEESSAKSASVYYSQLMCQPILLLDQALVSDVGDSAEVAVKMFADYVNTFSSTFNVPMEKLKTLVATAEELAKNVLDNVLSTFISAARQG 2640
2 NTKGSLPINVIVFDGSKCEESSAKSASVYYSQLMCQPILLLDQALVSDVGDSAEVAVKMFADYVNTFSSTFNVPMEKLKTLVATAEELAKNVLDNVLSTFISAARQG 2640
3 NTKGSLPINVIVFDGSKCEESSAKSASVYYSQLMCQPILLLDQALVSDVGDSAEVAVKMFADYVNTFSSTFNVPMEKLKTLVATAEELAKNVLDNVLSTFISAARQG 2640

FVDSDVETKDVVECLKLHQSDIEVTGDSNNYMLTYNKVENMTPRDLGACIDCSARHINAQVAKSHNIALIWNVKDFMSLSEQLRKQIRSAAKNNLPFKLTCAATTRQV

1 FVDSDVETKDVVECLKLHQSDIEVTGDSNNYMLTYNKVENMTPRDLGACIDCSARHINAQVAKSHNIALIWNVKDFMSLSEQLRKQIRSAAKNNLPFKLTCAATTRQV 2750
2 FVDSDVETKDVVECLKLHQSDIEVTGDSNNYMLTYNKVENMTPRDLGACIDCSARHINAQVAKSHNIALIWNVKDFMSLSEQLRKQIRSAAKNNLPFKLTCAATTRQV 2750
3 FVDSDVETKDVVECLKLHQSDIEVTGDSNNYMLTYNKVENMTPRDLGACIDCSARHINAQVAKSHNIALIWNVKDFMSLSEQLRKQIRSAAKNNLPFKLTCAATTRQV 2750

VNVVTTKIALKGGKIVNNWLKQLIKVTLVFLVAAIFYLITPVHVM SKHTDFSSEIIIGYKAIDGGVTRDIASTDTCFANKHADFDTWFSQRGGSYTNDKACPLIAAVITR

1 VNVVTTKIALKGGKIVNNWLKQLIKVTLVFLVAAIFYLITPVHVM SKHTDFSSEIIIGYKAIDGGVTRDIASTDTCFANKHADFDTWFSQRGGSYTNDKACPLIAAVITR 2860
2 VNVVTTKIALKGGKIVNNWLKQLIKVTLVFLVAAIFYLITPVHVM SKHTDFSSEIIIGYKAIDGGVTRDIASTDTCFANKHADFDTWFSQRGGSYTNDKACPLIAAVITR 2860
3 VNVVTTKIALKGGKIVNNWLKQLIKVTLVFLVAAIFYLITPVHVM SKHTDFSSEIIIGYKAIDGGVTRDIASTDTCFANKHADFDTWFSQRGGSYTNDKACPLIAAVITR 2860

EVGFVVPGPGTILRTTNGDFLHFLPRVFSAVGNICYTPSKLIEYTDAT SACVLAAECTIFKDASGKPVPYC YDTNVLEG SVAYE SLRPDTRYVLM DGSI IQFPNTYLE

1 EVGFVVPGPGTILRTTNGDFLHFLPRVFSAVGNICYTPSKLIEYTDAT SACVLAAECTIFKDASGKPVPYC YDTNVLEG SVAYE SLRPDTRYVLM DGSI IQFPNTYLE 2970
2 EVGFVVPGPGTILRTTNGDFLHFLPRVFSAVGNICYTPSKLIEYTDAT SACVLAAECTIFKDASGKPVPYC YDTNVLEG SVAYE SLRPDTRYVLM DGSI IQFPNTYLE 2970
3 EVGFVVPGPGTILRTTNGDFLHFLPRVFSAVGNICYTPSKLIEYTDAT SACVLAAECTIFKDASGKPVPYC YDTNVLEG SVAYE SLRPDTRYVLM DGSI IQFPNTYLE 2970

GSRVVTTFDSEYCRHGT CERSEAGVCVSTS GRWVLNNNDYYRS LPGVFCGV DAVNLLTNMFTPLI QPI GALDIS ASIV AGGIV AIVVTCLAYYFMR RRAFGEYSHVVAF

1 GSVRVVTTFDSEYCRHGT CERSEAGVCVSTS GRWVLNNNDYYRS LPGVFCGV DAVNLLTNMFTPLI QPI GALDIS ASIV AGGIV AIVVTCLAYYFMR RRAFGEYSHVVAF 3080
2 GSVRVVTTFDSEYCRHGT CERSEAGVCVSTS GRWVLNNNDYYRS LPGVFCGV DAVNLLTNMFTPLI QPI GALDIS ASIV AGGIV AIVVTCLAYYFMR RRAFGEYSHVVAF 3080
3 GSVRVVTTFDSEYCRHGT CERSEAGVCVSTS GRWVLNNNDYYRS LPGVFCGV DAVNLLTNMFTPLI QPI GALDIS ASIV AGGIV AIVVTCLAYYFMR RRAFGEYSHVVAF 3080

NTLLFLMSFTVLCLTPVYSFLPGVYVIYLTFYLTDVSFLAHIQWMVMFTPPLVPFWITIAYIICISTKHFYWFFSNYLKRRVVFNGVSFSTFEEAALCTFLLNKEMY
1 NTLLFLMSFTVLCLTPVYSFLPGVYVIYLTFYLTDVSFLAHIQWMVMFTPPLVPFWITIAYIICISTKHFYWFFSNYLKRRVVFNGVSFSTFEEAALCTFLLNKEMY 3190
2 NTLLFLMSFTVLCLTPVYSFLPGVYVIYLTFYLTDVSFLAHIQWMVMFTPPLVPFWITIAYIICISTKHFYWFFSNYLKRRVVFNGVSFSTFEEAALCTFLLNKEMY 3190
3 NTLLFLMSFTVLCLTPVYSFLPGVYVIYLTFYLTDVSFLAHIQWMVMFTPPLVPFWITIAYIICISTKHFYWFFSNYLKRRVVFNGVSFSTFEEAALCTFLLNKEMY 3190

LKLRSVLLPLTQYNRYLALYNKYKYFSGAMDTSYREAACCHLAKALNDFNSNSGDVLYQPPQTSITSAVLQSGFRKMAFFSGKVEGCMVQVTCGTTLNLWLDDVYY
1 LKLRSVLLPLTQYNRYLALYNKYKYFSGAMDTSYREAACCHLAKALNDFNSNSGDVLYQPPQTSITSAVLQSGFRKMAFFSGKVEGCMVQVTCGTTLNLWLDDVYY 3300
2 LKLRSVLLPLTQYNRYLALYNKYKYFSGAMDTSYREAACCHLAKALNDFNSNSGDVLYQPPQTSITSAVLQSGFRKMAFFSGKVEGCMVQVTCGTTLNLWLDDVYY 3300
3 LKLRSVLLPLTQYNRYLALYNKYKYFSGAMDTSYREAACCHLAKALNDFNSNSGDVLYQPPQTSITSAVLQSGFRKMAFFSGKVEGCMVQVTCGTTLNLWLDDVYY 3300

CPRHVICTSEDMLNPNEYEDLLIRKSNNFLVQAGNVQLRVIGHSMQNCVLKLKVDTANPKTPKYKFVRIQPGQTFSVLACYNGSPSGVYQCAMRPNFTIKGSFLNGSCGS
1 CPRHVICTSEDMLNPNEYEDLLIRKSNNFLVQAGNVQLRVIGHSMQNCVLKLKVDTANPKTPKYKFVRIQPGQTFSVLACYNGSPSGVYQCAMRPNFTIKGSFLNGSCGS 3410
2 CPRHVICTSEDMLNPNEYEDLLIRKSNNFLVQAGNVQLRVIGHSMQNCVLKLKVDTANPKTPKYKFVRIQPGQTFSVLACYNGSPSGVYQCAMRPNFTIKGSFLNGSCGS 3410
3 CPRHVICTSEDMLNPNEYEDLLIRKSNNFLVQAGNVQLRVIGHSMQNCVLKLKVDTANPKTPKYKFVRIQPGQTFSVLACYNGSPSGVYQCAMRPNFTIKGSFLNGSCGS 3410

VGFNIDYDCSFCYMHMHMELPTGVHAGTDLEGNFYGPFFVDRQTAQAAGTDTTITVNVLAWLYAAVINGDRWFLNRFTTLNDFNLVAMKYNYEPLTQDHVDILGPLSAQT
1 VGFNIDYDCSFCYMHMHMELPTGVHAGTDLEGNFYGPFFVDRQTAQAAGTDTTITVNVLAWLYAAVINGDRWFLNRFTTLNDFNLVAMKYNYEPLTQDHVDILGPLSAQT 3520
2 VGFNIDYDCSFCYMHMHMELPTGVHAGTDLEGNFYGPFFVDRQTAQAAGTDTTITVNVLAWLYAAVINGDRWFLNRFTTLNDFNLVAMKYNYEPLTQDHVDILGPLSAQT 3520
3 VGFNIDYDCSFCYMHMHMELPTGVHAGTDLEGNFYGPFFVDRQTAQAAGTDTTITVNVLAWLYAAVINGDRWFLNRFTTLNDFNLVAMKYNYEPLTQDHVDILGPLSAQT 3520

GIAVLDMCASLKE LLQNGMNGRTI LG SALLE D E F T P F D V V R Q C S G V T F Q S A V K R T I K G T H H W L L L T I L T S L L V L V Q S T Q W S L F F F L Y E N A F L P F A M G I I A M S A F A M M F V K
GIAVLDMCASLKE LLQNGMNGRTI LG SALLE D E F T P F D V V R Q C S G V T F Q S A V K R T I K G T Q H W L L L T I L T S L L V L V Q S T Q W S L F F F L Y E N A F L P F A M G I I A M S A F A M M F V K 3630
GIAVLDMCASLKE LLQNGMNGRTI LG SALLE D E F T P F D V V R Q C S G V T F Q S A V K R T I K G T H H W L L L T I L T S L L V L V Q S T Q W S L F F F L Y E N A F L P F A M G I I A M S A F A M M F V K 3630
GIAVLDMCASLKE LLQNGMNGRTI LG SALLE D E F T P F D V V R Q C S G V T F Q S A V K R T I K G T H H W L L L T I L T S L L V L V Q S T Q W S L F F F L Y E N A F L P F A M G I I A M S A F A M M F V K 3630

HKH AFLC L F L L P S L A T V A Y F N M V Y M P A S W V M R I M T W L D M V D T S L S G F K L K D C V M Y A S A V V L L I L M T A R T V Y D D G A R R V W T L M N V L T L V Y K V Y Y G N A L D Q A I S M W A L I I S V
HKH AFLC L F L L P S L A T V A Y F N M V Y M P A S W V M R I M T W L D M V D T S L S G F K L K D C V M Y A S A V V L L I L M T A R T V Y D D G A R R V W T L M N V L T L V Y K V Y Y G N A L D Q A I S M W A L I I S V 3740
HKH AFLC L F L L P S L A T V A Y F N M V Y M P A S W V M R I M T W L D M V D T S L -- K L K D C V M Y A S A V V L L I L M T A R T V Y D D G A R R V W T L M N V L T L V Y K V Y Y G N A L D Q A I S M W A L I I S V 3737
HKH AFLC L F L L P S L A T V A Y F N M V Y M P A S W V M R I M T W L D M V D T S L S G F K L K D C V M Y A S A V V L L I L M T A R T V Y D D G A R R V W T L M N V L T L V Y K V Y Y G N A L D Q A I S M W A L I I S V 3740

T S N Y S G V V T T V M F L A R G I V F M C V E Y C P I F F I T G N T L Q C I M L V Y C F L G Y F C T C Y F G L F C L L N R Y F R L T L G V Y D Y L V S T Q E F R Y M N S Q G L L P P K N S I D A F K L N I K L L G V G G K
T S N Y S G V V T T V M F L A R G I V F M C V E Y C P I F F I T G N T L Q C I M L V Y C F L G Y F C T C Y F G L F C L L N R Y F R L T L G V Y D Y L V S T Q E F R Y M N S Q G L L P P K N S I D A F K L N I K L L G V G G K 3850
T S N Y S G V V T T V M F L A R G I V F M C V E Y C P I F F I T G N T L Q C I M L V Y C F L G Y F C T C Y F G L F C L L N R Y F R L T L G V Y D Y L V S T Q E F R Y M N S Q G L L P P K N S I D A F K L N I K L L G V G G K 3847
T S N Y S G V V T T V M F L A R G I V F M C V E Y C P I F F I T G N T L Q C I M L V Y C F L G Y F C T C Y F G L F C L L N R Y F R L T L G V Y D Y L V S T Q E F R Y M N S Q G L L P P K N S I D A F K L N I K L L G V G G K 3850

P C I K V A T V Q S K M S D V K C T S V V L L S V L Q Q L R V E S S S K L W A Q C V Q L H N D I L L A K D T T E A F E K M V S L L S V L L S M Q G A V D I N K L C E E M L D N R A T L Q A I A S E F S S L P S Y A A F A T A
P C I K V A T V Q S K M S D V K C T S V V L L S V L Q Q L R V E S S S K L W A Q C V Q L H N D I L L A K D T T E A F E K M V S L L S V L L S M Q G A V D I N K L C E E M L D N R A T L Q A I A S E F S S L P S Y A A F A T A 3960
P C I K V A T V Q S K M S D V K C T S V V L L S V L Q Q L R V E S S S K L W A Q C V Q L H N D I L L A K D T T E A F E K M V S L L S V L L S M Q G A V D I N K L C E E M L D N R A T L Q A I A S E F S S L P S Y A A F A T A 3957
P C I K V A T V Q S K M S D V K C T S V V L L S V L Q Q L R V E S S S K L W A Q C V Q L H N D I L L A K D T T E A F E K M V S L L S V L L S M Q G A V D I N K L C E E M L D N R A T L Q A I A S E F S S L P S Y A A F A T A 3960

QEAYEQAVANGDSEVVLKKLKKSLNVAKSEFDRDAAMQRKLEKMAQAMTQMYKQARSEDKRAKVTSAMQTMLFTMLRKLDNDALNNIINNARDGCVPLNIIPLTAAKL
1 QEAYEQAVANGDSEVVLKKLKKSLNVAKSEFDRDAAMQRKLEKMAQAMTQMYKQARSEDKRAKVTSAMQTMLFTMLRKLDNDALNNIINNARDGCVPLNIIPLTAAKL 4070
2 QEAYEQAVANGDSEVVLKKLKKSLNVAKSEFDRDAAMQRKLEKMAQAMTQMYKQARSEDKRAKVTSAMQTMLFTMLRKLDNDALNNIINNARDGCVPLNIIPLTAAKL 4067
3 QEAYEQAVANGDSEVVLKKLKKSLNVAKSEFDRDAAMQRKLEKMAQAMTQMYKQARSEDKRAKVTSAMQTMLFTMLRKLDNDALNNIINNARDGCVPLNIIPLTAAKL 4070

MVVIPDYNTYKNTCDGTTFTYASALWEIQQVVDADSKIVQLSEISMDNSPNLAWPLIVTALRANSAVKLQNNELSPVALRQMSCAAGTTQACTDDNALAYYNTTKGGRF
1 MVVIPDYNTYKNTCDGTTFTYASALWEIQQVVDADSKIVQLSEISMDNSPNLAWPLIVTALRANSAVKLQNNELSPVALRQMSCAAGTTQACTDDNALAYYNTTKGGRF 4180
2 MVVIPDYNTYKNTCDGTTFTYASALWEIQQVVDADSKIVQLSEISMDNSPNLAWPLIVTALRANSAVKLQNNELSPVALRQMSCAAGTTQACTDDNALAYYNTTKGGRF 4177
3 MVVIPDYNTYKNTCDGTTFTYASALWEIQQVVDADSKIVQLSEISMDNSPNLAWPLIVTALRANSAVKLQNNELSPVALRQMSCAAGTTQACTDDNALAYYNTTKGGRF 4180

VLALLSDLQDLKWARFPKSDGTGTIYTELEPPCRFVTDTPKGPVKYLYFIKGGLNNLNRMVLGSLAATVRLQAGNATEVPANSTVLSFCAFAVDAAKAYKDYLASGGQP
1 VLALLSDLQDLKWARFPKSDGTGTIYTELEPPCRFVTDTPKGPVKYLYFIKGGLNNLNRMVLGSLAATVRLQAGNATEVPANSTVLSFCAFAVDAAKAYKDYLASGGQP 4290
2 VLALLSDLQDLKWARFPKSDGTGTIYTELEPPCRFVTDTPKGPVKYLYFIKGGLNNLNRMVLGSLAATVRLQAGNATEVPANSTVLSFCAFAVDAAKAYKDYLASGGQP 4287
3 VLALLSDLQDLKWARFPKSDGTGTIYTELEPPCRFVTDTPKGPVKYLYFIKGGLNNLNRMVLGSLAATVRLQAGNATEVPANSTVLSFCAFAVDAAKAYKDYLASGGQP 4290

ITNCVKMLCTHTGTGQAITVTPEANMDQESFGGASCCLYCRCHIDHPNPKGFCDLKGKYVQIPTTCANDPGFTLKNTVCTVGMWKGYGCSCDQLREPMLQSADAQSFL
1 ITNCVKMLCTHTGTGQAITVTPEANMDQESFGGASCCLYCRCHIDHPNPKGFCDLKGKYVQIPTTCANDPGFTLKNTVCTVGMWKGYGCSCDQLREPMLQSADAQSFL 4400
2 ITNCVKMLCTHTGTGQAITVTPEANMDQESFGGASCCLYCRCHIDHPNPKGFCDLKGKYVQIPTTCANDPGFTLKNTVCTVGMWKGYGCSCDQLREPMLQSADAQSFL 4397
3 ITNCVKMLCTHTGTGQAITVTPEANMDQESFGGASCCLYCRCHIDHPNPKGFCDLKGKYVQIPTTCANDPGFTLKNTVCTVGMWKGYGCSCDQLREPMLQSADAQSFL 4400

NRVCGVSAARLTPCGTGTSTDVVYRAFDIYNDKVAGFAKFLKTNCCRFQEKDDEDDNLIDSYFVVKRHTFSNYQHEETIYNLLKDCPAVAKHDFFKFRIDGDMVPHISRQR

1 NRVCGVSAARLTPCGTGTSTDVVYRAFDIYNDKVAGFAKFLKTNCCRFQEKDDEDDNLIDSYFVVKRHTFSNYQHEETIYNLLKDCPAVAKHDFFKFRIDGDMVPHISRQR 4510

2 NRVCGVSAARLTPCGTGTSTDVVYRAFDIYNDKVAGFAKFLKTNCCRFQEKDDEDDNLIDSYFVVKRHTFSNYQHEETIYNLLKDCPAVAKHDFFKFRIDGDMVPHISRQR 4507

3 NRVCGVSAARLTPCGTGTSTDVVYRAFDIYNDKVAGFAKFLKTNCCRFQEKDDEDDNLIDSYFVVKRHTFSNYQHEETIYNLLKDCPAVAKHDFFKFRIDGDMVPHISRQR 4510

LTKYTADLVYALRHFDEGNCCTLKEILVTYNCDDDFNKKDWYDFVENPDILRVYANLGERVRQALLKTVQFC DAMRNAGIVGVLTLDNQDLNGNWYDFGDFIQTTPG

1 LTKYTADLVYALRHFDEGNCCTLKEILVTYNCDDDFNKKDWYDFVENPDILRVYANLGERVRQALLKTVQFC DAMRNAGIVGVLTLDNQDLNGNWYDFGDFIQTTPG 4620

2 LTKYTADLVYALRHFDEGNCCTLKEILVTYNCDDDFNKKDWYDFVENPDILRVYANLGERVRQALLKTVQFC DAMRNAGIVGVLTLDNQDLNGNWYDFGDFIQTTPG 4617

3 LTKYTADLVYALRHFDEGNCCTLKEILVTYNCDDDFNKKDWYDFVENPDILRVYANLGERVRQALLKTVQFC DAMRNAGIVGVLTLDNQDLNGNWYDFGDFIQTTPG 4620

SGVPVVDSYYSLMPILTTLTRALTAESHVDLTKPYIKW DLLKYDFT EERLKLFDRYFKYWDQTYHPNCVNCLDDRCILHCANFNVL FSTVFPLTSFGPLVRKIFVDGV

1 SGVPVVDSYYSLMPILTTLTRALTAESHVDLTKPYIKW DLLKYDFT EERLKLFDRYFKYWDQTYHPNCVNCLDDRCILHCANFNVL FSTVFPLTSFGPLVRKIFVDGV 4730

2 SGVPVVDSYYSLMPILTTLTRALTAESHVDLTKPYIKW DLLKYDFT EERLKLFDRYFKYWDQTYHPNCVNCLDDRCILHCANFNVL FSTVFPLTSFGPLVRKIFVDGV 4727

3 SGVPVVDSYYSLMPILTTLTRALTAESHVDLTKPYIKW DLLKYDFT EERLKLFDRYFKYWDQTYHPNCVNCLDDRCILHCANFNVL FSTVFPLTSFGPLVRKIFVDGV 4730

PFVVSTGYHRELGVVHNQDVNLHSSRLSF KELLVYAADPAMHAASGNLLLDKRTTCSVAALTNNVAFQTVKPGNFNKDFYDFAVSKGFFKEGSSVELKHFFF A QDGNA

1 PFVVSTGYHRELGVVHNQDVNLHSSRLSF KELLVYAADPAMHAASGNLLLDKRTTCSVAALTNNVAFQTVKPGNFNKDFYDFAVSKGFFKEGSSVELKHFFF A QDGNA 4840

2 PFVVSTGYHRELGVVHNQDVNLHSSRLSF KELLVYAADPAMHAASGNLLLDKRTTCSVAALTNNVAFQTVKPGNFNKDFYDFAVSKGFFKEGSSVELKHFFF A QDGNA 4837

3 PFVVSTGYHRELGVVHNQDVNLHSSRLSF KELLVYAADPAMHAASGNLLLDKRTTCSVAALTNNVAFQTVKPGNFNKDFYDFAVSKGFFKEGSSVELKHFFF A QDGNA 4840

AISDYDYYRYNLPTMCDIRQLLFVVEVVVDKYFDGYDGGCINANQIVVNLDKSAGFPNKGKARLYYDSMSYEDQDALFAYTKRNVIPITITQMNLKYAISAKNRARTVA
1 AISDYDYYRYNLPTMCDIRQLLFVVEVVVDKYFDGYDGGCINANQIVVNLDKSAGFPNKGKARLYYDSMSYEDQDALFAYTKRNVIPITITQMNLKYAISAKNRARTVA 4950
2 AISDYDYYRYNLPTMCDIRQLLFVVEVVVDKYFDGYDGGCINANQIVVNLDKSAGFPNKGKARLYYDSMSYEDQDALFAYTKRNVIPITITQMNLKYAISAKNRARTVA 4947
3 AISDYDYYRYNLPTMCDIRQLLFVVEVVVDKYFDGYDGGCINANQIVVNLDKSAGFPNKGKARLYYDSMSYEDQDALFAYTKRNVIPITITQMNLKYAISAKNRARTVA 4950

GVSICSTMTNRQFHQKLLKSIAATRGATVVIIGTSKFYGGWHNMLKTVSDVENPHLMGDYPKCDRAMPNMLRIMASLVLARKHTCCSLSHRFYRLANECAQVLSEVM
1 GVSICSTMTNRQFHQKLLKSIAATRGATVVIIGTSKFYGGWHNMLKTVSDVENPHLMGDYPKCDRAMPNMLRIMASLVLARKHTCCSLSHRFYRLANECAQVLSEVM 5060
2 GVSICSTMTNRQFHQKLLKSIAATRGATVVIIGTSKFYGGWHNMLKTVSDVENPHLMGDYPKCDRAMPNMLRIMASLVLARKHTCCSLSHRFYRLANECAQVLSEVM 5057
3 GVSICSTMTNRQFHQKLLKSIAATRGATVVIIGTSKFYGGWHNMLKTVSDVENPHLMGDYPKCDRAMPNMLRIMASLVLARKHTCCSLSHRFYRLANECAQVLSEVM 5060

CGGSLYVKPGGTSSGDATTAYANSVFNICQAVTANVNALLSTDGNKIADKYVRNLQHRLYECLYRNRDVTDFTNEFYAYLRKHFSMMILSDDAVVCFNSTYASQGLVAS
1 CGGSLYVKPGGTSSGDATTAYANSVFNICQAVTANVNALLSTDGNKIADKYVRNLQHRLYECLYRNRDVTDFTNEFYAYLRKHFSMMILSDDAVVCFNSTYASQGLVAS 5170
2 CGGSLYVKPGGTSSGDATTAYANSVFNICQAVTANVNALLSTDGNKIADKYVRNLQHRLYECLYRNRDVTDFTNEFYAYLRKHFSMMILSDDAVVCFNSTYASQGLVAS 5167
3 CGGSLYVKPGGTSSGDATTAYANSVFNICQAVTANVNALLSTDGNKIADKYVRNLQHRLYECLYRNRDVTDFTNEFYAYLRKHFSMMILSDDAVVCFNSTYASQGLVAS 5170

IKNFKSVLYQQNNVFMSEAKCWTETDLTKGPHEFCQSHTMLVKQGDDYVLPYPDPSRILGAGCFVDDIVKTDTLMIERFVSLAIDAYPLTKHPNQEYADVFLYLQYI
1 IKNFKSVLYQQNNVFMSEAKCWTETDLTKGPHEFCQSHTMLVKQGDDYVLPYPDPSRILGAGCFVDDIVKTDTLMIERFVSLAIDAYPLTKHPNQEYADVFLYLQYI 5280
2 IKNFKSVLYQQNNVFMSEAKCWTETDLTKGPHEFCQSHTMLVKQGDDYVLPYPDPSRILGAGCFVDDIVKTDTLMIERFVSLAIDAYPLTKHPNQEYADVFLYLQYI 5277
3 IKNFKSVLYQQNNVFMSEAKCWTETDLTKGPHEFCQSHTMLVKQGDDYVLPYPDPSRILGAGCFVDDIVKTDTLMIERFVSLAIDAYPLTKHPNQEYADVFLYLQYI 5280

RKLHDELTGHMLDMYSVMLTNDNTSRYWEPEFYEAMYTPHTVLQAVGACVLCNSQTSLRCGACIRRPFLLCCKCCYDHVISTSHKLVL SVNPNPYVCNAPGCDVTDTQLYLG

1 RKLHDELTGHMLDMYSVMLTNDNTSRYWEPEFYEAMYTPHTVLQAVGACVLCNSQTSLRCGACIRRPFLLCCKCCYDHVISTSHKLVL SVNPNPYVCNAPGCDVTDTQLYLG 5390

2 RKLHDELTGHMLDMYSVMLTNDNTSRYWEPEFYEAMYTPHTVLQAVGACVLCNSQTSLRCGACIRRPFLLCCKCCYDHVISTSHKLVL SVNPNPYVCNAPGCDVTDTQLYLG 5387

3 RKLHDELTGHMLDMYSVMLTNDNTSRYWEPEFYEAMYTPHTVLQAVGACVLCNSQTSLRCGACIRRPFLLCCKCCYDHVISTSHKLVL SVNPNPYVCNAPGCDVTDTQLYLG 5390

GMSYYCKSHKPPISFPLCANGQVFGLYKNTCVGSDNVTFNIAITCDWTNAGDYILANTCTERLKLFAAETLKATEETFKLSYGIATREVLSDRELHLSWEVGKPRPPL

1 GMSYYCKSHKPPISFPLCANGQVFGLYKNTCVGSDNVTFNIAITCDWTNAGDYILANTCTERLKLFAAETLKATEETFKLSYGIATREVLSDRELHLSWEVGKPRPPL 5500

2 GMSYYCKSHKPPISFPLCANGQVFGLYKNTCVGSDNVTFNIAITCDWTNAGDYILANTCTERLKLFAAETLKATEETFKLSYGIATREVLSDRELHLSWEVGKPRPPL 5497

3 GMSYYCKSHKPPISFPLCANGQVFGLYKNTCVGSDNVTFNIAITCDWTNAGDYILANTCTERLKLFAAETLKATEETFKLSYGIATREVLSDRELHLSWEVGKPRPPL 5500

NRNYVFTGYRVTKNSKVQIGEYTFEKGDYGDADVYRGTTTYKLNVDYFVLTSHVMPLSAPTLVPQEHYVRITGLYPTLNISDEFSSNVANYQKVGMQKYSTLQGPPGT

1 NRNYVFTGYRVTKNSKVQIGEYTFEKGDYGDADVYRGTTTYKLNVDYFVLTSHVMPLSAPTLVPQEHYVRITGLYPTLNISDEFSSNVANYQKVGMQKYSTLQGPPGT 5610

2 NRNYVFTGYRVTKNSKVQIGEYTFEKGDYGDADVYRGTTTYKLNVDYFVLTSHVMPLSAPTLVPQEHYVRITGLYPTLNISDEFSSNVANYQKVGMQKYSTLQGPPGT 5607

3 NRNYVFTGYRVTKNSKVQIGEYTFEKGDYGDADVYRGTTTYKLNVDYFVLTSHVMPLSAPTLVPQEHYVRITGLYPTLNISDEFSSNVANYQKVGMQKYSTLQGPPGT 5610

GKSHFAIGLALYYP SARIVYTACSHAADV DALCEKALKYL PIDKCSRII PARARVE CFDKFKVN STLEQYVFC TVNALPETTADIVV FDEISMAT NYDLSVVNARLRAKH Y

1 GKSHFAIGLALYYP SARIVYTACSHAADV DALCEKALKYL PIDKCSRII PARARVE CFDKFKVN STLEQYVFC TVNALPETTADIVV FDEISMAT NYDLSVVNARLRAKH Y 5720

2 GKSHFAIGLALYYP SARIVYTACSHAADV DALCEKALKYL PIDKCSRII PARARVE CFDKFKVN STLEQYVFC TVNALPETTADIVV FDEISMAT NYDLSVVNARLRAKH Y 5717

3 GKSHFAIGLALYYP SARIVYTACSHAADV DALCEKALKYL PIDKCSRII PARARVE CFDKFKVN STLEQYVFC TVNALPETTADIVV FDEISMAT NYDLSVVNARLRAKH Y 5720

VYIGDPAQLPAPRTLLTKTLEPEYFNSVCRLMKTIGPDMFLGTCRRCPAEIVDTVSALVYDNKLKAHKDKSAQCFKMFYKGVITHDVSSAINRPQIGVVREFLTRNPAW

1 VYIGDPAQLPAPRTLLTKTLEPEYFNSVCRLMKTIGPDMFLGTCRRCPAEIVDTVSALVYDNKLKAHKDKSAQCFKMFYKGVITHDVSSAINRPQIGVVREFLTRNPAW 5830
2 VYIGDPAQLPAPRTLLTKTLEPEYFNSVCRLMKTIGPDMFLGTCRRCPAEIVDTVSALVYDNKLKAHKDKSAQCFKMFYKGVITHDVSSAINRPQIGVVREFLTRNPAW 5827
3 VYIGDPAQLPAPRTLLTKTLEPEYFNSVCRLMKTIGPDMFLGTCRRCPAEIVDTVSALVYDNKLKAHKDKSAQCFKMFYKGVITHDVSSAINRPQIGVVREFLTRNPAW 5830

RKAVFISPYNSQNAVASKILGLPTQVDSSQGSEYDYVIFTQTTEAHSCNVNRFNVAITRAKVGILCIMSDRDLYDKLQFTSLEIPRRNVATLQAENVTLFKDCSKVI

1 RKAVFISPYNSQNAVASKILGLPTQVDSSQGSEYDYVIFTQTTEAHSCNVNRFNVAITRAKVGILCIMSDRDLYDKLQFTSLEIPRRNVATLQAENVTLFKDCSKVI 5940
2 RKAVFISPYNSQNAVASKILGLPTQVDSSQGSEYDYVIFTQTTEAHSCNVNRFNVAITRAKVGILCIMSDRDLYDKLQFTSLEIPRRNVATLQAENVTLFKDCSKVI 5937
3 RKAVFISPYNSQNAVASKILGLPTQVDSSQGSEYDYVIFTQTTEAHSCNVNRFNVAITRAKVGILCIMSDRDLYDKLQFTSLEIPRRNVATLQAENVTLFKDCSKVI 5940

TGLHPTQAPTHLSVDTKFTEGLCVDIPGIPKDMTYRRLISMMGFKMNYQVNNGYPNMFITREEAIRHVRAWIGFDVEGCHATREAVGTNLPLQLGFSTGVNLVAVPTGYV

1 TGLHPTQAPTHLSVDTKFTEGLCVDIPGIPKDMTYRRLISMMGFKMNYQVNNGYPNMFITREEAIRHVRAWIGFDVEGCHATREAVGTNLPLQLGFSTGVNLVAVPTGYV 6050
2 TGLHPTQAPTHLSVDTKFTEGLCVDIPGIPKDMTYRRLISMMGFKMNYQVNNGYPNMFITREEAIRHVRAWIGFDVEGCHATREAVGTNLPLQLGFSTGVNLVAVPTGYV 6047
3 TGLHPTQAPTHLSVDTKFTEGLCVDIPGIPKDMTYRRLISMMGFKMNYQVNNGYPNMFITREEAIRHVRAWIGFDVEGCHATREAVGTNLPLQLGFSTGVNLVAVPTGYV 6050

DTPNNNTDSRVSAKPPPGDQFKHLIPLMYKGLPNVVRRIKIVQMLSRTLKNLSDRVVFVLWAHGFELTSMKYFVKIGPERTCCLCDRRATCFSTASDTYACWHHSIGFDY

1 DTPNNNTDSRVSAKPPPGDQFKHLIPLMYKGLPNVVRRIKIVQMLSRTLKNLSDRVVFVLWAHGFELTSMKYFVKIGPERTCCLCDRRATCFSTASDTYACWHHSIGFDY 6160
2 DTPNNNTDSRVSAKPPPGDQFKHLIPLMYKGLPNVVRRIKIVQMLSRTLKNLSDRVVFVLWAHGFELTSMKYFVKIGPERTCCLCDRRATCFSTASDTYACWHHSIGFDY 6157
3 DTPNNNTDSRVSAKPPPGDQFKHLIPLMYKGLPNVVRRIKIVQMLSRTLKNLSDRVVFVLWAHGFELTSMKYFVKIGPERTCCLCDRRATCFSTASDTYACWHHSIGFDY 6160

VYNPFMIDVQQWGFTGNLQSNHDLYCQVHGNAHVASCDAIMTRCLAVHECFVKRVDWTIEYPIIGDELKINAACRKVQHMVVAALLADKFPVLHDIGNPKAIKCPQAD
1 VYNPFMIDVQQWGFTGNLQSNHDLYCQVHGNAHVASCDAIMTRCLAVHECFVKRVDWTIEYPIIGDELKINAACRKVQHMVVAALLADKFPVLHDIGNPKAIKCPQAD 6270
2 VYNPFMIDVQQWGFTGNLQSNHDLYCQVHGNAHVASCDAIMTRCLAVHECFVKRVDWTIEYPIIGDELKINAACRKVQHMVVAALLADKFPVLHDIGNPKAIKCPQAD 6267
3 VYNPFMIDVQQWGFTGNLQSNHDLYCQVHGNAHVASCDAIMTRCLAVHECFVKRVDWTIEYPIIGDELKINAACRKVQHMVVAALLADKFPVLHDIGNPKAIKCPQAD 6270

VEWKFYDAQPCSDKAYKIEELFYSYATHSDKFTDGVCFLFWNCNVDRYPANSIVCRFDTRLVSLNLPGCDGGSLYVNKHAFHTPAFDKSAFVNLKQLPFFYSDSPCESH
1 VEWKFYDAQPCSDKAYKIEELFYSYATHSDKFTDGVCFLFWNCNVDRYPANSIVCRFDTRLVSLNLPGCDGGSLYVNKHAFHTPAFDKSAFVNLKQLPFFYSDSPCESH 6380
2 VEWKFYDAQPCSDKAYKIEELFYSYATHSDKFTDGVCFLFWNCNVDRYPANSIVCRFDTRLVSLNLPGCDGGSLYVNKHAFHTPAFDKSAFVNLKQLPFFYSDSPCESH 6377
3 VEWKFYDAQPCSDKAYKIEELFYSYATHSDKFTDGVCFLFWNCNVDRYPANSIVCRFDTRLVSLNLPGCDGGSLYVNKHAFHTPAFDKSAFVNLKQLPFFYSDSPCESH 6380

GKQVVSDIDYVPLKSATCITRCNLGGAVCRHHANEYRLYLDAYNMMISAGFSLWVYKQFDTYNLWNTFTRLQSLENVAFNVNKGHFDGQQGEVPVSIINNTVYTKVDGV
1 GKQVVSDIDYVPLKSATCITRCNLGGAVCRHHANEYRLYLDAYNMMISAGFSLWVYKQFDTYNLWNTFTRLQSLENVAFNVNKGHFDGQQGEVPVSIINNTVYTKVDGV 6490
2 GKQVVSDIDYVPLKSATCITRCNLGGAVCRHHANEYRLYLDAYNMMISAGFSLWVYKQFDTYNLWNTFTRLQSLENVAFNVNKGHFDGQQGEVPVSIINNTVYTKVDGV 6487
3 GKQVVSDIDYVPLKSATCITRCNLGGAVCRHHANEYRLYLDAYNMMISAGFSLWVYKQFDTYNLWNTFTRLQSLENVAFNVNKGHFDGQQGEVPVSIINNTVYTKVDGV 6490

DVELFENKTTLPVNVAFELWAKRNIPVPEVKILNNLGVDIAANTVIWDYKRDPAPAHISTIGVCSMTDIACKPTETICAPLTFFDGRVDGQVDFRNARNGVLITEGSV
1 DVELFENKTTLPVNVAFELWAKRNIPVPEVKILNNLGVDIAANTVIWDYKRDPAPAHISTIGVCSMTDIACKPTETICAPLTFFDGRVDGQVDFRNARNGVLITEGSV 6600
2 DVELFENKTTLPVNVAFELWAKRNIPVPEVKILNNLGVDIAANTVIWDYKRDPAPAHISTIGVCSMTDIACKPTETICAPLTFFDGRVDGQVDFRNARNGVLITEGSV 6597
3 DVELFENKTTLPVNVAFELWAKRNIPVPEVKILNNLGVDIAANTVIWDYKRDPAPAHISTIGVCSMTDIACKPTETICAPLTFFDGRVDGQVDFRNARNGVLITEGSV 6600

KGLQPSVGPQASLNGVTLIGEAVKTQFNYYKKVDGVVQQLPETYFTQSRNLQEFKPRSQMEIDFLEAMDEFIERYKLEGYAFEHIVYGDFSHSQLGLHLIGLAKRF
1 KGLQPSVGPQASLNGVTXXXXXXXXXXXXXXVQQLPETYFTQSRXXXXXXXXSQXXXXXXELAMDEFIERYKLEGYAFEHIVYGDFSHSQLGLHLIGLAKRF 6710
2 KGLQPSVGPQASLNGVTLIGEAVKTQFNYYKKVDGVVQQLPETYFTQSRNLQEFKPRSQMEIDFLEAMDEFIERYKLEGYAFEHIVYGDFSHSQLGLHLIGLAKRF 6707
3 KGLQPSVGPQASLNGVTLIGEAVKTQFNYYKKVDGVVQQLPETYFTQSRNLQEFKPRSQMEIDFLEAMDEFIERYKLEGYAFEHIVYGDFSHSQLGLHLIGLAKRF 6710

KESPFLEDFIPMDSTVKNYFITDAQTGSSKCVCSVIDLLLDDFVEIIKSQDLSVVSKVVKVTIDYTEISFMLWCKDGHVETFYPKLQSSQAWQPGVAMPNLYKMQRMLL
1 RESPFELEDFIPMDSTVKNYFITDAQTGSSKCVCSVIDLLLDDFVEIIKSQDLSVVSKVVKVTIDYTEISFMLWCKDGHVETFYPKLQSSQAWQPGVAMPNLYKMQRMLL 6820
2 KESPFLEDFIPMDSTVKNYFITDAQTGSSKCVCSVIDLLLDDFVEIIKSQDLSVVSKVVKVTIDYTEISFMLWCKDGHVETFYPKLQSSQAWQPGVAMPNLYKMQRMLL 6817
3 KESPFLEDFIPMDSTVKNYFITDAQTGSSKCVCSVIDLLLDDFVEIIKSQDLSVVSKVVKVTIDYTEISFMLWCKDGHVETFYPKLQSSQAWQPGVAMPNLYKMQRMLL 6820

EKCDLQNYGDSATLPKGIMMNVAKYTQLCQYLNTLTLAVPYNMRVIHFGAGSDKGVAPGTAVLRQWLPTGTLLVSDLDNDFVSDADSTLIGDCATVHTANKWDLIISDMY
1 EKCDLQNYGDSATLPKGIMMNVAKYTQLCQYLNTLTLAVPYNMRVIHFGAGSDKGVAPGTAVLRQWLPTGTLLVSDLDNDFVSDADSTLIGDCATVHTANKWDLIISDMY 6930
2 EKCDLQNYGDSATLPKGIMMNVAKYTQLCQYLNTLTLAVPYNMRVIHFGAGSDKGVAPGTAVLRQWLPTGTLLVSDLDNDFVSDADSTLIGDCATVHTANKWDLIISDMY 6927
3 EKCDLQNYGDSATLPKGIMMNVAKYTQLCQYLNTLTLAVPYNMRVIHFGAGSDKGVAPGTAVLRQWLPTGTLLVSDLDNDFVSDADSTLIGDCATVHTANKWDLIISDMY 6930

DPKTKNVTKENDSKEGFFTYICGFIQQKLAALGGSVAIKITEHSWNADLYKLMGHFAWWTAFTVNVNASSSEAFLIGCNYLGKPREQIDGYVMHANYIFWRNTNPIQLSSY
1 DPKTKNVTKENDSKEGFFTYICGFIQQKLAALGGSVAIKITEHSWNADLYKLMGHFAWWTAFTVNVNASSSEAFLIGCNYLGKPREQIDGYVMHANYIFWRNTNPIQLSSY 7040
2 DPKTKNVTKENDSKEGFFTYICGFIQQKLAALGGSVAIKITEHSWNADLYKLMGHFAWWTAFTVNVNASSSEAFLIGCNYLGKPREQIDGYVMHANYIFWRNTNPIQLSSY 7037
3 DPKTKNVTKENDSKEGFFTYICGFIQQKLAALGGSVAIKITEHSWNADLYKLMGHFAWWTAFTVNVNASSSEAFLIGCNYLGKPREQIDGYVMHANYIFWRNTNPIQLSSY 7040

SLFDMSKFPLKLRGTAVMSLKEGQINDMILSLLSKGRLIIRENNRVVISSDVLVNN	
1 SLFDMSKFPLKLRGTAVMSLKEGQINDMILSLLSKGRLIIRENNRVVISSDVLVNN	7096
2 SLFDMSKFPLKLRGTAVMSLKEGQINDMILSLLSKGRLIIRENNRVVISSDVLVNN	7093
3 SLFDMSKFPLKLRGTAVMSLKEGQINDMILSLLSKGRLIIRENNRVVISSDVLVNN	7096

Figure S6. Schematic view of contigs of the ORF1ab polyprotein of 1. Alpha Variant (B.1.1.7) (UDQ41836.1) and 2. Delta Variant (B.1.617.21) (UDU36744.1) of SARs-CoV-2 with 3. reference Strain (Wuhan) (YP_009724389.1).

7. ORF3a protein

MDLFMRIFTIGTVTLKQGEIKDATPSDFVRATATIPIQASLPFGWLIVGVALLAVFQSASKIITLKKRWQLALSKGVHFVCNLLLLFVTVYSHLLLVAAGLEAPFLYLYA	
1 MDLFMRIFTIGTVTLKQGEIKDATPSDFVRATATIPIQASLPFGWLIVGVALLAVFQSASKIITLKKRWQLALSKGVHFVCNLLLLFVTVYSHLLLVAAGLEAPFLYLYA	110
2 MDLFMRIFTIGTVTLKQGEIKDATPSDFVRATATIPIQASLPFGWLIVGVALLAVFQSASKIITLKKRWQLALSKGVHFVCNLLLLFVTVYSHLLLVAAGLEAPFLYLYA	110
3 MDLFMRIFTIGTVTLKQGEIKDATPSDFVRATATIPIQASLPFGWLIVGVALLAVFQSASKIITLKKRWQLALSKGVHFVCNLLLLFVTVYSHLLLVAAGLEAPFLYLYA	110

LVYFLQSINFVRIIMRLWLCKCRSKNPLLYDANYFLCWHTNCYDYCIPYNSVTSSIVITS GD GTT SPISEHDYQIGGYTEKWESGVKDCVVLHSYFTSDYYQLYSTQLS	
1 LVYFLQSINFVRIIMRLWLCKCRSKNPLLYDANYFLCWHTNCYDYCIPYNSVTSSIVITS GD GTT SPISEHDYQIGGYTEKWESGVKDCVVLHSYFTSDYYQLYSTQLS	220
2 LVYFLQSINFVRIIMRLWLCKCRSKNPLLYDANYFLCWHTNCYDYCIPYNSVTSSIVITS GD GTT SPISEHDYQIGGYTEKWESGVKDCVVLHSYFTSDYYQLYSTQLS	220
3 LVYFLQSINFVRIIMRLWLCKCRSKNPLLYDANYFLCWHTNCYDYCIPYNSVTSSIVITS GD GTT SPISEHDYQIGGYTEKWESGVKDCVVLHSYFTSDYYQLYSTQLS	220

TDTGVEHVTFFIYNKIVDEPEEHVQIHTIDGSSGVVNPNPMEPIYDEPTTTTSVPL	
1 TDTGVEHVTFFIYNKIVDEPEEHVQIHTIDGSSGVVNPNPMEPIYDEPTTTTSVPL	275
2 TDTGVEHVTFFIYNKIVDEPEEHVQIHTIDGSSGVVNPNPMEPIYDEPTTTTSVPL	275
3 TDTGVEHVTFFIYNKIVDEPEEHVQIHTIDGSSGVVNPNPMEPIYDEPTTTTSVPL	275

Figure S7. Schematic view of contigs of the ORF3a protein of 1. Alpha Variant (B.1.1.7) (UDQ41839.1) and 2. Delta Variant (B.1.617.21) (UDU36747.1) of SARs-CoV-2 with 3. reference Strain (Wuhan) (YP_009724391.1).

8. ORF6 protein

The figure shows a schematic representation of the ORF6 protein contigs. A red bar at the top represents the reference strain (Wuhan). Below it are three yellow bars representing the Alpha Variant (B.1.1.7), Delta Variant (B.1.617.21), and another Delta Variant (B.1.617.21). The sequence for each variant is identical: MFHLVDFQVTIAEILLIIMRTFKVSIWNLDYIINLIIKNLSKSLTENKYSQLDEEQPMEI. The length of the sequence is indicated as 60 units for each variant.

MFHLVDFQVTIAEILLIIMRTFKVSIWNLDYIINLIIKNLSKSLTENKYSQLDEEQPMEI
1 MFHLVDFQVTIAEILLIIMRTFKVSIWNLDYIINLIIKNLSKSLTENKYSQLDEEQPMEI 60
2 MFHLVDFQVTIAEILLIIMRTFKVSIWNLDYIINLIIKNLSKSLTENKYSQLDEEQPMEI 60
3 MFHLVDFQVTIAEILLIIMRTFKVSIWNLDYIINLIIKNLSKSLTENKYSQLDEEQPMEI 60

Figure S8. Schematic view of contigs of the ORF6 protein of 1. Alpha Variant (B.1.1.7) (UDQ41842.1) and 2. Delta Variant (B.1.617.21) (UDU36750.1) of SARs-CoV-2 with 3. reference Strain (Wuhan) (YP_009724394.1).

9. ORF7a protein

The figure shows a schematic representation of the ORF7a protein contigs. A red bar at the top represents the reference strain (Wuhan). Below it are three yellow bars representing the Alpha Variant (B.1.1.7), Delta Variant (B.1.617.21), and another Delta Variant (B.1.617.21). The sequence for each variant is identical: MKIILFLALITLATCELYHQECVRGTTVLLKEPCSSGTYEGNSPFHPLADNKFALTFCSTQFAFACPDGVKHVYQLRARSVSPKL FIRQEEVQELYSPIFLIVAAIVFI. The length of the sequence is indicated as 110 units for each variant.

MKIILFLALITLATCELYHQECVRGTTVLLKEPCSSGTYEGNSPFHPLADNKFALTFCSTQFAFACPDGVKHVYQLRARSVSPKL FIRQEEVQELYSPIFLIVAAIVFI
1 MKIILFLALITLATCELYHQECVRGTTVLLKEPCSSGTYEGNSPFHPLADNKFALTFCSTQFAFACPDGVKHVYQLRARSVSPKL FIRQEEVQELYSPIFLIVAAIVFI 110
2 MKIILFLALITLATCELYHQECVRGTTVLLKEPCSSGTYEGNSPFHPLADNKFALTFCSTQFAFACPDGVKHVYQLRARSVSPKL FIRQEEVQELYSPIFLIVAAIVFI 110
3 MKIILFLALITLATCELYHQECVRGTTVLLKEPCSSGTYEGNSPFHPLADNKFALTFCSTQFAFACPDGVKHVYQLRARSVSPKL FIRQEEVQELYSPIFLIVAAIVFI 110

The figure shows a schematic representation of the ORF7a protein contigs. A red bar at the top represents the reference strain (Wuhan). Below it are three yellow bars representing the Alpha Variant (B.1.1.7), Delta Variant (B.1.617.21), and another Delta Variant (B.1.617.21). The sequence for each variant is identical: TLCFTLKRKT. The length of the sequence is indicated as 120 units for each variant.

TLCFTLKRKT
1 TLCFTLKRKT 120
2 TLCFTLKRKT 120
3 TLCFTLKRKT 120

Figure S9. Schematic view of contigs of the ORF7a protein of 1. Alpha Variant (B.1.1.7) (UDQ41843.1) and 2. Delta Variant (B.1.617.21) (UDU36751.1) of SARs-CoV-2 with 3. reference Strain (Wuhan) (YP_009724395.1).

10. ORF7b protein

MIELSLIDFYLCFLAFLLFVLVLIIMLIIFWFSLELQDHNETCHA
1 MIELSLIDFYLCFLAFLLFVLVLIIMLIIFWFSLELQDHNETCHA 43
2 MIELSLIDFYLCFLAFLLFVLVLIIMLIIFWFSLELQDHNETCHA 43
3 MIELSLIDFYLCFLAFLLFVLVLIIMLIIFWFSLELQDHNETCHA 43

Figure S10. Schematic view of contigs of the ORF7b protein of 1. Alpha Variant (B.1.1.7) (UDQ41844.1) and 2. Delta Variant (B.1.617.21) (UDU36752.1) of SARs-CoV-2 with 3. reference Strain (Wuhan) (YP_009725318.1).

11. ORF8 protein

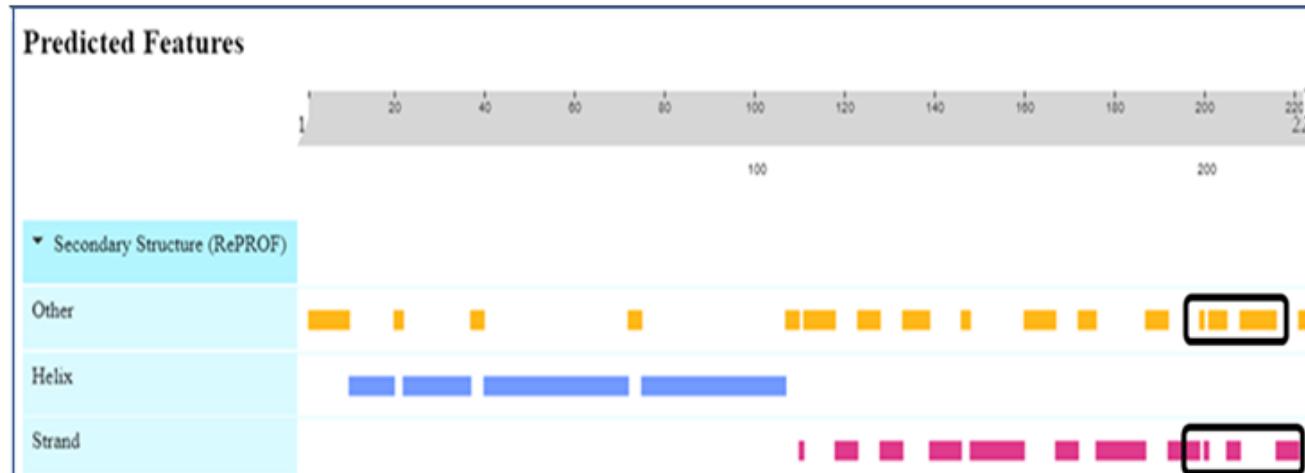
MKFLVFLGIITTVAAFHQECSLQSCTHQPYVVDDPCPIHFYSKWyIRVGARKSAPLIELCVDEAGSKSPIQYIDIGNYTVSCLPFTINCQEPKLGSVVRCFSFYEDFLE 110
1 MKFLVFLGIITTVAAFHQECSLQSCTHQPYVVDDPCPIHFYSKWyIRVGARKSAPLIELCVDEAGSKSPIQYIDIGNYTVSCLPFTINCQEPKLGSVVRCFSFYEDFLE
2 MKFLVFLGIITTVAAFHQECSLQSCTHQPYVVDDPCPIHFYSKWyIRVGARKSAPLIELCVDEAGSKSPIQYIDIGNYTVSCLPFTINCQEPKLGSVVRCFSFYEDFLE 110

YHDVRVVLDFI 121
1 YHDVRVVLDFI
2 YHDVRVVLDFI 121

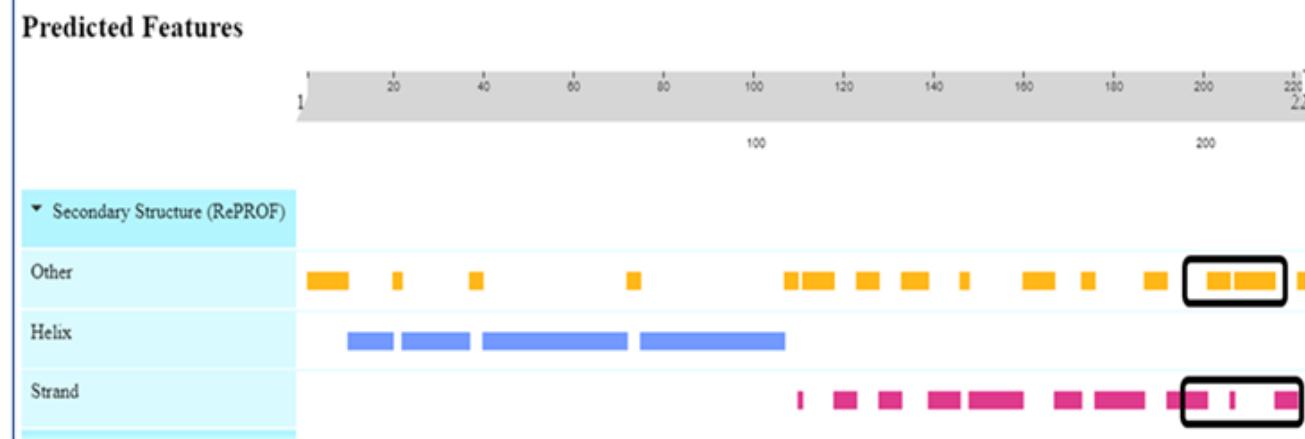
Figure S11. Schematic view of contigs of the ORF8 protein of 1. Delta Variant (B.1.617.21) (UDU36753.1) of SARs-CoV-2 with 2. reference Strain (Wuhan) (YP_009724396.1).

Membrane Protein

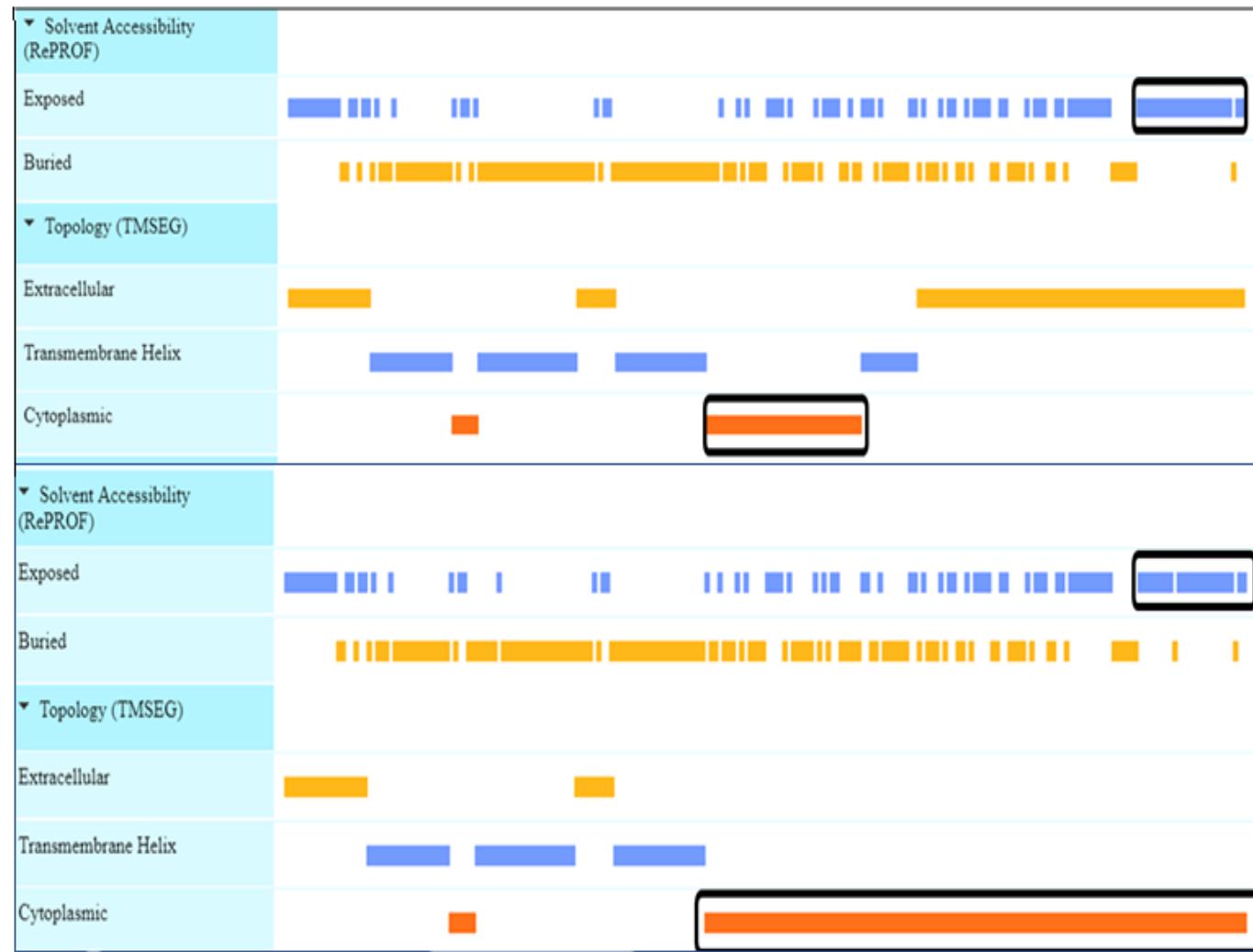
Alpha (B.1.617.21)
UDU36749.1



Wuhan
YP_009724393.1



Alpha (B.1.617.21)
UDU36749.1



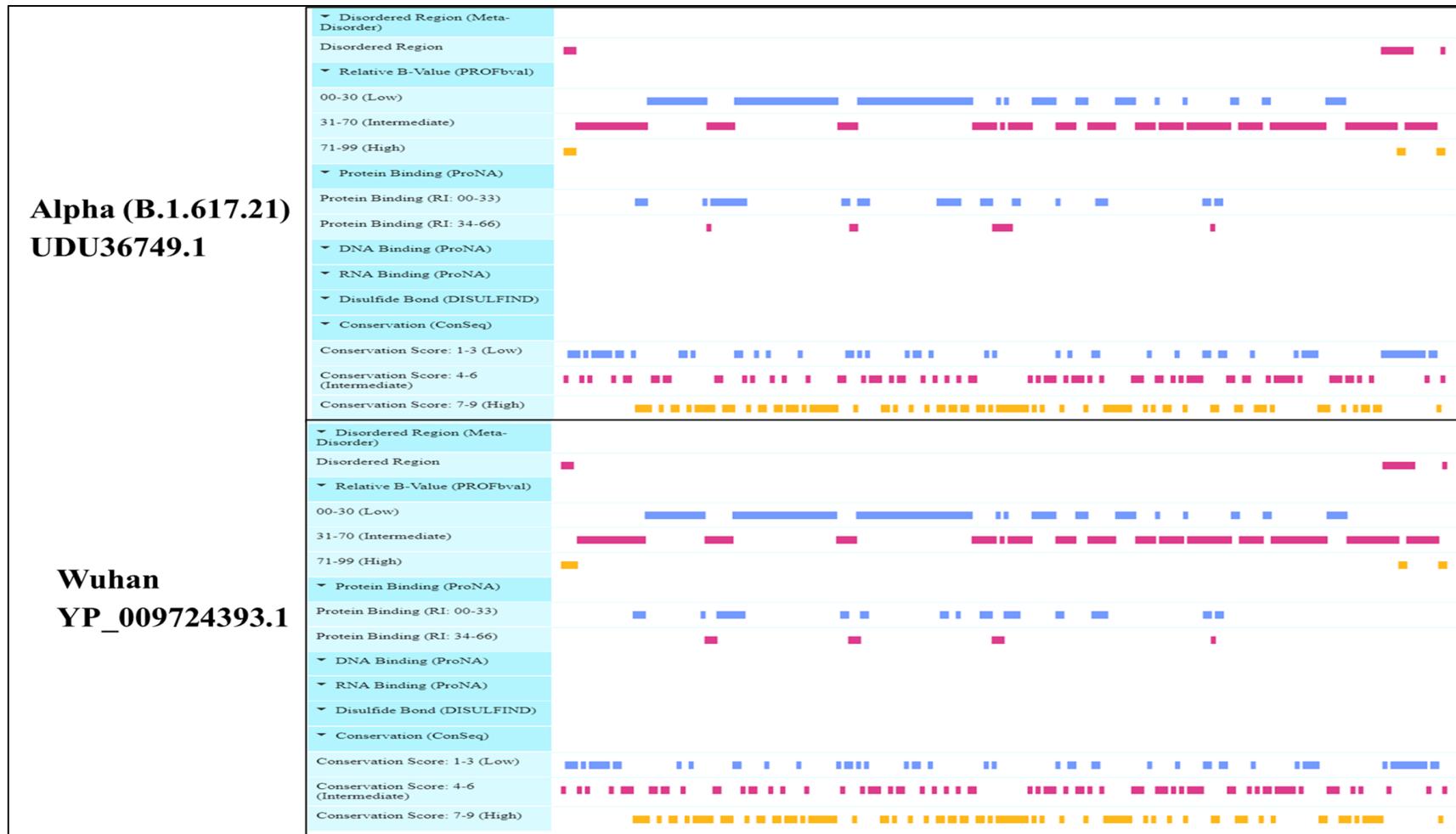
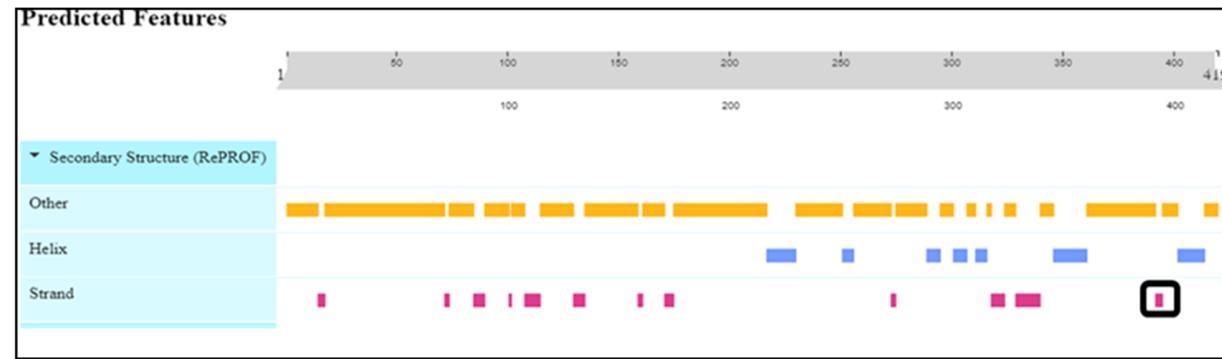


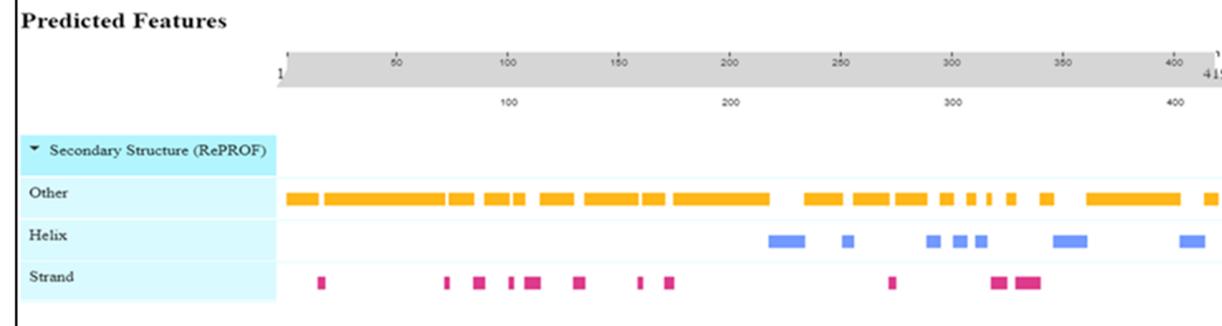
Figure S12. Viewer lays out predicted features of protein structural and functional features of Membrane Glycoproteins.

Nucleocapsid phosphoprotein

Alpha (B.1.617.21)
UDU36754.1



Delta (B.1.1.7)
UDQ41846.1



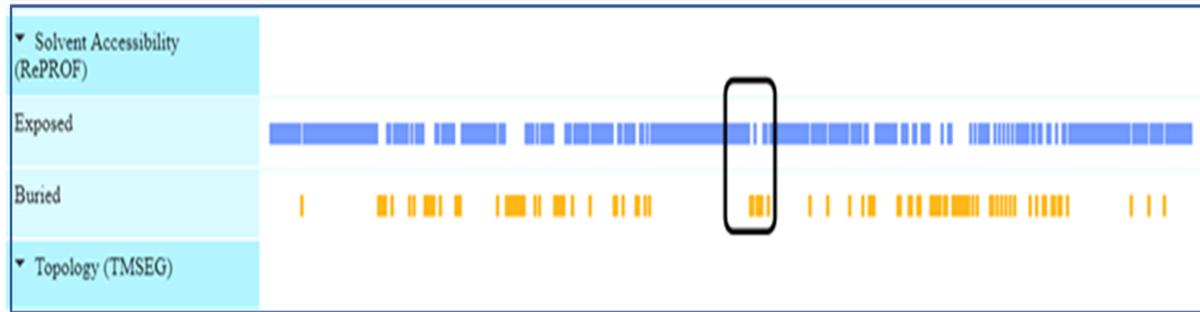
Wuhan
YP_009724397.2



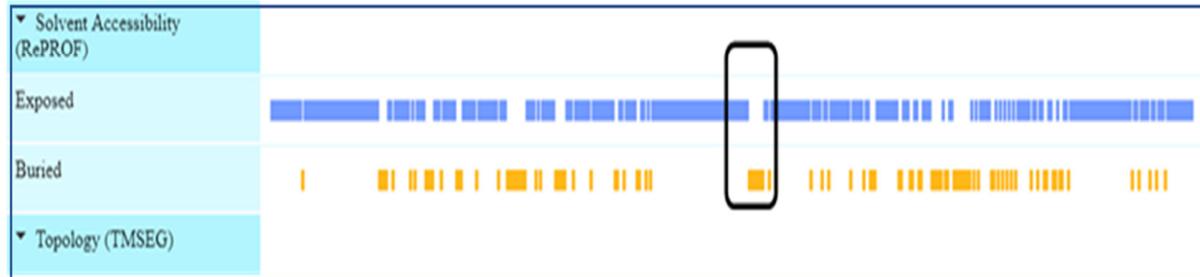
Alpha (B.1.617.21)
UDU36754.1



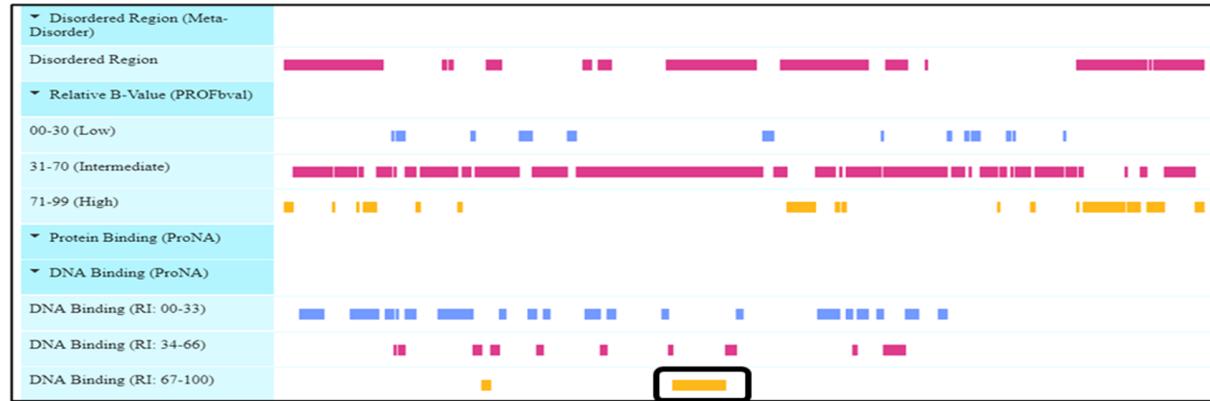
Delta (B.1.1.7)
UDQ41846.1



Wuhan
YP_009724397.2



Alpha (B.1.617.21)
UDU36754.1



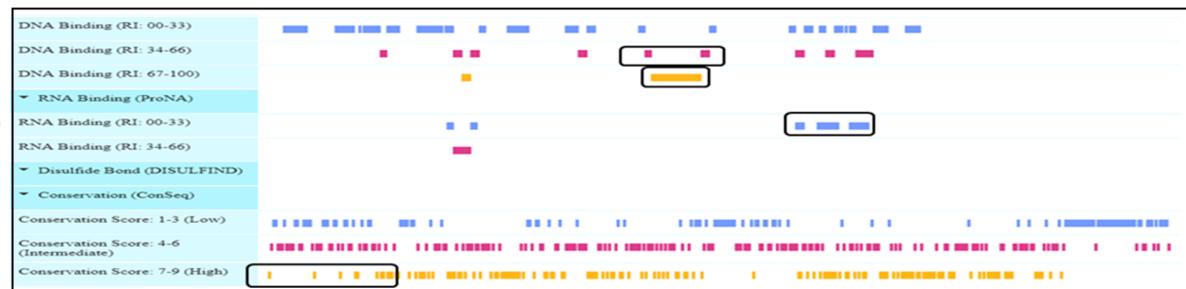
Delta (B.1.1.7)
UDQ41846.1



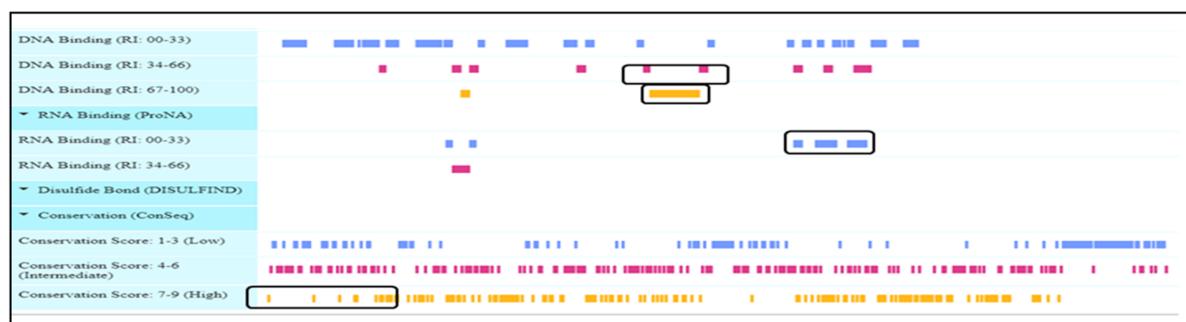
Wuhan
YP_009724397.2



Alpha (B.1.617.21)
UDU36754.1



Delta (B.1.1.7)
UDQ41846.1



Wuhan
YP_009724397.2

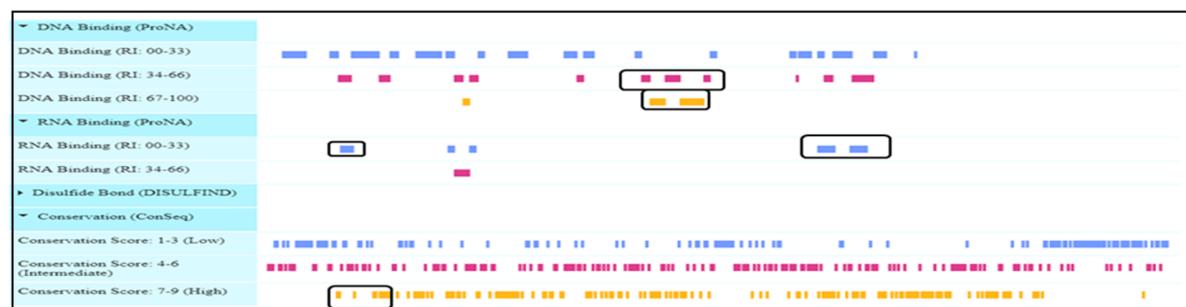
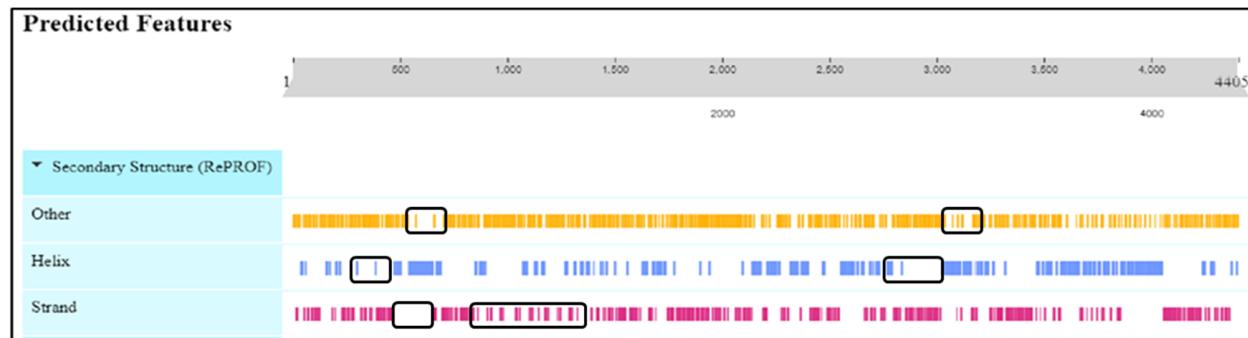


Figure S13. Viewer lays out predicted features of protein structural and functional features of Nucleocapsid phosphoprotein.

1. ORF1a Polyprotein

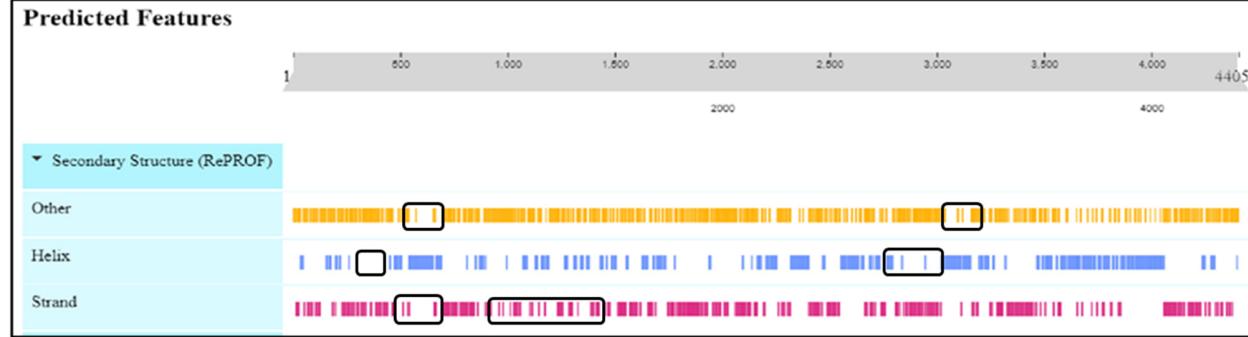
Alpha
B.1.617.21
UDU36745.1



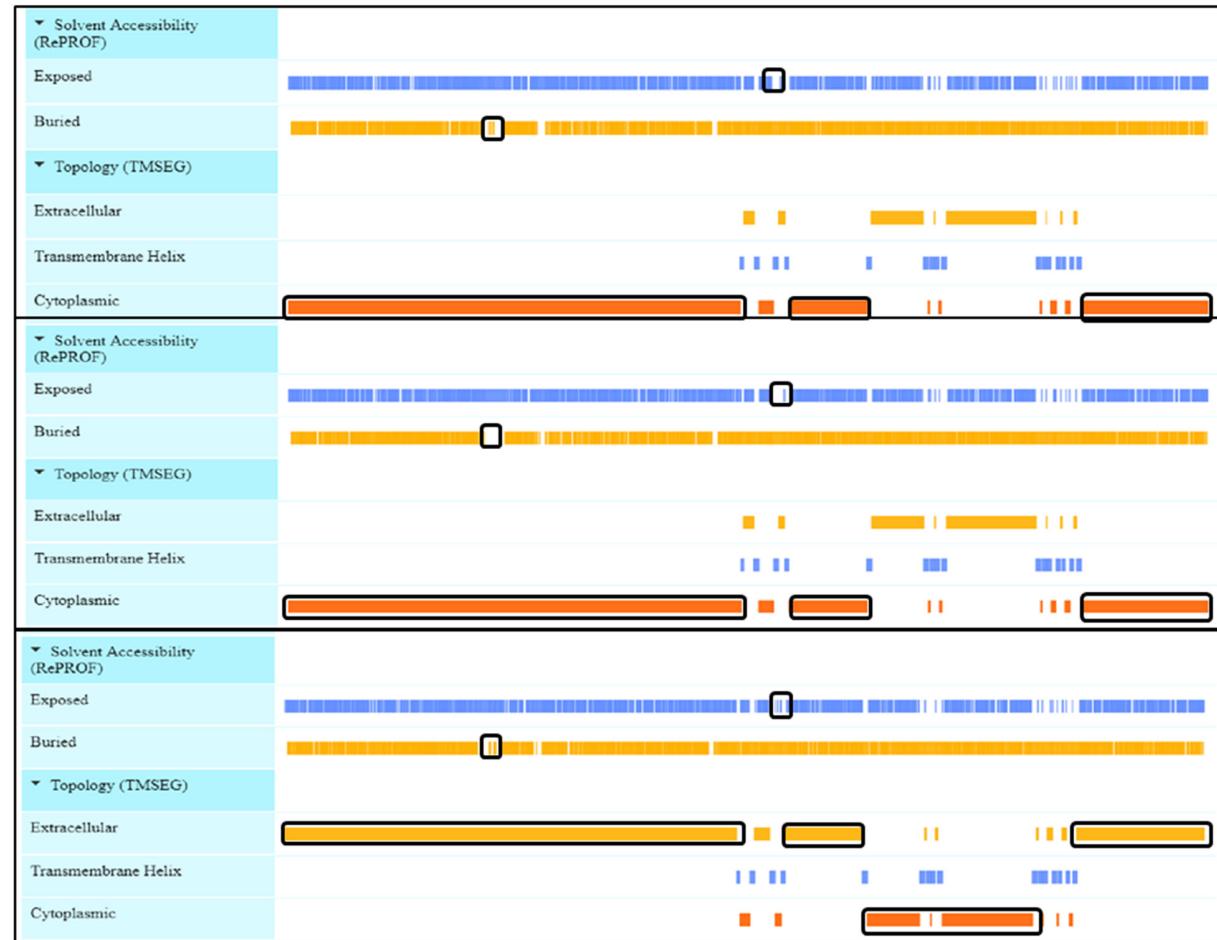
Delta
B.1.1.7
UDQ41837.1



Wuhan
YP_009725295.1



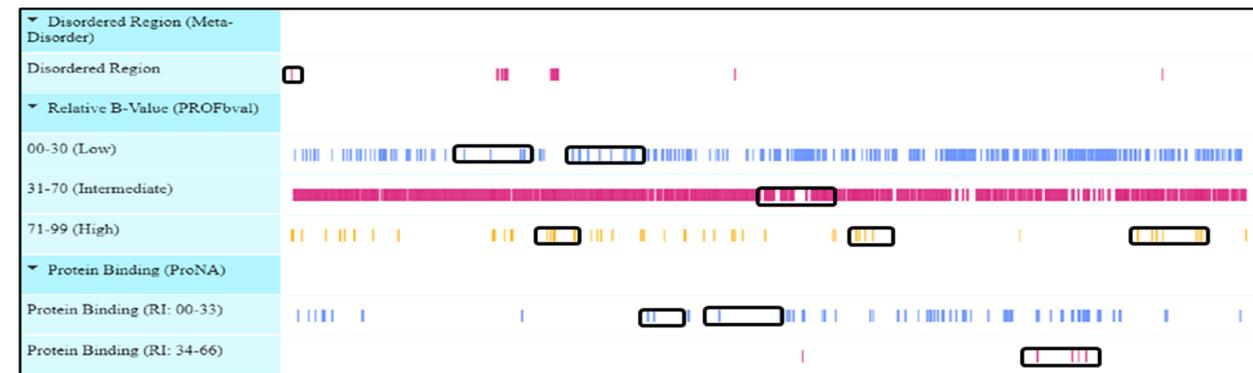
Alpha
B.1.617.21
UDU36745.1



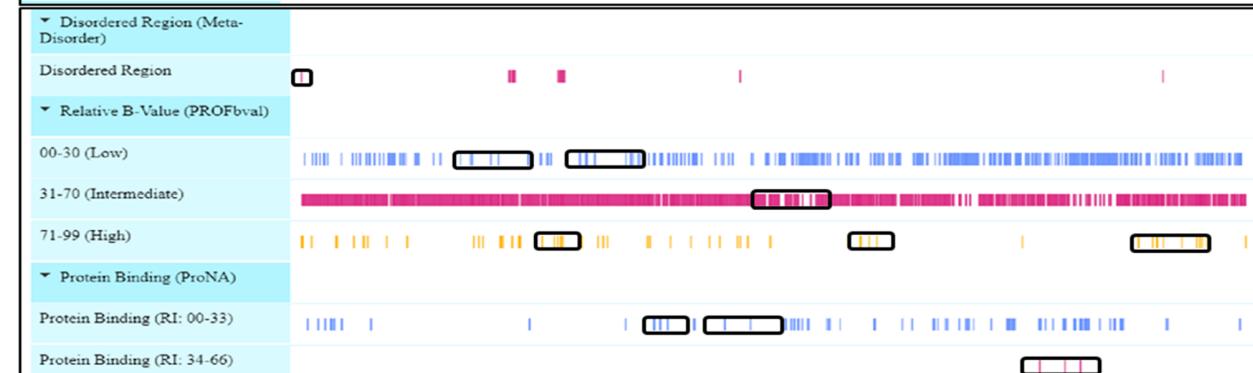
Delta
B.1.1.7
UDQ41837.1

Wuhan
YP_009725295.1

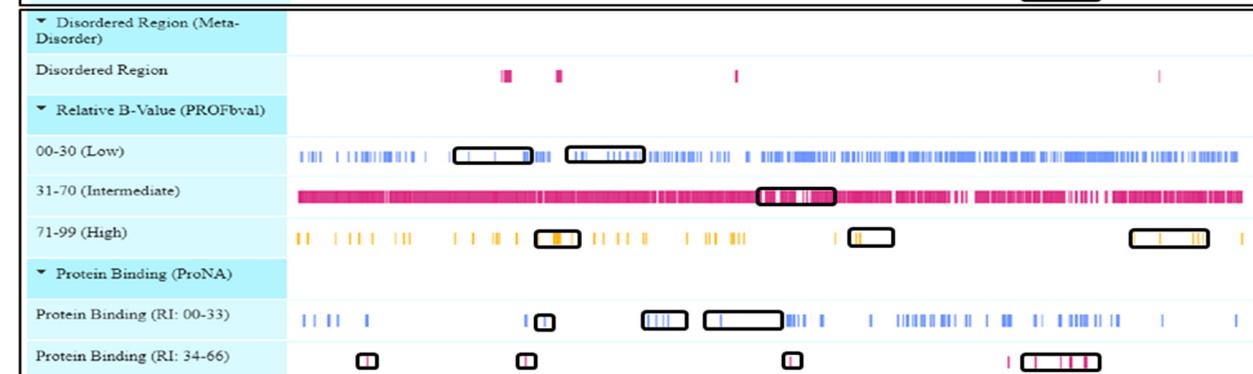
Alpha
B.1.617.21
UDU36745.1



Delta
B.1.1.7
UDQ41837.1



Wuhan
YP_009725295.1



Alpha
B.1.617.21
UDU36745.1

Delta
B.1.1.7
UDQ41837.1

Wuhan
YP_009725295.1

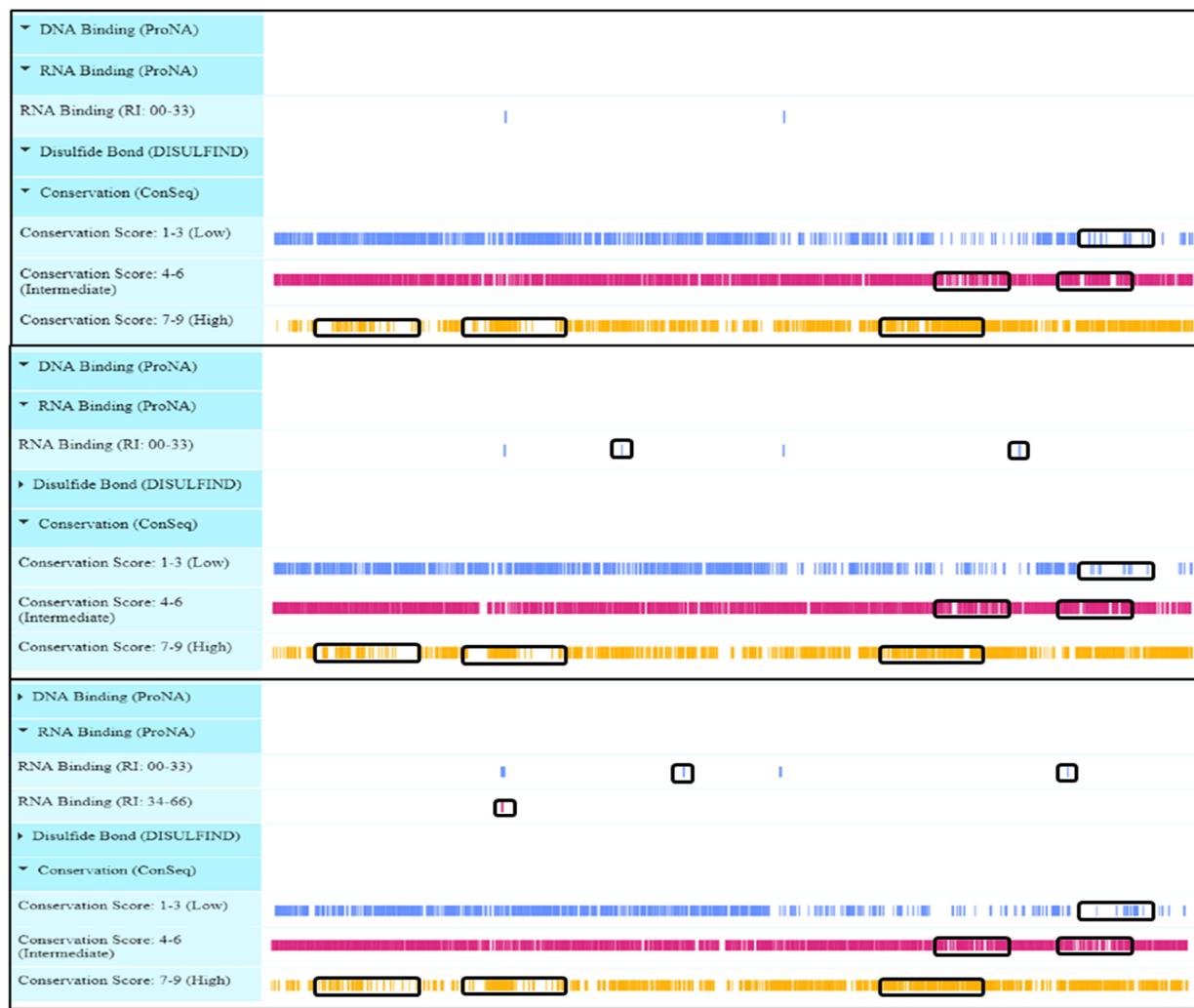
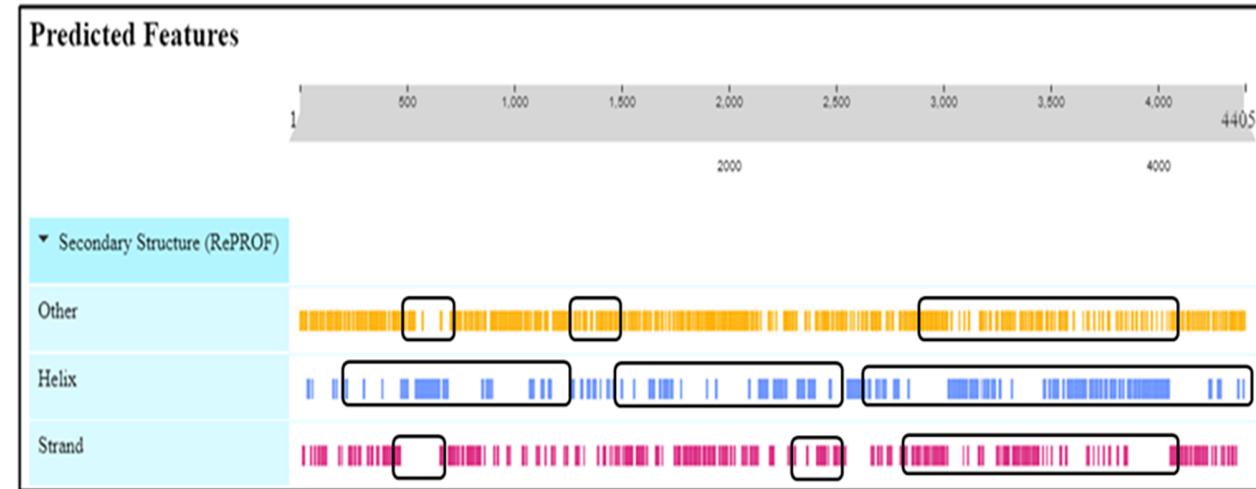


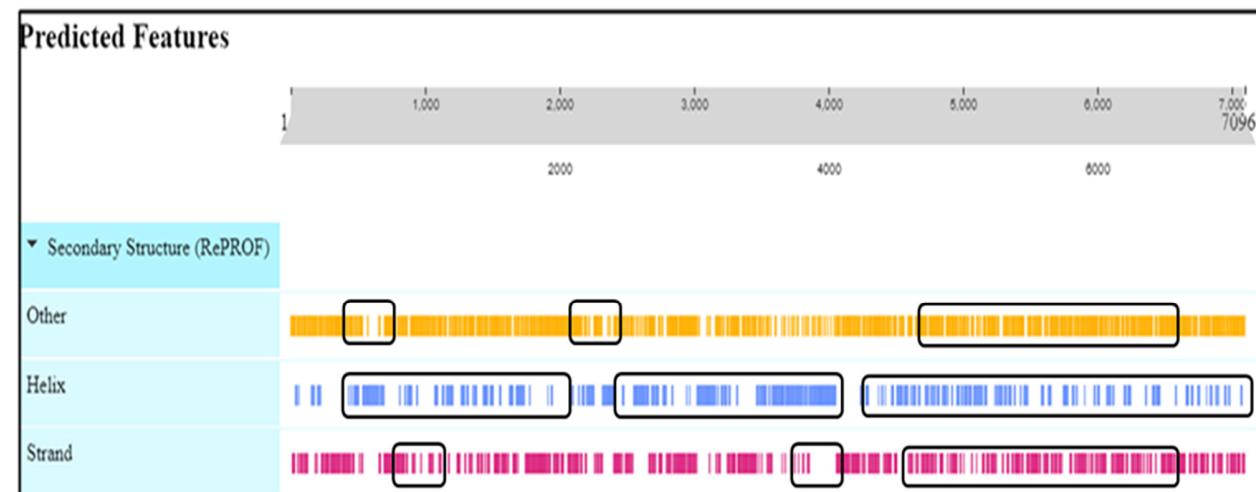
Figure S14. Viewer lays out predicted features of protein structural and functional features of ORF1a Polyprotein.

ORF1ab Polyprotein

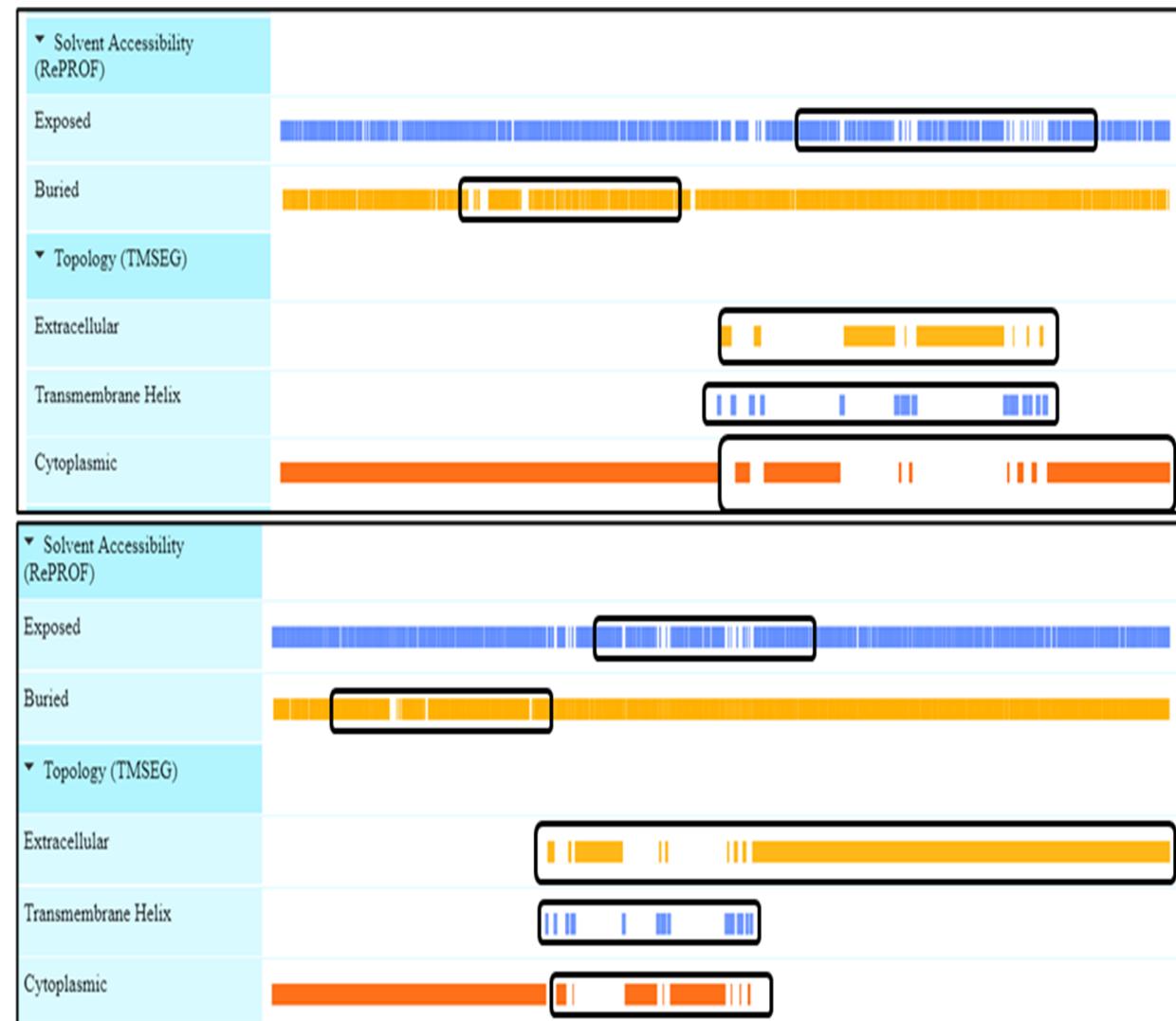
Delta
B.1.1.7
UDQ41836.1



Wuhan
YP_009724389.1

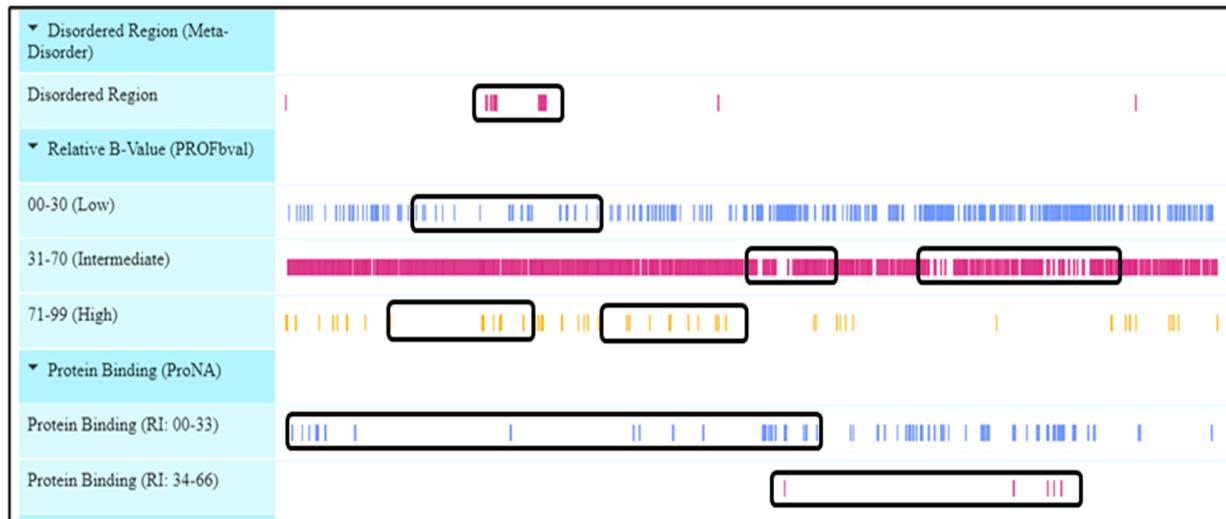


Delta
B.1.1.7
UDQ41836.1



Wuhan
YP_009724389.1

Delta
B.1.1.7
UDQ41836.1



Wuhan
YP_009724389.1

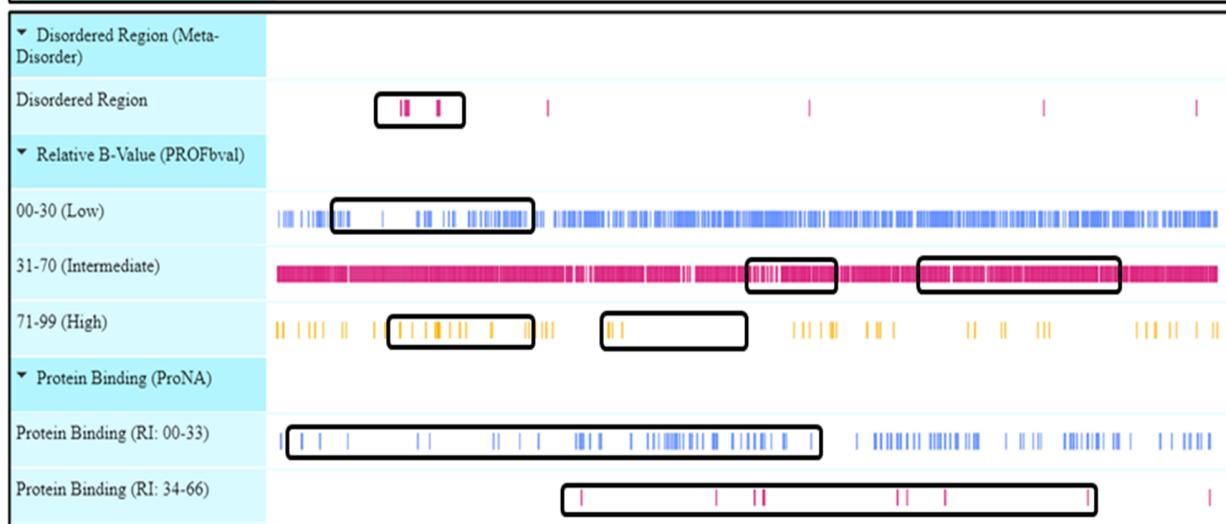


Figure S15. Viewer lays out predicted features of protein structural and functional features of ORF1ab Polyprotein.

2. ORF7a protein

Alpha

B.1.617.21

UDU36751.1

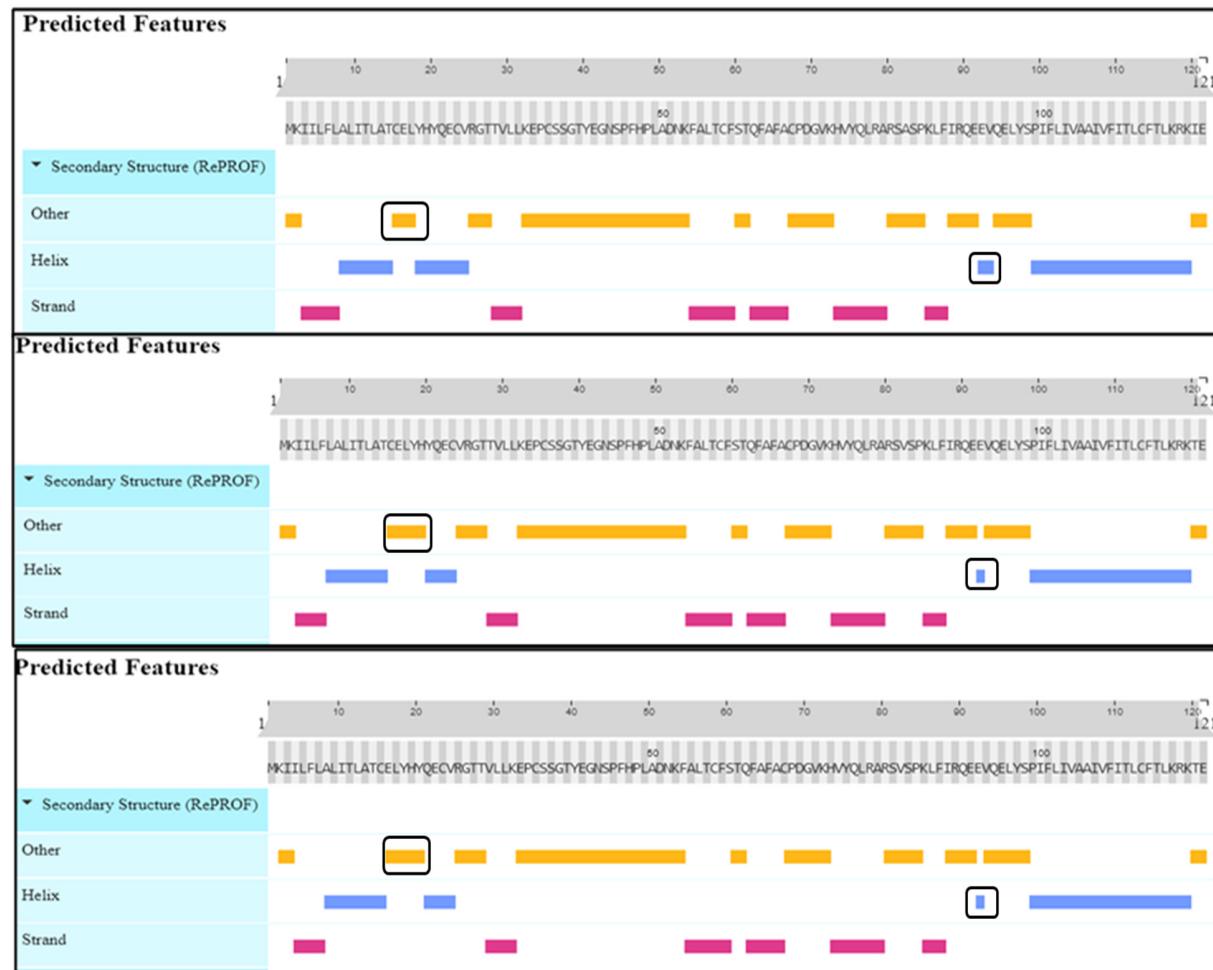
Delta

B.1.1.7

UDQ41843.1

Wuhan

YP_009724395.1



Alpha

B.1.617.21

UDU36751.1



Delta

B.1.1.7

UDQ41843.1

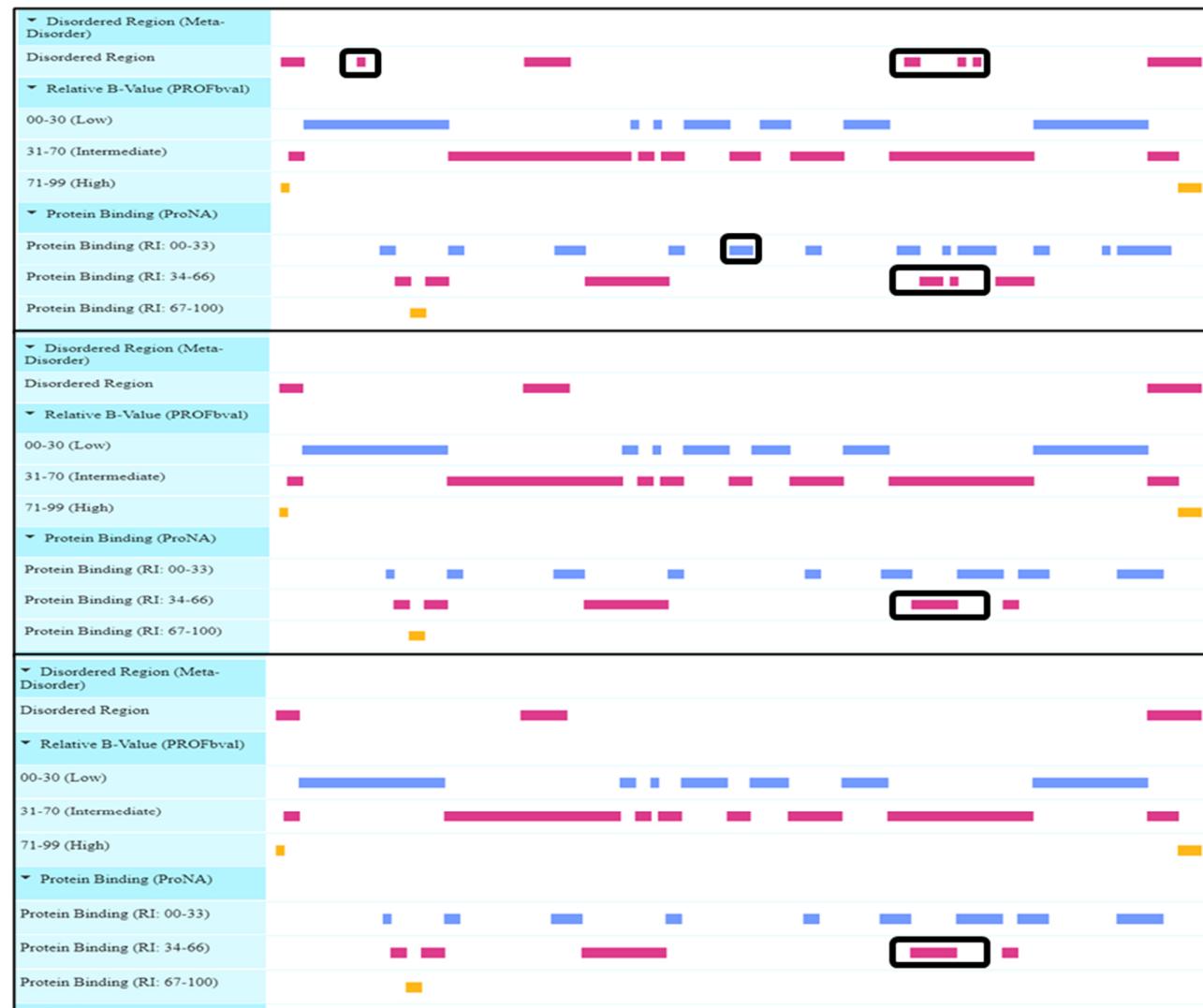


Wuhan

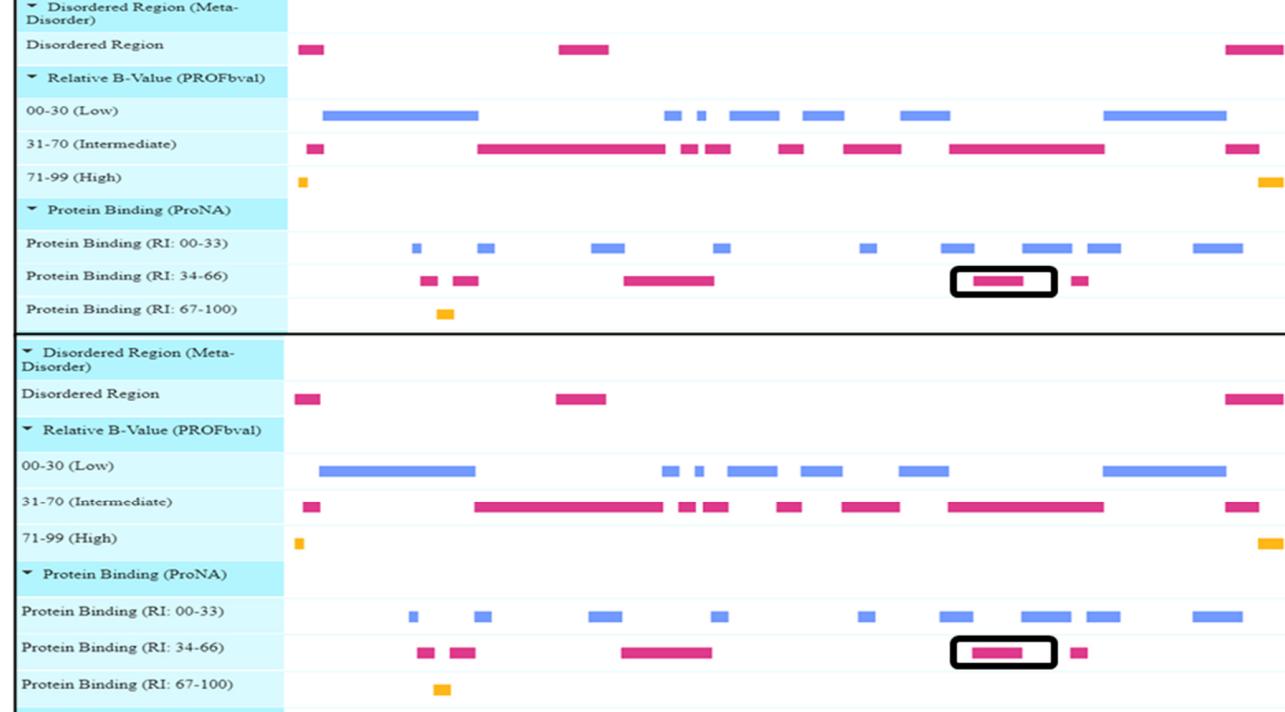
YP_009724395.1



Alpha
B.1.617.21
UDU36751.1



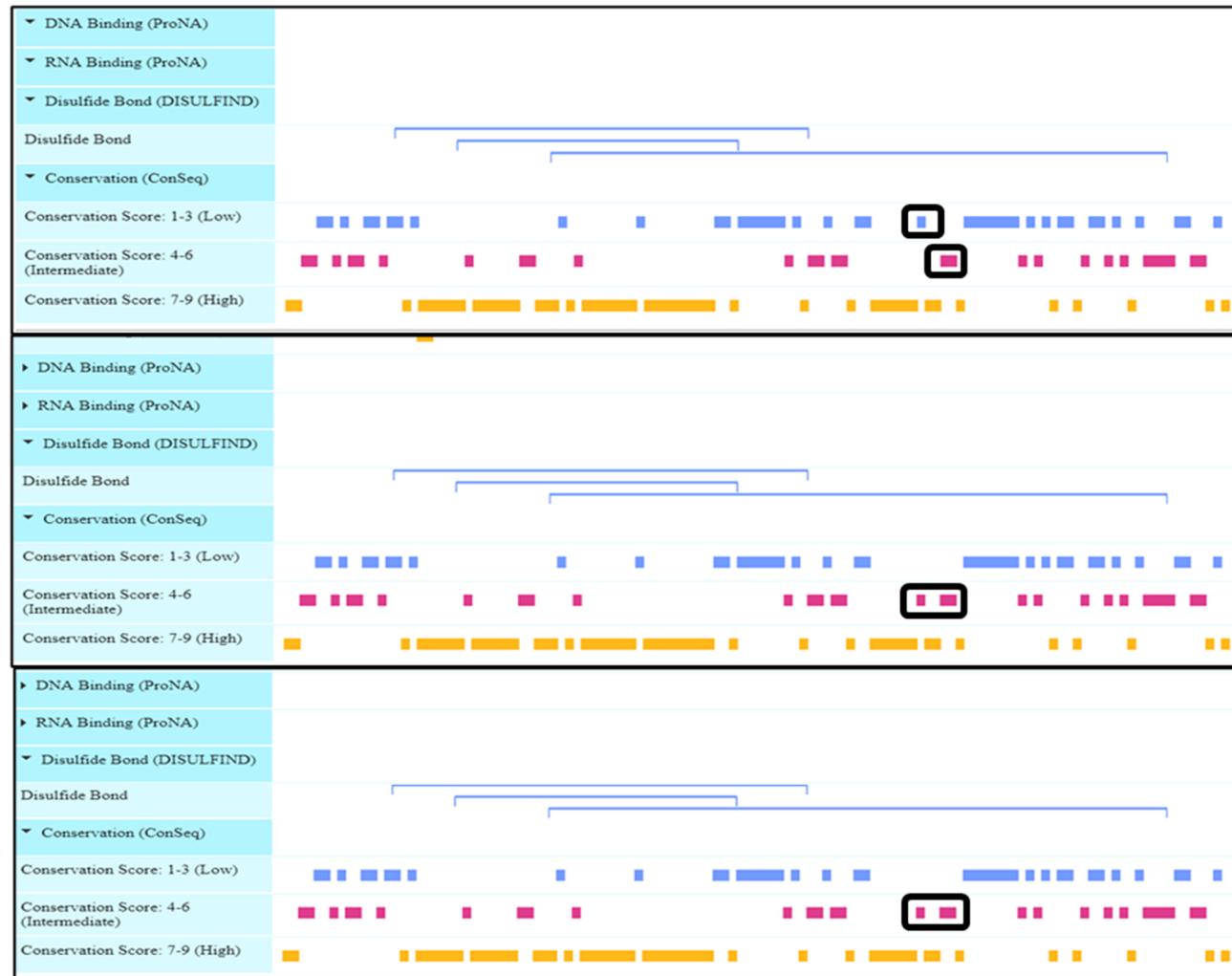
Delta
B.1.1.7
UDQ41843.1



Wuhan
YP_009724395.1



Alpha
B.1.617.21
UDU36751.1



Wuhan
YP_009724395.1

Figure S16. Viewer lays out predicted features of protein structural and functional features of ORF7a protein.

Supplementary Tables

Table S1: Mutation of amino acids in Alpha & Delta Variant of SARs-CoV-2 from Pakistan with reference strain (hCoV-19/Wuhan/WIV04/2019).

Alpha		Delta	
Mutation	Count	Mutation	Count
Envelope			
		E_V62F	1
Membrane			
		M_I82T	8
Nucleocapsid phosphoprotein			
N_D3L	5	N_A90S	1
N_G204R	5	N_D377Y	8
N_Q389H	1	N_D63G	8
N_R203K	5	N_G215C	4
N_S235F	5	N_H300Y	1
		N_R203M	8
		N_R385K	1
NS3			
NS3_K16N	1	NS3_A23V	1
		NS3_G49V	1
		NS3_I118T	1
		NS3_I62F	1
		NS3_K16T	1
		NS3_L65I	1
		NS3_L73I	1
		NS3_Q116H	1
		NS3_S26L	8
		NS3_T221K	1
		NS3_Y211H	1
NS7a			
		NS7a_L116F	2
		NS7a_T120I	8
		NS7a_V82A	8
NS7b			
		NS7b_T40I	4
NS8			
NS8_R52I	5	NS8_Q27stop	5

NS8_V62L	1		
NS8_Y73C	5		
NSP12			
NSP12_P323L	5	NSP12_G228S	
		NSP12_G671S	
		NSP12_P323L	
		NSP12_Q357H	
		NSP12_V111L	
NSP13			
		NSP13_M576I	
		NSP13_P77L	
		NSP13_R392C	
		NSP13_S350L	
NSP14			
		NSP14_A394V	
		NSP14_D144Y	
		NSP14_M72I	
		NSP14_P46L	
		NSP14_T113I	
NSP15			
		NSP15_G229C	
		NSP15_H234Y	
		NSP15_V66L	
NSP16			
		NSP16_K160R	
		NSP16_M270I	
NSP2			
NSP2_E345K	1	NSP2_A386S	
NSP2_L550F	1	NSP2_P129L	
		NSP2_Y16H	
NSP3			
NSP3_A1321V	1	NSP3_A416V	1
NSP3_A1819V	1	NSP3_A488S	4
NSP3_A1941V	1	NSP3_H1274Y	1
NSP3_A890D	5	NSP3_K1693N	1
NSP3_I1412T	5	NSP3_P1228L	4
NSP3_P153L	1	NSP3_P1469S	4
NSP3_R586C	1	NSP3_P822L	4

NSP3_T183I	5	NSP3_S1285F	1
NSP3_T423I	1	NSP3_S1370F	1
NSP3_T779I	1	NSP3_S1424F	1
	NSP3_V245F		
NSP4			
		NSP4_A446V	4
		NSP4_T492I	4
		NSP4_V167L	4
NSP5			
		NSP5_V86L	1
NSP6			
NSP6_F108del	5	NSP6_T181I	2
NSP6_G107del	5	NSP6_T77A	4
NSP6_S106del	5	NSP6_V149A	4
Spike			
Spike_A570D	5	Spike_A1078V	1
Spike_A67S	1	Spike_A222V	2
Spike_A688V	1	Spike_C1250W	1
Spike_D1118H	5	Spike_D138Y	1
Spike_D614G	5	Spike_D215H	1
Spike_H69del	5	Spike_D574Y	1
Spike_N501Y	5	Spike_D614G	8
Spike_P681H	5	Spike_D950N	6
Spike_S982A	5	Spike_E156G	8
Spike_S98F	1	Spike_E484Q	1
Spike_T716I	5	Spike_F157del	8
Spike_V70del	5	Spike_G142D	6
Spike_S98F	1	Spike_I850L	1
Spike_Y144del	5	Spike_L1141W	1
		Spike_L452R	8
		Spike_P681R	8
		Spike_Q613H	1
		Spike_R158del	8
		Spike_T19R	8
		Spike_T478K	8
		Spike_T95I	4
		Spike_V483A	1