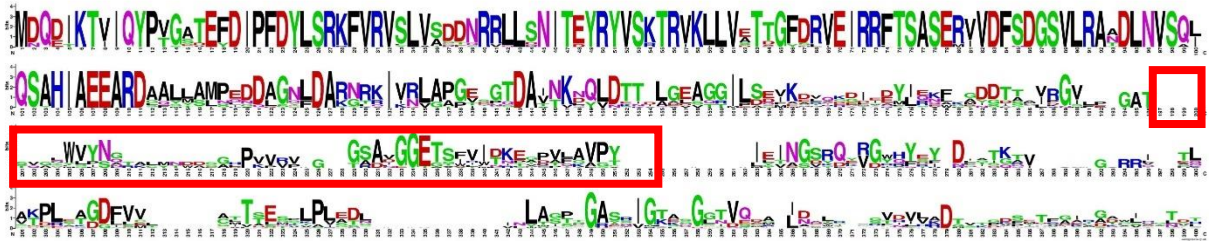
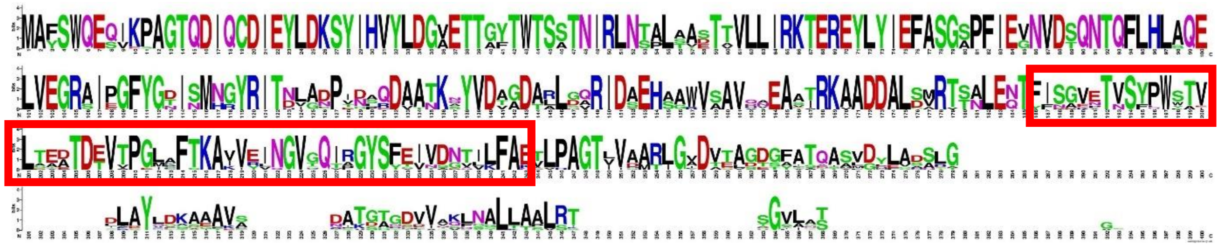
A



B

C



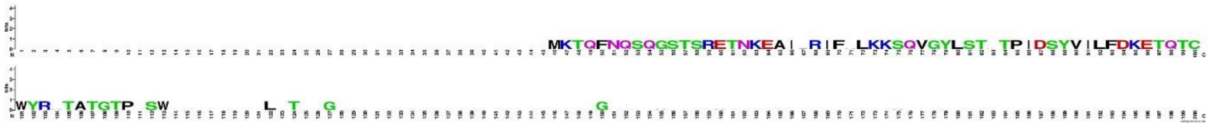
D

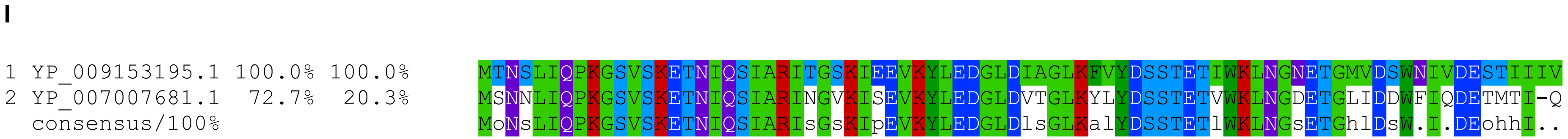
E

F

G

H





I

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1 YP_009153195.1 100.0% 100.0%    MTNSLIQPKGSVSKETNIQSIARITGSKIEEVKYLEDGLDIAGLKFVYDSSTETIWKLNGNETGMVDSWNIVDESTIIIV
2 YP_007007681.1  72.7%  20.3%    MSNNLIQPKGSVSKETNIQSIARINGVKISEVKYLEDGLDVTGLKYLYDSSTETVWKLNGDETGLIDDWFIQDETMTI-Q
  consensus/100%                 MoNsLIQPKGSVSKETNIQSIARIsGsKIpEVKYLEDGLDlsGLKalYDSSTETlWKLNGsETGhlDsW.I.DEohhI..
```

J

```
1 YP_009153197.1 100.0% 100.0%    MANKLTQPKGSISKETNKEAIARLFGIKKTAVGYISTSVLIDPYTILYDESTET-CWYRGTATGTPISWIITNGSLTLQT
2 YP_007007682.1  95.0%  23.7%    MTNKLTQPKGSVSKQLNIQTISRICGCNENEVSYIYNQLDIFNIKYLYDPISEKICISNG--SGLVLSYTVSENSIMVIT
  consensus/100%                 MsNKLTQPKGSlSKphNhpsIuRlhGhpcstVuYI.spl.I.shphLYD..oEp.Ch.pG..oGhslSahlopsSlhl.T
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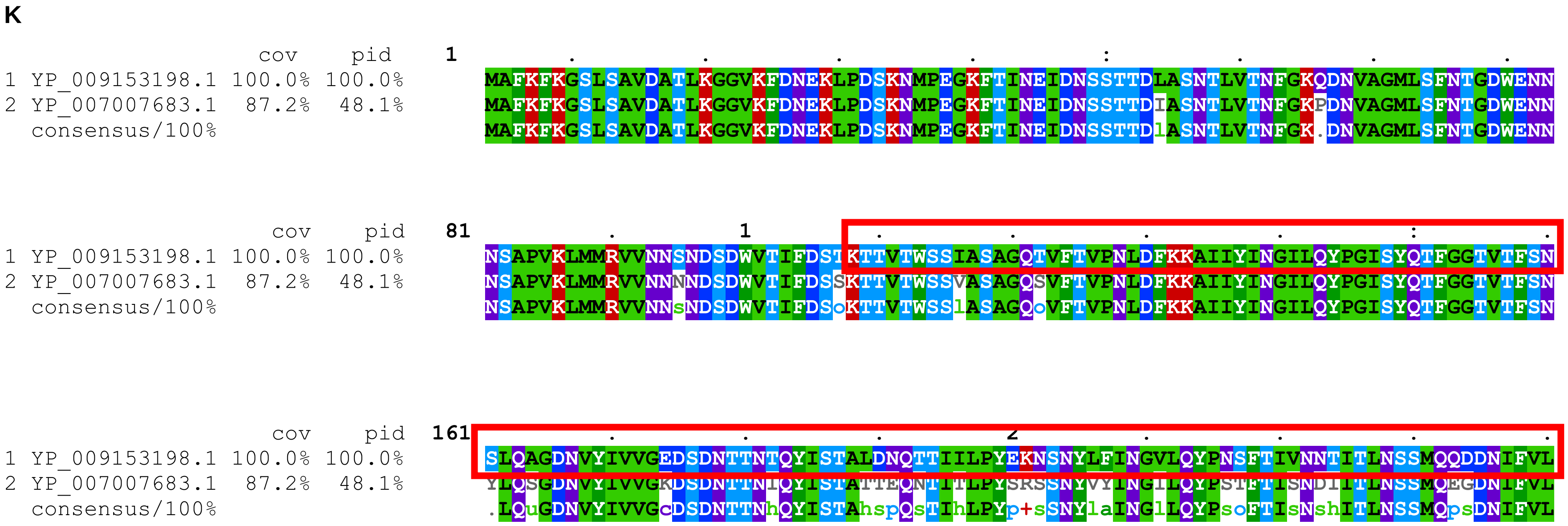

K

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                             cov    pid     1          .         .         .         .         :         .         .         .
1 YP_009153198.1 100.0% 100.0%             MAFKFKGSLSAVDATLKGGVKFDNEKLPDSKNMPEGKFTINEIDNSSTTDLASNTLVTNFGKQDNVAGMLSFNTGDWENN
2 YP_007003683.1  87.2%  48.1%             MAFKFKGSLSAVDATLKGGVKFDNEKLPDSKNMPEGKFTINEIDNSSTTDIASNTLVTNFGKPDNVAGMLSFNTGDWENN
  consensus/100%                            MAFKFKGSLSAVDATLKGGVKFDNEKLPDSKNMPEGKFTINEIDNSSTTDlASNTLVTNFGK.DNVAGMLSFNTGDWENN

                             cov    pid     81         .         1         .         .         .         .         :         .
1 YP_009153198.1 100.0% 100.0%             NSAPVKLMMRVVNNSNDSDWVTIFDSTKTTVTWSSIASAGQTVFTVPNLDFKKAIIYINGILQYPGISYQTFGGTVTFSN
2 YP_007007683.1  87.2%  48.1%             NSAPVKLMMRVVNNNNDSDWVTIFDSSKTTVTWSSVASAGQSVFTVPNLDFKKAIIYINGILQYPGISYQTFGGTVTFSN
  consensus/100%                            NSAPVKLMMRVVNNsNDSDWVTIFDSoKTTVTWSSlASAGQoVFTVPNLDFKKAIIYINGILQYPGISYQTFGGTVTFSN

                             cov    pid     161        .         .         .         2         .         .         .         .
1 YP_009153198.1 100.0% 100.0%             SLQAGDNVYIVVGEDSDNTTNTQYISTALDNQTTIILPYEKNSNYLFINGVLQYPNSFTIVNNTITLNSSMQQDDNIFVL
2 YP_007007683.1  87.2%  48.1%             YLQSGDNVYIVVGKDSDNTTNIQYISTATTEQNTITLPYSRSSNYVYINGILQYPSTFTISNDIITLNSSMQEGDNIFVL
  consensus/100%                            .LQuGDNVYIVVGcDSDNTTNhQYISTAhspQsTIhLPYp+sSNYlaINGlLQYPsoFTIsNshITLNSSMQpsDNIFVL
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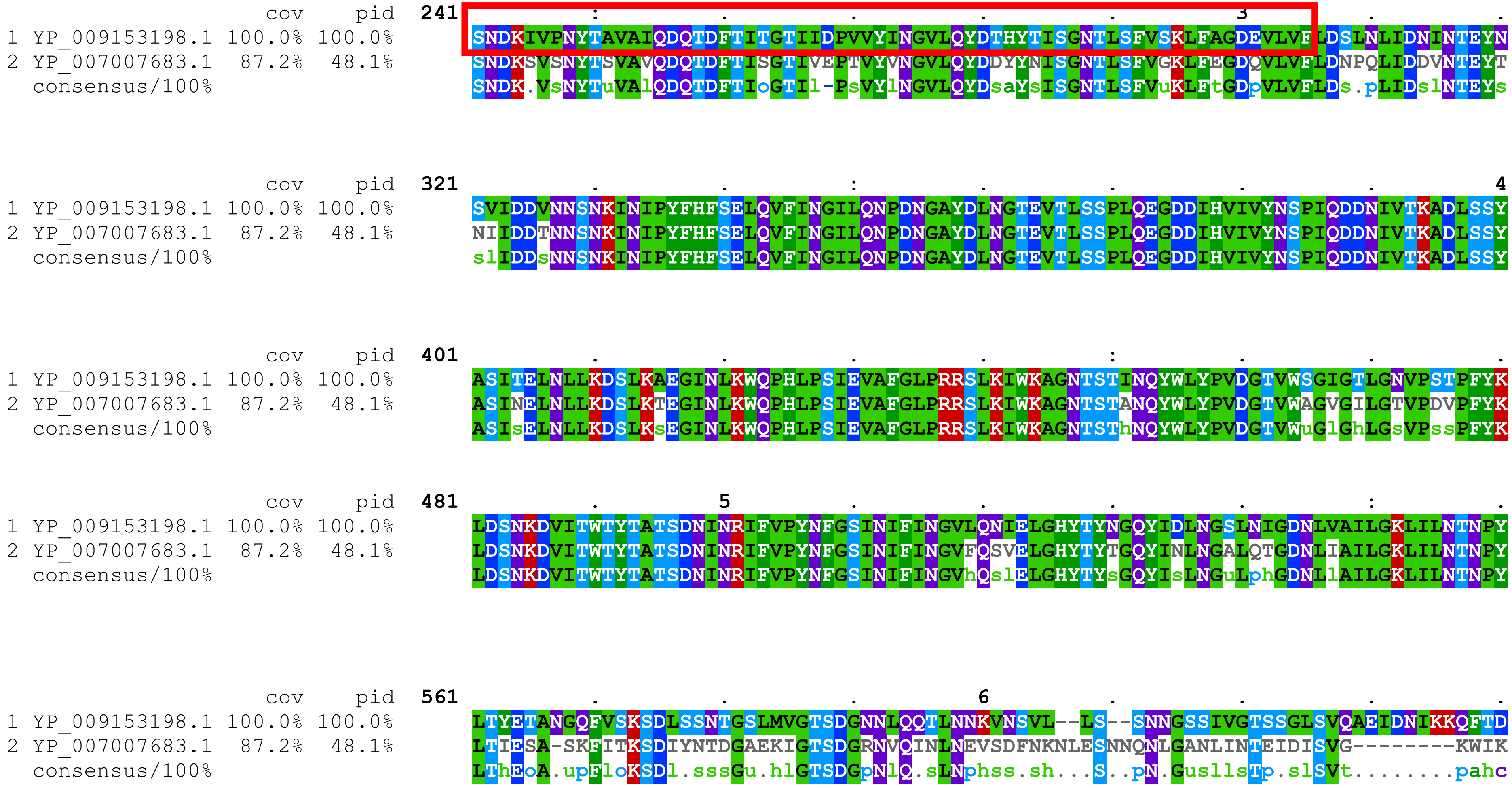

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                   cov     pid 241          :         .         .         .         .         3         .         .
1 YP_009153198.1 100.0% 100.0%     SNDKIVPNYTAVAIQDQTDFTITGTIIDPVVYINGVLQYDTHYTISGNTLSFVSKLFAGDEVLVFLDSLNLIDNINTEYN
2 YP_007007683.1  87.2%  48.1%     SNDKSVSNYTSVAVQDQTDFTISGTIVEPTVYVNGVLQYDDYYNISGNTLSFVGKLFEGDQVLVFLDNPQLIDDVNTEYT
  consensus/100%                   SNDK.VsNYTuVAlQDQTDFTIoGTIl-PsVYlNGVLQYDsaYsISGNTLSFVuKLFtGDpVLVFLDs.pLIDslNTEYs

                   cov     pid 321          .         .         :         .         .         .         .         4
1 YP_009153198.1 100.0% 100.0%     SVIDDVNNSNKINIPYFHFSELQVFINGILQNPDNGAYDLNGTEVTLSSPLQEGDDIHVIVYNSPIQDDNIVTKADLSSY
2 YP_007007683.1  87.2%  48.1%     NIIDDTNNSNKINIPYFHFSELQVFINGILQNPDNGAYDLNGTEVTLSSPLQEGDDIHVIVYNSPIQDDNIVTKADLSSY
  consensus/100%                   slIDDsNNSNKINIPYFHFSELQVFINGILQNPDNGAYDLNGTEVTLSSPLQEGDDIHVIVYNSPIQDDNIVTKADLSSY

                   cov     pid 401          .         .         .         .         :         .         .         .
1 YP_009153198.1 100.0% 100.0%     ASITELNLLKDSLKAEGINLKWQPHLPSIEVAFGLPRRSLKIWKAGNTSTINQYWLYPVDGTVWSGIGTLGNVPSTPFYK
2 YP_007007683.1  87.2%  48.1%     ASINELNLLKDSLKTEGINLKWQPHLPSIEVAFGLPRRSLKIWKAGNTSTANQYWLYPVDGTVWAGVGILGTVPDVPFYK
  consensus/100%                   ASIsELNLLKDSLKsEGINLKWQPHLPSIEVAFGLPRRSLKIWKAGNTSThNQYWLYPVDGTVWuGlGhLGsVPssPFYK

                   cov     pid 481          .         5         .         .         .         .         :         .
1 YP_009153198.1 100.0% 100.0%     LDSNKDVITWTYTATSDNINRIFVPYNFGSINIFINGVLQNIELGHYTYNGQYIDLNGSLNIGDNLVAILGKLILNTNPY
2 YP_007007683.1  87.2%  48.1%     LDSNKDVITWTYTATSDNINRIFVPYNFGSINIFINGVFQSVELGHYTYTGQYINLNGALQTGDNLIAILGKLILNTNPY
  consensus/100%                   LDSNKDVITWTYTATSDNINRIFVPYNFGSINIFINGVhQslELGHYTYsGQYIsLNGuLphGDNLlAILGKLILNTNPY

                   cov     pid 561          .         .         .         6         .         .         .         .
1 YP_009153198.1 100.0% 100.0%     LTYETANGQFVSKSDLSSNTGSLMVGTSDGNNLQQTLNNKVNSVL--LS--SNNGSSIVGTSSGLSVQAEIDNIKKQFTD
2 YP_007007683.1  87.2%  48.1%     LTIESA-SKFITKSDIYNTDGAEKIGTSDGRNVQINLNEVSDFNKNLESNNQNLGANLINTEIDISVG--------KWIK
  consensus/100%                   LThEoA.upFloKSDl.sssGu.hlGTSDGpNlQ.sLNphss.sh...S..pN.GusllsTp.slSVt........pahc
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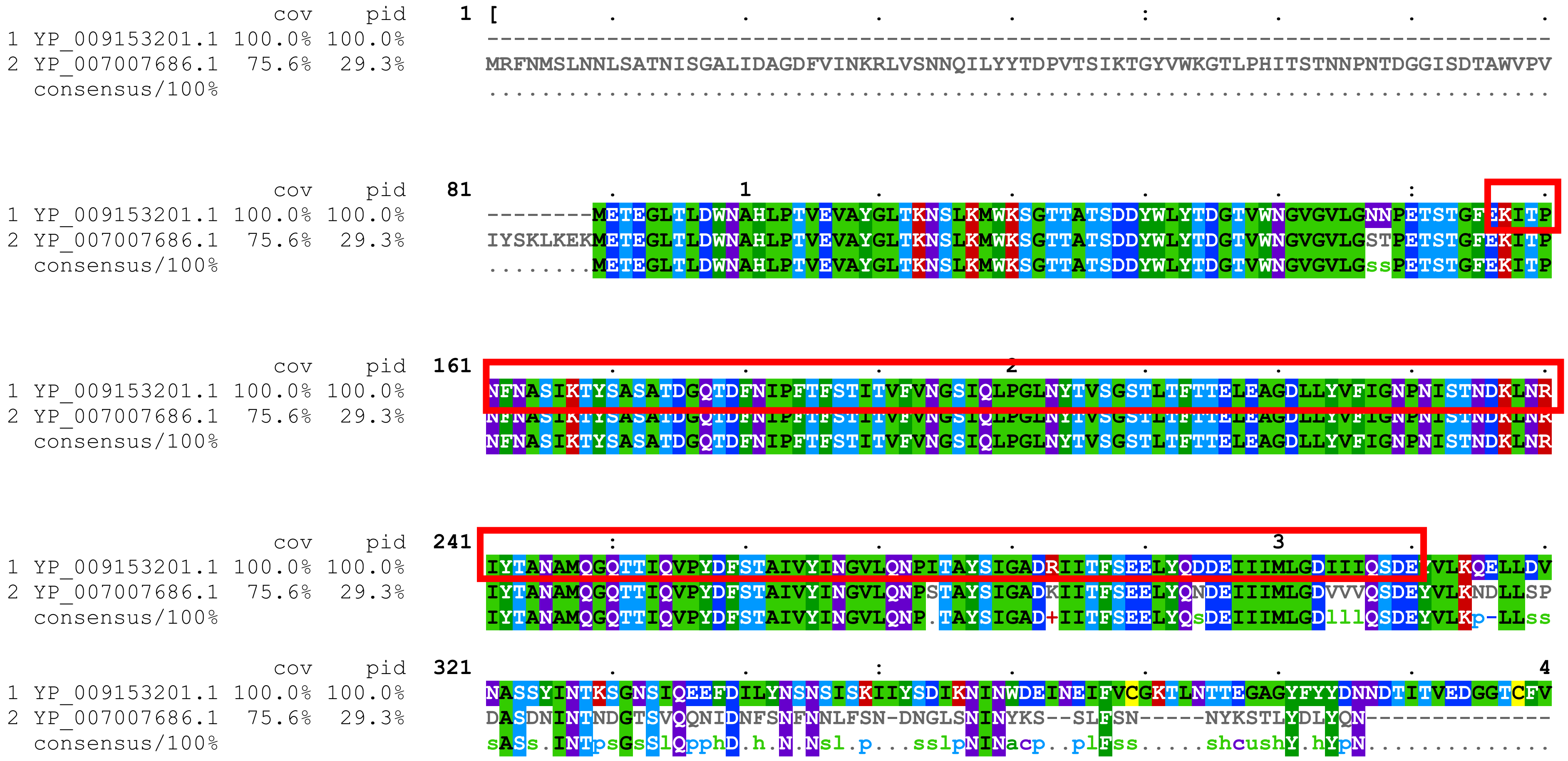
L



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                         cov     pid   1 [       .         .         .         .         :         .         .         .
1 YP_009153201.1 100.0% 100.0%           --------------------------------------------------------------------------------
2 YP_007007686.1  75.6%  29.3%           MRFNMSLNNLSATNISGALIDAGDFVINKRLVSNNQILYYTDPVTSIKTGYVWKGTLPHITSTNNPNTDGGISDTAWVPV
  consensus/100%                         ................................................................................

                         cov     pid  81         .         1         .         .         .         .         :         .
1 YP_009153201.1 100.0% 100.0%           --------METEGLTLDWNAHLPTVEVAYGLTKNSLKMWKSGTTATSDDYWLYTDGTVWNGVGVLGNNPETSTGFEKITP
2 YP_007007686.1  75.6%  29.3%           IYSKLKEKMETEGLTLDWNAHLPTVEVAYGLTKNSLKMWKSGTTATSDDYWLYTDGTVWNGVGVLGSTPETSTGFEKITP
  consensus/100%                         ........METEGLTLDWNAHLPTVEVAYGLTKNSLKMWKSGTTATSDDYWLYTDGTVWNGVGVLGssPETSTGFEKITP

                         cov     pid 161         .         .         .         2         .         .         .         .
1 YP_009153201.1 100.0% 100.0%           NFNASIKTYSASATDGQTDFNIPFTFSTITVFVNGSIQLPGLNYTVSGSTLTFTTELEAGDLLYVFIGNPNISTNDKLNR
2 YP_007007686.1  75.6%  29.3%           NFNASIKTYSASATDGQTDFNIPFTFSTITVFVNGSIQLPGLNYTVSGSTLTFTTELEAGDLLYVFIGNPNISTNDKLNR
  consensus/100%                         NFNASIKTYSASATDGQTDFNIPFTFSTITVFVNGSIQLPGLNYTVSGSTLTFTTELEAGDLLYVFIGNPNISTNDKLNR

                         cov     pid 241         :         .         .         .         .         3         .         .
1 YP_009153201.1 100.0% 100.0%           IYTANAMQGQTTIQVPYDFSTAIVYINGVLQNPITAYSIGADRIITFSEELYQDDEIIIMLGDIIIQSDEYVLKQELLDV
2 YP_007007686.1  75.6%  29.3%           IYTANAMQGQTTIQVPYDFSTAIVYINGVLQNPSTAYSIGADKIITFSEELYQNDEIIIMLGDVVVQSDEYVLKNDLLSP
  consensus/100%                         IYTANAMQGQTTIQVPYDFSTAIVYINGVLQNP.TAYSIGAD+IITFSEELYQsDEIIIMLGDlllQSDEYVLKp-LLss

                         cov     pid 321         .         .         :         .         .         .         .         4
1 YP_009153201.1 100.0% 100.0%           NASSYINTKSGNSIQEEFDILYNSNSISKIIYSDIKNINWDEINEIFVCGKTLNTTEGAGYFYYDNNDTITVEDGGTCFV
2 YP_007007686.1  75.6%  29.3%           DASDNINTNDGTSVQQNIDNFSNFNNLFSN-DNGLSNINYKS--SLFSN-----NYKSTLYDLYQN--------------
  consensus/100%                         sASs.INTpsGsSlQpphD.h.N.Nsl.p...sslpNINacp..plFss.....shcushY.hYpN..............
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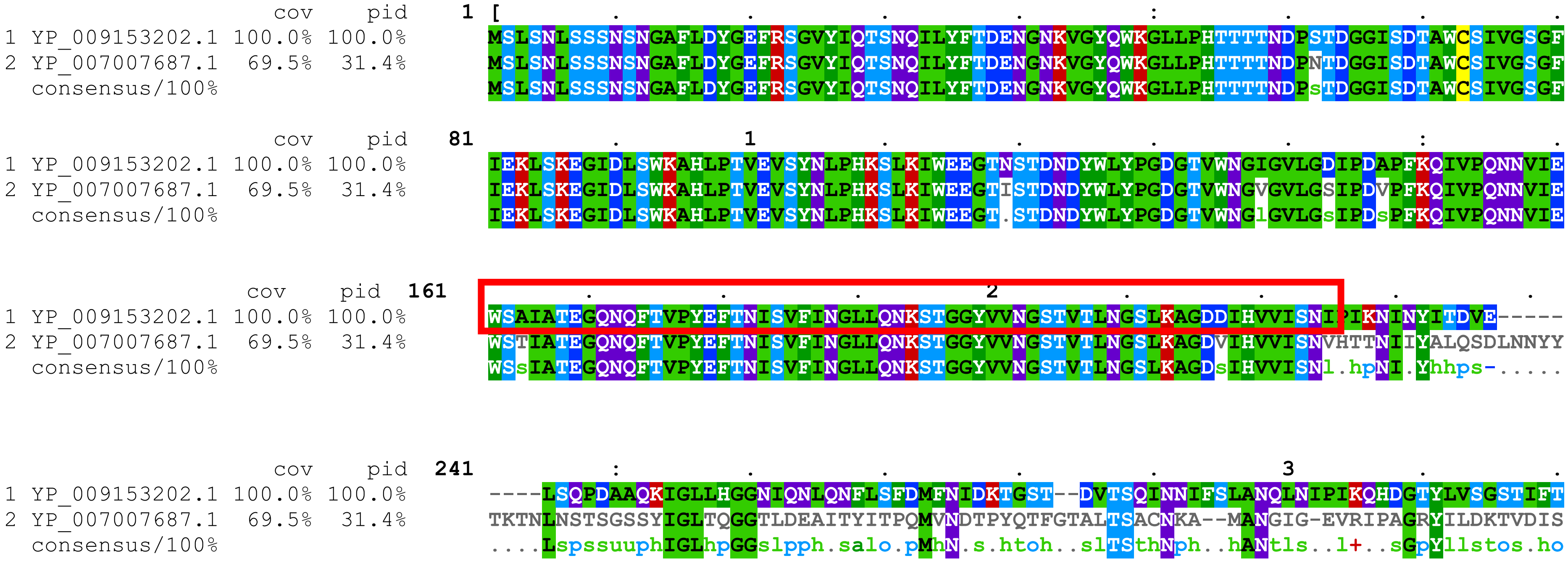
M



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                       cov     pid     1 [       .         .         .         .         :         .         .         .
1 YP_009153202.1 100.0% 100.0%      MSLSNLSSSNSNGAFLDYGEFRSGVYIQTSNQILYFTDENGNKVGYQWKGLLPHTTTTNDPSTDGGISDTAWCSIVGSGF
2 YP_007007687.1  69.5%  31.4%      MSLSNLSSSNSNGAFLDYGEFRSGVYIQTSNQILYFTDENGNKVGYQWKGLLPHTTTTNDPNTDGGISDTAWCSIVGSGF
  consensus/100%                    MSLSNLSSSNSNGAFLDYGEFRSGVYIQTSNQILYFTDENGNKVGYQWKGLLPHTTTTNDPsTDGGISDTAWCSIVGSGF

                       cov     pid    81         .         1         .         .         .         .         :         .
1 YP_009153202.1 100.0% 100.0%      IEKLSKEGIDLSWKAHLPTVEVSYNLPHKSLKIWEEGTNSTDNDYWLYPGDGTVWNGIGVLGDIPDAPFKQIVPQNNVIE
2 YP_007007687.1  69.5%  31.4%      IEKLSKEGIDLSWKAHLPTVEVSYNLPHKSLKIWEEGTISTDNDYWLYPGDGTVWNGVGVLGSIPDVPFKQIVPQNNVIE
  consensus/100%                    IEKLSKEGIDLSWKAHLPTVEVSYNLPHKSLKIWEEGT.STDNDYWLYPGDGTVWNGlGVLGsIPDsPFKQIVPQNNVIE

                     cov     pid  161          .         .         .         2         .         .         .         .
1 YP_009153202.1 100.0% 100.0%      WSAIATEGQNQFTVPYEFTNISVFINGLLQNKSTGGYVVNGSTVTLNGSLKAGDDIHVVISNIPIKNINYITDVE-----
2 YP_007007687.1  69.5%  31.4%      WSTIATEGQNQFTVPYEFTNISVFINGLLQNKSTGGYVVNGSTVTLNGSLKAGDVIHVVISNVHTTNIIYALQSDLNNYY
  consensus/100%                    WSsIATEGQNQFTVPYEFTNISVFINGLLQNKSTGGYVVNGSTVTLNGSLKAGDsIHVVISNl.hpNI.Yhhps-.....

                       cov     pid   241         :         .         .         .         .         3         .         .
1 YP_009153202.1 100.0% 100.0%      ----LSQPDAAQKIGLLHGGNIQNLQNFLSFDMFNIDKTGST--DVTSQINNIFSLANQLNIPIKQHDGTYLVSGSTIFT
2 YP_007007687.1  69.5%  31.4%      TKTNLNSTSGSSYIGLTQGGTLDEAITYITPQMVNDTPYQTFGTALTSACNKA--MANGIG-EVRIPAGRYILDKTVDIS
  consensus/100%                    ....LspssuuphIGLhpGGslpph.salo.pMhN.s.htoh..slTSthNph..hANtls..l+..sGpYllstos.ho
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N

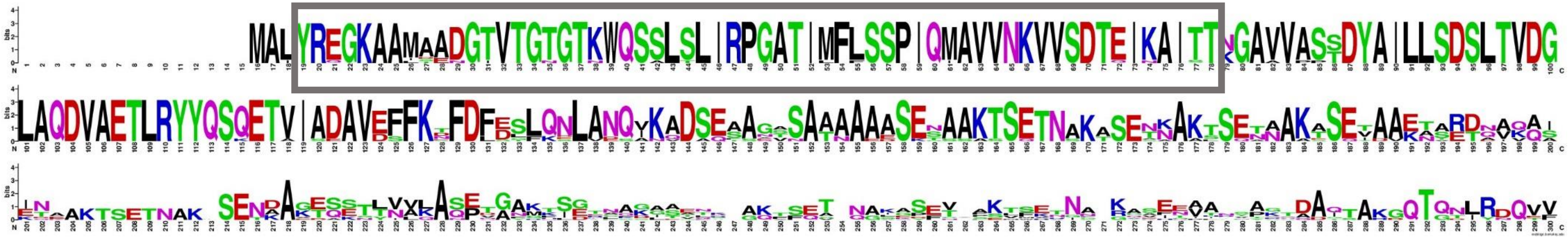

Figure S1. Conserved sequences at the N-terminus of the *Klebsiella* RBPs per family using a WebLogo when multiple RBP sequences are available, or a pairwise alignment when only two RBP sequences are available. (A) N-terminal anchor of the first RBP of KP32viruses; (B) conserved peptide of the second RBP of KP32viruses; (C) N-terminal anchor of the first RBP of KP34viruses; (D) conserved peptide of the second RBP of KP34viruses; (E) N-terminal anchor of the first RBP of viruses belonging to the Menlow group; (F) conserved peptide of the second RBP of viruses belonging to the Menlow group; (G) conserved peptide of the third RBP of viruses belonging to the Menlow group; (H) conserved peptide of the fourth RBP of viruses belonging to the Menlow group; (I) conserved peptide of the second RBP of viruses belonging to the ΦK64-1; (J) conserved peptide of the fourth RBP of viruses belonging to the ΦK64-1 group; (K) anchor of the fifth RBP of viruses belonging to the ΦK64-1 group; (L) conserved peptide of the eighth RBP of viruses belonging to the ΦK64-1 group; (M) conserved peptide of the ninth RBP of viruses belonging to the ΦK64-1 group; (N) N-terminal anchor of the first RBP of KP36viruses. The red frames indicate the region of RBPs detected to be homologous to T4gp10. In the case of KP36viruses, the region homologous to the T5 distal tail protein domain B was indicated with grey frame.