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NTDB id 1100 NMB RS09455 WP 002225652.1  
 NTDB id 1092 CAD91899.1 1..2286( )  
 NTDB id 1115 OK783 RS00485 WP 003698035.1  
 NTDB id 1186 GTF74 RS01320 WP 000788426.1  
 NTDB id 1175 A1552VC RS12105 WP 000788426.1  
 NTDB id 1408 DSB67 RS13980 WP 010643500.1  
 NTDB id 1009 ACIAD RS15175 WP 004923730.1  
 NTDB id 1039 HON27 RS01460 WP 031993779.1  
 NTDB id 1052 ABD1 RS15850 WP 001017033.1  
 NTDB id 1284 ACE17W RS12370 WP 010946666.1  
 NTDB id 1257 GC085 RS04855 WP 163621000.1  
 NTDB id 1027452 AB4Y39 RS20590 WP 052675472.1  
 NTDB id 1193 PAKAF RS26665 WP 003161249.1  
 consensus

MNTKLTK.....IISGLFVATAAFQTASAGNITDIKVVSLPNKQKIVKVSFDKEIV.NPTGFVVTSSPARIALDFEQ 70  
 MNTKLTK.....IISGLFVATAAFQTASAGNITDIKVVSLPNKQKIVKVSFDKEIV.NPTGFVVTSSPARIALDFEQ 70  
 MNTKLTK.....IISGLFVATAAFQTASAGNITDIKVVSLPNKQKIVKVSFDKEIV.NPTGFVVTSSPARIALDFEQ 70  
 ..... 0  
 ..... 0  
 ..... 0  
 MKQIIRQFSIGTVAYAIMQ.....VASAQVAITNVVPMNIPGQGTEIRVMFNGLPP.QPQAYQLEQPARLILDFDK 70  
 MNHVFRQFSMGAVAIAIMQ.....AASAQVSMTNIVPMQIAGQGTEIRVMFNGLPP.QPQAYQLENPSRLILDFDK 70  
 MNHVFRQFSMGAVAIAIMQ.....AASAQVSMTNIVPMQIAGQGTEIRVMFNGLPP.QPQAYQLENPSRLILDFDK 70  
 .....MR.....KIIAILILIS.ASLSMAYSKDNSLISVKVLPENRVRIDFQFSKPLKQLPASFITQKPPRLVLDLFIS 69  
 .....MR.....KIIAILILIS.ASLSLAYSKDNSLISVKVLPENRVRIDFQFSKPLKQLPASFITQKPPRLVLDLFIS 69  
 ..... 0  
 MNSGLSR.....LGIALI AAMF.....APALLAADLEKLDVAALPGDRVELKLFQFDEPVAA.PRGYTIEQPARIALDLPG 69  
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 consensus

TGISMD..QQVLEYADPLLSKISAAQNSSRARLVNLNKPQQYNTEVRGNKVVWIFINESDDTVSAPARPAVKAAPAAPAK 148  
 TGISMD..QQVLEYADPLLSKISAAQNSSRARLVNLNKPQQYNTEVRGNKVVWIFINESDDTVSAPARPAVKAAPAAPAK 148  
 TGISMD..QQVLEYADPLLSKISAAQNSSRARLVNLNKPQQYNTEVRGNKVVWIFINESDDTVSAPARPAVKAAPAAPAK 148  
 .....MKNGLKT..YVAQTWLTWVGLALCAS..... 25  
 .....MKNGLKT..YVAQTWLTWVGLALCAS..... 25  
 .....MKMRHGLTLTPRKLTLGFLSFWLWVGLALCAS..... 28  
 AGQKIAK..SLIPVTTNEASSIDVSSDDKRRARVVNLDKAGAFITTRVEGNVFIKINNIQSTATP.....V.....A... 135  
 AQQGLKQ..SKISVATNEASSVDVTSDDQRSRLTVNLKDTGAFITTRVEGNTFILKINSAQTSNKP.....L.....P... 135  
 AQQGLKQ..SKISVATNEASSVDVTSDDQRSRLTVNLKDTGAFITTRVEGNTFILKINSAQTSNKP.....L.....P... 135  
 TDMQIPSDQKTKTIQLGSLHSYNIVAVGDRVRAILELDRSVSYSGSTAGSIYSLVNLGKSNL.F.....EN. 135  
 TDMQIPSDQKTKTIQLGSLHSYNIVAVGDRVRAILELDRSVSYSGSTAGSIYSLVNLGKSNL.F.....EN. 135  
 ..... 0  
 VQNKI..GTKNRELSVGNTRSVTVVEAKDRTRLINLITLSSYTTRVEGNLFFVVGNSPAGASVASTAPVKASPAPAS. 146  
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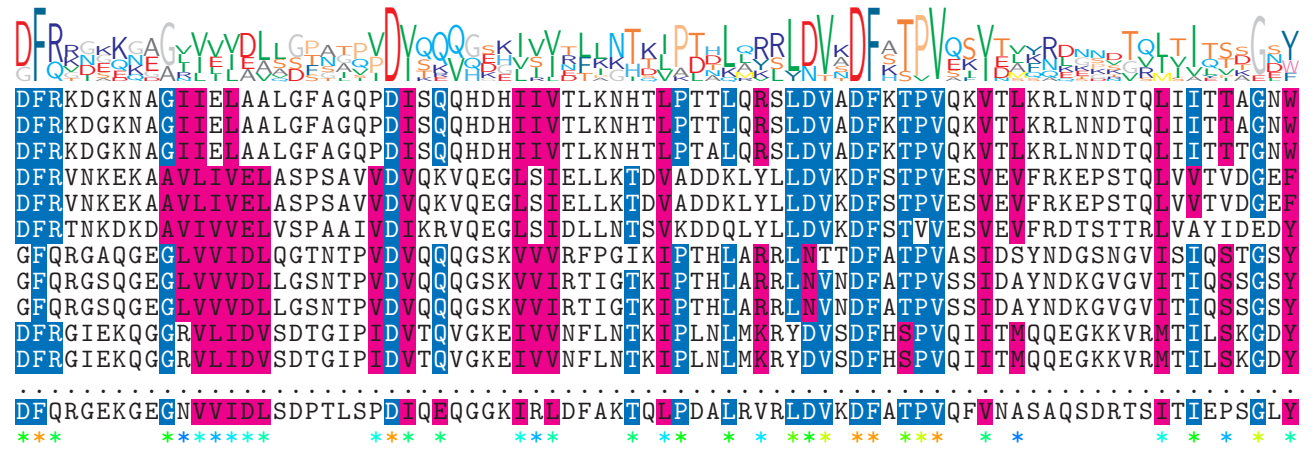
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 consensus

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 QQAAPSTKSAVSVSEPFPAKQQAAPFTESVSVSAPFSPAKQQAASAKQQAAPAKQQAAPAKQQAAPAKQTN 220  
 QQA.....AAPFTESVSVSAPFSPAKQQA.....AASAKQTN 182  
 .....S.....MVFSAESATANQLENI 42  
 .....S.....MVFSAESATANQLENI 42  
 .....FVAEEVQSNLSKSI 43  
 .....TSAPAPQGGIGNI 148  
 .....VVS.AQPQGVSN 147  
 .....VVS.AQPQGVSN 147  
 .....SKEV.....FITNQVNAKHEIKRI 155  
 .....SKEV.....FITNQVNAKHEIKRI 155  
 ..... 0  
 .....YAQP.....IKPKPYVPAGRAIRNI 166  
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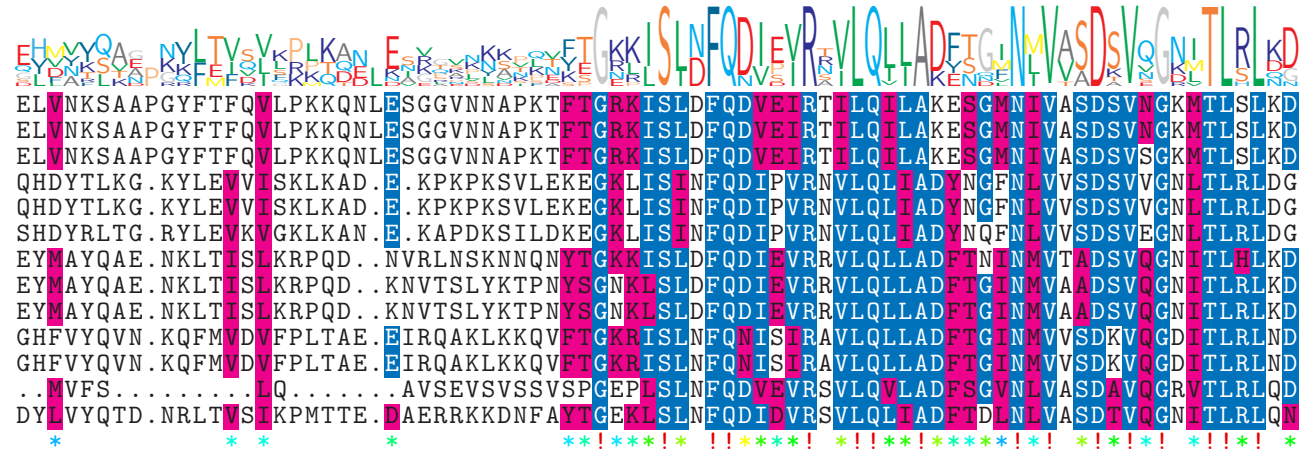
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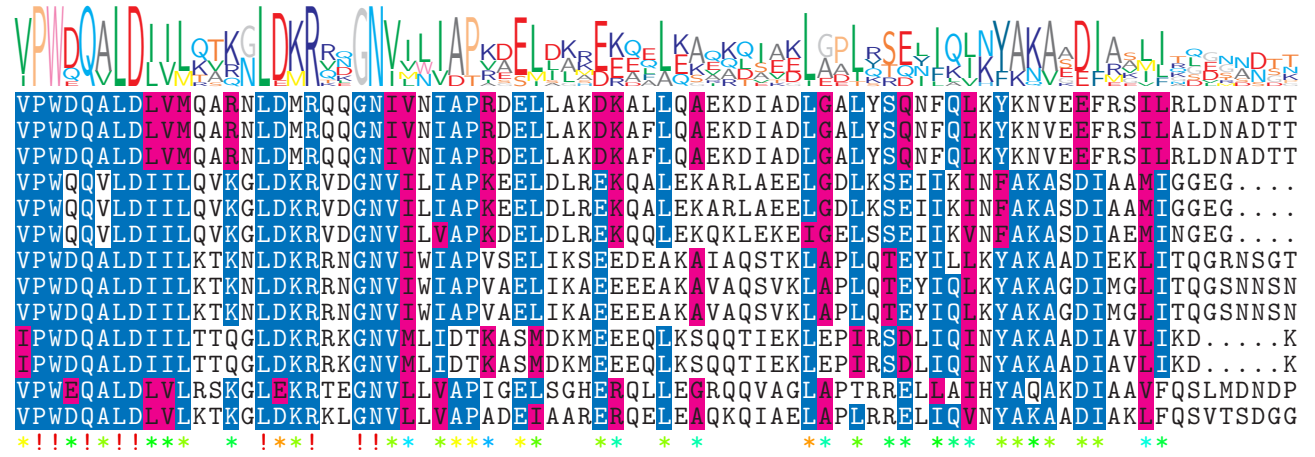
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