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 NTDB id 1100 NMB RS09455 WP 002225652.1
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 NTDB id 1186 GTF74 RS01320 WP 000788426.1
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 NTDB id 1257 GC085 RS04855 WP 163621000.1
 NTDB id 82511 PRtIB026 RS04855 WP 267813897.1
 NTDB id 1193 PAKAF RS26665 WP 003161249.1
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MNTKLTK.....IISGLFVATAAFQTASAGNITDIKVVSLPNKQKIVKVSFDKEIV.NPTGFVVTSSPARIALDFEQ 70
 MNTKLTK.....IISGLFVATAAFQTASAGNITDIKVVSLPNKQKIVKVSFDKEIV.NPTGFVVTSSPARIALDFEQ 70
 MNTKLTK.....IISGLFVATAAFQTASAGNITDIKVVSLPNKQKIVKVSFDKEIV.NPTGFVVTSSPARIALDFEQ 70
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 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....APALLAADLEKLDVAAALPGDRVELKQLQFDEPVAA.PRGYTIEQPARIALDLPG 69
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 consensus

TGISM..DQQVLEYADPLLSKISAAQNSSRARLVNLNKPQQYNTEVRGNKVVWIFINESDDTVSAPARPAVKAAPAAPAK 148
 TGISM..DQQVLEYADPLLSKISAAQNSSRARLVNLNKPQQYNTEVRGNKVVWIFINESDDTVSAPARPAVKAAPAAPAK 148
 TGISM..DQQVLEYADPLLSKISAAQNSSRARLVNLNKPQQYNTEVRGNKVVWIFINESDDTVSAPARPAVKAAPAAPAK 148
MKNGLKT..YVAQTWLTWVGLALCAS..... 25
MKNGLKT..YVAQTWLTWVGLALCAS..... 25
MKMRHGLTLTPRKLTLGFLSFWLWVGLALCAS..... 28
 AGQKIAK..SLIPVTTNEASSIDVSSDDKRRARVVNLDKAGAFTRRVEGNVFLKINNIQSTATP.....V.....A... 135
 AQQGLKQ..SKISVATNEASSVDVTSDDQRSRLTVNLDKAGAFTRRVEGNVFLKINSAQTSNKP.....L.....P... 135
 AQQGLKQ..SKISVATNEASSVDVTSDDQRSRLTVNLDKAGAFTRRVEGNVFLKINSAQTSNKP.....L.....P... 135
 TDMQIPSDQKTKTIQLGSLHSYNIVAVGDRVRAILELDRSVSYSGSTAGSIYSLVNLGKSNL.F.....ENS 136
 TDMQIPSDQKTKTIQLGSLHSYNIVAVGDRVRAILELDRSVSYSGSTAGSVSYSLVNLGKSNL.F.....ENS 136
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 VQNKI..GTKNRELSVGNTRSVTVVEAKDRRLIINLTTLSYTTTRVEGNLFFVVGNSPAGASVASTAPVKASPAPASY 147
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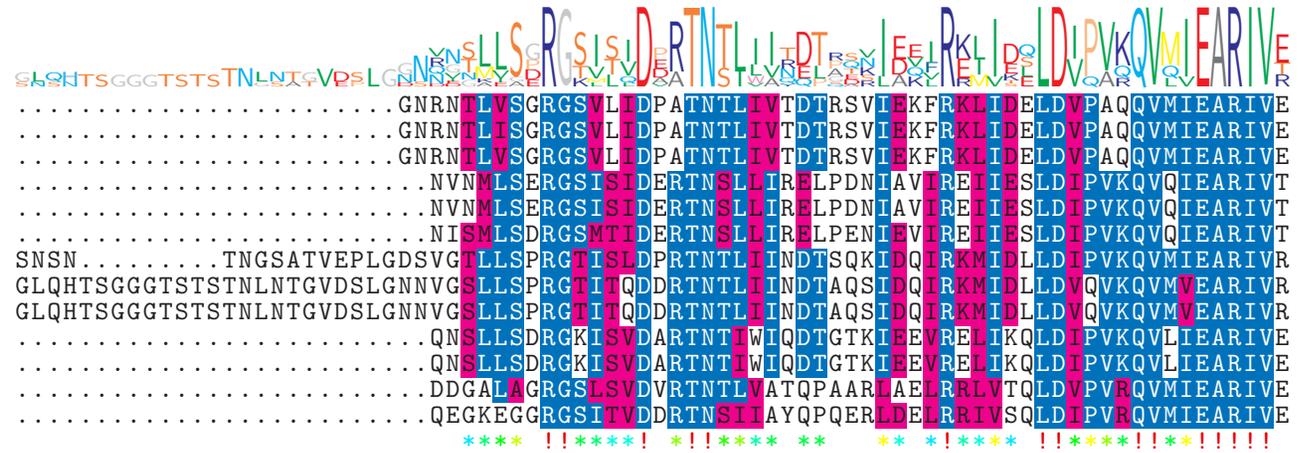
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 consensus

QQAAPSTKSAVSVSEPFPAKQQAAPFESVSVSAVSPAKQQAASAASAKQQA...AASAKQTNI 182
 QQAAPSTKSAVSVSEPFPAKQQAAPFESVSVSAVSPAKQQAASAASAKQQA...AASAKQTNI 228
 QQAAPSTKSAVSVSEPFPAKQQAAPFESVSVSAVSPAKQQAASAASAKQQA...AASAKQTNI 220
SM.....VFSAESATANQLENI 42
SM.....VFSAESATANQLENI 42
FVAEEVQSNLSIKSI 43
TSAPAPQGGIGNI 148
VVS.AQPQGVSN 147
VVS.AQPQGVSN 147
KE.....VF.....ITNQVVNAKHEIKRI 155
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AQ.....PI.....KPKPYVPAGRAIRNI 166
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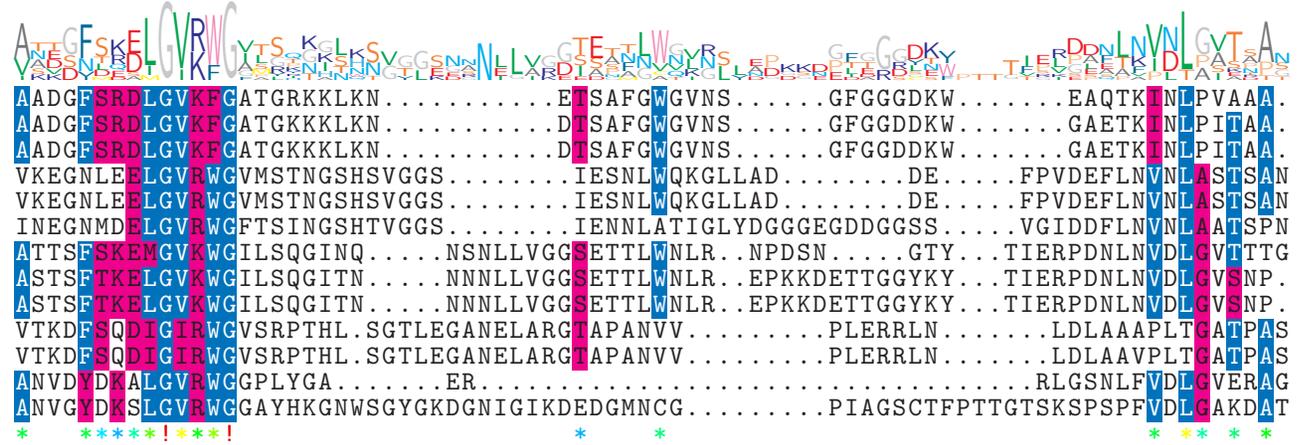
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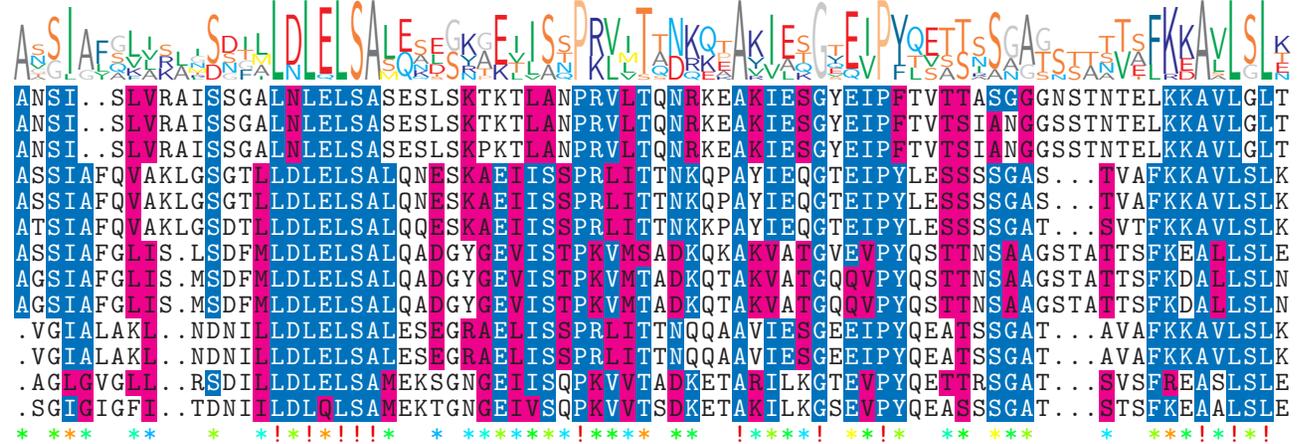
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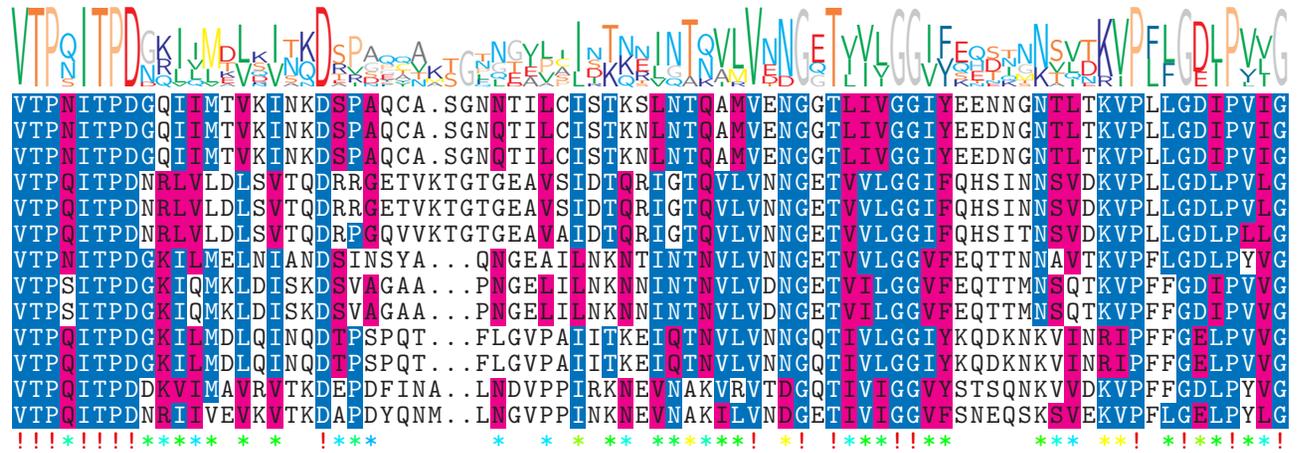
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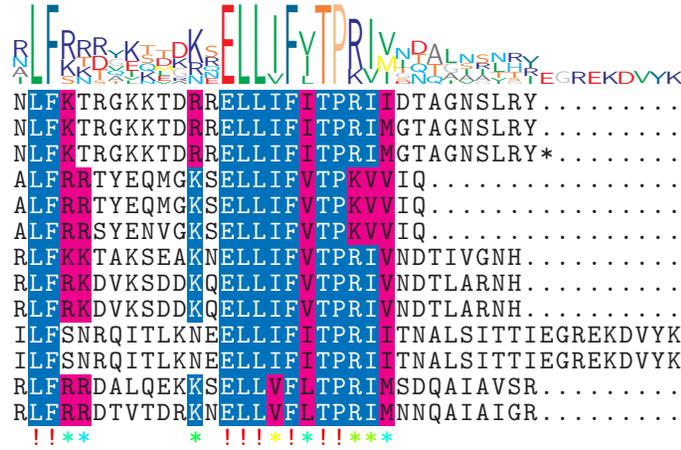


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 consensus



723
769
761
571
571
580
709
721
721
698
698
407
714

X non conserved
X similar
X ≥ 50% conserved