

logo

NTDB id 50070 HT085 RS07555 WP 003693549.1
NTDB id 1107 VT05 RS06875 WP 003693549.1
consensus

MKQSARIKMDQTLKNTLGICALLAFCFGAAIASGYHLEYEYGYRYSAVGALASVFLLLLARGFPRVSSVLLIYVGTALYLP
 MKQSARIKMDQTLKNTLGICALLAFCFGAAIASGYHLEYEYGYRYSAVGALASVFLLLLARGFPRVSSVLLIYVGTALYLP
 MKQSARIKMDQTLKNTLGICALLAFCFGAAIASGYHLEYEYGYRYSAVGALASVFLLLLARGFPRVSSVLLIYVGTALYLP

85
85

logo

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consensus

VGMLYGAPSYQIVGSILESNPAEAREFVGNLPGSLYFVQALFFIFGLTVWKYCVSVGVFADVKMKRRSKIWL TILL TLILSCAV
 VGMWLYGAPSYQIVGSILESNPAAEAREFVGNLPGSLYFVQALFFIFGLTVWKYCVSVGVFADVKMKRRRSKIWL TILL TLILSCAV
 VGMWLYGAPSYQIVGSILESNPAAEAREFVGNLPGSLYFVQALFFIFGLTVWKYCVSVGVFADVKMKRRRSKIWL TILL TLILSCAV

170
170

logo

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consensus

MEKIAGDKDWRPDAGLLLNIFDLYYDLASAPAQYAAKRAHILEAAKKASTWHIRHVAPKYKNYVWVIGESARSDYMNVYGFPLP
MEKIAGDKDWRPDAGLLLNIFDLYYDLASAPAQYAAKRAHILEAAKKASTWHIRHVAPKYKNYVVVIGESARSDYMNVYGFPLP
MEKIAGDKDWRPDAGLLLNIFDLYYDLASAPAQYAAKRAHILEAAKKASTWHIRHVAPKYKNYVVVIGESARSDYMNVYGFPLP

255
255

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DTPFLSRTKGLLINGYQSTAHATNLSLPQTLGLPGEPNNNIVSLAKQAGFRTAWLSNQGMLGHFANEISTYALRSDYPWFTQRGD
DTPFLSRTKGLLINGYQSTAHATNLSLPQTLGLPGEPNNNIVSLAKQAGFRTAWLSNQGMLGHFANEISTYALRSDYPWFTQRGD
DTPFLSRTKGLLINGYQSTAHATNLSLPQTLGLPGEPNNNIVSLAKQAGFRTAWLSNQGMLGHFANEISTYALRSDYPWFTQRGD

340
340

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YKGSAGLSDRLLLPAFKRVL TGNAGTKPRLIMHLMGSHSDFCTRLDKDARRFQYQTEKISCYVSTIAQTDKFLEDTVKILNENK
YKGSAGLSDRLLLPAFKRVL TGNAGTKPRLIMHLMGSHSDFCTRLDKDARRFQYQTEKISCYVSTIAQTDKFLEDTVKILNENK
YKGSAGLSDRLLLPAFKRVL TGNAGTKPRLIMHLMGSHSDFCTRLDKDARRFQYQTEKISCYVSTIAQTDKFLEDTVKILNENK

425
425

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ESWSLVYFSDHGLMHVGKGGERTLT HGEWK RQSYGVPLVKISSDDTRREMIKVRRSAFNFLRGFGSWTGIETDEL PDDGYDFWGN
ESWSLVYFSDHGLMHVGKGGERTLT HGEWK RQSYGVPLVKISSDDTRREMIKVRRSAFNFLRGFGSWTGIETDEL PDDGYDFWGN
ESWSLVYFSDHGLMHVGKGGERTLT HGEWK RQSYGVPLVKISSDDTRREMIKVRRSAFNFLRGFGSWTGIETDEL PDDGYDFWGN

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510

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consensus

VPDVPGE⁺NNLAFIDRQSD⁺DDPAPWYAGK⁺GKSAKNTSKK

548
548

 non conserved
 similar
 $\geq 50\%$ conserved