

logo

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 1381 A4U84 RS02010 WP 021113424.1
NTDB id 1065123 ACHWS5 RS02095 WP 015702713.1
NTDB id 1347 HI 0435 AAC22094.1
NTDB id 1373 NTHI RS02645 WP 011272046.1
consensus

MKNGLKT..YVAQTWLTLWVGLALCASSMVFSAESATANQLENIDFRVNKEKA AVL LVELASPSAVVDVQKVQEGLSI
..MKNGLKT..YVAQTWLTLWVGLALCASSMVFSAESATANQLENIDFRVNKEKA AVL LVELASPSAVVDVQKVQEGLSI
MKMRHGLTLTPRKLTGLFSLWFSLLLAP...FVAAEEVQSNLSKSIDFRTNKDKDAVIVVELVSPAAIVDIKRVQEGLSI
.....
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consensus

ELLKTDVADDKLYLLDVKDFSTPVESVEVFRKEPSTQLVVTVDGEFQHDYTLKGYLEVVISKIKADEKPKPKSVLEKEG
ELLKTDVADDKLYLLDVKDFSTPVESVEVFRKEPSTQLVVTVDGEFQHDYTLKGYLEVVISKIKADEKPKPKSVLEKEG
DLLNTSVKDDQLYLLDVKDFSTVVESVEVFRDSTTRLVAYIDEDYSHDYRLTGRYLEVVKVGIKAN EKAPDKSILDKEG
.....MRYLFL.....F.....FATFPVLAN
.....MWRAFRKIS.FVYFLCGVAY.....VGSQAQDA
.....MKKYFLKCGYFLVCFCLPLI.....VFANPKTDN
.....MKKYFLKCGYFLVCFCLPLI.....VFANPKTDN
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consensus

KLISINFQDIPVRNVQLQLIADYNGFNLVSDSVVGNLTLRLDGVPWQQVLDIILQVKGLDKRVDGNVIL IAPKEELDLRE
KLISINFQDIPVRNVQLQLIADYNGFNLVSDSVVGNLTLRLDGVPWQQVLDIILQVKGLDKRVDGNVIL IAPKEELDLRE
KLISINFQDIPVRNVQLQLIADYNGFNLVSDSVVGNLTLRLDGVPWQQVLDIILQVKGLDKRVDGNVIL IAPKEELDLRE
QQISLSIRNAPTAEIISYLAETGKNITISDEIKDTKNFRVEKSHFDEILNSLIKTHQLNLKKENG IYYIHQAQEH....
EHFYLRKQAPLIVEMQLYALQHQDLLIDDHLEGTLSLQMKKTTFEKCLQSIARMKQLELHQECKSYLTSPSG....
ERFFTRL SQAPLAQTLEQLAFQQDVNLVIGDILENKISLKLNNIDMPRLQITIAKSKHLTLNKKDDG IYYLNGSQSG....
ECFFTRL SQAPLAQTLEQLAFQQDVNLVIGERLEGNISLKLNNIDMPRLKIIAKSKHLTLNKKDDG VYYLNGSQSG....
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consensus

KQALEKARLAEE LGDLKSEI IKINFAKASDIAAMIGGEGNVNMLSERGSISIDERTNSLLIRELPDNI IAVIREIIESLDI
KQALEKARLAEE LGDLKSEI IKINFAKASDIAAMIGGEGNVNMLSERGSISIDERTNSLLIRELPDNI IAVIREIIESLDI
KQALEKARLAEE LGDLKSEI IKINFAKASDIAAMIGGEGNVNMLSERGSISIDERTNSLLIRELPDNI IAVIREIIESLDI
...VAANDTHPTSLMTSSIKLHFAKAEVVKSLT.SCGSLLSVGSSLSFDERTNLLIQDEPQSIQRIKALVAEMDK
...VAANDTHPTSLMTSSIKLHFAKAEVVKSLT.SCGSLLSVGSSLSFDERTNLLIQDEPQSIQRIKALVAEMDK
...VAANDTHPTSLMTSSIKLHFAKAEVVKSLT.SCGSLLSVGSSLSFDERTNLLIQDEPQSIQRIKALVAEMDK
...VAANDTHPTSLMTSSIKLHFAKAEVVKSLT.SCGSLLSVGSSLSFDERTNLLIQDEPQSIQRIKALVAEMDK
* * * * *

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