

logo

NTDB id 1314 DR RS00625 WP 010886768.1
NTDB id 1037 TT RS09535 WP 011174226.1
NTDB id 626 LCA RS04960 WP 011374694.1
NTDB id 114 BSU 16110 NP 389493.1
NTDB id 1361 HI 0985 AAC22646.1
NTDB id 1388 A4U84 RS04945 WP 062924099.1
NTDB id 1043 HON27 RS16615 WP 168727007.1
NTDB id 1073 ABD1 RS00865 WP 015451369.1
NTDB id 1021 ACIAD RS00975 WP 004930462.1
NTDB id 599 KW2 RS05940 WP 021037268.1
NTDB id 407 SMU RS04605 WP 002262865.1
NTDB id 525 SMSK321 RS06295 WP 000705298.1
NTDB id 267 KZH43 RS05590 WP 000705306.1
NTDB id 226 SPD RS05990 WP 000705306.1
NTDB id 192 SPR RS05715 WP 000705306.1
NTDB id 157 SP RS06205 WP 000705306.1
NTDB id 497 SM12261 RS05565 WP 000705318.1
NTDB id 1094 KZH42 RS01320 WP 002224767.1
NTDB id 1089 NMB RS00600 WP 002224767.1
NTDB id 1120 NGFG RS10355 WP 020997408.1
NTDB id 1122 OK783 RS09595 WP 003705341.1
NTDB id 1152 A1552VC RS00200 WP 000654772.1
NTDB id 1399 DSB67 RS15600 WP 010645755.1
NTDB id 1145195 DXE44 RS09355 WP 114654192.1
NTDB id 1250 GCO85 RS13065 WP 027219989.1
consensus

QDVLTEINWGLAPA...P...AVP.DLPPEQARVLRALQ..TPAT..LDDLAATTG 342
EDVLSYLGMSARPK...P...LP.GLSPEEEALYALLQ..EKKEALP...AMALG 304
NILIEELRYFD..... 288
EDIFEELPERNVQYTEPF..... 297
KDILETLQYHS.....IHSQ.TEIDFDQIA...VPNYTPPPDPR...RL.VEAPSHPKLYSRIGYTPVSI...DAEEFN 344
EDILEATAWQR...QSVHIQ.PSL.FDTKP...KQAVKSEPKFAKNLPELTACQQQLFEQISLEPISVDDLAKATD 346
EQIIEIDLALPTQWQSQQNQ...EET...NTNTP...EIPHEHLIDLYQSL...DWVGQNI...VVHHN 345
EQIIEIDLALPTQWQSQQNQ...EEA...NTNTP...EIREHLIDLYQSL...DWVGQNI...VVHHN 345
EQIIEIDLALPTHWHSQSTASGEANADDSG...KTDDA...DLPDDLPLYQLL...DWQGQDL...LAQHYQ 350
QDILEEYLYN..... 282
FDILNEFNF..... 280
QDVLAEFEF..... 282
QDVLAEFEF..... 282
QDVLAEFEF..... 282
QDVLAEFEF..... 282
QDVLAEFEF..... 282
QDVLAEFEF..... 282
DDILNECPGLLQNTGASSYSINKGIPEKRITAVQTASDQLSLPEGKMPSEKTENRPVGGSIILDRMGFDPVHPDVL...AGQLA 365
DDILNECPGLLQNTGASSYSINKGIPEKRITAVQTASDQLSLPEGKMPSEKTENRPVGGSIILDRMGFDPVHPDVL...AGQLA 365
DDILNECPGLLQNTGASSYSINKDTPDTGRRRTVQTAY..APPPAAKMPSEGAAGGTAVGGIILDKMGFDPVHPDVL...AGQLA 363
DDILNECPGLLQNTGASSYSINKDTPDTGRRRAVQTAY..APPPAAKMPSEGAAGGTAVGGIILDKMGFDPVHPDVL...AGQLA 363
QQIHQELKNALTWS.....LSEQVPYQA.....TLFSAVQSD.....EELPFPELLANVGIATPIDILASRTQ 339
QEVINEIQSLLDWS.....INQSL.....DLFSAPIDE.....EELPFPELLANVGNATPVDILASRTN 337
KDILEELKNW..... 224
ADVLEELKIEHHQF.....T.....SNK.....PIFSLASGK.....E.....NLVKFIGFETTTIDQ...IDRS 328
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 consensus



LSIPETLQTALVMLQLQGLAYEV.GGRWSR... 370
 IPPERVLSLTLLELKLARALPGGRYGGP... 334
 288
 297
 LSVDVLLVQLLDLELQDLIISENGLYKRV... 373
 MAVETALIELLNLELLGVVKQVRGGYVIT... 375
 IPVSELTSSLMELLELLGLCMQQSGLYLRCRS.. 376
 IPVSELTSSLMELLELLGLCMQQSGLYLRCRS.. 376
 GSTAELTAQLMELELLGVCIQQSGRYLRCRSPY 383
 282
 280
 282
 282
 282
 282
 282
 282
 282
 MPAADLYAALLELELDGSVAAMPGRYQRIRT. 397
 MPAADLYAALLELELDGSVAAMPGRYQRIRT. 397
 MPAADLYAALLELELDGSVAAMPGRYQRIRT. 395
 MPAADLYAALLELELDGSVAAMPGRYQRIRT. 395
 IPVQDITMMQLLELELLCHVVAVPGGYIRKGRG. 371
 IPVQEVMMQLLELELSCHVVAVSGGYIRKGRG. 369
 224
 YGMEQVTSGLAELELKGAVIAVPGGYIRCEYER 361
 * * *** * *

[X] non conserved
 [X] similar
 [X] ≥ 50% conserved