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logo
NTDB id 1073 ABD1 RS00865 WP 015451369.1     MLTQLSSHHYHTLKVWYLVQHSLVSFKKIIDYFGNCEKATQPDGLAKWSSLGLHANHLKRVNEFQTTQG.QAQFEQLV.Q   78
NTDB id 1043 HON27 RS16615 WP 168727007.1    MLTQLSSHQYHTLKVWYLVQHSLVSFKKIIDYFGNCEKATQPDGLAKWSSLGLHANHLKRVNEFQTPQG.QAQFEQLV.Q   78
NTDB id 1021 ACIAD RS00975 WP 004930462.1    MITILSSHHYHTIKVWYVLQHSLSGFKKLIHYFGDCETALQPQRLSDWQKLGLHANHLKRLEEVHTLQG.QQQFEKML.A   78
NTDB id 1094 KZH42 RS01320 WP 002224767.1    ...MTEDERFAWLQLAFTPYIGAESFLLLMRRFGSAQNALSA.PAEQVAALIRHKQALEAWRNAEKRALARQAAEAALEW   76
NTDB id 1089 NMB RS00600 WP 002224767.1      ...MTEDERFAWLQLAFTPYIGAESFLLLMRRFGSAQNALSA.PAEQVAALIRHKQALEAWRNAEKRALARQAAEAALEW   76
NTDB id 1122 OK783 RS09595 WP 003705341.1    ...MTEDERFAWLQLAFTPYIGAESFLLLMRSFGSAQNALSA.PAEQVAPAVRHKHALEAWRNAEKRALARQAAEAALEW   76
NTDB id 1120 NGFG RS10355 WP 020997408.1     ...MTEDERFAWLQLAFTPYIGAESFLLLMRSFGSAQNALSA.PAEQVAPAVRHKHALEAWRNAEKRALARQAAEAALEW   76
NTDB id 1250 GCO85 RS13065 WP 027219989.1    .....MNNLQPLLALNRMKRIGPRTVLKLQKRWPDLNLMFQL.SSVDLEEAGLPSWLAQTIKNFD.....PDFIKTDLNW   69
NTDB id 1152 A1552VC RS00200 WP 000654772.1 ...MKDQDLAAWLALCFTPKLGSKTISHLLATR.LPAQLQSF.TPKQWLACGLKPEQLVFLTTQA.....AKQAEQCLQW   70
NTDB id 103540 QUF19 RS16865 WP 286295179.1 ...MNEQQLSAWLTLSFVPQLGGKRLARLLSID.SPSNIVGY.SSHQLQAIGLSAKQIAYLREQA.....PREVEACLEW   70
NTDB id 1399 DSB67 RS15600 WP 010645755.1    MTPQNDIDLAAWLKLSCLPGIGGVKMNKLLSKD.TPSNIVQY.STEQLQLLGLTAKQLQAW.SQV.....DKEVDACLTW   72
NTDB id 1388 A4U84 RS04945 WP 062924099.1    .....MTHLTKLLALLQVPQLGAQRIGRLLSEV.DFGEFCQY.DKTALKQMGWNERQIQRWFNPE.....HKWIDQALQW   68
NTDB id 1361 HI 0985 AAC22646.1              ....MNDITYTLLRLMQVPKLGGVGIDKILSNI.TLNELLNY.DDVAFRQMGWGAIQIRRWFKPE.....AKFIEPALVW   69
consensus                                      *  * * *** *** *  ***  *      *      *  **      *                  *  * *
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logo
NTDB id 1073 ABD1 RS00865 WP 015451369.1     QVRQHTDFILTPDDSGYPTQLLPYTDHPPIIFGKGQAQALLQPQIAIVGSRKPSPHGRQVAYDFAYYLSEKGFFISSGLA   158
NTDB id 1043 HON27 RS16615 WP 168727007.1    QVRQHTDFILTPDDSGYPTQLLPYTDHPPIIFGKGQAQALLQPQIAIVGSRKPSPHGRQVAYDFAYYLSEKGFFISSGLA   158
NTDB id 1021 ACIAD RS00975 WP 004930462.1    QLQTHTDFIVTPDDPAYPSQLIPYQDRPPILFGQGSIQSLIQPQIAVVGSRKPSPHGRQVAYDFSYFLSEKGFYITSGLA   158
NTDB id 1094 KZH42 RS01320 WP 002224767.1    EMRD.GCRLMLLQDEDFPEMLTQGLTAPPVLFLRGNVQLLHKPSAAIVGSRHATPQAMRIAKDFGKSLGGKGIPVVSGMA   155
NTDB id 1089 NMB RS00600 WP 002224767.1      EMRD.GCRLMLLQDEDFPEMLTQGLTAPPVLFLRGNVQLLHKPSAAIVGSRHATPQAMRIAKDFGKSLGGKGIPVVSGMA   155
NTDB id 1122 OK783 RS09595 WP 003705341.1    EMRD.GCRLMLLQDEDFPEMLTQGLTAPPVLFLRGNVRLLHKPSAAIVGSRHATPQAMRIAKDFGRALGGKGIPTVSGMA   155
NTDB id 1120 NGFG RS10355 WP 020997408.1     EMRD.GCRLMLLQDEDFPEMLTQGLTAPPVLFLRGNVRLLHKPSAAIVGSRHATPQAMRIAKDFGRALGGKGIPTVSGMA   155
NTDB id 1250 GCO85 RS13065 WP 027219989.1    LSSSENHHILTWDSPYYPALLKEIADPPFILYAKGELSALTQPSLAIVGSRNASVTGNENARAFSREISRHGVSIVSGLA   149
NTDB id 1152 A1552VC RS00200 WP 000654772.1 RSAANNRYIVTPHCPLYPRLLKEINSSPPVLFIEGIWEAVHDPAVAIVGSRNASVDGRQIARQFATELAQSGLVVTSGLA   150
NTDB id 103540 QUF19 RS16865 WP 286295179.1 QARQPNHHIITPNCSHYPKLLNEIASAPSVLFVKGHVEKLIEPQIAMVGSRNASIEGLQTAKSFAKEFVQNGLIVTSGLA   150
NTDB id 1399 DSB67 RS15600 WP 010645755.1    VAASSHHHILTLADALYPPLLKQTVAPPPLLFVKGEASCLPQPQIAMVGSRNASVDGLQHTRTFASDLVQHDLIVTSGLA   152
NTDB id 1388 A4U84 RS04945 WP 062924099.1    AEQD.QQQILTLFDEDYPFLLKQISTAPPVLFVRGNVESLSLPQIAIVGSRDYSHYGEHWAGHFSAELVKHQLAVTSGLA   147
NTDB id 1361 HI 0985 AAC22646.1              SQKE.GNHLVNYFSPFYPFLLKQTASFPPLLFVKGNLTALSQRQMAMVGSRYCTTYGEYWAKHFATELSLAGFTITSGLA   148
consensus                                     *     ***  *  *! *!    * !*******!**  *  * *!*!!!! **  *  *** !*  *   ** **!!*!
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logo
NTDB id 1073 ABD1 RS00865 WP 015451369.1     YGIDEAAHQGASA.HQRTIAVTGTGLDTTYPAQNKKLAEYILAQNGAIITEFLPGTPPLQQHFPRRNRIVSGLSLGVLVV   237
NTDB id 1043 HON27 RS16615 WP 168727007.1    YGIDEAAHQGAST.HQRTIAVTGTGLDTTYPAQNKKLAEHILAKNGAIITEFLPGTPPLQQHFPRRNRIVSGLSLGVLVV   237
NTDB id 1021 ACIAD RS00975 WP 004930462.1    HGIDEAAHQGSLV.HHRAIAVVGTGLDLCYPSGNKALKQHIRDQQGAIVSEFLPGTPPLQAHFPRRNRIVSGLSLGVLVV   237
NTDB id 1094 KZH42 RS01320 WP 002224767.1    SGIDTAAHQGALQAEGGTIAVWGTGIDRIYPPVNKNLAYEIAE.KGLIVSEFPIGTRPYAGNFPRRNRLIAALSQVTLVV   234
NTDB id 1089 NMB RS00600 WP 002224767.1      SGIDTAAHQGALQAEGGTIAVWGTGIDRIYPPVNKNLAYEIAE.KGLIVSEFPIGTRPYAGNFPRRNRLIAALSQVTLVV   234
NTDB id 1122 OK783 RS09595 WP 003705341.1    SGIDTAAHQGALEAEGGTVAVWGTGIDRIYPPANKNLAYEIAE.KGLIVSEFPIGTRPYAGNFPRRNRLIAALSQVTLVV   234
NTDB id 1120 NGFG RS10355 WP 020997408.1     SGIDTAAHQGALEAEGGTIAVWGTGIDRIYPPANKNLAYEIAE.KGLIVSEFPIGTRPYAGNFPRRNRLIAALSQVTLVV   234
NTDB id 1250 GCO85 RS13065 WP 027219989.1    LGIDAHAHLGCLEGGGKTIAVLGTGIDCIYPRRHLKLAEQITE.NGLLLSEFPLKSPPIAGHFPLRNRIISGLSLCILVI   228
NTDB id 1152 A1552VC RS00200 WP 000654772.1 LGIDGYAHDGALQAQGQTVAVLGSGLAQVYPKQHQGLAERIIA.QGALVSEFAPHTPPKADHFPRRNRIISGLSLGVVVV   229
NTDB id 103540 QUF19 RS16865 WP 286295179.1 LGIDGYAHDGALDKGGETFAVLGSGLDSIYPARHRNLAERICE.NGALISEFRPSAKPRPEHFPRRNRIISGLSLGTLVV   229
NTDB id 1399 DSB67 RS15600 WP 010645755.1    LGIDGHAHDGALLAGGKTIAVLGSGLEQVYPARHRGLAQRVAE.NGALVSEFRPDAKPRAENFPRRNRIISGLSLGVLVV   231
NTDB id 1388 A4U84 RS04945 WP 062924099.1    IGIDGFCHQRAANENGITIAVLGSGLDQVYPARHKKLAEQIVETSGALVSEFFPSQPPIAENFPRRNRIISGLSLGTLVI   227
NTDB id 1361 HI 0985 AAC22646.1              LGIDGHCHQAVVNIQGQTIAVLGSGLEQIYPSKHQRLSAQIIENNGALVSEFLPNQAPIAANFPRRNRIISGLSVGTLVV   228
consensus                                     !!!   *!****   *  **!! !*!** *!!   * !*  * *  !***!! * * ! *  !!*!!!****!!** *!*
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logo
NTDB id 1073 ABD1 RS00865 WP 015451369.1     EATLKSGSLITANKAAEQGKTVFAIPGHIYSEFHQGCHQLIREGAILIDHPEQIIEDLALPTQ.........WQSQQQNQ   308
NTDB id 1043 HON27 RS16615 WP 168727007.1    EATLKSGSLITANKAAEQGKTVFAIPGHIYSEFHQGCHQLIREGAILIDHPEQIIEDLALPTQ.........WQSQQQNQ   308
NTDB id 1021 ACIAD RS00975 WP 004930462.1    EATLKSGSLITANKAAEQGKVVFAIPGHIYSEFHQGCHQLIREGAILVDHPEQIIEDLALPTH.........WHSQSTAS   308
NTDB id 1094 KZH42 RS01320 WP 002224767.1    EAALESGSLITARLAAEMGREVMAVPGSIDNPHSKGCHKLIKDGAKLVECLDDILNECPGLLQNTGA...SSYSINKGIP   311
NTDB id 1089 NMB RS00600 WP 002224767.1      EAALESGSLITARLAAEMGREVMAVPGSIDNPHSKGCHKLIKDGAKLVECLDDILNECPGLLQNTGA...SSYSINKGIP   311
NTDB id 1122 OK783 RS09595 WP 003705341.1    EAALESGSLITAGLAAEMGREVMAVPGSIDNPHSKGCHKLIKDGAKLTECLDDILNECPGLLQNTGA...SSYSINKDTP   311
NTDB id 1120 NGFG RS10355 WP 020997408.1     EAALESGSLITAGLAAEMGREVMAVPGSIDNPHSKGCHKLIKDGAKLTECLDDILNECPGLLQNTGA...SSYSINKDTP   311
NTDB id 1250 GCO85 RS13065 WP 027219989.1    EAAIKSGSLITARMALEQNRDVLAIPGSIHNPLARGCHYLLQQGAKLVTSVADVLDELKIEHHQFTS.............  295
NTDB id 1152 A1552VC RS00200 WP 000654772.1 EAAEKSGSLITARYAAEQGREVFVVPGSIFNAASQGSNQLIRQGACLVQSVQQIHQELKNA.........LTWSLSEQVP   300
NTDB id 103540 QUF19 RS16865 WP 286295179.1 EAAEKSGSLITARYAMEQGREVFALPGSIHSPTSRGGNSLIKAGACLVQNAQDVLIEIRSL.........LDWSIDQQPS   300
NTDB id 1399 DSB67 RS15600 WP 010645755.1    EAAEKSGSLITARYALEQGREVFALPASINAPNASGGNQLIQNGACLVQNTQEVLNEIQSL.........LDWSINQSLD   302
NTDB id 1388 A4U84 RS04945 WP 062924099.1    EATVNSGSLITARYALEQGREVFALPNSVQNPYSEGCHKLIKEGALLVENVEDILEAIAWQRQSVHIQPSL.FDTKP..K   304
NTDB id 1361 HI 0985 AAC22646.1              EATEKSGSLITARYALEQNREVFAVPGNIQNKSSQGCHRLIKQGAMLVENAKDILETLYQHS..IHSQTEIDFDQIAVPN   306
consensus                                    !!***!!!!!!!* !*!****!***!*** ** * !** !***!! !**  **** **              *  *
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logo
NTDB id 1073 ABD1 RS00865 WP 015451369.1     T..........EEA.......NTNTPEIREHLIDLYQSLDWVGQNIDQLVVHHNIPVSELTSSLMELELLGLCMQQSGLY   371
NTDB id 1043 HON27 RS16615 WP 168727007.1    T..........EET.......NTNTPEIPEHLIDLYQSLDWVGQNIDQLVVHHNIPVSELTSSLMELELLGLCMQQSGLY   371
NTDB id 1021 ACIAD RS00975 WP 004930462.1    GEA.....NADDSG.......KTDDADLPDDLLPLYQLLDWQGQDLDQLAQHYQGSTAELTAQLMELELLGVCIQQSGRY   376
NTDB id 1094 KZH42 RS01320 WP 002224767.1    EKRITAVQTASDQLSLPEGKMPSEKTENRPVGGSILDRMGFDPVHPDVLAGQLAMPAADLYAALLELELDGSVAAMPGGR   391
NTDB id 1089 NMB RS00600 WP 002224767.1      EKRITAVQTASDQLSLPEGKMPSEKTENRPVGGSILDRMGFDPVHPDVLAGQLAMPAADLYAALLELELDGSVAAMPGGR   391
NTDB id 1122 OK783 RS09595 WP 003705341.1    DTGRRAVQTAY..APPPAAKMPSEGAAGGTAVGGILDKMGFDPVHPDVLAGQLAMPAADLYAALLELELDGSVAAMPGGR   389
NTDB id 1120 NGFG RS10355 WP 020997408.1     DTGRRTVQTAY..APPPAAKMPSEGAAGGTAVGGILDKMGFDPIHPDVLAGQLAMPAADLYAALLELELDGSVAAMPGGR   389
NTDB id 1250 GCO85 RS13065 WP 027219989.1    ................NKPIFS.....LASGKENLVKFIGFETTTIDQIIDRSGYGMEQVTSGLAELELKGAVIAVPGGY   354
NTDB id 1152 A1552VC RS00200 WP 000654772.1 ............Y...QATLFSAVQSDEELPFPELLANVGIEATPIDILASRTQIPVQDIMMQLLELELLGHVVAVPGGY   365
NTDB id 103540 QUF19 RS16865 WP 286295179.1 ............L...FEPT.PNEGENEQLPFPQLLANVGLEATPVDILAQRTHIPVHEVMMQLLELELSGHVVAVSGGY   364
NTDB id 1399 DSB67 RS15600 WP 010645755.1    ............L...FSAP.I...DEEELPFPQLLANVGNEATPVDILASRTNIPVQEVMMQLLELELSGHVVAVSGGY   363
NTDB id 1388 A4U84 RS04945 WP 062924099.1    ............QAVKSEPKFAKNLPELTACQQQLFEQISLEPISVDDLAKATDMAVETALIELLNLELLGVVKQVRGGY   372
NTDB id 1361 HI 0985 AAC22646.1              ............YTPPPDPR...RL.VEAPSHPKLYSRIGYTPVSIDDLAEEFNLSVDVLLVQLLDLELQDLIISENGLY   370
consensus                                                              *        **  ****   *! **    *** **   !**!!! * **** !**
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logo
NTDB id 1073 ABD1 RS00865 WP 015451369.1     LRCRS..   376
NTDB id 1043 HON27 RS16615 WP 168727007.1    LRCRS..   376
NTDB id 1021 ACIAD RS00975 WP 004930462.1    LRCRSPY   383
NTDB id 1094 KZH42 RS01320 WP 002224767.1    YQRIRT.   397
NTDB id 1089 NMB RS00600 WP 002224767.1      YQRIRT.   397
NTDB id 1122 OK783 RS09595 WP 003705341.1    YQRIRT.   395
NTDB id 1120 NGFG RS10355 WP 020997408.1     YQRIRT.   395
NTDB id 1250 GCO85 RS13065 WP 027219989.1    IRCEYER   361
NTDB id 1152 A1552VC RS00200 WP 000654772.1 IRKGRG.   371
NTDB id 103540 QUF19 RS16865 WP 286295179.1 IRKGRG.   370
NTDB id 1399 DSB67 RS15600 WP 010645755.1    IRKGRG.   369
NTDB id 1388 A4U84 RS04945 WP 062924099.1    VIT....   375
NTDB id 1361 HI 0985 AAC22646.1              KRV....   373
consensus                                    **
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X non conserved
X similar
X $\geq$ 50% conserved