logo

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NTDB id 298553 DOM24 RS00540 WP 106439152.1   MIAELSQLHYHSLKLWYLVQHSVSSFNQLVEYFGSAEQATTPAALARWGNLKLHANHS...KRAQEFYSATGQAEFEQLT   77
NTDB id 1043 HON27 RS16615 WP 168727007.1     MLTQLSSHQYHTLKVWYLVQHSLVSFKKIIDYFGNCEKATQPDGLAKWSSLGLHANHL...KRVNEFQTPQGQAQFEQLV   77
NTDB id 1073 ABD1 RS00865 WP 015451369.1      MLTQLSSHHYHTLKVWYLVQHSLVSFKKIIDYFGNCEKATQPDGLAKWSSLGLHANHL...KRVNEFQTTQGQAQFEQLV   77
NTDB id 1021 ACIAD RS00975 WP 004930462.1     MITILSSHHYHTIKVWYVLQHSLSGFKKLIHYFGDCETALQPQRLSDWQKLGLHANHL...KRLEEVHTLQGQQQFEKML   77
NTDB id 1152 A1552VC RS00200 WP 000654772.1   ...MKDQDLAAWLALCFTPKLGSKTISHLLATRLPAQLQSFT..PKQWLACGLKPEQLVF......LTTQAAKQAEQCLQ   69
NTDB id 1094 KZH42 RS01320 WP 002224767.1     ...MTEDERFAWLQLAFTPYIGAESFLLLMRRFGSAQNALSA..PAEQVAALIRHKQALEAWRNAEKRALARQAAEAALE   75
NTDB id 1089 NMB RS00600 WP 002224767.1       ...MTEDERFAWLQLAFTPYIGAESFLLLMRRFGSAQNALSA..PAEQVAALIRHKQALEAWRNAEKRALARQAAEAALE   75
NTDB id 1120 NGFG RS10355 WP 020997408.1      ...MTEDERFAWLQLAFTPYIGAESFLLLMRSFGSAQNALSA..PAEQVAPAVRHKHALEAWRNAEKRALARQAAEAALE   75
NTDB id 1122 OK783 RS09595 WP 003705341.1     ...MTEDERFAWLQLAFTPYIGAESFLLLMRSFGSAQNALSA..PAEQVAPAVRHKHALEAWRNAEKRALARQAAEAALE   75
consensus                                        * * * **** * *** **  **  **  *********    ****** ***  * *   *  *  *********  *
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NTDB id 298553 DOM24 RS00540 WP 106439152.1   QRVLASCDFILVPEDILYPQQLHPYTDKPPILFGQGSAQALSQPQIAIVGSRKPSPHGRQVAYDFAYYLSEKGFYITSGL  157
NTDB id 1043 HON27 RS16615 WP 168727007.1     QQVRQHTDFILTPDDSGYPTQLLPYTDHPPIIFGKGQAQALLQPQIAIVGSRKPSPHGRQVAYDFAYYLSEKGFFISSGL  157
NTDB id 1073 ABD1 RS00865 WP 015451369.1      QQVRQHTDFILTPDDSGYPTQLLPYTDHPPIIFGKGQAQALLQPQIAIVGSRKPSPHGRQVAYDFAYYLSEKGFFISSGL  157
NTDB id 1021 ACIAD RS00975 WP 004930462.1     AQLQTHTDFIVTPDDPAYPSQLIPYQDRPPILFGQGSIQSLIQPQIAVVGSRKPSPHGRQVAYDFSYFLSEKGFYITSGL  157
NTDB id 1152 A1552VC RS00200 WP 000654772.1   WRSAANNRYIVTPHCPLYPRLLKEINSSPPVLFIEGIWEAVHDPAVAIVGSRNASVDGRQIARQFATELAQSGLVVTSGL  149
NTDB id 1094 KZH42 RS01320 WP 002224767.1     WEMRDGCRLMLL.QDEDFPEMLTQGLTAPPVLFLRGNVQLLHKPSAAIVGSRHATPQAMRIAKDFGKSLGGKGIPVVSGM  154
NTDB id 1089 NMB RS00600 WP 002224767.1       WEMRDGCRLMLL.QDEDFPEMLTQGLTAPPVLFLRGNVQLLHKPSAAIVGSRHATPQAMRIAKDFGKSLGGKGIPVVSGM  154
NTDB id 1120 NGFG RS10355 WP 020997408.1      WEMRDGCRLMLL.QDEDFPEMLTQGLTAPPVLFLRGNVRLLHKPSAAIVGSRHATPQAMRIAKDFGRALGGKGIPTVSGM  154
NTDB id 1122 OK783 RS09595 WP 003705341.1     WEMRDGCRLMLL.QDEDFPEMLTQGLTAPPVLFLRGNVRLLHKPSAAIVGSRHATPQAMRIAKDFGRALGGKGIPTVSGM  154
consensus                                     * **   *******  *  *! *!    * !!**!**!***  ** ! *!*!!!!  ***  ****!**!*  !* *!*  **!!*
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logo

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NTDB id 298553 DOM24 RS00540 WP 106439152.1   ALGIDEAAHQGALQHQ.RTIAVVGTGLDLVYPAHNRKLQEQILQYGGTIVSEFLPGTQPLKHHFPRRNRIVSGLSLGVLV  236
NTDB id 1043 HON27 RS16615 WP 168727007.1     AYGIDEAAHQGASTHQ.RTIAVTGTGLDTTYPAQNKKLAEHILAKNGAIITEFLPGTPPLQQHFPRRNRIVSGLSLGVLV  236
NTDB id 1073 ABD1 RS00865 WP 015451369.1      AYGIDEAAHQGASAHQ.RTIAVTGTGLDTTYPAQNKKLAEYILAQNGAIITEFLPGTPPLQQHFPRRNRIVSGLSLGVLV  236
NTDB id 1021 ACIAD RS00975 WP 004930462.1     AHGIDEAAHQGSLVHH.RAIAVVGTGLDLCYPSGNKALKQHIRDQGGAIVSEFLPGTPPLQAHFPRRNRIVSGLSLGVLV  236
NTDB id 1152 A1552VC RS00200 WP 000654772.1   ALGIDGYAHDGALQAQGQTVAVLGSGLAQVYPKQHQGLAERIIA.QGALVSEFAPHTPPKADHFPRRNRIISGLSLGVVV  228
NTDB id 1094 KZH42 RS01320 WP 002224767.1     ASGIDTAAHQGALQAEGGTIAVWGTGIDRIYPPVNKNLAYEIAE.KGLIVSEFPIGTRPYAGNFPRRNRLIAALSQVTLV  233
NTDB id 1089 NMB RS00600 WP 002224767.1       ASGIDTAAHQGALQAEGGTIAVWGTGIDRIYPPVNKNLAYEIAE.KGLIVSEFPIGTRPYAGNFPRRNRLIAALSQVTLV  233
NTDB id 1120 NGFG RS10355 WP 020997408.1      ASGIDTAAHQGALEAEGGTIAVWGTGIDRIYPPANKNLAYEIAE.KGLIVSEFPIGTRPYAGNFPRRNRLIAALSQVTLV  233
NTDB id 1122 OK783 RS09595 WP 003705341.1     ASGIDTAAHQGALEAEGGTVAVWGTGIDRIYPPANKNLAYEIAE.KGLIVSEFPIGTRPYAGNFPRRNRLIAALSQVTLV  233
consensus                                     ! !!! *!!*!** * * **!! !*!** *!!  ** !*  ! *  ! ***!! **! ! ***!!!!!!*****!!****!
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NTDB id 298553 DOM24 RS00540 WP 106439152.1   AEAALESGSLITAQRAADQGKIIFAIPGHIYSEHHQGCHQLIREGAILVDHPEQLIEDLALPT......QWHSQQQKIS.  309
NTDB id 1043 HON27 RS16615 WP 168727007.1     VEATLKSGSLITANKAAEQGKTVFAIPGHIYSEFHQGCHQLIREGAILIDHPEQIIEDLALPT......QWQSQQQNQT.  309
NTDB id 1073 ABD1 RS00865 WP 015451369.1      VEATLKSGSLITANKAAEQGKTVFAIPGHIYSEFHQGCHQLIREGAILIDHPEQIIEDLALPT......QWQSQQQNQT.  309
NTDB id 1021 ACIAD RS00975 WP 004930462.1     VEATLKSGSLITANKAAEQGKVVFAIPGHIYSEFHQGCHQLIREGAILVDHPEQIIEDLALPT......HWHSQSTASGE  310
NTDB id 1152 A1552VC RS00200 WP 000654772.1   VEAAEKSGSLITARYAAEQGREVFVVPGSIFNAASQGSNQLIRQGACLVQSVQQIHQELKNAL......TWSLSEQVPYQ  302
NTDB id 1094 KZH42 RS01320 WP 002224767.1     VEAALESGSLITARLAAEMGREVMAVPGSIDNPHSKGCHKLIKDGAKLVECLDDILNECPGLLQNTGASSYSINKGIPEK  313
NTDB id 1089 NMB RS00600 WP 002224767.1       VEAALESGSLITARLAAEMGREVMAVPGSIDNPHSKGCHKLIKDGAKLVECLDDILNECPGLLQNTGASSYSINKGIPEK  313
NTDB id 1120 NGFG RS10355 WP 020997408.1      VEAALESGSLITAGLAAEMGREVMAVPGSIDNPHSKGCHKLIKDGAKLTECLDDILNECPGLLQNTGASSYSINKDTPDT  313
NTDB id 1122 OK783 RS09595 WP 003705341.1     VEAALESGSLITAGLAAEMGREVMAVPGSIDNPHSKGCHKLIKDGAKLTECLDDILNECPGLLQNTGASSYSINKDTPDT  313
consensus                                     *!!**!!!!!!!  !!**!*****!!*!** ***!***!!**!! !** ********   *       *****   *
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logo

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NTDB id 298553 DOM24 RS00540 WP 106439152.1  ......SVPEPA.........QVPEHLF...ELYQQLDWVGLDLDQIALKLPLPTAELTGHLMELELLGLCVQQSGRY.L  370
NTDB id 1043 HON27 RS16615 WP 168727007.1    ....EETNTNTP.........EIPEHLI...DLYQSLDWVGQNIDQLVVHHNIPVSELTSSLMELELLGLCMQQSGLY.L  372
NTDB id 1073 ABD1 RS00865 WP 015451369.1     ....EEANTNTP.........EIREHLI...DLYQSLDWVGQNIDQLVVHHNIPVSELTSSLMELELLGLCMQQSGLY.L  372
NTDB id 1021 ACIAD RS00975 WP 004930462.1    ANADDSGKTDDA.........DLPDDLL...PLYQLLDWQGQDLDQLAQHYQGSTAELTAQLMELELLGVCIQQSGRY.L  377
NTDB id 1152 A1552VC RS00200 WP 000654772.1 ATLFSA...............VQSDEELPFPELLANVGIEATPIDILASRTQIPVQDIMMQLLELELLGHVVAVPGGYIR  367
NTDB id 1094 KZH42 RS01320 WP 002224767.1    RITAVQTASDQLSLPEGKMPSEKTENRPVGGSILDRMGFDPVHPDVLAGGQLAMPAADLYAALLELELDGSVAAMPGGRYQ  393
NTDB id 1089 NMB RS00600 WP 002224767.1      RITAVQTASDQLSLPEGKMPSEKTENRPVGGSILDRMGFDPVHPDVLAGGQLAMPAADLYAALLELELDGSVAAMPGGRYQ  393
NTDB id 1120 NGFG RS10355 WP 020997408.1     GRRTVQTAY..APPPAAKMPSEGAAGGTAVGGILDKMGFDPIHPDVLAGGQLAMPAADLYAALLELELDGSVAAMPGGRYQ  391
NTDB id 1122 OK783 RS09595 WP 003705341.1    GRRAVQTAY..APPPAAKMPSEGAAGGTAVGGILDKMGFDPVHPDVLAGGQLAMPAADLYAALLELELDGSVAAMPGGRYQ  391
consensus                                          * *            *  *       **  ****** *!***  * ** *** * !*!!!!*! *****!**
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logo

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NTDB id 298553 DOM24 RS00540 WP 106439152.1  RCRPGF  376
NTDB id 1043 HON27 RS16615 WP 168727007.1    RCRS..  376
NTDB id 1073 ABD1 RS00865 WP 015451369.1     RCRS..  376
NTDB id 1021 ACIAD RS00975 WP 004930462.1    RCRSPY  383
NTDB id 1152 A1552VC RS00200 WP 000654772.1 KGRG..  371
NTDB id 1094 KZH42 RS01320 WP 002224767.1    RIRT..  397
NTDB id 1089 NMB RS00600 WP 002224767.1      RIRT..  397
NTDB id 1120 NGFG RS10355 WP 020997408.1     RIRT..  395
NTDB id 1122 OK783 RS09595 WP 003705341.1    RIRT..  395
consensus                                    * !*
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X non conserved

X similar

X $\geq$ 50% conserved