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NTDB id 1028 TT RS08215 WP 011173991.1	MSXLSIGDRLGAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1306 DR RS10060 WP 027479822.1	.MALSIGDRLGAILLDQG YLGDN DLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAAL	79
NTDB id 1168 A1552VC RS11070 WP 000957200.1		0
NTDB id 1401 DSB67 RS12665 WP 010643259.1		0
NTDB id 1293 VP RS12240 WP 005479695.1		0
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 200634 BJK09 RS07385 WP 027227022.1		0
NTDB id 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
consensus		

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NTDB id 1028 TT RS08215 WP 011173991.1	RLTPEERKELRAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLLEYPSPGK	158
NTDB id 1306 DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLLEIVVPSGA	157
NTDB id 1168 A1552VC RS11070 WP 000957200.1		0
NTDB id 1401 DSB67 RS12665 WP 010643259.1		0
NTDB id 1293 VP RS12240 WP 005479695.1		0
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consensus		

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NTDB id 1028 TT RS08215 WP 011173991.1	SGEGQKDLKLGELL LQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	237
NTDB id 1306 DR RS10060 WP 027479822.1	SDAGRTGGKLGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVL	237
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NTDB id 1401 DSB67 RS12665 WP 010643259.1		0
NTDB id 1293 VP RS12240 WP 005479695.1		0
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NTDB id 1028 TT RS08215 WP 011173991.1	LRLSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYLAALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSR	317
NTDB id 1306 DR RS10060 WP 027479822.1	GSMLRADALRLLAVPVDETEQGVTVLTSDPRKRPDIDALIGRPVQLMLTRPRDIERLIEQFYPPQRGRLLGEQLVQEGTLSR	317
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NTDB id 1110 NGFG RS09235 WP 003689817.1		0
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NTDB id 1028 TT RS08215 WP 011173991.1	EALKEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAAQAVATQLGYPYVDPEE	397
NTDB id 1306 DR RS10060 WP 027479822.1	DQLREALQVQAREGKVKPLGEVITELGFASPDVEDSALQKQNVGGGRLEDTLVQSGKLSPEMLARSLAAQLGYEFLDPIQ	397
NTDB id 1168 A1552VC RS11070 WP 000957200.1	MLTNLVAILRQAEILISATQEQAIVTVQVSASGTSVPEALLELSIFHAQELTEQLSHIFGLPETDLSR	66
NTDB id 1401 DSB67 RS12665 WP 010643259.1	MLTNLSTVLRQAGILTFSSQEESSLLEQVKASGISMPEALLSSGFFQSHLTELHSSVFGLSCTSLNQ	66
NTDB id 1293 VP RS12240 WP 005479695.1	MHSNLSTILRQKGLTFSQEESSLIEQVKASGISMPEALLSSGFFTSSSLAEHLSSIFGLSQPELSQ	66
NTDB id 1110 NGFG RS09235 WP 003689817.1	MSVGLLRILVQNQVVTVEQAHHYHN.ESQAGKEVLPMLFSDGVISPKSLAALIARVFSYSILDLRH	65
NTDB id 200634 BJK09 RS07385 WP 027227022.1	MALATDEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLVQYLVKNKILSAEQIALTAAQNFQVPMMDINC	74
NTDB id 1251 GC085 RS07725 WP 011946523.1	MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVKNKILSAEQIALTAAQNFQVPMMDINC	74
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MSALHTSPKFTGFFRRLVEEKHVSAAATMQTALDAAKRAKQDVTAVYLIEEVHLSPSLAETISAEFAEPYFDLDV	74
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQALEKAKKFKQDIPYPLIDNFSISPLTIAEIIISLEFGEPLLDLGV	74
consensus	* ***** *** ***** ** * * * ** * ***** ** * *** *** * ***** ***	

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NTDB id 1028 TT RS08215 WP 011173991.1	DPPDPGAPLLIPEDLCRRYGVFPHRLEGNRLVLLMKDPRNIALDDVRLALKRKGLNVEVAPAVATEAAITKLIERYFGK	477
NTDB id 1306 DR RS10060 WP 027479822.1	NPPDPKVALMPEATARRYVVVPVRLQGNSLVVAMKDPRNVFALDDLKLITG.....KEILPAVMAEKDIIRLIERYFGE	472
NTDB id 1168 A1552VC RS11070 WP 000957200.1	YDYANLCQQGLGLRELITRYDALPIAKQGNLLLLAVSDPTLLQAEFEFRFATG.....LQVELALADHRALQAAIRRLYGR	141
NTDB id 1401 DSB67 RS12665 WP 010643259.1	YEYASLCQTLGLRLDLITRHNAIPLNRTSSTLILAVADPTNLQAEDDFRFATG.....LQVELVLADFRELTAAIRRLYGR	141
NTDB id 1293 VP RS12240 WP 005479695.1	YEYASLCQQGLGLRELITRHNAIPLHRTPTSTLLLAVADPTNQQAEDDFRFATG.....LQVELVLADFRELSTAIRRLYGR	141
NTDB id 1110 NGFG RS09235 WP 003689817.1	YPRHRVLMGVLTEEQMVEFHCVPVVFRRGDKVFFAVSDPTQMPQIQKTVSAAG.....IAVELVIVEDDQLAGLLDWVGR	140
NTDB id 200634 BJK09 RS07385 WP 027227022.1	IEVDSIPASLVNEKLIKRRHAMVPLFSRGTNLYLATDDPSKQASLKEIQFHTG.....LNTHAIVVETDKLSSLIDNLLTA	149
NTDB id 1251 GC085 RS07725 WP 011946523.1	IDVGTIPVNLVNEKLIKRRHAMVPLFSRGTNLYLATDDPSKQASLKEIQFHTG.....LNTHAIVVETDKLSALIDNLLTA	149
NTDB id 1058 ABD1 RS01615 WP 001274986.1	YDTSQIPKDLVDQKLILKHRILPLIQRGQILYVATSNPSNIEAIDAIRFNSK.....LLVEPVIVEHHKLEKVLGQHFAE	149
NTDB id 1018 ACIAD RS01685 WP 004920473.1	FDPALFLKDKIDEKLIQKYRIMPLVHRGHVLYVATSNPTNIEAMDAIRFNSK.....LKVEPIIVEHDKLERLLSEHFVE	149
consensus	** * * ** ***** ** *! * ** * ***** *! *** ***** ***** ***** ***** ** ***** *****	

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consensus



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consensus



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consensus



889
887
562
561
561
558
574
574
570
570

☒ non conserved
☒ similar
☒ ≥ 50% conserved