

logo

		MSXLSIGDRLGAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	
NTDB id 1028	TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1306	DR RS10060 WP 027479822.1	.MALSIGDRLGAALLDQGYLGDNLDLRALERHSEVGGR LADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAAL	79
NTDB id 1168	A1552VC RS11070 WP 000957200.1		0
NTDB id 1293	VP RS12240 WP 005479695.1		0
NTDB id 1401	DSB67 RS12665 WP 010643259.1		0
NTDB id 1110	NGFG RS09235 WP 003689817.1		0
NTDB id 1058	ABD1 RS01615 WP 001274986.1		0
NTDB id 1018	ACIAD RS01685 WP 004920473.1		0
NTDB id 419589	GWK36 RS13490 WP 166271863.1		0
NTDB id 1251	GCO85 RS07725 WP 011946523.1		0
consensus			

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		RLTPEERKELRPFALDEEAGVVRVAFLNPLDLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLLEVPSPGK	
NTDB id 1028	TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLLEVPSPGK	158
NTDB id 1306	DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLLEIVVPSGA	157
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NTDB id 419589	GWK36 RS13490 WP 166271863.1		0
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consensus			

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		SGEGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	
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NTDB id 1306	DR RS10060 WP 027479822.1	SDAGRTGGKLGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVL	237
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consensus			

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NTDB id 1028 TT RS08215 WP 011173991.1	LEMLRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYALALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSR	317
NTDB id 1306 DR RS10060 WP 027479822.1	LSMLRADALRLLAVPVDETEQGVTVLTSDPRKRPDIDALIGRPVQLMLTRPRDIERLIEQFYPPQRGRLLGEQLVQEGTLSR	317
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NTDB id 1251 GC085 RS07725 WP 011946523.1		0
consensus		

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NTDB id 1028 TT RS08215 WP 011173991.1	EALKEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATQLGYPYVDPEE	397
NTDB id 1306 DR RS10060 WP 027479822.1	DQLREALQVQAREGKVKPLGEVITELGFASPDVEDSALQKQNVGGGRLEDTLVQSGKLSPEMLARSLAAQLGYEFLDPIQ	397
NTDB id 1168 A1552VC RS11070 WP 000957200.1	MLTNLVAILRQAEILISATQEQAQVVTQVSASGTSVPEALLELSIFHAQELTEQLSHIFGLPETDLSR	66
NTDB id 1293 VP RS12240 WP 005479695.1	MHSNLSITLRQKGLLTFSQEEESLIEQVKASGISMPEALLSSGFFTSSELAEHLSSIFGLSQPELSQ	66
NTDB id 1401 DSB67 RS12665 WP 010643259.1	MLTNLSTVLRQAGILTFSQEEESLLEQVKASGISMPEALLSSGFFQSHELTEHLSSVFGLSCTSLNQ	66
NTDB id 1110 NGFG RS09235 WP 003689817.1	MSVGLLRILVQNQVVTVEQAQEHYYNE.SQAGKEVLPMLFSDGVISPKSLAALIARVFSYSILDLRH	65
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MSALHTSPKFTGFFRRLVEEKHVSAAATMGTALDAAKRAKQDVTAYLIEEVHLSPLSLAETISAEFAEPYFDLDV	74
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MSAFTTTPPKFSGFIRRLVEEGYVNAQNMQALEKAKKFKQDIVPYLIDNFSISPLTIAEIIISLEFGEPLLDLGV	74
NTDB id 419589 GWK36 RS13490 WP 166271863.1	MAKDQATFKPSGLAWRLVKEQLISESQMHAAYQEARAKGRFTVQHLVTENILEPRRIAVLASHEFGVPLLDLDA	74
NTDB id 1251 GC085 RS07725 WP 011946523.1	MALATEEYRLQIGQLLVLEKLLDKTKAIELHLKLAEEKISLLQYIVKNKILSAEQIALTAQNFQVPMPLDINC	74
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NTDB id 1028 TT RS08215 WP 011173991.1	DPPDPGAPLLIPEDLCRRYGVFPHRLEGNRLVLLMKDPRNIALDDVRLALKRGLNVEVAPAVATEAAITKLIERYFGK	477
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NTDB id 1168 A1552VC RS11070 WP 000957200.1	YDYANLCQQLGLRELITRYDALPIAKQGNLLLLAVSDPTLLQAEFEFRFATG.....LQVELALADHRALQAIRRLYGR	141
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NTDB id 1401 DSB67 RS12665 WP 010643259.1	YEYASLCQQLGLRLDLITRHNALPLNRTSSTLILAVADPTNLQAEDDFRFATG.....LQVELVLADFRELTAIRRLYGR	141
NTDB id 1110 NGFG RS09235 WP 003689817.1	YPRHRVLMGVLTEEQMVEFHCVPVFRRGDKVFFAVSDPTQMPQIQKTVSAAG.....IATELVIVEDDQLAGLLDVGSR	140
NTDB id 1058 ABD1 RS01615 WP 001274986.1	YDTSQIPKDLVDQKLILKHLRILPLIQRGQILYVATSNPSNIEAIDAIRFNSK.....LLVEPVIVEHHKLEKVLGQHFAE	149
NTDB id 1018 ACIAD RS01685 WP 004920473.1	FDPALFLKDKIDEKLIQKYRIMPLVHRGHVLYVATSNPTNIEAMDAIRFNSK.....LKVEPIIVEHDKLERLLSEHFVE	149
NTDB id 419589 GWK36 RS13490 WP 166271863.1	FDPGLMPMNLVDERLITKHLRALPLMRGNRLFLALSDPTNEQAIEEIRFNTG.....LITEPIIVEDHKLGAIDKTLHA	149
NTDB id 1251 GC085 RS07725 WP 011946523.1	IDVGTIPVNLVNEKLIKRHAMVPLFSRGTNLYLATDPSKQASLKEIQFHTG.....LNTHAIVVETDKLSALIDNLLTA	149
consensus	* * * * *	

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NTDB id 1028 TT RS08215 WP 011173991.1
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consensus

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consensus

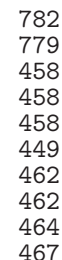
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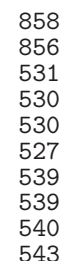
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consensus

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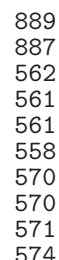
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consensus
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NTDB id 1251 GC085 RS07725 WP 011946523.1
consensus

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-  non conserved
-  similar
-  >50% conserved