

logo

NTDB id 1306 DR RS10060 WP 027479822.1	MSXLSIGDRRLGAILLDQGYLGDNLDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAAL	79
NTDB id 1028 TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
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 190609 A6L61 RS07070 WP 002221967.1		0
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
consensus		

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NTDB id 1306 DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLIYVPSGA	157
NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDRTLSEEEVDTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPP..P	158
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NTDB id 1306 DR RS10060 WP 027479822.1	SDAGRTGGKLGRLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVL	237
NTDB id 1028 TT RS08215 WP 011173991.1	SGEGQKDLKLGELLQKGWISREALEEALVEQKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	237
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NTDB id 1293 VP RS12240 WP 005479695.1		0
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NTDB id 1306 DR RS10060 WP 027479822.1	LSMRLSDALRYLAVPYGEISSEVIVYSDPRKREXYRLYRPXSHMLTSPSYEELLESYYPQRRLGELVQEGELSR	317
NTDB id 1028 TT RS08215 WP 011173991.1	GSMLRADALRLLAVPVDETEQGVTVLTS DPRKRPDIDALIGRPVQLMLTRPRDIERLIEQFYPPQRGRLLGEQLVQEGTLSR	317
NTDB id 1168 A1552VC RS11070 WP 000957200.1	LLLLRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSR	0
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NTDB id 1306 DR RS10060 WP 027479822.1	DQLREALQVQAREGKVKPLGEVITELGFASPDVDSALQKQNVGGRLLEDTLVQSGKLSPEMLARSLAAQLGYEFLDPIQ	397
NTDB id 1028 TT RS08215 WP 011173991.1	EALKEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGRLLEDTLVQSGKLRPEALAAQAVATQLGYPPVDPEE	397
NTDB id 1168 A1552VC RS11070 WP 000957200.1	MLTNLVAAILRQAEILISATQEQAVVTQVSASGTSVPEALLELSIFHAQELTEQLSHIFGLPETDLSR	66
NTDB id 1293 VP RS12240 WP 005479695.1	MHSNLSTILRQKGLLTFSQEESLIEQVKASGISMPEALLSSGFFTSSSELAEHLSSIFGLSQPELSQ	66
NTDB id 1401 DSB67 RS12665 WP 010643259.1	MLTNLSTVLRQAGILTFSQEESSLIEQVKASGISMPEALLSSGFFQSHELTEHLSSVFGLSCTSLNQ	66
NTDB id 190609 A6L61 RS07070 WP 002221967.1	MSVGLLRILVQNQVVTVEQAEHYY.NESQAGKEVLPMLFSDGVISPKSLAALIARVFSYSILDLRH	65
NTDB id 1110 NGFG RS09235 WP 003689817.1	MSVGLLRILVQNQVVTVEQAEHYY.NESQAGKEVLPMLFSDGVISPKSLAALIARVFSYSILDLRH	65
NTDB id 1251 GC085 RS07725 WP 011946523.1	MALATEEYRLQGIGQLLVLEKLLDKTKAIELHLKLA AEKISLLQYIVKNKILSAEQIALTAAQNFQGVPMLDINC	74
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQALEKAKKFKQDIVPYLIDNFSISPLTIAEIIISLEFGEPLLDLGV	74
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MSALHTSPKFTGFFRRLVEEKHVSAAATMTALDAAKRAKQD TVAYLIEEVHLSPSLLAETISAEFAEYPFDLDV	74
consensus	* * * * *	

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NTDB id 1306 DR RS10060 WP 027479822.1	NPPDPKVALMIP EATARRYVVVVRQLQGNLSLVVAMKDPNRNVFALDDLKLITG.....KEILPAVMAEKDIIRLIERYFGE	472
NTDB id 1028 TT RS08215 WP 011173991.1	DPPDPGAPLLIPEDLCRRYGVFPHRLEGNRLVLLMKDPRNIALDDVRLALKRKGLNVEVAPAVATEAAITKLIERFYGK	477
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NTDB id 1251 GC085 RS07725 WP 011946523.1	IDVGTIPVNLVNEKLIKRRHAMVPLFSRGTNLYLATDDPSKQASLKEIQFHTG.....LNTHAIVVETDKLSALIDNLLTA	149
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NTDB id 1058 ABD1 RS01615 WP 001274986.1	YDTSQIPKDLVDQKLLILKHRILPLIQRGQILYVATSNPSNIEAIDAIRFNSK.....LLVEPVIVEHHKLEKVLGQHFAE	149
consensus	* * * * *	

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consensus

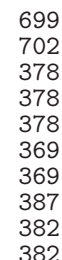
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consensus

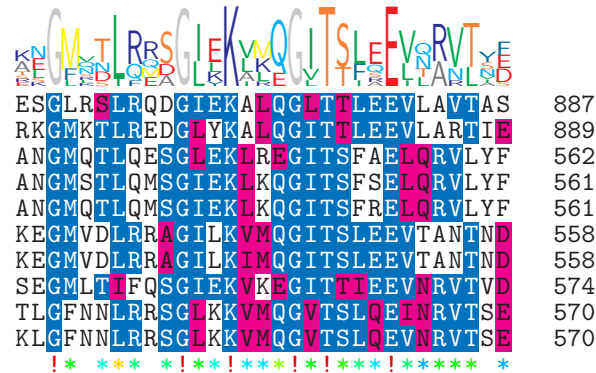
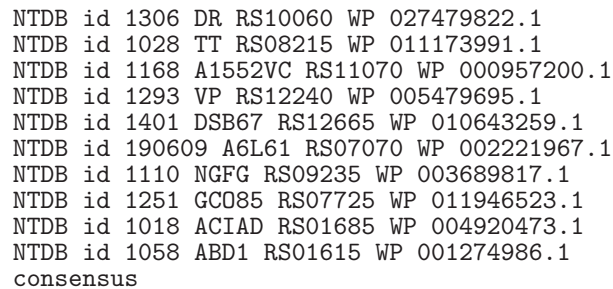
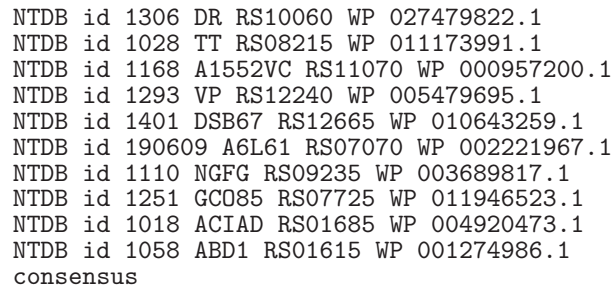
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consensus

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-  non conserved
-  similar
-  > 50% conserved