

logo

NTDB id 1306 DR RS10060 WP 027479822.1	MSXLSIGDRLGAALLDQGYLGDNDLQRALERHSEVGGRLADVLDIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAAL	79
NTDB id 1028 TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
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 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 403650 GMX02 RS19685 WP 156020398.1		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 1306 DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLIYVPPSGA	157
NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPP..P	158
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
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NTDB id 1293 VP RS12240 WP 005479695.1		0
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consensus		

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NTDB id 1306 DR RS10060 WP 027479822.1	SDAGRTGGKLGRLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVL	237
NTDB id 1028 TT RS08215 WP 011173991.1	SGEGQKDLKLGELLQKQWISREALEEALVEQKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	237
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 1168 A1552VC RS11070 WP 000957200.1		0
NTDB id 1293 VP RS12240 WP 005479695.1		0
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Sequence	Position 1	Position 2	Position 3	Position 4	Position 5	Position 6	Position 7	Position 8	Position 9	Position 10
ALREQNSFPKGA	A	Q	K	M	S	L	R	L	K	M
ALRPYSTLPKGA	L	N	A	I	M	G	L	D	I	A
ALREVVPQPIA	R	V	P	Q	P	I	A	R	V	P
ILVETQQPASH	L	S	R	L	A	A	R	I	K	I
ILIETQQPPNH	L	S	R	L	A	A	R	I	K	I
ILIEIQQPPSH	L	S	R	L	A	A	R	I	K	I
ILHEVATPPAS	L	S	R	L	A	A	R	I	K	I
ILHEVSEPPIS	L	S	R	L	A	A	R	I	K	I
VLRLQIANPPL	L	S	R	L	A	A	R	I	K	I
VLRLIATPPLQ	L	S	R	L	A	A	R	I	K	I

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consensus

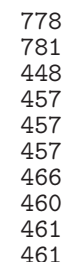
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[illegible]

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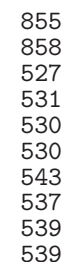
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consensus

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-  non conserved
-  similar
-  > 50% conserved