

logo

NTDB id 1306 DR RS10060 WP 027479822.1	MSXLSIGDRRLGAALLDQGYLGNDLQRALERHSEVGGRLAEVLVDMSGMLLSERRIAQTIEDRFGIPLVELHRVEIPPVKV	79
NTDB id 1028 TT RS08215 WP 011173991.1	.MALSIGDRRLGAILLDQGYLGNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAAL	80
NTDB id 1168 A1552VC RS11070 WP 000957200.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPVKV	0
NTDB id 1401 DSB67 RS12665 WP 010643259.1		0
NTDB id 1293 VP RS12240 WP 005479695.1		0
NTDB id 1020457 ABU188 RS00985 WP 370469869.1		0
NTDB id 1110 NGFG RS09235 WP 003689817.1		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 1306 DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGA	157
NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPP..P	158
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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NTDB id 1306 DR RS10060 WP 027479822.1	SDAGRTGGKLGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVL	237
NTDB id 1028 TT RS08215 WP 011173991.1	SGEGQKDKLKGELLLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	237
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 1020457 ABU188 RS00985 WP 370469869.1		0
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EFMLRADALRLLAVPVDETEQGVTVLTSDPRKRPDIDALIGRPVQLMLTRPDIERLIEQFYPQRGRLGEQLVQEGTLSR LLLLRSDALRYGAVPIGFQNGEVEVLSDPRHKEAVAQLLNRPARFYLALPQAWELFRRAYPQKNRLGEVLVQEGKLSR	317 317
..... 	0 0 0 0 0 0 0 0 0

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[illegible]

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NPPDPKVAL	MIP	E	A	T	A	R	R	V	V	V	P	V	P	L	R	Q	G	N	S	L	V	A	M	K	D	P	R	N	V	F	A	L	D	D	L	K	L	I	T	G	...	K	E	L	P	A	V	M	A	E	K	D	I	R	L	T	E	R	Y	F	G	E	472							
DPDPDGAPL	L	I	P	E	D	L	C	R	R	Y	G	V	F	P	H	R	L	E	G	N	R	L	V	L	M	K	D	P	R	N	I	L	A	L	D	D	V	R	L	A	L	K	R	K	G	L	N	Y	E	V	A	P	A	V	A	T	E	A	A	T	K	L	J	E	R	F	Y	G	K	477
YDYANLCQQ	L	G	L	R	E	L	I	T	R	Y	D	A	L	P	T	A	K	Q	G	N	L	L	L	A	V	S	D	P	T	L	L	Q	A	E	E	E	F	R	F	A	T	G	...	L	Q	V	E	L	A	L	A	D	H	R	A	L	Q	A	A	T	R	R	L	Y	G	R	141			
YEYASLCQT	L	G	L	R	D	L	I	T	R	H	N	A	L	P	I	N	R	T	S	S	T	L	I	L	A	V	A	D	P	T	N	L	Q	A	E	D	D	F	R	F	A	T	G	...	L	Q	V	E	L	V	L	A	D	F	R	E	L	T	A	A	T	R	R	L	Y	G	R	141		
YEYASLCQD	L	G	L	R	E	L	I	T	R	H	N	A	L	P	L	H	R	T	P	S	T	L	L	A	V	A	D	P	T	N	Q	A	E	D	D	F	R	F	A	T	G	...	L	Q	V	E	L	V	L	A	D	F	R	E	L	S	T	A	T	R	R	L	Y	G	R	141				
YNQSLVPQD	L	I	N	L	K	I	M	Q	Y	I	C	V	P	I	F	K	R	G	N	R	L	F	L	A	V	S	D	P	T	S	I	Q	H	Y	Q	K	L	A	T	D	A	G	...	C	I	L	N	L	V	I	V	R	D	D	Q	L	R	I	L	E	N	L	G	Q	E	140				
YPRHRVLMG	V	L	T	E	E	Q	M	V	F	H	C	V	P	V	F	R	G	D	K	V	F	F	A	V	S	D	P	T	Q	M	P	Q	I	Q	K	T	V	S	A	A	G	...	T	A	V	E	L	V	I	V	E	D	D	Q	L	A	G	L	D	W	G	S	R	140						
IDVGTIPVN	L	V	N	E	K	L	I	K	R	H	A	M	V	P	L	F	S	R	G	T	N	L	Y	L	A	T	D	D	P	S	K	Q	A	S	L	K	E	I	Q	F	H	T	G	...	L	N	T	H	A	I	V	E	T	D	K	L	S	A	L	I	D	N	L	T	A	149				
YDTSQIPKD	L	V	D	Q	K	L	I	L	K	H	R	I	L	P	L	I	Q	R	G	Q	I	L	V	A	T	S	N	P	S	N	I	E	A	I	D	A	I	R	F	N	S	K	...	L	L	V	E	P	V	I	V	E	H	H	K	L	E	K	V	I	G	H								

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