

NTDB id	1169	A1552VC	RS11075	WP	000648511.1	MKATQ.....TLPLKNYRWKGINSNGKK.VSGQLLAISEIEVRDKLKDQHITQIKKLKKGVSVLAR.LTHRVKSKDITI	72
NTDB id	973129	AABD50	RS02885	WP	005479682.1	.MKTTT.....TPQLKNFRWKGVNSSGKK.TSGQTLLAMSEIEVRRERLDAQHIKIKKLKKSSISFLTK.LSHRVKGGK DITV	71
NTDB id	1402	DSB67	RS12670	WP	010643257.1	.MKTII.....APQ LKNYRWKGINSNGKK.TSGNVLAMTEIEVRRERLDAQHIKIKKLKKGSISFITK.ISHRVKGK DITI	71
NTDB id	1112	NAGF	RS09215	WP	003689811.1	.MAKNGGFSLF AKKEKR FIFEGRHSASDKLVNGEVS AFTEE EARKKLAKRGIRPLQITRV.....KTSSRKKITQEDITV	74
NTDB id	1113	AAA85695.1	219..1451()			.MAKNGGFSLF AKKEKR FIFEGRHSASDKLVNGEVS AFTEE EARKKLAKRGIRPLQITRV.....KTSSRKKITQEDITV	74
NTDB id	1252	GCO85	RS07730	WP	011213805.1	.MDKN.....SPP LTFHYQGINKAGQK.MEGDIQARS LAIAKADLRKQGIVTNKVVKRRKP LFD R.KNKKITQA DITV	71
NTDB id	1198	PSJM300	03950	AFN	76868.1	.MAQQ.....AIKNSVF TWEGLDRQGAK.IKGE LSCVSPALVKAQLRKQGINPQKVKKKSIS LFS..AGKKIKPMDIAL	70
NTDB id	1016	ACTIAD	RS01680	WP	004920476.1	MAA KK.....TQVM P VFAYEGVD RKGIK.LKGE LPARNMALAKVT LRKQG ITIRTIREKRKN IFEGLLKKVKVPL DIAI	73
NTDB id	1059	ABD1	RS01610	WP	000279215.1	MAVKK.....AQMMPTFAYEGVD RKGVK.IKGE LPAKNMALAKVT LRKQGVTVNR IREKRKNILEGLFKKKVTTLDITI	73
consensus						* * * * *	

NTDB id 1169 A1552VC RS11075 WP 000648511.1	LTRQLATM LTTGVP IVQALKLVGDNRHKAEMK SILAQITKSVEAGTPLSKAMRTASAHFDLTLYVDLVETGEMSGNLP	152
NTDB id 973129 AABD50 RS02885 WP 005479682.1	FTRQISTM LVTGVPLVQALKLVSDNHKKAEMK SILMSVTRAVEAGTPMSKAMRTASNHFDPLYTDLIATGEQSGNLA	151
NTDB id 1402 DSB67 RS12670 WP 010643257.1	FTRQIATM LMTGVP IVQALKLVSENHKKAEMK SILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLSQ	151
NTDB id 1112 NGFG RS09215 WP 003689811.1	FTRQLSTM IKA GLPLMQAFEIVARGHGNSMTEMLMEIRGQVEQGSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLL	154
NTDB id 1113 AAA85695.1 219..1451()	FTRQLSTM INAG LPLMQAFEIVARGHGNSMTEMLMEIRGQVEQGSLSRAFSNHPKYFDRFYCNLVAAAGTGGVLESLL	154
NTDB id 1252 GC085 RS07730 WP 011213805.1	FSRQLATM IESG IPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLDIML	151
NTDB id 1198 PSJM300 03950 AFN76868.1	FTRQMATM MKAGVP LQSFDIIGEGFDNPNMRKLVDDLKQEVAAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLETLL	150
NTDB id 1016 ACTIAD RS01680 WP 004920476.1	FTRQLATM MKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVECGNIFAGALRKYPQYFDNLFCSLIESGEQSGSLEIML	153
NTDB id 1059 ABD1 RS01610 WP 000279215.1	FTRQLATM MKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALETML	153
consensus	***I***K***G***L***V***Q***A***L***K***L***V***G***D***N***H***K***A***E***M***K***S***I***L***A***Q***I***T***K***S***V***E***A***G***T***P***L***S***K***A***M***R***T***A***S***A***H***F***D***L***T***L***Y***V***D***L***V***E***T***G***E***M***S***G***N***L***P***E***V***F***	

NTDB id	1169	A1552VC	RS11075	WP	000648511.1	E	R	L	A	T	A	T	S	E	K	S	E	Q	L	R	A	K	V	I	K	A	L	I	P	S	M	V	L	V	A	L	G	V	S	Y	L	M	L	T	M	V	I	P	E	F	E	S	M	F	K	G	F	G	A	E	L	P	W	F	T	Q	Q	V	L	K	L	S	H	V	Q	A	Y	S	L	W	A	F	I		
NTDB id	973129	AABD50	RS02885	WP	005479682.1	E	R	L	A	T	A	T	S	E	K	N	E	Q	L	R	A	K	V	I	K	A	L	I	P	A	M	V	I	L	V	A	L	G	V	S	F	I	M	L	T	K	V	I	P	E	F	E	K	M	F	V	G	F	G	A	E	L	P	W	F	T	R	Q	V	D	L	S	A	W	T	Q	N	W	S	P	F	I	A	L	
NTDB id	1402	DSB67	RS12670	WP	010643257.1	E	R	L	A	T	A	T	S	E	K	S	E	Q	L	R	A	K	V	I	K	A	L	I	P	A	M	V	I	L	V	A	L	G	V	S	Y	L	M	L	T	R	V	I	P	E	F	E	K	M	F	T	G	F	G	A	D	L	P	A	F	T	Q	M	V	L	N	L	S	A	W	T	Q	N	W	G	P	F	I	G	L
NTDB id	1112	NGFG	RS09215	WP	003689811.1	D	K	L	A	I	Y	K	E	K	T	Q	A	I	R	K	K	V	K	T	A	L	T	P	V	S	V	I	A	V	A	I	G	L	V	F	V	M	I	F	V	L	P	A	F	K	E	V	Y	A	N	M	G	A	E	L	P	L	T	Q	T	V	M	D	S	D	F	V	S	Y	G	M	V	L	I						
NTDB id	1113	AAA85695.1	219..1451()			D	K	L	A	I	Y	K	E	K	T	Q	A	I	R	K	K	V	K	T	A	L	T	P	V	S	V	I	A	V	A	I	G	L	V	F	V	M	I	F	V	L	P	A	F	K	E	V	Y	A	N	M	G	A	E	L	P	L	T	Q	T	V	M	D	S	D	F	V	S	Y	G	M	V	L	I						
NTDB id	1252	GC085	RS07730	WP	011213805.1	D	K	V	A	T	A	T	S	E	K	E	I	E	I	K	K	K	T	I	K	K	A	L	T	P	I	A	V	M	V	A	L	L	V	T	A	G	L	L	I	Y	V	V	P	Q	F	E	S	L	F	K	G	F	G	A	D	L	P	A	M	T	R	A	V	I	T	M	S	E	F	M	Q	A	Y	W	Y	I	I	F	G
NTDB id	1198	PSJM300	03950	AFN76868.1		D	R	V	A	T	A	T	S	E	K	T	E	A	L	K	A	K	I	K	K	A	M	N	P	I	A	V	V	L	V	A	V	I	T	A	I	L	L	I	K	V	V	P	Q	F	D	V	F	A	N	F	G	A	E	L	P	A	F	T	L	M	V	I	G	L	S	E	A	L	Q	A	W	Y	V	V	L	A			
NTDB id	1016	ACTAD	RS01680	WP	004920476.1	D	R	V	A	T	A	T	S	E	K	S	E	V	L	K	K	I	K	K	A	M	K	P	A	T	V	I	V	V	A	I	V	V	T	I	L	M	V	K	V	V	P	V	F	K	D	L	F	T	S	F	G	A	D	L	P	A	F	T	Q	L	V	N	M	S	N	W	M	Q	D	Y	W	F	I	L	I				
NTDB id	1059	ABD1	RS01610	WP	000279215.1	D	R	V	A	T	A	T	S	E	K	S	E	L	L	K	K	I	K	K	A	M	K	P	A	T	V	I	V	V	A	I	V	V	T	I	L	M	V	K	V	V	P	V	F	Q	D	L	F	A	S	F	G	A	D	L	P	A	F	T	Q	M	V	N	M	S	K	W	M	Q	E	Y	W	F	I	M	I				

NTDB id 1169	A1552VC	RS11075	WP 000648511.1	AIAAAITGLKALRKNSFQIRLKTSTRGLKFPITIGNVLAKASTIAKFSRTLATSFAAGIPILASLKTITAKTSGNVHFETA	IN	312
NTDB id 973129	AABD50	RS02885	WP 005479682.1	CSISVVFISARVLSKRSDSFRLMLNRSVLKFPVLGAVLSKAAIAKFSRTLATSFTAGIPILTSLKTTSTKSGNMHYQLA	IE	311
NTDB id 1402	DSB67	RS12670	WP 010643257.1	SFVSLISGKIMSQRSDSFRLLAARSSLRVPIILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSTKSGNMHYQLA	IE	311
NTDB id 1112	NGFG	RS09215	WP 003689811.1	ALGFAIYGLFLKLKARSIKIQRMRDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEATR	314	
NTDB id 1113	AAA85695.1	219..1451()		ALGFAIYRFLKLKARSIKIQRMRDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEATR	314	
NTDB id 1252	GC085	RS07730	WP 011213805.1	ALGGVYVSFFYAKNHSLEFAQTTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKATD	311	
NTDB id 1198	PSJM300	03950	AFN76868.1	CFVGAAYAFKQAHTRSEKFRNWFDRLLMLKVPVVGDIYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVERSATN	310	
NTDB id 1016	ACIAD	RS01680	WP 004920476.1	VITGAATAGFLEARKRSKRFRDQDLRLVLRPLIVGDLVYKAITARYSRTLATTFAGVPLIDALASTAGATNNIVYEQAVL	313	
NTDB id 1059	ABD1	RS01610	WP 000279215.1	AIGAVIAAFLEAKRSKRKFRDGLDKLALKLPFGDLVYKAITARYSRTLATTFAGVPLIDALESTAGATNNVIYEKAVM	313	
consensus				*****		

