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NTDB id	587 KW2 RS10850 WP 042211510.1	. . . MQT	DILRLLRPKGKKLALIKQAKLIQLMGNLLNNGFNLGVEVINFLALSKLVEKEFVFKMHQGGLSSGKSLSEILESLFSKN	81
NTDB id	83035 H7680 RS00735 WP 015057201.1	.MTFLQR	DISVRSKQGLKKLSKEEQYKLIQLLANILLTGFNLAETIAFLTSSHLPPEPYVLRMEEALLKGGRGLADMLAGTGFSDA	84
NTDB id	395 FSA28 RS09400 WP 257638827.1	.MTFLQQ	DISLKEKHKKQKKLKIKQKRKIQLFNNLFSTSGFNLTETIIDFLERSHLLAEIYTCKMRQGLNLGLHLAEIMSSLGFSDDD	84
NTDB id	386 SMU RS09030 WP 255262721.1	.MTFLQQ	DISLKEKHKKQKKLKIKQKRKIQLFNNLFSTSGFNLTETIIDFLERSHLLAEIYTCKMRQGLNLGLHLAEIMSSLGFSDDD	84
NTDB id	430 SGO RS09415 WP 012130941.1	MISFLQG	DISILSKQKQKQLGTSAKQKVIELFNNLFSSGFHLAETVFDFLGRSALLEKNYYVQQMMRQGLANGQAFAFEIMASLGFSDA	85
NTDB id	271 KZH43 RS09260 WP 074196785.1		MDISQVFRLLRRKKLATAQKNIITLFNNLFSSGFHLVETISFLDRSALLDKQCVTQMVRVGLSQGKSFFSEMMESELGCSSA	79
NTDB id	230 SPD RS09890 WP 074196785.1		MDISQVFRLLRRKKLATAQKNIITLFNNLFSSGFHLVETISFLDRSALLDKQCVTQMVRVGLSQGKSFFSEMMESELGCSSA	79
NTDB id	196 SPR RS09425 WP 074196785.1		MDISQVFRLLRRKKLATAQKNIITLFNNLFSSGFHLVETISFLDRSALLDKQCVTQMVRVGLSQGKSFFSEMMESELGCSSA	79
NTDB id	161 SP RS10375 WP 074196785.1		MDISQVFRLLRRKKLATAQKNIITLFNNLFSSGFHLVETISFLDRSALLDKQCVTQMVRVGLSQGKSFFSEMMESELGCSSA	79
NTDB id	529 SMSK321 RS09235 WP 080550783.1		MDISQVFRLLRRKKLATAQKNIITLFNNLFSSGFHLVETISFLDRSALLDKQCVTQMRTDLSQGGSFFSEMMESELGFSSA	79
NTDB id	501 SM12261 RS00950 WP 004238896.1		MDISQVFRLLRRKKLATAQKNIITLFNNLFSSGFHLVETISFLDRSALLDKQCVTQMRAGLSQGKSFFSEMMESELGFSSA	79
consensus			* ! * ! * * * * * * * ! * * * * * ! * * * ! * * * ! * * * ! * ! * ! * * * * ! * * ! * ! * * * * * * * ! *	

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NTDB id	587	KW2	RS10850	WP	042211510.1	VVTQLALVEVHGNLVGTMQQLVELHLKKQLKVKKKLEI	VATYTPVVL	LLVFLIGIMWGGLKNYLLPQLDKGN	NFATLILNHLPVFFSV	166																																																																															
NTDB id	83035	H7680	RS00735	WP	015057201.1	ILTQISLADGHGNIETTLVNI	IQGYLNQMAKLRKRTIEV	VVTYPIILLVFLFVMI	LGLRHYVMPQLEAQ	.NQLTIFITHFPALFFGI	168																																																																														
NTDB id	395	FSA28	RS09400	WP	257638827.1	VVTQLALSEVHGNTQKSL	LKIESYLNLIIVKKKLVEV	ITYPIILLIFLVVIM	LGLKNYLLPQLEKG	.NFATRLISNFPILFLLG	168																																																																														
NTDB id	386	SMU	RS09030	WP	255262721.1	VVTQLALSEVHGNTQKSL	LKIESYLNLIIVKKKLVEV	ITYPIILLIFLVVIM	LGLKNYLLPQLERG	.NFATRLISNFPILFLLG	168																																																																														
NTDB id	430	SGO	RS09415	WP	012130941.1	VVTQLSLAEHLGNLSL	ALLKIEEYLDNLAKVKKKLEI	VATYPMML	LGFLVLIMIGLRNYLLPQLSSQ	.NFATQLIGHLPITFLLT	169																																																																														
NTDB id	271	KZH43	RS09260	WP	074196785.1	I	V	T	Q	L	S	L	A	E	V	H	G	N	L	H	L	S	L	G	K	I	E	E	Y	L	D	N	L	A	K	V	K	K	L	E	I	V	A	T	Y	P	L	I	L	L	G	F	L	L	L	I	M	L	G	L	R	N	Y	L	L	P	Q	L	D	S	S	.	N	I	A	T	Q	I	I	G	N	L	P	Q	I	F	L	G	M
NTDB id	230	SPD	RS09890	WP	074196785.1	I	V	T	Q	L	S	L	A	E	V	H	G	N	L	H	L	S	L	G	K	I	E	E	Y	L	D	N	L	A	K	V	K	K	L	E	I	V	A	T	Y	P	L	I	L	L	G	F	L	L	L	I	M	L	G	L	R	N	Y	L	L	P	Q	L	D	S	S	.	N	I	A	T	Q	I	I	G	N	L	P	Q	I	F	L	G	M
NTDB id	196	SPR	RS09425	WP	074196785.1	I	V	T	Q	L	S	L	A	E	V	H	G	N	L	H	L	S	L	G	K	I	E	E	Y	L	D	N	L	A	K	V	K	K	L	E	I	V	A	T	Y	P	L	I	L	L	G	F	L	L	L	I	M	L	G	L	R	N	Y	L	L	P	Q	L	D	S	S	.	N	I	A	T	Q	I	I	G	N	L	P	Q	I	F	L	G	M
NTDB id	161	SP	RS10375	WP	074196785.1	I	V	T	Q	L	S	L	A	E	V	H	G	N	L	H	L	S	L	G	K	I	E	E	Y	L	D	N	L	A	K	V	K	K	L	E	I	V	A	T	Y	P	L	I	L	L	G	F	L	L	L	I	M	L	G	L	R	N	Y	L	L	P	Q	L	D	S	S	.	N	I	A	T	Q	I	I	G	N	L	P	Q	I	F	L	G	M
NTDB id	529	SMSK321	RS09235	WP	080550783.1	I	V	T	Q	L	S	L	A	E	V	H	G	N	L	H	L	S	L	G	K	I	E	E	Y	L	D	N	L	A	K	V	K	K	L	E	I	V	A	T	Y	P	L	I	L	L	G	F	L	L	L	I	M	L	G	L	R	N	Y	L	L	P	Q	L	D	S	S	.	N	I	A	T	Q	I	I	G	N	L	P	Q	I	F	L	G	M
NTDB id	501	SM12261	RS00950	WP	004238896.1	I	V	T	Q	L	S	L	A	E	V	H	G	N	L	H	L	S	L	G	K	I	E	E	Y	L	D	N	L	A	K	V	K	K	L	E	I	V	A	T	Y	P	L	I	L	L	G	F	L	L	L	I	M	L	G	L	R	N	Y	L	L	P	Q	L	D	S	S	.	N	I	A	T	Q	I	I	G	N	L	P	Q	I	F	L	G	M
consensus						* * ! * ! * * ! * * * ! ! * * * * * * * ! * * * * * * * ! * * * ! * ! * ! * ! * ! * ! * ! * * ! * * * ! * * ! * * * ! * * ! * * *																																																																																			

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NTDB id 587	KW2 RS10850 WP 042211510.1	GALIVLLTSLSIIIIFKHHISALTNFTFLVKVPLVSSFIRLYLTAYFSREWGNLIAQGVVELRQIIELMKKKQKSRIFAEVGIKLDLGL	251
NTDB id 83035	H7680 RS00735 WP 015057201.1	ILFIGVLLGGIWLHWRSSQRLKLFTHFSAYPVLGKLLQQYLTAYYAREWGTLIGQGLELPVILDIMAMEKSLFMQELAEIDIRVSL	253
NTDB id 395	FSA28 RS09400 WP 257638827.1	CCFFILLVGIIFTTFFSRKISRHLIGFCSHLPFVGKYLQLYLTAYYAREWGNLIGQGVEMAQIVRLMQDKKSQQLFREICYDMEKAL	253
NTDB id 386	SMU RS09030 WP 255262721.1	CCFFILLVGIIFTTFFSRKISRHLIGFCSHLPFAGKYLQLYLTAYYAREWGNLIGQGVEMAQIVRLMQDKKSQQLFREICYDMEKAL	253
NTDB id 430	SGO RS09415 WP 012130941.1	VLMLLGLLTGAIYLVFKGQKRPVYSFLARLPFVGSFVRIYLTAYYAREWGNMIGQGLELSQIFQIMQEQRSVLFQEQIGQDLGQAL	254
NTDB id 271	KZH43 RS09260 WP 074196785.1	VGLVSVLALLALTIFYKRSKMSVFSILARLPFIGIFVQTYLTAYYAREWGNMISQGMELTQIFQMMQEQQSQLFKEVGQDLAQTL	248
NTDB id 230	SPD RS09890 WP 074196785.1	VGLVSVLALLALTIFYKRSKMSVFSILARLPFIGIFVQTYLTAYYAREWGNMISQGMELTQIFQMMQEQQSQLFKEVGQDLAQTL	248
NTDB id 196	SPR RS09425 WP 074196785.1	VGLVSVLALLALTIFYKRSKMSVFSILARLPFIGIFVQTYLTAYYAREWGNMISQGMELTQIFQMMQEQQSQLFKEVGQDLAQTL	248
NTDB id 161	SP RS10375 WP 074196785.1	VGLVSVLALLALTIFYKRSKMSVFSILARLPFIGIFVQTYLTAYYAREWGNMISQGMELTQIFQMMQEQQSQLFKEVGQDLAQTL	248
NTDB id 529	SMSK321 RS09235 WP 080550783.1	VGLVSLTLLALTIFYKRSKMRVFSILARIPFLGIFVQTYLTAYYAREWGNMISQGMELTQIFQIMQEQQSQLFKEVGQDLAQSL	248
NTDB id 501	SM12261 RS00950 WP 004238896.1	VGFSVSGVLLALTIFYKRGSKMRVFSILARIPFLGIFVQTYLTAYYAREWGNMISQGMELTQIFQIMQEQQSQLFKEVGQDMAHAL	248
consensus		***** * 248	

