

NTDB id 587	KW2 RS10850 WP 042211510.1	MQTDILRLLRPKGKKLALIKQAKLIQLMGNLLNNGFNLGEVINFLALSKLVEKEFVFKMHQGLS	64
NTDB id 430	SGO RS09415 WP 012130941.1	MISFLQQDISILSKQKQKKLGTSKQKQVIELFNNLFSSGFHLAETVDFLGRSALLEKNYVQQMRQGLA	68
NTDB id 271	KZH43 RS09260 WP 074196785.1	MDISQVFRLRRKKLATAKQKNIITLFNNLFSSGFHLVETISFLDRSALLDKQCVTQMRVGLS	62
NTDB id 230	SPD RS09890 WP 074196785.1	MDISQVFRLRRKKLATAKQKNIITLFNNLFSSGFHLVETISFLDRSALLDKQCVTQMRVGLS	62
NTDB id 196	SPR RS09425 WP 074196785.1	MDISQVFRLRRKKLATAKQKNIITLFNNLFSSGFHLVETISFLDRSALLDKQCVTQMRVGLS	62
NTDB id 161	SP RS10375 WP 074196785.1	MDISQVFRLRRKKLATAKQKNIITLFNNLFSSGFHLVETISFLDRSALLDKQCVTQMRVGLS	62
NTDB id 529	SMSK321 RS09235 WP 080550783.1	MDISQVFRLRRKKLATAKQKNIITLFNNLFSSGFHLVETISFLDRSALLDKQCVTQMRDLS	62
NTDB id 501	SM12261 RS00950 WP 004238896.1	MDISQVFRLRRKKLATAKQKNIITLFNNLFSSGFHLVETISFLDRSALLDKQCVTQMRAGLS	62
NTDB id 36166	GALLQ RS00635 WP 012961328.1	MLKKTTLKVTDQSAGIQKLKVLLKTDISQINLKQKSKKLFPFKKQKRVQLFNNLFESGFNLTEIVSFLRRSQLLLDIYVERMQESLL	85
NTDB id 395	FSA28 RS09400 WP 257638827.1	MTFLQQDISLKEKHKQKKLKIKKQKRVQLFNNLFTSGFNLTEIIDFLERSHLLAEIYTKKMRQGL	67
NTDB id 386	SMU RS09030 WP 255262721.1	MTFLQQDISLKEKHKQKKLKIKKQKRVQLFNNLFTSGFNLTEIIDFLERSHLLAEIYTKKMRQGLL	67
consensus		* * * * *	

Sequence	Accession
SGKSLSEILESLSFSKNVVTQLALVEVHGNLVGTMQLVELHLKKQLKVKKKKLEIEMATYPVVLLVFLIGIMWGLKNYLLPQLDKGN	149
NGQAFSEIMASLGFSDAVVTQLSLAEVHGNLSLALLKIEEYLDNLAKVKKKKLEIEMATYPMMLLGLFLIMTGLRNYLLPQLSSQ	152
QGKSFSEMMESLGCSSAIVTQLSLAEVHGNLHLSLGKIEEYLDNLAKVKKKKLEIEMATYPLILLGFLLLIMLGLRNYLLPQLDSS	146
QGKSFSEMMESLGCSSAIVTQLSLAEVHGNLHLSLGKIEEYLDNLAKVKKKKLEIEMATYPLILLGFLLLIMLGLRNYLLPQLDSS	146
QGKSFSEMMESLGCSSAIVTQLSLAEVHGNLHLSLGKIEEYLDNLAKVKKKKLEIEMATYPLILLGFLLLIMLGLRNYLLPQLDSS	146
QGKSFSEMMESLGCSSAIVTQLSLAEVHGNLHLSLGKIEEYLDNLAKVKKKKLEIEMATYPLILLGFLLLIMLGLRNYLLPQLDSS	146
QGKSFSEMMESLGCSSAIVTQLSLAEVHGNLHLSLGKIEEYLDNLAKVKKKKLEIEMATYPLILLGFLLLIMLGLRNYLLPQLDSS	146
QGKSFSEMMESLGCSSAIVTQLSLAEVHGNLHLSLGKIEEYLDNLAKVKKKKLEIEMATYPLILLGFLLLIMLGLRNYLLPQLDSS	146
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NGLHLAEIIMSSLGFSDDVVTQLALSEVHGNTQKSLKIESYLNLLILVKKKLVVETITYPITILLIFLVVIMLGLKNYLLPQLBKG	151

N	A	T	Q	I	G	N	L	P	Q	I	F	L	G	M	V	G	L	V	S	V	L	A	L	L	T	F	Y	K	R	S	S	K	M	V	S	I	L	A	R	L	P	E	G	I	F	V	Q	T	Y	L	T	A	Y	A	R	E	W	G	N	M	I	S	Q	G	E	L	Q	I	F	Q	M	Q	E								
E	R	L	G	M	V	G	L	V	S	V	L	A	L	L	T	F	Y	K	R	S	S	K	M	V	S	I	L	A	R	L	P	E	G	I	F	V	Q	T	Y	L	T	A	Y	A	R	E	W	G	N	M	I	S	Q	G	E	L	Q	I	F	Q	M	Q	E																		
N	F	A	T	L	I	N	H	L	P	L	V	F	S	V	G	A	L	I	V	L	T	S	L	S	I	I	F	K	H	I	S	A	L	T	N	F	T	F	L	V	K	V	P	L	V	S	S	F	I	R	L	Y	L	T	A	Y	F	S	R	E	W	G	N	L	I	A	Q	G	V	E	L	R	Q	I	F	E	L	M	K	K	234
N	F	A	T	Q	I	G	H	L	P	T	I	F	L	L	T	V	L	M	L	G	L	T	G	A	I	L	V	F	K	G	K	R	I	P	V	S	F	L	A	R	L	P	F	V	G	S	F	V	R	I	Y	L	T	A	Y	A	R	E	W	G	N	M	I	S	Q	G	E	L	S	Q	I	F	Q	M	Q	E	237				
N	I	A	T	Q	I	G	N	L	P	Q	I	F	L	G	M	V	G	L	V	S	V	L	A	L	L	T	F	Y	K	R	S	S	K	M	S	V	S	I	L	A	R	L	P	F	I	G	I	F	V	Q	T	Y	L	T	A	Y	A	R	E	W	G	N	M	I	S	Q	G	M	E	L	T	Q	I	F	Q	M	Q	E	231		
N	I	A	T	Q	I	G	N	L	P	Q	I	F	L	G	M	V	G	L	V	S	V	L	A	L	L	T	F	Y	K	R	S	S	K	M	S	V	S	I	L	A	R	L	P	F	I	G	I	F	V	Q	T	Y	L	T	A	Y	A	R	E	W	G	N	M	I	S	Q	G	M	E	L	T	Q	I	F	Q	M	Q	E	231		
N	I	A	T	Q	I	G	N	L	P	Q	I	F	L	G	M	V	G	L	V	S	V	L	A	L	L	T	F	Y	K	R	S	S	K	M	S	V	S	I	L	A	R	L	P	F	I	G	I	F	V	Q	T	Y	L	T	A	Y	A	R	E	W	G	N	M	I	S	Q	G	M	E	L	T	Q	I	F	Q	M	Q	E	231		
N	I	A	T	Q	I	G	N	L	P	Q	I	F	L	G	M	V	G	L	V	S	V	L	L	T	L	L	T	F	Y	K	R	S	S	K	M	R	V	S	I	L	A	R	I	P	F	L	G	I	F	V	Q	T	Y	L	T	A	Y	A	R	E	W	G	N	M	I	S	Q	G	M	E	L	T	Q	I	F	Q	M	Q	E	231	
N	I	A	T	Q	I	G	N	L	P	Q	I	F	L	G	M	V	G	F	V	S	V	G	V	L	L	T	F	Y	K	R	S	S	K	M	R	V	S	I	L	A	R	I	P	F	L	G	I	F	V	Q	T	Y	L	T	A	Y	A	R	E	W	G	N	M	I	S	Q	G	M	E	L	T	Q	I	F	Q	M	Q	E	231		
N	V	A	T	Q	I	I	T	H	F	P	T	I	F	L	L	S	I	F	S	I	G	V	L	L	V	C	A	T	F	Y	A	R	R	L	S	Q	I	D	L	Y	S	R	I	S	R	I	P	L	V	G	N	Y	V	R	L	Y	L	T	A	Y	A	R	E	W	G	N	L	I	G	Q	G	E	L	M	A	I					

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consensus



- X non conserved
- X similar
- X $\geq 50\%$ conserved