

NTDB id 587 KW2 RS10850 WP 042211510.1	MQT	DILRLLRPKGKKLALIKQAKLIQLMGNLLNNGFNLGEVINFLALSKLVEKEFVFKMHQGLSSGKSLSEIL	73
NTDB id 395 FSA28 RS09400 WP 257638827.1	MTFLQQ	DISLKEKHKKKKLKIKQRKVVIQLFN NFLTS GFNLTEIIDFLERSHLLAEIYTKKMRQG LL NGLHL AEIM	76
NTDB id 386 SMU RS09030 WP 255262721.1	MTFLQQ	DISLKEKHKKKKLKIKQRKVVIQLFN NFLTS GFNLTEIIDFLERSHLLAEIYTKKMRQG LL NGLHL AEIM	76
NTDB id 252370 CR542 RS00805 WP 255195823.1	MRKLI AF LQQ	DISVLGRQKQKKLP AR QRVIELFN NFLASGFHLGEIVDFLKRSQLLADLYTVQLSD GLLAGKPFSSLL	80
NTDB id 430 SGO RS09415 WP 012130941.1	...MISFLQQ	DISILSKQKQKKLG TSKQKQVIELFN NFLFS SGFH LAETVD FLGRSALL EKKNYVQKMRQGLANGQA FSEIM	77
NTDB id 271 KZH43 RS09260 WP 074196785.1		M DISQVFRLRRKKLAT AKQKNIITLFN NFLFS SGFHL VETISFLDRS ALLDKQC VTQM RVGLSQGKS FSEM M	71
NTDB id 230 SPD RS09890 WP 074196785.1		M DISQVFRLRRKKLAT AKQKNIITLFN NFLFS SGFHL VETISFLDRS ALLDKQC VTQM RVGLSQGKS FSEM M	71
NTDB id 196 SPR RS09425 WP 074196785.1		M DISQVFRLRRKKLAT AKQKNIITLFN NFLFS SGFHL VETISFLDRS ALLDKQC VTQM RVGLSQGKS FSEM M	71
NTDB id 161 SP RS10375 WP 074196785.1		M DISQVFRLRRKKLAT AKQKNIITLFN NFLFS SGFHL VETISFLDRS ALLDKQC VTQM RVGLSQGKS FSEM M	71
NTDB id 529 SMSK321 RS09235 WP 080550783.1		M DISQVFRLRRKKLAT AKQKNIITLFN NFLFS SGFHL VETISFLDRS ALLDKQC VTQM RTDLSQGKS FSEM M	71
NTDB id 501 SM12261 RS00950 WP 004238896.1		M DISQVFRLRRKKLAT AKQKNIITLFN NFLFS SGFHL VETISFLDRS ALLDKQC VTQM RA GLSQGKS FSEM M	71
consensus		* ! ! * * * * * * * * ! ! * * * * ! * * * ! * ! * * * ! ! * * * ! ! * * * * * * * * * ! * * * ! * * * * * * * * *	

NTDB	id	587	KW2	RS10850	WP	042211510.1	ESLSFSKNVVTQLALVEVHGNLVGTMQLVELHLKKQLKVKKKLIEVATYPVVLLVFLIGIMWGLKNYLLPQLDKGN	NFAT	153
NTDB	id	395	FSA28	RS09400	WP	257638827.1	SSLGFSDDVVTQLALSEVHGNTQKSLLKIESYLNLIILVKKKLVEVITYPITILLIFLVVIMLGLKNYLLPQL	EKG.NFAT	155
NTDB	id	386	SMU	RS09030	WP	255262721.1	SSLGFSDDVVTQLALSEVHGNTQKSLLKIESYLNLIILVKKKLVEVITYPITILLIFLVVIMLGLKNYLLPQL	ERG.NFAT	155
NTDB	id	252370	CR542	RS00805	WP	255195823.1	ADLRFSDDAVVTQVALAEVHGNTSLSLSHIQSYLENVSKVRKKLIEVATYPIILLGFLFLIMLGLKNYLLPQL	EEG.NAAT	159
NTDB	id	430	SGO	RS09415	WP	012130941.1	ASLGFSDDAVVTQLSLAEHLGNLSLALLKIEEYLDNLAKVKKKLEIATYPMMLLGLFLVIMIGLRNYLLPQL	SSQ.NFAT	156
NTDB	id	271	KZH43	RS09260	WP	074196785.1	ESLGCSSAIVTQLSLAEVHGNLHLSLGKIEEYLDNLAKVKKKLEIATYPLILLGFLLLIMLGLRNYLLPQL	DSS.NIAT	150
NTDB	id	230	SPD	RS09890	WP	074196785.1	ESLGCSSAIVTQLSLAEVHGNLHLSLGKIEEYLDNLAKVKKKLEIATYPLILLGFLLLIMLGLRNYLLPQL	DSS.NIAT	150
NTDB	id	196	SPR	RS09425	WP	074196785.1	ESLGCSSAIVTQLSLAEVHGNLHLSLGKIEEYLDNLAKVKKKLEIATYPLILLGFLLLIMLGLRNYLLPQL	DSS.NIAT	150
NTDB	id	161	SP	RS10375	WP	074196785.1	ESLGCSSAIVTQLSLAEVHGNLHLSLGKIEEYLDNLAKVKKKLEIATYPLILLGFLLLIMLGLRNYLLPQL	DSS.NIAT	150
NTDB	id	529	SMSK321	RS09235	WP	080550783.1	ESLGFSSAIVTQLSLAEVHGNLHLSLGKIEEYLDNLAKVKKKLEIATYPLILLGFLLLIMLGLRNYLLPQL	DSS.NIAT	150
NTDB	id	501	SM12261	RS00950	WP	004238896.1	ESLGFSSAIVTQLSLAEVHGNLHLSLGKIEEYLDNLAKVKKKLEIATYPLILLGFLLLIMLGLRNYLLPQL	DSS.NIAT	150
consensus							***!!**!*!!**!!**!!**!!**!!**!!**!!**!!**!!**!!**!!**!!**!!**!!**!!**!!**!!**!!**!!**!!	!!**!!	

[illegible]

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consensus

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