

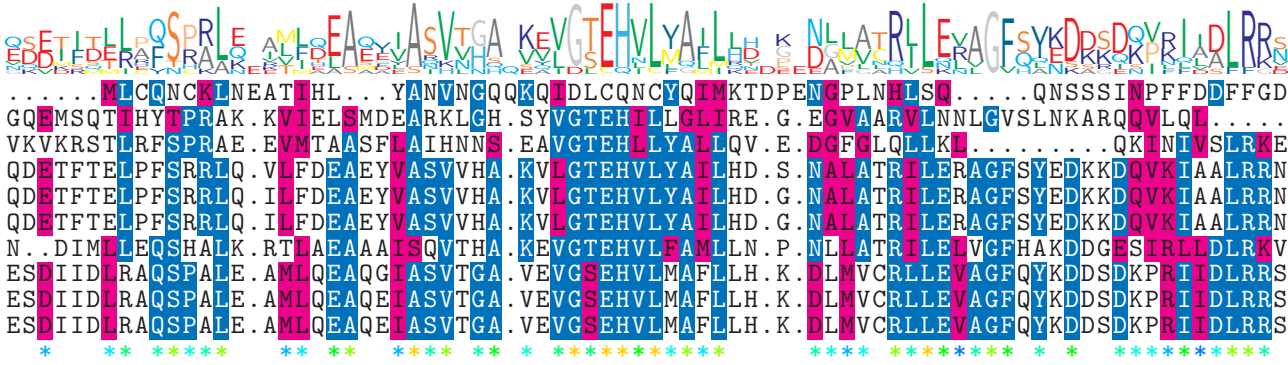
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NTDB id 85 BSU 00860 NP 387967.1
NTDB id 610 V4T04 RS10165 WP 012897346.1
NTDB id 287 SP RS11210 WP 001109712.1
NTDB id 290 KZH43 RS10025 WP 001109677.1
NTDB id 289 SPD RS10700 WP 001109677.1
NTDB id 377 SMU RS09275 WP 002262344.1
NTDB id 329 STU RS10020 WP 011225298.1
NTDB id 260905 CR921 RS00520 WP 101415506.1
NTDB id 297 STER RS00545 WP 011680614.1
consensus



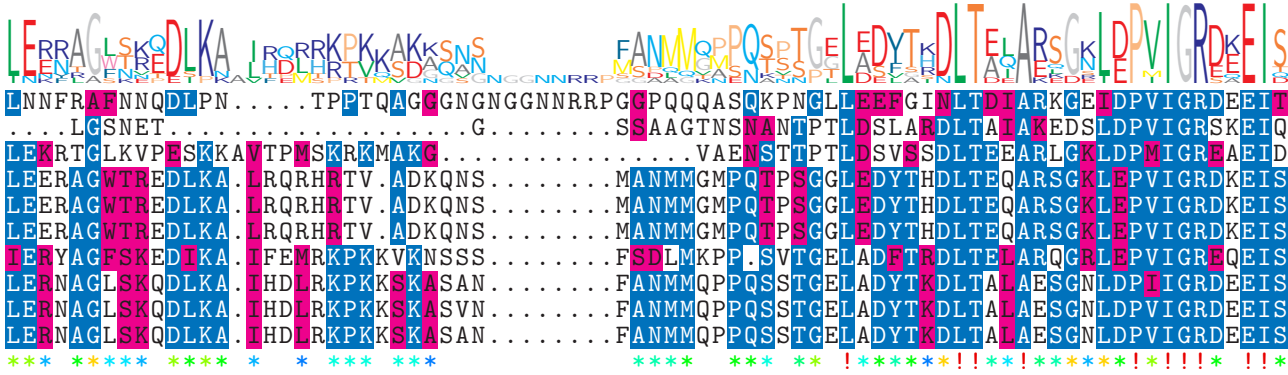
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Sequence 1	R	V	I	E	L	N	R	R	T	K	N	N	P	V	L	G	E	A	G	V	G	K	T	A	L	A	L	G	L	A	Q	R	I	A	S	G	E	V	P	F	E	L	A	D	M	R	I	L	E	D	M	S	V	V	A	G	T	R	F	R	G	D	F	E	E	R	M	N	Q	I	I	D	E	I	E	A																								
Sequence 2	R	V	I	E	L	N	R	R	T	K	N	N	P	V	L	G	E	A	G	V	G	K	T	A	L	A	L	G	L	A	Q	R	I	A	S	G	E	V	P	F	E	L	A	D	M	R	I	L	E	D	M	S	V	V	A	G	T	R	F	R	G	D	F	E	E	R	M	N	Q	I	I	D	E	I	E	A																								
Sequence 3	R	V	I	E	L	N	R	R	T	K	N	N	P	V	L	G	E	A	G	V	G	K	T	A	L	A	L	G	L	A	Q	R	I	A	S	G	E	V	P	F	E	L	A	D	M	R	I	L	E	D	M	S	V	V	A	G	T	R	F	R	G	D	F	E	E	R	M	N	Q	I	I	D	E	I	E	A																								
Sequence 4	R	V	I	E	L	N	R	R	T	K	N	N	P	V	L	G	E	A	G	V	G	K	T	A	L	A	L	G	L	A	Q	R	I	A	S	G	E	V	P	F	E	L	A	D	M	R	I	L	E	D	M	S	V	V	A	G	T	R	F	R	G	D	F	E	E	R	M	N	Q	I	I	D	E	I	E	A																								
Sequence 5	R	V	I	E	L	N	R	R	T	K	N	N	P	V	L	G	E	A	G	V	G	K	T	A	L	A	L	G	L	A	Q	R	I	A	S	G	E	V	P	F	E	L	A	D	M	R	I	L	E	D	M	S	V	V	A	G	T	R	F	R	G	D	F	E	E	R	M	N	Q	I	I	D	E	I	E	A																								
Sequence 6	R	V	I	E	L	N	R	R	T	K	N	N	P	V	L	G	E	A	G	V	G	K	T	A	L	A	L	G	L	A	Q	R	I	A	S	G	E	V	P	F	E	L	A	D	M	R	I	L	E	D	M	S	V	V	A	G	T	R	F	R	G	D	F	E	E	R	M	N	Q	I	I	D	E	I	E	A																								
Sequence 7	R	V	I	E	L	N	R	R	T	K	N	N	P	V	L	G	E	A	G	V	G	K	T	A	L	A	L	G	L	A	Q	R	I	A	S	G	E	V	P	F	E	L	A	D	M	R	I	L	E	D	M	S	V	V	A	G	T	R	F	R	G	D	F	E	E	R	M	N	Q	I	I	D	E	I	E	A																								
Sequence 8	R	V	I	E	L	N	R	R	T	K	N	N	P	V	L	G	E	A	G	V	G	K	T	A	L	A	L	G	L	A	Q	R	I	A	S	G	E	V	P	F	E	L	A	D	M	R	I	L	E	D	M	S	V	V	A	G	T	R	F	R	G	D	F	E	E	R	M	N	Q	I	I	D	E	I	E	A																								
Sequence 9	R	V																																																																																																		

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RQD	V	I	L	F	I	D	E	L	H	T	I	I	G	S	G	S	G	I	D	S	T	L	D	A	A	N	I	L	K	P	A	L	A	R	G	T	L	R	T	V	G	A	T	T	L	N	E	Y	R	.	I	E	K	D	A	A	L	S	R	R	F	A	K	Y	T	I	E	E	P	S	V	A	E	I	T	300																								
AC	N	I	L	F	I	D	E	L	H	T	I	I	G	A	G	.	A	E	G	A	I	D	A	S	N	I	L	K	P	S	L	A	R	G	E	L	Q	C	I	G	A	T	T	L	D	E	Y	R	K	Y	I	E	K	D	A	A	L	S	R	R	F	A	K	Y	T	I	E	E	P	S	V	D	E	S	I	Q	349																							
D	P	D	V	I	T	I	F	I	D	E	L	H	T	I	I	G	A	G	G	M	D	S	V	N	D	A	A	N	I	L	K	P	A	L	A	R	G	T	D	F	Q	M	V	G	A	T	T	Y	H	E	Y	K	Y	I	E	K	D	E	A	L	S	R	R	F	A	K	Y	T	I	E	E	P	S	V	D	E	A	I	A	363																				
D	G	Q	V	I	L	F	I	D	E	L	H	T	I	I	G	S	G	S	G	I	D	S	T	L	D	A	A	N	I	L	K	P	A	L	A	R	G	T	L	R	T	V	G	A	T	T	Q	E	Y	Q	K	H	I	E	K	D	A	A	L	S	R	R	F	A	K	Y	T	I	E	E	P	S	V	A	D	S	M	T	376																					
D	G	Q	V	I	L	F	I	D	E	L	H	T	I	I	G	S	G	S	G	I	D	S	T	L	D	A	A	N	I	L	K	P	A	L	A	R	G	T	L	R	T	V	G	A	T	T	Q	E	Y	Q	K	H	I	E	K	D	A	A	L	S	R	R	F	A	K	Y	T	I	E	E	P	S	V	A	D	S	M	T	376																					
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Position	Sequence	Accession
1	ATRDEY	AK12KENTP
2	AYQSQ	AK12KENTP
3	AVIKL	AK12KENTP
4	ALMDG	AK12KENTP
5	ALMDG	AK12KENTP
6	ALMDG	AK12KENTP
7	ALITN	AK12KENTP
8	ALISG	AK12KENTP
9	ALISG	AK12KENTP
10	ALISG	AK12KENTP

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VIGQD	AVSAISRAIRRNQSGIR	TKRP	IGSFMFLGPTGVGKTELAKALAEVLFDD	ESALIR	EDMSEYMEKFAASRLN	GA	
↓	↓	↓	↓	↓	↓	↓	
VIGQDA	AVDKTAKAIRRN	RVGIGTPN	RPIGSFLFV	GPTGVGKTEL	SKQLAIELFG	SEDSMIR	FDMS
VIGQDE	AVAVAKAVRRAR	AGLKDPR	KRPIGSFIFL	GPTGVGKTEL	AKALAESIFG	DESMIR	IDMS
VIGQE	EAVTSAV	SRAIRRN	ARSGVADSR	PMGSGFMFLGPTGVGKTEL	AKALAEVLF	GEDNMI	RVDM
VIGQD	QAVSSISRAIRRN	NQSGIRSH	KRPIGSFMFLGPTGVGKTEL	AKALAEVLFDD	ESALIR	FDMS	EYMEKFAASRLN
VIGQD	QAVSSISRAIRRN	NQSGIRSH	KRPIGSFMFLGPTGVGKTEL	AKALAEVLFDD	ESALIR	FDMS	EYMEKFAASRLN
VIGQD	QAVSSISRAIRRN	NQSGIRSH	KRPIGSFMFLGPTGVGKTEL	AKALAEVLFDD	ESALIR	FDMS	EYMEKFAASRLN
VIGQD	DAVSSISRAIRRN	NQSGIRV	HKRPIGSFMFLGPTGVGKTEL	AKALAEVLFDD	ESALIR	FDMS	EYMEKFAASRLN
VIGQDE	AVSAISRAIRRN	NQSGIRTG	KRPIGSFMFLGPTGVGKTEL	AKALAEVLFDD	ESALIR	FDMS	EYMEKFAASRLN
VIGQDE	AVSAISRAIRRN	NQSGIRTG	KRPIGSFMFLGPTGVGKTEL	AKALAEVLFDD	ESALIR	FDMS	EYMEKFAASRLN
VIGQDE	AVSAISRAIRRN	NQSGIRTG	KRPIGSFMFLGPTGVGKTEL	AKALAEVLFDD	ESALIR	FDMS	EYMEKFAASRLN
*	*	*	*	*	*	*	*

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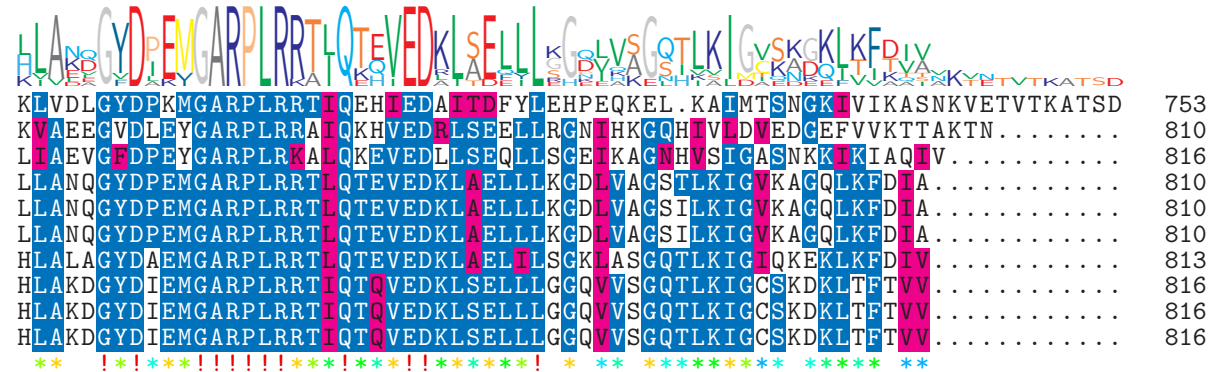
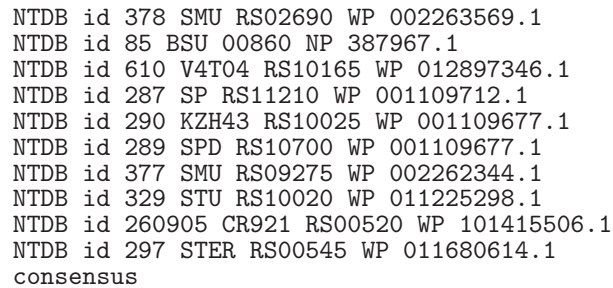
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-  non conserved
-  similar
-  $\geq 50\%$ conserved