

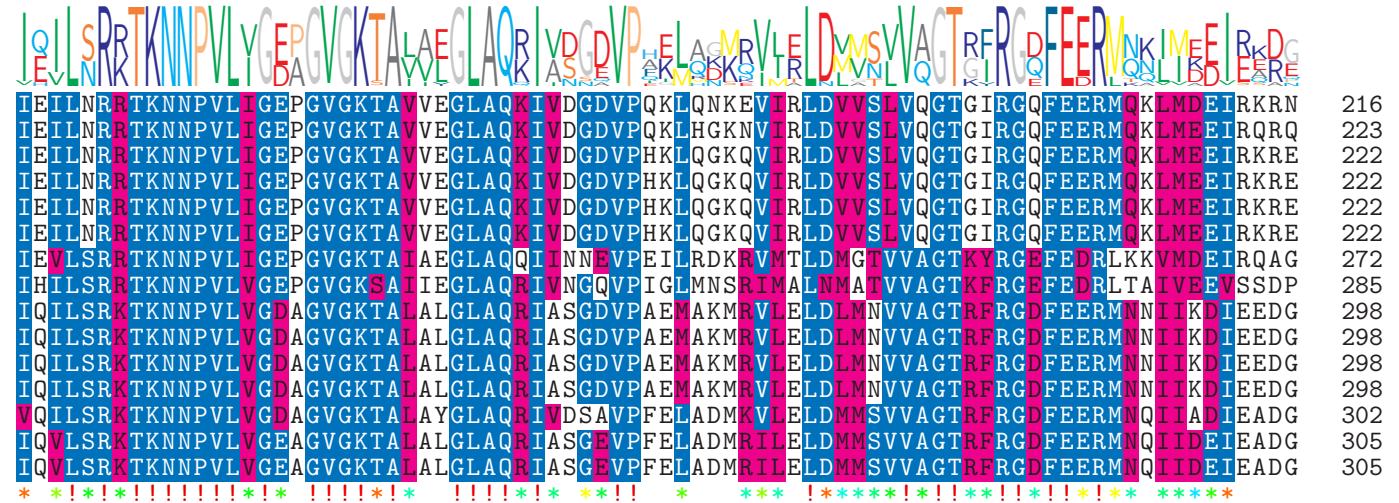
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NTDB id	378	SMU	RS02690	WP	002263569.1	MLCQNCKINEA.....	11
NTDB id	281	KZH43	RS03550	WP	000882517.1	MLCQNCKINDS.....	11
NTDB id	245	SPD	RS03860	WP	000882517.1	MLCQNCKINDS.....	11
NTDB id	243	SPR	RS03635	WP	000882517.1	MLCQNCKINDS.....	11
NTDB id	241	SP	RS04015	WP	000882523.1	MLCQNCKINDS.....	11
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NTDB id	287	SP	RS11210	WP	001109712.1	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYS	70
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NTDB id	297	STER	RS00545	WP	011680614.1	MTIYSRKMQAIFHRAQLEAERFESPFLLETWHVILLAMVEVTGSVAYLTFDTDFEDRIHSEEIETA AVLAMEKRPKDLS	76
NTDB id	329	STU	RS10020	WP	011225298.1	MTIYSRKMQAIFHRAQLEAERFESPFLLETWHVILLAMVEVPGSVAYLTFDTDFEDRIHSEEIETA AVLAMEKRPKDLS	76
consensus						*** * * **** **	

Accession	Species	Gene	Protein	Sequence	Score
NTDB id 601	KW2	RS02615	WP 021036805.1	...TIHLYTSVNGQKKQIDLCQNCYQI...MKS G REALFGAGNASNGNSDE.....PFNP.FNDIFSA L QGG	72
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NTDB id 281	KZH43	RS03550	WP 000882517.1	...TIHLYTNLNGKQKQIDLCQNCYKI...IKTD P NNSLFKGMT L LNNRD.....FDP.FG D FFND L LNNF	69
NTDB id 245	SPD	RS03860	WP 000882517.1	...TIHLYTNLNGKQKQIDLCQNCYKI...IKTD P NNSLFKGMT L LNNRD.....FDP.FG D FFND L LNNF	69
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NTDB id 85	BSU	O0860	NP 387967.1	GQEMSQT I HYTPRAKKVIELSMDEARKLGHSYV G TEH L LLGLIREGEGVAARV L NNLGVSLNKARQQVLQL.....	141
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NTDB id 287	SP	RS11210	WP 001109712.1	QDET F TEL P FSRR L QVL F DEAEYVASV V HAKV L GTEH V LYAILH D GNALATRI L ERAGFSYEDKKDQVKIAA L RRN L EER	150
NTDB id 116228	E0F39	RS11500	WP 001109696.1	QDET F TEL P FSRR L QVL F DEAEYVASV V HAKV L GTEH V LYAILH D GNALATRI L ERAGFSYEDKKDQVKIAA L RRN L EER	150
NTDB id 290	KZH43	RS10025	WP 001109677.1	QDET F TEL P FSRR L QVL F DEAEYVASV V HAKV L GTEH V LYAILH D GNALATRI L ERAGFSYEDKKDQVKIAA L RRN L EER	150
NTDB id 289	SPD	RS10700	WP 001109677.1	QDET F TEL P FSRR L QVL F DEAEYVASV V HAKV L GTEH V LYAILH D GNALATRI L ERAGFSYEDKKDQVKIAA L RRN L EER	150
NTDB id 377	SMU	RS09275	WP 002262344.1	N...D I M L LEQSHALKRTLA E AAAI S QVTHAKEV G TEH V L F AM L LNP N LLATRI L ELVG F HAKDDGESIRLL D RKV T ERY	154
NTDB id 297	STER	RS00545	WP 011680614.1	ESDI D DLRAQSPAL E AM L QEAQEI A SVTGAVE V GSEH V LM A FL L LHK D LMVCR L LEVAGFQYKDDSDKPRI D RRS L ERN	156
NTDB id 329	STU	RS10020	WP 011225298.1	ESDI D DLRAQSPAL E AM L QEAQGI A SVTGAVE V GSEH V LM A FL L LHK D LMVCR L LEVAGFQYKDDSDKPRI D RRS L ERN	156
consensus				*** * * * * *	

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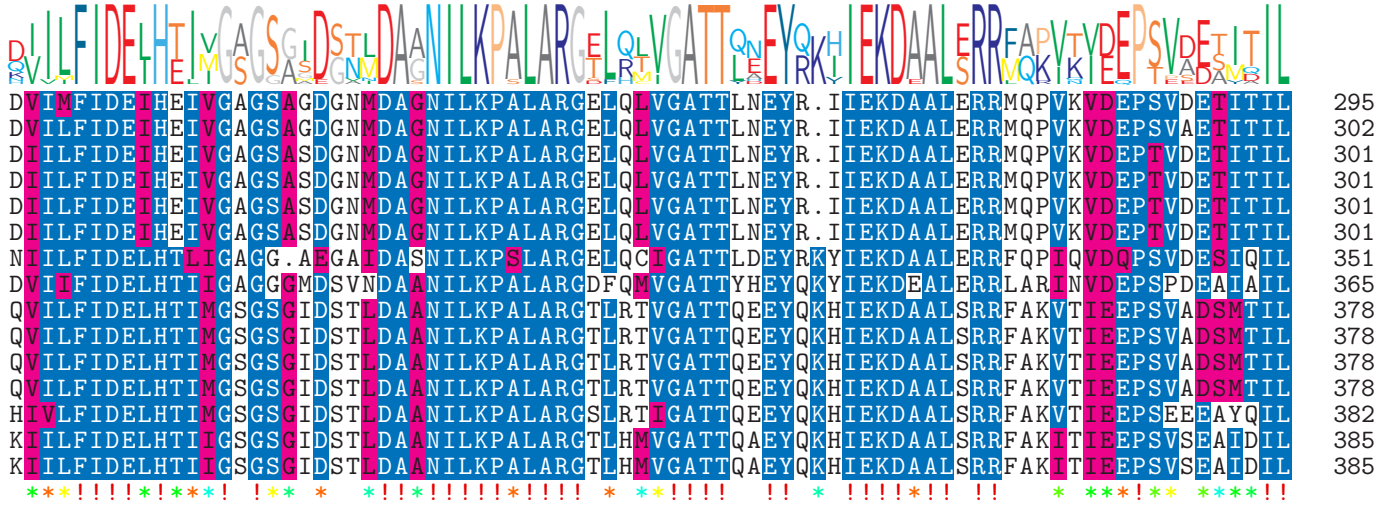
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NTDB id 241 SP RS04015 WP 000882523.1
NTDB id 85 BSU 00860 NP 387967.1
NTDB id 610 V4T04 RS10165 WP 012897346.1
NTDB id 287 SP RS11210 WP 001109712.1
NTDB id 1126228 EOF39 RS11500 WP 001109696.1
NTDB id 290 KZH43 RS10025 WP 001109677.1
NTDB id 289 SPD RS10700 WP 001109677.1
NTDB id 377 SMU RS09275 WP 002262344.1
NTDB id 297 STER RS00545 WP 011680614.1
NTDB id 329 STU RS10020 WP 011225298.1
consensus

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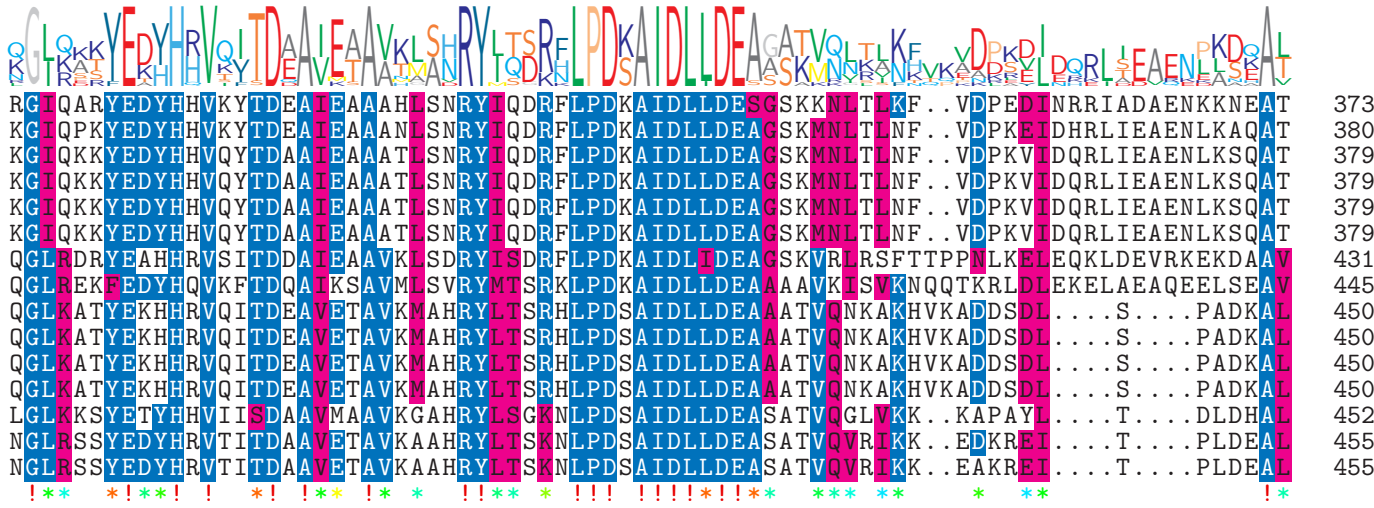
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NTDB	id	297	STER	RS00545	WP	011680614.1
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consensus						




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NTDB id 297 STER RS00545 WP 011680614.1
NTDB id 329 STU RS10020 WP 011225298.1
consensus

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NTDB id 241 SP RS04015 WP 000882523.1	VDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKD.LKAVMTSKCNIIQIKSAKK.AEVKSSEKEK.	752
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consensus	* !*****!!!!!!*!! *!! *** * * * * * * * * *	

- non conserved
- similar
- ≥ 50% conserved