

logo

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NTDB id 601 KW2 RS02615 WP 021036805.1
NTDB id 378 SMU RS02690 WP 002263569.1
NTDB id 216211 BZG42 RS02345 WP 155969646.1
NTDB id 281 KZH43 RS03550 WP 000882517.1
NTDB id 245 SPD RS03860 WP 000882517.1
NTDB id 243 SPR RS03635 WP 000882517.1
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
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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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Position	Sequence	Score
1	MLCQNCNINEA	11
2	MLCQNCNINEA	11
3	MLCKNCNINDA	11
4	MLCQNCNINDS	11
5	MLCQNCNINDS	11
6	MLCQNCNINDS	11
7	MLCQNCNINDS	11
8	MLCQNCNINDS	11
9	MMFGRFTERAQKVLALAQEEALRLGHNNIGTEHILLGLVREGEGLAAKALQALGLGSEKIQKEVESLIG	70
10	MKFENIKYPTPTLDRILEKAEEYAHQYQYGTIESAHLAAMATTSGSIAYSLLAGMNVDDSSDLLIDL	72
11	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYS	70
12	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYS	70
13	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYS	70
14	...MTDYSKLMQEVFRLAQFEAARFESSYLESWHVLLAMVEIDSSVAGLSFAEFADVRFEDYQAAAILAIGKKPKSSS	76
15	...MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVTGSAAYLTFTDFEDRIHSEEIETA AVLAMEKRPKDL	76
16	...MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVPGSAYLTFTDFEDRIHSEEIETA AVLAMEKRPKDL	76

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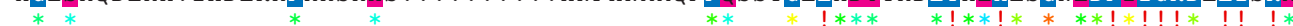
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[illegible]

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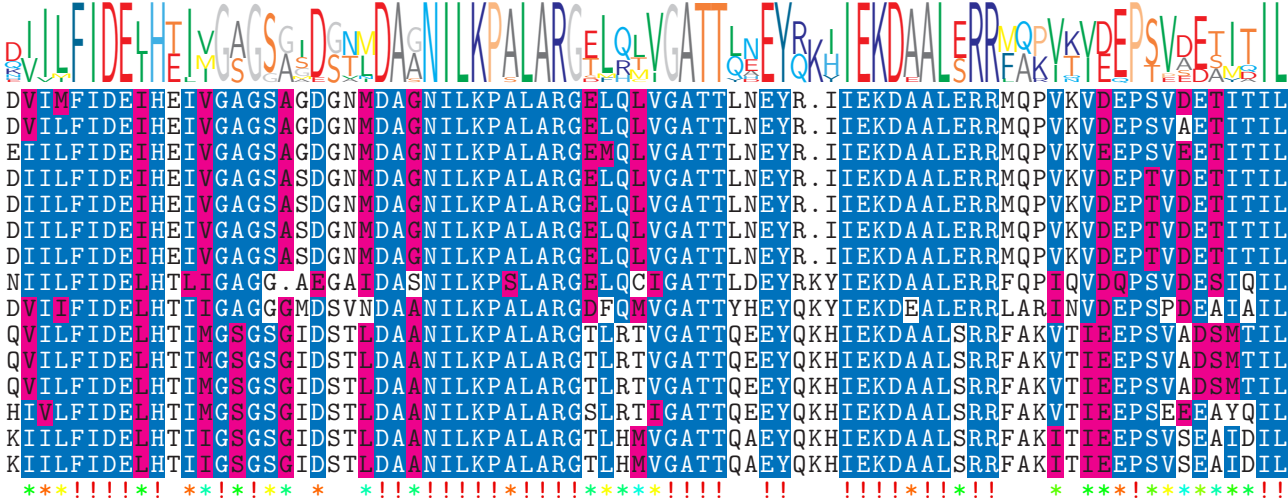
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consensus

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logo

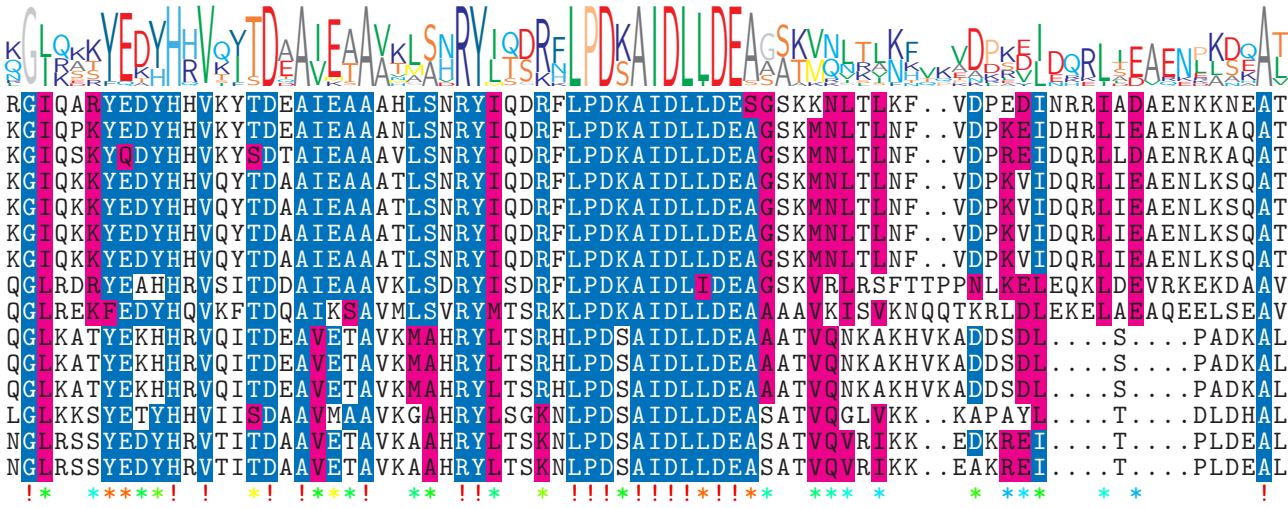
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NTDB id	297	STER	RS00545	WP	011680614.1
NTDB id	329	STU	RS10020	WP	011225298.1
consensus					



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logo

NTDB id	601	KW2	RS02615	WP	021036805.1
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consensus					



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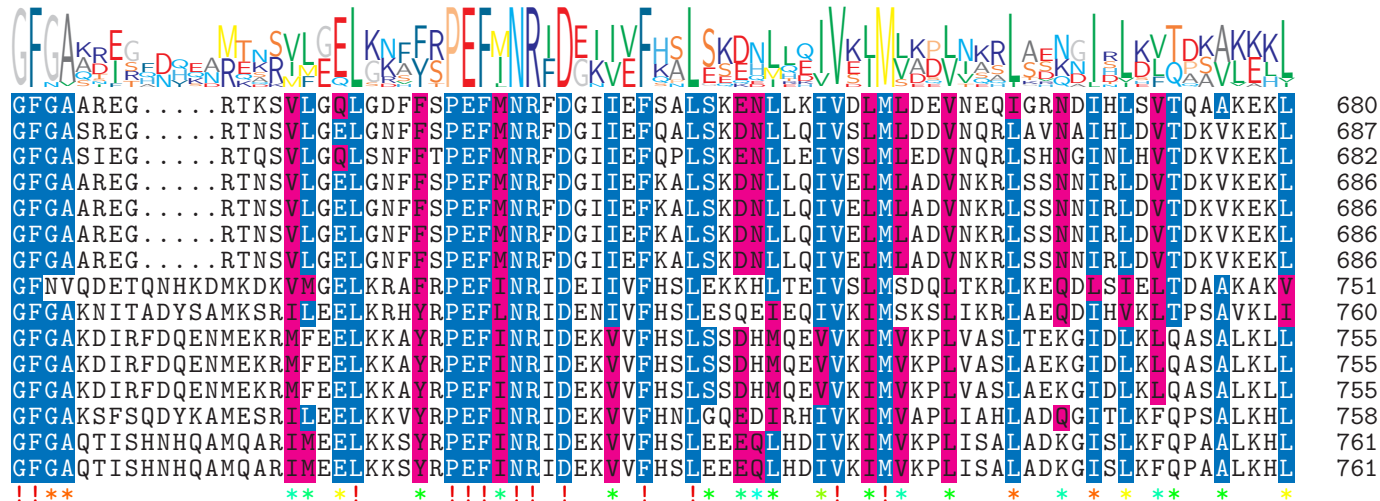
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logo



X non conserved
X similar
X ≥ 50% conserved