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NTDB id 601 KW2 RS02615 WP 021036805.1
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
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NTDB id 378 SMU RS02690 WP 002263569.1
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 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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Position	Sequence	Score
1	MLCQNCNINEAT	12
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4	MLCQNCNINEAT	12
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8	MLCQNCNINEAT	12
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10	MLCQNCNINEAT	12
11	MMFGRFTERAQKVLALAQEEALRLGHNNIGTEHILLGLVREGEGLAAKALQALGLGSEKIQKEVESLIG	70
12	MKFENIKYPTPTLDRILEKAEEYAHQYQYGTIESAHLIAAMATTSGSIAYSLLAGMNVDSDDLIDL	72
13	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYS	70
14	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYS	70
15	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYS	70
16	...MTDYSLKMQEVFRLAQFEAARFESSYLESWHVLLAMVEIDSSVAGLSFAEFEDVRFEDYQAAAILAIGKKPKSSS	76
17	...MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVTGSAVAYLTFTDFEDRIHSEEIETA AVLAMEKRPKDL	76
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logo

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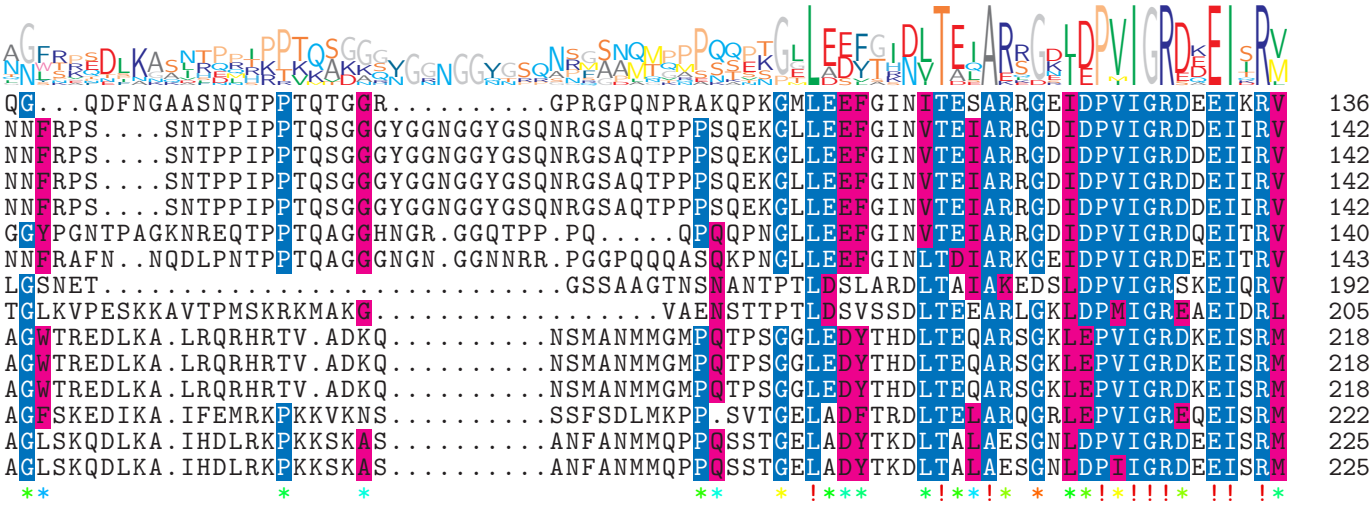
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NTDB id 329 STU RS10020 WP 011225298.1
consensus

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Sequence	Position
....IHL ^{1.0} Y ^{0.8} T ^{0.5} N ^{0.5} L ^{0.5} NG ^{0.5} KK ^{0.5} Q ^{0.5} Q ^{0.5} IDL ^{1.0} CQ ^{0.5} NC ^{0.5} Y ^{0.5} Q...IM ^{0.5} K ^{0.5} SG ^{0.5} G ^{0.5} Q ^{0.5} EAL ^{0.5} FCAGNASNGNSDEPFNP.....FND ^{0.5} IFSAL ^{0.5} ...	69
....IHL ^{1.0} Y ^{0.8} T ^{0.5} N ^{0.5} L ^{0.5} NG ^{0.5} KK ^{0.5} Q ^{0.5} Q ^{0.5} IDL ^{1.0} CQ ^{0.5} NC ^{0.5} Y ^{0.5} K...II ^{0.5} K ^{0.5} TD ^{0.5} P ^{0.5} NN ^{0.5} SL ^{0.5} FK ^{0.5} G ^{0.5} MTD ^{0.5} ...LNNRD ^{0.5} .FDP.....FGD ^{0.5} FF ^{0.5} ND ^{0.5} L ^{0.5} ...	66
....IHL ^{1.0} Y ^{0.8} T ^{0.5} N ^{0.5} L ^{0.5} NG ^{0.5} KK ^{0.5} Q ^{0.5} Q ^{0.5} IDL ^{1.0} CQ ^{0.5} NC ^{0.5} Y ^{0.5} K...II ^{0.5} K ^{0.5} TD ^{0.5} P ^{0.5} NN ^{0.5} SL ^{0.5} FK ^{0.5} G ^{0.5} MTD ^{0.5} ...LNNRD ^{0.5} .FDP.....FGD ^{0.5} FF ^{0.5} ND ^{0.5} L ^{0.5} ...	66
....IHL ^{1.0} Y ^{0.8} T ^{0.5} N ^{0.5} L ^{0.5} NG ^{0.5} KK ^{0.5} Q ^{0.5} Q ^{0.5} IDL ^{1.0} CQ ^{0.5} NC ^{0.5} Y ^{0.5} K...II ^{0.5} K ^{0.5} TD ^{0.5} P ^{0.5} NN ^{0.5} SL ^{0.5} FK ^{0.5} G ^{0.5} MTD ^{0.5} ...LNNRD ^{0.5} .FDP.....FGD ^{0.5} FF ^{0.5} ND ^{0.5} L ^{0.5} ...	66
....IHL ^{1.0} Y ^{0.8} T ^{0.5} N ^{0.5} L ^{0.5} NG ^{0.5} KK ^{0.5} Q ^{0.5} Q ^{0.5} IDL ^{1.0} CQ ^{0.5} NC ^{0.5} Y ^{0.5} K...II ^{0.5} K ^{0.5} TD ^{0.5} P ^{0.5} NN ^{0.5} SL ^{0.5} FK ^{0.5} G ^{0.5} MTD ^{0.5} ...LNNRD ^{0.5} .FDP.....FGD ^{0.5} FF ^{0.5} ND ^{0.5} L ^{0.5} ...	66
....IHL ^{1.0} Y ^{0.8} T ^{0.5} N ^{0.5} L ^{0.5} NG ^{0.5} KK ^{0.5} Q ^{0.5} Q ^{0.5} VD ^{0.5} LCH ^{0.5} NC ^{0.5} Y ^{0.5} Q...IM ^{0.5} K ^{0.5} TD ^{0.5} PH ^{0.5} NA ^{0.5} IL ^{0.5} RG ^{0.5} LG ^{0.5} ...LTNPN ^{0.5} NMD ^{0.5} P.....FSE ^{0.5} FN ^{0.5} NH ^{0.5} L ^{0.5} ...	67
....IHL ^{1.0} Y ^{0.8} AN ^{0.5} V ^{0.5} NG ^{0.5} KK ^{0.5} Q ^{0.5} Q ^{0.5} IDL ^{1.0} CQ ^{0.5} NC ^{0.5} Y ^{0.5} Q...IM ^{0.5} K ^{0.5} TD ^{0.5} P ^{0.5} ENG ^{0.5} PL ^{0.5} NH ^{0.5} LS ^{0.5} Q...QN ^{0.5} SS ^{0.5} IN ^{0.5} PF.....FD ^{0.5} DF ^{0.5} FG ^{0.5} DL ^{0.5} ...	67
GQEMSQTIIHYTPRAKKVIELSMDEARKLGHSYVGT ^{1.0} EH ^{1.0} ILL ^{1.0} GL ^{1.0} IREGEGVAARVIN ^{0.5} NL ^{0.5} GVSLN ^{0.5} KARQQVLQL.....	141
VKVKRSTLRFSPRAFEVMTAASFLAIHNNSEAVGT ^{1.0} EH ^{1.0} LL ^{1.0} YALL ^{1.0} QVEDGFG ^{0.5} LQL ^{0.5} KL.....QKINIVSLRKEL ^{0.5} EKR	143
QDETFTFLPFSRRLLQVLFD ^{0.5} EAEYVASV ^{0.5} VHAKVL ^{0.5} GT ^{1.0} EH ^{1.0} VLYAIL ^{1.0} HDGNALATRI ^{0.5} LERAGFSYEDKKDQVKIAALRRNLEER	150
QDETFTFLPFSRRLLQILFD ^{0.5} EAEYVASV ^{0.5} VHAKVL ^{0.5} GT ^{1.0} EH ^{1.0} VLYAIL ^{1.0} HDGNALATRI ^{0.5} LERAGFSYEDKKDQVKIAALRRNLEER	150
QDETFTFLPFSRRLLQILFD ^{0.5} EAEYVASV ^{0.5} VHAKVL ^{0.5} GT ^{1.0} EH ^{1.0} VLYAIL ^{1.0} HDGNALATRI ^{0.5} LERAGFSYEDKKDQVKIAALRRNLEER	150
N..D ^{0.5} IM ^{0.5} LL ^{0.5} EQSHALKRTLA ^{0.5} EA ^{0.5} AA ^{0.5} ISQVTHAKEVGT ^{1.0} EH ^{1.0} VL ^{1.0} FAMLLNPNLLATRI ^{0.5} LELVGFHAKDDGESIRLLD ^{0.5} LRKV ^{0.5} TERY	154
ESDIIDLRAQSPALEAM ^{0.5} LQEAQEIASVTGAVEVGS ^{0.5} EH ^{0.5} VL ^{0.5} MAFLLHKDLMVCRLL ^{0.5} EVAGFQYKDDSDKPRIIDLRRSLERN	156
ESDIIDLRAQSPALEAM ^{0.5} LQEAQGIASVTGAVEVGS ^{0.5} EH ^{0.5} VL ^{0.5} MAFLLHKDLMVCRLL ^{0.5} EVAGFQYKDDSDKPRIIDLRRSLERN	156

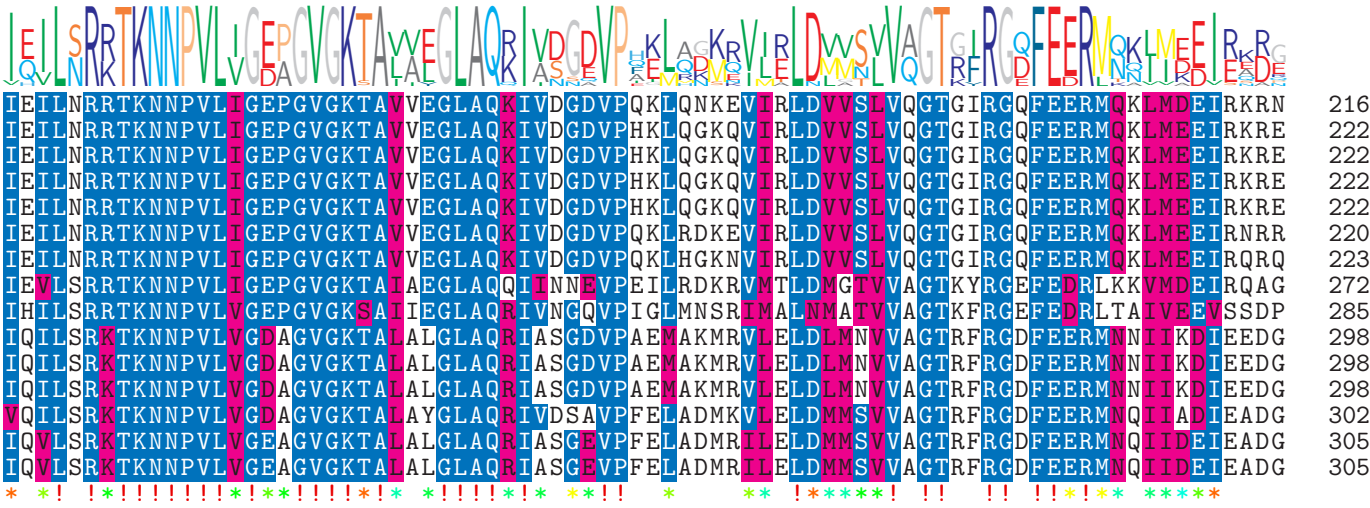
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NTDB id	85	BSU	00860	NP	387967.1
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NTDB id	297	STER	RS00545	WP	011680614.1
NTDB id	329	STU	RS10020	WP	011225298.1
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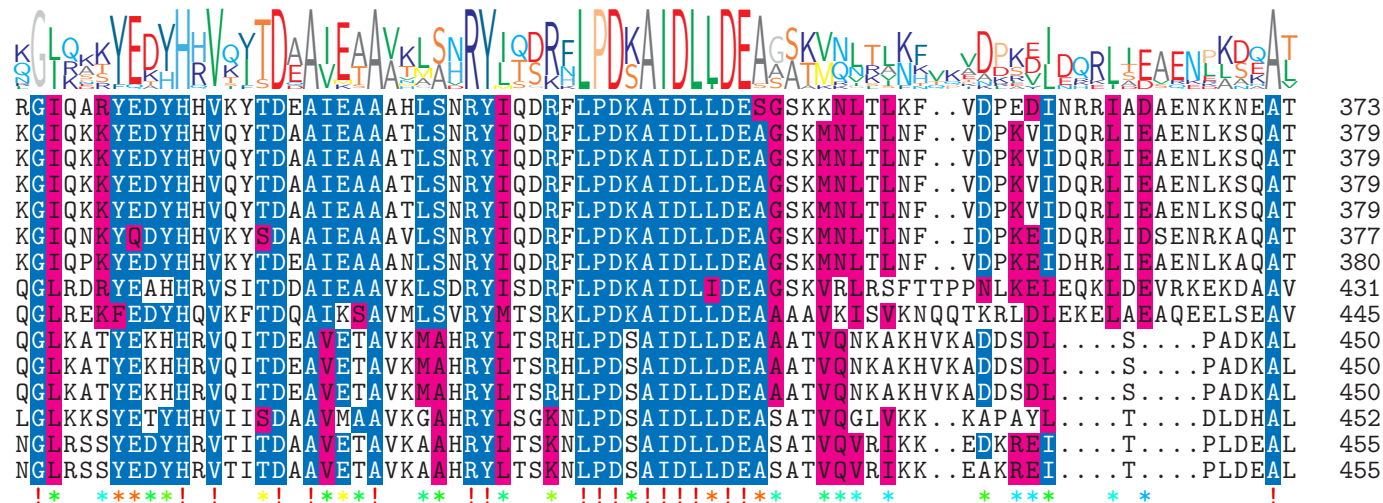
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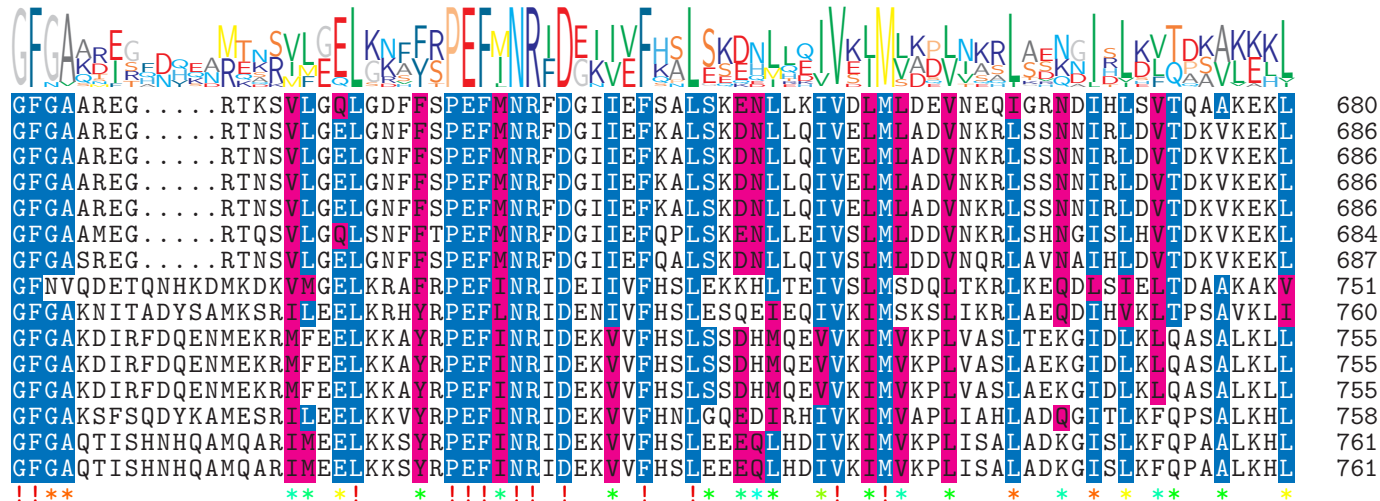
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consensus

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logo



 non conserved
 similar
 ≥ 50% conserved