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NTDB id 114 BSU 16110 NP 389493.1
NTDB id 626 LCA RS04960 WP 011374694.1
NTDB id 599 KW2 RS05940 WP 021037268.1
NTDB id 525 SMSK321 RS06295 WP 000705298.1
NTDB id 497 SM12261 RS05565 WP 000705318.1
NTDB id 267 KZH43 RS05590 WP 000705306.1
NTDB id 226 SPD RS05990 WP 000705306.1
NTDB id 192 SPR RS05715 WP 000705306.1
NTDB id 157 SP RS06205 WP 000705306.1
NTDB id 1131152 H0513 RS04865 WP 100262427.1
NTDB id 407 SMU RS04605 WP 002262865.1
consensus

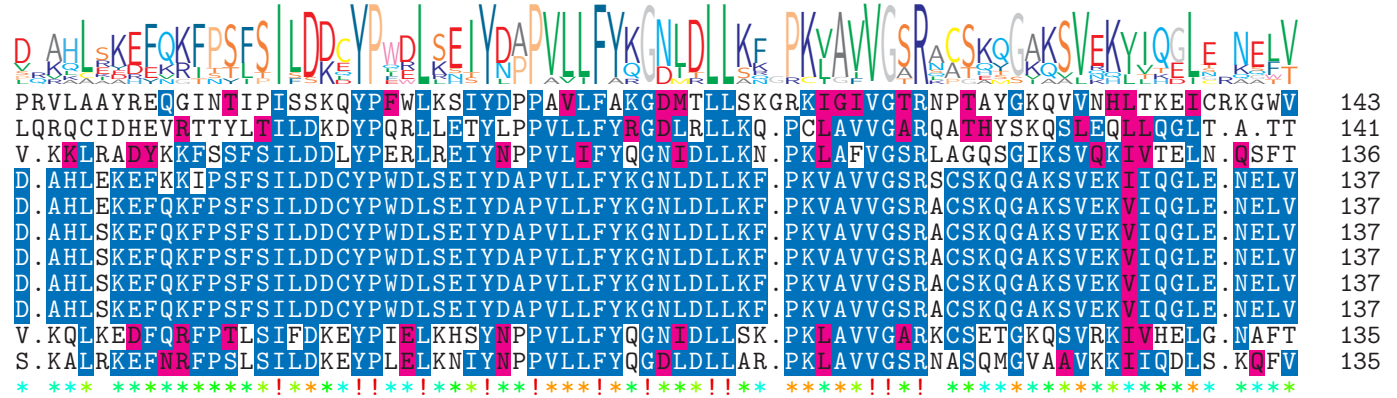
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NTDB id 114 BSU 16110 NP 389493.1
NTDB id 626 LCA RS04960 WP 011374694.1
NTDB id 599 KW2 RS05940 WP 021037268.1
NTDB id 525 SMSK321 RS06295 WP 000705298.1
NTDB id 497 SM12261 RS05565 WP 000705318.1
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NTDB id 192 SPR RS05715 WP 000705306.1
NTDB id 157 SP RS06205 WP 000705306.1
NTDB id 1131152 H0513 RS04865 WP 100262427.1
NTDB id 407 SMU RS04605 WP 002262865.1
consensus

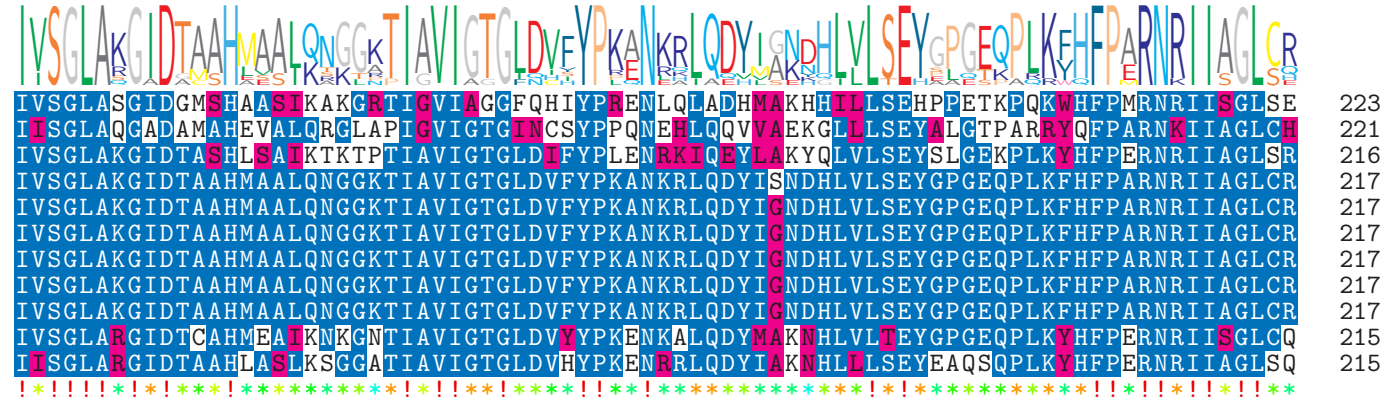
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NTDB id 114 BSU 16110 NP 389493.1
NTDB id 626 LCA RS04960 WP 011374694.1
NTDB id 599 KW2 RS05940 WP 021037268.1
NTDB id 525 SMSK321 RS06295 WP 000705298.1
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NTDB id 226 SPD RS05990 WP 000705306.1
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NTDB id 157 SP RS06205 WP 000705306.1
NTDB id 1131152 H0513 RS04865 WP 100262427.1
NTDB id 407 SMU RS04605 WP 002262865.1
consensus

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logo

NTDB id 114	BSU 16110 NP 389493.1	GVIVVQCKEKSGSLITAYQALECGREVFVPGSIFDPYAGGPIKLIQCGAKA	WSAEDIFEELPERNVQYTEPF	297
NTDB id 626	LCA RS04960 WP 011374694.1	SLIVTEARHKSGSLITANLALQANRNVYAIPGRIDQSLSQGCNQLIAAGATPLLDKNILIEELRYFD		288
NTDB id 599	KW2 RS05940 WP 021037268.1	GVVVVEAKLRSGSLITCERALEEGRDIFAIPGNIADGTS	SDGCNHLIQCGAKLVYQAQDILIEVLYN	282
NTDB id 525	SMSK321 RS06295 WP 000705298.1	GVIVAEAKMRSGSLITCERAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF		282
NTDB id 497	SM12261 RS05565 WP 000705318.1	GVIVAEAKMRSGSLITCERAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF		282
NTDB id 267	KZH43 RS05590 WP 000705306.1	GVIVAEAKMRSGSLITCERAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF		282
NTDB id 226	SPD RS05990 WP 000705306.1	GVIVAEAKMRSGSLITCERAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF		282
NTDB id 192	SPR RS05715 WP 000705306.1	GVIVAEAKMRSGSLITCERAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF		282
NTDB id 157	SP RS06205 WP 000705306.1	GVIVAEAKMRSGSLITCERAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF		282
NTDB id 1131152	H0513 RS04865 WP 100262427.1	GVVMVVEAKIRSGSLITCERAMEEGRDVFAIPGNI	LDGKSDGCHYLIQEGAKCITTCFDTISEFS	279
NTDB id 407	SMU RS04605 WP 002262865.1	GVVMVAEAKIRSGSLITCERAMEEGRDVFAIPGNI	LDGQSEGCHHLIQEGAKCITSCFDILNEFN	280
consensus		*****!*****! ! ! ! ! !*****!*****!*****! !*****!*****!*****! !*****!*****!*****!*****!*****!		

- non conserved
- similar
- ≥ 50% conserved