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NTDB id 601 KW2 RS02615 WP 021036805.1
NTDB id 378 SMU RS02690 WP 002263569.1
NTDB id 281 KZH43 RS03550 WP 000882517.1
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NTDB id 329 STU RS10020 WP 011225298.1
consensus

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Position	Sequence	Score
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3	AQEEA	70
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8	IAAKALQALGLGSEKIQKEVESLI	70
9	GR	70
10	MKFENIKYIPTLDRILEK	72
11	AEEYA	72
12	AHQYQYGTIESA	72
13	HLAAMATTSGS	72
14	IAYSLLAGMNVDSDDLII	72
15	DL	72
16	SSH	72
17	MNYSKALNECIES	70
18	AYMV	70
19	AGHFGARYLES	70
20	WHLLIAMSNHSYS	70
21	VAGATLNDYPYEMDRLE	70
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39	VAGLSFAEF	76
40	EADVRFEDYQAAAILAIGKKPKSSS	76
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48	AQLEA	76
49	AERFESPFL	76
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51	VAYLTF	76
52	TFDFEDRIHSEEIETAAVLAMEKRPKDLS	76

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NTDB id 329 STU RS10020 WP 011225298.1
consensus

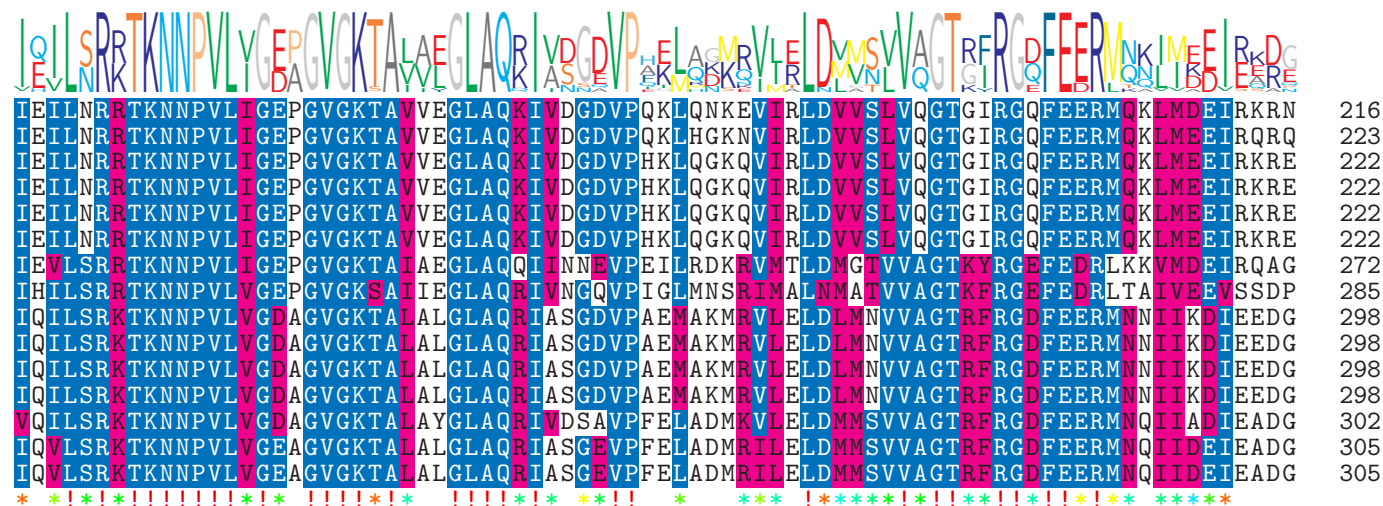
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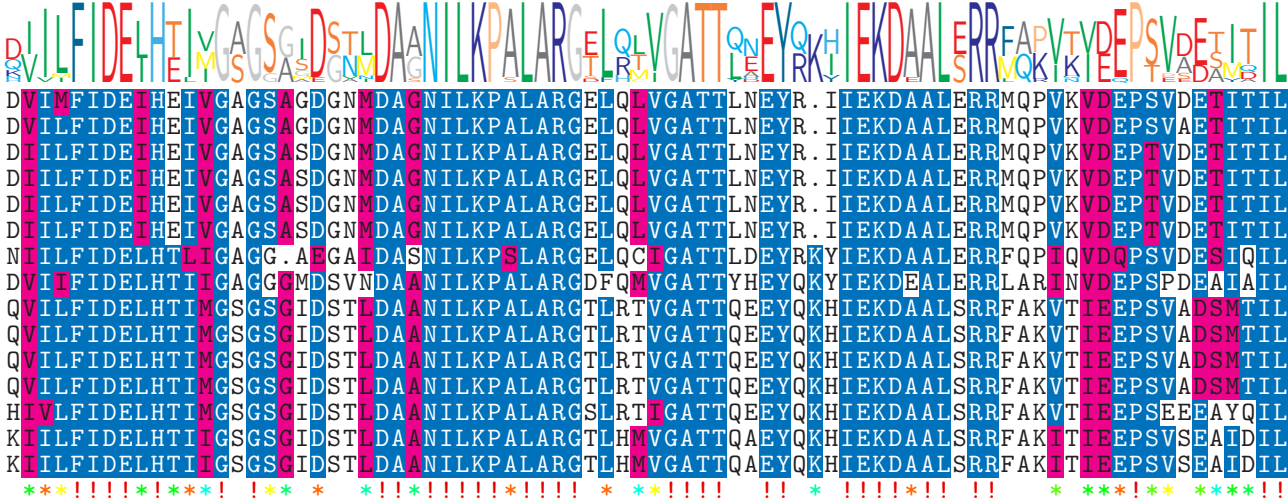
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logo

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consensus



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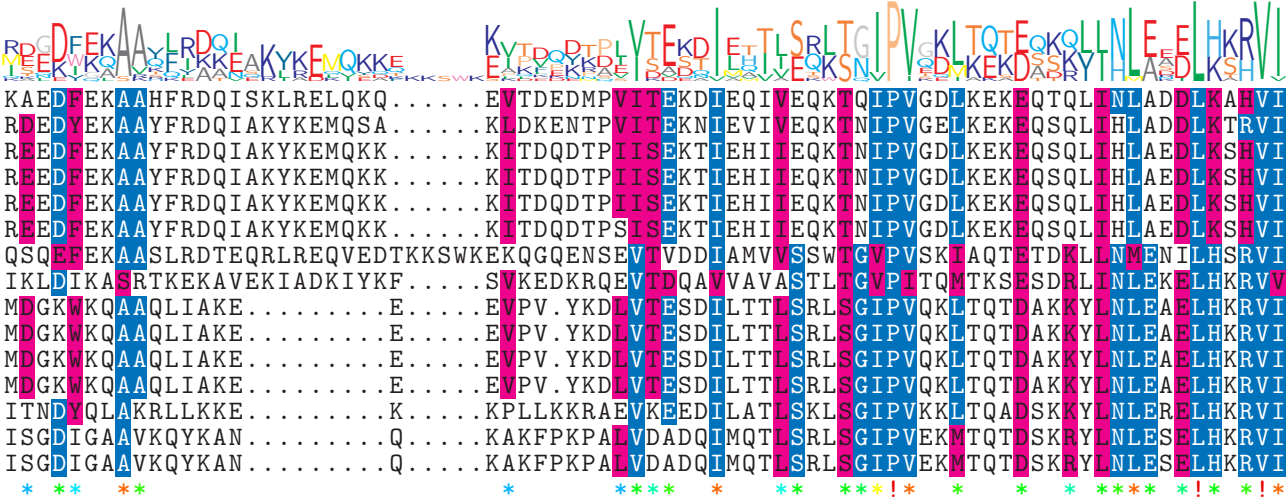
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consensus



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consensus					



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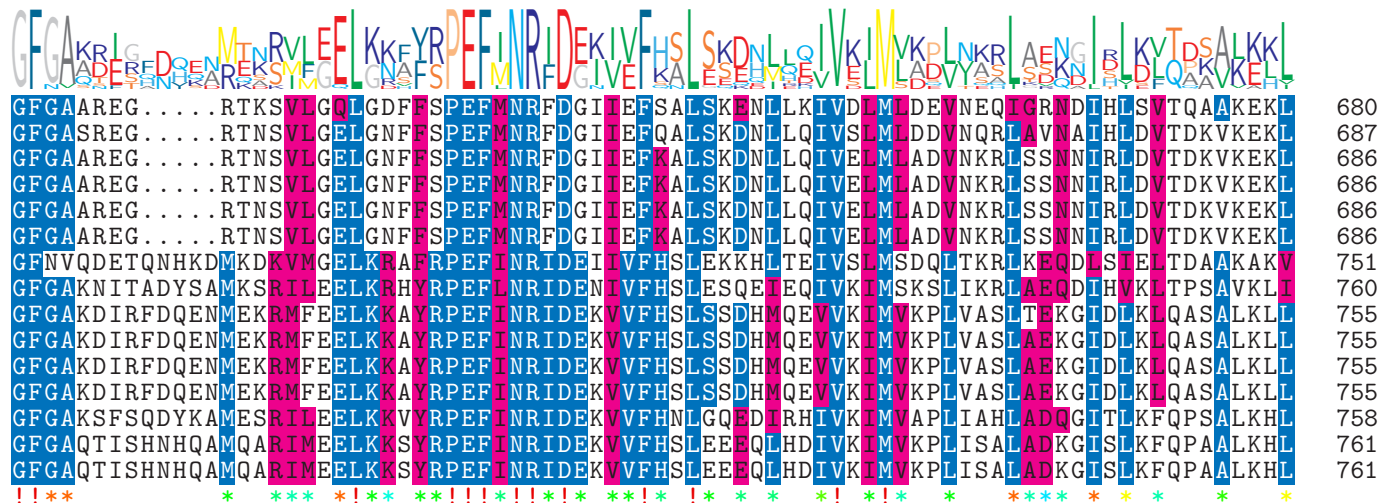


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NTDB id 297 STER RS00545 WP 011680614.1
NTDB id 329 STU RS10020 WP 011225298.1
consensus

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logo

NTDB id 601 KW2 RS02615 WP 021036805.1	VDLGYNPAMGARPLRRTIQENIEDSTADFYIEHPEYKQ.LVADLIDDKIVISNQTQETAETTDEEVP	748
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NTDB id 281 KZH43 RS03550 WP 000882517.1	VDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKD.LKAVMTSKGNIQIKSAKK.AEVKSSEKEK.	752
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NTDB id 243 SPR RS03635 WP 000882517.1	VDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKD.LKAVMTSKGNIQIKSAKK.AEVKSSEKEK.	752
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consensus	* !*****!!!!!!*!! *!! *** ** * * * * * *	

- non conserved
- similar
- ≥ 50% conserved