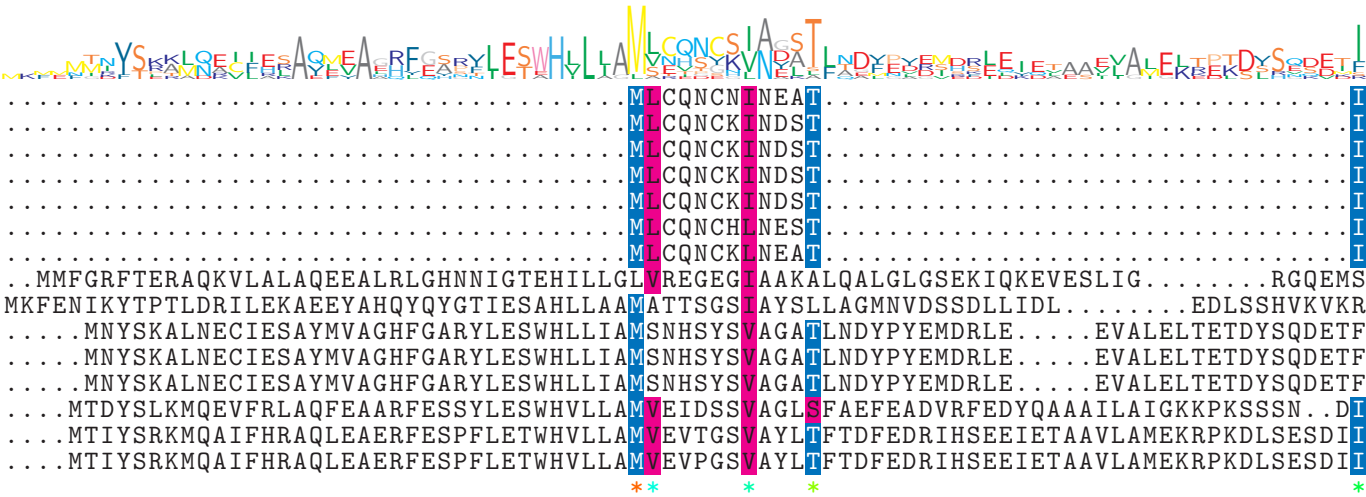


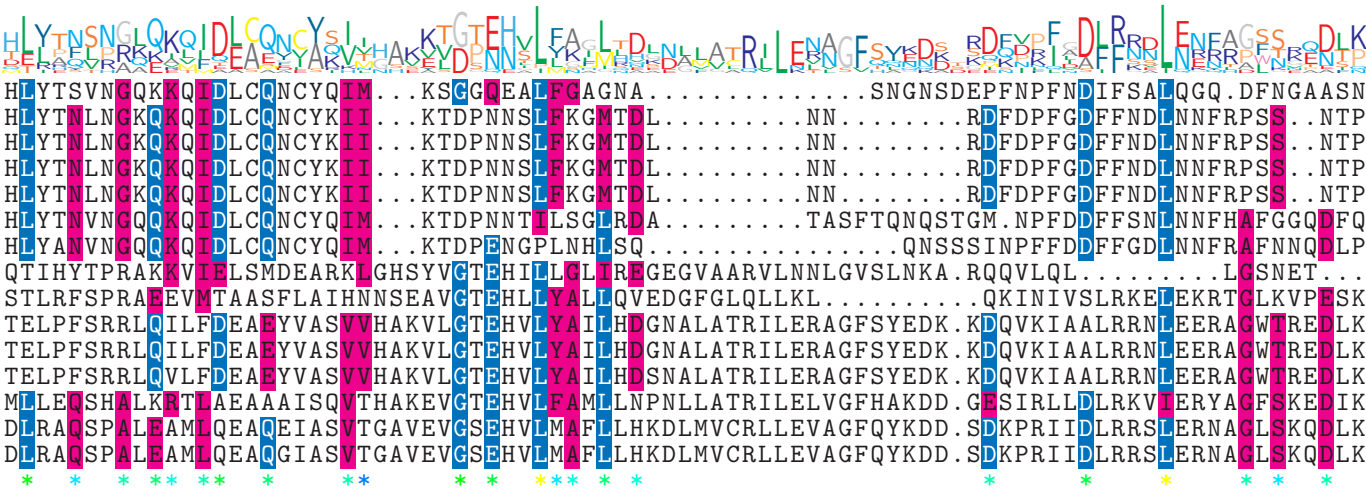
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consensus



logo

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logo

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consensus

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logo

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NTDB id 329 STU RS10020 WP 011225298.1
consensus

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Sequence	Score
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IGEPGVGKTA ^W VEGLA ^Q R ^I VDGDVP ^H KLQ ^G KQ ^V IRLD ^V VS ^L VQ ^G TGIRG ^Q FEERM ^Q KL ^M E ^E IR ^K RED ^I ILFID ^E IHEIVGAGS ^A S	241
IGEPGVGKTA ^W VEGLA ^Q R ^I VDGDVP ^H KLQ ^G KQ ^V IRLD ^V VS ^L VQ ^G TGIRG ^Q FEERM ^Q KL ^M E ^E IR ^K RED ^I ILFID ^E IHEIVGAGS ^A S	241
IGEPGVGKTA ^W VEGLA ^Q R ^I VDGDVP ^H KLQ ^G KQ ^V IRLD ^V VS ^L VQ ^G TGIRG ^Q FEERM ^Q KL ^M E ^E IR ^K RED ^I ILFID ^E IHEIVGAGS ^A S	241
IGEPGVGKTA ^W VEGLA ^Q R ^I VDGDVP ^H KLQ ^G KQ ^V IRLD ^V VS ^L VQ ^G TGIRG ^Q FEERM ^Q KL ^M E ^E IR ^K RED ^I ILFID ^E IHEIVGAGS ^A S	241
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IGEPGVGKTA ^W VEGLA ^Q R ^I VDGDVP ^Q KLH ^G KNV ^I RLD ^V VS ^L VQ ^G TGIRG ^Q FEERM ^Q KL ^M E ^E IR ^Q RQD ^V ILFID ^E IHEIVGAGS ^A G	242
IGEPGVGKTA ^I AEGLAQ ^Q IINNE ^V PEIL ^R DKRV ^M TLDM ^G TVAG ^T KYRG ^E FE ^D RLKK ^V MDEIR ^Q AGN ^I ILFID ^E LHT ^L IGAG ^G .A	290
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VGEAGVGKTA ^L ALGLAQ ^R IASGE ^V VPFELADM ^R ILELD ^M MSV ^V AGTRFRG ^D FEERM ^N Q ^I IDE ^I EADGK ^I ILFI ^D ELHT ^L IGSGSG ^I	324
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logo

[illegible]

logo

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consensus						** ! ! *	* ! ! ! * ! ! ! * ! ! ! * ! ! * * * * *	* * *	*	* *	!	* * *	* * *	*	*

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NTDB id 329 STU RS10020 WP 011225298.1
consensus

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logo

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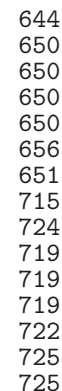
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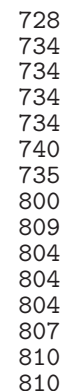
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NTDB id 297 STER RS00545 WP 011680614.1
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consensus

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logo

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consensus	*	*																				

- ⓧ non conserved
- ⓧ similar
- ⓧ ≥ 50% conserved