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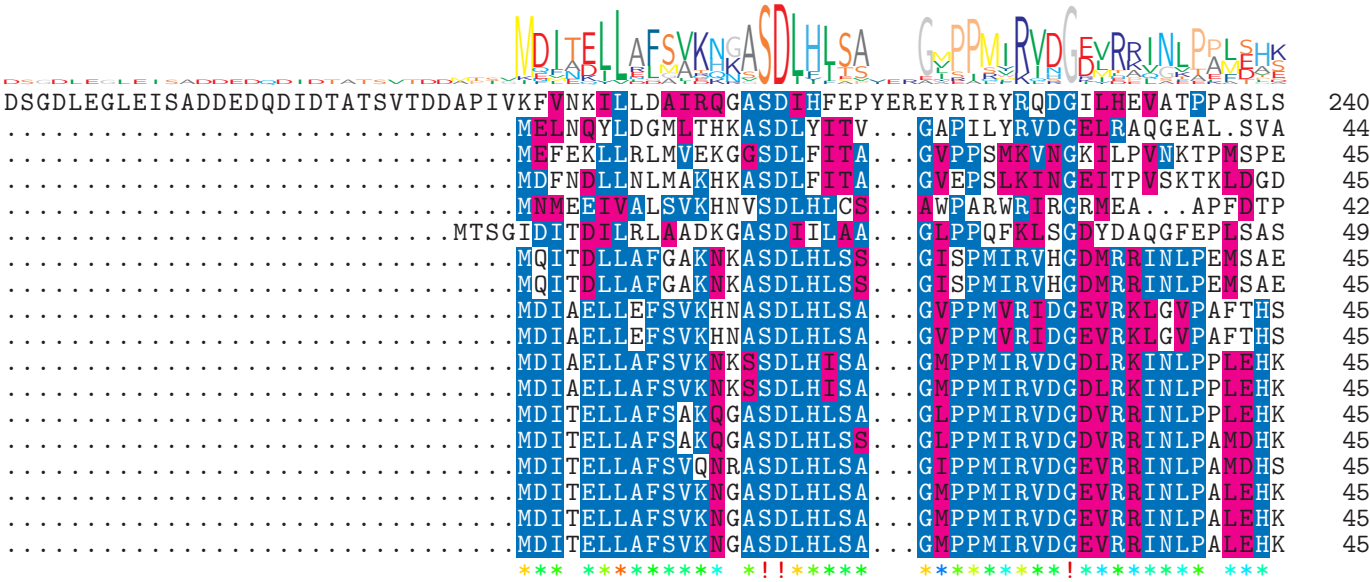
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NTDB id 1040 HON27 RS13360 WP 000355489.1		0
consensus		

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consensus		

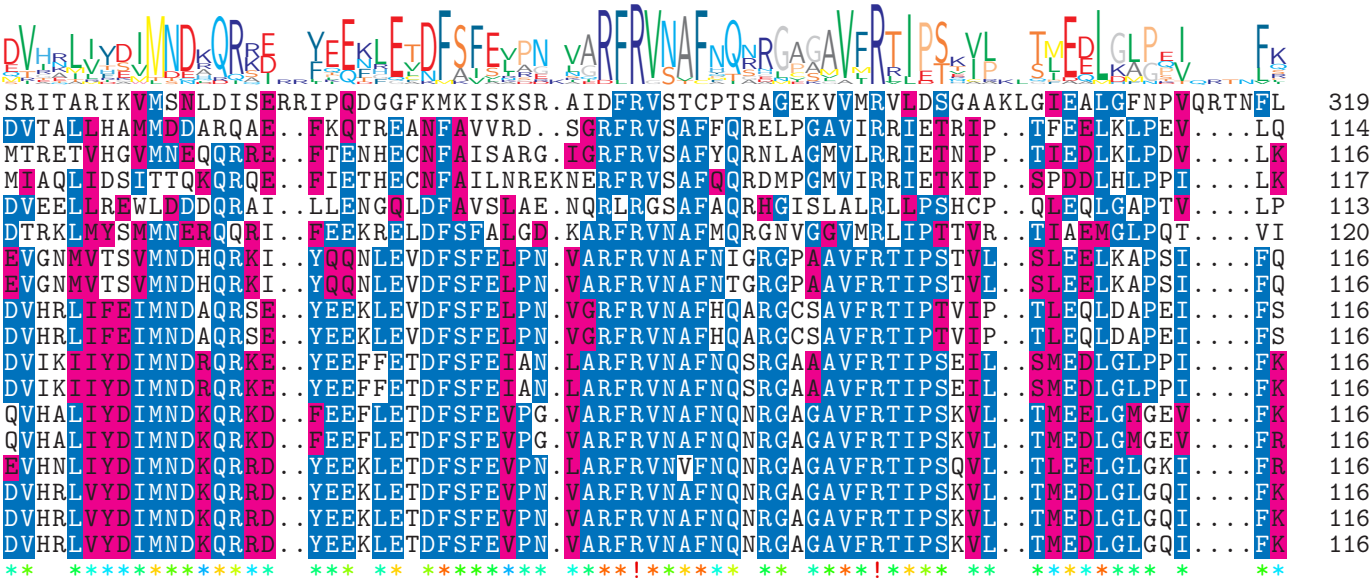
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NTDB	id	1194	PAKAF	RS01995	WP	003084552.1
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NTDB	id	1081	FDQ49	RS05335	WP	006581387.1
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NTDB id	1040	HON27	RS13360	WP	000355489.1
consensus					

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.....DKNKGRHGVEVLNSPRIADLIRRGELHELKATMARSQEVGM	312
.....TPDGKRRAVIEVLINTPLAADLIRKGEVHELKGLMKRSTDLCGM	314
.....THDQSSRRAAVEVLINTPLLSDYIRQGEITYKIKELMARSQELGM	315
.....D.KQEGRVALFELLINTPAVGNLIREGKTHQLPHVIQTGQQVGM	310
.....RADGQGRVLAYEILLANPAVRALIREGKTFQITSVMQTGAREGM	318
.....THDGNGRVASHEILIANPAVRNLIRENKITTQINSVLQTGGQASGM	314
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.....R.VGGGRVACHEIMLATPAIRNLIREDKVAQMYSIIQTGAAHGM	313
.....K.NKGG RVAALEIMMCTGAIRNLIREDKIAQMYSIIQTGQAKGM	313
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.....K.IGGGRVAAHEIMIGTPAIRNLIREDKVAQMYSIIQTGGSLSGM	313
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.....K.EGGGRVAAHEIMIGTPAIRNLIREGKVAQMYSIIQTGATHGM	313
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.....K.NGGGRVAAHEIMIGIPAIRNLIRENKVAQMYSIIQTGANHGM	313
.....K.NGGGRVAAHEIMIGIPAIRNLIRENKVAQMYSIIQTGANHGM	313
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QTFDQALYNLYVQGEITYEDALLHADSSNDLRLMIKLGSETDGEHLTSVS.QGLTL.....EMSDDDPGRSFR....	381
QTFDQALFDLYDHQHISYADALKHADSPNNLRLQIKLSEEANKPLDNRRERMSEMER.....KMTFDGQRRNLK....	383
ITFQQSYQHRVGEGRLL.....	326
VTMDAYLAGLFRHHLITYDKGLERAID.PKEFARLA..NDASAGL.GGASMTPAAPPVPAYNSASSSSTGRGGDFGRGAA	394
QTMDDQLQSLVRQGLIAPEVARRRAQNSESMSF.....	347
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QTLDDQLTELNVKNIIISKHTAHEAALN.KSLF.....	344
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QTLDSCLKGLLAKGLISRDSAKEKAKQ.PENF.....	344
TTLDDQLKQLLAKGIINLPTARAVAKS.PESF.....	344
TTLDDQLKGLVSRGVISPQTARTAAKQ.PESFL.....	345
TTLDDQLKGLVARGVISPQTARTAAKQ.PESFL.....	345
TTLDDQLKGLVARGVISPQTARTAAKQ.PESFL.....	345
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NTDB id 1251 GC085 RS07725 WP 011946523.1		574
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consensus		

-  non conserved
-  similar
-  ≥ 50% conserved