

logo

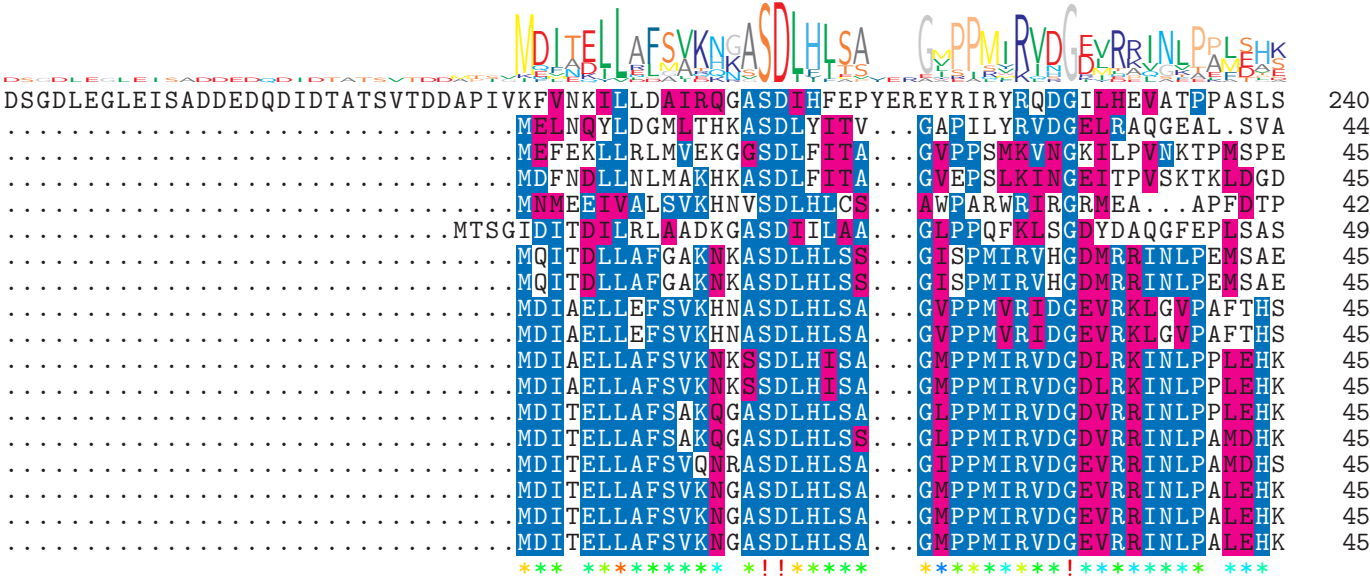
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NTDB id 1203 PSJM300 01605 AFN76401.1		0
NTDB id 1019 ACIAD RS04205 WP 004922051.1		0
NTDB id 64898 AYT25 RS15340 WP 001326494.1		0
NTDB id 1307 DR RS10055 WP 010888596.1		0
NTDB id 1086 NMV RS00245 WP 002218487.1		0
NTDB id 1116 NGFG RS10615 WP 003690200.1		0
NTDB id 1185 GTF74 RS11940 WP 000350195.1		0
NTDB id 1176 A1552VC RS01160 WP 000350195.1		0
NTDB id 1283 ACE17W RS02630 WP 010947729.1		0
NTDB id 1259 GC085 RS10305 WP 010947729.1		0
NTDB id 1194 PAKAF RS01995 WP 003084552.1		0
NTDB id 1202 PSJM300 01600 AFN76400.1		0
NTDB id 1020 ACIAD RS04210 WP 011182164.1		0
NTDB id 1081 FDQ49 RS05335 WP 006581387.1		0
NTDB id 1060 ABD1 RS04380 WP 000355489.1		0
NTDB id 1040 HON27 RS13360 WP 000355489.1		0
consensus		

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NTDB	id	1251	GC085	RS07725	WP	011946523.1
NTDB	id	1177	A1552VC	RS01165	WP	000422572.1
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NTDB	id	64898	AYT25	RS15340	WP	001326494.1
NTDB	id	1307	DR	RS10055	WP	010888596.1
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NTDB	id	1020	ACIAD	RS04210	WP	011182164.1
NTDB	id	1081	FDQ49	RS05335	WP	006581387.1
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NTDB id	1060	ABD1	RS04380	WP	000355489.1
NTDB id	1040	HON27	RS13360	WP	000355489.1
consensus					

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.....DKNKGRHG VFVLLNSPRIADLIRRGELHELKATMARSQEVGM	312
.....TPDGKRRAVIEVLINTPLAADLIRKGEVHELKGLMKRSTDLCGM	314
.....THDQSSRRAAVEVLINTPLLSDYIRQGEITYKIKELMARSQELGM	315
.....D.KQEGRVALFELLINTPAVGNLIREGKTHQLPHVIQTGGQQVGM	310
.....RADGQGRVLAYEILLANPAVRALIREGKTFQITSVMQTGAREGM	318
.....THDGNGRVASHEILIANPAVRNLIRENKITQINSVLQTGGQASGM	314
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.....R.VGGGRVACHEIMLATPAIRNLIREDKVAQMYSIIQTGA AHGM	313
.....R.VGGGRVACHEIMLATPAIRNLIREDKVAQMYSIIQTGA AHGM	313
.....K.NKGG RVAALEIMMCTGAIRNLIREDKIAQMYSIIQTGQAKGM	313
.....K.NKGG RVAALEIMMCTGAIRNLIREDKIAQMYSIIQTGQAKGM	313
.....K.IGGGRVAAHEIMIGTPAIRNLIREDKVAQMYSIIQTGGS LGM	313
.....K.VGGGRVAAHEIMIGTPAIRNLIREDKVAQMYSIIQTGGS LGM	313
.....K.EGGGRVAAHEIMIGTPAIRNLIREGKVAQMYSIIQTGATHGM	313
.....K.NGGGRVAAHEIMIGIPAIRNLIRENKVAQMYSIIQTGANHGM	313
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.....K.NGGGRVAAHEIMIGIPAIRNLIRENKVAQMYSIIQTGANHGM	313
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NTDB id	1060	ABD1	RS04380	WP	000355489.1
NTDB id	1040	HON27	RS13360	WP	000355489.1
consensus					

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QTFDQALYNLYVQGEITYEDALLHADSSNDLRLMIKLGSETDGEHLTSVS.QGLTL.....EMSDDDPGRSFR....	381
QTFDQALFDLYDHQHISYADALKHADSPNNLRLQIKLSEEANKPLDNRERMSEMER.....KMTFDGQRRNLK....	383
ITFQQSYQHRVGEGRLL.....	326
VTMDAYLAGLFRHHLITYDKGLERAID.PKEFARLA..NDASAGL.GGASMTPAAPPVPAYNSASSSSTGRGGDFGRGAA	394
QTMDDQLQSLVRQGLIAPEVARRRAQNSESMSF.....	347
QTMDDQLQSLVRQGLIAPEAARRRAQNSESMSF.....	347
QTMEQNAKQLIARGVVDAQEVQSKIELDLKAF.....	345
QTMEQNAKQLIARGVVDAQEVQSKIELDLKAF.....	345
QTLDDQLTELNVNKNIISKHTAHEAALN.KSLF.....	344
QTLDDQLTELNVNKNIISKHTAHEAALN.KSLF.....	344
QTLDMCLKGLVAKGLISRENAREKAKI.PENF.....	344
QTLDSCLKGLLAKGLISRDSAKEKAKQ.PENF.....	344
TTLDDQLKQLLAKGIINLPTARAVAKS.PESF.....	344
TTLDDQLKGLVSRGVISPQTARTAAKQ.PESFL.....	345
TTLDDQLKGLVARGVISPQTARTAAKQ.PESFL.....	345
TTLDDQLKGLVARGVISPQTARTAAKQ.PESFL.....	345
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consensus		

-  non conserved
-  similar
-  ≥ 50% conserved