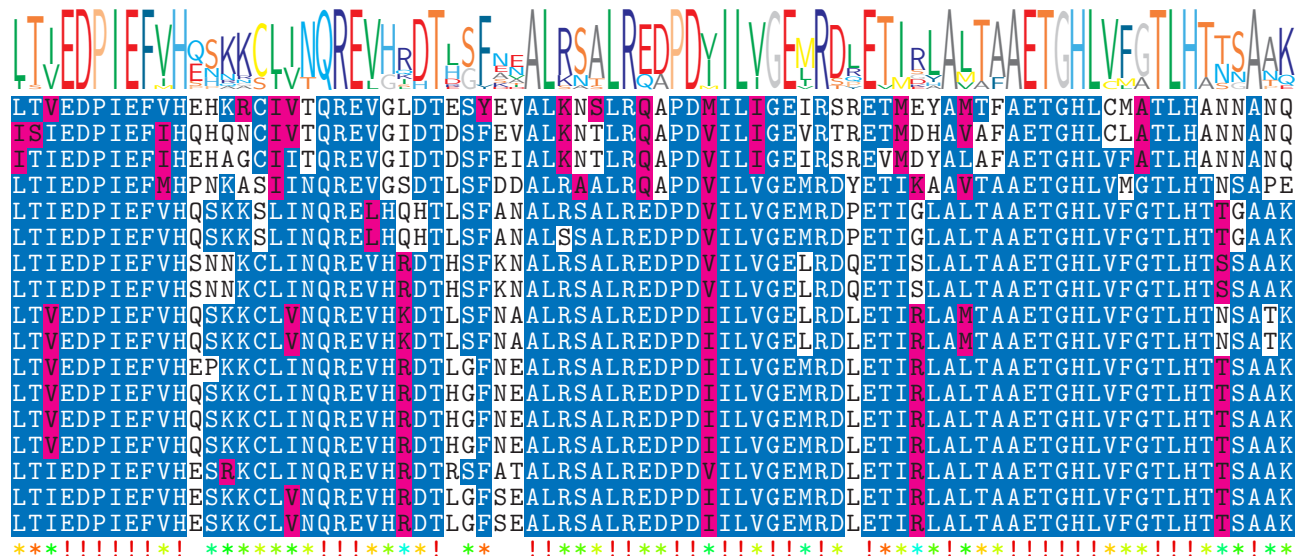



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NTDB id 1259 GCO85 RS10305 WP 010947729.1
NTDB id 1020 ACIAD RS04210 WP 011182164.1
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NTDB id 1194 PAKAF RS01995 WP 003084552.1
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consensus

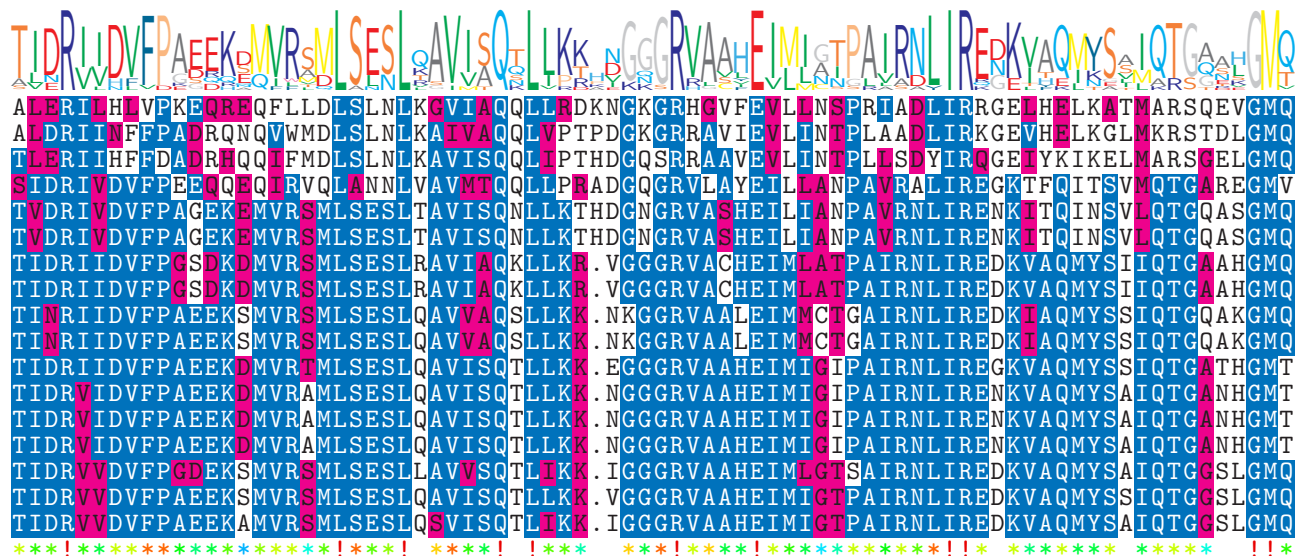


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NTDB id 1020 ACIAD RS04210 WP 011182164.1
NTDB id 1081 FDQ49 RS05335 WP 006581387.1
NTDB id 1060 ABD1 RS04380 WP 000355489.1
NTDB id 1040 HON27 RS13360 WP 000355489.1
NTDB id 239244 CCX46 RS28625 WP 095049465.1
NTDB id 1202 PSJM300 01600 AFN76400.1
NTDB id 1194 PAKAF RS01995 WP 003084552.1

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consensus



Protein	Sequence	Score
TFDQALYQLVDDKLS	EQDALHSADSANLRLMLKT.KRGDDY...GSGSLQNVKI.....DME.....	368
TFDQALYNLYVQGETI	YEDALLHADSSNMLRLMIKL.GSETDGEHLTSVS.QGLTLL.....EMSDDDPGRSFR....	381
TFDQALFDLYDHQHIS	YADALKHADSPNNLRLQIKL.SEEANKPLDNRERMSEMER.....KMTFDGQRRNLK....	383
TMDAYLAGLFRHLLIT	YDKLERAIIDPKFARLANDASAGLGG....ASMTPAAPPVPAYNSASSSSSTGRGGDFGRGAA	394
TMDQSLQSLVVRQGLI	APEVARRRRAQNSSEMSF.....	347
TMDQSLQSLVVRQGLI	APEAARRRAQNSSEMSF.....	347
TMEQNAKQLIARGVVD	AQEVQSKIELDLKAF.....	345
TMEQNAKQLIARGVVD	AQEVQSKIELDLKAF.....	345
TLDQHLTELVNKNIIS	SKHTAHEAALNK.SLF.....	344
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TLDQSLKQLLAKGLI	NLPATARAVAKSP.ESF.....	344
TLDQSLKGLVSRGVIS	PQTARTAAKQP.ESFL.....	345
TLDQSLKGLVARGVIS	PQTARTAAKQP.ESFL.....	345
TLDQSLKGLVARGVIS	PQTARTAAKQP.ESFL.....	345
TLDMCLKDLLTKGLIS	REHAREKARTP.DNF.....	344
TLDSCLKGLLAKGLIS	RDSAKEKAKQP.ENF.....	344
TLDMCLKGLVAKGLIS	RENAREKAKIP.ENF.....	344

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NTDB	id	1086	NMV	RS00245	WP	002218487.1		347
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NTDB	id	1176	A1552VC	RS01160	WP	000350195.1		345
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NTDB	id	1202	PSJM300	01600	AFN76400.1		344	
NTDB	id	1194	PAKAF	RS01995	WP	003084552.1		344
consensus								

-  non conserved
-  similar
-  $\geq 50\%$ conserved