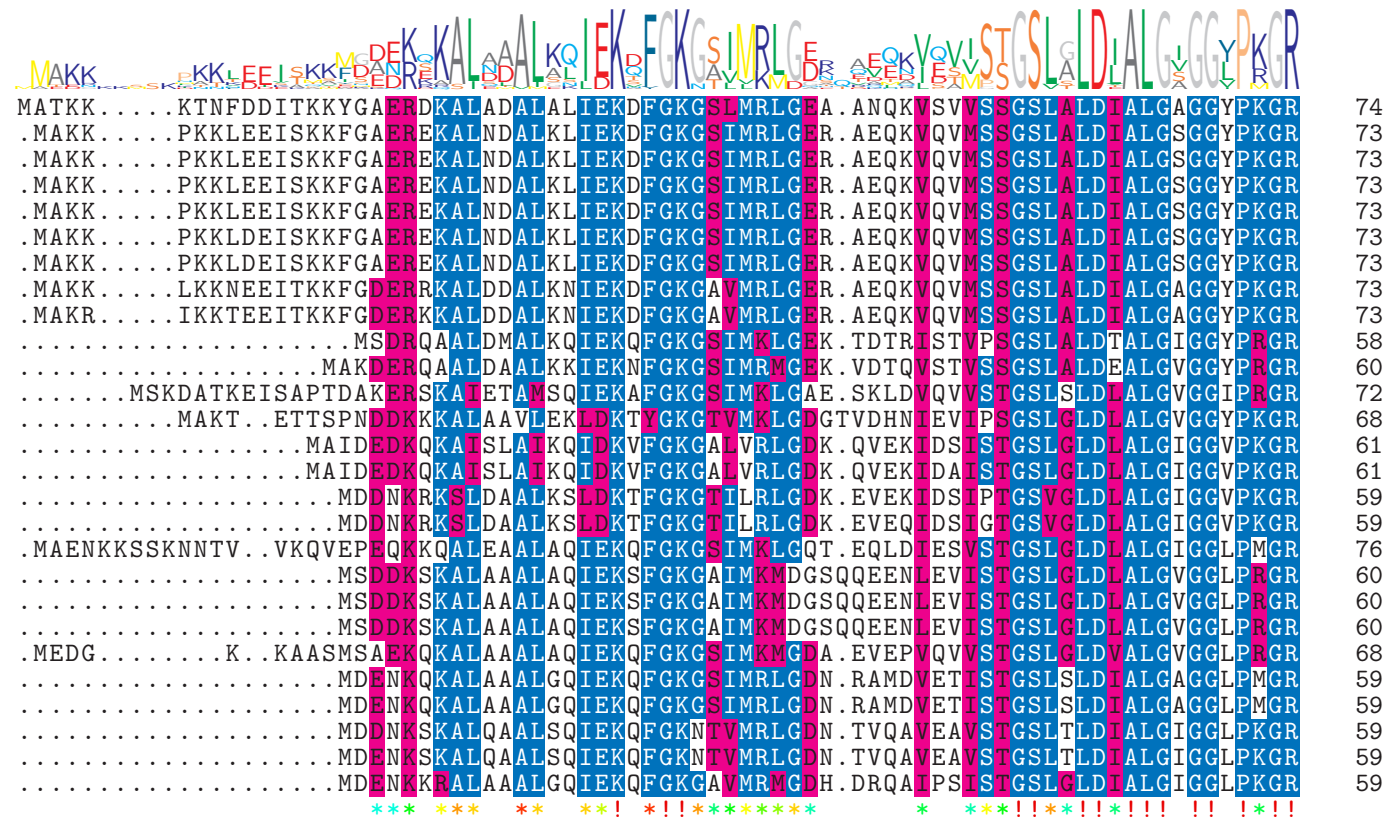
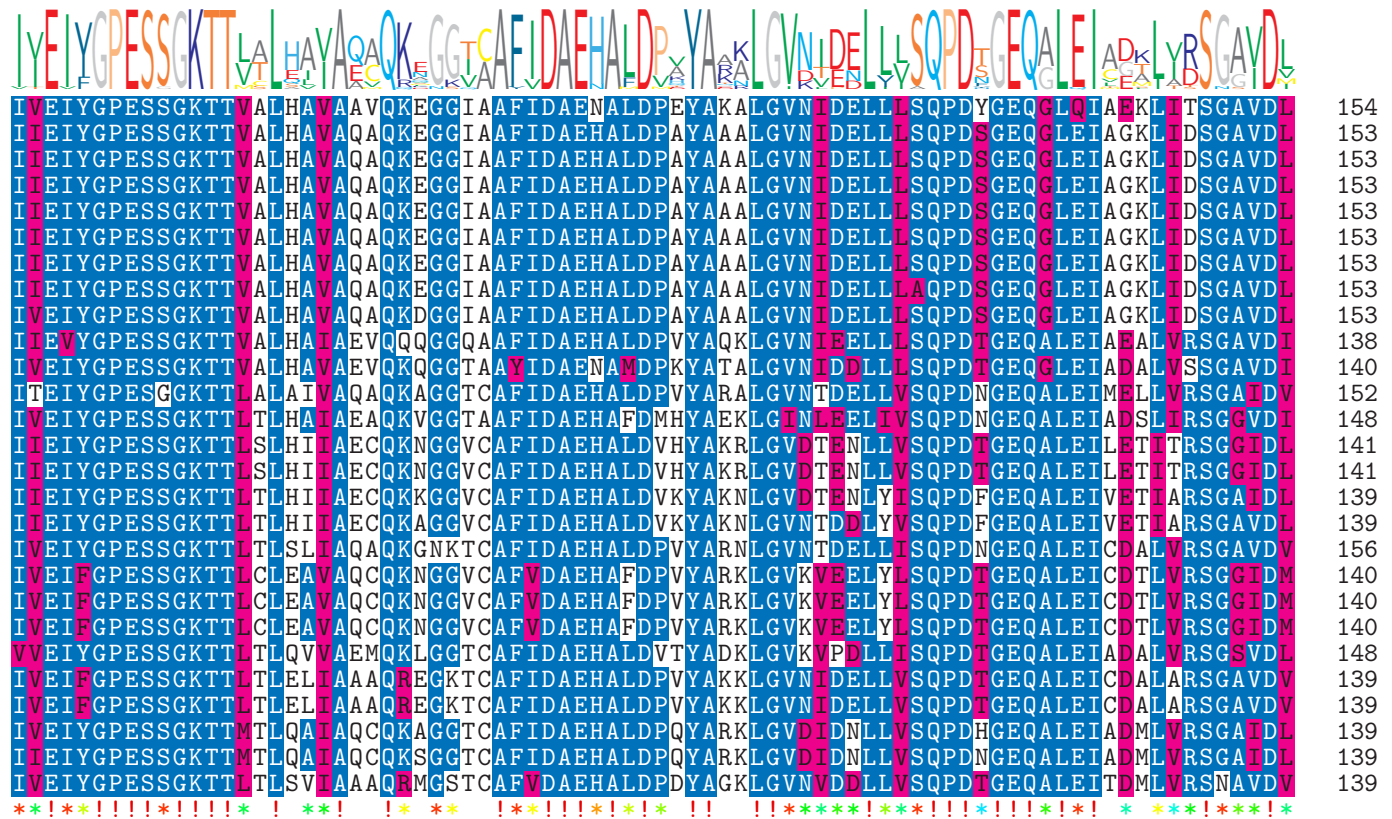


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NTDB id 1074 ABD1 RS10195 WP 000344167.1	SVRLDIR	RIGQ....	V.KEG	DEIIG	SETKV	IKVVKNK	MAPPF	REAI	FQILY	GKGV	NQLG	ELVD	LAV	QQN	I	V	QKAGAW	SYQ	293									
NTDB id 1205 PSJM300 05545 AFN77183.1	SVRLDIR	RTGA....	V.KEG	DEVVG	SETRV	IKVVKNKV	VAPPFR	QAEFQI	LYGK	GIYR	NGEI	IIDL	GV	QQG	L	V	EKS	GAWAYK	293									
consensus	*!!***!*													* ** *****!*****!*****!*					* *****!*!***** ***** *					***** ! !*****!				

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consensus

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Sequence	Score
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DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EH ⁺ PE ⁺ IF ⁺ DE ⁺ ID ⁺ KQ ⁺ VR ⁺ VQF ⁺ CL ⁺ IDGEEIAES....KKDE....AAQVDS..VNEEVPLDLGDELEIE	381
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GEKIGQGS ⁺ ENAK ⁺ RYLAD ⁺ HP ⁺ QL ⁺ IF ⁺ DE ⁺ ID ⁺ RK ⁺ VR ⁺ VKF ⁺ CL ⁺ LEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGS ⁺ ENAK ⁺ KFLAD ⁺ NPE ⁺ IF ⁺ DD ⁺ ID ⁺ DH ⁺ KV ⁺ RV ⁺ VQY ⁺ CL ⁺ IEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EE ⁺ RL ⁺ LGQGR ⁺ ENAK ⁺ QFL ⁺ KEN ⁺ KD ⁺ IM ⁺ LM ⁺ IQE ⁺ QIRE ⁺ HY ⁺ CL ⁺ DNNGVVQQQA ⁺ EETQEEL.EFE.E.....	348
SERIGQGRENAK ⁺ NYLAD ⁺ HED ⁺ VED ⁺ EV ⁺ RL ⁺ KV ⁺ RAAY ⁺ CT ⁺ SDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGQGREK ⁺ TIAYIA ⁺ ER ⁺ PE ⁺ ME ⁺ QE ⁺ IED ⁺ RV ⁺ MAAIRAGNAGEAPALAPAPAAPEAAAA.....	363
DTKL ⁺ GGQGRD ⁺ TV ⁺ KE ⁺ L ⁺ IK ⁺ DN ⁺ PE ⁺ LA ⁺ EE ⁺ L ⁺ AK ⁺ IRE ⁺ KLQAK.....	343
DKKL ⁺ GGQGR ⁺ ENAK ⁺ ALL ⁺ KED ⁺ KALADE ⁺ ITL ⁺ KIKES ⁺ IGS ⁺ NEEI....MPLPDEPLEEME.....	347
DKKL ⁺ GGQGR ⁺ ENAK ⁺ ALL ⁺ KED ⁺ KALADE ⁺ ITL ⁺ KIKES ⁺ IGS ⁺ NEEI....MPLPDEPLEEME.....	347
ASKL ⁺ GGQGR ⁺ ENAK ⁺ AF ⁺ LKEN ⁺ PTIA ⁺ DE ⁺ ITQAI ⁺ QNS ⁺ IGT ⁺ DNVI....LGSKDDEEGEE.....	344
DKKL ⁺ GGQGR ⁺ ENAK ⁺ AF ⁺ LKEN ⁺ PEIA ⁺ DE ⁺ ITKAI ⁺ QNS ⁺ MG ⁺ IEGMI....SGSEDDEGEE.....	343
GTKIGQGK ⁺ NNAV ⁺ KVLKEN ⁺ PEIA ⁺ DK ⁺ KL ⁺ BE ⁺ QIR ⁺ NTLA ⁺ SNPNS....VLKATASDSNDESD..VEEFSEEEEL.....	372
GAKIGQGK ⁺ DNVR ⁺ VWLKEN ⁺ PEIS ⁺ DE ⁺ ID ⁺ AK ⁺ IRAL ⁺ NGVEMHI....TEGTQDET ⁺ DGER.....PEE.....	348
GAKIGQGK ⁺ DNVR ⁺ VWLKEN ⁺ PEIS ⁺ DE ⁺ ID ⁺ AK ⁺ IRAL ⁺ NGVEMHI....TEGTQDET ⁺ DGER.....PEE.....	348
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GE ⁺ RIGQGRD ⁺ NCREF ⁺ LRENA ⁺ EL ⁺ ARE ⁺ IE ⁺ NK ⁺ VR ⁺ EHL ⁺ CVTPMG....AVTLA.EEVEED.....	352
GDKIGQGK ⁺ ANACK ⁺ YLKEN ⁺ PEIA ⁺ AK ⁺ TL ⁺ DKK ⁺ IRE ⁺ MLLNPENM....QLIAETSSAADDVE..FGAVPEEF.....	354
GD ⁺ KIGQGK ⁺ ANACK ⁺ YLKEN ⁺ PEIA ⁺ AK ⁺ TL ⁺ DKK ⁺ IRE ⁺ MLLNPENM....QLIAETSSAADDVE..FGAVPEEF.....	354
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GNKIGQGK ⁺ NNVIR ⁺ YLEEN ⁺ PQIA ⁺ EIE ⁺ ERNIRE ⁺ QLLT ⁺ TGTN....GAVQ.I.EDEEEPD..LL..LES.....	349
GSKIGQGK ⁺ ANAACK ⁺ YLEEN ⁺ PIG ⁺ QIE ⁺ EQQIR ⁺ AKLL ⁺ YTSAN....TKATPVAEDLADAD..I.....	347

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NTDB id 1022 ACIAD RS06390 WP 004925639.1	...		349
NTDB id 1074 ABD1 RS10195 WP 000344167.1	...		349
NTDB id 1205 PSJM300 05545 AFN77183.1	...		347
consensus			

- X non conserved
- X similar
- X ≥ 50% conserved