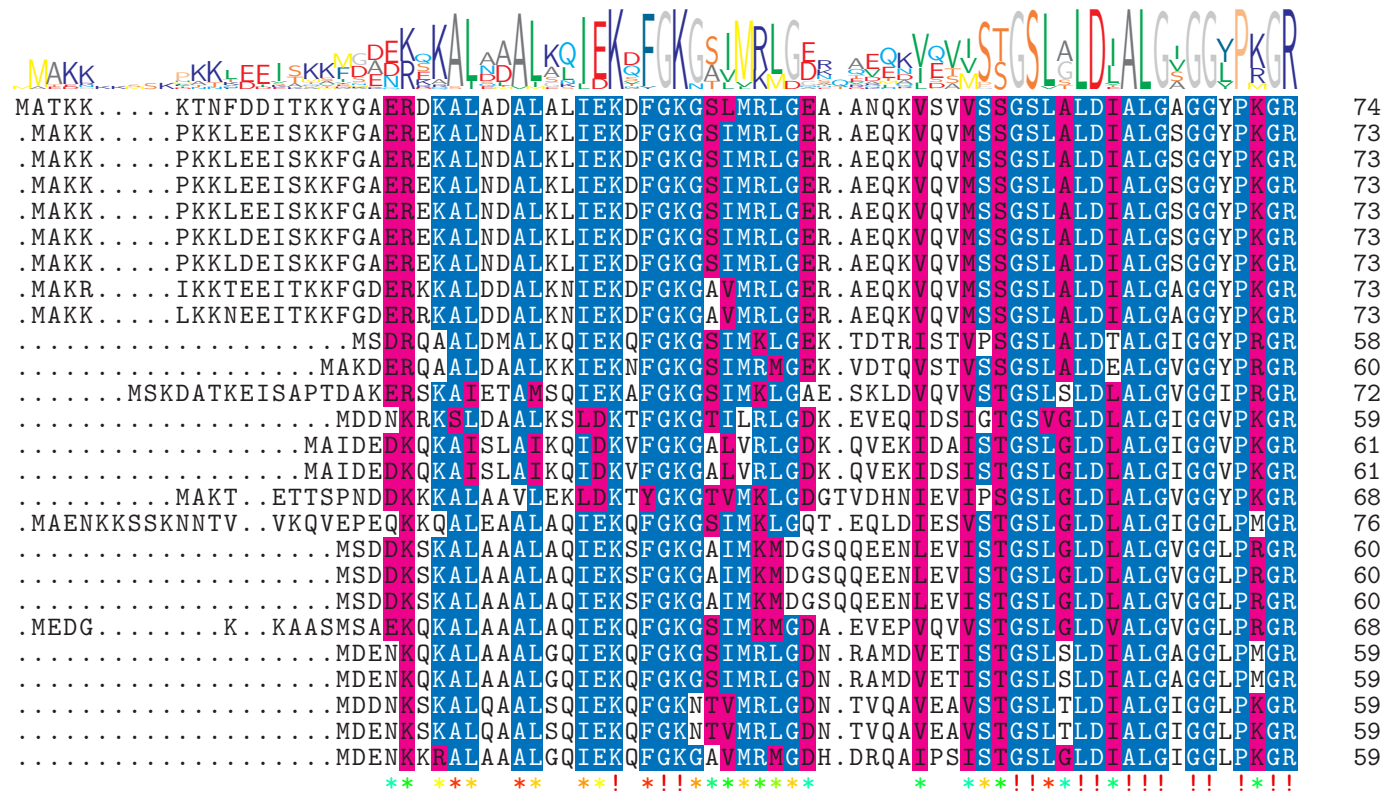


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consensus

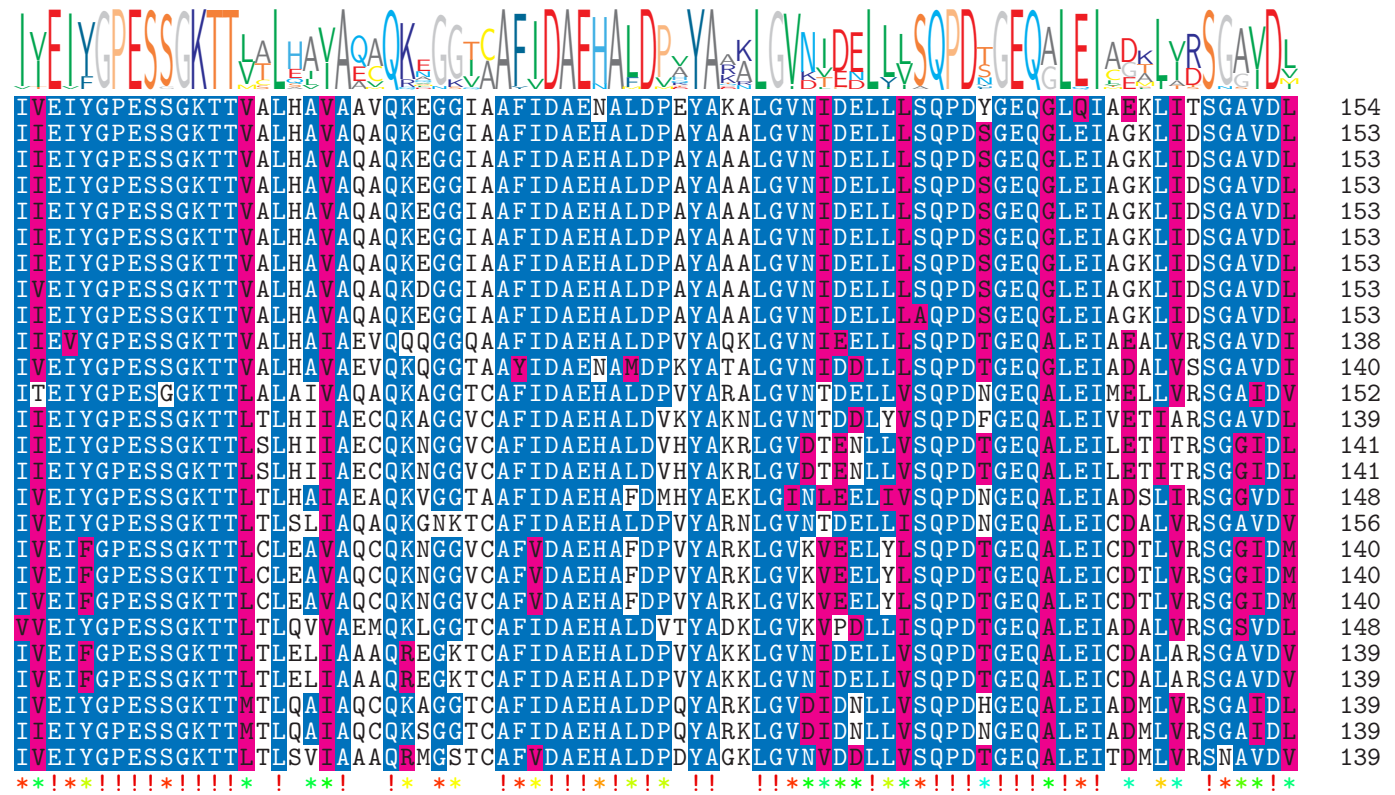
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consensus

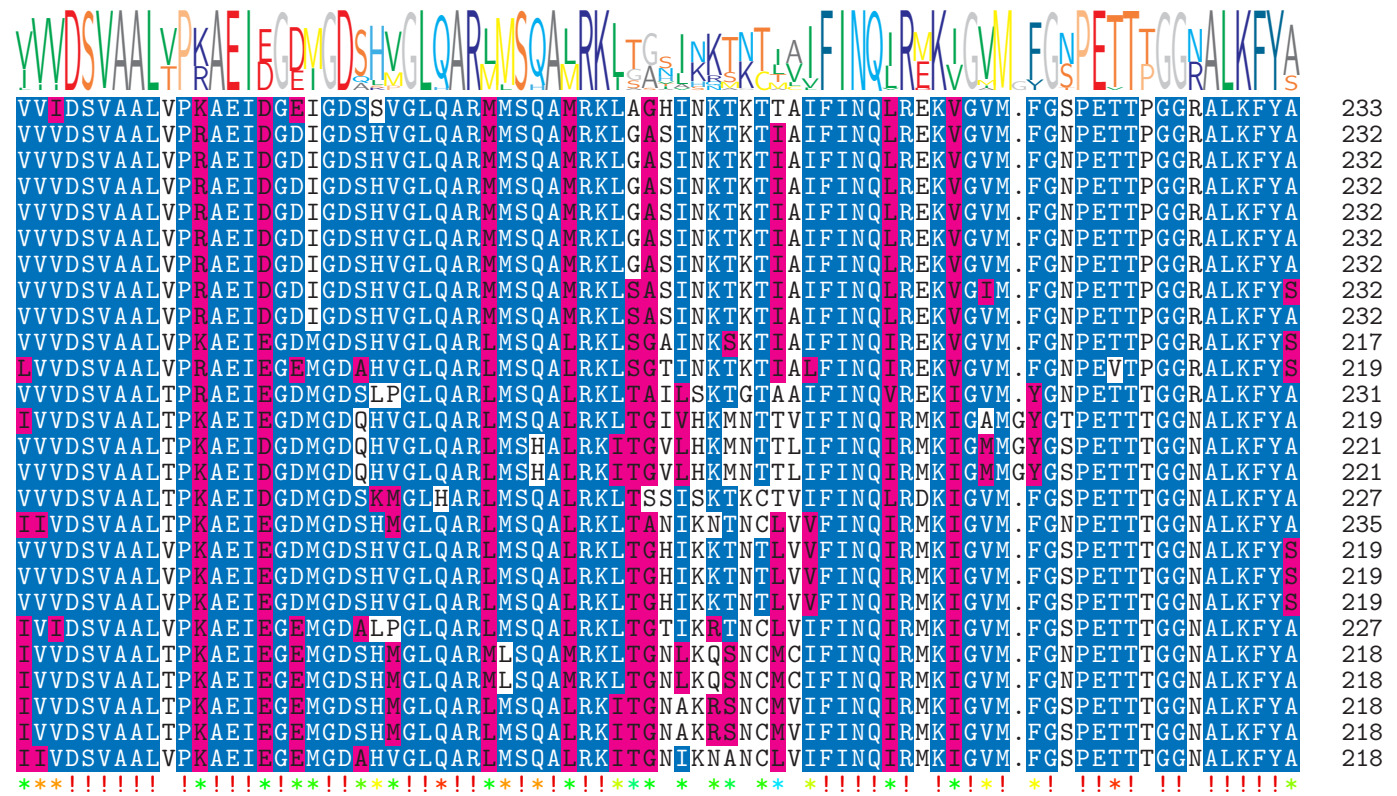
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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NTDB id 1389 A4U84 RS07560 WP 021112712.1	SVRLDIR	RCGV....	V.KDG	DEI	IGSET	KVKVVKNKVAPPF	REVQF	DIMY	GEGIS	RMNELL	ILAE	ANGF	I	KKSG	AW	FSYD	310									
NTDB id 1130 NGFG RS03960 WP 003688695.1	SVRLDIR	RTGS....	I.KKG	EEV	LGNET	RVKVI	KNKVAPPF	RQAEF	DILY	GEGIS	WE	GELID	IGV	KNDI	INKSG	AW	YSYN	294								
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NTDB id 1427 RS RS02760 WP 011000510.1	SVRLDIR	RIGS....	I.KKG	DEV	VGNET	KVKVVKNKVAPPF	REAI	FDILY	GAGV	S	REGE	ITDL	GV	EAKV	VVEK	SG	AWYSYN	302								
NTDB id 1165 A1552VC RS01565 WP 000344154.1	SVRLDIR	RTGA....	I.KEG	EEV	VGNET	RIKVVKNK	IAAPF	KEANTQ	IMY	QG	GFNR	EGEL	IDL	GVKHK	MVEK	SG	AWYSYN	293								
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	SVRLDIR	RIGQ....	V.KEG	DEI	VGSET	KVKVVKNK	MAPPF	KEAI	FQILY	GKGT	NQL	GEL	VDL	AVQQ	DIV	QK	AGAW	YSYQ	293							
NTDB id 1205 PSJM300 05545 AFN77183.1	SVRLDIR	RTGA....	V.KEG	DEV	VGS	ETRVKVVKNKVAPPF	RQAEF	QILY	GKGI	YRN	GE	ITDL	GV	QQGL	VEK	SG	AWY	AYK	293							
consensus	*!!***!* *														* ** ***!***!!*!!*!!* * *				*****!***!*** ***** **				***** ! !*****!			

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consensus

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Sequence	Score
DEKIGQGA ¹ E ² KA ³ KN ⁴ YL ⁵ KE ⁶ HQ ⁷ DV ⁸ F ⁹ DE ¹⁰ ID ¹¹ HK ¹² V ¹³ RA ¹⁴ AH ¹⁵ GI ¹⁶ LDDSEVAETEETTASKTKAKAKKEEKAVETEEIELELED....	387
DEKIGQGS ¹ EN ² AK ³ KYL ⁴ AE ⁵ HP ⁶ EIF ⁷ DE ⁸ ID ⁹ DK ¹⁰ QV ¹¹ RS ¹² KF ¹³ GLIDGEEVSEQD ¹⁴ TEN ¹⁵ KKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ EN ² AK ³ KYL ⁴ AE ⁵ HP ⁶ EIF ⁷ DE ⁸ ID ⁹ DK ¹⁰ QV ¹¹ RS ¹² KF ¹³ GLIDGEEVSEQD ¹⁴ TEN ¹⁵ KKDE...PKKEEA..VNEEVPLDLGDELEIE	385
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DEKIGQGS ¹ EN ² AK ³ KYL ⁴ AD ⁵ NPE ⁶ VFAE ⁷ ID ⁸ HQ ⁹ V ¹⁰ VQ ¹¹ F ¹² GLIDGEEAAE...SKKDE...VAQVDS..VNEEVTLDLGDELEIE	381
DEKIGQGS ¹ EN ² AK ³ KYL ⁴ AD ⁵ NPE ⁶ VFAE ⁷ ID ⁸ HQ ⁹ V ¹⁰ VQ ¹¹ F ¹² GLIDGEEIAE...SKKDE...AAQVDS..VNEEVTLDLGDELEIE	381
GEKIGQGS ¹ EN ² AK ³ KFL ⁴ AD ⁵ NPE ⁶ IFDD ⁷ ID ⁸ HK ⁹ V ¹⁰ VQ ¹¹ Y ¹² CLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIEIE	382
GEKIGQGS ¹ EN ² AK ³ KRYL ⁴ AD ⁵ HP ⁶ Q ⁷ LFDE ⁸ ID ⁹ DK ¹⁰ V ¹¹ VK ¹² F ¹³ GLLEESEEEESAMAVASE.....E.....TDDLALDLNNGIEIE	377
EER ¹ LGGGREN ² AK ³ FL ⁴ KEN ⁵ KD ⁶ I ⁷ ML ⁸ MI ⁹ Q ¹⁰ IRE ¹¹ HY ¹² CLDNNGVVQQQAETQEEL.EFE.E.....	348
SERIGQGR ¹ EN ² AK ³ NYL ⁴ AD ⁵ HED ⁶ VE ⁷ DEV ⁸ LR ⁹ KV ¹⁰ RAAY ¹¹ GISDVPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
DERIGQGE ¹ K ² E ³ KT ⁴ IAY ⁵ I ⁶ AER ⁷ PEME ⁸ Q ⁹ EIRDRVMAAIRAGNAGEAPALAPAPAAPEAAE..A.....	363
DKKLGGGREN ¹ SKA ² FL ³ KEN ⁴ PEI ⁵ AD ⁶ EIT ⁷ KAI ⁸ QNSM ⁹ GTIEGMI....SGSEDD..EGE..E.....	343
DKKLGGGREN ¹ AK ² ALL ³ KED ⁴ KAL ⁵ AD ⁶ EIT ⁷ LK ⁸ IKES ⁹ GSNEEI....MPLPDE..PLE..EME.....	347
DKKLGGGREN ¹ AK ² ALL ³ KED ⁴ KAL ⁵ AD ⁶ EIT ⁷ LK ⁸ IKES ⁹ GSNEEI....MPLPDE..PLE..EME.....	347
DTKLGGGRD ¹ TV ² KE ³ L ⁴ IKD ⁵ NPE ⁶ LAEE ⁷ LEAK ⁸ IREKLQAK.....	343
GTKIGQGK ¹ NNAV ² KWL ³ KEN ⁴ PEI ⁵ AD ⁶ KL ⁷ EQ ⁸ IRNTLASNPNS.....VLKATASDSND..ESDVEEFSEEEL.....	372
GAKIGQGK ¹ KDN ² VR ³ VWL ⁴ KEN ⁵ PEI ⁶ SDEI ⁷ DAK ⁸ IRALN ⁹ GVEMHI....TEGTQDET ¹⁰ DGE..R.....PEE.....	348
GAKIGQGK ¹ KDN ² VR ³ VWL ⁴ KEN ⁵ PEI ⁶ SDEI ⁷ DAK ⁸ IRALN ⁹ GVEMHI....TEGTQDET ¹⁰ DGE..R.....PEE.....	348
GAKIGQGK ¹ KDN ² VR ³ VWL ⁴ KEN ⁵ PEI ⁶ SDEI ⁷ DAK ⁸ IRALN ⁹ GVEMHI....TEGTQDET ¹⁰ DGE..R.....PEE.....	348
GERIGQGRD ¹ NCRE ² FL ³ RENAE ⁴ LARE ⁵ EN ⁶ KV ⁷ REHL ⁸ GVTPMG.....AVTLA.EEEVE..D.....	352
GDKIGQGK ¹ ANACK ² YL ³ KEN ⁴ PEI ⁵ AKT ⁶ LD ⁷ KKL ⁸ REMLLN ⁹ PNEM....QLIAETSSAAD..DVEFGAVPEEF.....	354
GDKIGQGK ¹ ANACK ² YL ³ KEN ⁴ PEI ⁵ AKT ⁶ LD ⁷ KKL ⁸ REMLLN ⁹ PNEM....QLIAETSSAAD..DVEFGAVPEEF.....	354
GNKIGQGK ¹ NNVIR ² YLEEN ³ PQISTE ⁴ IEAVIREQLLTKASD....QTAA.HDETEE..EPDLL..ES.....	349
GNKIGQGK ¹ NNVIR ² YFEENN ³ QIAEEIERNIREQLLTGTN....GAVQ.I.EDEE..EPDLL..LES.....	349
GSKIGQGK ¹ ANAAK ² YLEEN ³ PEI ⁴ GQEIEQQIRAKLLVTSAN....TKATPVAEDLA..DADI.....	347

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NTDB id 194 SPR RS08825 WP 001085462.1	IEE	388
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NTDB id 499 SM12261 RS08315 WP 078228268.1	IEE	384
NTDB id 408 SMU RS09530 WP 002262392.1	D..	383
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consensus

 non conserved
 similar
 ≥ 50% conserved