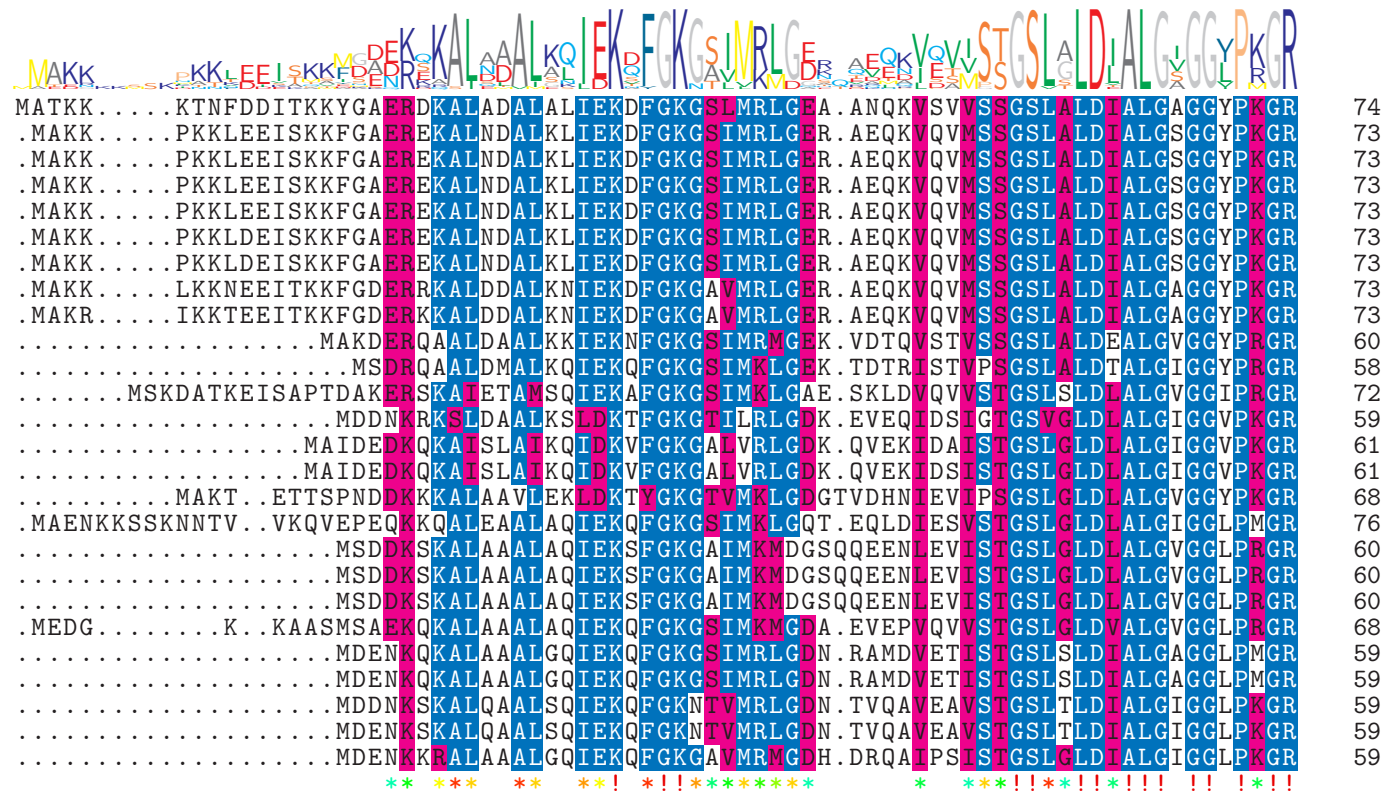
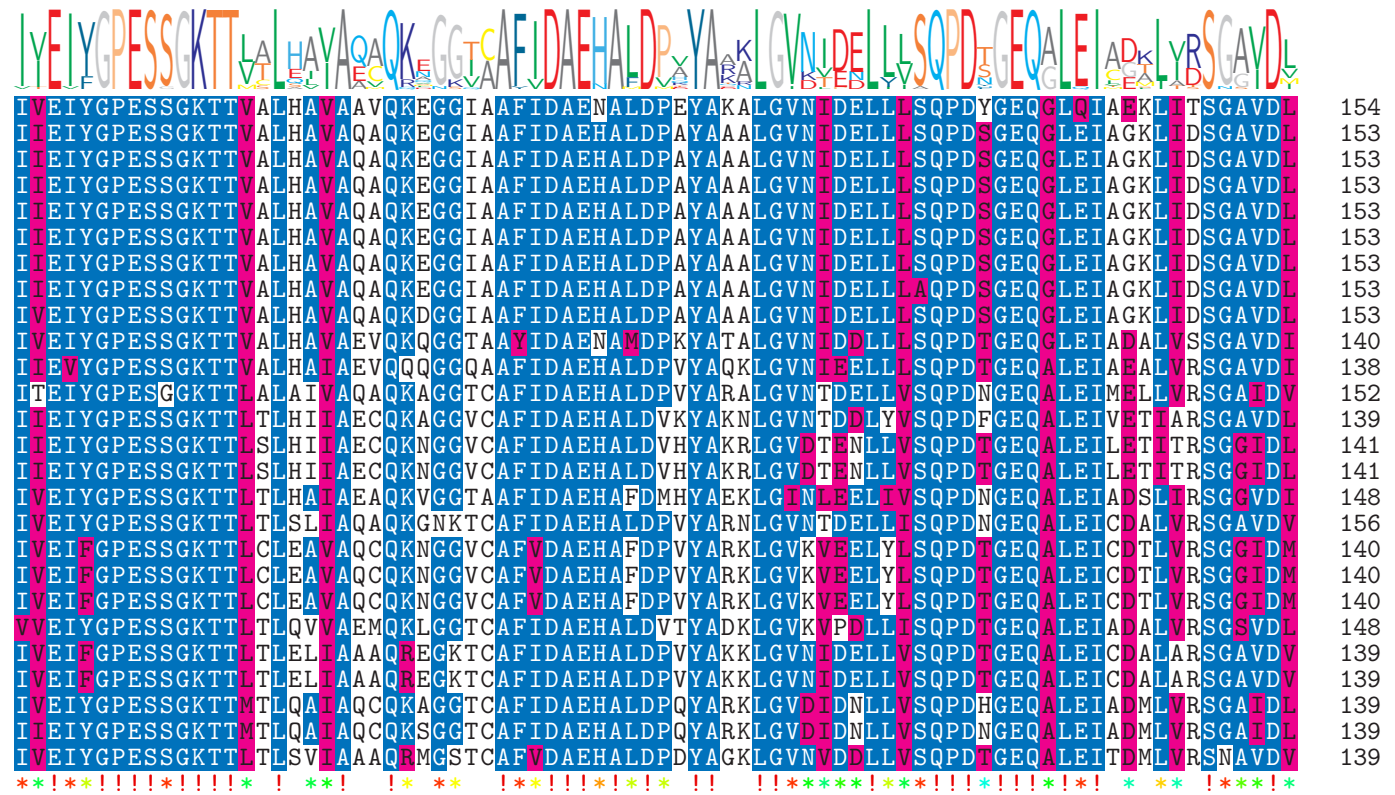


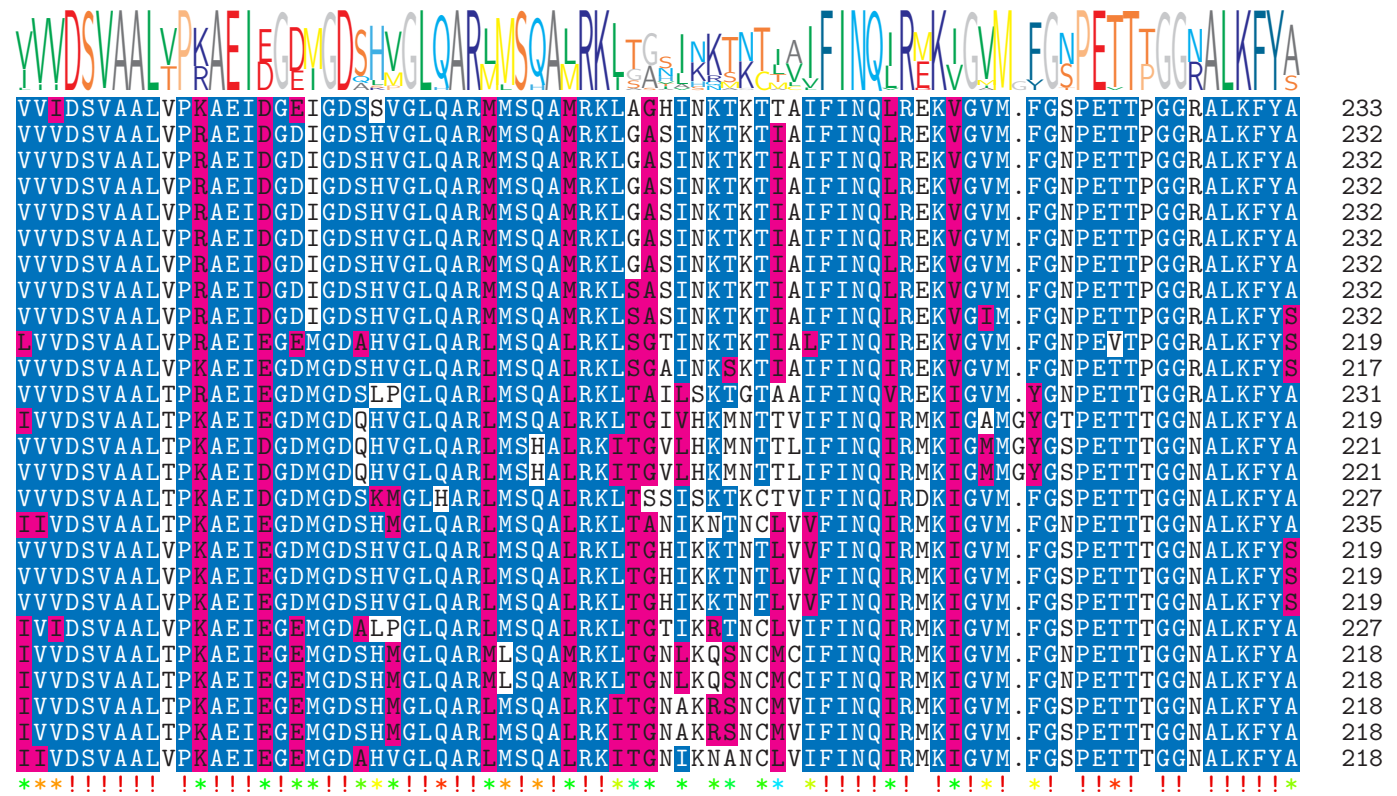
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consensus



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NTDB id 600 KW2 RS01765 WP 011675413.1	SVRLDVRG	STKIEEGS	.GDNKTQ	IGKITK	IKVVKNKVAPPF	KVALV	DIMF	GEGIS	STGEL	INIAVEEG	ITKK	SGAW	FAYN	312						
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NTDB id 194 SPR RS08825 WP 001085462.1	SVRLDVRG	NTQIKGTG	.DQKETN	VGKETK	IKVVKNKVAPPF	KEAVV	EIMY	GEGIS	KTGEL	LKIASDL	DIKK	KAGAW	YSYK	311						
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NTDB id 453 Spy49 1753c ACI62003.1	SVRLDVRG	TQTQIKGTG	.DQKDS	IGKETK	IKVVKNKVAPPF	KVAEV	EIMY	GEGIS	RTGEL	VKIASDL	DIQK	KAGAW	FSYN	311						
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NTDB id 115 BSU 16940 NP 389576.2	SVRLEV	RRRAEQLK	QGN....DV	MGNKTKI	IKVVKNKVAPPF	RTAEV	DIMY	GEGIS	KEGE	IIDL	LGTEL	DIVQ	KSG	SWYSYE	292					
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NTDB id 1211 C694 RS00795 WP 000963128.1	SVRIDIR	RIAS....L	KQNEQH	IGNRAKA	VVVKNKVAPPF	REAEF	DIMF	GEGIS	KEGE	IIDL	GVKL	DIV	DKSG	AW	LSYQ	296				
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NTDB id 1130 NGFG RS03960 WP 003688695.1	SVRLDIR	RTGS....I	KKGE	EV	LGNETRV	KVIKNKVAPPF	RQAEF	DILY	GEGIS	WEGEL	ID	IGVKN	DI	INKSG	AW	SYN	294			
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NTDB id 1123 OK783 RS03845 WP 003688695.1	SVRLDIR	RTGS....I	KKGE	EV	LGNETRV	KVIKNKVAPPF	RQAEF	DILY	GEGIS	WEGEL	ID	IGVKN	DI	INKSG	AW	SYN	294			
NTDB id 1427 RS RS02760 WP 011000510.1	SVRLDIR	RIGS....I	KKGDEV	VGNETKV	VVVKNKVAPPF	REAI	FIDILY	GAGV	SREGE	IIDL	GV	EAKV	VVEK	SG	AW	SYN	302			
NTDB id 1165 A1552VC RS01565 WP 000344154.1	SVRLDIR	RTGA....I	KEGE	EV	VGNETRI	KVVKNKIA	APFKE	ANTQ	IMY	QG	GFN	REGEL	ID	LG	VKHK	MVEK	SG	AW	SYN	293
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NTDB id 1022 ACIAD RS06390 WP 004925639.1	SVRLDIR	RIGQ....V	KEGDEI	IGSETKV	VVVKNKMAPPF	REAI	FQILY	GKGV	NQLGEL	VDLAV	QQN	IV	QK	AG	AW	SYQ	293			
NTDB id 1074 ABD1 RS10195 WP 000344167.1	SVRLDIR	RIGQ....V	KEGDEI	VGSETKV	VVVKNKMAPPF	KEAI	FQILY	GKGT	NQLGEL	VDLAV	QQD	IV	QK	AG	AW	SYQ	293			
NTDB id 1205 PSJM300 05545 AFN77183.1	SVRLDIR	RTGA....V	KEGDEV	VGS	ETKV	VVVKNKVAPPF	RQAEF	QILY	GKGI	YRNGE	IIDL	GV	QQGL	V	EK	SG	AW	YAYK	293	
consensus	*!!***!*														*	**	*****!			


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Sequence	Score
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DEKIGQGS E NA K KYLA E HP E IF F DEID K QVRSK F GLIDGEEVSEQD T ENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
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DEKIGQGS E NA K KYLA D NPEIF F DEID H QVRSVQ F GLIDGEEIAES....KKDE....AAQVDS..VNEEVTLDLGDELEIE	381
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GEKIGQGS E NA K RYLADHP Q L F DEID R KVRVK F GLLEESEESAMAVASE.....E.....TDDLALDLNNGIEIE	377
GEKIGQGS E NA K KFLADNPEIF D DDID H KVRVQY C LIEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
SERIGQG R ENAKNYLADH D VE D EVRLK V RAAY G ISDVPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
EERLGGGREN A K F LKENK D IM L MIQ E IREHY G LDNNGVVQQQAETQEEL.EFE.E.....	348
DERIGQG E K T IAYIA E RPEME Q EIRDRVMAAIRAGNAGEAPALAPAPAAPEAAE..A.....	363
DKKLGGGREN S KA F LKENPEIA D EITKAIQNSM G TEGMI....SGSEDD..EGE..E.....	343
DKKLGGGREN A KALLKEDKALADEITLKIKESIGSNEEI....MPLPDE..PLE..EME.....	347
DKKLGGGREN A KALLKEDKALADEITLKIKESIGSNEEI....MPLPDE..PLE..EME.....	347
DTKLGGGRD T V K ELIK D NPEIA E ELEAKIREKLQAK.....	343
GTKIGQGK N NAV K WLKENPEIA D AKLEIQEI R NTLASNPNS.....VLKATASDSND..ESDVEEFSEEEEL.....	372
GAKIGQGK D NVRVWLKENPEIS D EIDAKIRALNGVEMHI....TEGTQDET D GDE..R.....PEE.....	348
GAKIGQGK D NVRVWLKENPEIS D EIDAKIRALNGVEMHI....TEGTQDET D GDE..R.....PEE.....	348
GAKIGQGK D NVRVWLKENPEIS D EIDAKIRALNGVEMHI....TEGTQDET D GDE..R.....PEE.....	348
GERIGQGRD N CREFLREN A ELAREIENKVR E HLGVTPMG....AVTLA.EEEVE..D.....	352
GDKIGQGK A NA C KYLKENPEIA K TLDKKLREMLLNPNEM....QLIAETSSAAD..DVEFGAVPEEF.....	354
GDKIGQGK A NA C KYLKENPEIA K TLDKKLREMLLNPNEM....QLIAETSSAAD..DVEFGAVPEEF.....	354
GNKIGQGK N NVIRYLEEN P QISTEIEAVIREQLLTKASD....QTAA.HDETEE..EPDLL..ES.....	349
GNKIGQGK N NVIRYFEEN N QIAEIEIRNIREQLLTTGTN....GAVQ.I.EDEE..EPDLL..LES.....	349
GSKIGQGK A NA A KYLEENPEI G QIEQQIRAKLLVTSAN....TKATPVAEDLA..DADI.....	347

logo

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NTDB id 269 KZH43 RS08665 WP 001085462.1	IEE	388
NTDB id 228 SPD RS09265 WP 001085462.1	IEE	388
NTDB id 194 SPR RS08825 WP 001085462.1	IEE	388
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NTDB id 499 SM12261 RS08315 WP 078228268.1	IEE	384
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consensus

 non conserved
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 ≥ 50% conserved