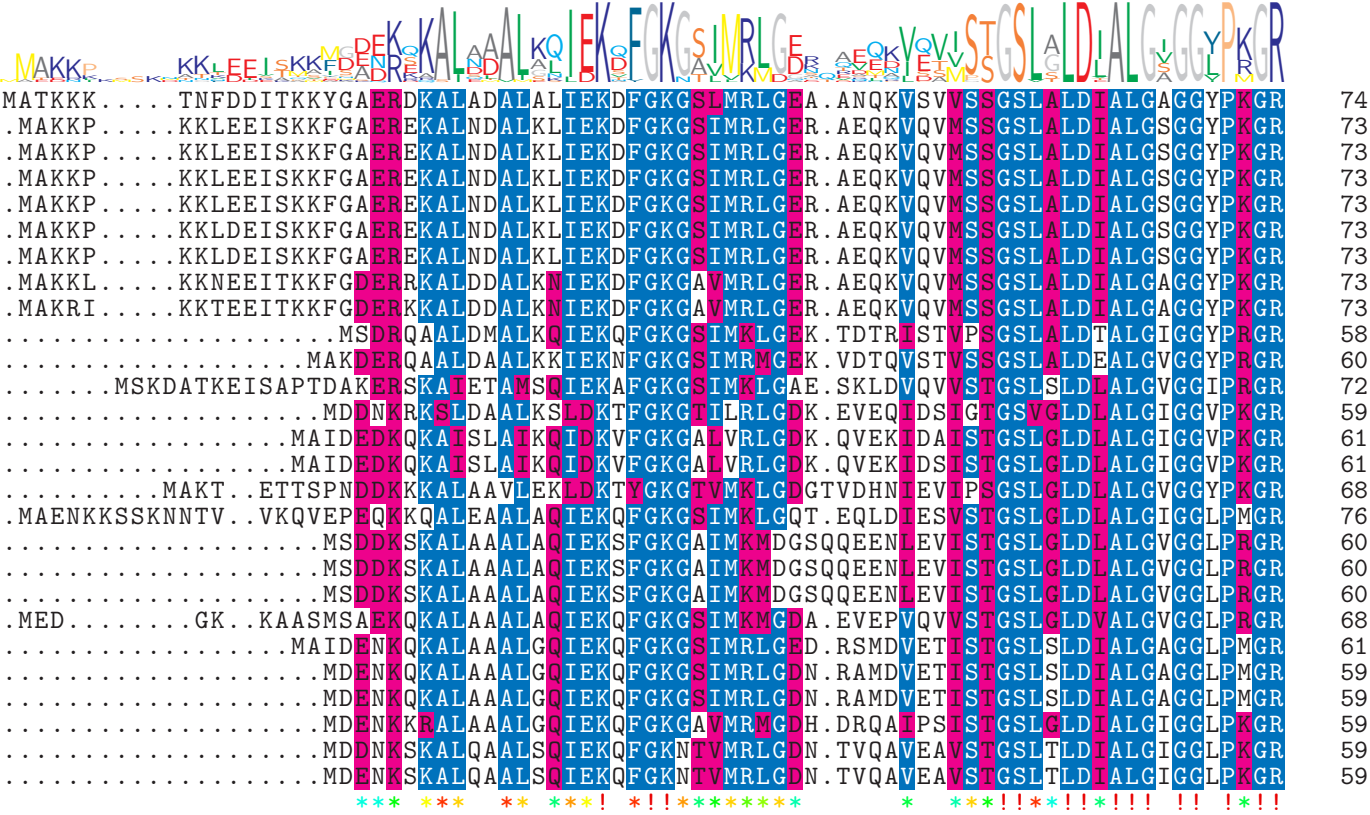


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NTDB id 159 SP RS09750 WP 001085462.1
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus



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consensus

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logo

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NTDB id 228 SPD RS09265 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPFKAEAVVEIMYEGEGISKTGELLKIASDL	D	IIKKAGAWYSYK	311						
NTDB id 194 SPR RS08825 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPFKAEAVVEIMYEGEGISKTGELLKIASDL	D	IIKKAGAWYSYK	311						
NTDB id 159 SP RS09750 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPFKAEAVVEIMYEGEGISKTGELLKIASDL	D	IIKKAGAWYSYK	311						
NTDB id 527 SMSK321 RS11065 WP 001085454.1	SVRLDVRGSTQIKGTG.DQKDTN	VGKETKIKVVKNKVAPPFKAEAFVEIMYEGEGISKTGELLKIASDL	D	IIKKAGAWYSYK	311						
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NTDB id 1313 DR RS12030 WP 010888966.1	SVRLDVRKIGQ....PTKVGND	AVANTVKIKTVKNKVAAPFKEVELALVYGKGF	QDLS	DLVGLAADMDI	IKKAGSFYSYG	307					
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NTDB id 1334 RAOC RS04870 WP 004918236.1	SVRIDIRRLSDTGKIKDKSGEV	IGNRTKVVKNKVAPPFKSA	AEFDIMYEGEGVSKVGEILD	VAT	DL	DI	IQKSGSWFSYQ	307			
NTDB id 1389 A4U84 RS07560 WP 021112712.1	SVRLDIRRCGV....V.KDGDEI	IGSETKVVKNKVAPPFR	EV	QFDIMYEGEGISRMNELL	ILAEANGFI	KKSGAWFSYD	310				
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NTDB id 362776 FD428 RS04900 WP 012134806.1	SVRLDIRRIGA....V.KEGENV	VGSETRVKVVKNKIAAPFKQAEFQ	ILYGE	GINFY	GELVD	LG	VKEK	LI	EKAGAWYSYN	295	
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NTDB id 1022 ACIAD RS06390 WP 004925639.1	SVRLDIRRIGQ....V.KEGDEI	IGSETKVVKNKMAPPFR	EA	IFQILYGKGV	NQLGELVD	LAV	QQ	N	I	VQKAGAWYSYQ	293
NTDB id 1074 ABD1 RS10195 WP 000344167.1	SVRLDIRRIGQ....V.KEGDEI	VGSETKVVKNKMAPPFK	EA	IFQILYGKGT	NQLGELVD	LAV	QQ	D	I	VQKAGAWYSYQ	293
consensus	*!!**!* *	*	**	*****!*****!!*!!*!!* *	*****!!*!!*!!* ***** *	***** !!*****!	***** !!*****!				

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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
DEKIGQGA ⁺ AKAK ⁺ NYLKEHQ ⁺ DV ⁺ FDEIDHKV ⁺ RAAH ⁺ GLDDSEVAETEEETTAS ⁺ KTAKAK ⁺ KE ⁺ FAVETEEIELELED	387
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPEIF ⁺ DEIDKQ ⁺ VR ⁺ SKFGLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPEIF ⁺ DEIDKQ ⁺ VR ⁺ SKFGLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPEIF ⁺ DEIDKQ ⁺ VR ⁺ SKFGLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ DNPEVFA ⁺ EIDH ⁺ QVRVQFGLIDGEEAAE . . . SKKDE . . . VAQVDS . VNEEVTLDLGDLEIE	381
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ DNPEIF ⁺ DEIDH ⁺ QVRVQFGLIDGEEIAE . . . SKKDE . . . AAQVDS . VNEEVTLDLGDLEIE	381
GEKIGQGS ⁺ ENAK ⁺ RYLADHPQLF ⁺ DEIDRK ⁺ VR ⁺ VKFLLEESEEEESAMAVASE E TDDLALDLNGIEIE	377
GEKIGQGS ⁺ ENAK ⁺ KFLADNPEIF ⁺ DDIDHK ⁺ VRVQYGLIEEDNTEEKQSSKEK ETDEK . ADKNLVLELDDTIELE	382
EERLGGGREN ⁺ AKQFLKENKDIMLMIQEQIREHYGLDNGGVVQQAEETQEEL.EFE.E	348
SERIGQGSREN ⁺ AKNYLADHEDVEDEVRLK ⁺ VR ⁺ AAYGISDVPEEDLPTTEDE.QI.NILPDDST EE	355
DERIGGQKEKTIA ⁺ YIAERPMEQEIRDRVMQAIRAGNAGEAPALAPAPAPEAA . . . EA	363
DKKLGQGSREN ⁺ SKAFLKENPEIAD ⁺ EITKAIQNSMGI ⁺ EGMI SGSEDD EGEE	343
DKKLGQGSREN ⁺ AKALLKEDKALADEITLKIKESIGSNEEI MPLPDE PLEEME	347
DKKLGQGSREN ⁺ AKALLKEDKALADEITLKIKESIGSNEEI MPLPDE PLEEME	347
DTKLGQGRD ⁺ TVKELIKDNPELAE ⁺ ELEAKIREKLQAK	343
GTKIGQGKNN ⁺ AVKVLKENPEIADKLEQEI ⁺ RNTLASNPNS VLKATASDSN . . . DESDVEEFSEEL	372
GAKIGGQKDN ⁺ VRVWLKENPEISDEIDAKIRALNGVEMHI TE GT . . . QDET ⁺ DGERPEE	348
GAKIGGQKDN ⁺ VRVWLKENPEISDEIDAKIRALNGVEMHI TE GT . . . QDET ⁺ DGERPEE	348
GAKIGGQKDN ⁺ VRVWLKENPEISDEIDAKIRALNGVEMHI TE GT . . . QDET ⁺ DGERPEE	348
GERIGQGRDN ⁺ CREFLRENAELAREIENK ⁺ VREHLGVTPMG AVTLA.EEVE . . . ED	352
GEKIGQGANATA ⁺ WLKENPATAKIEKKVRELLSNQDS TPDFSVDNN . . . GEGVKETNEDF	354
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPNEM QLIAETSSAA . . DDVEFGAVPEEF	354
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPNEM QLIAETSSAA . . DDVEFGAVPEEF	354
GSKIGGQKANA ⁺ AKYLEENPEIGQIEEQIRAKLLVTSAN TKATPVAEDL . . ADADI	347
GNKIGQGKNN ⁺ VIRYLEENPQISTEIEAVIREQLLTKASD QTAA.HDETE . . EEPDLLES	349
GNKIGQGKNN ⁺ VIRYLEENPQIAEIEIERNIREQLLTGTN GAVQ.I.EDE . . EEPDLLES	349

logo

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NTDB id 1022 ACIAD RS06390 WP 004925639.1	...	349
NTDB id 1074 ABD1 RS10195 WP 000344167.1	...	349

consensus

 non conserved
 similar
 ≥ 50% conserved