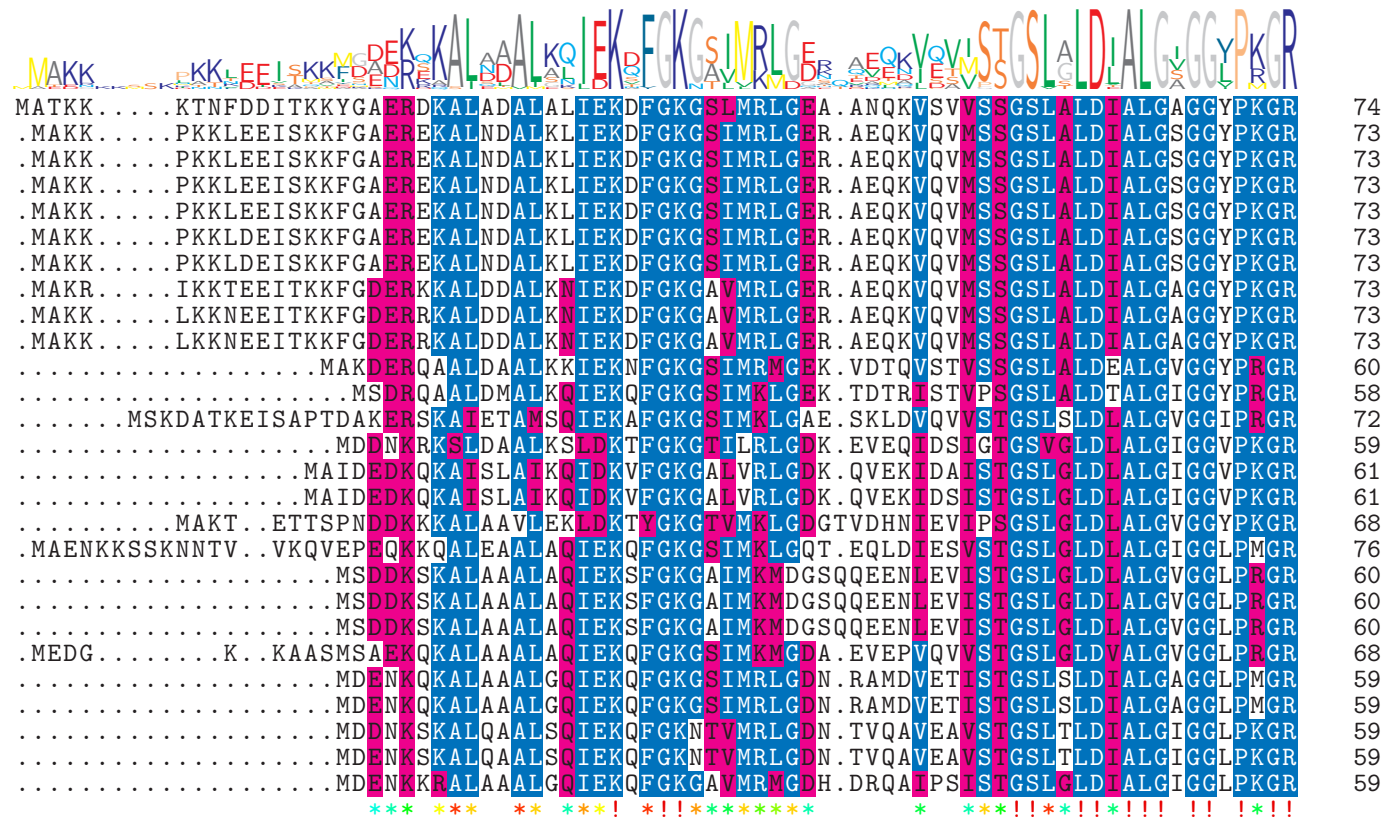


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consensus

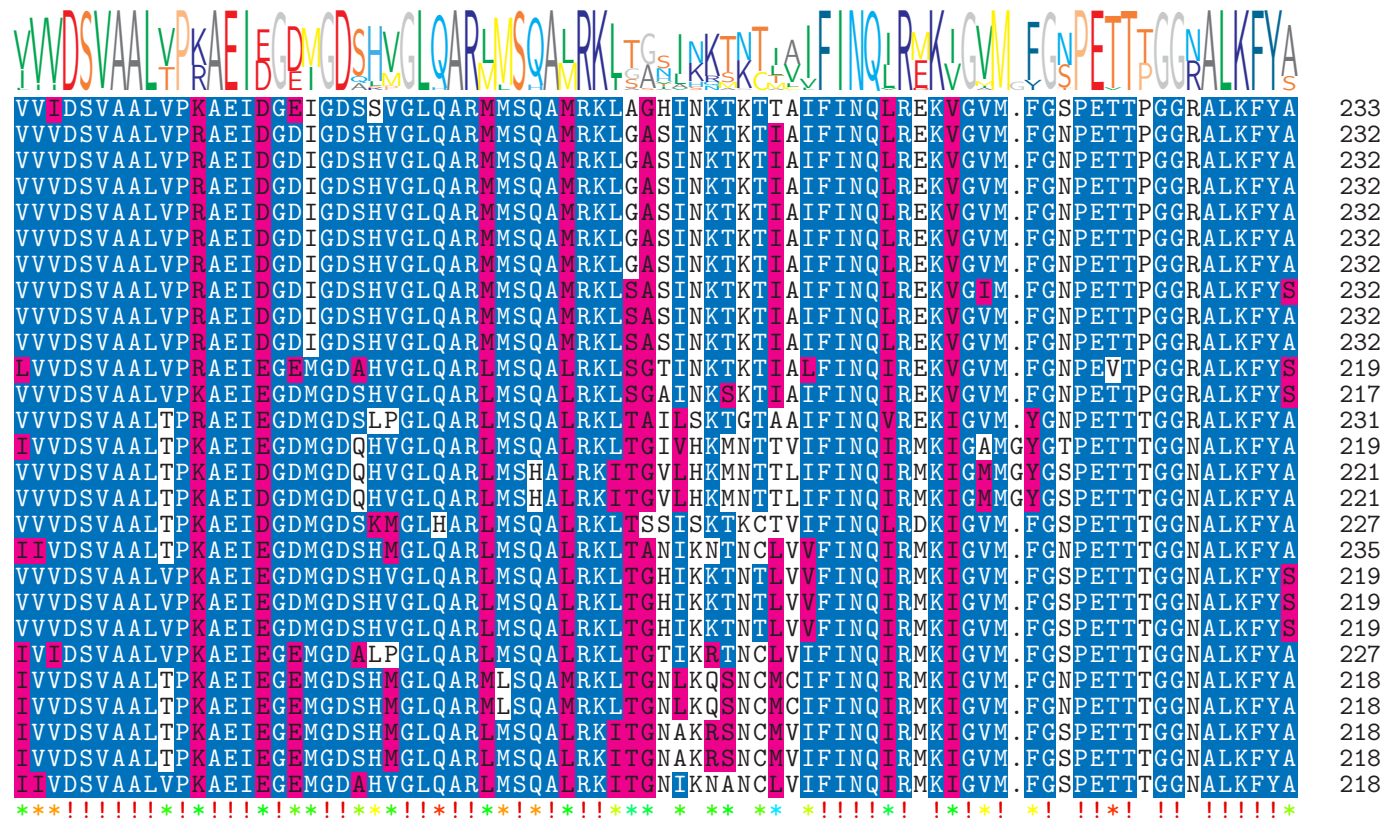
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consensus

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logo

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NTDB id 228 SPD RS09265 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPFKEA	AVVEIMYEGEGISKTGELL	KIASDLIIKKAGAWYSYK	311
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NTDB id 115 BSU 16940 NP 389576.2	SVRLEVRRAEQLKQGN.....DV	MGNKTKIKVVKNKVAPPFRTA	EAEDIMYEGEGISKEGEIT	IDLGTELDIIQKSGSWYSYE	292
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NTDB id 1211 C694 RS00795 WP 000963128.1	SVRIDIRRIAS....L.KQNEQH	IGNRAKAKVVKNKVAPPFRE	AEFDIMFGEGISKEGEIT	IDYGVKLDIVDKSGAWLSYQ	296
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NTDB id 1142 GTF74 RS11550 WP 000344154.1	SVRLDIRRTGA....I.KEGEEV	VGNETRIKVVKNKIAAPFKE	ANTQIMYGGGFNREGEL	IDLGVKHKMVEKSGAWYSYN	293
NTDB id 1022 ACIAD RS06390 WP 004925639.1	SVRLDIRRIGQ....V.KEGDEI	IGSETKVVKNKMAPPFRE	AIFFQILYGKGVNQLGEL	VDLAVQQNIVQKAGAWYSYQ	293
NTDB id 1074 ABD1 RS10195 WP 000344167.1	SVRLDIRRIGQ....V.KEGDEI	VGSETKVVKNKMAPPFKE	AIFFQILYGKGTNQLGEL	VDLAVQQDIVQKAGAWYSYQ	293
NTDB id 1205 PSJM300 05545 AFN77183.1	SVRLDIRRTGA....V.KEGDEV	VGSETRVVKNKVAPPFRQA	EFQILYGKGIYRNGEIT	DLGVQQGLVEKSGAWAYK	293
consensus	*!!**!* *	* ** *****!*****!*****!*	* *****!*!***** ***** *	***** ! !*****!	

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consensus

Sequence	Score
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GEKIGQGSSENAKKFLADNPEIFDDIDHKVRVQFGLIEEDNTEEKQSSKEKE...TDEK..ADKNLVLELDDTIELE	382
GEKIGQGSSENAKRYLADHPPELFEIDRKVRVKFGLLEESEEEESAMAVA.....AE..GTTDLVLDLDNNGIEIE	377
GEKIGQGSSENAKRYLADHPQLFEIDRKVRVKFGLLEESEEEESAMAVA.....SE..ETDDLALDLDNNGIEIE	377
SERIGQGRENAKNYLADHEDVEDEVRLKVRAAAGISDVPEEDLPTTEDE.QINI.....LPDDSTEE..	355
EERLGGGRENAKQFLKENDKIMLTIQEIQIREHYGLDNNGVVQQQAETQEELEF.....E.E.....	348
DERIGQGEKTIAYIAIERPEMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAA...EA.....	363
DKKLGGGRENKAFLENPEIADKITKAIQNSMGIEGMI.....SGSEDD..EG.....EE.....	343
DKKLGGGRENKALLKEDKALADEITLKIKESIGSNEEI...MPLPDE..PL.....EEME	347
DKKLGGGRENKALLKEDKALADEITLKIKESIGSNEEI...MPLPDE..PL.....EEME	347
DTKLGGGRDITVKELIKDNPPELAELEAKIREKLQAK.....	343
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GAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI...TEGTQDETGD...ER...PEE....	348
GAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI...TEGTQDETGD...ER...PEE....	348
GERIGQGRDNCREFLRENALEIENKVRHGLVTPMG...AVTLA.EEVE...ED.....	352
GDKIGQGKANACKYLKENPEIAKTLDKKLREMLLNPNEM...QLIAETSSAA...DDVEFGAVPEEF...	354
GDKIGQGKANACKYLKENPEIAKTLDKKLREMLLNPNEM...QLIAETSSAA...DDVEFGAVPEEF...	354
GNKIGQGKNNVIRYLEENPQISTEIEAVIREQLLTKASD...QTAA.HDETE...EEDPLL..ES.....	349
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GSKIGQGKANAAKYLEENPEIQEIEQQIRAKLLVTSAN...TKATPVAEDL...ADADI.....	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
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consensus		

-  non conserved
-  similar
-  ≥ 50% conserved