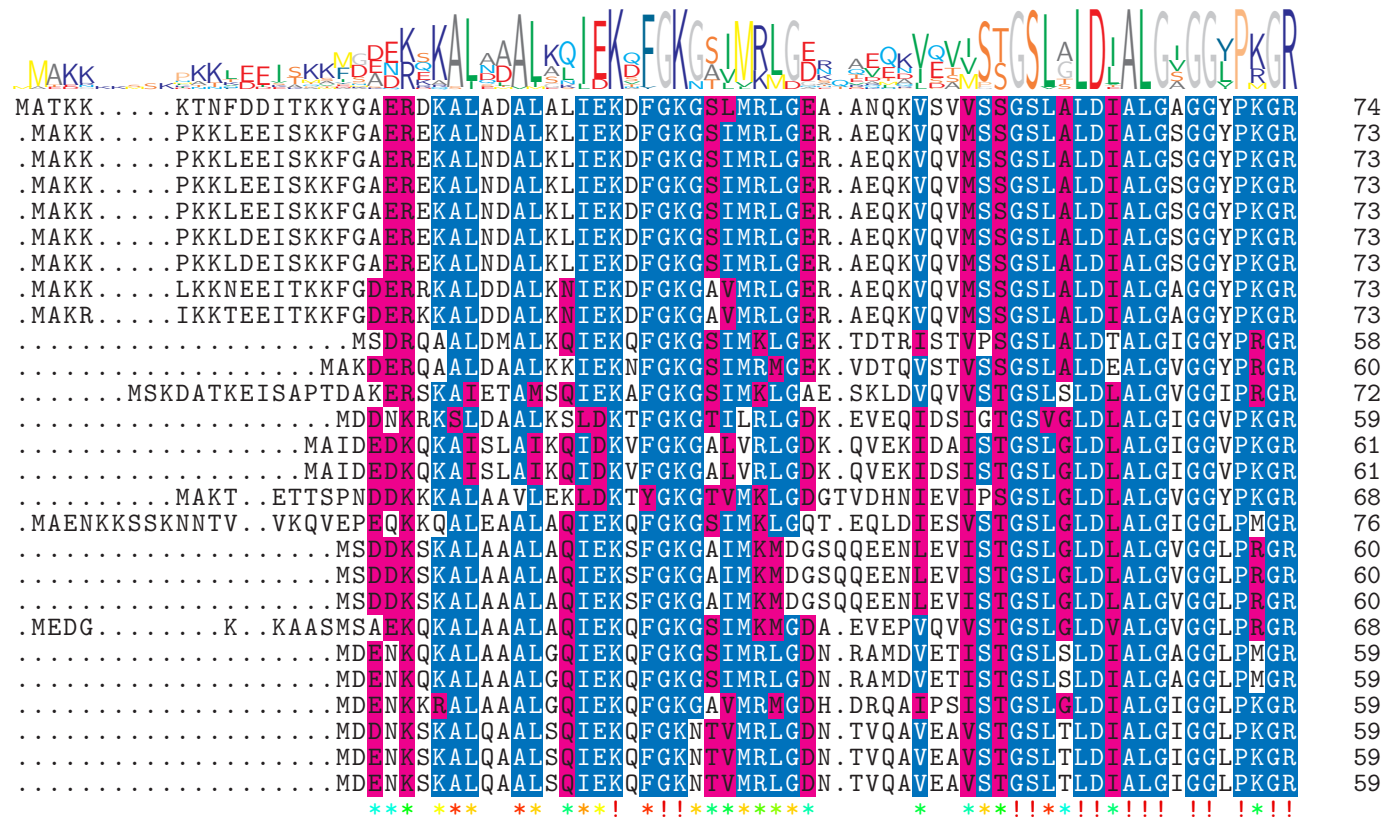


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NTDB id 600 KW2 RS01765 WP 011675413.1
NTDB id 269 KZH43 RS08665 WP 001085462.1
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NTDB id 194 SPR RS08825 WP 001085462.1
NTDB id 159 SP RS09750 WP 001085462.1
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NTDB id 499 SM12261 RS08315 WP 078228268.1
NTDB id 453 Spy49 1753c ACI62003.1
NTDB id 408 SMU RS09530 WP 002262392.1
NTDB id 115 BSU 16940 NP 389576.2
NTDB id 625 LCA RS02525 WP 011374196.1
NTDB id 1313 DR RS12030 WP 010888966.1
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NTDB id 1214 NCTC11637 00359 SQJ03206.1
NTDB id 1211 C694 RS00795 WP 000963128.1
NTDB id 1334 RAOC RS04870 WP 004918236.1
NTDB id 1389 A4U84 RS07560 WP 021112712.1
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NTDB id 1123 OK783 RS03845 WP 003688695.1
NTDB id 1427 RS RS02760 WP 011000510.1
NTDB id 1165 A1552VC RS01565 WP 000344154.1
NTDB id 1142 GTF74 RS11550 WP 000344154.1
NTDB id 1205 PSJM300 05545 AFN77183.1
NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 377422 FR838 RS02450 WP 002115680.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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NTDB id 269 KZH43 RS08665 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPFKEAVVE	IMYEGEGISKTGELLKIASDLDI	IKKAGAWYSYK	311				
NTDB id 228 SPD RS09265 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPFKEAVVE	IMYEGEGISKTGELLKIASDLDI	IKKAGAWYSYK	311				
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NTDB id 453 Spy49 1753c ACI62003.1	SVRLDVRGTTQIKGTG.DQKDSN	IGKETKIKVVKNKVAPPFKEAEVE	IMYEGEGISRTGELVKIASDLDI	IKKAGAWFSYN	311				
NTDB id 408 SMU RS09530 WP 002262392.1	SVRLDVRGNTQIKGTG.EQKDSN	IGKETKIKVVKNKVAPPFKEAFVE	IYEGEGISRTGELVKIASDLGI	IKKAGAWYSYN	311				
NTDB id 115 BSU 16940 NP 389576.2	SVRLEVRRAEQLKQGN.....DVMGNKTKIKVVKNKVAPPFR	TAEVDIMYEGEGISKEGEIIDLGTEL	DIVQKSGSWYSYE	292					
NTDB id 625 LCA RS02525 WP 011374196.1	TVRLEVRRAETIKNGT.....DMIGNRARIKVVKNKVAPPFKEAEVD	IMYGGISRTGELVDMAVEKDI	INKSGSWYSYG	294					
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NTDB id 1245 Cj1673c YP 002345041.1	SVRLDVRKVAT.....L.KQNEEP	IGNRVKVVKNKVAPPFRQAEF	DVMFGEGLSREGELIDYGV	KLDIVDKSGAWFSYK	294				
NTDB id 1214 NCTC11637 00359 SQJ03206.1	SVRIDIRRIAA.....L.KQNEQH	IGNRAKAKVVKNKVAPPFR	EAFFDIMFGEGISKEGEIIDYGV	KLDIVDKSGAWLSYQ	296				
NTDB id 1211 C694 RS00795 WP 000963128.1	SVRIDIRRIAS.....L.KQNEQH	IGNRAKAKVVKNKVAPPFR	EAFFDIMFGEGISKEGEIIDYGV	KLDIVDKSGAWLSYQ	296				
NTDB id 1334 RAOC RS04870 WP 004918236.1	SVRIDIRRLSDTGKIKDKSGEV	IGNRTKVVKNKVAPPFKSAEF	FDIMYEGEGVSKVGEILD	VATDLDI	IKKSGSWFSYQ	307			
NTDB id 1389 A4U84 RS07560 WP 021112712.1	SVRLDIRRCGV.....V.KDGDEI	IGSETKVVKNKVAPPFREVQF	DIMYEGEGISRMNELLILAEANG	FIKKS	GAWF	SYD	310		
NTDB id 1130 NGFG RS03960 WP 003688695.1	SVRLDIRRTGS.....I.KKGE	EEVLGNETRVKVIKNKVAPPFR	QAEFDILYEGEGISWEGELID	IGVKNDI	INKSGAWYSYN	294			
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NTDB id 1123 OK783 RS03845 WP 003688695.1	SVRLDIRRTGS.....I.KKGE	EEVLGNETRVKVIKNKVAPPFR	QAEFDILYEGEGISWEGELID	IGVKNDI	INKSGAWYSYN	294			
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NTDB id 1165 A1552VC RS01565 WP 000344154.1	SVRLDIRRTGA.....I.KEG	EEVVGNETRIKVVKNKIAAPFKE	ANTQIMYGQGFNR	REGELIDLG	VKHKMVEK	SGAWYSYN	293		
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NTDB id 1205 PSJM300 05545 AFN77183.1	SVRLDIRRTGA.....V.KEG	DEVVGS	ETRVKVVKNKVAPPFRQAEFQ	ILYGGKIYRNGEIIDLG	VQQGLVEK	SGAWYAYK	293		
NTDB id 1022 ACIAD RS06390 WP 004925639.1	SVRLDIRRIGQ.....V.KEG	DEIIGSETKVVKNKMAPPFREAI	FIQILYGGKVTNQLGEL	VDLAVQQNIVQK	AGAWYSYQ	293			
NTDB id 377422 FR838 RS02450 WP 002115680.1	SVRLDIRRIGQ.....V.KEG	DEIIGSETRVKVVKNKMAPPFKEAIFQ	ILYGGKVTNQLGEL	VDLAVQQDIVQK	AGAWYSYQ	293			
NTDB id 1074 ABD1 RS10195 WP 000344167.1	SVRLDIRRIGQ.....V.KEG	DEIIGSETKVVKNKMAPPFKEAIFQ	ILYGGKVTNQLGEL	VDLAVQQDIVQK	AGAWYSYQ	293			
consensus	*!!**!* *	*	**	*****!*****!*****	*****!*!*****	*****	***	***	! !*****!


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NTDB id 600 KW2 RS01765 WP 011675413.1
NTDB id 269 KZH43 RS08665 WP 001085462.1
NTDB id 228 SPD RS09265 WP 001085462.1
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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 377422 FR838 RS02450 WP 002115680.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
DEKIGGGA ⁺ E ⁺ KA ⁺ KN ⁺ YL ⁺ KE ⁺ HQ ⁺ DV ⁺ FD ⁺ EI ⁺ DH ⁺ KV ⁺ RAAH ⁺ CI ⁺ LDDSEVAETEETTASKTKAKAKKEEKAVETEEIELELED....	387
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EI ⁺ FD ⁺ EI ⁺ DK ⁺ VR ⁺ SKF ⁺ GLIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EI ⁺ FD ⁺ EI ⁺ DK ⁺ VR ⁺ SKF ⁺ GLIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EI ⁺ FD ⁺ EI ⁺ DK ⁺ VR ⁺ SKF ⁺ GLIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AD ⁺ NPE ⁺ VFA ⁺ EI ⁺ DH ⁺ QV ⁺ RVQF ⁺ GLIDGEEAAE....SKKDE....VAQVDS..VNEEVTLDLGDELEIE	381
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AD ⁺ NPE ⁺ IF ⁺ EI ⁺ DH ⁺ QV ⁺ RVQF ⁺ GLIDGEEIAE....SKKDE....AAQVDS..VNEEVTLDLGDELEIE	381
GEKIGGGS ⁺ EN ⁺ AK ⁺ RYL ⁺ AD ⁺ HP ⁺ QI ⁺ FD ⁺ EI ⁺ DR ⁺ KV ⁺ VKF ⁺ GLLEESEESAMAVASE.....E.....TDDLALDLNNGIEIE	377
GEKIGGGS ⁺ EN ⁺ AK ⁺ KFL ⁺ AD ⁺ NPE ⁺ IF ⁺ DD ⁺ IDH ⁺ KV ⁺ RVQY ⁺ GLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EE ⁺ RL ⁺ GGGREN ⁺ AK ⁺ QFL ⁺ KEN ⁺ KD ⁺ IMLM ⁺ IQEQ ⁺ IREHY ⁺ CLDNNGVVQQQA ⁺ EETQEEL.EFE.E.....	348
SERIGGGREN ⁺ AK ⁺ NYL ⁺ AD ⁺ HED ⁺ VE ⁺ DV ⁺ RLK ⁺ VRAAY ⁺ CI ⁺ SDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGGQKEKTIAYIA ⁺ ERP ⁺ EME ⁺ QE ⁺ IRDR ⁺ VMAAIRAGNAGEAPALAPAAPEAA..EA.....	363
DKKLGGGREN ⁺ SKA ⁺ FL ⁺ KEN ⁺ PEI ⁺ AD ⁺ EITKAT ⁺ IQNSM ⁺ TEGMIS....GSEDDGEE.....	343
DKKLGGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ AD ⁺ EITLKI ⁺ KESIG ⁺ SNEEIM....PLPDEPLEE..ME.....	347
DKKLGGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ AD ⁺ EITLKI ⁺ KESIG ⁺ SNEEIM....PLPDEPLEE..ME.....	347
DTKLGGGRD ⁺ TV ⁺ KEL ⁺ IKD ⁺ NPE ⁺ LAE ⁺ ELEAK ⁺ IREKLQAK.....	343
GTKIGGQKNN ⁺ AVK ⁺ WL ⁺ KEN ⁺ PEI ⁺ AD ⁺ KL ⁺ EQ ⁺ IRNTL ⁺ ASNPNSV....LKATASDSN..DESDVEEFSEEEEL.....	372
GAKIGGQKDN ⁺ RV ⁺ VL ⁺ KEN ⁺ PEI ⁺ SD ⁺ EIDAK ⁺ IRALN ⁺ GVEMHIT....EG.....T..QDET ⁺ DGERPEE.....	348
GAKIGGQKDN ⁺ RV ⁺ VL ⁺ KEN ⁺ PEI ⁺ SD ⁺ EIDAK ⁺ IRALN ⁺ GVEMHIT....EG.....T..QDET ⁺ DGERPEE.....	348
GAKIGGQKDN ⁺ RV ⁺ VL ⁺ KEN ⁺ PEI ⁺ SD ⁺ EIDAK ⁺ IRALN ⁺ GVEMHIT....EG.....T..QDET ⁺ DGERPEE.....	348
GERIGGGRD ⁺ NCRE ⁺ FLREN ⁺ AEL ⁺ ARE ⁺ EI ⁺ ENK ⁺ VREHL ⁺ GVTPMGA....VTLAE.EVE..ED.....	352
GDKIGGQKAN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PEI ⁺ AKT ⁺ LDKKL ⁺ REMLLN ⁺ PENMQ....LIAETSSAA..DDVEFGAVPEEF.....	354
GDKIGGQKAN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PEI ⁺ AKT ⁺ LDKKL ⁺ REMLLN ⁺ PENMQ....LIAETSSAA..DDVEFGAVPEEF.....	354
GSKIGGQKANA ⁺ AKY ⁺ LEEN ⁺ PEI ⁺ GQ ⁺ EIEQQ ⁺ IRAKLL ⁺ TSANT....KATPVAEDL..ADA...DI.....	347
GNKIGGQKNN ⁺ VIR ⁺ YLEEN ⁺ PQ ⁺ ISTE ⁺ IEAV ⁺ IREQLLTKASDQ....TAAHD.ETE..EEP...DLLES.....	349
GNKIGGQKNN ⁺ VIR ⁺ HFEEN ⁺ PQ ⁺ MAGE ⁺ IEK ⁺ IIREQLLTTGTNG....AVQVE.DEE..ED...LLLES.....	348
GNKIGGQKNN ⁺ VIR ⁺ YFEEN ⁺ NQ ⁺ IAE ⁺ EIER ⁺ NIREQLLTTGTNG....AVQIE.DEE..EPD...LLLES.....	349

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		IEE	
NTDB id 600 KW2 RS01765 WP 011675413.1	...	387	
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	
NTDB id 159 SP RS09750 WP 001085462.1	IEE	388	
NTDB id 527 SMSK321 RS11065 WP 001085454.1	IEE	384	
NTDB id 499 SM12261 RS08315 WP 078228268.1	IEE	384	
NTDB id 453 Spy49 1753c ACI62003.1	D..	378	
NTDB id 408 SMU RS09530 WP 002262392.1	D..	383	
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NTDB id 1205 PSJM300 05545 AFN77183.1	...	347	
NTDB id 1022 ACIAD RS06390 WP 004925639.1	...	349	
NTDB id 377422 FR838 RS02450 WP 002115680.1	...	348	
NTDB id 1074 ABD1 RS10195 WP 000344167.1	...	349	
consensus			

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