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NTDB id 601 KW2 RS02615 WP 021036805.1
NTDB id 378 SMU RS02690 WP 002263569.1
NTDB id 241 SP RS04015 WP 000882523.1
NTDB id 281 KZH43 RS03550 WP 000882517.1
NTDB id 245 SPD RS03860 WP 000882517.1
NTDB id 243 SPR RS03635 WP 000882517.1
NTDB id 50574 MY9 RS00580 WP 014475592.1
NTDB id 85 BSU 00860 NP 387967.1
NTDB id 610 V4T04 RS10165 WP 012897346.1
NTDB id 290 KZH43 RS10025 WP 001109677.1
NTDB id 289 SPD RS10700 WP 001109677.1
NTDB id 287 SP RS11210 WP 001109712.1
NTDB id 377 SMU RS09275 WP 002262344.1
NTDB id 297 STER RS00545 WP 011680614.1
NTDB id 329 STU RS10020 WP 011225298.1
consensus

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Protein	Sequence	Length
MLCQNCN	MLCQNCNINEAT	13
MLCQNCI	MLCQNCIINEAT	13
MLCQNCI	MLCQNCIINDST	13
MLCQNCI	MLCQNCIINDST	13
MLCQNCI	MLCQNCIINDST	13
MLCQNCI	MLCQNCIINDST	13
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MMFGR	MMFGRFTERAQKVLALAQEEALRLGHNNIGTEHILLGLVREGEGIAAKALQALGLGSEKIQKEVESLIG.....RGQEMS	75
MKFENIK	MKFENIKYPTLDRILEKAEEYAHQYQYGTIESAHLIAAMATTSGSIAYSLLAGMNVDSDDLIDL.....EDLSSHVKVKR	77
MN	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNSYSVAGATLNDYPYEMDRLE....EVALELTETDYSQDET	75
MN	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNSYSVAGATLNDYPYEMDRLE....EVALELTETDYSQDET	75
MN	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNSYSVAGATLNDYPYEMDRLE....EVALELTETDYSQDET	75
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MTI	MTIYSRKMQAIFHRAQLEAERFESPFLLETWHVLLAMVEVTGSVAYLTFTDFEDRIHSEEIETAAVLAMEKRPKDLSEDI	81
MTI	MTIYSRKMQAIFHRAQLEAERFESPFLLETWHVLLAMVEVPGSVAYLTFTDFEDRIHSEEIETAAVLAMEKRPKDLSEDI	81

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NTDB id 601 KW2 RS02615 WP 021036805.1
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NTDB id 297 STER RS00545 WP 011680614.1
NTDB id 329 STU RS10020 WP 011225298.1
consensus

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Sequence	Score
HL ^Y TSVN ^G Q ^Q K ^K Q ^I DL ^C QCNCY ^Q I...MKS ^G G ^G Q ^E AL ^F FGAGNAS ^N GN ^S DE...PFNP.FND ^I FSAL ^Q GG ^G .DFNGAAS ^N .	80
HL ^Y ANVN ^G Q ^Q K ^K Q ^I DL ^C QCNCY ^Q I...MKTDP ^E NGPLN ^L LSQ ^N S ^S S...INPFFD ^F FFGDL ^N NFN ^R FA ^F NNQDL ^P .	79
HL ^Y TN ^L N ^L GK ^Q K ^Q I ^D LCQNCY ^K I...IKTDP ^N NS ^L FKG ^M TD ^L LN ^N RD...FDP.FG ^D FFND ^L LNNFR ^P SS ^N ..TP.	76
HL ^Y TN ^L N ^L GK ^Q K ^Q I ^D LCQNCY ^K I...IKTDP ^N NS ^L FKG ^M TD ^L LN ^N RD...FDP.FG ^D FFND ^L LNNFR ^P SS ^N ..TP.	76
HL ^Y TN ^L N ^L GK ^Q K ^Q I ^D LCQNCY ^K I...IKTDP ^N NS ^L FKG ^M TD ^L LN ^N RD...FDP.FG ^D FFND ^L LNNFR ^P SS ^N ..TP.	76
HL ^Y TN ^L N ^L GK ^Q K ^Q I ^D LCQNCY ^K I...IKTDP ^N NS ^L FKG ^M TD ^L LN ^N RD...FDP.FG ^D FFND ^L LNNFR ^P SS ^N ..TP.	76
QTIHY ^T PRAK ^K V ^I ELSMDEARK ^L GHSY ^V GT ^E HI ^L LLGLIREGEGVAAR ^V LNNLGVSLN ^K ARQ ^Q VL ^Q L...LGSNET....	147
QTIHY ^T PRAK ^K V ^I ELSMDEARK ^L GHSY ^V GT ^E HI ^L LLGLIREGEGVAAR ^V LNNLGVSLN ^K ARQ ^Q VL ^Q L...LGSNET....	147
STLRFSPRAEEV ^M TAASFLAIHN ^N SEAV ^G TEH ^L LYALLQ ^V EDG ^F GL ^Q L ^L KL...QKINIVSLR ^K EL ^E KRTGLK ^V PES ^K K	153
TELPFSRRLQILF ^D EAEYVAS ^V VHAKVLG ^T EHVLYAIL ^H DGNALATRI ^L ERAGFSYEDKKDQVKIAALRRN ^L EERAG ^W TREDL ^K A	160
TELPFSRRLQILF ^D EAEYVAS ^V VHAKVLG ^T EHVLYAIL ^H DGNALATRI ^L ERAGFSYEDKKDQVKIAALRRN ^L EERAG ^W TREDL ^K A	160
TELPFSRRLQVLF ^D EAEYVAS ^V VHAKVLG ^T EHVLYAIL ^H DSNALATRI ^L ERAGFSYEDKKDQVKIAALRRN ^L EERAG ^W TREDL ^K A	160
MLLEQSHALK ^R TLAEAAAI ^S QVTHAKEVG ^T EHVLFAMLLNP ^N LLATRI ^L ELVG ^F HA ^K DDGESIR ^L LLDL ^R KV ^I ERYAG ^F SKEDI ^K A	164
DLRAQSPALEAMLQEAQEIAS ^V TGAVEVG ^S EHVLM ^A FL ^L HK ^D LMVCRL ^L EVAG ^F QYK ^D SD ^S KPRI ^I DL ^R RS ^L ERNAG ^L SKQDL ^K A	166
DLRAQSPALEAMLQEAQGIAS ^V TGAVEVG ^S EHVLM ^A FL ^L HK ^D LMVCRL ^L EVAG ^F QYK ^D SD ^S KPRI ^I DL ^R RS ^L ERNAG ^L SKQDL ^K A	166

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NTDB id 601 KW2 RS02615 WP 021036805.1	QTPPTQTGG.....RGPGRGPQNPRAKQPKGMLLEFGINITESARRGEIDPVIIGRDEEIKRVIEILNRRTKNNPVL	151
NTDB id 378 SMU RS02690 WP 002263569.1	NTPPTQAGCGNGNGGN.N.RRPGGPQQQASQKPNGLLEFGINLTDIARKGEIDPVIIGRDEEITRVIEILNRRTKNNPVL	158
NTDB id 241 SP RS04015 WP 000882523.1	PIPTQSGGGYGGNGGYGSQNRGSAQTTPPSQEKGLLEFGINVTETIARRGDIIDPVIIGRDEEITRVIEILNRRTKNNPVL	157
NTDB id 281 KZH43 RS03550 WP 000882517.1	PIPTQSGGGYGGNGGYGSQNRGSAQTTPPSQEKGLLEFGINVTETIARRGDIIDPVIIGRDEEITRVIEILNRRTKNNPVL	157
NTDB id 245 SPD RS03860 WP 000882517.1	PIPTQSGGGYGGNGGYGSQNRGSAQTTPPSQEKGLLEFGINVTETIARRGDIIDPVIIGRDEEITRVIEILNRRTKNNPVL	157
NTDB id 243 SPR RS03635 WP 000882517.1	PIPTQSGGGYGGNGGYGSQNRGSAQTTPPSQEKGLLEFGINVTETIARRGDIIDPVIIGRDEEITRVIEILNRRTKNNPVL	157
NTDB id 50574 MY9 RS00580 WP 014475592.1	GSSAAGTNSNANTPTLDSLARDLTAIAKEDSLDPVIGRSKEIQRVIEVLSRRTKNNPVL	207
NTDB id 85 BSU 00860 NP 387967.1	GSSAAGTNSNANTPTLDSLARDLTAIAKEDSLDPVIGRSKEIQRVIEVLSRRTKNNPVL	207
NTDB id 610 V4T04 RS10165 WP 012897346.1	AVTPMSKRKMAKG.....VAENSTPTLDSVSSDLTEEARLGKLDPMIGRAEIDRLIHILSRRTKNNPVL	220
NTDB id 290 KZH43 RS10025 WP 001109677.1	.LRQRHRTV.ADK.....QNSMANMMGMPTTPSGGLEDYTHDLTEQARSCKLEPVIIGRDKIEISRMIIQLSRKTKNNPVL	233
NTDB id 289 SPD RS10700 WP 001109677.1	.LRQRHRTV.ADK.....QNSMANMMGMPTTPSGGLEDYTHDLTEQARSCKLEPVIIGRDKIEISRMIIQLSRKTKNNPVL	233
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NTDB id 377 SMU RS09275 WP 002262344.1	.IFEMRKPKKVKN.....SSSFSDLMKPP.SVTGELADFTRLDELARQGRLPEVIGREQEISRMVQILSRKTKNNPVL	237
NTDB id 297 STER RS00545 WP 011680614.1	.IHDLRKPKKSKA.....SANFANMMQPPQSSITGELADYTKDLTALAESGNLDPVIGRDEEISRMIIQLSRKTKNNPVL	240
NTDB id 329 STU RS10020 WP 011225298.1	.IHDLRKPKKSKA.....SANFANMMQPPQSSITGELADYTKDLTALAESGNLDPVIGRDEEISRMIIQLSRKTKNNPVL	240
consensus	* * ** * !*** **!*!*!* * **!*!!!!* !! !** *!*****	

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NTDB id 601 KW2 RS02615 WP 021036805.1	GEPGVGKTAIVVEGLAQKIVDGDVPQKILQNKEVIRLDVVSIVVQGTGIRGQFEERMQKLMDEIRKRNDVIMFIDEITHEIVGAGSAGD	236
NTDB id 378 SMU RS02690 WP 002263569.1	GEPGVGKTAIVVEGLAQKIVDGDVPQKILHGKNVIRLDVVSIVVQGTGIRGQFEERMQKLMDEIRKRNDVIMFIDEITHEIVGAGSAGD	243
NTDB id 241 SP RS04015 WP 000882523.1	GEPGVGKTAIVVEGLAQKIVDGDVPHKLQGGKQVIRLDVVSIVVQGTGIRGQFEERMQKLMDEIRKRNDVIMFIDEITHEIVGAGSAGD	242
NTDB id 281 KZH43 RS03550 WP 000882517.1	GEPGVGKTAIVVEGLAQKIVDGDVPHKLQGGKQVIRLDVVSIVVQGTGIRGQFEERMQKLMDEIRKRNDVIMFIDEITHEIVGAGSAGD	242
NTDB id 245 SPD RS03860 WP 000882517.1	GEPGVGKTAIVVEGLAQKIVDGDVPHKLQGGKQVIRLDVVSIVVQGTGIRGQFEERMQKLMDEIRKRNDVIMFIDEITHEIVGAGSAGD	242
NTDB id 243 SPR RS03635 WP 000882517.1	GEPGVGKTAIVVEGLAQKIVDGDVPHKLQGGKQVIRLDVVSIVVQGTGIRGQFEERMQKLMDEIRKRNDVIMFIDEITHEIVGAGSAGD	242
NTDB id 50574 MY9 RS00580 WP 014475592.1	GEPGVGKTAIAEGLAQKIIINNEVPEILRDKRVMITLDMGTIVVAGTKYRGEFEDRLKKVMDIEIRQAGNIILFIDELHTLIGAGG.AE	291
NTDB id 85 BSU 00860 NP 387967.1	GEPGVGKTAIAEGLAQKIIINNEVPEILRDKRVMITLDMGTIVVAGTKYRGEFEDRLKKVMDIEIRQAGNIILFIDELHTLIGAGG.AE	291
NTDB id 610 V4T04 RS10165 WP 012897346.1	GEPGVGKSAIIIEGLAQRIIVNGQVPIGLMNSRIMALNMATVVAGTKYRGEFEDRLTAIVEEVSSDPDVIIIFIDELHTIIGAGGMD	305
NTDB id 290 KZH43 RS10025 WP 001109677.1	GDAGVGKTALALGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFRGDFEERMNNIIKDIEEDGQVILFIDELHTIMSGSGID	318
NTDB id 289 SPD RS10700 WP 001109677.1	GDAGVGKTALALGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFRGDFEERMNNIIKDIEEDGQVILFIDELHTIMSGSGID	318
NTDB id 287 SP RS11210 WP 001109712.1	GDAGVGKTALALGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFRGDFEERMNNIIKDIEEDGQVILFIDELHTIMSGSGID	318
NTDB id 377 SMU RS09275 WP 002262344.1	GDAGVGKTALAYGLAQRIIVDSAVPFELADMKVLELDMMSSVAGTRFRGDFEERMNNIIEADIEADGHIVLFIDELHTIMSGSGID	322
NTDB id 297 STER RS00545 WP 011680614.1	GEAGVGKTALALGLAQRIASGEVPFELADMRIILELDMMSSVAGTRFRGDFEERMNNIIEADIEADGKIILFIDELHTIIGSGSGID	325
NTDB id 329 STU RS10020 WP 011225298.1	GEAGVGKTALALGLAQRIASGEVPFELADMRIILELDMMSSVAGTRFRGDFEERMNNIIEADIEADGKIILFIDELHTIIGSGSGID	325
consensus	!*****!* *!!!!!* *!!!! * ** !*****!*****!*****!*****!*****!*****!*****!*****!*****!	

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NTDB id 329 STU RS10020 WP 011225298.1
consensus



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NTDB id 329 STU RS10020 WP 011225298.1
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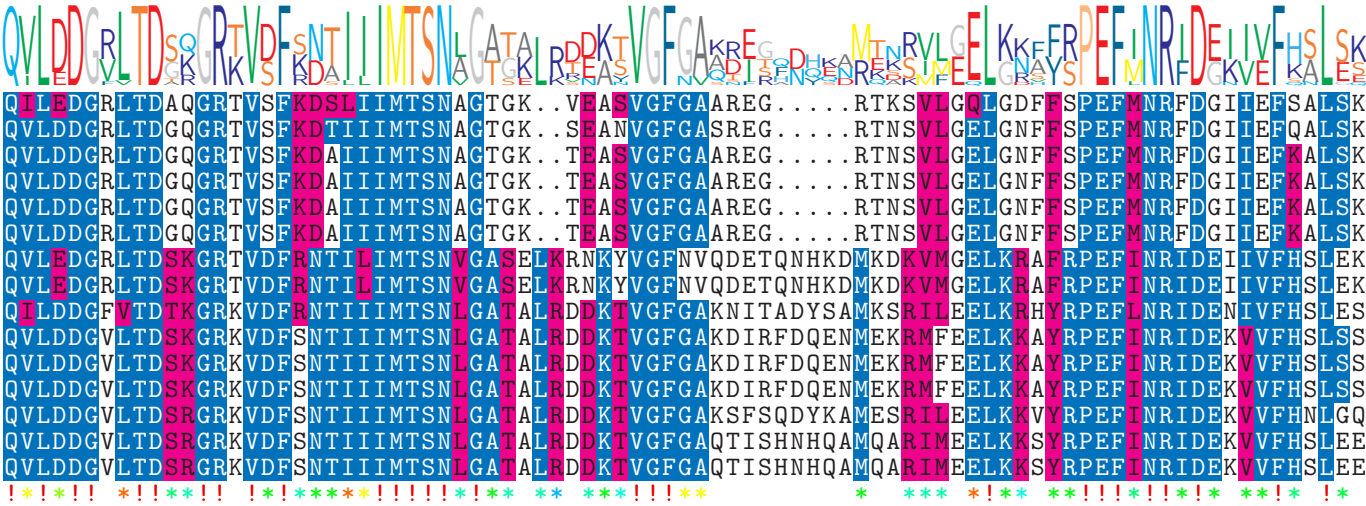
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NTDB id 378 SMU RS02690 WP 002263569.1	KLDKENTPVITEKNI	IEVIVEQKTN	IPVIGEL	LKEKE	EQSQLI	HLADDL	KTRVIGQDA	AVDKI	IAKAIRNRVGL	GTPNRP	IGSFL	LVGVP	489			
NTDB id 241 SP RS04015 WP 000882523.1	KITDQDTPSI	IESEKTI	IEHII	EQKTN	IPVIGDL	LKEKE	EQSQLI	HLAEDL	KSHVIGQDD	AVDKI	IAKAIRNRVGL	GTPNRP	IGSFL	488		
NTDB id 281 KZH43 RS03550 WP 000882517.1	KITDQDTP	IIESEKTI	IEHII	EQKTN	IPVIGDL	LKEKE	EQSQLI	HLAEDL	KSHVIGQDD	AVDKI	IAKAIRNRVGL	GTPNRP	IGSFL	488		
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NTDB id 50574 MY9 RS00580 WP 014475592.1	EKQGGENSEVT	IVDDIAM	VVSSWT	GV	VPVSKI	IAQTETD	KLLNMENI	LHSRVIGQDE	AVVAV	AKAVRRARAGL	KDPK	RPIGSF	IFLGP	546		
NTDB id 85 BSU 00860 NP 387967.1	EKQGGENSEVT	IVDDIAM	VVSSWT	GV	VPVSKI	IAQTETD	KLLNMENI	LHSRVIGQDE	AVVAV	AKAVRRARAGL	KDPK	RPIGSF	IFLGP	546		
NTDB id 610 V4T04 RS10165 WP 012897346.1	.VKEDGRQEV	TDQAV	VAVAST	LT	GVPI	QMTKSE	SDRLIN	LEKELH	KRVIGQEE	AI	SAVSRA	IRRARSG	VADSRPM	GSMF	FLGP	555
NTDB id 290 KZH43 RS10025 WP 001109677.1	.VPV.YKDL	LVTESD	ILTTLS	RSLSG	IPVQKL	TQTD	AKKYLN	LEAELH	KRVIGQDQ	AVSS	ISRAIRRN	QSGIR	SHKR	RPIGSF	MFLGP	550
NTDB id 289 SPD RS10700 WP 001109677.1	.VPV.YKDL	LVTESD	ILTTLS	RSLSG	IPVQKL	TQTD	AKKYLN	LEAELH	KRVIGQDQ	AVSS	ISRAIRRN	QSGIR	SHKR	RPIGSF	MFLGP	550
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NTDB id 377 SMU RS09275 WP 002262344.1	.PLLKKRAE	VKEED	ILATLS	SKLSG	IPVKKL	TQAD	SKKYLN	LERELH	KRVIGQDD	AVSS	ISRAIRRN	QSGIR	VGKR	RPIGSF	MFLGP	553
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consensus	*	*****	*	***	*****	*	*	*****	*!*	*!?!*!?!*	*	*!?!*!?!*	*!	*!?!*!?!*!?!*	*!	*!?!*!?!*!?!*

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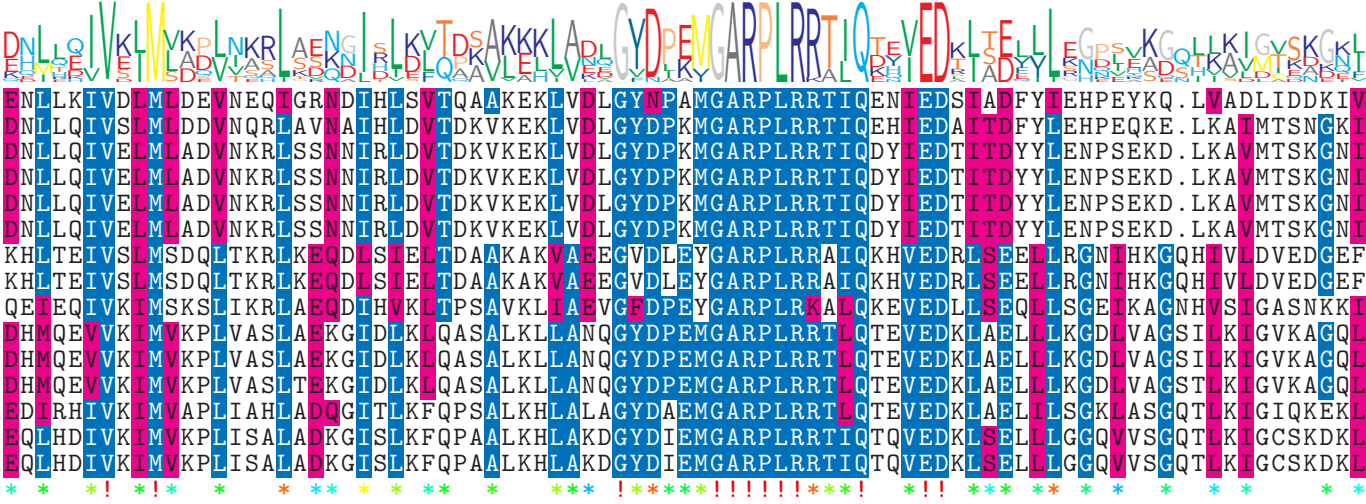
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NTDB id 297 STER RS00545 WP 011680614.1	TFTVV.....	816
NTDB id 329 STU RS10020 WP 011225298.1	TFTVV.....	816
consensus		

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