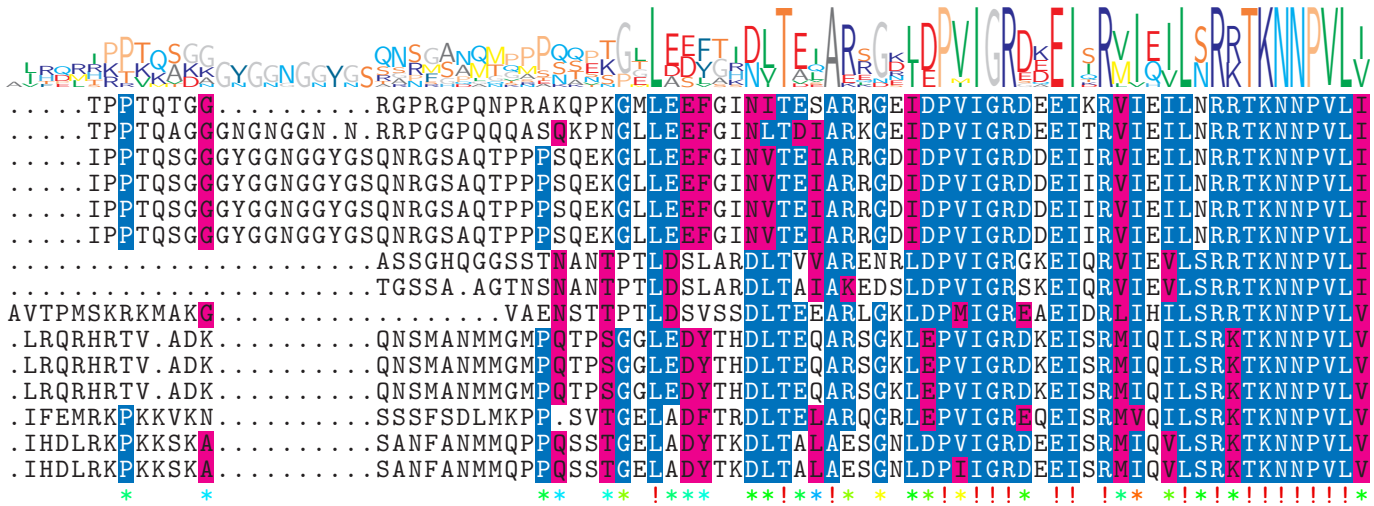


Accession	Gene	Protein	Sequence	Position
NTDB id 601 KW2 RS02615 WP 021036805.1	...	MLCQNCNINEA	TI	13
NTDB id 378 SMU RS02690 WP 002263569.1	...	MLCQNCNINEA	TI	13
NTDB id 241 SP RS04015 WP 000882523.1	...	MLCQNCNINDS	TI	13
NTDB id 281 KZH43 RS03550 WP 000882517.1	...	MLCQNCNINDS	TI	13
NTDB id 245 SPD RS03860 WP 000882517.1	...	MLCQNCNINDS	TI	13
NTDB id 243 SPR RS03635 WP 000882517.1	...	MLCQNCNINDS	TI	13
NTDB id 94725 AOD63 RS00470 WP 000971179.1	..MMFGRFTERAQKVLALSQEEAIRIGHNNIGTEHILLGLVREGEGLAAKALIALGLSPEKVQKEVEALIG.....RGTEAS			75
NTDB id 85 BSU 00860 NP 387967.1	..MMFGRFTERAQKVLALAQEEALRLGHNNIGTEHILLGLVREGEGLAAKALQALGLGSEKIQKEVESLIG.....RGQEMS			75
NTDB id 610 V4T04 RS10165 WP 012897346.1	MKFENIKYPTPLDRILEKAEYEAHQYQYGTIESAHLAAMATTSGSIAYSLLAGMNVDDSSDLLIDL.....EDLSSHVKVKR			77
NTDB id 290 KZH43 RS10025 WP 001109677.1	MNYSKALNECIESAYMVAAGHFGARYLESWHLLIAMSNNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYSQDET			75
NTDB id 289 SPD RS10700 WP 001109677.1	MNYSKALNECIESAYMVAAGHFGARYLESWHLLIAMSNNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYSQDET			75
NTDB id 287 SP RS11210 WP 001109712.1	MNYSKALNECIESAYMVAAGHFGARYLESWHLLIAMSNNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYSQDET			75
NTDB id 377 SMU RS09275 WP 002262344.1	...MTDYSLKMQEVFRLAQFEAARFESSYLESWHVLLAMVEIDSSVAGLSFAEFADVRVFEDYQAAAILAIGKKPKSSSN..DI			79
NTDB id 329 STER RS00545 WP 011680614.1	...MTIYSRKMQAIFHRAQLEAERFESPFLTWHVLLAMVEVTGSAVYLTFTDFEDRIHSEEIETAAVLAMEKRPKDLSES			81
NTDB id 327 STU RS10020 WP 011225298.1	...MTIYSRKMQAIFHRAQLEAERFESPFLTWHVLLAMVEVPGSAVYLTFTDFEDRIHSEEIETAAVLAMEKRPKDLSES			81
consensus	***			

NTDB	id	601	KW2	RS02615	WP	021036805.1	HLYTSVNGQKKQIDLCQCNCYQI...MKSGGQEALFGAGNASNGNSDE.....PFNP.FNDIFSALQGQ.DFNGAASNQ	81
NTDB	id	378	SMU	RS02690	WP	002263569.1	HLVANVNGQKKQIDLCQCNCYQI...MKTDPENGPLNHSQQNSSS.....INPFFDDFFGDLNNFRAFNNQDLPN	80
NTDB	id	241	SP	RS04015	WP	000882523.1	HLYTNLNGKQKKQIDLCQCNCYKI...IKTDPNNSLFKGMTDLNNRD.....FDP.FGDFFNDLNNFRPSSN..TPP	77
NTDB	id	281	KZH43	RS03550	WP	000882517.1	HLTYNLNGKQKKQIDLCQCNCYKI...IKTDPNNSLFKGMTDLNNRD.....FDP.FGDFFNDLNNFRPSSN..TPP	77
NTDB	id	245	SPD	RS03860	WP	000882517.1	HLYTNLNGKQKKQIDLCQCNCYKI...IKTDPNNSLFKGMTDLNNRD.....FDP.FGDFFNDLNNFRPSSN..TPP	77
NTDB	id	243	SPR	RS03635	WP	000882517.1	HLYTNLNGKQKKQIDLCQCNCYKI...IKTDPNNSLFKGMTDLNNRD.....FDP.FGDFFNDLNNFRPSSN..TPP	77
NTDB	id	94725	AOD63	RS00470	WP	000971179.1	QTVHYTPRAKKVIELSMDEARKLGHSYVGTEHILLGLIREGEGVAARVLNNLGVSLNKARQQVLQ..LLGSNE.....	146
NTDB	id	85	BSU	O0860	NP	387967.1	QTIHYTPRAKKVIELSMDEARKLGHSYVGTEHILLGLIREGEGVAARVLNNLGVSLNKARQQVLQ..LLGSNE.....	146
NTDB	id	610	V4T04	RS10165	WP	012897346.1	STLRFSPPRAEEVMTAASFLAIHNNSEAVGTEHLLYALLQVEDGFGLQLKL.....QKINIVSLRKELEBKRTGLKVPESKK	153
NTDB	id	290	KZH43	RS10025	WP	001109677.1	TELPFSRRRLQILFDEAEYVASVVHAKVLGTEHVLYAILHDGNALATRILERAGFSYEDKKDQVKIAALRRNLEERAGWTREDLKA	160
NTDB	id	289	SPD	RS10700	WP	001109677.1	TELPFSRRRLQILFDEAEYVASVVHAKVLGTEHVLYAILHDGNALATRILERAGFSYEDKKDQVKIAALRRNLEERAGWTREDLKA	160
NTDB	id	287	SP	RS11210	WP	001109712.1	TELPFSRRRLQVLFDEAEYVASVVHAKVLGTEHVLYAILHDSNALATRILERAGFSYEDKKDQVKIAALRRNLEERAGWTREDLKA	160
NTDB	id	377	SMU	RS09275	WP	002262344.1	MILEQSHALKRTLAEAAAISQVTHAKEVGTEHVLFAMLLNPNLLATRIILELVGFHAKDDGESIRLLDLRKVIERYAGFSKEDIKA	164
NTDB	id	329	STER	RS00545	WP	011680614.1	DLRAQSPALEARMLQEAQEIASVTGAVEVGSEHVLMAFLLHKDLMVCRLLEVAGFQYKDDSDKPRIIDLRRSLERNAGLSKQDLKA	166
NTDB	id	297	STU	RS10020	WP	011225298.1	DLRAQSPALEARMLQEAQGIASVTGAVEVGSEHVLMAFLLHKDLMVCRLLEVAGFQYKDDSDKPRIIDLRRSLERNAGLSKQDLKA	166
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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 94725 AOD63 RS00470 WP 000971179.1
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
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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 94725 AOD63 RS00470 WP 000971179.1
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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NTDB id 601 KW2 RS02615 WP 021036805.1	GNMDAGNILKPALARGEELQLVGATTLNEYR.IIEKDAALERRMQPVKVDEPSVDETITILRGIQARYEDYHHVKYTDEAIEAAAH	320
NTDB id 378 SMU RS02690 WP 002263569.1	GNMDAGNILKPALARGEELQLVGATTLNEYR.IIEKDAALERRMQPVKVDEPSVAETITILKGIQPKYEDYHHVKYTDEAIEAAAN	327
NTDB id 241 SP RS04015 WP 000882523.1	GNMDAGNILKPALARGEELQLVGATTLNEYR.IIEKDAALERRMQPVKVDEPTVDETITILKGIQKKYEDYHHVQYTDAAIEAAAT	326
NTDB id 281 KZH43 RS03550 WP 000882517.1	GNMDAGNILKPALARGEELQLVGATTLNEYR.IIEKDAALERRMQPVKVDEPTVDETITILKGIQKKYEDYHHVQYTDAAIEAAAT	326
NTDB id 245 SPD RS03860 WP 000882517.1	GNMDAGNILKPALARGEELQLVGATTLNEYR.IIEKDAALERRMQPVKVDEPTVDETITILKGIQKKYEDYHHVQYTDAAIEAAAT	326
NTDB id 243 SPR RS03635 WP 000882517.1	GNMDAGNILKPALARGEELQLVGATTLNEYR.IIEKDAALERRMQPVKVDEPTVDETITILKGIQKKYEDYHHVQYTDAAIEAAAT	326
NTDB id 94725 AOD63 RS00470 WP 000971179.1	GAIDASNILKPSLARGEELQCIGATTLDDEYRKYIEKDAALERRFQPIHVDEPSLDESTQILKGLRDRYEAAHHRVSIITDDAIDA AVK	377
NTDB id 85 BSU 00860 NP 387967.1	GAIDASNILKPSLARGEELQCIGATTLDDEYRKYIEKDAALERRFQPIQVDQPSVDESIQILQGLRDRYEAAHHRVSIITDDAIEAAV K	376
NTDB id 610 V4T04 RS10165 WP 012897346.1	SVNDAANILKPALARGDFQMVGATTYHEYQKYIEKDEALERRLARINVDEPSPDEAIAAILQGLREKFEDYHQVKFTDQAIKS AVM	390
NTDB id 290 KZH43 RS10025 WP 001109677.1	STLDAANILKPALARGTLRTVGATTQEEYQKHIEKDAALSRRFAKVTIEEPSVADSMTILQGLKATYEKHHRVQITDEAVETAVK	403
NTDB id 289 SPD RS10700 WP 001109677.1	STLDAANILKPALARGTLRTVGATTQEEYQKHIEKDAALSRRFAKVTIEEPSVADSMTILQGLKATYEKHHRVQITDEAVETAVK	403
NTDB id 287 SP RS11210 WP 001109712.1	STLDAANILKPALARGTLRTVGATTQEEYQKHIEKDAALSRRFAKVTIEEPSVADSMTILQGLKATYEKHHRVQITDEAVETAVK	403
NTDB id 377 SMU RS09275 WP 002262344.1	STLDAANILKPALARGSLRTIGATTQEEYQKHIEKDAALSRRFAKVTIEEPSEEEAYQILLGLKKS YET YHHV IISDAAVMAAVK	407
NTDB id 297 STER RS00545 WP 011680614.1	STLDAANILKPALARGTLHVMVGATTQA EYQKHIEKDAALSRRFAKITIEEPSVSEATDILNGLRSSYEDYHRVTITDAAVETAVK	410
NTDB id 329 STU RS10020 WP 011225298.1	STLDAANILKPALARGTLHVMVGATTQA EYQKHIEKDAALSRRFAKITIEEPSVSEATDILNGLRSSYEDYHRVTITDAAVETAVK	410
consensus	*!!!!!!!!*!!!!*****!!!!!! !! * !!!!!*!!!!!! * ****!*****!! !** *!****! *! !****!	

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NTDB id 601 KW2 RS02615 WP 021036805.1	LSNRYIQDRFLPDKAIDLLDEAGSKVNLTILKEV.DPKEIDHRLIEAENLKAQATRDDEYEKAAYFRDQIAKYKEMQS.....Q	397
NTDB id 378 SMU RS02690 WP 002263569.1	LSNRYIQDRFLPDKAIDLLDEAGSKMNLTLNFV..DPKEIDHRLIEAENLKAQATRDDEYEKAAYFRDQIAKYKEMQS.....A	404
NTDB id 241 SP RS04015 WP 000882523.1	LSNRYIQDRFLPDKAIDLLDEAGSKMNLTLNFV..DPKVIDQRLIEAENLKSQATREEDFEKAAYFRDQIAKYKEMQK.....K	403
NTDB id 281 KZH43 RS03550 WP 000882517.1	LSNRYIQDRFLPDKAIDLLDEAGSKMNLTLNFV..DPKVIDQRLIEAENLKSQATREEDFEKAAYFRDQIAKYKEMQK.....K	403
NTDB id 245 SPD RS03860 WP 000882517.1	LSNRYIQDRFLPDKAIDLLDEAGSKMNLTLNFV..DPKVIDQRLIEAENLKSQATREEDFEKAAYFRDQIAKYKEMQK.....K	403
NTDB id 243 SPR RS03635 WP 000882517.1	LSNRYIQDRFLPDKAIDLLDEAGSKMNLTLNFV..DPKVIDQRLIEAENLKSQATREEDFEKAAYFRDQIAKYKEMQK.....K	403
NTDB id 94725 AOD63 RS00470 WP 000971179.1	LSDRYITDRFLPDKAIDLLDEAASKVRLRSYTTTPPNLKELEVKLEEIRKEKDAAVQSQEF EKAASLRDMEQRLREKLEDTKRQWK	462
NTDB id 85 BSU 00860 NP 387967.1	LSDRYISDRFLPDKAIDLLDEAGSKVRLRSFTTPPNLKELEQKLDEVRKEKDAAVQSQEF EKAASLRDTEQRLREQVEDTKKSWK	461
NTDB id 610 V4T04 RS10165 WP 012897346.1	LSVRYMTSRKLPDKAIDLLDEAAA AVKISVKNQQT KRLDLEKELAEAEQEELSEAVIKLDIKASRTKEKAVEKIADKIYKFS....	471
NTDB id 290 KZH43 RS10025 WP 001109677.1	MAHRYLTSRHL PDS AIDLLDEAAATVQNKAKHV KADDSDL.....S....PADKALMDGKWKQAAQLIAKEE.....E....	467
NTDB id 289 SPD RS10700 WP 001109677.1	MAHRYLTSRHL PDS AIDLLDEAAATVQNKAKHV KADDSDL.....S....PADKALMDGKWKQAAQLIAKEE.....E....	467
NTDB id 287 SP RS11210 WP 001109712.1	MAHRYLTSRHL PDS AIDLLDEAAATVQNKAKHV KADDSDL.....S....PADKALMDGKWKQAAQLIAKEE.....E....	467
NTDB id 377 SMU RS09275 WP 002262344.1	GAHRYLSGKNLPDS AIDLLDEASATVQGLVKK..KAPAYL....T....DLDHALITNDYQLAKRLLKKEK.....K....	469
NTDB id 297 STER RS00545 WP 011680614.1	AAHRYLTSKNLPDS AIDLLDEASATVQVR IKK..EDKREI....T....PLDEALISGDIGAAVKQYKANQ.....K....	472
NTDB id 329 STU RS10020 WP 011225298.1	AAHRYLTSKNLPDS AIDLLDEASATVQVR IKK..EAKREI....T....PLDEALISGDIGAAVKQYKANQ.....K....	472
consensus	** !!!!! * !!!!!*!!!!!!*!!!!* **** * * * **** * * !* ** *	

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NTDB id 601 KW2 RS02615 WP 021036805.1	EVTDEDMPVITEKDI	IEQIVEQKTQIPVGD	LKEKEQQTQLINL	ADDLKAHVIGQDE	AVDKISK	AI	RRSRVGL	GKPNRPIGSFL	LVGP	482
NTDB id 378 SMU RS02690 WP 002263569.1	KLDKENTPVITEKNI	IEVIVEQKTNIPV	GELKEKEQSQLI	HLADDLKTR	VIGQDA	AVDKIA	KAIRNRVGL	GTPNRPIGSFL	LVGP	489
NTDB id 241 SP RS04015 WP 000882523.1	KITDQDTPSISEKTI	IEHIIIEQKTNIP	VGD	LKEKEQSQLI	HLAEDLKSH	VIGQDD	AVDKIA	KAIRNRVGL	GTPNRPIGSFL	LVGP
NTDB id 281 KZH43 RS03550 WP 000882517.1	KITDQDTP	IIESEKTI	IEHIIIEQKTNIP	VGD	LKEKEQSQLI	HLAEDLKSH	VIGQDD	AVDKIA	KAIRNRVGL	GTPNRPIGSFL
NTDB id 245 SPD RS03860 WP 000882517.1	KITDQDTP	IIESEKTI	IEHIIIEQKTNIP	VGD	LKEKEQSQLI	HLAEDLKSH	VIGQDD	AVDKIA	KAIRNRVGL	GTPNRPIGSFL
NTDB id 243 SPR RS03635 WP 000882517.1	KITDQDTP	IIESEKTI	IEHIIIEQKTNIP	VGD	LKEKEQSQLI	HLAEDLKSH	VIGQDD	AVDKIA	KAIRNRVGL	GTPNRPIGSFL
NTDB id 94725 AOD63 RS00470 WP 000971179.1	EQQKGENSEVT	VEDIANVVSTW	TRIPVSKLAQ	TETDKLLN	LESILH	DRVIGQDE	AVVA	AKAVRRARAGL	KDPKRP	IGSFIFLGP
NTDB id 85 BSU 00860 NP 387967.1	EKQGGENSEVT	VDDIAMVVSSW	TGVPVSKIAQ	TETDKLLN	MENILH	SRVIGQDE	AVVA	AKAVRRARAGL	KDPKRP	IGSFIFLGP
NTDB id 610 V4T04 RS10165 WP 012897346.1	VKEDKRQEV	TDQAVVA	VASTLTGVPIT	QMTKSE	SDRLIN	LEKELH	KRVVQ	EEAISA	VSRA	IRRARS
NTDB id 290 KZH43 RS10025 WP 001109677.1	VPV.YKD	LVTESD	ILTTLSRLSG	IPVQKLT	TQTD	AKKYL	NLEAEL	LHKRVIGQDQ	AVSSIS	RAIRRNQSGIR
NTDB id 289 SPD RS10700 WP 001109677.1	VPV.YKD	LVTESD	ILTTLSRLSG	IPVQKLT	TQTD	AKKYL	NLEAEL	LHKRVIGQDQ	AVSSIS	RAIRRNQSGIR
NTDB id 287 SP RS11210 WP 001109712.1	VPV.YKD	LVTESD	ILTTLSRLSG	IPVQKLT	TQTD	AKKYL	NLEAEL	LHKRVIGQDQ	AVSSIS	RAIRRNQSGIR
NTDB id 377 SMU RS09275 WP 002262344.1	PLKKRAE	VKEED	ILATLSKLSG	IPVKKLT	QAD	SKKYL	NLEREL	LHKRVIGQDD	AVSSIS	RAIRRNQSGIR
NTDB id 297 STER RS00545 WP 011680614.1	AKFPKPAL	VDADQ	IMQTLSRLSG	IPVEKMT	QTDSK	RYLN	LESEL	LHKRVIGQDE	AVSAIS	RAIRRNQSGIR
NTDB id 329 STU RS10020 WP 011225298.1	AKFPKPAL	VDADQ	IMQTLSRLSG	IPVEKMT	QTDSK	RYLN	LESEL	LHKRVIGQDE	AVSAIS	RAIRRNQSGIR
consensus	*	*****	*	***	*	!* *	*	*****	!* *	*****

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NTDB id 601 KW2 RS02615 WP 021036805.1	TGVGKTELAKALAE	VLFGDEDSMIR	EDMSEYMEKHS	VSRLNG	APPGYVGYDE	EGQLTEKVR	NKPYSV	LLDEVEKAHPD	VFNIM	567
NTDB id 378 SMU RS02690 WP 002263569.1	TGVGKTELAKALAE	VLFGDEDSMIR	EDMSEYMEKHS	VSRLNG	APPGYVGYDE	EGQLTEKVR	NKPYSV	LLDEVEKAHPD	VFNIM	574
NTDB id 241 SP RS04015 WP 000882523.1	TGVGKTELAKALAE	VLFGDEDSMIR	EDMSEYMEKHS	VSRLNG	APPGYVGYDE	EGQLTEKVR	NKPYSV	LLDEVEKAHPD	VFNIM	573
NTDB id 281 KZH43 RS03550 WP 000882517.1	TGVGKTELAKALAE	VLFGDEDSMIR	EDMSEYMEKHS	VSRLNG	APPGYVGYDE	EGQLTEKVR	NKPYSV	LLDEVEKAHPD	VFNIM	573
NTDB id 245 SPD RS03860 WP 000882517.1	TGVGKTELAKALAE	VLFGDEDSMIR	EDMSEYMEKHS	VSRLNG	APPGYVGYDE	EGQLTEKVR	NKPYSV	LLDEVEKAHPD	VFNIM	573
NTDB id 243 SPR RS03635 WP 000882517.1	TGVGKTELAKALAE	VLFGDEDSMIR	EDMSEYMEKHS	VSRLNG	APPGYVGYDE	EGQLTEKVR	NKPYSV	LLDEVEKAHPD	VFNIM	573
NTDB id 94725 AOD63 RS00470 WP 000971179.1	TGVGKTELAKALAE	VLFGDEDSMIR	EDMSEYMEKHS	VSRLNG	APPGYVGYDE	EGQLTEKVR	NKPYSV	LLDEVEKAHPD	VFNIM	632
NTDB id 85 BSU 00860 NP 387967.1	TGVGKTELAKALAE	VLFGDEDSMIR	EDMSEYMEKHS	VSRLNG	APPGYVGYDE	EGQLTEKVR	NKPYSV	LLDEVEKAHPD	VFNIM	631
NTDB id 610 V4T04 RS10165 WP 012897346.1	TGVGKTELAKALAE	VLFGDEDSMIR	EDMSEYMEKHS	VSRLNG	APPGYVGYDE	EGQLTEKVR	NKPYSV	LLDEVEKAHPD	VFNIM	640
NTDB id 290 KZH43 RS10025 WP 001109677.1	TGVGKTELAKALAE	VLFGDEDSMIR	EDMSEYMEKHS	VSRLNG	APPGYVGYDE	EGQLTEKVR	NKPYSV	LLDEVEKAHPD	VFNIM	635
NTDB id 289 SPD RS10700 WP 001109677.1	TGVGKTELAKALAE	VLFGDEDSMIR	EDMSEYMEKHS	VSRLNG	APPGYVGYDE	EGQLTEKVR	NKPYSV	LLDEVEKAHPD	VFNIM	635
NTDB id 287 SP RS11210 WP 001109712.1	TGVGKTELAKALAE	VLFGDEDSMIR	EDMSEYMEKHS	VSRLNG	APPGYVGYDE	EGQLTEKVR	NKPYSV	LLDEVEKAHPD	VFNIM	635
NTDB id 377 SMU RS09275 WP 002262344.1	TGVGKTELAKALAE	VLFGDEDSMIR	EDMSEYMEKHS	VSRLNG	APPGYVGYDE	EGQLTEKVR	NKPYSV	LLDEVEKAHPD	VFNIM	638
NTDB id 297 STER RS00545 WP 011680614.1	TGVGKTELAKALAE	VLFGDEDSMIR	EDMSEYMEKHS	VSRLNG	APPGYVGYDE	EGQLTEKVR	NKPYSV	LLDEVEKAHPD	VFNIM	641
NTDB id 329 STU RS10020 WP 011225298.1	TGVGKTELAKALAE	VLFGDEDSMIR	EDMSEYMEKHS	VSRLNG	APPGYVGYDE	EGQLTEKVR	NKPYSV	LLDEVEKAHPD	VFNIM	641
consensus	!!!!!!!!!!	*****	*	!* *	*	*****	!* *	*****	!!!!!!!!!!	*****

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NTDB id 601 KW2 RS02615 WP 021036805.1	ISNQTQETAETTDDEEVPAE	748
NTDB id 378 SMU RS02690 WP 002263569.1	VIKASNK.VETVTKATSD.	753
NTDB id 241 SP RS04015 WP 000882523.1	QIKSAKK.AEVKSSEKEK.	752
NTDB id 281 KZH43 RS03550 WP 000882517.1	QIKSAKK.AEVKSSEKEK.	752
NTDB id 245 SPD RS03860 WP 000882517.1	QIKSAKK.AEVKSSEKEK.	752
NTDB id 243 SPR RS03635 WP 000882517.1	QIKSAKK.AEVKSSEKEK.	752
NTDB id 94725 AOD63 RS00470 WP 000971179.1	VIHSAEKVK.....	811
NTDB id 85 BSU 00860 NP 387967.1	VVKTTAKTN.....	810
NTDB id 610 V4T04 RS10165 WP 012897346.1	KIAQIV.....	816
NTDB id 290 KZH43 RS10025 WP 001109677.1	KFDIA.....	810
NTDB id 289 SPD RS10700 WP 001109677.1	KFDIA.....	810
NTDB id 287 SP RS11210 WP 001109712.1	KFDIA.....	810
NTDB id 377 SMU RS09275 WP 002262344.1	KFDIV.....	813
NTDB id 297 STER RS00545 WP 011680614.1	TFTVV.....	816
NTDB id 329 STU RS10020 WP 011225298.1	TFTVV.....	816
consensus		



-  non conserved
-  similar
-  ≥ 50% conserved