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NTDB id	Accession	Sequence	Position
NTDB id 1474	Cj1108 YP 002344501.1	MLCQNCNINEA.....TI	0
NTDB id 601	KW2 RS02615 WP 021036805.1	MLCQNCNINEA.....TI	13
NTDB id 241	SP RS04015 WP 000882523.1	MLCQNCNINEA.....TI	13
NTDB id 243	SPR RS03635 WP 000882517.1	MLCQNCNINEA.....TI	13
NTDB id 245	SPD RS03860 WP 000882517.1	MLCQNCNINEA.....TI	13
NTDB id 281	KZH43 RS03550 WP 000882517.1	MLCQNCNINEA.....TI	13
NTDB id 378	SMU RS02690 WP 002263569.1	MLCQNCNINEA.....TI	13
NTDB id 85	BSU 00860 NP 387967.1	..MMFGRFTERAQKVLALAQEEALRLGHNNIGTEHILLGLVREGGIAAKALQALGLGSEKIQKEVESLIG.....RGQEMS	75
NTDB id 610	V4T04 RS10165 WP 012897346.1	MKFENIKYPTPTLDRILEKAEEYAHQYQYGTIESAHLAAMATTSGSIAYSLLAGMNVDDSSDLLIDL.....EDLSSHVKVKR	77
NTDB id 289	SPD RS10700 WP 001109677.1	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYSQDET	75
NTDB id 290	KZH43 RS10025 WP 001109677.1	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYSQDET	75
NTDB id 287	SP RS11210 WP 001109712.1	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYSQDET	75
NTDB id 377	SMU RS09275 WP 002262344.1	MTDYSLKMQEVFRLAQFEAARFESSYLESWHVLLAMVEIDSSVAGLSFAEFADVRFEDYQAAAILAIGKKPKSSSN..DI	79
NTDB id 297	STER RS00545 WP 011680614.1	MTIYSRKMQAIFHRAQLEAERFESPFLFETWHVLLAMVEVTGSAVYLTFTDFEDRIHSEEIETAAVLAMEKRPKDLSESDI	81
NTDB id 329	STU RS10020 WP 011225298.1	MTIYSRKMQAIFHRAQLEAERFESPFLFETWHVLLAMVEVPGSAVYLTFTDFEDRIHSEEIETAAVLAMEKRPKDLSESDI	81
consensus		*.....*	**

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NTDB id 1474 Cj1108 YP 002344501.1	..MKYQENLQKYLIDNAKNLSLINHHEFVTCHEVLFALLKLSTDFKDIFFEEFSDGDLELLETELKNYISQNNQVIKQEIEPTISVV	83
NTDB id 601 KW2 RS02615 WP 021036805.1	HLVTSVNGQKKQIDLCQNCYQ...IMKSGGQEQALFGAGNASNGNSDEP	58
NTDB id 241 SP RS04015 WP 000882523.1	HLYTNLNGKQKQIDLCQNCYK...IIKTDPNNSLFKGMTDLNNRD	55
NTDB id 243 SPR RS03635 WP 000882517.1	HLTYTNLNGKQKQIDLCQNCYK...IIKTDPNNSLFKGMTDLNNRD	55
NTDB id 245 SPD RS03860 WP 000882517.1	HLYTNLNGKQKQIDLCQNCYK...IIKTDPNNSLFKGMTDLNNRD	55
NTDB id 281 KZH43 RS03550 WP 000882517.1	HLTYTNLNGKQKQIDLCQNCYK...IIKTDPNNSLFKGMTDLNNRD	55
NTDB id 378 SMU RS02690 WP 002263569.1	HLVANVNGQKKQIDLCQNCYQ...IMKTDPENGPLNHLISQQNSSS	55
NTDB id 85 BSU 00860 NP 387967.1	QTIHYTPRAKKVIELSMDEARKLGHSYVGTEHILLGLIREGEGVAARVLNN	126
NTDB id 610 V4T04 RS10165 WP 012897346.1	STLRFSPRAEEVMTAASFLAIHNNSEAVGTEHLLYALLQVEDGFGLQLLKL	128
NTDB id 289 SPD RS10700 WP 001109677.1	TELPFSRRLQILFDEAEYVASVVHAKVLGTEHVLYAILHDGNALATRILER	126
NTDB id 290 KZH43 RS10025 WP 001109677.1	TELPFSRRLQILFDEAEYVASVVHAKVLGTEHVLYAILHDGNALATRILER	126
NTDB id 287 SP RS11210 WP 001109712.1	TELPFSRRLQVLFDEAEYVASVVHAKVLGTEHVLYAILHDSNALATRILER	126
NTDB id 377 SMU RS09275 WP 002262344.1	MLLEQSHALKRTLAEAAAISQVTHAKEVGTEHVLFAMLLNPNLLATRILEL	130
NTDB id 297 STER RS00545 WP 011680614.1	DLRAQSPALEAMLQEAQEIASVTGAVEVGSSEHVLMFAFLHKKDLMVCRLLLEV	132
NTDB id 329 STU RS10020 WP 011225298.1	DLRAQSPALEAMLQEAQGIASVTGAVEVGSSEHVLMFAFLHKKDLMVCRLLLEV	132
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NTDB id 290 KZH43 RS10025 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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Sequence	Score
LDEILLSSKNKNNEIKIIFLEKLIQDSRSYSSYLLKKHN.....INLNKIQLQNHENIQNLNNHTSD	147
.....FNP.FNDIFSALQ.G.QDFNGAASN.....QTPPTQTGG.....RGRPGPQNPRAKQPKGMLLEFGIN	113
.....FDP.FGDFFNLDN.NFRPSSN..TP....PIPTQSGGGYGGNGGYGSQNRGSAQTTPPSQEKGLLEFGIN	119
.....FDP.FGDFFNLDN.NFRPSSN..TP....PIPTQSGGGYGGNGGYGSQNRGSAQTTPPSQEKGLLEFGIN	119
.....FDP.FGDFFNLDN.NFRPSSN..TP....PIPTQSGGGYGGNGGYGSQNRGSAQTTPPSQEKGLLEFGIN	119
.....FDP.FGDFFNLDN.NFRPSSN..TP....PIPTQSGGGYGGNGGYGSQNRGSAQTTPPSQEKGLLEFGIN	119
.....INPFFDFFFGDLN.NFRFNNQDLP....NTPPTQAGCGNGNGGN.N.RRPGGPQQQASQKPNGLLEFGIN	120
...LGVSLNKAQQVLQL.....LGSNET.....GSSAAGTNSNANTPTLDSLARD	169
.....QKINIVSLRKELE.KRTGLKVPESKKAVTPMSKRKMAKG.....VAENSTPTLDSVSSD	182
..AGFSYEDKKDQVKIAALRRNLE.ERAGWTREDLKA.LRQRHRTV.ADK.....QNSMANMMGMPQTTPSGGLEDYTHD	195
..AGFSYEDKKDQVKIAALRRNLE.ERAGWTREDLKA.LRQRHRTV.ADK.....QNSMANMMGMPQTTPSGGLEDYTHD	195
..AGFSYEDKKDQVKIAALRRNLE.ERAGWTREDLKA.LRQRHRTV.ADK.....QNSMANMMGMPQTTPSGGLEDYTHD	195
..VGFHAKDDGESIRLLDLRKVLE.RYAGFSKEDIKA.IFEMRKPKKVKN.....SSSFSDLMKPP.SVTGELADFTRD	199
..AGFQYKDDSDKPRIIDLRRSLE.RNAGLSKQDLKA.IHDLRKPKKSKA.....SANFANMMQPPQSSTGELADYTKD	202
..AGFQYKDDSDKPRIIDLRRSLE.RNAGLSKQDLKA.IHDLRKPKKSKA.....SANFANMMQPPQSSTGELADYTKD	202

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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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Sequence	Score
LTLLAQNGKIDPLIGRKFEIERMMQILSRRTKNNPVLVGEAGVGKTAIVEGLALATAIEKKVPKNLQNAKIFSLDMASILAGTKYR	232
ITESARRGEIDPVIGRDEEIKRVIEILNRRRTKNNPVLIGEPGVGKTAVVEGLAQKIVDGDVPQKLQNKEVIRLDVVSILVQGTGIR	198
VTEIARRGDIIDPVIGRDEEIRVIEILNRRRTKNNPVLIGEPGVGKTAVVEGLAQKIVDGDVPHKLQGGKQVIRLDVVSILVQGTGIR	204
VTEIARRGDIIDPVIGRDEEIRVIEILNRRRTKNNPVLIGEPGVGKTAVVEGLAQKIVDGDVPHKLQGGKQVIRLDVVSILVQGTGIR	204
VTEIARRGDIIDPVIGRDEEIRVIEILNRRRTKNNPVLIGEPGVGKTAVVEGLAQKIVDGDVPHKLQGGKQVIRLDVVSILVQGTGIR	204
VTEIARRGDIIDPVIGRDEEIRVIEILNRRRTKNNPVLIGEPGVGKTAVVEGLAQKIVDGDVPHKLQGGKQVIRLDVVSILVQGTGIR	204
LTDIARKGEIDPVIGRDEEITRVIEILNRRRTKNNPVLIGEPGVGKTAVVEGLAQKIVDGDVPQKLHGKNVIRLDVVSILVQGTGIR	205
LTATAKEDSLDPVIGRSKEIQRVIEVLSRRTKNNPVLIGEPGVGKTAVVEGLAQKIVDGDVPEILRDKRVMITLDMGTVVAGTKYR	254
LTEEARLGLKIDMIGRAEIDRLIHLSRRTKNNPVLIGEPGVGKSAIEGLAQKIVDGDVPEILMNSRIMALNMATVVAGTKFR	267
LTEQARSCKLEPVIGRDKIEISRMQILSRKTNNPVLVGDAGVGKTALALGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFR	280
LTEQARSCKLEPVIGRDKIEISRMQILSRKTNNPVLVGDAGVGKTALALGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFR	280
LTEQARSCKLEPVIGRDKIEISRMQILSRKTNNPVLVGDAGVGKTALALGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFR	280
LTELARQGRLEPVIGREQEISRMVQILSRKTNNPVLVGDAGVGKTALAYGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFR	284
LTALAESGNLDPVIGRDEEISRMQVLSRKTNNPVLVGEAGVGKTALALGLAQRIASGEVPFELADMRIEELDMMSVVAGTRFR	287
LTALAESGNLDPVIGRDEEISRMQVLSRKTNNPVLVGEAGVGKTALALGLAQRIASGEVPFELADMRIEELDMMSVVAGTRFR	287

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NTDB id 290 KZH43 RS10025 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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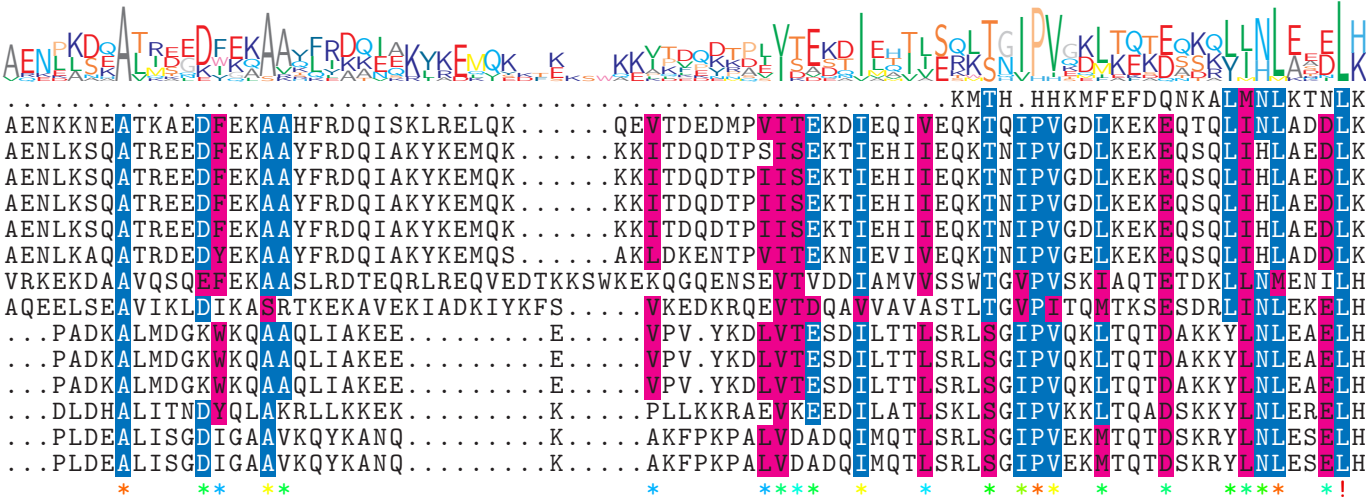
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consensus



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NTDB id 1474 Cj1108 YP 002344501.1
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consensus



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NTDB id	1474 Cj1108 YP_002344501.1	YIGFEEGGLLSNAIRKNPFSLVLFDEIEKAHPDLSNITFLQIFDNAELTDNSGLKVDFKNTIIIMTSNLGLKE...SNELGFLSKN	590
NTDB id	601 KW2 RS02615 WP_021036805.1	YVGVEEAGQLTERVRRNPYSLLILDEIEKAHPDVMMHFLQILEDGRLTDAQGRTVSFKDSLIIIMTSNAGTGK..VEASVGFGAAR	611
NTDB id	241 SP_RS04015 WP_000882523.1	YVGYDEAGQLTEKVRHNYPYSLLILDEVEKAHPDVMMHFLQVLDDGRLTDGGQGRTVSFKDAIIMTSNAGTGK..TEASVGFGAAR	617
NTDB id	243 SPR_RS03635 WP_000882517.1	YVGYDEAGQLTEKVRHNYPYSLLILDEVEKAHPDVMMHFLQVLDDGRLTDGGQGRTVSFKDAIIMTSNAGTGK..TEASVGFGAAR	617
NTDB id	245 SPD_RS03860 WP_000882517.1	YVGYDEAGQLTEKVRHNYPYSLLILDEVEKAHPDVMMHFLQVLDDGRLTDGGQGRTVSFKDAIIMTSNAGTGK..TEASVGFGAAR	617
NTDB id	281 KZH43_RS03550 WP_000882517.1	YVGYDEAGQLTEKVRHNYPYSLLILDEVEKAHPDVMMHFLQVLDDGRLTDGGQGRTVSFKDAIIMTSNAGTGK..TEASVGFGAAR	617
NTDB id	378 SMU_RS02690 WP_002263569.1	YVGVEEAGQLTEKVRRNYPYSLLILDEVEKAHPDVMMHFLQVLDDGRLTDGGQGRTVSFKDTIIIMTSNAGTGK..SEANVGF GASR	618
NTDB id	85 BSU_00860 NP_387967.1	YVGYDEGGQLTEKVRRKYPYSVLLLEIEKAHPDVFNILLQVLEDGRLTDSKGRTVDFRNTILIMTSNVGASELKR NKYVGVNFVQD	677
NTDB id	610 V4T04_RS10165 WP_012897346.1	YVGYDEGGQLTERVVRNKYPYSVLLLEVEKAHPDVFNIMLQLDDGFVTDTKGRKVDFRNTIIIMTSNLGATALRDDKT VGFGAKN	686
NTDB id	289 SPD_RS10700 WP_001109677.1	YVGVEEGGELTEKVRNKYPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDKT VGFGAKD	681
NTDB id	290 KZH43_RS10025 WP_001109677.1	YVGVEEGGELTEKVRNKYPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDKT VGFGAKD	681
NTDB id	287 SP_RS11210 WP_001109712.1	YVGVEEGGELTEKVRNKYPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDKT VGFGAKD	681
NTDB id	377 SMU_RS09275 WP_002262344.1	YVGVEEGGELTEKVRNKYPYSVLLFDEVEKAHPDIFNILLQVLDDGVLTDSRG RKVDFSNTIIIMTSNLGATALRDDKT VGFGAKS	684
NTDB id	297 STER_RS00545 WP_011680614.1	YVGYDEGGELTEKVRNKYPYSVLLFDEIEKAHPDIFNILLQVLDDGVLTDSRG RKVDFSNTIIIMTSNLGATALRDDKT VGFGAQT	687
NTDB id	329 STU_RS10020 WP_011225298.1	YVGYDEGGELTEKVRNKYPYSVLLFDEIEKAHPDIFNVLLQVLDDGVLTDSRG RKVDFSNTIIIMTSNLGATALRDDKT VGFGAQT	687
consensus		!*~**~*! ~***** !*~***! !!~!!!!!!* *~* !~***** *!! ~*~*!~*****!!!!!!* ~*~*~*~*	

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NTDB id	1474 Cj1108 YP 002344501.1	EKK.....SNRAIKDFFAFEFINRIDKI LHFNDLNDAILVKITIEKELDEISKNL...NNTIKLSVDDKAKIYLAKKAAYNKEFGV	665
NTDB id	601 KW2 RS02615 WP 021036805.1	EG.....RTKSVLGQLIGDFFSPEFMNRFDGI IEFSAISKENLLKIVDLMLDEVNEQIGRNDIHLSVTQAAKEKLVDLGYNPAMGA	691
NTDB id	241 SP RS04015 WP 000882523.1	EG.....RTNSVLGELGNFFSPEFMNRFDGI IEFKALSKDNLLQIVELMLADVKNRLSSNNIRLDVTDKVKEKLVLDGYDPKMGA	697
NTDB id	243 SPR RS03635 WP 000882517.1	EG.....RTNSVLGELGNFFSPEFMNRFDGI IEFKALSKDNLLQIVELMLADVKNRLSSNNIRLDVTDKVKEKLVLDGYDPKMGA	697
NTDB id	245 SPD RS03860 WP 000882517.1	EG.....RTNSVLGELGNFFSPEFMNRFDGI IEFKALSKDNLLQIVELMLADVKNRLSSNNIRLDVTDKVKEKLVLDGYDPKMGA	697
NTDB id	281 KZH43 RS03550 WP 000882517.1	EG.....RTNSVLGELGNFFSPEFMNRFDGI IEFKALSKDNLLQIVELMLADVKNRLSSNNIRLDVTDKVKEKLVLDGYDPKMGA	697
NTDB id	378 SMU RS02690 WP 002263569.1	EG.....RTNSVLGELGNFFSPEFMNRFDGI IEFQALSKDNLLQIVSLMLDDVNQRILAVNAIHLDVTDKVKEKLVLDGYDPKMGA	698
NTDB id	85 BSU 00860 NP 387967.1	ETQNHKDMKDVMGELKRAFREFEINRIIDEI IVFHSLEKKHLTEIVSLMSDQLTKRLKEQDLSTIELTDAAKAKVAEEGVLDLEYGA	762
NTDB id	610 V4T04 RS10165 WP 012897346.1	ITADYSAMKSRILEELKRHYRPEFLNRIDENIVFHSLESQEITEIQVIMSKSLIKRLAEQDIHVKLTPSAVKLIAEVGFDPPEYGA	771
NTDB id	289 SPD RS10700 WP 001109677.1	IRFDQENMEKRMFEELKKAYRPEFLNRIDEKVVFHSLSDDHMQEVVKIMVKPLVASLAEEKIDLKLQASALKLLANQGYDPEMGA	766
NTDB id	290 KZH43 RS10025 WP 001109677.1	IRFDQENMEKRMFEELKKAYRPEFLNRIDEKVVFHSLSDDHMQEVVKIMVKPLVASLAEEKIDLKLQASALKLLANQGYDPEMGA	766
NTDB id	287 SP RS11210 WP 001109712.1	IRFDQENMEKRMFEELKKAYRPEFLNRIDEKVVFHSLSDDHMQEVVKIMVKPLVASLTEKGIDLKLQASALKLLANQGYDPEMGA	766
NTDB id	377 SMU RS09275 WP 002262344.1	FSQDYKAMESRILEELKKVYRPEFLNRIDEKVVFNHLQGEDI RHIVKIMVAPLIAHLADQG ITLKFKQPSALKHLALAGYDAEMGA	769
NTDB id	297 STER RS00545 WP 011680614.1	ISHNHQAMQARIMEELKKSYPREFINRIIDEKVVFHSLLEEQLHDIVKIMVKPLISALADKG ISLKFKQPAALKHLAKDGYDIEMGA	772
NTDB id	329 STU RS10020 WP 011225298.1	ISHNHQAMQARIMEELKKSYPREFINRIIDEKVVFHSLLEEQLHDIVKIMVKPLISALADKG ISLKFKQPAALKHLAKDGYDIEMGA	772
consensus		** * ** * ! ! ! ! ! ! ! * ! ! * * * * * * * * * *	

NTDB	id	1474	Cj1108	YP	002344501.1	RLLKRIITSEEIGEKISDEILFCKIKKCGIAKIKLGKNEK	EFIF.....	709	
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NTDB	id	241	SP	RS04015	WP	000882523.1	RPLRRTIQDYIEDTITDYYLENPSEKDLKAVMTSKGN	IQIKSAKKA.EVKSSSEKEK	752
NTDB	id	243	SPR	RS03635	WP	000882517.1	RPLRRTIQDYIEDTITDYYLENPSEKDLKAVMTSKGN	IQIKSAKKA.EVKSSSEKEK	752
NTDB	id	245	SPD	RS03860	WP	000882517.1	RPLRRTIQDYIEDTITDYYLENPSEKDLKAVMTSKGN	IQIKSAKKA.EVKSSSEKEK	752
NTDB	id	281	KZH43	RS03550	WP	000882517.1	RPLRRTIQDYIEDTITDYYLENPSEKDLKAVMTSKGN	IQIKSAKKA.EVKSSSEKEK	752
NTDB	id	378	SMU	RS02690	WP	002263569.1	RPLRRTIQEHIEDAITDFYLEHPEQKELKAIMTSMCK	IVIKASNKV.ETVTKATSD	753
NTDB	id	85	BSU	00860	NP	387967.1	RPLRRAIQKHVEDRLSEELLRGNTHKQGHIVLDVEDGE	FVVKTTAKTN.....	810
NTDB	id	610	V4T04	RS10165	WP	012897346.1	RPLRKALQKEVEDLLSEQLLSGEIKACNHVSTIGASNKK	LKIAQIV.....	816
NTDB	id	289	SPD	RS10700	WP	001109677.1	RPLRRTLQTEVEDKLAELLKGDIVAGSILKIGVKAGQ	LKFDIA.....	810
NTDB	id	290	KZH43	RS10025	WP	001109677.1	RPLRRTLQTEVEDKLAELLKGDIVAGSILKIGVKAGQ	LKFDIA.....	810
NTDB	id	287	SP	RS11210	WP	001109712.1	RPLRRTLQTEVEDKLAELLKGDIVAGSTLKIGVKAGQ	LKFDIA.....	810
NTDB	id	377	SMU	RS09275	WP	002262344.1	RPLRRTLQTEVEDKLAELLSCQLKIGIQKEK	LKFDIV.....	813
NTDB	id	297	STER	RS00545	WP	011680614.1	RPLRRTIQTEVEDKLSLELLGQGVVSCQTLKIGCSKDK	LTFTVV.....	816
NTDB	id	329	STU	RS10020	WP	011225298.1	RPLRRTITQVEDKLSLELLGQGVVSCQTLKIGCSKDK	LTFTVV.....	816
consensus						!*!*****	*** * * * *	*** * * *	816

-  non conserved
-  similar
-  $\geq 50\%$ conserved