NOTES

Characterization of the groEL-Like Genes in Streptomyces albus

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Three GroEL-like heat shock proteins (HSP56, HSP58, and HSP18) have been observed in *Streptomyces albus* (G. Guglielmi, P. Mazodier, C. J. Thompson, and J. Davies, J. Bacteriol. 173:7374–7381, 1991). Here we report the cloning and complete nucleotide sequence of *groEL1*, which encodes HSP18 and HSP58, and *groEL2*, which encodes HSP56. Both nucleotide sequences predicted proteins of 56,680 Da that were 70% identical. The 5' nucleotide sequence of *groEL1* coded for a protein corresponding to HSP18 that may be a processed gene product. At least two *groEL1*-like genes were present in all 12 *Streptomyces* species tested; they were not closely linked in the genome. *groEL1*, but not *groEL2*, was adjacent to a *groES*-like gene.

Pleiotropic genetic phenotypes and biochemical properties have demonstrated that the heat shock proteins of the GroEL family have physiologically diverse functions (for reviews, see references 13, 17, and 20). GroEL was originally named for the role it plays in bacteriophage virion assembly (7, 28), although its more general function was suggested by the fact that it is essential for viability of Escherichia coli at all temperatures (5) and that overproduction of GroEL suppresses defects in various enzymes (24). These apparently disparate phenotypes are presumed to be indirect and a reflection of the primary activity of GroEL in stabilizing intermediates in protein folding pathways that may lead to the export or assembly of enzyme complexes (12). Apparently, GroEL cannot provide this function for all proteins; SecB, DnaK, and the trigger factor seem to play similar roles but have different substrate specificities (1, 12). In spite of these diverse functions, which overlap with those of other proteins controlling protein renaturation, only one groEL gene has been reported so far in the numerous eubacteria that have been studied. Our observation of three GroEL-like proteins (HSP18, HSP56, and HSP58) in Streptomyces albus (8) implied that there are multiple copies of groEL-like genes in this organism. Although the amino acid sequence of the N-terminal region of HSP18 was similar to that of GroEL from various bacteria, its size (18 kDa) and basic charge were very different from those of all other GroEL proteins described to date, which, like HSP56 and HSP58, are acidic and have apparent molecular masses ranging from 55 to 65 kDa.

Cloning of two S. *albus groEL*-like genes. *XhoI* fragments (1.2 and 1.8 kb) that contained different *S. albus groEL*-like genes (8) were partially purified from genomic DNA by agarose gel electrophoresis and cloned into the *SalI* site of pUC19 (25). Plasmid pGM1, containing a 1.8-kb insert, was isolated by screening with a *groEL1*-specific probe (OL1 [8]); pGM2, containing a 1.2 kb insert, was isolated by screening with a probe corresponding to the 5' region of the

Mycobacterium leprae groEL gene (15). DNA inserts in pGM1 and pGM2 were then used as probes to screen a genomic bank generated with cosmid pHC79 (11). Recombinant cosmids were obtained that hybridized to the 1.8-kb (pGM3) or 1.2-kb (pGM4) XhoI fragment. The fragments of pGM3 and pGM4 that corresponded to the region within and adjacent to the XhoI fragments were determined by Southern blot hybridization and subcloned into M13 for dideoxy sequencing reactions (19).

Sequence of groEL1. The nucleotide sequence of the region of pGM3 that corresponded to OL1, HSP18, and HSP58 is shown in Fig. 1. Codon usage analysis (data not shown) predicted a functional open reading frame (groEL1) that encoded an acidic protein (a pI of 4.60 was predicted by using the University of Wisconsin sequence analysis program Isoelectric) of 56,681 Da whose N-terminal amino acids corresponded to Edman degradation products of the N terminus of HSP58 (10 residues analyzed) and N-terminal and internal V8-generated peptides of HSP18 (48 of 49 residues analyzed). Although these amino acid sequence identities were unexpected, they provided strong evidence that HSP18 was the product of the groEL1 gene. The hybridization data cited above (8) indicated that S. albus has only two groEL-like genes; nucleotide sequence analysis described below showed that the second gene did not encode HSP18. Nevertheless, the nucleotide sequence of groEL1 (which has been determined from two independent clones, pGM1 and pGM3) had no in-frame stop codon that could give rise to an 18-kDa peptide. Since the predicted N-terminal 21-kDa polypeptide of GroEL (HSP18 migrates as a 21-kDa band under some denaturing conditions [8]) is acidic (estimated from the first 201 amino acids of groEL1; pI 4.43), the basic charge of HSP18 (8) also cannot be explained directly from the primary sequence of groEL1.

The synthesis of a truncated basic protein (HSP18) could be explained by ribosomal frameshifting at a site within groEL1. Frameshifting can generate unexpected alternative gene products (2) that are sometimes functional. For example (4, 6, 23), in the *E. coli dnaX* gene that encodes DNA

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1	ACACAGCGACGGGCAGGTCCGGCACCGCGACGACGGACGACCTGGTCGCCACACTCAG
61	ATCAGTTAACCCCGTGATCTCCGAAGGGGGAGGTCGGATCGTGACGACCGCCAGCTCCAA V T T A S S K
121	GGTTGCCATCAAGCCGCTCGAGGACCGCATCGTGGTCCAGCCGCTCGACGCCGAGCAGAC V A I K P L E D R I V V Q P L D A E Q T
181	CACGGCTTCGGGCCTGGTCATCCCGGACACCGCGAAGGAAG
241	CCTCGCGGTCGGCCCGCGCCGCCTTCGAGAACGGCGAGCGCCTGCCCTCGACGTCGAGACGC L A V G P G R F E N G E R L P L D V K T
301	CCCCCACGTCCTCCTCTACAGCAAGCAACGTACGCCGAGGCCCAAGCAACGACGACGACGACGACGACGAC
361	GTACCTCGTCCTCTCGGCCCGCGACGTTCTCGCCATCATCGAGAAGTAGCAGGCCGGAGC Y L V L S A R D V L A T T F K
421	GGTCCGGGGCGCGAGCCCGGACGCCAGACTCCACCTTTTTCCTGAAGCGCGCCCCTGGCCC
481	CCCCCGAGTGTTTGCCGGGTGGCGAGGGGCGCGTTTCATTTCGAGAGCGCGGCGGCAGGCC
541	GCTCCGAGAGGATTCGAAAAGCTCCCATGGCGAAGATTCTGAAGTTCGACGACGCCC M A K I L K F D E D A R
601	GTCGCGCCCTTGAGCGGCGCGAACACCAGCGGCCGACACCGTCAAGGTGACCATCGGCC
661	CCNAGGCCCCCAACGTCGTCATCGACAAGAAGTTCGGCCGCCCCGACCATCACCAACGACG
721	CCETCACCATCECCCETERGETCERETCERCETCETCERCET
781	TCGTCAAGGAGGTGGCGACCAAGACCAACGACCACCACCACCACCACCACCAC
• • •	<u>V K E V A T K T N D I A G D G T T T A T</u>
041	<u><u>U</u> L A Q A L V R E G L R N V A A G A S P</u>
901	CGGCCGCCCTGAAGAAGGGCATCGACGCCGCCGTCGCCGCCGTCTCCGCCGAGCTGCTCG A A L K K G I D A A V A A V S A E L L D
961	ACACCECEGCECCEATCEACEACAAGTCCEACEATCECCEGCEGTCCECCEGCECTCCCCEGCE T A R P I D D K S D I A A V A A L S A Q
1021	AGGACAAGCAGGTCGGCGAGCTCATCGCCGAGGCGATGGACAAGGTCGGCCAAGGACGGCG D K Q V G E L I A E A M D K V G K D G V
1081	TCATCACCGTCGAGGAGTCCAACACCTTCGGTGTCGACCTGGACTTCACCGAGGGCATGG I T V E E S N T F G V D L D F T E G M A
1141	CCTTCGACAAGGGCTACCTGTCCCCGTACATGGTGACCGACC
1201	TOCTOGACGACCCGTACATCCTGATCCACCAGGCCAAGATCGGTTCGATCCAGGACTGC L D D P Y I L I H O G K I G S I O D L L
1261	TOCCCCTCCTCCAGAGGTCATCCAGCCCCCTCCCAACCCCCTCCAACACCCCCCCC
1321	AGGACGTCGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
1381	ACCOUNT A V K A P G F G P C P C COUNT CONTRACTOR
1441	TEGECACCETCACCEGTEATCSCCCEAEGAGETCGSCCTCAACCTCGACCAGE A T L T G A T V I A E E V G L K L D O A

1501 CCGGTCTGGACGTGCTGGGCACCGCCGCCGCGTCACCGTCACCAAGGACGACACGACCA G L D V L G T A R R V T V T K D D T T 1561 TCGTGGACGGCGGCGGCGAACGCCGAGGACGTCCAGGGCCGCGTCGCCCAGATCAAGGCCG V D G G G N A E D V Q G R V A Q I K A

1621 AGATCGAGTCGACCGACTCGGACTGGGACCGCGAGAAGCTCCAGGAGCGCCTCGCCAAGC I E S T D S D W D R E K L Q E R L A K L G G V C V I R V G A A T E V E L K E R K H R L E D A I S A T R A A v EEG 1801 TCTCCGGTGGTGGCTCCGCGCTGGTCCACGCCGTCAAGGTCCTGGACGACAACCTCGGCC K V L ΗA DD L

polymerase III, the in-frame translational stop signal encodes a 71-kDa polymerase subunit. A -1 translational frameshift occurs in 50% of the transcripts at a site within the gene; as a result, ribosomes terminate early in the new frame NOTES 7383

W I A E N A G L E G Y V I T 1981 TCGACAAGGGCCAGGGCTACAGGGGCGACGACGGGGGAGTACGGC -D K G Q G F N A A T G E Y G 2041 GCGTCATCGACCCGGTCAAGGTCAACGCCCTCGGCGCTGGGAGAAC	TKVAEL
1981 TCGACAAGGGCCAGGGCTTCAACGCGGCCACCGGCGAGTACGGC _D K G Q G F N A A T G E Y G 2041 GCGTCATCGACCCGGTCAAGGTCAACGCCCCGCCCTGGAGAAC	
-D K G Q G F N A A T G E Y G 2041 GCGTCATCGACCGGGTCAAGGTCACCGGCTCGGCGCTGGAGAAC	CGACCTGGTCAAGGCCG
2041 GCGTCATCGACCCGGTCAAGGTCACCCGCTCGGCCTGGAGAA	DLVKAG
VIDPVKVTPSAIPN	CGCGGCCTCCATCGCCT
· · · · · · · · · · · · · · · · · · ·	λλ S Ι λ S
2101 CCCTGCTCCTGACGACCGAGACCCTGGTCGTCGAGAAGCCGGCC	CGAGGAGGAGCCCGAGG
LLLTTETLVVEKPA	ΕΕΕΡΕλ
2161 CCGGTCACGGTCACGGGCACAGCCACTGAGGCTGACCCCTTCCC	GCAGCOGAGGCCCGGCT
GHGHGHSH *	
	CGGGACGCGCGACGCCT
2281 ACCGCGGCCCGTACTTGCGGCCGGTACGCGAGGTCATCCCGGTC	CAGCAGGGCCCGCGGGG
2341 TCAGCTTCACCAGGCCCATCAGCGCCTTGTACCGAGGGTCCGGG	GAT 2386

FIG. 1. Nucleotide sequence of groEL1 and groES. Arrows indicate imperfect inverted repeat sequences. Underlining indicates experimental amino acid sequence data (8). The double-underlined T (threonine) residue indicates the only inconsistency with the experimentally determined peptide sequence (P2) (8).

to yield a 52-kDa protein. Both the 52- and 71-kDa products are thought to have physiological roles. In the case of groEL1, which can be translated as a full-sized protein of 58 kDa (8), a +2 or -1 frameshift would generate a stop codon to produce a 21-kDa basic protein. Alternatively, posttranslational cleavage and modification of GroEL1 are possible. We are carrying out C-terminal amino acid analysis of HSP18 to distinguish between these possibilities.

Codon usage analyses predict that the region upstream of groEL1 contains a functional open reading frame encoding a 10,948-Da protein that is homologous to GroES found in a variety of bacteria, including E. coli, Coxiella spp., Legionella spp., cyanobacteria, Mycobacterium tuberculosis, and M. bovis (data not shown). The groES-like gene is separated from the groEL-like gene by a long inverted repeat sequence that contains a motif (TTTCAT[16 N]TTGCCG) that is also present upstream of the *M. tuberculosis*, *M. bovis*, and *M.* leprae groEL-like genes (3).

Sequence of groEL2. The nucleotide sequence of the region of pGM4 that hybridized to the M. leprae probe (Fig. 2) showed that it was different from groEL1. Codon usage analysis (data not shown) predicted a functional open reading frame that encoded an acidic protein (predicted pI, 4.61; GroEL2) of 56,682 Da whose N-terminal amino acids corresponded to the 10 N-terminal residues of HSP56 (8). Inspection of the sequence within 200 bp of groEL2 did not reveal a groES-like gene like that near groEL1.

Similarities between GroEL1, GroEL2, and eubacterial GroEL proteins. Although GroEL1 and GroEL2 were 70% identical, there were significant differences. GroEL1 did not contain the Gly-Gly-Met motif found near the C terminus of these procaryotic proteins and in all reported eucaryotic HSP56-58 proteins (with the exception of chloroplast rubisco-binding protein). Instead, the C terminus of GroEL1 contained the motif Gly-His-Gly-His-Gly-His-Ser-His.

A comparison of GroEL1, GroEL2 and other eubacterial GroEL proteins is shown in Fig. 3. With this alignment, the percent amino acid identity for all pairwise combinations was calculated and presented as a dendrogram (Fig. 4). This analysis revealed that, although GroEL1 clearly belonged to the actinomycete group, it was distinguishable from all other members, which formed a distinct family.

Multiple groEL-like genes in streptomycete genomes. Southern blots of genomic DNA isolated from 12 different Streptomyces spp. (S. albus and S. coelicolor A3 [2] [John Innes 7384 NOTES J. BACTERIOL.

		S. sp. B. coli
-		C. burn L. paet M. bovi
1 61		N. tube N. leps S. ALM
	МАКІІАР	S. ALBO
121	CGACGAGGAGGCGCGCGCGCGCGCGCGCGCGGGATGAACCAGCTCGCCGACGCCGTCAA D E E A R R G L E R G M N Q L A D A V K	S. sp. E. coli
181	GGTCACCCTTGGCCCCAAGGCCGCAACGTCGTCCTCGAGAAGAAGTGGGGGGCCCCCCAC V T L G P K G R N V V L E K K W G A P T	L. paet N. bovi
241	GATCACCAACGATGGTGTCTCCATCGCCAAGGAGATCGAGCTCGAAGACCCGTACGAGAA I T N D G V S I A K E I E L E D P Y E K	N. lepi S. ALBC
301	GATCGGCGCCGAGCTGGTCAAGGAGGTCGCGAAGAAGACGGACG	CONSER
361		E. col. C. burn
	T T T A T V L A Q A L V R E G L R N V A	N. bov. N. tub
421	CCCGGGTGCCAACCCGATGCCCTGAGCCGCGCATCGAGAGCCCTCGAGCCGTUTC A G A N P M A L K R G I E K A V E A V S	S. ALB S. ALB
481	CTCCGCCCTGCTGGAGCAGGCGAAGGACGTGGAGACCAAGGAGCAGATCGCCTCCACCGC S A L L E Q A K D V E T K E Q I A S T A	CONSER S. sp.
541	CTCCATCTCCGCCGCCGACACCCAGATCGGCGAGCTGATCGCCGAGGCCATGGACAAGGT S I S A A D T O I G E L I A E A M D K V	E. col: C. burn L. pnes
601	CGGCAAGGAAGGCGTCATCACCGTCGAGGAGTCCCAGACCTTCGGTCTGGAGCTGGAGCT	N. bov. N. tube N. leps
661	G R E G V I T V E E S O T F G L E L E L CACCEAGGGTATECGCTTCGACAAGGGCTACATCTCGGCGTACTTCGCCACCGACATGGA	S. ALB S. ALB CONSERV
771	TEGMRFDKGYISAYFATDME	S. sp. E. col.
/21	R M E A S L D D P Y I L I V N S K I G N	C. bur L. pne N. bov
781	CGTGAAGGACCTGCTCCCGCTGCTGGAGAAGGTCATGCAGTCGGGCAAGCCGCTGCTGAT V K D L L P L L E K V M Q S G K P L L I	H. tub H. lep S. ALB
841	CATCGCCGAGGACGTCGAGGCGAGGCCCTGTCGACCTGGTGGTCAACAAGATCCGTGG I A E D V E G E A L S T L V V N K I R G	S. ALB CONSER
901	CACCTTCAAGTCCGTCGCCGTCAAGGCCCCCGGGCTTCGGCGACCGCCGCAAGGCCATGCT	S. sp. E. col C. bur
961	CGGTGACATCGCCATCCTCACGGCGGCGCCACGGTCATCTCCGAGGAGGTCGGCCTCAAGGT	L. pne N. bov N. tub
1021	G D I A I L T G G T V I S E E V G L K L	M. lep S. ALB S. ALB
1021	E N A G L D L L G R A R K V V I T K D E	CONSER
1081	GACCACGATCGTCGACGGTGCCGGCGACACGGACCAGGTCAACGGCCGCGTCGCGCAGAT T T I V D G λ G D T D Q V N G R V λ Q I	E. col C. bur L. pae
1141	CCGCCCCGAGATCGAGAACAGCGACTACGACTGCGCGAGAAGCTCCAGGAGCGTCT R A E I E N S D S D Y D R E K L Q E R L	N. bov N. tub M. lez
1201	GCGANCGTGGCCGGCGCGGCGCGCGCCGCCACCGACGCCGCGCGCG	S. ALB S. ALB CONSER
1 261	GAAGGAGCECAAGCACCGCATCGAGGACGCGGTGCGCAACGCCAAGGCCGCCGTCGAGGA	S. sp. K. col
1 3 2 1		C. bur L. pne
1361	G I V A G G G V A L L Q A S S V F E K L	N. tub N. lep
1381	CGAGCTCGAGGGCGACGAGGCCACCGGTGCCGCCGCCGCCGCGCGTGGAGGCCCC E L E G D E A T G A A A V K L A L E A P	S. ALE CONSER
1441	CCTCAAGCAGATCGCCGTCAACGGTGGCGCGCGCGGGGGGGG	S. sp. E. col
1501	CAACCTCTCCGTGGGCCCACGGCCTGAACGCCGCGCCGC	L. pne N. boy
1561	CGAGGGCATCCTCGACCCGGCCAAGGTGACGCGTTCCGCGCGCCCCAGAACGCCGCGTCGAT	n. tub N. lep S. ALB
1621	E G I L D P A K V T R S A L Q N A A S I	S. ALB CONSER
1061	A A L F L T T E A V I A D K P E K A A A	S. sp. E. col C. bur
1681	CGCTGCCCCGGGTGGCATGCCCGGCGGTGACATGGACTTCTGACCGGACCCGCCTTCCGG A A P G G M P G G D M D F *	L. pne N. bov N. tub
1741	TCGGCCCGTCCGGCACCACGCCCCACCGGGGCGGTGTCCCTCTTCCGAGGATGCCGCCCC	M. lep S. Alb S. Alb
1901	GETGEGETTEETTEE 1814	CONSER

FIG. 2. Nucleotide sequence of groEL2. The arrows indicate the position of an imperfect inverted repeat.

5. sp. 7942	
-	MAKRII-YNENARRALEKGIDILAEAVAVTLGPKGRNVVLEKKFGAPQIINDGVTIAKEI
. coli	MAARDVKFGNDARVKNLRGVNVLADAVKVTLGPRGRNVVLDKSFGAPTITKDGVSVARE I
. burnet i	MAAKVI KUSHEVI HAMENGUEVI ANAVEVTI CONCOMVU DESTCAPTI TEDCUSVAKE I
. portadoro.	In The Address of the Article And the Article Address of the Addre
·	
. CUDWICUL.	nn-alialusikanalanalahavavilipninuvilarnikartiitkogvilarei
. leprae	PA-KIIAIDEEARRCLERGLERGLERGLERGLERGERVVLERREGEPTIIRDGVSIAKEI
. ALBUS-30	nn-allar di sakrigi leningi adavavi ligerigri ve lerrigapti trogvsi ake i
. ALSUS-58	NA-ALLAF DEDARKALENGVINDLADTVKVTIGPRENNVVIDKRFGAPTITNDGVTIAREV
CONSERVED	NA G. LA. V VT.GP.GRNVV. K. GAP DGV. A.E.
5. sp. 7942	ELEDHIENTGVALIRQAASKTNDAAGDGTTTATVLAHAVVKEGLENVAAGANAILLERGI
. coli	ELEDIG EINGAONVKEVAEKANDAAGDGTTTATVLAGALITTEGLKAVAAGNIPHDLKRGI
C. burneti	Eledkfenncaqnykevasrteddagdgtttatvlaqailyegikavlagnnphdlkrgi
L. paeumono.	EFEBRFIOINGAQNVKEVASKTSDTAGDGTTTATVLARSILVEGEKAVAAGHIPHDLKRGI
4. bovis	ELEOPYERIGAELVKEVAKKTODVAGDGTTTATVLAQALVREGLENVAAGAMPLGLKRGI
W. tubercul.	ELEDPYERIGAELVREVARKTDOVAGDGTTTATVLAQALVREGLANVAAGANPLGLRRGI
4. lepree	ELEDPYERICAELVKEVAKKTODVACDCTTTATVLAQALVKECLENVAAGANPLCLKRCI
S. ALBUS-56	ELEDPYEKIGAELVKEVAKKTDDVAGDGTTTATVLAQALVREGLRNVAAGANPHALKRGI
S. ALBUS-58	ECDDPYENLGAQLVKEVATKINDIAGDGTTTATVLAQALVREGLRNVAAGASPAALKKGI
CONSERVED	E G A D AGDGTTTATVLA EGV AG LK.GI
	· · · · · · · · · · · · · · · · · · ·
5. sp. 7942	DKATNFLYEQIKSEARPYEDSKSIAQYGAISAGNDFEYGQMIADAMDKYGKEGYISIEEG
. coli	DKAVTAAVEELKALSVPCSDSKAIAQVGTISANSDETVGKLIAEAMDKVGKEGVITVEDG
C. burneti	DRAVTAAVAELKKISKPCKDQKAIAQVGTISANSDKSIGDIIAEAMEKVGKBGVITVEDG
L. paeumoao.	DKAVLAVTKKLQAMEKPCKDEKAIAQVGTISANSDEAIGAIIAEANEKVGKEGVITVEDG
M. bovis	EKAVEKVTETLLEGAKEVETKEQIAATAAISAG-DQBIGDLIAEANDKVGNEGVITVEES
M. tubercul.	ERAVERVTETLLRGAREVETREQIAATAAISAG-DQSIGDLIAEANDRVGNEGVITVEES
M. leprae	EKAVDKVTETLLKDAKEVETKEQIAATAAISAG-DQSIGDLIAEANDKVGNEGVITVEES
S. ALBUS-56	ERAVEAVSSALLEOARDVETKEOIASTASISAA-DTOICELIAEANDRVGREGVITVEES
S. ALBUS-58	DAAVAAVSAELLDTARPIDOKSDIAAVAALSAQ-DKQVGELIAEAMDKVGKDGVITVEES
CONSERVED	. A IASA D .F .IA.AM.KVGGVIE.
S. sp. 7942	KSMTTELEVTEGNRPDRGYISPYFATDTERMEAVFDEPFILITDKKIGLVCDLVPVLEOV
. coli	TGLQDELDVVEGNOFDRGYLSPYFINKPETGAVELESPFILLADKKISNIREMLPVLEAV
C. burneti	SGLENALEVVECHOFDRGYLSPYF INNOCHMEAELEMPF ILLVDERT ENTRELTPLLENV
L. paeumozo.	NGLENELSVVECHOLI-AVESPYFINNOCHMECELEHPFILLVDKEVESIBENLSVLRCV
M. bovis	NTFCLOLELTECNEFDEGYISCYFVTDPERORAVLEDPYILLVSEEVSTVEDLLPLLEEV
M. tubercul.	NTFELOLELTECHEFOREVISCYFVTDPERORAVLEDPYILLVSSEVSTVKDLLPLLEKV
M. leprae	NTFCLOLELTECHEFORCY I SCYFYTDARBORAVLERPYTLLVSSEVSTVKDLLPLLRKV
S. ALBUS-56	OTTCLELELTECHEPDECYTSAYPATOMERIEASLODPYTLTWSETCOVEDLLPLLEKV
S ALBUS-SE	VTPCVDI DPTPCNA PDECVI SPVNUTOPPNPANI DDPVI I TEOCHICSTODI I DI LEV
CONSERVED	I. FCM C V D TI. K IPV
S. sp. 7942	ARAC
E. coli	AKAGKPLLI I A ROVECTALATAVANTI BETVEVAAVKA DEPERAMIOD LATITE
C. burneti	AKSC
L. nneumono.	AKSC
N. bovis	TGAC
M. tubercul.	IGAC
M. lenrae	TOAC
5. AT.B/15-56	MORC
C AT.B//C-58	TALCCEPTIAT TERROT OF UNIT DOPPHEVENUE BORCODDENIA COMPTING
CONSERVED	C I THEO F FAT T VAN DC AVENDERDERAMI C A IT
F	
L. paeumono.	QVISEIGABLEGATLEDIGBARKI VVTRENTTI IDGEGAATEINAKI TUIKAQMEETTS
	QVISESVELTLEMADLELLEMARKVVVTRUETTIVEGAGDTDALAGKVAQINGEIENSUS
C AT.B/76_56	The second of the second secon
S AT.B/18-58	TVI SPEVCI EI DOSCI DVI CTA DBUTUTUDOCTUSCICUS POUCOBUSCI ES ET POTO
CONSERVED	
CONDERVED	
S. en. 7842	SYDEFELOED ANT SCOUNTERANTPREMEDRED TO POATNATE AUPPOTUDCCOTT
E. coli	DYDRENJERAL ACCUANT FUCA ATTENENT FARMENT AT A ATTENE TO OUT I
C. burneti	
	DYDKERLOERLAKLAGGVAVI KVGAATEVENKEKKARVEDALEATRAAVERGVVPGGGVA
L. paeumono.	DYDKEKLQERLAKLAGGVAVI KVGAATEVENKEKKARVEDALEATRAAVEEGVVPGGGVA DYDREKLQERVAKLAGGVAVI KVGAATEVENKEKKARVEDALEATRAAVEEGIVAGGGVA
L. pneumono. M. bovis	DYDREKLOEFLAKLAGGVAVI KVCAATEVENKEKKARVEDALLATEAAVEEGVVAGGGVA DYDREKLOEFLAKLAGGVAVI KVCAATEVENKEKKARVEDALLATEAAVEEGIVAGGGVA DYDREKLOEFLAKLAGGVAVI KAGAATEVEL KEEKEE IDAAVMAKAAVEGIVAGGGVA
L. pneumono. M. bovis M. tubercul.	DYDREKLOERLAKLAGCVAVIKVQAATEVENEKKAAVEDALAATEAAVEECVVPGGCVA DYDREKLOERVAKLAGCVAVIKVQAATEVENEKKAAVEDALAATEAAVEECIVAGGVA DYDREKLOERLAKLAGCVAVIKVQAATEVELKEERIERIEDAVMARAAVEECIVAGGVT DYDREKLOERLAKLAGCVAVIKVQAATEVELKEERIERIEDAVMARAAVEECIVAGGVT
L. pneumono. M. bovis M. tubercul. M. leprae	DYDREKLOERLAKLAGCVAVI KOGAATEVENEKKRARVEDALAATEAAVEEG VVPCGGVA DYDREKLOERVAKLAGCVAVI KOGAATEVENEKKRARVEDALAATEAAVEEG VVCGGVA DYDREKLOERLAKLAGCVAVI KOGAATEVELKERKIIRI EDAVMARAAVEEG VVCGGVT DYDREKLOERLAKLAGCVAVI KOGAATEVELKERKIIRI EDAVMARAAVEEG VVCGGVT
L. pneumono. M. bovis M. tubercul. M. leprae S. ALBUS-56	DYDREKLOERLANLAGGVAVI KVGAATTYSHEIKIKARVEDALAATTAAVEEGVVPGGGVA DYDREKLOERVANLAGGVAVI KVGAATTYSHEIKIKARVEDALAATTAAVEEGVVGGGVA DYDREKLOERVANLAGGVAVI KVGAATTYSHEIKIKARVEDALAATTAAVEEG VVGGGVT DYDREKLOERLANLAGGVAVI KVGAATTYSLIKERKERIE EDAVMARAAVEEG VVGGGVT DYDREKLOERLANLAGGVAVI KKGAATTYSLIKERKERIE EDAVMARAAVEEG VVGGGVA
L. pneumono. M. bovis M. tubercul. M. leprae S. ALBUS-56 S. ALBUS-58	DYDREKLGERLAKLAGGVAVI KVGAATTYENEKKKARVEDALLATPAAVEGYVPGGGVA DYDREKLGERVAKLAGGVAVI KVGAATTYENEKKRARVEDALLATPAAVEGYVPGGGVA DYDREKLGERLAKLAGGVAVI KVGAATTYELKERKERI EDAVMAARAAVEGYVAGGVT DYDREKLGERLAKLAGGVAVI KAGAATTYELKERKERI EDAVMAARAAVEGYVAGGVT DYDREKLGERLAKLAGGVAVI KAGAATTYELKERKERI EDAVMAARAAVEGYVAGGVT DYDREKLGERLAKLAGGVAVI KAGAATTYELKERKERI EDAVMAARAAVEGYVAGGVT
L. pheumono. M. bovis M. tubercul. M. leprae S. ALBUS-56 S. ALBUS-58 CONSERVED	DYDREKLGERLAKLAGGVAVI KNGAATEVENEKKRAKVEDALAATEAAVEEGVVPGGGVA DYDREKLGERLAKLAGGVAVI KNGAATEVELKERKERI EDAVMARAAVEEG IVAGGGVA DYDREKLGERLAKLAGGVAVI KNGAATEVELKERKERI EDAVMARAAVEEG IVAGGGVT DYDREKLGERLAKLAGGVAVI KNGAATEVELKERKERI EDAVMARAAVEEG IVAGGGVT DYDREKLGERLAKLAGGVAVI KNGAATEVELKERKERI EDAVMARAAVEEG IVAGGGVT DYDREKLGERLAKLAGGVO, KNGAATEVELKERKERI EDAVMARAAVEEG IVAGGGVT DYDREKLGERLAKLAGGVO, VGAATE DELER BANANGGVAVI KNGAATEVELKERKERI EDAVMARAAVEEG IVAGGGVA DYDREKLGERLAKLAGGVO,GAATE
L. pheumono. N. bovis M. tubercul. M. leprae S. ALBUS-56 S. ALBUS-58 CONSERVED	DYDREKLGERLAKLAGGVAVIKVGAATEVENEKKRARVEDALAATAAAVEGGVVPGGGVA DYDREKLGERLAKLAGGVAVIKVGAATEVENEKKRARVEDALAATAAVEGG DYDREKLGERLAKLAGGVAVIKVGAATEVELKERKERIEDAVMARAAVEGGIVAGGGVT DYDREKLGERLAKLAGGVAVIKAGATEVELKERKERIEDAVMARAAVEGGIVAGGGVT DYDREKLGERLAKLAGGVAVIKAGATEVELKERKERIEDAVMARAAVEGGIVAGGGVT DYDREKLGERLAKLAGGVQIVKAGATEVELKERKERIEDAVMARAAVEGGIVAGGGVT DYDREKLGERLAKLAGGVQIVKAGATEVELKERKERIEDAVMARAAVEGGIVAGGGVG DMDREKLGERLAKLAGGVVIKVGATEVELKERKERIEDAVMARAAVEGGIVAGGGVG DMDREKLGERLAKLAGGVVIKVGATEVELKERKERIEDAVMARAAVEGGIVAGGGVG DMDREKLGERLAKLAGGVVIKVGATEVELKERKERIEDAVMARAAVEGGIVAGGGG
L. pneumono. M. bovis M. tubercul. M. lepree S. ALBUS-56 S. ALBUS-58 CONSERVED S. sp. 7942	DYDREKLGERLAKLAGGVAVIKVGAATTYENEKEKKARVEDALAATPAAVEEGVVPGGGVA DYDREKLGERLAKLAGGVAVIKVGAATTVENEKEKRARVEDALAATPAAVEEGIVAGGGVA DYDREKLGERLAKLAGGVAVIKVGAATEVELKERKERIEDAVMARAAVEEGIVAGGGVT DYDREKLGERLAKLAGGVAVIKVGAATEVELKERKERIEDAVMARAAVEEGIVAGGGVT DYDREKLGERLAKLAGGVAVIKVGAATEVELKERKERIEDAVMARAAVEEGIVAGGGVT DYDREKLGERLAKLAGGVUVIKVGAATEVELKERKERIEDAIVMARAAVEEGIVAGGGVT DMDREKLGERLAKLAGGVUVIKVGAATEVELKERKERIEDAIVMARAAVEEGIVAGGGVT DMDREKLGERLAKLAGGVUVIKVGAATEVELKERKERIEDAIVMARAAVEEGIVAGGGVT DMDREKLGERLAKLAGGVUVIKVGAATEVELKERKERIEDAIVMARAAVEEGIVAGGGVT LABLAPQLEEMATAMLSGEELTGAQIV-ALTARLERAEMAGLMGAVISERVKELPFDE
L. pneumono. N. bovis M. tubercul. N. leprae S. ALBUS-56 S. ALBUS-56 CONSERVED S. sp. 7942 E. coli	DYDREKLGERLAKLAGGVAVIKVGAATTYENEKEKKARVEDALAATTAAVEEGVVPGGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYENEKEKARVEDALAATTAAVEEG VVGGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYELKERERIE EDAVMARAAVEEG VVGGGVT DYDREKLGERLAKLAGGVAVIKAGAATTYELKERERIE EDAVMARAAVEEG VVGGGVT DYDREKLGERLAKLAGGVAVIKAGAATTYELKERERIENDAVMARAAVEEG VVGGGVT DYDREKLGERLAKLAGGVVIKKGAATTYELKERERIENDAVMARAAVEEG VVGGGVA DMDREKLGERLAKLAGGVVIKKGAATTYELKERERIENDAVMARAAVEEG VVGGGVA DMDREKLGERLAKLAGGVVIKKGAATTYELKERERIENDAVMARAAVEEG VVGGGVA LDEKLGERLAKLAGGVVIKKGAATTYELKERERIENDAVMARAAVEEG VVGGGVA LDEKLGERLAKLAGGVVIKKGAATTYELKERERIENDAVEEGVAAVEEG VVGGGVA LDEKLGERLAKLAGGVVIKKGAATTYELKERERIENDAVEEGVAAVEEG VVGGGVA LDEKLGERLAKLAGGVVIKKGAATTYELKERERIENDAVEEGVAAVEEGVAAGGVA LDEKLGERLAKLAGGVVIKKGAATTYELKERERIENDAVEEGVAAVEEGVAAGGVA LLEKLGERLAKLAGGVGVIKKGAATTYELKERERIENDAVEEGVAAVEEGVAAGGVA
L. pneumono. M. bovis M. tubercul. M. tuberce S. ALBUS-56 S. ALBUS-56 CONSERVED S. sp. 7942 E. coli C. burneti	DYDREKLGERLAKLAGGVAVIKVGAATEVENEKKRAKVEDALAATAAAVEGGVVPGGGVA DYDREKLGERLAKLAGGVAVIKVGAATEVENEKKRAKVEDALAATAAVEGGVAGGV DYDREKLGERLAKLAGGVAVIKVGAATEVELKERKERIEDAVMMARAAVEGGIVAGGVT DYDREKLGERLAKLAGGVAVIKAGAATEVELKERKERIEDAVMMARAAVEGGIVAGGVT DYDREKLGERLAKLAGGVAVIKAGAATEVELKERKERIEDAVMMARAAVEGGIVAGGVT DYDREKLGERLAKLAGGVAVIKAGAATEVELKERKERIEDAISANAAVEGGIVAGGGV DMDREKLGERLAKLAGGVAVIKAGAATEVELKERKERIEDAISANAAVEGGIVAGGGV DMDREKLGERLAKLAGGVAVIKAGAATEVELKERKERIEDAISANAAVEGGIVAGGGV DMDREKLGERLAKLAGGVIKVALAKELKERKERIEDAISANAAVEGGIVAGGGV LABLAPOLEENATANLSGEELTGAQIV-ALTARLKRIARENAGLMGAVISERVKELPFDE LIRVASKLAD-LAGGHEDGNVGIKVALRAMERIPLOJVINGGEEFSVANTY-KGGCON LIRVIKSDS-VEVENEDGNVGIKVALRAMERIPLOJVINGGEEFSVANTY-KGGOG
L. pneumono. M. bovis M. tubercul. M. leprse S. ALBUS-56 S. ALBUS-56 CONSERVED S. sp. 7942 E. coli C. burneti L. pneumono.	DYDREKLGERLAKLAGGVAVIKVGAATEVENEKKAAVEDALAATAAVEEGVVPGGGVA DYDREKLGERVAKLAGGVAVIKVGAATEVENEKKAAVEDALAATAAVEEGVVGGGVA DYDREKLGERLAKLAGGVAVIKVGAATEVELKERERIERIEDAVMAKAAVEEGVAGGGVT DYDREKLGERLAKLAGGVAVIKKGAATEVELKERERIERIEDAVMAKAAVEEGVAGGGVT DYDREKLGERLAKLAGGVAVIKKGAATEVELKERERIEDEDAVMAKAAVEEGVAGGGV DYDREKLGERLAKVAGGVAVIKKGAATEVELKERERIEDEDAVMAKAAVEEGVAGGGV DYDREKLGERLAKVAGGVGVIKKGAATEVELKERERIEDEDAVMAKAAVEEGVAGGGV DYDREKLGERLAKVAGGVGVIKGAATEVELKERERIEDEDAVMAKAAVEEGVAGGGV DHDREKLGERLAKVAGGOVGVIKGAATEVELKERERIEDEDAVMAKAAVEEGVAGGGV LABLAPOLEEMATAMISGEELTGAQIV-ALTARIKEIDAVEAKAKVEGVAGVAKVAFV LIKVASLAD-LKGOBOVGVIKVALRAMEAPIGGVVGGGVAVAGVAVATVANEKOVM LIKVKSLDS-LKGDDOGWGVIKVALRAMEAPIGGVVATVAGGAVADKVANEKOVM
L. pneumono. M. bovis M. tubercul. M. tupercul. M. tepres S. ALSUS-56 S. ALSUS-56 CONSERVED S. sp. 7942 S. coli C. burneti L. pneumono. M. bovis	DYDREKLGERLAKLAGGVAVIKVGAATEVENEKKRAKVEDALAATAAAVEGGVVPGGGVA DYDREKLGERLAKLAGGVAVIKVGAATEVENEKKRAKVEDALAATAAAVEGGVPGGGVA DYDREKLGERLAKLAGGVAVIKVGAATEVELKERKERIEDAVMARAAVEGGVAGGGVT DYDREKLGERLAKLAGGVAVIKAGAATEVELKERKERIEDAVMARAAVEGGVAGGGVT DYDREKLGERLAKLAGGVAVIKAGAATEVELKERKERIEDAVMARAAVEGGVAGGGVT DYDREKLGERLAKLAGGVAVIKAGAATEVELKERKERIEDAVMARAAVEGGVAGGGVT DYDREKLGERLAKLAGGVAVIKAGAATEVELKERKERIEDAVMARAAVEGGVAGGGVT DYDREKLGERLAKLAGGVUIKVGAATEVELKERKERIEDAISATAAAVEGGVAGGGV DIDREKLGERLAKLAGGVUIKVGAATEVELKERKERIEDAISATAAAVEGGVAGGGV LIBLAFLGERLAKLAGGVUIKVGAATEVELKERKERIEDAISATAAAVEGGVAGGG LAELAPOLEENATAMISGEELTGAQIV—ALTARLERIAELADISATAAVEGGVVGGGA LIRLASIGJD—LAGGNEDGRVGIKVILAANERLAGIVIKTGVGAAVADKVANEKUD LIRVIKSIGS—VEVENDOGRVGIKILBERIEDIGVTKAGTERSVANTV-KGDGG
L. pneumono. M. bovis M. tubercul. M. tupercul. S. ALBUS-56 S. ALBUS-56 CONSERVED S. sp. 7942 E. coli C. burneti L. pneumono. M. bovis M. tubercul.	DYDREKLGERLAKLAGGVAVIKVGAATEVENEKKAAVEDALAATAAVEEGVVPGGGVA DYDREKLGERLAKLAGGVAVIKVGAATEVENEKKAAVEDALAATAAVEEGVVGGGVA DYDREKLGERLAKLAGGVAVIKVGAATEVELKERKERLEDAVMARAAVEEGIVAGGGV DYDREKLGERLAKLAGGVAVIKVGAATEVELKERKERLEDAVMARAAVEEGIVAGGV DYDREKLGERLAKLAGGVAVIKVGAATEVELKERKERLEDAVMARAAVEEGIVAGGV DYDREKLGERLAKLAGGVAVIKVGAATEVELKERKERLEDAVMARAAVEEGIVAGGGV DYDREKLGERLAKVAGGVGVIKVGAATEVELKERKERLEDAVMARAAVEEGIVAGGGV DYDREKLGERLAKVAGGVGVIKVGAATEVELKERKERLEDAVMARAAVEEGIVAGGGV DHDREKLGERLAKVAGGVGVIKVGAATEVELKERKERLEDAVEANAAVEEGIVAGGGV LABLAPOLEEMATAMLSGEELTGAQIV-ALTARLERIABINAGINGAVISEVVAKVAKELPDDE LIKVASILAD-LAGGHEOGNGVIKVALRAMEAPLAQIVINGGEFFSVVANTV-KGGCON LIKVIKSLDS-LKGDMEOGNGVIKIARATESLGIVKINGGVAAVADKVVNKVAKELDED LIRVASHLAD-LLAGGHEOGNGVIKIARATESLGIVKINGGAAVADKVVNKVVNKVVNKVVNKVVNKVVNKVVNKVVNKVVNKVV
L. pneumono. M. bovis M. tubercul. M. lepree S. ALBUS-56 S. ALBUS-56 CONSERVED S. sp. 7942 B. coli C. burneti L. pneumono. M. bovis M. tubercul. M. lepree	DYDREKLGERLÄKLÄGGVAVIKVGÄATEVENEKKAAVEDALAATAAVEEGVPGGGVA DYDREKLGERLÄKLÄGGVAVIKVGÄATEVENEKKAAVEDALAATAAVEEG VAGGGVT DYDREKLGERLÄKLÄGGVAVIKVGÄATEVELKERKERIEDAVMAKAAVEEG VAGGGVT DYDREKLGERLÄKLÄGGVAVIKAGATEVELKERKERIEDAVMAKAAVEEG VAGGGVT DYDREKLGERLÄKLÄGGVAVIKAGATEVELKERKERIEDAVMAKAAVEEG VAGGGVT DYDREKLGERLÄKLÄGGVAVIKAGATEVELKERKERIEDAVMAKAAVEEG VAGGGVT DYDREKLGERLÄKLÄGGVUIKVGÄATEVELKERKERIEDAVMAKAAVEEG VAGGGVT DYDREKLGERLÄKLÄGGVUIKVGÄATEVELKERKERIEDAVAMAKAAVEEG VAGGGVT DYDREKLGERLÄKLÄGGVUIKVGÄATEVELKERKERIEDAVAMAKAAVEEG VAGGGVT DIDREKLGERLÄKLÄGGVUIKVGÄATEVELKERKERIEDAVAMAKAAVEEG VAGGGVT LIRVASKLAD-LEGOMEDGINGIKVALKAMEAPLAGIVAKVEEDAVANTO-KGGGAN LIRVASKLAD-LEGOMEDGINGIKVALKAMEAPLAGIVAKVESKAAVAAKVEEG LIRVASKLAD-LEGOMEDGINGIKVALKAMEAPLAGIVAKVEKGVASKVANKVAEKO-N LIRVASKLADS-LKGDMEDGINGUIKVALKAPHENGIVTIMAGYEASVANKVAKVAEKO-N LIRVASKLADS-LKGDMEDGINGUIKVALKAPHENGIVTIMAGYERSVAKVAKVAEKO-N LIQAAPTIDELKLGDERATAMIVVALEAPLENGIVATAVESKLAGVVAKVARKINLPAGE LLGAAPTIDELKLGDERATAMIVVALEAPLENGIAPHSELFEGVVAKVARKINLPAGE
L. pheumono. M. bovis M. tubercul. M. tupercul. S. ALBUS-56 S. ALBUS-56 S. ALBUS-56 CONSERVED S. sp. 7942 E. coli C. burneti L. pheumono. M. tubercul. M. tubercul. M. tuperce S. ALBUS-56	DYDREKLGERLÄKLÄGGVAVIKVGAATTYNNEKKRÄKVEDALAATTAAVEEGVVPGGGVA DYDREKLGERLÄKLÄGGVAVIKVGAATTYNNEKKRÄKVEDALAATTAAVEEGVVGGGVA DYDREKLGERLÄKLÄGGVAVIKVGAATTYELKERKERIEDAVMMARAAVEEGIVAGGGVT DYDREKLGERLÄKLÄGGVAVIKVGAATTYELKERKERIEDAVMMARAAVEEGIVAGGGV DYDREKLGERLÄKLÄGGVAVIKVGAATTYELKERKERIEDAVMARAAVEEGIVAGGGV DYDREKLGERLÄKLÄGGVAVIKVGAATTYELKERKERIEDAVMARAAVEEGIVAGGGV DYDREKLGERLÄKLÄGGVAVIKVGAATTYELKERKERIEDAVMARAAVEEGIVAGGGV LABLAPQLEEKATAMISGERLIGAQIV-ALTARIKERKERIEDAVMARAAVEEGIVAGGGV LIKUGELANVAGGVVIKVGAATTYELKERKERIEDAVMARAAVEEGIVAGGGV LIKUGELANVAGGVVIKVGAATTYELKERKERIENIEDAVMARAAVEEGIVAGGGV LIKUGELANVAGGVVIKVGAATTYELKERKERIENIEDAVMARAAVEEGIVAGGGV LIKUGELANVAGGVVIKVGAATTYELKERKERIENIEDAVMARAAVEEGIVAGGGV LIKUGELANVAGGVVIKVGATTYELKERKERIENIEDAVMARAVEEGIVAGGU LIKUASILAD-LAGGNEDGNVCIKVALRAMERPLODIVIKCEEFFSVAMITV-KGCDGN LIKUKKELDS-LKGODENGVCIKVALRAMERPLODIVIKCEEFFSVAMITV-KGCDG LIDAAPTIDS-LLKDGDEATCAMIVKVALERPLRQIATENSGLERGVVAEKVNENLPAGE LIQAAPTIDSLKUGDEATCAMIVKVALERPLRQIAPHSGERGEGVVAEKVNENLPAGE LIQAAPTER
L. pneumono. M. bovis M. tubercul. M. lepree S. ALBUS-56 S. ALBUS-56 CONSERVED S. sp. 7942 E. coli C. burneti L. pneumono. M. bovis M. tubercul. M. lepree S. ALBUS-56 S. ALBUS-58	DYDREKLGERLAKLAGGVAVIKVGAATTYENEKKKARVEDALAATAAVEEGVVPGGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYENEKKRARVEDALAATAAVEEGVVGGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMMARAAVEEGIVAGGGVT DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMMARAAVEEGIVAGGGVT DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMMARAAVEEGIVAGGGVT DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMMARAAVEEGIVAGGGVT DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMMARAAVEEGIVAGGGVT DYDREKLGERLAKLAGGVVIKVGAATTYELKERKERIEDAVMMARAAVEEGIVAGGGVT DYDREKLGERLAKLAGGVUIKVGAATTYELKERKERIEDAVMMARAAVEEGIVAGGGVT LIDAKLGERLAKLAGGVUIKVGAATTYELKERKERIEDAVMARAAVEEGIVAGGGVT LIDAKLGERLAKLAGGVIKVAKATTYELKERKERIEDAVMARAAVEEGIVAGGGVT LIDAKSTUD-UFGORDOWGIVAIRAMERLEGIVAGGVAVATTSERVKELFPDE LITVASLAD-UFGORDOWGIVAIRAMERLEGIVALGEEFSVANTY-KGGGON LIRVIKSLDS-UFVENEDGWCGVEIARMATFILGUINGEEFSVANTY-KGGGON LIRVIKSLDS-UFVENEDGWCGVEIARRAMATFILGUINSLEFGVVAKVAKKALEND-N LIDAAFTDE
L. pheumono. M. bovis M. tubercul. M. tuperes S. ALBOS-56 S. ALBOS-56 CONSERVED S. sp. 7942 E. coli C. burneti L. pheumono. M. tubercul. M. tubercul. M. tuperes S. ALBOS-56 S. ALBOS-58 CONSERVED	DYDREKLGERLAKLAGGVAVIKVGAATTYENEKEKKARVEDALAATAAAVEGYVPGGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYENEKEKARVEDALAATAAVEGYVAGGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMMARAAVEGYVAGGGVT DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVEGYVAGGGVT DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVEGYVAGGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVEDAVAAVEGYVAGGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVEGYVAGGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVEDAVAAVEGYVAGGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVEDAVAAVEGYVAGGGVA LIKASKLAG-LGGVAVIKVGAATTYELKERKERIEDAVEGAVAVEGYVAGGVA LIKASKLAG-LGGVAVIKVGAATTYELKERKERIEDAVEGAVISTUSGGSA LIKASKLAG-LGGVAVIKVGAATTYELKERKERIEDAVEGAVISTUSGGSA LIKASKLAG-LGGVAVIKVGATTYELGERIETAVAVEGYVAKVAKIELFFOL LIKASKLAG-LGGVAVIKVGATAFFIGJVAVISTUSGEFFISVAAVISTUSGGGA LIKAVKIKSLDS-LKGDMOGUMCIHLARAISISHMGUTVIGGTANSGLFGVVAKVAKVALMEDAV LIQAAFTDE-LLALGDEATCAMIVKVALERIPIGJANNSGLFGVVAKVAKVANISVGE LUGAAFTLDE-LLKIGDEATCAMIVKVALERIPIGJANNSGLFGVVAKVAKVAKVAKISVGE LUGAAFKUDD-HLGFTGERATGAVVAVVAKRAFFISJIANNGGLGFGVVAKVAKNISVGE LUGAAFKUDD-HLGFTGERATGAVVAVVAKRAFFISJIANNGGLFGVVAKVAKKNISVGE
L. pneumono. M. bovis M. tubercul. M. loprae S. ALBUS-56 S. ALBUS-56 CONSERVED S. sp. 7942 E. coli C. burneti L. pneumono. M. bovis M. tubercul. M. loprae S. ALBUS-56 CONSERVED	DYDREKLGERLAKLAGGVAVIKVGAATTYENEKKRAKVEDALAATAAAVEEGVVPGGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYENEKKRAKVEDALAATAAVEEGVVGGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERLEDAVMMARAAVEEGVVGGGVT DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERLEDAVMARAAVEEGVVGGGVT DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERLEDAVMARAAVEEGVVGGGVA DYDREKLGERLAKVAGGVGVIKVGAATTYELKERKERLEDAVEANAAVEEGVVGGGVA DYDREKLGERLAKVAGGVGVIKVGAATTYELKERKERLEDAVMARAAVEEGVVGGGVA DYDREKLGERLAKVAGGVGVIKVGAATTYELKERKERLEDAVMARAAVEEGVVGGGVA DYDREKLGERLAKVAGGVGVIKVGAATTYELKERKERLEDAVMARAAVEEGVVGGGVA DYDREKLGERLAKVAGGVGVIKVGAATTYELKERKERLEDAVMARAAVEEGVVGGGVA DYDREKLGERLAKVAGGVGVIKVGAATTYELKERKERLEDAVEANAAVEEGVVGGGVA DYDREKLGERLAKVAGGVGVIKVGAATTYELKERKERLEDAVEANAAVEEGVVGGGVA LIKVASLDS-UKGDDONNGVIKUALEARERLEGVVGAAVVADKVANEGVVA LIKVASLDS-UKGDDONNGVIKUALEARERLEGIAFVGGAAVVADKVANEHGOVN LIDAATIDS-LLKEDDEATGANIVKVALEAPLEGIAFNSGLEFGVVAEKVRNLPAGE LIQAAPTIDE-ILKEGDEATGANIVKVALEAPLEGIAFNSGLEFGVVAEKVRNLPAGE LIQAAFIDE-ILKEDEATGANIVKVALEAPLEGIAFNSGLEFGVVAEKVRNLSVGE LIQASSVFRKILKLEGDEATGANIVKVALEAPLEGIAFNSGLEFGVVAEKVRNLSVGE LIQASSVFRKILKLEGDEATGANIVKVALEAPLEGIAFNSGLEGGVVEKVRNLSVGE LIQASSVFTKILKLEGDEATGANIVKVALEAPLEGIAFNSGLEGGVVEKVRNLSVGE LIQASSVFTKILKLEGDEATGANIVKVALEAPLEGIAFNSGLEGGVVEKVRNLSVGE LIQASSVFTKILKLEGDEATGANIVKVALEAPLEGIAFNSGLEGGVVEKVRNLSVGE LIQASSVFTKILKLEGDEATGANIVKVALEAPLEGIAFNSGLEGGVVEKVRNLSVGE LIQASSVFTKILKLEGDEATGANIVKVALEAPLEGIAFNSGLEGGVVEKVRNLSVGE
L. pseumono. M. bovis M. tubercul. M. tuperes S. ALBOS-56 S. ALBOS-56 S. ALBOS-58 CONSERVED S. sp. 7942 E. coli C. burneti L. pseumoso. M. tubercul. M. tubercul. M. tubercul. M. tubercul. S. ALBOS-56 S. ALBOS-58 CONSERVED S. sp. 7942	DYDREKLGERLAKLAGGVAVIKVGAATTYENEKKRARVEDALAATAAVTEGVVGGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYENEKKRARVEDALAATAAVTEGIVAGGGV DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMMARAAVTEGIVAGGGV DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVTEGIVAGGV DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVTEGIVAGGV DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVTEGIVAGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVTEGIVAGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVTEGIVAGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVTEGIVAGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVTEGIVAGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVTEGIVAGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVTEGIVAGGVA DIDEKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVTEGIVAGGVA DIDEKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVTEGIVAGGVA DIDEKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVTEGIVAGGVA DIDEKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARVATEGIVAGGVA DIDEKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAV DIDAATTIDE-VIKTEGGRAGVVSIRARMATPLGGIVAKVAVAVKVKVAKABROVN DIDAATTIDE-VIKLEGDEATCAMIVKVALERIEDAGINAMSELFGVVAEKVARKVNISVGE DIGAAPLDR
L. pneumono. M. bovis M. tubercul. M. tupercul. S. ALBUS-56 S. ALBUS-56 CONSERVED S. sp. 1942 E. coli C. burneti L. pneumono. M. bovis M. tubercul. M. tubercul. M. tubercul. M. tubercul. S. ALBUS-56 S. ALBUS-58 CONSERVED S. sp. 7942 E. coli	DYDREKLGERLAKLAGGVAVIKVGAATEVENEKKRAKVEDALAATAAVEEGVVPGGGVA DYDREKLGERLAKLAGGVAVIKVGAATEVENEKKRAKVEDALAATAAVEEGVVGGGVA DYDREKLGERLAKLAGGVAVIKVGAATEVELKERERIERIEDAVMARAAVEEGIVAGGGVT DYDREKLGERLAKLAGGVAVIKVGAATEVELKERERIEDAVMARAAVEEGIVAGGGVT DYDREKLGERLAKLAGGVAVIKVGAATEVELKERERIEDAVMARAAVEEGIVAGGGVT DYDREKLGERLAKVAGGVGVIKVGAATEVELKERERIEDAVMARAAVEEGIVAGGGVA DWDREKLGERLAKVAGGVGVIKVGAATEVELKERERIEDAVMARAAVEEGIVAGGGVA DWDREKLGERLAKVAGGVGVIKVGAATEVELKERERIEDAVMARAAVEEGIVAGGGVA DWDREKLGERLAKVAGGVGVIKVGAATEVELKERERIEDAVMARAAVEEGIVAGGGVA DWDREKLGERLAKVAGVGVIKVGAATEVELKERERIEDAVMARAAVEEGIVAGGGVA DWDREKLGERLAKVAGVGVIKVGAATEVELKERERIEDAVMARAAVEGIVAGGGVA DWDREKLGERLAKVAGVGVIKVGAATEVELKERERIEDAVANAAVEGIVAGGGVA LIKVKSLDS-UKGDOGVGVIKVALEARIKGIVINGGEEFSVARTV-KGGCON LIKVKSLDS-UKGDOGVGVIKVALEARISJOVINGGEEFSVARTV-KGGCON LIKVKSLDS-UKGDOGMGCHILTERAITESPHGIVINGGEAFSVARTVNKVALERIG-N LLGAAPTLDSLKLGEDEATGANIVKVALEARIJENGIAPHSGEFGVVARKVNHIPAGE LLGAAPTLDSLKLGEDEATGANIVKVALEARIJENGIAPHSGEFGVVARKVNHIPAGE LLGAAPALDR
L. pseumeno. M. bovis M. tubercul. M. tuperes S. algova-56 S. algova-56 S. algova-58 CONSERVED S. sp. 7942 E. coli C. burneti L. pseumono. M. bovis M. tubercul. M. loprae S. algova-56 S. algova-58 CONSERVED S. sp. 7942 E. coli C. burneti	DYDREKLGERLAKLAGGVAVIKVGAATTYENEKKKARVEDALAATAAVTEGVVPGGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYENEKKRARVEDALAATAAVTEGIVAGGV7 DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVTEGIVAGGV7 DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVTEGIVAGGV7 DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVTEGIVAGGV7 DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVTEGIVAGGV7 DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVTEGIVAGGV7 DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVTEGIVAGGV7 DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVTEGIVAGGV7 DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMARAAVTEGIVAGGV7 DYDREKLGERLAKLAGGVIKVAATTYELKERKERIEDAVMARAAVTEGIVAGGV7 LIDEKUGERLAKLAGGVIKVAATTELKERKERIEDAVMARAAVTEGIVAGGV7 LITVASUAD-LCOGNEGUNIKVALKELBARVALKATAVIKATEGIVAGVAKVALKELFPDG LITVASUAD-LCOGNEGIVIINGARTSENGUVIKUGEEFSVANTV-KKGGGCN LITVASUAD-LCOGNEGIVIINGARTSENGUVIKUGEEFSVANTV-KKARENO- LIQAAPTIDELKLGGDEATCANIVKVALKERPIGJINNSGLEFGVVAEKVNELPAGE LIGAAPTIDEILKLGDEATCANIVKVALERPIGIZAMISGLEGGVVEKVNENLSVGE LIGAASSVFEKLKLGDEATCANIVKVALERPIGIZAMISGLEGGVVEKVNENLSVGE LUGAASSVFEK
L. pheumono. M. bovis M. tubercul. M. tubercul. M. tubercul. M. tubercul. S. ALBUS-56 S. ALBUS-56 CONSERVED S. sp. 7942 E. coli M. tubercul. M. tubercul. M. tubercul. M. tubercul. S. ALBUS-56 S. ALBUS-56 CONSERVED S. sp. 7942 E. coli C. burneti L. pneumono.	DYDREKLQERLAKLAGGVAVIKVGAATEVENEKKRAKVEDALAATAAVEEGVVGGGVA DYDREKLQERVAKLAGGVAVIKVGAATEVENEKKRAKVEDALAATAAVEEGVVGGGVA DYDREKLQERVAKLAGGVAVIKVGAATEVELKERKERIEDAVMAKAAVEEGIVAGGGV DYDREKLQERLAKLAGGVAVIKVGAATEVELKERKERIEDAVMAKAAVEEGIVAGGVT DYDREKLQERLAKLAGGVAVIKVGAATEVELKERKERIEDAVMAKAAVEEGIVAGGGV DYDREKLQERLAKLAGGVAVIKVGAATEVELKERKERIEDAVMAKAAVEEGIVAGGGV DYDREKLGERLAKLAGGVGVIKVGAATEVELKERKERIEDAVMAKAAVEEGIVAGGGV DYDREKLGERLAKLAGGVGVIKVGAATEVELKERKERIEDAVMAKAAVEEGIVAGGGV DYDREKLGERLAKLAGGVGVIKVGAATEVELKERKERIEDAVMAKAAVEEGIVAGGGV DYDREKLGERLAKLAGGVGVIKVGAATEVELKERKERIEDAVEANAAVEEGIVAGGGV DYDREKLGERLAKLAGGVGVIKVGAATEVELKERKERIEDAVEANAAVEEGIVAGGGV LIRAVKIAD-LAGGEEOGNGVGIVALKAATEVELKERKERIEDAVEANAAVEEGIVAGGGV LIRAVKALDS-LKGDDEEDGRVGVIKVALKARADIVINGGEEFSVVANTV-KGGOGN LIRAVKSLDS-LKGDDEOGNGVGIKVALKARATEJEGIVINGGEEFSVVANTVAVENKVANEIGUN LIDAAPIDS-LLKDGDEETGANIVKVALKAPIGJIVINGGEEFSVVAKVANEIGUN LIDAAPIDS-LLKIEDEATGANIVKVALKAPIGJIAPNSGLEFGVVAKVNENLPAGE LIDAAPIDS-LKIEDGEATGANIVKVALKAPIGJIAPNSGLEFGVVAKVNENLPAGE LIDAAPIDR-LLKIEGEATGANIVKVALKAPIGJIAPNSGLEFGVVAKKVNENLPAGE LIDAAPIDR-LKIEDEATGANIVKVALKAPIGJIAPNSGLEFGVVAKKVNENLPAGE LIDAAPIDR-LKIEDEATGANIVKVALKAPIGJIAPNSGLEFGVVAKKVNENLPAGE LIDAAPIDR-LLKIGDEATGANIVKVALKAPIGJIAPNSGLEGGVVEKVNENLPAGE LIDAAPIDR-LLEJGDEATGANIVKVALKAPIGJIAPNSGLEGGVVEKVNENLPAGE LIDAAPIDR-LLEJGDEATGANIVKVALKAPIGJIAPNSGLEGGVVEKVNENLPAGE LIDAAPIDR-LLEJGDEATGANIVKVALKAPIGJIAPNSGLEGGVVEKVNENLPAGE LIDAAPIDR-LLEJGDEATGANIVKVALKAPIGJIAPNSGLEGGVVEKVNENLPAGE LIDAAPIDR-LLEJGDEATGANIVKVALKAPIGJIAPNSGLEGGVVEKVNENLPAGE LIDAAPIDR-LLEJGDEATGANIVKVALKAPIGJIAPNSGLEGGVVEKVNENLPAGE LIDAAPIDR-LLEJGDEATGANIVKVALKAPIGJIAPNSGLEGGVVEKVNENLPAGE LIDAAPIDR-LLEJGDEATGANIVKVALKAPIGJIAPNSGLEGGVVEKVNENLPAGE LIDAAPIDR-LLEJGDEATGANIVKVALKAPIGJIAPIGJIAPNSGLEGGVVEKVNENLPAGE LIDAAPIDR-LLEJGDEATGANIVKVALKAPIGJIAPIGJIAPNGLEGGVVEKVNENLPAGA LIDAAPIDR-LLEJGDEATGANIVKALKAPIGJIAPIGJIAPIGJIGGGVVEKVNENLPAGA LIDAAPIDR-LLEJGDEATGANIVKVALKAPIGJIAPIGJIAPIGJIGGVVEKVNENLFGGVGVEKVENLSVG
L. pseumeno. M. bovis M. tubercul. M. tuperes S. algoy-56 S. algoy-56 S. algoy-56 S. algoy-58 CONSERVED S. sp. 7942 E. coli C. burneti L. pseumono. M. tubercul. M. topras S. algoy-56 S. algoy-56 S. algoy-58 S. algoy-58 S	DYDREKLGERLAKLAGGVAVIKVGAATTYENEKKKARVEDALAATAAVEEGVVPGGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYENEKKKARVEDALAATAAVEEGVVGGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMAAAVEEGIVAGGGVT DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMAAAVEEGIVAGGGVT DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMAAAVEEGIVAGGGVT DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERIEDAVMAAAVEEGIVAGGGVT DYDREKLGERLAKLAGGVVIKVGAATTYELKERKERIEDAVMAAAVEEGIVAGGGVT DYDREKLGERLAKLAGGVVIKVGAATTYELKERKERIEDAVMAAAVEEGIVAGGGVT DYDREKLGERLAKLAGGVVIKVGAATTYELKERKERIEDAVMAAAVEEGIVAGGGVT DYDREKLGERLAKLAGGVVIKVGAATTYELKERKERIEDAVMAAAVEEGIVAGGGVA INDREKLGERLAKLAGGVVIKVGAATTYELKERKERIEDAVMAAAVEEGIVAGGGVA INDREKLGERLAKLAGGVVIKVAATERLEKTAENAGINGAVISERVKELFPDE LIKVASLAD-LKOOBOONGIVGIVALRAMERLEGIVANGGVAAVADVTJNEDUN LIRAGALDS-LKGDDONGIVGIVALRAMERLEGIJVHIGTERSVAATVAKKELFDDE LIGAAPTIDEILKIGDEATGANIVKVALRAPLGIJAMISGLEGGVVEKVNHVAERDEU LIGAAPTIDEILKIGDEATGANIVKVALRAPLGIJAMISGLEFGVVAEKVNHLPAGE LIGAAPTIDEILKIGDEATGANIVKVALRAPLGIJAMISGLEFGVVAEKVNHLPAGE LIGAASSVFEKILKIGDEATGANIVKVALRAPLGIJAMISGLEGGVVIKVNHLSVGE LUAASSVFEKILKIGDEATGANIVKVALRAPLGIJAMISGLEGGVVIKTVHLSVGE LUAASSVFEKILKIGDEATGANIVKALRAPLGIJAMISGLEGGVVIKTVHLSVGE LUAASSVFEKILKIGDEATGANIVKALRAPLGIJAMISGLEGGVVIKTVHLSVGE LUAASSVFEKILKIGDEATGANIVKALRAPLKGIAMISKABHGATITEKVHELDKO CSYNASTERGONDOWNIGILDPTKVTRALQMASSIAAVLITEGIVAEKVANLSVGE LUAASSVFEKILKIGDEATGANIVKALRAPLKGIAMISKABHGATTEGVAEKVANLSVGE LUAASSVFEKILKIGDEATGANIVKALRAPLKGIAMISKABHGATTEGVAEKVANLSVGE LUAASSVFEKILKIGDEATGANIVKALRAPLKGIAMISKABHGATTEGVAEKVANLSVGE LUAASSVFEK
L. pseumono. M. bovis M. tubercul. M. tupercul. M. tupercul. S. ALBOS-56 S. ALBOS-56 CONSERVED S. sp. 7942 E. coli C. burneti L. pseumono. M. tubercul. M. tupercul. S. sp. 7942 E. coli C. burneti L. pseumono. M. bovis M. tubercul.	DYDREKLQERLAKLAGGVAVIKVGAATEVENEKKRAKVEDALAATAAVEEGVVPGGGVA DYDREKLQERVAKLAGGVAVIKVGAATEVENEKKRAKVEDALAATAAVEEGVVPGGGVA DYDREKLQERVAKLAGGVAVIKVGAATEVELKERKERIEDAVMMARAAVEEGIVAGGGV DYDREKLQERLAKLAGGVAVIKVGAATEVELKERKERIEDAVMMARAVEEGIVAGGGV DYDREKLQERLAKLAGGVAVIKVGAATEVELKERKERIEDAVMMARAVEEGIVAGGGV DYDREKLQERLAKVGGVAVIKVGAATEVELKERKERIEDAVMARAAVEEGIVAGGGV DYDREKLQERLAKVGGVOIRVGANTEVELKERKERIEDAVMARAAVEEGIVAGGGV DYDREKLGERLAKSGVOIRVGAATEVELKERKERIEDAVMARAAVEEGIVAGGGV DYDREKLGERLAKSGVOIRVGAATEVELKERKERIEDAVMARAAVEEGIVAGGGV DIDEKLGERLAKSGVOIRVGAATEVELKERKERIEDAVMARAAVEGIVAGGGV DIDEKLGERLAKSGVOIRVGAATEVELKERKERIEDAVMARAAVEGIVAGGGV LABLAPQLEEKATAMISGERITGAQIV-ALTARIKENEMIGIVAICGEFFSVAMITV-KGGCG LIRVAKIJAD-LGGGHEOGNVGIKVAIRAMERIGDIVIACGEFFSVAMITV-KGGCG LIRVAKIJAD-LGGOHEOGNVGIKVAIRAMERIGDIVIACGEFFSVAMITV-KGGCG LIRVAKIJAD-LGGDEEOGNVGIKVAIRAMERIGDIVIACGEFFSVAMITV-KGGCG LIDAAPTIDS-LKICODENTIAMITKAALERIFISGIUVIACGEFFSVAMITV-KGGCG LIQAAPTIDS-LKICDERATGAMIVKVAILERIFISGIZAFNSGLEFGVVAKKVRHIJSGE LJQAAPTIDSLKICGERATGAMIVKVAILERIFISGIZAFNSGLEFGVVAKKVRHIJSGE LJQAAPTIDSLKICGERATGAMIVKVAILERIFISGIZAFNSGLEFGVVAKKVRHIJSGE LJQAAPTUR
L. pseumono. M. bovis M. bovis M. tubercul. M. loprae S. ALBO3-56 S. ALBO3-56 S. ALBO3-56 S. ALBO3-56 CONSERVED S. sp. 7942 E. coli C. burneti L. pseumono. M. loprae S. ALBO3-56 S. ALBO3-56 S. ALBO3-56 S. ALBO3-56 CONSERVED S. sp. 7942 E. coli C. burneti L. pseumono. M. bovis M. tubercul. M. loprae	DYDREKLGERVARLAGGVAVIKVGAATTVENEKKRANVEDALAATAAVTEGVVPGGGVA DYDREKLGERVARLAGGVAVIKVGAATTVENEKKRANVEDALAATAAVTEG TVAGGGVT DYDREKLGERVARLAGGVAVIKVGAATTVELKEREKERIEDAVMMARAAVTEG TVAGGGVT DYDREKLGERVARLAGGVAVIKVGAATTVELKEREKERIEDAVMARAAVTEG TVAGGGVT DYDREKLGERVARLAGGVAVIKVGAATTVELKEREKERIEDAVMARAAVTEG TVAGGGVT DYDREKLGERVARLAGGVAVIKVGAATTVELKEREKERIEDAVMARAAVTEG TVAGGGVT DYDREKLGERVARLAGGVAVIKVGAATTVELKEREKERIEDAVMARAAVTEG TVAGGGVT DYDREKLGERVARLAGGVAVIKVGAATTVELKEREKERIEDAVMARAAVTEG TVAGGGVT DYDREKLGERVARLAGGVAVIKVGAATTVELKEREKERIEDAVMARAAVTEG TVAGGGVT DYDREKLGERVARLAGGVAVIKVGAATTVELKEREKERIEDAVMARAAVTEG TVAGGGVA EKUGER.AGGV VGAATT.E.K.K.R.EDAAVTEG V.GGC LIATADATAD-LGGOBGDWGIVGIVALKAMERPLGGIVVACCEEPS VAMTV-KGGCN LIKVASLDB-LKCEMDOGWCIVILARAMERPLGGIVVACCEEPS VAMTV-KGGCN LIKVASLDB-LKCEMDOGWCIVILARAMERPLGGIVVEKVANDAVADKVANKURLERD- LIDAAPTLDB-LLGDDATCAMIVKVALEAPLRGIAPHSGLEFGVARKVMNLPAGE LIQAAPTLDBLKLEGDEATGAMIVKVALEAPLRGIAPHSGLEFGVARKVMNLPAGE LIQAAPTLDBLKLEGDEATGAMIVKVALEAPLRGIAPHSGLEFGVARKVMNLPAGE LIQAAPTLDBG AI.N.G.V.V.V. -GIDASSNFEKLKLEGDEATGAMIVKVALEAPLRGIAPHSGLEGGVVEKVKNLSVGE LVGASSVFEKG AI.N.G.V.V.V. -GIDASSNDFVNHFTAGIVDPAKVTERALJMAASIAAVTITECIVVDKPEPKEKAPGA YGTWAATEFIGHNINGILDPTKVTRALGMASVASIALTTECWTDLPRODADL- GLAMAGTVFEDLIAGVADPVKVTRALGMASVASIALTTECWTDLPRORADAL
L. pseumono. M. bovis M. tubercul. M. tuperes S. ALBOS-56 S. ALBOS-56 S. ALBOS-58 CONSERVED S. sp. 7942 E. coli L. pseumono. M. tubercul. M. tubercul. M. tupercul. S. ALBOS-56 S. ALBOS-56 CONSERVED S. sp. 7942 E. coli L. pseumono. M. bovis M. tubercul. M. tubercul. M. tubercul. M. tuperes S. ALBUS-56 S. S. S	DYDREKLQERLAKLAGGVAVIKVGAATEVENEKKRAKVEDALAATAAVEEGVVPGGGVA DYDREKLQERVAKLAGGVAVIKVGAATEVENEKKRAKVEDALAATAAVEEG'VAGGGVA DYDREKLQERVAKLAGGVAVIKVGAATEVELKERKERIEDAVMMARAAVEEG'VAGGGVT DYDREKLQERLAKLAGGVAVIKVGAATEVELKERKERIEDAVMARAAVEEG'VAGGGVA DYDREKLQERLAKLAGGVAVIKVGAATEVELKERKERIEDAVMARAAVEEG'VAGGGVA DYDREKLQERLAKVGGVAVIKVGAATEVELKERKERIEDAVMARAAVEEG'VAGGGVA DYDREKLGERLAKLAGGVAVIKVGAATEVELKERKERIEDAVMARAAVEEG'VAGGGVA DYDREKLGERLAKVGGVOIKVGATEVELKERKERIEDAVMARAAVEEG'VAGGGVA DYDREKLGERLAKSGVOIKVGAATEVELKERKERIEDAVMARAAVEEG'VAGGGVA DYDREKLGERLAKGGVOIKVGAATEVELKERKERIEDAVMARAAVEEG'VAGGGVA DYDREKLGERLAKGGVOIKVGAATEVELKERKERIEDAVMARAAVEEG'VAGGGVA LABLAPQLEEMATAMLSGERLTGAQIV-ALTARIKAELEDAVEGVAKVATEGVAGGUN LIKVKSLDSVECMOOMOG'NILARAINEPLOQIVIKGGEKEFSVVAKVAELEPDE LIKVASILDSLGGOMEOMIVGIKVALRAMERPLOQIVIKGGEKEFSVVAKVAELEPDE LIQAAPTDELKLGODEATCANIVKVALRAPLGQITAMSGIEGVVAKVARNIJSGE LIQAAPTDELKLGDEATCANIVKVALRAPLGQIATMSGIEGVVAKVARNIJSGE LIQAAPTDELKLGDEATCANIVKVALRAPLGQIATMSGIEGVVAKVARNIJSGUE LIQAAPTADENLGEDEATCANIVKVALRAPLGQIATMSGIEGVVAKVARNIJSGUE VGINAATEETGINIDMSI LDPTKVTRALGAANSIJAMVLITTECWTDEPEKEAPAGA
L. pseumono. M. bovio M. bovio M. tubercul. M. loprae S. ALBOJ-56 S. ALBOJ-56 S. ALBOJ-56 S. ALBOJ-56 CONSERVED S. ap. 7942 E. coli C. burneti M. leprae S. ALBOJ-56 S. ALBOJ-56 C. burneti L. pseumono. M. bovis M. bovis M. tubercul. M. tubercul. M. tuberes S. ALBOJ-56 S. ALBOJ-56 S. ALBOJ-56 S. ALBOJ-56 S. ALBOJ-56	DYDREKLGERLAKLAGGVAVIKVGAATTYENEKKKAAVEDALAATAAVEEGVVPGGGVA DYDREKLGERLAKLAGGVAVIKVGAATTYENEKKKAAVEDALAATAAVEEG'VAGGGVT DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERLEDAVMARAAVEEG'VAGGGVT DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERLEDAVMARAAVEEG'VAGGGVT DYDREKLGERLAKLAGGVAVIKVGAATTYELKERKERLEDAVMARAAVEEG'VAGGGVT DYDREKLGERLAKVAGGVGVIKVGAATTYELKERKERLEDAVMARAAVEEG'VAGGGVT DYDREKLGERLAKVAGGVGVIKVGAATTYELKERKERLEDAVMARAAVEEG'VAGGGVA DYDREKLGERLAKVAGGVGVIKVGAATTYELKERKERLEDAVMARAAVEEG'VAGGGVA DYDREKLGERLAKVAGGVGVIKVGAATTYELKERKERLEDAVMARAAVEEG'VAGGGVA LIDEKLGERLAKVAGGVGVIKVGAATTYELKERKERLEDAVMARAAVEEG'VAGGGVA DYDREKLGERLAKVAGGVGVIKVGAATTYELKERKERLEDAVMARAAVEEG'VAGGGVA LIDEKLGERLAKVAGGVGVIKVGAATTYELKERKERLEDAVMARAAVEEG'VAGGGVA LIDAATAD - LEGGDENGVGVIVALEARLEANGLAGVAVADKVANTSERVKELPEDE LITVASLDS - VEVENEDGRVGVIXIARAMERPLGO'VANGVANVADKVANEDGV LIDAATAD - LEGGDENGVIKVALEARLEARLEANGGLAGVAVADKVANEDG LIDAAPTIDE
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L. preumono. M. bovis M. tubercul. M. lopree S. ALBUS-56 S. ALBUS-56 CONSERVED S. sp. 7942 E. coli C. burneti L. preumono. M. tubercul. M. tubercul. M. tubercul. S. ALBUS-56 S. ALBUS-56 CONSERVED M. tubercul. M. bovis M. tubercul. M. bovis S. sp. 7942 E. coli C. burneti L. pneumono. M. bovis M. tubercul. M. lopree S. ALBUS-56 S. ALBUS-56 S. ALBUS-56 CONSERVED	DYDREKLGERLAKLAGGVAVIKVGAATYSHEKKKARVEDALAATAAVEEGVVPGGGVA DYDREKLGERLAKLAGGVAVIKVGAATYSHEKKRARVEDALAATAAVEEG'VAGGGVT DYDREKLGERLAKLAGGVAVIKVGAATYSLHEKKRERIEDAVMMARAAVEEG'VAGGGVT DYDREKLGERLAKLAGGVAVIKVGAATYSLHEKKRERIEDAVMMARAAVEEG'VAGGGVT DYDREKLGERLAKLAGGVAVIKVGAATSVELKERERIEDAVMARAAVEEG'VAGGGVT DYDREKLGERLAKLAGGVGVIKVGAATSVELKERERIEDAVMARAAVEEG'VAGGGVT DYDREKLGERLAKLAGGVGVIKVGAATSVELKERERIEDAVMARAAVEEG'VAGGGVT DYDREKLGERLAKLAGGVGVIKVGAATSVELKERERIEDAVMARAAVEEG'VAGGGVA DMDREKLGERLAKLAGGVGVIKVGAATSVELKERERIEDAVMARAAVEEG'VAGGGVA DMDREKLGERLAKLAGGVGVIKVGAATSVELKERERIEDAVMARAAVEG'VAGGGVA DMDREKLGERLAKLAGGVGVIKVGAATSVELKERERIEDAVMARAAVEG'VAGGGVA DMDREKLGERLAKLAGGVGVIKVGAATSVELKERERIEDAVMARAAVEG'VAGGGVA LIKVASLDS-UKZDDOMVG'IVIKVALEMERIEDAVENVAKVANEG'VAGGVA LIKVASLDS-UKZDDOMVG'IVIKVALEMERIEDIGVIKVGVAGVAVDKVANEHGUN LIGAAPTIDS-UKLDDOMVG'IVIKVALEMEISDEGGVVEKVNENVENVENVENVEN LIGAAPTIDS-UKLDDEATGAMIVKVALEMEISDEGGVVEKVNENVENVENVEN LIGAAPTIDS-UKLDDEATGAMIVKVALEMEISDEGGVVEKVNENVENVEN LIGAAPTIDS-UKLDDEATGAMIVKVALEMEISDEGGVVEKVNENVENVEN LIGAAPTIDS-UKLDDEATGAMIVKVALEMEISDEGGVVEKVNENVEN LIGAAPTADS-UKLDDEATGAMIVKVALEMEISDEGGVVEKVNENVEN LIGAAPTADS-UKLDDEATGAMIVKVALEMEISDEGGVVEKVNENUSSGE LIGAAPADD-UKLFGDEATGAMIVKVALEMEISDEGGVVEKVNENUSSGE LIGAAPTADS-UKLDDEATGAMIVKVALEMEISDEGGVVEKVNENUSSGE LIGAAPADD-UKLFGDEATGAMIVKVALEMEISDEGGVVEKVNENUSSGE LIGAAPADD-UKLFGDEATGAMIVKVALEMEISGAMITTEGVVEKVNENUSSGE LIGAAPADD-UKLFGDEATGAMIVKVALEMEISGAMITTEGVDEGGVDEKVNENUSSGE LIGAAPADD-UKLFGDEATGAMIVKVALEMEISGAMITTEGVVEKVNENUSSGE LIGAAPADD-UKLFGDEATGAMIVKVALEMEISGAMITTEGVVEKVNENUSSGE LIGAAPADD-UKLFGDEATGAMIVKVALEMEISGAMITTEGVVEKVNENUSSGE LIGAAPADD-VNENTALDEATAMIVKTERALGMASSIAMITTEGVVEKVNENUSSGE CONAMIGETGDHIMGILDPTIVTITALGMASSIAMITTEGVVEKVNENUSSGE GEGMAATGETGDHIMGULDPTIVTITALGMASSIAMITTEGVVERVEKVMENSGEVGG GEGMAATGETGDHIMGULDPTIVTTALGMASSIAMITTEGVVERVERVERMERSGE GEGMAATGETGDHIMGULDPTIVTTALGMASSIAMITTEGVVERVERMERSGEGGGGVERGVEKVERVERMERSGE GEGMAATGETGDHIMGULDPTIVTTALGMASSIAMIGTTTEGVVERMERSMERSGEGGGGVERGVERGVERKAMAPEGG GEGMAATGETGDUKKGVERGUPVERTERALGMASSIAMITT
L. pseumono. M. bovis M. tubercul. M. tupercul. M. tupercul. M. tupercul. S. ALBOS-56 S. ALBOS-56 CONSERVED S. sp. 7942 E. coli C. burneti L. pneumono. M. tubercul. M. tupercul. S. ALBOS-56 S. ALBOS-58 CONSERVED S. sp. 7942 E. coli C. burneti L. pseumono. M. tubercul. M. tubercul. M. tubercul. M. tupercul. S. ALBOS-56 S. ALBOS-56 S. ALBOS-56 S. ALBOS-56 S. ALBOS-58 CONSERVED S. ALBOS-54 CONSERVED S. Sp. 7942	DYDREKLGERLAKLAGGVAVIKVGAATYSHEKKRARVEDALAATAAAVEEGVVGGGVA DYDREKLGERLAKLAGGVAVIKVGAATYSHEKKRARVEDALAATAAVEEG'VGGGVA DYDREKLGERLAKLAGGVAVIKVGAATYSLKERKRERIEDAVMMARAAVEEG'VAGGGVT DYDREKLGERLAKLAGGVAVIKVGAATYSLKERKRERIEDAVMARAAVEEG'VAGGGVA DYDREKLGERLAKLAGGVAVIKVGAATYSLKERKRERIEDAVMARAAVEEG'VAGGGVA DYDREKLGERLAKLAGGVAVIKVGAATYSLKERKRERIEDAVMARAAVEEG'VAGGGVA DYDREKLGERLAKLAGGVAVIKVGAATYSLKERKRERIEDAVMARAAVEEG'VAGGGVA DYDREKLGERLAKLAGGVAVIKVGAATYSLKERKRERIEDAVMARAAVEEG'VAGGGVA DYDREKLGERLAKLAGGVAVIKVGAATYSLKERKRERIEDAVMARAAVEEG'VAGGGVA DYDREKLGERLAKLAGGVAVIKVGAATYSLKERKRERIEDAVMARAAVEEG'VAGGGVA DYDREKLGERLAKLAGGVAVIKVGAATYSLKERKRERIEDAVMARAAVEEG'VAGGGVA DYDREKLGERLAKLAGGVAVIKVGAATYSLKERKRERIEDAVMARAAVEEG'VAGGGVA LIKVAKLDSVEVENEDGRAVGVALARMEAPLGVIXLGEEFFSVAMTY-KGCGGN LIKVAKLDSVEVENEDGRAVGVIXIARAMEAPLGVIXHGGEVGVAKVANDIVAL LIQAAPIDSLLCDOEATCAMIVKVALEAPLGVIXHGSLEFGVVAKVANDINGVA LIQAAPIDSLKUGDEATCAMIVKVALEAPLGVIXHVGLAGVVAKVAKVNISVGE LIQAAPIDSLKUGDEATCAMIVKVALEAPLGVIXHVGLEGVGVAKVANLSVGE LIQAAPIDSKUGDEATCAMIVKVALEAPLGVIXHVGLEGVAKVAKVNISVGE LIQAAPIDSKUGDEATCAMIVKVALEAPLGVIXHVGLEGVGVEKVAKVNISVGE VEVEAVKVLDD
L. pheumono. M. bovis M. tubercul. M. tubercul. M. tubercul. M. tubercul. S. ALBOS-56 S. ALBOS-58 CONSERVED S. sp. 7942 E. coli C. burneti L. pheumono. M. tubercul. M. tubercul. M. tubercul. J. paeumono. M. bovis S. sp. 7942 E. coli C. burneti L. pheumono. M. tubercul. M. tubercul. M. tubercul. M. tubercul. M. tubercul. M. tubercul. S. ALBOS-58 CONSERVED S. ALBOS-58 CONSERVED S. S. ALBOS-58 CONSERVED S. S. P. 7942 E. coli	DYDREKLQERLAKLAGGVAVIKVGAATYSHEKKKARVEDALAATAAVEEGVVGGGVA DYDREKLQERVAKLAGGVAVIKVGAATYSHEKKRARVEDALAATAAVEEGIVGGGVA DYDREKLQERVAKLAGGVAVIKVGAATYSHEKKRARVEDALAATAAVEEGIVAGGVA DYDREKLQERLAKLAGGVAVIKVGAATYSLAKERKERLEDAVMAKAAVEEGIVAGGVA DYDREKLQERLAKLAGGVAVIKVGAATYSLAKERKERLEDAVMAKAAVEEGIVAGGVA DYDREKLQERLAKLAGGVAVIKVGAATSVELKERKERLEDAVMAKAAVEEGIVAGGVA DYDREKLGERLAKLAGGVGVIRVGAATSVELKERKERLEDAVMAKAAVEEGIVAGGVA DYDREKLGERLAKLAGGVGVIRVGAATSVELKERKERLEDAVMAKAAVEEGIVAGGVA DYDREKLGERLAKLAGGVGVIRVGAATSVELKERKERLEDAVEANAAVEEGIVAGGVA DYDREKLGERLAKLAGGVGVIRVGAATSVELKERKERLEDAVMAKAAVEEGIVAGGGVA DYDREKLGERLAKLAGGVGVIRVGAATSVELKERKERLEDAVEANAAVEEGIVAGGGVA DYDREKLGERLAKLAGGVGVIRVGAATSVELKERKERLEDAVEANAAVEEGIVAGGGVA DYDREKLGERLAKLAGGVGVIRVGAATSVELKERKERLEDAVEANAAVEEGIVAGGGVA DYDREKLGERLAKLAGGVGVIRVGAATSVELKERKERLEDAVEANAAVEEGIVAGGGVA DYDREKLGERLAKLAGGVGVIRVGAATSVELKERKERLEDAVEANAAVEEGIVAGGGVA DYDREKLGERLAKLAGGVGVIRVGAATSVELKERKERLEDAVEANAAVEEGIVAGGVA DYDREKLGERLAKLAGGVGVIRVGAATSVELKERKERLEDAVENISA DYDREKLGERLAKLAGGVGVIRVGAATSVELKERKERLEDAVENIS DYDREKLGERLAKLAGGVGVIRVGAATSVELKERKERLEDAVENIS DYDREKLGERLAKANVELGERGENGVYIKVALERPLAGIVINGGERSVENVENVENIS DYDREKLGERGERGERGVAIVVALERPLAGIVINGGERSVAKVENISTAGE DJAAPALDKLEUGDERTGANIVKVALERPLAGIAPINGAERGVVAKVENISJGGE DJAAPALDK
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FIG. 3. Alignment of eubacterial GroELs from Synechococcus sp. (S. sp.) strain PCC 7942 (27), E. coli (9), Coxiella burnetii (26), Legionella pneumophila (18), M. tuberculosis (21), and M. bovis (22). Alignment was done by using Clustal programs (10). Conserved amino acids are indicated; dots show conservation of similar amino acids. A block of conserved amino acids, a portion of which was used to construct a degenerated probe (see Fig. 5), is underlined.



FIG. 4. Dendrogram representation of the similarities between eubacterial GroEL proteins. Analyses were carried out on the alignment shown in Fig. 3 by using CLUSTAL programs (10). Abbreviations and references are as described in the legend to Fig. 3.

Culture Collection]; S. citricolor, S. colombiensis, S. endus, S. polychromogenes, S. rimosus, and S. spectabilis (culture collection of Elizabeth Wellington]; S. fradiae ATCC 10745; S. griseus [ETH, SS-1198]; S. kanamyceticus ATCC 12853;



FIG. 5. Detection of two groEL-like genes in actinomycetes. Restriction endonuclease-digested genomic DNA of S. viridochromogenes (lane 1; XhoI), S. parvulus (lane 2; XhoI), S. albus (lane 3; XhoI), S. lividans (lane 4; XhoI), S. coelicolor (lane 5; XhoI), M. smegmatis (lane 6; PstI), and E. coli (lane 7; PstI) were screened with an OL3, a degenerate 30-mer oligonucleotide probe (GGCTTCGG[CT]GACCG CCGCAAGGC[CG]ATGCTC) conserved among actinomycete groEL genes (a portion of a block of conserved amino acids, underlined in Fig. 3). The positions and sizes (in kilobases) of molecular size markers (bacteriophage lambda cleaved with PstI) are indicated by arrows.

S. parvulus ATCC 12434; and S. viridochromogenes GCC 40736) were hybridized with an oligonucleotide probe representing a sequence that is highly conserved among actinomycete groEL genes (Fig. 5; not all species are shown). Two strong bands of hybridization were observed with high-stringency conditions (60° C, $0.5 \times$ SSC [1 \times SSC is 0.15 M NaCl plus 0.015 M sodium citrate]) in every Streptomyces sp. tested. One band was observed in Mycobacterium smeg matis and no bands were observed in E. coli under these conditions of hybridization.

The observation that the probe hybridized to two restriction fragments after digestion with either XhoI (Fig. 5) or SstI (data not shown) strongly suggested that the two genes are not closely linked on the streptomycete chromosome. This was confirmed by using Southern blots (data not shown), which indicated that neither cosmid pGM3 nor pGM4 contained both genes. Finally, digestion of the *S. albus* genome by SspI followed by pulsed-field electrophoresis, blotting, and hybridization showed that the two genes were present on different 700- and 200-kb fragments (data not shown).

Streptomyces spp. are gram-positive mycelial eubacteria that are well known for their ability to produce antibiotics, secrete proteins, and differentiate during starvation; such conditions probably involve stress heat shock proteins (8). GroEL synthesis is induced in stationary-phase cultures of *E. coli* (16) starved for carbon, phosphate, or nitrogen (14). The observation that most *Streptomyces* species have two groEL-like genes that express three gene products supports the notion that multiple GroEL proteins (probably comparable to those observed in *S. albus*) fulfill physiologically distinct and important roles. Specialized functions may be required for substrate (protein or possibly peptide antibiotic) recognition, subcellular localization, or physiological changes associated with differentiation.

Nucleotide sequence accession numbers. The nucleotide sequence data shown in Fig. 1 and 2 have been submitted to GenBank under accession numbers M76657 and M76658, respectively.

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