We are IntechOpen, the world's leading publisher of Open Access books Built by scientists, for scientists



122,000





Our authors are among the

TOP 1%





WEB OF SCIENCE

Selection of our books indexed in the Book Citation Index in Web of Science™ Core Collection (BKCI)

Interested in publishing with us? Contact book.department@intechopen.com

Numbers displayed above are based on latest data collected. For more information visit www.intechopen.com



Unique Biochemical Features of the Cytokinetic Protein FtsZ of Mycobacteria

Prabuddha Gupta, Atul Pradhan and Parthasarathi Ajitkumar

Additional information is available at the end of the chapter

http://dx.doi.org/10.5772/intechopen.70540

Abstract

FtsZ, the bacterial cytokinetic protein, a structural homologue of mammalian β-tubulin, is present in bacteria of diverse genera, including mycobacteria. The FtsZ protein of *Mycobacterium tuberculosis* (*M. tuberculosis* FtsZ), the causative agent of tuberculosis, is the most studied among the mycobacterial FtsZ proteins as it is a potential anti-tuberculosis drug target. *M. tuberculosis* FtsZ possesses many unique biochemical features, which include slow polymerisation kinetics, presence of charged amino acids in the C-terminal domain that interacts with a variety of other cell division proteins, and the presence of specific amino acids at unique locations that makes it distinct from the FtsZ of other mycobacterial species and of other bacterial genera. On the other hand, although the FtsZ of *Mycobacterium leprae* (*M. leprae* FtsZ), the causative agent of leprosy, shows high level of conservation with *M. tuberculosis* FtsZ due to the difference in specific amino acid residues at critical locations on the protein. The present review focuses on these structural features of *M. tuberculosis* FtsZ, as studied by others and by us, in comparison to those of the FtsZ of other mycobacterial species and of other mycobacterial species and of other species and of other species and protein.

Keywords: mycobacteria, FtsZ, biochemical features, polymerisation, GTPase, GTP binding, bacterial cytokinesis

1. Introduction

IntechOpen

Bacterial cell division involves karyokinesis and cytokinesis. The replication and segregation of genetic material occur in karyokinesis. In cytokinesis, the cytoplasm and its contents increase in quantity and get partitioned between two daughter cells with the development of the septum between them and formation of new cell membrane and cell wall in the sacculus.

© 2018 The Author(s). Licensee IntechOpen. This chapter is distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/3.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

The process of septation is guided by the cytokinetic protein, FtsZ [1, 2], which is the bacterial structural homologue of mammalian β -tubulin [3]. Polymeric FtsZ, as the inner membrane bound FtsZ ring at the mid-cell site [1, 2], guides septation. A large number of cell division proteins interact with FtsZ at the median (reviewed in [4, 5]). The duration of the whole process of cell division varies from bacterium to bacterium, with different strains of Escherichia coli completing cell division in 18-55 min [6], Bacillus subtilis taking 120 min [7], whereas Mycobacterium smegmatis taking 3 h [8], M. tuberculosis 18 h in vivo [9] and 24 h in vitro [10], and M. leprae completing it in 13.5 days once [11]. Accordingly, since the septation process takes only a part of the whole cell division duration, the polymerisation and depolymerisation dynamics of FtsZ of each bacterium need to be different in different bacteria to suit the septation duration in the bacterium. The required modifications in the polymerisation and depolymerisation dynamics of the cytokinetic protein to suit the time span of septation need to be effected through specific changes in the amino acid residues of FtsZ. Such changes, which can influence polymerisation and depolymerisation dynamics of FtsZ, can be vividly discerned from the evolutionarily purposeful placement of specific amino acid residues at specific structural locations on the protein. Here, we have tried to point out this particular aspect of the structure-function correlation of FtsZ from mycobacteria with that of FtsZ from other mycobacterial species and bacterial genera.

2. Basic common structural features of FtsZ of other bacteria

The biochemical identity of FtsZ was first established through the demonstration of the GTP binding and GTPase activities of *Escherichia coli* FtsZ (*E. coli* FtsZ) [12, 13]. Both the authors showed the presence of a peptide motif (105 GGGTGTG 111), similar to the tubulin signature motif (140 GGGTGSG 147), and postulated that it would form a phosphate-binding loop like in β -tubulin [14]. The GGGTGTG motif is crucial for GTP binding as its change to SGGTGTG in the FtsZ84 mutant of the temperature-sensitive *E. coli* (*ftsZ84*) strain markedly reduced GTP binding ability (by crosslinking) [13] and converted FtsZ into an ATPase *in vitro* [12]. Tubulin and FtsZ share poor primary sequence homology of 10–18%, except in two sequence regions (amino acids 95–175 in β -tubulin and 65–135 in *E. coli* FtsZ, and 305–350 in β -tubulin and 255–300 in *E. coli* FtsZ) where they show clear sequence homology of 85–87 and 51–78%, respectively [15]. The first region contains β -tubulin/FtsZ signature motif, flanked by identical looking secondary structural elements [15]. However, the overall three-dimensional structures of FtsZ and β -tubulin are almost similar [16, 17], which is reflected in the GTP-dependent polymerisation of *E. coli* FtsZ *in vitro* [18, 19] like β -tubulin polymerisation [20].

The crystal structures of the FtsZ proteins of *Methanococcus jannaschii* [16], *Thermotoga maritima* [21], *Bacillus subtilis, Pseudomonas aeruginosa*, and *Aquifex aeolicus* [22] essentially showed independently folding N- and C-terminal domains arranged around a central helix. The N-terminal domain contains GTP-binding site and an incomplete GTPase active site. During the course of polymerisation, the T7 loop of one monomer is supplied in *trans* to the GTPbinding pocket of the next, thus forming the active site for GTP hydrolysis [23–28]. From the co-crystal structure of SulA-FtsZ, it was found that SulA, a cell division inhibitor [29], binds the T7 loop surface of FtsZ, thereby blocking polymer formation as a part of SOS response [30]. Thus, the T7 loop seems to be critically required for FtsZ polymerisation, thereby carrying the potential to be an antibacterial inhibitor target.

In all the solved structures of FtsZ of *M. jannaschii* [16], *P. aeruginosa* [22], *A. aeolicus* [22], *T. maritima* [21], and of *B. subtilis* [31], the end part of the C-terminus has been found to be unstructured and containing variable residues. It has been found to be a platform for the interaction of a large number of cell division proteins, ZipA [32], FtsA [33], EzrA [34], SepF [35, 36], ZapD [37], and with FtsZ itself [4, 5, 38].

2.1. Specific residues required for the biochemical activities of FtsZ

GTP-binding residues are best conserved between FtsZ and β -tubulin [39]. Monomeric FtsZ binds GTP tightly with a K_d of 5 μ M [40]. The FtsZ84 (G105S) mutant protein has an impaired GTPase activity in vitro [12]. In other examples, while the mutant FtsZ6460 (G109S) showed nil GTPase activity, FtsZ9124 (P203L) possessed reduced GTPase activity, and both the mutants failed to polymerise in vitro [41]. Extensive work has been carried out on the characterisation of FtsZ mutants in vitro and in vivo [42-44]. Based on a model structure of E. coli FtsZ, which was built on the crystal structure of M. jannaschii FtsZ [16], the mutants were found to be primarily of three classes [43]. (i) On the front and back surface of protofilament and few on the top and bottom surfaces not in contact with GTP, which were termed as benign mutants as all of them could complement ftsZ84 strain at non-permissive temperature. Few examples of these mutants are A70T, A81V/F268C (Z100), D158A, D158N, D187A, F268C (Z114), D269A, and D299A. (ii) GTP contact mutants, e.g., N43D, D45A, D45N, D209A, did not complement ftsZ84 and could polymerise only in the presence of DEAE-dextran. (iii) Mutants, D86K, D96A, E238A, S245F, and E250A, where the mutations were thought to be on the lateral surface of protofilaments and therefore believed to play role in inter-protofilament interactions. These mutants could polymerise *in vitro*, but none of them could complement *ftsZ84* at nonpermissive temperature.

Further studies showed that the mutations on the top surface of *E. coli* FtsZ model (e.g., G21K, L68C\D\W, F182C) have far less disturbing effect on the complementation (in plate and liquid culture) and GTPase activity of FtsZ compared to those of the mutations on the bottom surface (e.g. D96A, N207C, D209A\C\K, F210A) [44]. Interestingly, one top surface mutant Q47K that binds GTP at more than 1:1 ratio and having around 30-fold less GTPase activity, compared to that of wild-type FtsZ, failed to complement cell division, both in plate and in liquid culture [44]. The E83 and R85 in the helix H3 bend and lateral residues of *E. coli* FtsZ were found to be important for the polymerisation, GTPase activity, and cellular viability [45]. E93R substitution in *E. coli* FtsZ induces bundling of protofilaments, reduces GTPase activity, ity, and impairs bacterial cytokinesis [46]. Similarly, R191 of *B. subtilis* FtsZ was found to be required for polymerisation [47].

The residue D212G of the T7 loop is conserved among all FtsZ sequences known [48] and all the mutations D212ANC, D212G (FtsZ2) impaired GTPase activity [42–44]. The location of FtsZ2 mutation was later validated by the crystallography data that SulA binds to T7 loop

region of FtsZ and a mutation in T7 loop might prevent binding of SulA to block FtsZ polymerisation [30]. There was no other structural abnormality of FtsZ2 to bind GTP and therefore could polymerise in the presence of DEAE-dextran *in vitro* [19] or co-polymerise with wildtype FtsZ [25].

The C-terminal variable (CTV) region residues in *E. coli* FtsZ and *B. subtilis* FtsZ were found to mediate electrostatic interactions to facilitate lateral association of the FtsZ protofilaments to form polymers *in vitro* and *in vivo* [39] and for interaction with other proteins such as ZapD ([49], reviewed in [4, 5]).

2.2. Polymerisation properties of FtsZ in vitro and in vivo

FtsZ has been found to exist mostly as dimers [50, 51]. FtsZ assembly process leading to polymerisation has also been found to involve a dimer nucleus [52]. Among the wide variety of FtsZ structures visualised by various methods till date, the simplest one is the protofilament constituted by FtsZ subunits stacked one above the other with a diameter of 5 nm, with each subunit placed at 4.3 nm apart [53]. While straight protofilaments were favoured by high concentration of GTP or by GTPase inhibition, curved conformation was triggered by GTP hydrolysis or in the presence of GDP [54]. Examination of the FtsZ polymers using atomic force microscopy (AFM) showed that individual protofilaments can fragment and re-anneal on a surface [55]. Also, individual protofilaments were found to have tendency to form bundles in the presence of GTP and singular curved protofilaments were observed in the presence of GDP-AlF₃ [55]. This observation might have implications on the assembly dynamics of FtsZ ring on the inner cell membrane during bacterial cell division.

The *E. coli* FtsZ-Q47K mutant, which does not support cell division [44], formed bundles and rings in yeast cytoplasm [56]. They found that the double mutant *E. coli* FtsZ-Q47K-**D86K**, which carries a lateral mutation (indicated in bold letters) formed long linear cables but did not assemble into a ring. In a separate observation, the authors have reported that FtsZ cables laterally assemble to form bundles in yeast cytoplasm. Thus, these observations indicated that the lateral contacts in FtsZ are important *in vivo* for FtsZ polymeric ring formation. Interestingly, it was found that the C-terminal unstructured tail, or region equivalent to it, is completely dispensable for *in vitro* and/ or *in vivo* polymerisation of *E. coli* FtsZ [57, 58], *P. aeruginosa* FtsZ [30], and *B. subtilis* FtsZ [34].

In *in vivo* studies, FtsZ rings constituted by FtsZ polymers have been observed at the midcell site using fluorescence microscopy [1, 2] and super resolution 3D-structured illumination microscopy (3D-SIM) [59]. *In vivo* studies in *E. coli* [60] and *B. subtilis* [61] have shown oscillation of FtsZ in a helical pattern throughout the length in the presence of FtsZ ring in *E. coli* [60] and later constricting to the median as the Z-ring form in *B. subtilis* [61].

3. Unique structural features of mycobacterial FtsZ and their role in biochemical activities

Like in the case of FtsZ from other bacterial systems [50–52], *M. tuberculosis* FtsZ exists as a dimer [62] and the assembly process leading to polymerisation has also been found to involve

a dimer nucleus [63]. Like in the case of FtsZ from other bacterial systems, the T7 loop of one monomer is supplied in *trans* to the GTP-binding pocket of the next, thus forming the active site for GTP hydrolysis [64]. In a FRET-based system, *M. tuberculosis* FtsZ was found to take about 60–100 s to reach polymerisation saturation, about 10 times slower compared to *E. coli* FtsZ [63]. At steady state also, subunit turnover and GTPase activity were about 8–10 times slower than those of *E. coli* FtsZ [63]. FRAP experiments showed that *M. tuberculosis* FtsZ has a slower recovery than *E. coli* FtsZ in yeast cytoplasm also [56], which is consistent with the slower polymerisation of *M. tuberculosis* FtsZ [65]. Thus, the FtsZ polymerisation and assembly dynamics of FtsZ of *M. tuberculosis*, which divides once in 18–24 h [9, 10], are much slower than those of the FtsZ of *E. coli*, the different strains of which divide once in 18–55 min [6].

3.1. The role of N-terminal domain residues

The N-terminal domain of the FtsZ proteins of all mycobacterial species is highly conserved (Figure 1). In spite of this conservation, conspicuous drastic differences exist at specific amino acid locations. A typical example is the glaring presence of T172 in M. leprae FtsZ as the lone exception in lieu of A172 in the FtsZ proteins of all the other mycobacterial species. M. leprae FtsZ was found to be polymerisation-lethargic in vitro, even in the presence of DEAE-dextran and under a variety of other conditions [66]. However, interestingly, change of T172 to A172, as it exists in M. tuberculosis FtsZ, showed dramatic polymerisation as in the case of M. tuberculosis FtsZ [66]. Conversely, the reciprocal replacement of A172 with T172 in *M. tuberculosis* FtsZ, as it exists in *M. leprae* FtsZ, completely abolished the polymerisation potential of *M. tuberculosis* FtsZ. These observations showed the crucial nature of A172 residue for polymerisation of FtsZ of all mycobacterial species that have generation time of 24 h or less. On the contrary, the change of A172 to T172, exclusively in M. leprae FtsZ, seems to be an evolution-driven modification, probably to dramatically tone down FtsZ polymerisation rate, as M. leprae divides only once in 13.5 days [11]. The positioning of T172, which can wield such dramatic influence on FtsZ polymerisation, is well justified to be in the N-terminal domain that is known to be important for polymerisation, as found in E. coli FtsZ [21, 57]. Modelling of M. leprae FtsZ and M. tuberculosis FtsZ showed that probably the presence of Thr, which is a hydrogen-bonding and branched residue, at 172 position in the T6 loop might have imposed rigidity on the T6 loop-H10 helix-T7 loop segment and thereby affecting the polymerisation potential of M. leprae FtsZ [66]. Conversely, at position 172, the presence of the non-branched residue Ala that does not engage in hydrogen bonding might not impose rigidity on the T6 loop-H10 helix-T7 loop, thereby facilitating polymerisation of M. tuberculosis FtsZ. The link of T6 loop, which contains the 172 residue, to the T7 loop, which might be crucial for polymerisation in vitro [66], via the H10 helix, supports this possibility. In view of these observations, it is needless to state that there have to be cellular factors that might enable polymerisation of M. leprae FtsZ in a very slow manner suiting the slow generation time of the bacterium when M. leprae divides inside human cells. The D84 and D94 of M. tuberculosis FtsZ are equivalent to D86 and D96 of E. coli FtsZ, respectively [42], and both the residues form salt bridge at the dimer interface [62]. The D94 and N22 form salt bridge with R181 and E136, respectively, in the other subunit [62]. Such interactions might be necessary for the protofilament association during M. tuberculosis FtsZ polymerisation as found necessary for the E. coli FtsZ polymerisation [42]. While G103 was found to be involved in GTP binding [67], C155 has also been found to play an important role in the assembly of M. tuberculosis FtsZ into protofilaments during polymerisation [68].

| | 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 | |
|--|---|--|--|---|--|--|---|--|--|
| | · · · · l · · · · l · · · | | | | | | . | | - |
| M. kansasii | | | MA-PPHNY | LAVIKVVGI | GGGGVNAVNRMI | EQGLKGVEFIA | INTDAQALLM | ISDADVK- 5 | 5 |
| M. IOTUITUM | | | MT PPHNY | | GGGGVNAVNRMJ | EQGLKGVEFIA | INTDAQALLA | ISDADVK- 5 | 5 |
| Mycobacterium sp. MMS | | | MT PPHNI | | GGGVNAVNRMI | | | | S C |
| Mycobacterium sp. MCS | | | | | M | T-IHKVKAVFG | | | 2 |
| M. gilvum | | | MT-PPHNY | AVTKVVGT | GGGVNAVNRMI | BOGLKGVEFTA | TNTDAOALLA | ISDADVK- 5 | 5 |
| M. vaccae | | | | -MIKVVGI | GGGGVNAVNRMI | EOGLKGVEFIA | INTDAOALLM | ASDADVK- 4 | 6 |
| M. vanbaalenii | | | MT-PPHNY | LAVIKVVGI | GGGGVNAVNRM I | EQGLKGVEFIA | INTDAQALLM | ISDADVK- 5 | 5 |
| M. chubuense | | | MT-PPHNY | LAVIKVVGI | GGGG <mark>VNA</mark> VNRMI | EQGLKGVEFIA | INTDAQALLM | ASDADVK- 5 | 5 |
| M. rhodesiae | | | MT-PPHNY | LAVIKVVGI | GGGG <mark>VNA</mark> VNRMI | EQGLKGVEFIA | INTDAQALLM | ISDADVK- 5 | 5 |
| M. thermoresistibile | | | MT-PPHNY | LAVIKVVGI | GGGGVN <mark>A</mark> VNRMI | EQGLKGVEFIA | INT <mark>D</mark> AQALLM | isdadvk- 5 | 5 |
| M. bovis-AF2122/97 | | | MT-PPHNY | LAVIKVVGI | 3GGGVNAVNRM1 | EQGLKGVEFIA | INTDAQALLM | ISDADVK - 5 | 5 |
| M. tuberculosis CDC1551 | | | MT-PPHNY | LAVIKVVGI | GGGGVNAVNRMI | EQGLKGVEFIA | INTDAQALLM | ISDADVK- 5 | 5 |
| M. canettii | | | MT PPHNY | LAVIKVVGI | GGGGVNAVNRMI | EQGLKGVEFIA | INTDAQALLM | ISDADVK- 5 | 5 |
| M. DOVIS BCG Str. Pasteur 117 | | | MT PPHNY | | GGGGVNAVNRMI | POCTKOVEFTA | TNTDAQALLE | | 5 |
| M. marinum | | | MT-PPHNY | AVTKVVGT | GGGVNAVNRMI | EOGLKGVEFTA | TNTDAOALLN | ISDADVK- 5 | 5 |
| M. ulcerans | | | MT-PPHNY | LAVIKVVGI | GGGVNAVNRMI | EOGLKGVEFIA | INTDAOALLA | SDADVK- 5 | 6 |
| M. liflandii | | | MT-PPHNY | LAVIKVVGI | GGGGVNAVNRMI | EOGLKGVEFIA | INTDAOALLM | ISDADVK- 5 | 5 |
| M. intracellulare | | N | MT-PPHNY | LAVIKVVGI | GGGGVNAVNRMI | EQGLKGVEFIA | INTDAQALLA | ISDADVK- 5 | 6 |
| M. indicus | | b | MT-PPHNY | LAVIKVVGI | GGGGVN <mark>A</mark> VNRMI | EQGLKGVEFIA | INTDAQALLM | ISDADVK- 5 | 6 |
| Mycobacterium sp. MOTT36Y | | | MT-PPHNY | LAVIKVVGI | GGGGVNAVNRMI | EQGLKGVEFIA | INTDAQALLM | ISDADVK- 5 | 5 |
| M. colombiense | | | MT PPHNY | LAVIKVVGI | GGGGVN <mark>A</mark> VNRMI | EQGLKGVEFIA | INTDAQALLM | ISDADVK- 5 | 5 |
| M. parascrofulaceum | | b | MT-PPHNYI | | GGGGVNAVNRMI | EQGLKGVEFIA | INTDAQALLM | ISDADVK- 5 | 6 |
| Mucobactorium ca TDM601 | | | MT PPHNY | | GGGGVNAVNRMI | EQGLKGVEFMA | TNTDAQALLM | ISDADVK- 5 | 5 |
| Mycobacterium sp. JDM601 M. hassiacum | | | MT PPHNY | AVTKVVCT | GGGVNAVNRMI | EOGLKGVEFIA | TNTDAOALLA | ISDADVK 5 | 5 |
| M. franklinii | | | | AVTKVVGT | GGGVNAVNRMI | FHGLKGVEFTA | TNTDAOALLN | ASDADVK - 5 | 5 |
| M. massiliense | | | MT-PPHNY | LAVIKVVGI | GGGGVNAVNRMI | BHGLKGVEFIA | INTDAOALLN | SDADVK- 5 | 5 |
| M. immunogenum | | | MT-PPHNY | LAVIKVVGI | GGGGVNAVNRM I | EHGLKGVEFIA | INTDAQALLM | ISDADVK- 5 | 5 |
| M. smegmatis | MVEVEGLQGRSAP | RAPNQGGRRS | MT-PPHNY | LAVIKVVGI | GGGG <mark>VNA</mark> VNRMI | EQGLKGVEFIA | INTDAQALLN | ASDADVK- 7 | 8 |
| M. tuberculosis H37Rv | | | MT-PPHNY | LAVIKVVGI | GGGG <mark>VNA</mark> VNRMI | EQGLKGVEFIA | INTDAQALLM | 1 <mark>SDADVK</mark> - 5 | 5 |
| M. tuberculosis H37Ra | | | MT-PPHNY | LAVIKVVGI | GGGG <mark>VNA</mark> VNRMI | EQGLKGVEFIA | INTDAQALLM | ISDADVK- 5 | 5 |
| Bacillus subtilis | | MLE | FE-TNIDG | LASIKVIGV | GGGG <mark>N</mark> NAVNRMI | ENEVQGVEYIA | VNTDAQAL <mark>N</mark> I | SKADVK- 5 | 8 |
| Streptomyces coelicolor | | | MA-APQNY | LAVIKVIGVO | GGGGVNAINRMI | EVGLKGVEFIA | INTDAQALLM | ISDADVK- 5 | 5 |
| Escherichia coli | | P | IFEPMELTNI | DAVIKVIGV | GGGGGNAVEHM | RERIECVEDFA | VNTDAQALRE | AVGQT- 5 | 1 |
| | | | | | | | | | |
| | 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 | |
| | 90 | 100 . | 110 | 120 • • • • • • • • • |) 130 | 140 | 150 . | 160 . | |
| M. kansasii | 90 LDVGRDSTRGLCA | 100 . CADPEVGRXI | 110 . . AEDAKDDI | 120 EELLR <mark>CAD</mark> M |) 130 / FVTA<mark>GEGGG</mark>TC | 140 | 150 . RKL <mark>CA</mark> LTV <mark>C</mark> V | 160 . /VTRP-F- 1 | 33 |
| M. kansasii M. fortuitum | 90 LDVGRDSTRGLCA LDVGRDSTRGLCA | 100 . GADPEVGRXI GADPEVGRKI | 110 | 120 |) 130 VFVTAGEGGGTC VFVTAGEGGGTC | 140 | 150 . RKL <mark>GA</mark> LTV <mark>G</mark> V RKL <mark>GA</mark> LTV <mark>G</mark> V | 160 | 33 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS | 90 I LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA | 100 GADPEVGRX/ GADPEVGRK/ GADPEVGRK/ | 110 AEDAKDDI AEDAKDDI AEDAKDDI | 120 EELLRGADM EELLRGADM EELLRGADM |) 130 VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT | 140 TGCAPVVASIA TGCAPVVASIA TGCAPVVASIA | 150 . RKLCALTVGV RKLCALTVGV RKLCALTVGV | 160 | 33 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS | 90 LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA YEDDDRAERGAAR | 100 ADPEVGRX GADPEVGRK GADPEVGRK GYARRI | 110 AEDAKDDI AEDAKDDI AEDAKDDI REDRFEE | 120 ELLRCADMU ELLRCADMU ELLRCADMU EQUIDRAGRE |) 130 VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT 2 | 140 TGCAPVVASIA TGCAPVVASIA TGCAPVVASIA TGCAPVVASIA -DDRPAPREY- | 150 RKLCALTVGV RKLCALTVGV RKLCALTVGV -DEPPITYRC | 160 | 333333 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS | 90 LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA YEDDDRAERGAAR YEDDDRAERGAAR | 100 GADPEVGRX GADPEVGRKA GADPEVGRKA GYARRI GYARRI GYARRI | 110 AEDAKDDI AEDAKDDI AEDAKDDI REDRFEE REDRFEE | 120 EELLRCADMU EELLRCADMU EELLRCADMU GYIDRAGRE GYIDRAGRE |) 130 VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT SY | 140 TGCAPVVASIA TGCAPVVASIA TGCAPVVASIA TGCAPVVASIA DDRPAPREY- DDRPAPREY- | 150 | 160 /VTRP-F- 1 /VTRP-F- 1 /VTRP-F- 1 SYDEPRFD 8 SYDEPRFD 8 | 3333555 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum | 90 LDVGRDSTRGLGA LDVGRDSTRGLGA YPDDDRAERCAAR YPDDDRAERCAAR LDVGRDSTRGLGA | 100 GADPEVGRX GADPEVGRX GADPEVGRX GYARR GADPEVGRX GADPEVGRX | 110 AEDAKDDI AEDAKDDI REDRFEE REDRFEE | 120 EELLRCADMU EELLRCADMU EELLRCADMU EGYIDRAGRE EGYIDRAGRE EELLRCADMU |) 130 VFVTAGEGGGTO VFVTAGEGGGTO VFVTAGEGGGTO VFVTAGEGGGTO VFVTAGEGGGTO | 140 TGCAPVVASIA TGCAPVVASIA TGCAPVVASIA TGCAPVVASIA -DDRPAPREY- TGCAPVVASIA | 150 RKLCALTVGV RKLCALTVGV -DEPPIYRCG -DEPPIYRCG RKLCALTVGV | 160 | 33 33 5 5 33 |
| M. kansasii M. fortuitum Mycobactarium sp. KMS Mycobactarium sp. JLS Mycobactarium sp. MCS M. gilvum M. vaccae M. yaphaalanii | 90 LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA YPDDDRAERCAAR YPDDDRAERCAAR LDVGRDSTRGLGA LDVGRDSTRGLGA | 100 GADPEVGRX GADPEVGRX GADPEVGRX GYARR GADPEVGRX GADPEVGRX GADPEVGRX | 110 AEDAKDDI AEDAKDDI AEDAKDDI REDRFEE REDRFEE AEDAKDDI AEDAKDDI | 120 EELLRCADMU EELLRCADMU EGLIRCADMU EGYIDRAGRE EGYIDRAGRE EELLRCADMU EELLRCADMU | 130 VFVTAGEGGGTQ VFVTAGEGGGTQ VFVTAGEGGGTQ VFVTAGEGGGTQ VFVTAGEGGGTQ | 140 TGGAPVVASIA TGGAPVVASIA -DDRPAPREY- DDRPAPREY- TGGAPVVASIA TGGAPVVASIA | 150 RKLCALTVGV RKLCALTVGV RKLCALTVGV -DEPPTYRCG RKLCALTVGV RKLCALTVGV RKLCALTVGV | 160 VTRP-F- 1 VTRP-F- 1 VTRP-F- 1 STDE PR-D 8 STDE PR-D 8 VTRP-F- 1 VTRP-F- 1 | 33 33 5 5 33 24 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense | 90 LDVGRDSTRGLGA LDVGRDSTRGLGA VDDDRAERCAAR YDDDRAERCAAR LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA | 100 CADPEVGRX7 CADPEVGRX7 CADPEVGRX7 CADPEVGRX7 CADPEVGRX7 CADPEVGRX7 CADPEVGRX7 CADPEVGRX7 CADPEVGRX7 | 110 AEDAKDDT AEDAKDDT AEDAKDDT REDRFEE- REDRFEE- AEDAKDDT AEDAKDDT AEDAKDDT | 120 ELLIRGADMY EELLIRGADMY EGYIDRAGRE EGYIDRAGRE EELLIRGADMY EELLIRGADMY EELLIRGADMY | 130 VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT | 140 TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA -DDRPAPREY- TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA | 150 RKLCALTVCV RKLCALTVCV RKLCALTVCV -DEPPTYRCC RKLCALTVCV RKLCALTVCV RKLCALTVCV | 160 VTRP-F-1 VTRP-F-1 SYDE-RED 8 SYDE-RED 8 VTRP-F-1 VTRP-F-1 VTRP-F-1 | 33 33 5 5 33 24 33 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae | 90 LDVGRDSTRGLGA LDVGRDSTRGLGA VGDDTRGLGA VGDDDRAERCAAR VGDDDRAERCAAR LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA | 100 CA DEVCRX CA DEVCRX CA DEVCRX CA DEVCRX CA DEVCRX CA DEVCRX CA DEVCRX CA DEVCRX CA DEVCRX | 110 AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI | 120 EELLRGADM EELLRGADM GYIDRAGRE EELLRGADM EELLRGADM EELLRGADM EELLRGADM | 130 VFVTACEGGGT VFVTACEGGGT VFVTACEGGGT VFVTACEGGGT VFVTACEGGGT VFVTACEGGGT VFVTACEGGGT | 140 TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA | 150 RKLCALTVCV RKLCALTVCV RKLCALTVCV PDEPPTYRCC DEPPTYRCC RKLCALTVCV RKLCALTVCV RKLCALTVCV RKLCALTVCV | 160 VVTRP-F-1 VVTRP-F-1 SVDEPR-P-1 SVDEPR-P-1 VVTRP-F-1 VVTRP-F-1 VVTRP-F-1 VVTRP-F-1 VVTRP-F-1 VVTRP-F-1 VVTRP-F-1 | 33 33 5 5 33 33 33 33 33 33 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile | 90 LDVGRDSTRGLGA LDVGRDSTRGLGA VPDDDRAERCAAR VPDDDRAERCAAR LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA | 100 CA DEVCRX2 CA DEVCRX3 CA DEVCRX3 C | 110 | 120 EELLRGADM EELLRGADM GYIDRAGRE GYIDRAGRE EELLRGADM EELLRGADM EELLRGADM EELLRGADM | 130 VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT | 140 TGCAPVVASIA TGCAPVVASIA TGCAPVVASIA TGCAPVVASIA TGCAPVVASIA TGCAPVVASIA TGCAPVVASIA TGCAPVVASIA TGCAPVVASIA TGCAPVVASIA | 150 RKLGALTVGV RKLGALTVGV -DEPPIYRC -DEPPIYRC RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV | 160 VVTRP G = 1 VVTRP G = 1 SYDE PR D 8 SYDE PR D 8 SYDE PR D 8 SYDE PR D 8 SYDE PR D 8 VVTRP G = 1 VVTRP G = 1 | 3333 335 532 333 333 333 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 | 90 LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA YSDDDRAERCAAR YSDDDRAERCAAR LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA | 100 GA DEVGRX GA DEVGRX | 110 | 120 EELLRGADM EELLRGADM GGTDRAGRE CGTDRAGRE EELLRGADM EELLRGADM EELLRGADM EELLRGADM | 130 VFVTA GEGGGT VFVTA GEGGGT VFVTA GEGGGT VFVTA GEGGGT VFVTA GEGGGT VFVTA GEGGGT VFVTA GEGGGT VFVTA GEGGGT VFVTA GEGGGT | 140 TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA | 150 RKLGALTVGV RKLGALTVGV -DEPPIYRC RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV | 160 VVTRP F VVTRP F VVTRP F SYDE R SYDE R VVTRP F | 3333 335 5324 333 333 333 333 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 | 90 LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA YDDDDRAERCAAR YDDDDRAERCAAR LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA | 100 C D PEVCRX C D PEVCRX | 110 AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDEI AEDAKDEI | 120 SELLRCADM SELLRCADM CGTDRAGRE CGTDRAGRE SELLRCADM SELLRCADM SELLRCADM SELLRCADM SELLRCADM SELLRCADM | yFVTAGEGGGT YFVTAGEGGGT YFVTAGEGGGT YFVTAGEGGGT YFVTAGEGGGT YFVTAGEGGGT YFVTAGEGGGT YFVTAGEGGGT YFVTAGEGGGT YFVTAGEGGGT | 140 TIGGAPUVASIA TIGGAPUVASIA TIGGAPUVASIA TIGGAPUVASIA TIGGAPUVASIA TIGGAPUVASIA TIGGAPUVASIA TIGGAPUVASIA TIGGAPUVASIA | 150 RKLCALTVCV RKLCALTVCV RKLCALTVCV RKLCALTVCV RKLCALTVCV RKLCALTVCV RKLCALTVCV RKLCALTVCV RKLCALTVCV RKLCALTVCV | 160 | |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii | 90 LDVGRD STRGLGA LDVGRD STRGLGA VDDDRAERCAAR YDDDRAERCAAR YDDDRAERCAAR LDVGRD STRGLGA LDVGRD STRGLGA LDVGRD STRGLGA LDVGRD STRGLGA LDVGRD STRGLGA LDVGRD STRGLGA LDVGRD STRGLGA | 100 CA DEVCRX CA DEVCRX | 110 AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI | 120 ELLRCADM EELLRCADM COIDRAGRE COIDRAGRE ELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM | 130 VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT | 140 TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TDRPAPREY- TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA | 150 RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV | 160 VVTRP = = 1 VVTRP = 1 VVTR | |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. thodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 | 90 LDVGRDSTRGLGA LDVGRDSTRGLGA VDDDRAERCAAR VDDDRAERCAAR LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA | 100 CA DEVCRX2 CA DEVCRX3 CA DEVCRX3 C | 110 AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI | 120 ELLRGADM ELLRGADM CGIDRGRE GGIDRGRE ELLRGADM EELLRGADM EELLRGADM EELLRGADM EELLRGADM EELLRGADM EELLRGADM EELLRGADM | 130 FVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT | 140 TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA | 150 RKLGALTVGV RKLGALTVGV -DEPPIYRCG -DEPPIYRCG RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV | 160 | |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. thodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum | 90 LDVGRDSTRGLGA LDVGRDSTRGLGA YDDDRAERCAAR YDDDRAERCAAR LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA | 100 GA DEVGRX GA DEVGRX | 110 | 120 ELLRGADM EELLRGADM COTDRAGRE COTDRAGRE EELLRGADM EELLRGADM EELLRGADM EELLRGADM EELLRGADM EELLRGADM EELLRGADM EELLRGADM | 130 VFVTACEGGGT VFVTACEGGGT VFVTACEGGGT VFVTACEGGGT VFVTACEGGGT VFVTACEGGT VFVTACEGGT VFVTACEGGT VFVTACEGGT VFVTACEGGT VFVTACEGGT | 140 TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA | 150 RKLGALTVGV RKLGALTVGV -DEPPIYRCC -DEPPIYRCC -DEPPIYRCC RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV | 160 | |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans | 90 LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA YDDDDRAERGAAR YDDDDRAERGAAR LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA | 100 | 110 AEDAKDDI AEDAKDDI AEDAKDDI REDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI | 120 EELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM | 130 VFVTAGEGGTO | 140 TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA | 150 RKLCALTVGV RKLCALTVGV -DEPPIYRCC RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV | 160 VVTRP F 1 VTRP 7 F 1 VTRP 9 P 9 VTRP 9 P 9 VTRP 9 P 10 VTRP 9 P 10 VTRP 11 VTRP 12 VTRP 14 VTRP 15 VTRP 16 VTRP 17 VTRP 10 VTRP 11 VTRP 12 VTRP 14 VTRP 15 VTRP 16 VTRP 17 VTRP 18 VTRP 19 VTRP 10 VTRP 10 VTRP 11 VTRP 12 VTRP 14 VTRP 15 VTRP 16 VTRP 17 VTRP 10 <th>333553233333333333333333333333333333333</th> | 333553233333333333333333333333333333333 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii | 90 LDVGRDSTRGLGA LDVGRDSTRGLGA YDDDDRAERCAAR YDDDDRAERCAAR LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA | 100 A DPEVGRX CA | 110 | 120 SELLRCADM SELLRCADM SELLRCADM SELLRCADM SELLRCADM SELLRCADM SELLRCADM SELLRCADM SELLRCADM SELLRCADM SELLRCADM SELLRCADM SELLRCADM SELLRCADM SELLRCADM | 130 VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGT | 140 TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA | 150 RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV | 160 VVTRP F 1 VTRP P 1 VTRP F VTRP F SYDE R SYDE R VTRP F VTRP F VTRP F VVTRP F | 333553233333333333333333333333333333333 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare | 90 LDVGRD STRCLCA LDVGRD STRCLCA LDVGRD STRCLCA YDDDRAERCAAR YDDDRAERCAAR LDVGRD STRCLCA LDVGRD STRCLCA | 100 CA DEVCRX CA DEV | 110 AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI | 120 ELLRCADM ELLRCADM CTIDRAGRE CTIDRAGRE ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM | 130 YFVTAGEGGGT | 140 TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA | 150 RKLCALTVGV RKLCALTVGV -DEPPIYRC -DEPPIYRC RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV | 160 VVTRP P VVTRP P VVTRP P SYDE PR SYDE PR VVTRP P | 333553233333333333333333333333333333333 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. thermoresistibile M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare M. indicus | 90 LDVGRD STRGLGA LDVGRD STRGLGA VDDDRAERCAAR YDDDRAERCAAR LDVGRD STRGLGA LDVGRD STRGLGA | 100 CA DEVCRX CA DEV | 110 | 120 ELLRGADM EELLRGADM CGIDRGRE CGIDRGRE ELLRGADM EELLRGADM EELLRGADM EELLRGADM EELLRGADM EELLRGADM EELLRGADM EELLRGADM EELLRGADM EELLRGADM EELLRGADM | 130 FVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGT | 140 TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA TGGAPVVASIA | 150 RKLGALTVGV RKLGALTVGV -DEPPIYRC -DEPPIYRC RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV RKLGALTVGV | 160 | |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. thodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare M. MOTT36Y | 90 LDVCRDSTRCLCA LDVCRDSTRCLCA VSDDDRAERCAAR VSDDDRAERCAAR LDVCRDSTRCLCA LDVCRDSTRCLCA LDVCRDSTRCLCA LDVCRDSTRCLCA LDVCRDSTRCLCA LDVCRDSTRCLCA LDVCRDSTRCLCA LDVCRDSTRCLCA LDVCRDSTRCLCA LDVCRDSTRCLCA LDVCRDSTRCLCA LDVCRDSTRCLCA LDVCRDSTRCLCA LDVCRDSTRCLCA LDVCRDSTRCLCA LDVCRDSTRCLCA | 100 | 110 ABDAKDDI ABDAKDDI ABDAKDDI ABDAKDDI ABDAKDDI ABDAKDDI ABDAKDDI ABDAKDDI ABDAKDEI | 120 ELLRCADM EELLRCADM EGTDRAGRE CGTDRAGRE EELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM EELLRCADM | 130 VFVTA GEGGGT VFVTA GEGGT | 140 TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA TICGAPVVASIA | 150 RKLCALTVGV RKLCALTVGV -DEPPIYRCC RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV RKLCALTVGV | 160 VVTRP F 1 VVTRP F 1 XVTRP F SYDE R VTRP F I VVTRP F 1 VVTRP F I 1 VVTRP F I 1 VVTRP F I I VVTRP F I I I I | |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare M. indicus Mycobacterium sp. MOTT36Y M. colombiense | 90 LDVGRD STRGLGA LDVGRD STRGLGA LDVGRD STRGLGA YDDDDRAERGAAR YDDDDRAERGAAR LDVGRD STRGLGA LDVGRD STRGLGA | 100 C D PEVCRX C | 110 AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI AEDAKDEI | 120 ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM | 130 VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT | 140 TICGAPUVASIA TICGAPUVASIA TICGAPUVASIA TICGAPUVASIA TICGAPUVASIA TICGAPUVASIA TICGAPUVASIA TICGAPUVASIA TICGAPUVASIA TICGAPUVASIA TICGAPUVASIA TICGAPUVASIA TICGAPUVASIA TICGAPUVASIA TICGAPUVASIA TICGAPUVASIA TICGAPUVASIA TICGAPUVASIA | 150 RKLCALTVCV | 160 VVTRP F 1 VTRP F 1 VTRP F SYDE R SYDE R VTRP F VTRP F VTRP F VTRP F VTRP F VTRP F VVTRP F | 33355323333333333333434433 |
| M. kansasii M. fortuitum Mycobacterium sp. JLS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare M. indicus Mycobacterium sp. MOTT36Y M. parascrofulaceum | 90 LDVGRDSTRGLGA LDVGRDSTRGLGA YDDDDRAERCAAR YDDDDRAERCAAR LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA | 100 A DPEVGRX CA | 110 AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDEI | 120 ELLRCADM | 130 VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT VFVTAGEGGT | 140 TGGAPVVASIA | 150 RKLCALTVGV | 160 VVTRP F 1 VTRP P 1 VTRP F VVTRP F IVVTRP F IVVTRP | 3335532333333333333334443334 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. indicus Mycobacterium sp. MOTT36Y M. colombiense M. parascrofulaceum M. leprae | 90 LDVGRD STRCLGA LDVGRD STRCLGA YDDDRAERCAAR YDDDRAERCAAR YDDDRAERCAAR LDVGRD STRCLGA LDVGRD STRCLGA | 100 CA DEVCRY CA DEV | 110 AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDDI AEDAKDEI A | 120 ELLRGADM ELLRGADM ELLRGADM ELLRGADM ELLRGADM ELLRGADM ELLRGADM ELLRGADM ELLRGADM ELLRGADM ELLRGADM ELLRGADM ELLRGADM ELLRGADM ELLRGADM ELLRGADM ELLRGADM ELLRGADM ELLRGADM | 130 FVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEG | 140 TGGAPVVASIA | 150 RKLCALTVGV | 160 VVTRP P | 333553233333333333334344333434 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. thermoresistibile M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare M. indicus Mycobacterium sp. MOTT36Y M. colombiense M. parascrofulaceum M. leprae Mycobacterium sp. JDM601 M. basiacum | 90 LDVCRDSTRCLCA LDVCRDSTRCLCA VCRDSTRCLCA VCRDSTRCLCA LDVCRDSTRCLCA | 100 | 110 | 120 ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM ELLRCADM | 130 VFVTA GEGGGT VFVTA GEGGT VFVTA GEG | 140 TGGAPVVASIA | 150 RKLGALTVGV RKLGALTVGV -DEPPIYRC -DEPPIYRC RKLGALTVGV | 160 VUTEP F VUTEP F VUTEP F SYDE R SYDE R SYDE R SYDE F VUTEP F IVVTEP F <tr td=""></tr> | 33355323333333333333343443344334 |
| | | | | | | | | | |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare M. indicus Mycobacterium sp. MOTT36Y M. colombiense M. parascrofulaceum M. leprae Mycobacterium sp. JDM601 M. hassiacum | 90 LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA YDDDDRAERGAAR YDDDDRAERGAAR LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA LDVGRDSTRGLGA | 100 C D PEVCRX C | 110 | 120 ELLRCADM | 130 VFVTA GEGGGT VFVTA GEGGT VFVTA GEGGT VFVTA VFVTA GEGGT VFVTA VFVTA VFVTA GEGGT VFVTA VFVTA GEGGT VFVTA GEGGT V | 140 TGCAPVVASIA | 150 RKLCALTVCV | 160 VVTRP F VVTRP F VTRP F SYDE R SYDE R VVTRP F VVTRP F IVVTRP F IVVTRP | 333553233333333333334443344333333333333 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare M. indicus Mycobacterium sp. MOTT36Y M. calombiense M. parascrofulaceum M. leprae Mycobacterium sp. JDM601 M. hassiacum M. franklinii | 90 LDVGRD STRCLGA LDVGRD STRCLGA LDVGRD STRCLGA YDDDDRAERCAAR YDDDDRAERCAAR LDVGRD STRCLGA LDVGRD STRCLGA | 100 A DPEVGRX CA | 110 | 120 SELLRCADM | 130 VFVTAGEGGGT VFVTAGEGGT VFVTAGE | 140 TGGA PVVAS IA TGGA PVVAS IA | 150 RKLCALTVCV | 160 VVTRP F VVTRP F VTRP F VVTRP F | 3 3 3 5 5 3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare M. indicus Mycobacterium sp. MOTT36Y M. calombiense M. parascrofulaceum M. leprae Mycobacterium sp. JDM601 M. franklinii M. massilense M. immunogenum | 90 LDVGRD STRCLGA LDVGRD STRCLGA YDDDDRAERCAAR YDDDDRAERCAAR YDDDDRAERCAAR LDVGRD STRCLGA LDVGRD STRCLGA | 100 A DPEVGRX CA | 110 | 120 ELLRCADM | 130 VFVTAGEGGGT VFVTAGEGGT VFVT | 140 TGGAPVVASIA | 150 RKLCALTVCV | 160 VVTRP F VVTRP F VTRP F VVTRP F VTRP F VTRP F VVTRP F VVTRP F VVTRP F VVTRP F VVTRP F VVTRP <th></th> | |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. indicus Mycobacterium sp. MOTT36Y M. colombiense M. jeprae Mycobacterium sp. JDM601 M. hassiacum M. franklinii M. massiliense M. immunogenum M. smegmatis | 90 LDVGRDSTRGLGA LDVGRDSTRGLGA VSDDDRAERGAAR VSDDDRAERGAAR LDVGRDSTRGLGA | 100 CA DEVCRY CA DEV | 110 | 120 ELLRGADM | 130 FVTA GEGGGT VFVTA GEGGT VFVTA GEGGT | 140 TGGAPVVASIA | 150 RKLCALTVGV | 160 VVTRP F VVTRP F VVTRP F SYDE R SYDE R SYDE R VVTRP F IVTRP F IVTRP F IVTRP </th <th></th> | |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. liflandii M. intracellulare M. indicus Mycobacterium sp. MOTT36Y M. colombiense M. parascrofulaceum M. laprae Mycobacterium sp. JDM601 M. hassiacum M. franklinii M. massiliense M. immunogenum M. smegmatis M. tuberculosis H37Rv | 90 LDVCRDSTRCLCA LDVCRDSTRCLCA VDDDRAERCAAR VDDDRAERCAAR LDVCRDSTRCLCA | 100 | 110 | 120 ELLIRGADM | 130 VFVTA GEGGGT VFVTA GEGGT VFVTA GEGGT VFV | 140 TGCA PVVA SIA TGCA PVVA SIA | 150 RKLCALTVCV | 160 VVTRP F VVTRP F SYDE R SYDY R SYDY < | |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare M. jarascrofulaceum M. leprae Mycobacterium sp. JDM601 M. hassilense M. immunogenum M. smegmatis M. tuberculosis H37Rv M. tuberculosis H37Ra | 90 LDVCRD STRCLCA LDVCRD STRCLCA VDDDRAERCAAR VDDDRAERCAAR LDVCRD STRCLCA LDVCRD STRCLCA | 100 C D PEVCRX C | 110 | 120 ELLRCADM | 130 VFVTA GEGGGT VFVTA GEGGT VFVTA GEGGT VFVT | 140 TIGA PVVASIA TIGA PVVASIA | 150 RKLCALTVCV | 160 VVTRP F VVTRP F VTRP F SYDE R SYDE R SYDE R VTRP F VTRP F VTRP F VYTRP F | |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare M. indicus Mycobacterium sp. MOTT36Y M. calombiense M. parascrofulaceum M. leprae Mycobacterium sp. JDM601 M. hassiacum M. franklinii M. massiliense M. immunogenum M. smegmatis M. tuberculosis H37Ra Bacillus subtilis | 90 LDVCRD STRCLCA LDVCRD STRCLCA VDDDRAERCAAR YDDDDRAERCAAR LDVCRD STRCLCA LDVCRD STRCLCA | 100 A DPEVGRX A DPEV | 110 | 120 ELIRGADM | 130 VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGEGGGT VFVTAGE | 140 TGGA PVVAS IA TGGA PVAS IA TGGA PV | 150 RKLGALTVGV | 160 VVTRP F VVTRP F VTRP F VVTRP F | |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare M. indicus Mycobacterium sp. MOTT36Y M. colombiense M. parascrofulaceum M. franklinii M. franklinii M. massilense M. immunogenum M. smegmatis M. tuberculosis H37Ra Bacillus subtilis | 90 LDVGRD STRCLGA LDVGRD STRCLGA YDDDDRAERCAAR YDDDDRAERCAAR YDDDDRAERCAAR LDVGRD STRCLGA LDVGRD STRCLGA | 100 A DPEVGRX CA | 110 | 120 ELLIRGADM | 130 VFVTAGEGGGT VFVTAGEGGT VFVTAG | 140 TGGA PVVAS IA TGGA PVAS IA TGGA | 150 RKLCALTVCV RKLCALVV RKLCALVV RKLCALVV RKLCALVV RKLCALVV | 160 VVTRP F VVTRP F VTRP F IVTRP F <th></th> | |

Figure 1. Homology comparison of the amino acid sequences in the N-terminal domain of FtsZ of various mycobacterial species.

3.2. The role of C-terminal domain residues

The C-terminal stretch of FtsZ protein has been found to have structural and functional roles in different bacterial systems (reviewed in [4, 5]). The crystal structure of *M. tuberculosis* FtsZ

did not contain the co-ordinates for the 66 residues at the C-terminal portion [62], indicating its unstructured nature like in the case of the C-terminal stretch of the full-length FtsZ of *M. jannaschii* [16], *Pseudomonas aeruginosa* [22], *Aquifex aeolicus* [22], *Thermococcus maritima* [21], and *B. subtilis* [31]. On the tubulin dimer template, the molecular model for the complete structure of *M. tuberculosis* FtsZ, inclusive of the extreme C-terminal 66 residues [69], the co-ordinates of which were not visible in the crystal structure of *M. tuberculosis* FtsZ [62], also showed an unstructured C-terminus [69].

Like in the case of *E. coli* FtsZ and *B. subtilis* FtsZ, the C-terminal region of the FtsZ proteins of all the mycobacterial species contain charged residues towards the C-terminal end. FtsZ of diverse mycobacterial species also shows wide variations in the nature of the residues in the C-terminal region (**Figure 2**). These residues show high levels of divergence from the residues on the FtsZ of *B. subtilis* (Gram-positive) and *E. coli* (Gram-negative) and even from the FtsZ of *Streptomyces coelicolor*, which is also an Actinobacteria like mycobacteria. Many mycobacterial species have an insertion of GGIAD in the C-terminal variable region, the function of which is under investigation.

The *M. tuberculosis* FtsZ dimer model showed a possible role for the C-terminal Arg residues (R378 and R379) on the stability of the dimer and hence on the polymerisation of the protein. In fact, biochemical studies showed that the deletion of the extreme C-terminal residues, R378 and R379 in the C-terminal extreme stretch of $_{373}$ PPFMRR $_{379}$ of *M. tuberculosis* FtsZ, completely abolished polymerisation *in vitro* [69]. Besides the deletion of R379, the deletion of the R378 or its replacement with Lys, His, Ala, or Asp completely abolished polymerisation activity, indicating the crucial nature of the residues in the unstructured region of the protein for polymerisation. However, the polymerisation potential of the protein was not affected by the deletion of the single R379 residue alone [69]. The C-terminus of most of the mycobacterial FtsZ ends with $_{377}$ MRR $_{379}$ and very few with $_{377}$ MRH $_{379}$, with the conservation of M377 (**Figure 2**).

M. tuberculosis FtsZ has been found to interact with *M. tuberculosis* FtsW *in vitro* [70] and *in vivo* [71]. The presence of three of the four aspartate residues, D367 to D370, was found to be critically required for the interaction of *M. tuberculosis* FtsZ with a cluster of positively charged residues in the C-terminal tail of *M. tuberculosis* FtsW *in vitro* [70] and *in vivo* [71] (**Figure 2**). Similarly, PknA-dependent phosphorylation of T343 in *M. tuberculosis* FtsZ is required for FtsZ function during oxidative stress [72]. Like in the case of FtsZ-SepF interaction in *B. subtilis* [35, 36], the C-terminal tail of *M. tuberculosis* FtsZ was found to be required for the interaction of SepF with FtsZ [73]. These and other studies showed that *M. tuberculosis* SepF is found to be an essential part of the mycobacterial cell division machinery [74], probably in assisting FtsZ localisation at the mid-cell site [73].

3.3. The role of other residues in the protein

Like in the case of the mutations D212A\N\C, D212G (FtsZ2) in *E. coli* FtsZ, which impair GTPase activity [42–44], the equivalent mutant D210G of *M. tuberculosis* FtsZ also showed impaired GTPase activity [67] (**Figure 3**). Although *M. tuberculosis* FtsZ-D210G polymerised *in vivo* to the mid-cell ring in a merodiploid *Mycobacterium smegmatis* background, it failed

| | 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 | |
|--|--|---------------------------------|-------------------------------------|--------------------------|--------------------------|----------------------------|------------------------|---------|-----|
| | | | | | | 1 | | 1 | 251 |
| M. kansasii M. fortuitum | AAHPEANIIFGTVIDDS | LGDEVRVTVI | AAGEDSAGE | SRKPVVSP- | | AAQTQPIASARA | CKVTTSL | DE PTDA | 351 |
| Mycobacterium sp. KMS | AAHPEANIIFGTVIDDS | LGDEVRVIVI | AAGEDSAGE | SRNPVVSP- | | AAATOPTAPGRA | GKVASPL | FEPADP | 351 |
| Mycobacterium sp. JLS | ATKVFLLSPADVD | VTADERRRIA | EACFYAYQ- | | | 2 | | | 220 |
| Mycobacterium sp. MCS | ATKVFLLSPADVD | VTADERRRIA | EACFYAYQ- | | | | | | 220 |
| M. gilvum | AAHPEANIIFGTVIDDS | L <mark>GDE</mark> VRVTVI | AAGFDAAGF | GRKPVTGE- | -AQQA-AAI | PAAAGQPIAPGKA | GRL <mark>N-</mark> SI | -FDPADP | 356 |
| M. vaccae | AAHPEANIIFGTVIDDS | LGDEVRVTVI | AAGEDAAGE | PGRKPVICE- | | | GRVNSSI | DPADP | 345 |
| M. chubuense | AAHPDANTTFGTVTDDS | | AAGEDAAGE | GRKPVIGE- | -ADAADAAI | | GRVNSSI. | | 358 |
| M. rhodesiae | AAHADANIIFGTVIDDS | LGDEVRVTVI | AAGFDSAGE | GRKPVVGA- | -G | QATAAGTA | GKVTSOL | FEPADA | 347 |
| M. thermoresistibile | SAHPEANIIFGTVIDDS | L <mark>GDE</mark> VRVTVI | AA <mark>GFD</mark> ASGF | SRKPVV <mark>NT-</mark> | -P | AASTOPIAPGRA | GSVSS-T | -FSPGEA | 351 |
| M. bovis-AF2122/97 | AAHPDANIIFGTVIDDS | L <mark>GDE</mark> VRVTVI | AAGFDVSGF | GRKPVMG | <mark>E</mark> 1 | -GGAHRIESAKA | GKLTSTL | -FEPVDA | 350 |
| M. tuberculosis CDC1551 | AAHPDANIIFGTVIDDS | | AAGEDVSGE | GRKPVMG | | -GCAHRIESAKA | GKLTSTL | FEPVDA | 350 |
| M. bovis BCG str. Pasteur 117 | AAHPDANIIFGTVIDDS | LGDEVRVIVI | AAGEDVSGE | GRKPVMG | | | GKLTSTL | FEPVDA | 350 |
| M. orygis | AAHPDANIIFGTVIDDS | LGDE VRVTVI | AAGFDVSGF | GRKPVMG | | -GCAHRIESAKA | GKLTSTL | -FEPVDA | 350 |
| M. marinum | AAHPDANIIFGTVIDDS | L <mark>GDE</mark> VRVTVI | AAGFDASGF | GRKPV <mark>AG</mark> A- | -TGAAPG <mark>B</mark> 1 | -G <mark>GAHRIESAKA</mark> | GKLSSTL | -FEPVDA | 357 |
| M. ulcerans | AAHPDANIIFGTVIDDS | LGDEVRVTVI | AAGFDASGF | GRKPVACA- | -TGAAPG | -GCAHRIESAKA | GKLSSTL | FEPVDA | 358 |
| M. intracellulare | AAHODANTIFGTVIDDS | LGDE VRVIVI | AAGEDASGE | GRKPVAGA- | -NADKEEK | | GKLSSTL | FEPVDA | 357 |
| M. indicus | AAHQDANIIFGTVIDDS | LGDEVRVTVI | AAGFDATGE | GRKPVIGG- | -NADKEEK | GAHRIESAKA | GKLTSTL | FEPVDA | 357 |
| Mycobacterium sp. MOTT36Y | AAH <mark>QD</mark> ANIIFGTVIDDS | L <mark>GDE</mark> VRVTVI | AAGF <mark>D</mark> ATGF | GRKPVI <mark>G</mark> G- | -NADKEEK | 7 <mark>GA</mark> HRIESAKA | GKLTSTL | -FEPVDA | 356 |
| M. colombiense | AAHQDANIIFGTVIDDS | LGDEVRVTVI | AAGFDAAGF | GRKPVIGG- | -SADKGEK | -GCAHRIESAKA | GKLTSTL | FEPVDA | 357 |
| M. loprao | AAHQDANIIFGTVIDDS | | AAGE SAAGE | | | | | FEPVDA | 350 |
| Mycobacterium sp. JDM601 | AAHPEANIIFGTVIDDS | LGDEVRVTVI | AAGFDSAGA | GRKPVTCA- | -TGQ | PRHAVAPGOA | GKVTSSL | FDPVDA | 351 |
| M. hassiacum | AAHPDANIIFGTVIDDS | L <mark>GDE</mark> VRVTVI | AAGFDANGF | SRKPIVSG- | -ATTAA | SACGQTIEPGRA | GRLSTSL | FEPADP | 355 |
| M. franklinii | SAHP <mark>E</mark> ANIIFGTVIDDS | L <mark>GDE</mark> VRVTVI | AAGFDAGGF | SRKPIS | -GTAAPGT | APCKA-GEVNGS | RANGISI | -FDTIDA | 355 |
| M. massiliense | SAHPEANIIFGTVIDDS | LGDEVRVTVI | AAGEDAGGI | SRKPITPG- | -GAAAPGT | APCKA-GOVNSG | | | 357 |
| M. smegmatis | AAHPEANTIFGTVIDDS | LGDEVRVTVT | AAGEDSAGE | SRKPVVSP- | -GAAAPGI | OAOTOPTASARA | CKVTTSL | FEPODA | 374 |
| M. tuberculosis H37Rv | AAHPDANIIFGTVIDDS | LGDEVRVTVI | AAGFDVSGF | GRKPVMG | | -GCAHRIESAKA | GKLTSTL | FEPVDA | 350 |
| M. tuberculosis H37Ra | AAHPDANIIFGTVIDDS | LGDEVRVTVI | AAGFD <mark>V</mark> SGF | GRKPVMG | <mark>E</mark> 1 | -G <mark>CAHRIESAKA</mark> | GKLTSTL | FEPVDA | 350 |
| Bacillus subtilis | ASDODVNMIFGSVINEN | LKDEIVVTVI | ATCEIEQEK | DVTKP | | QRPS NQ-SI | KTHNQSVI | PKREPKR | 348 |
| Escherichia coli | FASDNATVVTGTSLDPD | MNDELRVTVI | ATCIGNDKR | PSKRDNVLG | | OVOOPVMBRY | OHGMA-1 | | 351 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS | VSVPAHTNGATVSV VSVPAHTNGATVSV ASVPVHTNGATVSI | GGDGDGGI GGDGDGGI GGDDGGI | ADDVVDVPE ADDDVDVPE ADDDVDVPE | LMRR PFMRH PFMRH | 386 386 385 | | | | |
| Mycobacterium sp. JLS Mycobacterium sp. MCS | | | | | 220 | | | | |
| M. gilvum | ASVPAGNTNGATVRI | GGPDDGGI | SDDDVDVPF | FMRH | 392 | | | | |
| M. vaccae | ASVPAGHTNGATVRI | GGGDDGGI | S <mark>DDDVDV</mark> PF | FMR <mark>H</mark> | 381 | | | | |
| M. vanbaalenii | AAVPAGQTNCATVRI | GGGDDGGI | SDDDVDVPF | FMRH | 388 | | | | |
| M. chubuense M. rhodesiae | ASVPVHTNGATVRI ASVPVHTNGATVST | GGDGRDDGGI | | | 378 | | | | |
| M. thermoresistibile | TSVPVHSNGATVSV | GGED | DDDDVDVPF | FMRR | 382 | | | | |
| M. bovis-AF2122/97 | VSVPLHTNGATLSI | GGD | -DDDVDVPF | FMRR | 379 | | | | |
| M. tuberculosis CDC1551 | VSVPLHTNGATLSI | GGD | | FMRR | 379 | | | | |
| M. bovis BCG str. Pasteur 117 | VSVPLHTNGATLSI | GGD | | FMRR | 379 | | | | |
| M. orygis | VSVPLHTNGATLSI | GGD | -DDDVDVPF | FMRR | 379 | | | | |
| M. marinum | VSVPLHTNGATLSI | GGD | -DDDVDVPF | FMRR | 386 | | | | |
| M. ulcerans | VSVPLHTNGATLSI | GGD | -DDDVDVPF | FMRR | 387 | | | | |
| M. liflandii M. intracellulare | VSVPLHTNGATLSI | GGD | | | 386 | | | | |
| M. indicus | VSVPVHTNGSTLNI | GGD | | FMRR | 386 | | | | |
| Mycobacterium sp. MOTT36Y | VSVPVHTNGSTLNI | GGD | -DDDVDVPF | FMRR | 385 | | | | |
| M. colombiense | VSVPIHTNGSTLNI | GGE | -DDDVDVPF | FMRR | 386 | | | | |
| M. parascrofulaceum | VSVPVHTNGATLNI | GGD | | | 384 | | | | |
| Mycobacterium sp. JDM601 | VSVPAPTNCATVSV | CCRNG-DDGV | | FMRH | 387 | | | | |
| M. hassiacum | ASVPRPTNCATVSI | GGDDGPI | ADDDVDVPF | FMRR | 389 | | | | |
| M. franklinii | QSLPRDTNGSTVTI | .GG <mark>G</mark> | DEDDVDVPF | FMRR | 385 | | | | |
| M. massiliense | QSLPRDINGSTVTI | GGG | DEDDVDVPF | FMRR | 387 | | | | |
| M. 1mmunogenum M. smegmatis | QSLPRDTNCSTVTI | GGGDCCT | | | 387 | | | | |
| M. tuberculosis H37Rv | VSVPLHTNGATLSI | GGDGGI | | FMRR | 379 | | | | |
| M. tuberculosis H37Ra | VSVPLHTNGATLSI | GGD | -DDDVDVPF | FMRR | 379 | | | | |
| Bacillus subtilis | EPQQQ | NTVSRHTSQP | ADDTLDIPT | FLRNRNKRG | 382 | | | | |
| Streptomyces coelicolor | APVPEPVADLPVSPPP- | VPPSRTYSDS | AAEELDVPD | | 399 | | | | |

Figure 2. Homology comparison of the amino acid sequences in the C-terminal domain of FtsZ of various mycobacterial species.

to act as the sole source of FtsZ *in vivo* and showed 100-fold impaired GTPase activity *in vitro* [67]. The authors suggested that the mutation on the T7 loop might not prevent FtsZ self-association or association with the wild-type protein but rather specifically affect GTP

Unique Biochemical Features of the Cytokinetic Protein FtsZ of Mycobacteria 295 http://dx.doi.org/10.5772/intechopen.70540

| | 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 | |
|--|--|--|--|---|---|--|--|--|--|
| | | | | | •••• | | | | 000 |
| M. kansasii | | IQALRESC | DTLIVIPNDRLLQ | MGDAAVSLM- | | DAFRSADEVLI | | TDLITTPG | 202 |
| Mucobacterium sp. KMS | SFECKRRSNOAENG | TOSLEESC | DTLIVIPNDRLLQ | MGDAAVSLM- | | DAFRSADEVLI | | TDI.TTTPC | 202 |
| Mycobacterium sp. JLS | PRLRCPREFERPAPE | LGALRGST | RGALAMDPRRMAM | LEBEGSPLAK | ITTLRPKDY | SEARTIGEKEE | DGTPVI | MDLV | 161 |
| Mycobacterium sp. MCS | PRLRCPREFERPAPR | L <mark>GALR</mark> GST | RGALAMDPRRMAM | LF ^B EGSPLAK | ITTLRPKD | SEARTIGE KFF | DGTPVI | MDLV | 161 |
| M. gilvum | -SFEGKRRSNQAAEG | I <mark>Q</mark> ALRESC | DTLIVIPNDRLLQ | M <mark>GDAA</mark> VSLM- | | - <mark>DAF</mark> RSA <mark>DE</mark> VLI | NGVQGI | TDLITTPG | 202 |
| M. vaccae | -SFEGKRRSNQAADG | IASLRESC | DTLIVIPNDRLLQ | M <mark>GDAA</mark> VSLM- | | - <mark>DAFRSA</mark> DEVLI | 'NGAŐ I | TDLITTPG | 193 |
| M. vanbaalenii | -SFEGKRRSNQAADG | IAALRESC | DTLIVIPNDRLLQ | MGDAAVSLM- | | DAFRSADEVLI | NGVQGI | TDLITTPG | 202 |
| M. chubuense | -SFEGKRRSNQAENG | IQALRESC | DTLIVIPNDRLLQ | MEDAAVSLM- | | DAFRSADEVLI | | TDLITTPE | 202 |
| M. Thoussiae | | TAALRESC | DTLIVIPNDRLLQ | MGDAAVSLM- | | | | TDLITTPG | 202 |
| M. bovis-AF2122/97 | SFEGKRRSNOAENG | IAALRESC | DTLIVIPNDRLLO | MGDAAVSLM- | | DAFRSADEVLI | NGVOGI | TDLITTPG | 202 |
| M. tuberculosis CDC1551 | -SFEGKRRSNQAENG | IAALRESC | DTLIVIPNDRLLQ | MGDAAVSLM- | | DAFRSADEVLI | NGVQGI | TDLITTPG | 202 |
| M. canettii | -SFEGKRRSNQAENG | IAALRESC | DTLIVIPNDRLLQ | M <mark>GD</mark> AAVSLM- | | - <mark>D</mark> AFRSA <mark>DE</mark> VLI | NGVQGI | TDLITTPG | 202 |
| M. bovis BCG str. Pasteur 117 | -SFEGKRRSNQAENG | IAALRESC | DTLIVIPNDRLLQ | M <mark>GDAA</mark> VSLM- | | - <mark>DAFRSADE</mark> VLI | 'NGAÖL | TDLITTPG | 202 |
| M. orygis | -SFEGKRRSNQAENG | IAALRESC | DTLIVIPNDRLLQ | MGDAAVSLM- | | DAFRSADEVLI | NGVQGI | TDLITTPG | 202 |
| M. marinum | | IAALRESC | DTLIVIPNDRLLQ | MGDAAVSLM- | | DAFRSADEVLI | | TDLITTPE | 202 |
| M. liflandii | | TAALRESC | DTLIVIPNDRLLQ | MGDAAVSLM- | | DAFRSADEVLI | | TDLITTPG | 203 |
| M. intracellulare | -SFEGKRRGNOAESC | IAALRESC | DTLIVIPNDRLLO | MGDAAVSLM- | | DAFRSADEVLI | NGVOGI | TDLITTPG | 203 |
| M. indicus | -SFEGKRR <mark>G</mark> NQAESG | IAALRESC | DTLIVIPNDRLLQ | M <mark>GD</mark> AAVSLM- | | DAFRSADEVLI | м <mark>gvõ</mark> gi | TDLITTPG | 203 |
| Mycobacterium sp. MOTT36Y | -SFEGKRRGNQAESC | IAALRESC | DTLIVIPNDRLLQ | M <mark>GDAA</mark> VSLM- | | - <mark>DAF</mark> RSA <mark>DE</mark> VLI | NGVQGI | TDLITTPG | 202 |
| M. colombiense | -SFEGKRRSNQAEAG | INALRESC | DTLIVIPNDRLLQ | MGDAAVSLM- | | DAFRSADEVLI | NGVQGI | TDLITTPG | 202 |
| M. parascrofulaceum | -SFEGKRRGSQAEG | INTLRESC | DTLIVIPNDRLLQ | MGDAAVSLM- | | DAFRSADEVLI | NGVQGI | TDLITTPG | 203 |
| Mucobactorium an IDM601 | SFEGERRSNQAENG | | DTLIVIPNDRLLQ | MGDTAVSLM- | | DAFRSADEVLI | NGVQGI | TDLITTPG | 202 |
| M hassiacum | | TOALRESC | DTLIVIPNDRLLQ | MCDAAVSLM- | | DAFRAADEVLI | NGVOGT | TDT.TTTPG | 202 |
| M. franklinii | -SFEGKRRSGOAENG | IGSLRESC | DTLIVIPNDRLLO | MGDAAVSLM- | | DAFRSADEVLI | NGVOGI | TDLITTPG | 202 |
| M. massiliense | -SFEGKRRS <mark>G</mark> QAELC | ITSLRESC | DTLIVIPNDRLLQ | M <mark>GD</mark> AAVSLM- | | - <mark>D</mark> AFRSA <mark>DE</mark> VLI | NGVQGI | TDLITTPG | 202 |
| M. immunogenum | -SFEGKRRS <mark>G</mark> QAELG | I <mark>T</mark> SLRESC | DTLIVIPNDRLLQ | M <mark>GDAA</mark> VSLM- | | - <mark>DAF</mark> RSA <mark>DE</mark> VLI | л <mark>с</mark> vQ <mark>с</mark> і | TDLITTPG | 202 |
| M. smegmatis | -SFEGKRRSNQAEAG | IQALRESC | DTLIVIPNDRLLQ | M <mark>GD</mark> AAVSLM- | | -DAFRSADEVLI | и <mark>с</mark> ибат | TDLITTPG | 225 |
| M. tuberculosis H37Rv | -SFEGKRRSNQAENG | IAALRESC | DTLIVIPNDRLLQ | MGDAAVSLM- | | DAFRSADEVLI | | TDLITTPG | 202 |
| M. tuberculosis H3/Ra Bacillus subtilis | TECORDOLOAAC | TSAMKEAN | DTLIVIPNDRLLQ | | | | | SDITATPC | 202 |
| Streptomyces coelicolor | TFEGRRRANOAEDO | IAELREEV | DTLIVIPNDRLLS | IS ROVSVI- | | DAFKSADOVLI | SGVOGI | TDLITTPG | 202 |
| Escherichia coli | -NFEGKKRMAFAEQG | ITELSKHV | DSLITIPNDKLLK | VLGRGISLL- | | DAFGAANDVL | GAVQGI | AELITRPG | 204 |
| | | | | | | | | | |
| | | | | | | | | | |
| | 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 | |
| M kancacii | 250 | 260 • • • • • • • | 270 | 280 . | 290 | 300 | 310 | 320 | 281 |
| M. kansasii M. fortuitum | | | 270 . . GSARGDGRALKAA | 280 . ETATNSPLLE ETATNSPLLE | 290 A-SMEGAQ A-SMEGAQ | 300 | 310 CLFEIN CLFEIN | 320 | 281 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS | 250 | 260 AGTALMGI AGTALMGI AGTALMGI | 270 GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA | 280 | 290 A-SMEGAQO A-SMEGAQO A-SMEGAQO | 300 VLLSVAGGSDI VLLSVAGGSDI VLLSVAGGSDI | 310 GLFEIN GLFEIN GLFEIN | 320 EAASLVQD EAASLVQD EAASLVQD | 281 281 281 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG SMDNADAKRLVDF | 260 AGTALMGI AGTALMGI AGTALMGI AGTALMGI | 270 | 280 EIAINSPLLE EIAINSPLLE EIAINSPLLE | 290 A-SMECAQO A-SMECAQO A-SMECAQO | 300 VLLSVAGGSDI VLLSVAGGSDI VLLSVAGGSDI IAFALRCSFDI | 310 GLFEIN GLFEIN GLFEIN | 320 EAASLVQD EAASLVQD EAASLVQD | 281 281 281 189 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG -SMDNADKRLVDF -SMDNADKRLVDF | 260 AGTALMET AGTALMET AGTALMET A | 270 CSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA | 280 ETATNSPLLE ETATNSPLLE ETATNSPLLE | 290 A-SMECAQO A-SMECAQO A-SMECAQO A | 300 VLLSVAGGSD VLLSVAGGSD VLLSVAGGSD VLLSVAGGSD VLLSVAGGSD VLSVAGGSD VLSVAGGSD | 310 | 320 | 281 281 281 189 189 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum | 250 LINVDFADVKCVMSC LINVDFADVKCVMSC LINVDFADVKCVMSC SMDNADAKRLVDF SMDNADAKRLVDF LINVDFADVKCVMS | 260 AGTALMGT AGTALMGT AGTALMGT AGTALMGT A | 270 SARGDGRALKAA SARGDGRALKAA GSARGDGRALKAA CSARGDGRALKAA | 280 EIAINSPLLE EIAINSPLLE EIAINSPLLE EIAINSPLLE | 290 A-SMECAQ A-SMECAQ A-SMECAQ A A-SMECAQ | 300 VLLSVAGGSDI VLLSVAGGSDI VLLSVAGGSDI VAFALRCSFDF VLLSVAGGSDI | 310 GLFEIN .GLFEIN .V .CLFEIN | 320 | 281 281 281 189 189 281 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. waccae | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG SMDNADAKRUVDF SMDNADAKRUVDF LINVDFADVKGVMSS LINVDFADVKGVMSS | 260 ACTALMCI ACTALMCI ACTALMCI A ACTALMCI ACTALMCI | 270 GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA | 280 EIAINSPLLE EIAINSPLLE EIAINSPLLE EIAINSPLLE EIAINSPLLE EIAINSPLLE | 290 A-SMECAO A-SMECAO A-SMECAO A A A-SMECAO A-SMECAO A-SMECAO | 300 VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI JAFAIR GSF I VLLSVA GGSDI VLLSVA GGSDI | 310 GLFEIN GLFEIN GLFEIN V GLFEIN GLFEIN | 320 | 281 281 189 189 281 272 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG SMDNADAKRLVDF SMDNADAKRLVDF LINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSS | 260 ACTAING I ACTAING I ACTAING I ACTAING I ACTAING I ACTAING I ACTAING I ACTAING I | 270 GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA | 280 EIAINSPLLE EIAINSPLLE EIAINSPLLE EIAINSPLLE EIAINSPLLE EIAINSPLLE EIAINSPLLE EIAINSPLLE | 290 A-SMEGAQ A-SMEGAQ A-SMEGAQ A A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ | 300 VLLSVA GGS DI VLLSVA GGS DI VLLSVA GGS DI VLLSVA GGS DI VLLSVA GGS DI VLLSVA GGS DI VLLSVA GGS DI | 310 GLFEIN GLFEIN GLFEIN V GLFEIN GLFEIN GLFEIN GLFEIN | 320 BASLVOD BASLVOD BASLVOD BASLVOD BASLVOE BASLVOE BASLVOE BASLVOE BASLVOE | 281 281 189 189 281 272 281 281 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG SMDNADAKRLVDF SMDNADAKRLVDF LINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSS | 260 A CTAIMCT A CTAIMCT A CTAIMCT A CTAIMCT A CTAIMCT A CTAIMCT A CTAIMCT A CTAIMCT | 270 CSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA | 280 ETAINSPLIE ETAINSPLIE ETAINSPLIE ETAINSPLIE ETAINSPLIE ETAINSPLIE ETAINSPLIE ETAINSPLIE ETAINSPLIE | 290 A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ | 300 VLLSVACGSDI UAFALRCSFDI UAFALRCSFDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI | 310 GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN | BASLVQD BASLVQD BASLVQD BASLVQD BASLVQE BASLVQE BASLVQE BASLVQE BASLVQE BASLVQE BASLVQE | 281 281 189 189 281 272 281 281 281 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG SMDNADAKRLVDF SMDNADAKRLVDF LINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSS | 260 A CTAIMC I A CTAIMC I | 270 CSARGDGRALKAA GSARGDGRALKAA CSARGDGRALKAA CSARGDGRALKAA CSARGDGRALKAA CSARGDGRALKAA CSARGDGRALKAA CSARGDGRALKAA | 280 EIAINSPLLE EIAINSPLLE EIAINSPLLE EIAINSPLLE EIAINSPLLE EIAINSPLLE EIAINSPLLE EIAINSPLLE EIAINSPLLE EIAINSPLLE | 290 A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ | 300 VLLSVACGSDI VLLSVACGSDI IAFAIRCSFDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI | 310 GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN | 320 EASLVQD EASLVQD EASLVQD EASLVQE EASLVQE EASLVQE EASLVQE EASLVQE EASLVQE | 281 281 189 281 272 281 281 281 281 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG SMDNADAKRLVDF SMDNADAKRLVDF LINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG | 260 A CTAIME I A CTAIME I | 270 SARGDGRALKAA GSARGDGRALKAA CSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA | 280 E DAINSPLLE TAINSPLLE TAINSPLLE TAINSPLLE TAINSPLLE TAINSPLLE TAINSPLLE TAINSPLLE TAINSPLLE TAINSPLLE TAINSPLLE | 290 | 300 VLLSVACGSDI ULLSVACGSDI UAFALRCSFO VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI | 310 GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN | 320 BASLVQD BASLVQD BASLVQD BASLVQE BASLVQE BASLVQE BASLVQE BASLVQE BASLVQD BASLVQD | 281 281 189 281 272 281 281 281 281 281 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG SMDNADARRLVDF SMDNADARRLVDF LINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGIMSG | 260 A CTAIME T A CTAIME T | 270 SARGDGRALKAA GSARGDGRALKAA CSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA | 280 E TAINS PLLE E TAINS PLLE | 290 | 300 VLLSVACGSDI VLLSVACGSDI JAFALRCSFO VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI | 310 GLFEIN GLFEN GLFEN GLFEN GLFEN GLFEN GLFEN GLFEN GLFEN | 320 BASLVQD BASLVQD BASLVQD BASLVQE BASLVQE BASLVQE BASLVQE BASLVQD BASLVQD BASLVQD BASLVQD BASLVQD | 281 281 281 189 281 272 281 281 281 281 281 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bactoria PCC str. Datheme 117 | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG SMDNADAKRLVDF SMDNADAKRLVDF LINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG | 260 ACTAINCT ACTAINCT ACTAINCT ACTAINCT ACTAINCT ACTAINCT ACTAINCT ACTAINCT ACTAINCT ACTAINCT ACTAINCT ACTAINCT | 270 GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGEGRSLKAA GSARGEGRSLKAA | 280 E IAINSPLLE E IAINSPLLE | 290 A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ A-SMEGAQ | 300 VLLSVA GGSDI VLLSVA GGSDI VLMS I A GGSDI VLMS I A GGSDI | 310 GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN | BASLVQD BASLVQD BASLVQD BASLVQD BASLVQE BASLVQE BASLVQE BASLVQD BASLVQD BASLVQD BASLVQD BASLVQD BASLVQD BASLVQD | 281 281 189 281 281 281 281 281 281 281 281 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG SMDNADAKRLVDF SMDNADAKRLVDF LINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG | 260 A CTAIMCI A CTAIMCI | 270 GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA | 280 E JATNSPLLE E TAINSPLLE E TAINSPLE | 290 | 300 VLLSVA GGSD VLLSVA GGSD VLLSVA GGSD VLSVA GGSD VLSVA GGSD VLLSVA GGSD VLLSVA GGSD VLLSVA GGSD VLLSVA GGSD VLMS IA GGSD VLMS IA GGSD VLMS IA GGSD | 310 GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN | 320 BASLVQD BASLVQD BASLVQD BASLVQD BASLVQE BASLVQD BASLVQD BASLVQD BASLVQD BASLVQD BASLVQD BASLVQD BASLVQD BASLVQD BASLVQD BASLVQD | 281 281 189 281 272 281 281 281 281 281 281 281 281 281 28 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. thodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG SMDNADAKRLVDF SMDNADAKRLVDF LINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG | 260 A CTAIMCI A CTAIMCI | 270 CSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGGGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA | 280 E IAINSPLLE E TAINSPLLE E TAINSPLLE | 290 | 300 VLLSVA GGSDI VLLSVA GGSDI VLMS I A GGSDI VLMS I A GGSDI VLMS I A GGSDI VLMS I A GGSDI | 310 GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN | 320 BASLVQD EAASLVQD BAASLVQD BAASLVQD BAASLVQE EAASLVQE EAASLVQD BAASLVQD EAASLVQD EAASLVQD BAASLVQD BAASLVQD BAASLVQD BAASLVQD BAASLVQD | 281 281 281 281 281 281 281 281 281 281 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG SMDNADAKRLVDF SMDNADAKRLVDF LINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG | 260 A CTAIMC I A CTAIMC I | 270 CSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA | 280 E IAINSPLLE E IAINSPLLE | 290 | 300 VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLMSIACGSDI VLMSIACGSDI VLMSIACGSDI VLMSIACGSDI VLMSIACGSDI VLMSIACGSDI | 310 GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN | 320 BASLVQD BASLVQD BASLVQD BASLVQD BASLVQE BASLVQE BASLVQE BASLVQD BASLVQD BASLVQD BASLVQD BASLVQD BASLVQD BASLVQD BASLVQD BASLVQD | 281 281 189 281 272 281 281 281 281 281 281 281 281 281 28 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG -SMDNADARRUVDF DVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG | 260 A CTAIMC I A CTAIMC I | 270 GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA | 280 IAINSPLLE | 290 | 300 VILSVACGSDI VILSVACGSDI VILSVACGSDI VILSVACGSDI VILSVACGSDI VILSVACGSDI VILSVACGSDI VILSVACGSDI VILSVACGSDI VILSVACGSDI VIMSIACGSDI VIMSIACGSDI VIMSIACGSDI VIMSIACGSDI VIMSIACGSDI | 310 GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN | 320 EASLVQD EASLVQD EASLVQD EASLVQE EASLVQE EASLVQE EASLVQE EASLVQD EASLVQD EASLVQD EASLVQD EASLVQD EASLVQD EASLVQD EASLVQD | 281 281 189 189 272 281 281 281 281 281 281 281 281 281 28 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG SMDNADAKRLVDF SMDNADAKRLVDF ILINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG | 260 A CTAIMCT A CTAIMCT | 270 GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGDGRSLKAA GSARGDGRSLKAA | 280 IATNSPLLE | 290 | 300 VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLMS IA GGSDI | GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN | BASIVQD BASIVQD BASIVQD BASIVQD BASIVQE BASIVQE BASIVQD BASIVQD BASIVQD BASIVQD BASIVQD BASIVQD BASIVQD BASIVQD BASIVQD BASIVQD | 281 281 189 281 281 281 281 281 281 281 281 281 281 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis -AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare M. indicus | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG SMDNADAKRLVDF SMDNADAKRLVDF LINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG | 260 ACTAIMCI | 270 GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGDGRSLKAA GSARGDGRSLKAA GSARGDGRSLKAA GSARGEGRSLKAA | 280 E IAINSPLLE E IAINSPLLE | 290 | 300 VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLMS I A GGSDI | GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN | BASIVOD | 281 281 189 281 281 281 281 281 281 281 281 281 281 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. thermoresistibile M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. indicus Mycobacterium sp. MOTT36Y M. colombianse | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG SMDNADAKRLVDF SMDNADAKRLVDF SMDNADAKRLVDF LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG | 260 A CTAIMC I A | 270 CSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA CSARGDGRALKAA CSARGDGRALKAA CSARGDGRALKAA CSARGDGRALKAA CSARGDGRALKAA CSARGEGRSLKAA CSARGEGRSLKAA CSARGEGRSLKAA CSARGEGRSLKAA CSARGEGRSLKAA CSARGEGRSLKAA CSARGEGRSLKAA CSARGEGRSLKAA CSARGEGRSLKAA CSARGEGRSLKAA | 280 E JATNSPLLE E TAINSPLLE E TAINSPLLE | 290 | 300 VLLSVA GGSDI VLLSVA GGSDI JAFALR CSFO VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLMS I A GGSDI | 310 GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN | 320 PASLVQD PASLVQD PASLVQD PASLVQD PASLVQE PASLVQE PASLVQE PASLVQD PASLVQD PASLVQD PASLVQD PASLVQD PASLVQD PASLVQD PASLVQD PASLVQD PASLVQD PASLVQD PASLVQD PASLVQD PASLVQD PASLVQD | 281 281 189 281 272 281 281 281 281 281 281 281 281 281 28 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare M. indicus Mycobacterium sp. MOTT36Y M. colombiense | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG SMDNADAKRLVDF SMDNADAKRLVDF SMDNADAKRLVDF LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG LINVDFADVKGIMSG | 260 A CTAIMC I A | 270 CSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA | 280 E IAINSPLLE E TAINSPLLE E TAINSPLLE | 290 | 300 VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLMS IA GGSDI | 310 GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN | 320 BASLVQD BASLVQD BASLVQD BASLVQD BASLVQE BASLVQE BASLVQE BASLVQE BASLVQD | 281 281 189 281 281 281 281 281 281 281 281 281 281 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare M. indicus Mycobacterium sp. MOTT36Y M. colombiense M. parascrofulaceum M. leprae | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG -SMDNADARRUDF LINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSS LINVDFADVKGVMSG LINVDFADVKGIMSG | 260 A CTAIMC I A CTAIMC I | 270 GSARCDCRALKAA CSARCDCRALKAA CSARCDCRALKAA CSARCDCRALKAA CSARCDCRALKAA CSARCDCRALKAA CSARCDCRALKAA CSARCDCRALKAA CSARCECRSLKAA CSARCECRSLKAA CSARCECRSLKAA CSARCECRSLKAA CSARCECRSLKAA CSARCECRSLKAA CSARCECRSLKAA CSARCECRSLKAA CSARCECRSLKAA CSARCECRSLKAA CSARCECRSLKAA CSARCECRSLKAA CSARCECRSLKAA CSARCECRSLKAA CSARCECRSLKAA | 280 IAINSPLLE | 290 | 300 VLLSVACGSDI VLLSVACGSDI UAFALRCSFDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLLSVACGSDI VLSVACGSDI VLSVACGSDI VLSVACGSDI VLSVACGSDI VLSVACGSDI VLSVACGSDI VLSVACGSDI VLSVACGSDI VLSSIACGSDI | 310 GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN | 320 BASLVQD | 281 281 1899 281 281 281 281 281 281 281 281 281 282 282 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare M. indicus Mycobacterium sp. MOTT36Y M. colombiense M. parascrofulaceum M. leprae Mycobacterium sp. JDM601 | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGIMSG | 260 A CTAIMCT A CTAIMCT | 270 GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA | 280 I ATNSPLLE I ATNSPLLE | 290 | 300 VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLMS I A GGSDI | 310 GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN | BASIVOD | 281 281 1899 281 281 281 281 281 281 281 281 281 282 282 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis -AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare M. indicus Mycobacterium sp. MOTT36Y M. calombiense M. parascrofulaceum M. leprae Mycobacterium sp. JDM601 M. hassiacum | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG -SMDNADAKRLVDF -SMDNADAKRLVDF LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGIMSG | 260 ACTAIMCI | 270 GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGEGRSLKAA | 280 I ATNSPLLE I ATNSPLLE | 290 | 300 VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLMS I A GG | 310 GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN | 320 BASLVQD | 281 281 189 281 281 281 281 281 281 281 281 281 281 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare M. indicus Mycobacterium sp. MOTT36Y M. colombiense M. parascrofulaceum M. leprae Mycobacterium sp. JDM601 M. hassiacum M. franklinii | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG -SMDNADAKRLVDF -SMDNADAKRLVDF LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGIMSG | 260 A CTAIMC I A | 270 CSARCDCRALKAA CSARCDCRALKAA CSARCDCRALKAA CSARCDCRALKAA CSARCDCRALKAA CSARCDCRALKAA CSARCDCRALKAA CSARCDCRALKAA CSARCDCRALKAA CSARCECRSLKAA C | 280 E JATNSPLLE E TAINSPLLE E TAINSPLLE | 290 | 300 VLISVA GGSDI VLISVA GGSDI JAFALR SFOT ULSVA GGSDI VLISVA GGSDI VLISTA GGSDI | 310 GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN | BASIVOD BASIVOD BASIVOD BASIVOD BASIVOD BASIVOE BASIVOE BASIVOE BASIVOD | 281 281 1899 281 281 281 281 281 281 281 281 281 282 282 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. thermoresistibile M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. indicus Mycobacterium sp. MOTT36Y M. colombiense M. leprae Mycobacterium sp. JDM601 M. hassiacum M. franklinii M. massiliense M. indicus | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG -SMDNADAKRLVDF -SMDNADAKRLVDF -SMDNADAKRLVDF LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGIMSG LINVDFADVKSMSG | 260 A CTAIMC I A | 270 CSARGDGRALKAA CSARGDGRALKAA CSARGDGRALKAA CSARGDGRALKAA CSARGDGRALKAA CSARGDGRALKAA CSARGDGRALKAA CSARGDGRALKAA CSARGEGRSLKAA C | 280 E IAINSPLLE E TAINSPLLE E TAINSPLLE | 290 | 300 VILSVA GGSDI VILSVA GGSDI | 310 GLFE IN GLFE IN | 320 PASLVQD | 281 281 281 281 281 281 281 281 281 281 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. thodesiae M. rhodesiae M. thermoresistibile M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare M. jarascrofulaceum M. parascrofulaceum M. hassileinse M. franklinii M. massiliense M. immogenum M. smermatis | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG -SMDNADARRUDF LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGIMSG LINVDFADVKSVMSG LINVDFADVKGIMSG LINVDFADVKSVMSG LINVDFADVKSVMSG LINVDFADVKSVMSG | 260 | 270 GSARCDCRALKAA GSARCDCRALKAA GSARCDCRALKAA GSARCDCRALKAA GSARCDCRALKAA GSARCDCRALKAA GSARCDCRALKAA GSARCDCRALKAA GSARCDCRALKAA GSARCECRSLKAA G | 280 IAINSPLLE IAINSPLE | 290 A-SMEGAQ | 300 VLLSVAGGSDI VLLSVAGGSDI VLLSVAGGSDI VLLSVAGGSDI VLLSVAGGSDI VLLSVAGGSDI VLLSVAGGSDI VLLSVAGGSDI VLLSVAGGSDI VLMSIAGGSDI | 310 GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN GLFEIN | 320 BASIVOD BASIVOD BASIVOD BASIVOD BASIVOE BASIVOE BASIVOE BASIVOD | 281 281 189 281 281 281 281 281 281 281 281 282 282 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. toubuense M. rhodesiae M. thermoresistibile M. toberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare M. jarlacetum sp. MOTT36Y M. colombiense M. parascrofulaceum M. leprae Mycobacterium sp. JDM601 M. hassiacum M. franklinii M. franklinii M. smegmatis M. tuberculosis H37Rv | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGIMSG LINVDFADVKGMG LINVDFADVKGMG LINVDFADVKGMG LINVDFADVKGMG LINVDFADVKGMG LINVDFADVKGMG LINVDFADVKGMG LINVDFADVKGMG LINVDFADVKGMG LINVDFADVKGMG LINVDFADVKGMG LINVDFADVKGMG LINVDFADVKGMG LINVDFADVKGMG LINVDFADVKGMG LINVDFADVKGMG LINVDFADVKGMG L | 260 A CTAIMCT A CTAIMCTATAICTATACTATACTATACTATACTATACTAT | 270 GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGEGRSLKAA | 280 I ATNSPILE I | 290 | 300 VILSVA GGSDI VILSVA GGSDI VIMS I A GGSDI | 310 GLFBIN | 320 BASIVQD BASIVQD BASIVQD BASIVQD BASIVQE BASIVQE BASIVQE BASIVQD BA | 281 281 281 281 281 281 281 281 281 281 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare M. indicus Mycobacterium sp. MOTT36Y M. colombiense M. parascrofulaceum M. leprae Mycobacterium sp. JDM601 M. hassiacum M. franklinii M. massiliense M. immunogenum M. smegmatis M. tuberculosis H37Rx M. tuberculosis H37Ra | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGIMSG | 260 ACTAING I ACTAING I ACTAIN | 270 GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGDGRALKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGDGRALKAA GSARGDGRALKAA GSARGEGRSLKAA GSARGDGRALKAA GSARGEGRSLKAA GSARGDGRALKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGDGRALKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGDGRALKAA GSARGEGRSLKAA GSARGEGRSLKAA GSARGEGRSLKAA | 280 I ATNSPLLE I ATNSPLE | 290 | 300 VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLMS I A GGSDI | 310 GLFEIN | 320 BASIVQD | 281 281 189 281 281 281 281 281 281 281 281 282 282 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. rhodesiae M. thermoresistibile M. bovis-AF2122/97 M. tuberculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. intracellulare M. indicus Mycobacterium sp. MOTT36Y M. colombiense M. parascrofulaceum M. leprae Mycobacterium sp. JDM601 M. hassiacum M. franklinii M. massiliense M. immunogenum M. smegmatis M. tuberculosis H37Ra Bacillus subtilis | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG -SMDNADAKRLVDF -SMDNADAKRLVDF LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGIMSG LINVDFADVKG LINDFADVKG LINVDFADVKG LINVDFADVKG LINVDFADVKG LINVDFADVKG LINVDFADVKG LINVDFADVKG LINVDFADVKG LINVDFADVKG LINVDFADVKG LINVDFADVKG LINVDFADVKG LINVDFADVKG LINVFAN LINVDFADVKG LINVFADVKG LINVDFADVKG LINVFAN LINV | 260 A CTAIMC I A | 270 GSARGDCRALKAA GSARGDCRALKAA GSARGDCRALKAA CSARGDCRALKAA CSARGDCRALKAA CSARGDCRALKAA CSARGDCRALKAA CSARGDCRALKAA CSARGDCRALKAA CSARGECRSLKAA C | 280 I ATNSPLLE I TAINSPLLE I AINSPLLE I AINSPLE I | 290 | 300 VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLSVA GGSDI VLMS I A GGSDI | GLFEIN | 320 ASIVOD BASIVOD | 281 281 189 281 281 281 281 281 281 281 281 282 282 |
| M. kansasii M. fortuitum Mycobacterium sp. KMS Mycobacterium sp. JLS Mycobacterium sp. MCS M. gilvum M. vaccae M. vanbaalenii M. chubuense M. thermoresistibile M. thermoresistibile M. therculosis CDC1551 M. canettii M. bovis BCG str. Pasteur 117 M. orygis M. marinum M. ulcerans M. liflandii M. indicus Mycobacterium sp. MOTT36Y M. colombiense M. jeprae Mycobacterium sp. JDM601 M. hassiacum M. franklinii M. massiliense M. inmunogenum M. suberculosis H37Ra Bacillus subtilis Streptomyces coelicolor | 250 LINVDFADVKGVMSG LINVDFADVKGVMSG SMDNADAKRLVDF SMDNADAKRLVDF SMDNADAKRLVDF SMDNADAKRLVDF SMDNADAKRLVDF LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGVMSG LINVDFADVKGIMSG | 260 A CTAIMC I A | 270 CSARGD CRALKAA CSARGD CRALKAA CSARGD CRALKAA CSARGD CRALKAA CSARGD CRALKAA CSARGD CRALKAA CSARGD CRALKAA CSARGD CRALKAA CSARGE CRSLKAA CSARGE CR | 280 I ATNSPILE I TAINSPILE I | 290 | 300 VLLSVA GGSDI VLLSVA GGSDI JAFALR CSFOT SVLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLLSVA GGSDI VLMS I A G | 310 GLFEIN G | 320 PASLVQD PA | 281 281 281 281 281 281 281 281 281 281 |

Figure 3. Homology comparison of the amino acid sequences at other parts of FtsZ of various mycobacterial species.

hydrolysis, thereby uncoupling GTPase property from polymerisation. The specific residues, which have been found to be involved in the polymerisation or interaction of *M. tuberculosis* FtsZ with itself or with other cell division proteins, are listed in **Table 1**.

| Residue in <i>M. tuberculosis</i> FtsZ | Interacting protein of <i>M. tuberculosis</i> | Functional role of the interaction | Reference |
|---|---|------------------------------------|-----------|
| N22 | E136 of FtsZ | Polymerisation | [62] |
| D94 | R181 of FtsZ | Polymerisation | [62] |
| G103 | FtsZ | GTP binding | [67] |
| C155 | FtsZ | Polymerisation | [68] |
| A172 | FtsZ | Polymerisation | [66] |
| D210 | FtsZ | GTPase | [67] |
| T343 | PknA | FtsZ function* | [72] |
| D367-D370 | FtsW | FtsZ function* | [70] |
| R378, R379 | FtsZ | Polymerisation | [69] |
| C-terminal tail | SepF | FtsZ function* | [73] |

Table 1. Residues in *M. tuberculosis* FtsZ that interact with residues in another subunit or with other cell division proteins.

4. Correlation between FtsZ polymerisation kinetics and bacterial generation time

Mycobacterium leprae is one of the slowest growing bacteria with a generation time of 13.5 days in vivo [11]. The generation time of M. tuberculosis is 18 h in vivo [9] and 24 h in vitro [10]. Similarly, while M. smegmatis divides once in 3 h [8], S. coelicolor A3(2), which is classified under Actinobacteria like mycobacteria, has a generation time of 2.31 h, except that some of the strains grow as slow as 28.9 h depending upon growth conditions [75]. Meanwhile, different strains of *E. coli* show generation time of only 18–55 min [6]. In agreement with the slower generation time of M. tuberculosis, compared to that of E. coli, M. tuberculosis FtsZ showed slower polymerisation in vitro [63, 65]. Interestingly, the FtsZ of M. leprae, which divides once in 13.5 days [11], did not polymerise at all in vitro even in the presence of DEAE-dextran [66]. Comparatively, the time taken by M. smegmatis and S. coelicolor to reach steady state of FtsZ polymerisation is about 4 min [76]. Similarly, the time taken by the FtsZ of Caulobacter crescentus, which has a generation time of 3 h [77], to reach steady state of polymerisation is 5 min [78]. On the contrary, while E. coli FtsZ takes only 1–6 s to reach steady state of polymerisation [18, 79], FtsZ of B. subtilis, which divides once in 120 min [7], takes approximately 200 s [47]. These observations on the comparative polymerisation kinetics of FtsZ proteins of E. coli, M. tuberculosis, S. coelicolor, M. smegmatis, and M. leprae and the generation time of the respective bacterium (Table 2) probably allude to the existence of a correlation between the generation time of the bacterium and the time taken by the respective FtsZ to reach steady state kinetics *in vitro*, which may hold true *in vivo* as well. Mechanistically, such a correlation needs to be necessarily in-built so that kinetics of FtsZ polymerisation during division of the cell keeps pace with the overall generation time of the bacterium. The presence of A172 in the FtsZ of

| Bacterium | Time taken to reach steady state of FtsZ polymerisation (from light scattering data) ^a [with reference] | Generation time of the bacterium ^a [with reference] |
|-----------------|---|--|
| M. smegmatis | ~4 min [76] | 3 h [8] |
| S. coelicolor | ~4 min [76] | 2.31 h [75] |
| M. tuberculosis | ~6–10 min [65] | 24 h [10] |
| M. leprae | ND ^b [66] | 13.5 days [11] |
| E. coli | ~1-6 s [18] | 18–55 min [6] |
| B. subtilis | ~200 s [47] | 120 min [7] |
| C. crescentus | ~3 min [78] | 3 h [77] |

^aThe studies from which the respective values were taken are given in the parenthesis. ^bNot determined as *M. leprae* FtsZ does not polymerise *in vitro* [66].

Table 2. Correlation between the time taken to reach FtsZ polymerisation steady state and generation time of the bacterium.

all mycobacterial species, except in *M. leprae* where it is T172, is a typical example for such a correlation. The homology comparison of mycobacterial FtsZ sequence vividly shows the existence of several such minor differences in terms of specific amino acid residues at crucial positions that may play significant role in conferring differences in the polymerisation kinetics of the FtsZ protein of the respective bacterium. Structure-function studies on the polymerisation kinetics of a large number of FtsZ molecules from diverse bacterial genera differing widely in their generation time might establish such correlation.

5. Application of the FtsZ structure-function studies in public health

FtsZ being the principal essential cytokinetic protein in bacterial systems, it has been examined as a potential target for the design of inhibitory compounds that could be used as antibacterial drugs against diverse pathogenic bacteria (reviewed in [80]). Although the overall sequence conservation between FtsZ and β -tubulin is only 10–18% except at two stretches [15], it is important to ensure that anti-FtsZ compounds do not inhibit β -tubulin in humans. Owing to the overall conservation of the three-dimensional structure of FtsZ proteins from diverse bacterial genera, developing broad spectrum antibiotics, which are equally effective against the FtsZ of pathogenic bacteria of diverse genera, by designing inhibitor against the FtsZ molecule of a single bacterium, seems to be an attractive possibility [81].

6. Perspectives and challenges

The vast regions of homology and overall conservation of the three-dimensional structure of FtsZ proteins of diverse bacterial systems may seem attractive to design common inhibitors directed against these regions expecting them to be effective against the FtsZ proteins.

However, the structure-function studies on FtsZ revealing the subtle differences among the primary, secondary, and tertiary structures of FtsZ proteins from diverse bacteria give the hint that an anti-FtsZ inhibitor designed against the FtsZ of a select pathogenic bacterium may not act effectively with the same MIC/MBC against the FtsZ proteins of other pathogenic bacteria, as found [81]. Thus, the design of a common inhibitor that may be expected to act against FtsZ proteins from diverse pathogens remains a big challenge in the development of inhibitors against bacterial cytokinetic protein, FtsZ. Secondly, identification of the residues contributing to the structure that is required for the generation of force by FtsZ for cell wall/ membrane constriction [82] during the physical division of the mother cell also remains a challenge for future studies.

7. Conclusions

The essential cytokinetic protein, FtsZ, of different Mycobacterial species and of other bacteria has evolved to possess specific amino acid residues at crucial positions on the protein to suit the polymerisation kinetics that befit cell division duration. Thus, each FtsZ protein is unique in terms of the specific types of amino acid residues at crucial positions on the protein in spite of the regions of homology and overall conservation of the three-dimensional structure. It is these unique differences in the residues at specific crucial positions on the FtsZ protein that confer subtle differences on the FtsZ structure and hence on the cytokinetic function of the protein in the respective bacterium.

Acknowledgements

The work described in this review was supported by funding from the Department of Biotechnology, Govt. of India (BT/R&D/15/35/94, BT/PR7790/BRB/10/500/2006 and BT/ PR3787/MED/29/649/2012) to PA and infrastructure support from the DST-FIST, UGC Centre for Advanced Study in Molecular Microbiology, DBT-IISc Partnership Programme, ICMR Centre for Advanced Study in Molecular Medical Microbiology, and Indian Institute of Science. The authors apologise for missing citation of anyone's work on FtsZ relevant to this review due to any inadvertent error and/or space constraints.

Author details

Prabuddha Gupta^{1,2}, Atul Pradhan¹ and Parthasarathi Ajitkumar^{1*}

*Address all correspondence to: ajit@mcbl.iisc.ernet.in

1 Department of Microbiology and Cell Biology, Indian Institute of Science, Bengaluru, Karnataka, India

2 Amity University, Kolkata, West Bengal, India

References

- [1] Bi EF, Lutkenhaus J. FtsZ ring structure associated with division in *Escherichia coli*. Nature. 1991;**354**:161-164
- [2] Sun Q, Margolin W. FtsZ dynamics during the division cycle of live *Escherichia coli* cells. Journal of Bacteriology. 1998;**180**:2050-2056
- [3] Erickson HP. FtsZ, a prokaryotic homolog of tubulin? Cell 1995;80:367-370
- [4] Huang K-H, Durand-heredia J, Janakiraman A. FtsZ ring stability: Of bundles, tubules, crosslinks, and curves. Journal of Bacteriology. 2013;195:1859-1868. DOI: 10.1128/ JB.02157-12
- [5] Ortiz C, Natale P, Cueto L, Vicente M. The keepers of the ring: Regulators of FtsZ assembly. FEMS Microbiology Reviews. 2015;40:57-67. DOI: 10.1093/femsre/fuv040
- [6] Labrum EL. The effect of generation time on the delayed appearance of induced mutants in *Escherichia coli*. Proceedings of the National Academy of Sciences of the United States of America. 1953;39:1221-1227
- [7] Burdett ID, Kirkwood TB, Whalley JB. Growth kinetics of individual *Bacillus subtilis* cells and correlation with nucleoid extension. Journal of Bacteriology. 1986;**167**:219-230
- [8] Gadagkar R, Gopinathan KP. Growth of *Mycobacterium smegmatis* in minimal and complete media. Journal of Bioscience. 1980;**2**:337-348
- [9] Patterson RJ, Youmans GP. Multiplication of *Mycobacterium tuberculosis* within normal and "immune" mouse macrophages cultivated with and without streptomycin. Infection and Immunity. 1970;1:30-40
- [10] Hiriyanna KT, Ramakrishnan T. Deoxyribonucleic acid replication time in Mycobacterium tuberculosis H37Rv. Archives of Microbiology. 1986;144:105-109
- [11] Levy L. Death of *Mycobacterium leprae* in mice and the additional effect of dapsone administration. Proceedings of the Society for Experimental Biology and Medicine. 1970;135:745-749
- [12] RayChaudhuri D, Park JT. *Escherichia coli* cell-division gene *ftsZ* encodes a novel GTPbinding protein. Nature. 1992;**359**:251-254
- [13] De Boer P, Crossley R, Rothfield L. The essential bacterial cell-division protein FtsZ is a GTPase. Nature. 1992;359:254-256
- [14] Krauhs E, Little M, Kempf T, Hofer-Warbinek R, Ade W, Ponstingl H. Complete amino acid sequence of f8-tubulin from porcine brain. Proceedings of the National Academy of Sciences of the United States of America. 1981;78:4156-4160
- [15] De Pereda JM, Leynadier D, Evangelio JA, Chacón P, Andreu JM. Tubulin secondary structure analysis, limited proteolysis sites, and homology to FtsZ. Biochemistry. 1996;35:14203-14215

- [16] Lowe J, Amos LA. Crystal structure of the bacterial cell-division protein FtsZ. Nature. 1998;391:203-206
- [17] Nogales E, Wolf SG, Downing KH. Structure of the alpha beta tubulin dimer by electron crystallography. Nature. 1998;**391**:199-203
- [18] Bramhill D, Thompson CM. GTP-dependent polymerisation of *Escherichia coli* FtsZ protein to form tubules. Proceedings of the National Academy of Sciences of the United States of America. 1994;91:5813-5817
- [19] Mukherjee A, Lutkenhaus J. Guanine nucleotide-dependent assembly of FtsZ into filaments. Journal of Bacteriology. 1994;176:2754-2758
- [20] Wiche G, Cole RD. Reversible *in vitro* polymerisation of tubulin from a cultured cell line (rat glial cell clone C6). Proceedings of the National Academy of Sciences of the United States of America. 1976;73:1227-1231
- [21] Oliva MA, Cordell CC, Löwe J. Structural insight into FtsZ protofilament formation. Nature Structural & Molecular Biology. 2004;11:1243-1250
- [22] Oliva MA, Trambaiolo D, Löwe J. Structural insight into conformational variability of FtsZ. Journal of Molecular Biology. 2007;373:1229-1242
- [23] Scheffers DJ, den Blaauwen T, Driessen AJ. Non-hydrolysable GTPγS stabilizes the FtsZ polymer in a GDP-bound state. Molecular Microbiology. 2000;35:1211-1219
- [24] Rivas G, Lopez A, Mingorance J, Ferrandiz MJ, Zorrilla S, Minton AP, Vicente M, Andreu JM. Magnesium-induced linear self-association of the FtsZ bacterial cell division protein monomer. The primary steps for FtsZ assembly. The Journal of Biological Chemistry. 2000;275:11740-11749
- [25] Mukherjee A, Saez C, Lutkenhaus J. Assembly of an FtsZ mutant deficient in GTPase activity has implications for FtsZ assembly and the role of the Z ring in cell division. Journal of Bacteriology. 2001;183:7190-7197
- [26] Scheffers D-J, de Wit JG, den Blaauwen T, Driessen AJ. Substitution of a conserved aspartate allows cation-induced polymerization of FtsZ. FEBS Letters. 2001;**494**:34-37
- [27] Scheffers D-J, de Wit JG, den Blaauwen T, Driessen AJ. GTP hydrolysis of cell division protein FtsZ: Evidence that the active site is formed by the association of monomers. Biochemistry. 2002;41:521-529
- [28] Huecas S, Schaffner-Barbero C, García W, Yébenes H, Palacios JM, Díaz JF, Menéndez M, Andreu JM. The interactions of cell division protein FtsZ with guanine nucleotides. The Journal of Biological Chemistry. 2007;282:37515-37528
- [29] Huisman O, D'Ari R, Gottesman S. Cell-division control in *Escherichia coli*: Specific induction of the SOS function SfiA protein is sufficient to block septation. Proceedings of the National Academy of Sciences of the United States of America. 1984;81: 4490-4494

- [30] Cordell SC, Robinson EJ, Lowe J. Crystal structure of the SOS cell division inhibitor SulA and in complex with FtsZ. Proceedings of the National Academy of Sciences of the United States of America. 2003;**100**:7889-7894
- [31] Haydon DJ, Stokes NR, Ure R, Galbraith G, Bennett JM, Brown DR, Baker PJ, Barynin VV, Rice DW, Sedelnikova SE, Heal JR, Sheridan JM, Aiwale ST, Chauhan PK, Srivastava A, Taneja A, Collins I, Errington J, Czaplewski LG. An inhibitor of FtsZ with potent and selective anti-staphylococcal activity. Science. 2008;321:1673-1675
- [32] Mosyak L, Zhang Y, Glasfeld E, Haney S, Stahl M, Seehra J, Somers WS. The bacterial cell-division protein ZipA and its interaction with an FtsZ fragment revealed by X-ray crystallography. The EMBO Journal. 2000;**19**:3179-3191
- [33] Yan K, Pearce KH, Payne DJ. A conserved residue at the extreme C-terminus of FtsZ is critical for the FtsA-FtsZ interaction in *Staphylococcus aureus*. Biochemical and Biophysical Research Communications. 2000;270:387-392
- [34] Singh JK, Makde RD, Kumar V, Panda D. A membrane protein, EzrA, regulates assembly dynamics of FtsZ by interacting with the C-terminal tail of FtsZ. Biochemistry. 2007;46:11013-11022
- [35] Hamoen LW, Meile J-C, De Jong W, Noirot P, Errington J. SepF, a novel FtsZ-interacting protein required for a late step in cell division. Molecular Microbiology. 2006;59:989-999
- [36] Krol E, van Kessel SP, van Bezouwen LS, Kumar N, Boekema EJ, Scheffers D-J. Bacillus subtilis SepF Binds to the C-Terminus of FtsZ. PLoS One. 2012;7:e43293. DOI: 10.1371/ journal.pone.0043293
- [37] Durand-Heredia J, Rivkin E, Fan G, Morales J, Janakiraman A. Identification of ZapD as a cell division factor that promotes the assembly of FtsZ in *Escherichia coli*. Journal of Bacteriology. 2012;194:3189-3198
- [38] Buske PJ, Levin PA. Extreme C-terminus of bacterial cytoskeletal protein FtsZ plays fundamental role in assembly independent of modulatory proteins. The Journal of Biological Chemistry. 2012;287:10945-10957
- [39] Erickson HP. Atomic structures of tubulin and FtsZ. Trends in Cell Biology. 1998;8:133-137
- [40] Mukherjee A, Dai K, Lutkenhaus J. Escherichia coli cell division protein FtsZ is a guanine nucleotide binding protein. Proceedings of the National Academy of Sciences of the United States of America. 1993;90:1053-1057
- [41] Addinall SG, Small E, Whitaker D, Sturrock S, Donachie WD, Khattar MM. New temperature-sensitive alleles of *ftsZ* in *Escherichia coli*. Journal of Bacteriology. 2005;**187**:358-365
- [42] Lu C, Stricker J, Erickson HP. Site-specific mutations of FtsZ—Effects on GTPase and *in vitro* assembly. BMC Microbiology. 2001;1:7. PMCID: PMC32248
- [43] Stricker J, Erickson HP. In vivo characterization of Escherichia coli ftsZ mutants: Effects on Z-ring structure and function. Journal of Bacteriology. 2003;185:4796-4805

- [44] Redick SD, Stricker J, Briscoe G, Erickson HP. Mutants of FtsZ targeting the protofilament interface: Effects on cell division and GTPase activity. Journal of Bacteriology. 2005;187:2727-2736
- [45] Shin JY, Vollmer W, Lagos R, Monasterio O. Glutamate 83 and arginine 85 of helix H3 bend are key residues for FtsZ polymerisation, GTPase activity and cellular viability of *Escherichia coli*: Lateral mutations affect FtsZ polymerisation and *E. coli* viability. BMC Microbiology. 2013;13:26. DOI: 10.1186/1471-2180-13-26
- [46] Jaiswal R, Patel RY, Asthana J, Jindal B, Balaji PV, Panda D. E93R substitution of *Escherichia coli* FtsZ induces bundling of protofilaments, reduces GTPase activity and impairs bacterial cytokinesis. The Journal of Biological Chemistry. 2010;285:31796-31805
- [47] Dhaked HPS, Bhattacharya A, Yadav S, Dantu SC, Kumar A, Panda D. Mutation of Arg191 in FtsZ impairs cytokinetic abscission of *Bacillus subtilis* cells. Biochemistry. 2016;55:5754-5763. DOI: 10.1021/acs.biochem.6b00493
- [48] Vaughan S, Wickstead B, Gull K, Addinall SG. Molecular evolution of FtsZ protein sequences encoded within the genomes of archaea, bacteria, and eukaryota. Journal of Molecular Evolution. 2004;58:19-29
- [49] Huang K-H, Mychack A, Tchorzewski L, Janakiraman A. Characterisation of the FtsZ C-terminal variable region in Z-ring assembly and interaction with the Z-ring stabilizer ZapD in *E. coli* cytokinesis. PLoS One. 2016;11:e0153337. DOI: 10.1371/journal. pone.0153337
- [50] Di Lallo G, Anderluzzi D, Ghelardini P, Paolozzi L. FtsZ dimerisation *in vivo*. Molecular Microbiology. 1999;32:265-274
- [51] Justice SS, Garcia-Lara J, Rothfield LI. Cell division inhibitors SulA and MinC/MinD block septum formation at different steps in the assembly of the *Escherichia coli* division machinery. Molecular Microbiology. 2000;37:410-423
- [52] Chen Y, Bjornson K, Redick SD, Erickson HP. A rapid fluorescence assay for FtsZ assembly indicates cooperative assembly with a dimer nucleus. Biophysical Journal. 2005;88:505-514
- [53] Erickson HP, Taylor DW, Taylor KA, Bramhill D. Bacterial cell division protein FtsZ assembles into protofilament sheets and minirings, structural homologs of tubulin polymers. Proceedings of the National Academy of Sciences of the United States of America. 1996;93:519-523
- [54] Lu C, Reedy M, Erickson HP. Straight and curved conformations of FtsZ are regulated by GTP hydrolysis. Journal of Bacteriology. 2000;182:164-170
- [55] Mingorance J, Tadros M, Vicente M, Gonzalez JM, Rivas G, Velez M. Visualisation of single *Escherichia coli* FtsZ filament dynamics with atomic force microscopy. The Journal of Biological Chemistry. 2005;280:20909-20914

- [56] Srinivasan R, Mishra M, Wu L, Yin Z, Balasubramanian MK. The bacterial cell division protein FtsZ assembles into cytoplasmic rings in fission yeast. Genes & Development. 2008;22:1741-1746
- [57] Wang X, Huang J, Mukherjee A, Cao C, Lutkenhaus J. Analysis of the interaction of FtsZ with itself, GTP, and FtsA. Journal of Bacteriology. 1997;**179**:5551-5559
- [58] Ma X, Margolin W. Genetic and functional analyses of the conserved C-terminal core domain of *Escherichia coli* FtsZ. Journal of Bacteriology. 1999;181:7531-7544
- [59] Strauss MP, Liew ATF, Turnbull L, Whitchurch CB, Monahan LG, Harry EJ. 3D-SIM super resolution microscopy reveals a bead-like arrangement for FtsZ and the division machinery: Implications for triggering cytokinesis. PLoS Biology. 2012;10:e1001389. DOI: 10.1371/journal.pbio.1001389
- [60] Thanedar S, Margolin W. FtsZ exhibits rapid movement and oscillation waves in helixlike patterns in *Escherichia coli*. Current Biology. 2004;**14**:1167-1173
- [61] Peters PC, Migocki MD, Thoni C, Harry EJ. A new assembly pathway for the cytokinetic Z ring from a dynamic helical structure in vegetatively growing cells of *Bacillus subtilis*. Molecular Microbiology. 2007;64:487-499
- [62] Leung AK, Lucile White EL, Ross LJ, Reynolds RC, DeVito JA, Borhani DW. Structure of *Mycobacterium tuberculosis* FtsZ reveals unexpected, G protein-like conformational switches. Journal of Molecular Biology. 2004;342:953-970
- [63] Chen Y, Anderson DE, Rajagopalan M, Erickson HP. Assembly dynamics of *Mycobacterium tuberculosis* FtsZ. The Journal of Biological Chemistry. 2007;**282**:27736-27743
- [64] Borhani DW, White EL. Polymerisation of C-terminally truncated Mycobacterium tuberculosis FtsZ is unlikely to be physiologically relevant. Microbiology. 2004;**150**:3903-3906
- [65] White EL, Ross LJ, Reynolds RC, Seitz LE, Moore GD, Borhani DW. Slow polymerization of *Mycobacterium tuberculosis* FtsZ. Journal of Bacteriology. 2000;182:4028-4034
- [66] Gupta P, Srinivasan R, Rajeswari H, Indi S, Ajitkumar P. In vitro polymerisation of Mycobacterium leprae FtsZ or Mycobacterium tuberculosis FtsZ is revived or abolished respectively by reciprocal mutation of a single residue. Biochemical and Biophysical Research Communications. 2008;368:445-452
- [67] Rajagopalan M, Atkinson MA, Lofton H, Chauhan A, Madiraju MV. Mutations in the GTP-binding and synergy loop domains of *Mycobacterium tuberculosis ftsZ* compromise its function *in vitro* and *in vivo*. Biochemical and Biophysical Research Communications. 2005;**331**:1171-1177
- [68] Jaiswal R, Panda D. Cysteine 155 plays an important role in the assembly of *Mycobacterium tuberculosis* FtsZ. Protein Science. 2008;17:846-854
- [69] Gupta P, Rajeswari H, Arumugam M, Mishra S, Bhagavat R, Anand P, Chandra N, Srinivasan R, Indi SS, Ajitkumar P. *Mycobacterium tuberculosis* FtsZ requires at least one arginine residue at the C-terminal end for polymerisation *in vitro*. Acta Biochimica et Biophysics Sinica. 2010;**42**:58-69

- [70] Datta P, Dasgupta A, Bhakta S, Basu J. Interaction between FtsZ and FtsW of *Mycobacterium tuberculosis*. The Journal of Biological Chemistry. 2002;**277**:24983-24987
- [71] Rajagopalan M, Maloney E, Dziadek J, Poplawska M, Lofton H, Chauhan A, Madiraju MV. Genetic evidence that mycobacterial FtsZ and FtsW proteins interact, and colocalize to the division site in *Mycobacterium smegmatis*. FEMS Microbiology Letters. 2005;250:9-17
- [72] Sureka K, Hossain T, Mukherjee P, Chatterjee P, Datta P, Kundu M, Basu J. Novel role of phosphorylation-dependent interaction between FtsZ and FipA in mycobacterial cell division. PLoS One. 2010;5:e8590. DOI: 10.1371/journal.pone.0008590
- [73] Gupta S, Banerjee SK, Chatterjee A, Sharma AK, Kundu M, Basu J. Essential protein SepF of mycobacteria interacts with FtsZ and MurG to regulate cell growth and division. Microbiology. 2015;161:1627-1638. DOI: 10.1099/mic.0.000108
- [74] Gola S, Munder T, Casonato S, Manganelli R, Vicente M. The essential role of SepF in mycobacterial division. Molecular Microbiology. 2015;97:560-576. DOI: 10.1111/ mmi.13050
- [75] Cox RA. Quantitative relationships for specific growth rates and macromolecular compositions of *Mycobacterium tuberculosis, Streptomyces coelicolor* A3 (2) and *Escherichia coli* B/r: An integrative theoretical approach. Microbiology. 2004;**150**:1413-1426
- [76] Gupta P. Structure-function correlative studies on the biochemical properties (polymerisation, GTP binding, GTPase) of mycobacterial cytokinetic protein FtsZ *in vitro*. [PhD Thesis]. Indian Institute of Science, Bangalore, India. 2009; http://etd.ncsi.iisc.ernet.in/ handle/2005/661
- [77] Johnson RC, Ely B. Isolation of spontaneously derived mutants of *Caulobacter crescentus*. Genetics. 1977;86:25-32
- [78] Goley DE, Dye NA, Werner JN, Gitai Z, Shapiro L. Imaging-based identification of a critical regulator of FtsZ protofilament curvature in *Caulobacter*. Molecular Cell. 2010;39:975-987
- [79] Romberg L, Simon M, Erickson HP. Polymerisation of FtsZ, a bacterial homolog of tubulin. The Journal of Biological Chemistry. 2001;276:11743-11753
- [80] Haranahalli K, Tong S, Ojima I. Recent advances in the discovery and development of antibacterial agents targeting the cell-division protein FtsZ. Bioorganic & Medicinal Chemistry. 2016;24:6354-6362;9. DOI: 10.1016/j.bmc.2016.05.003
- [81] Panda D, Bhattacharya D, Gao QH, Oza PM, Lin HY, Hawkins B, Hibbs DE, Groundwater PW. Identification of agents targeting FtsZ assembly. Future Medicinal Chemistry. 2016;8:1111-1132. DOI: 10.4155/fmc-2016-0041
- [82] Erickson HP, Anderson DE, Osawa M. FtsZ in bacterial cytokinesis: Cytoskeleton and force generator all in one. Microbiology and Molecular Biology Reviews. 2010;74:504-528