Structure and subunit arrangement of Mycobacterial F1FO ATP synthase and novel features of the unique mycobacterial subunit δ

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1 **Structure and subunit arrangement of *Mycobacterial* F_1F_O ATP synthase and novel features**

2 **of the unique mycobacterial subunit δ**

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17 **Running title:** The novel 111-residues domain of mycobacterial δ

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19 **Keywords:** F-ATP synthase, subunit δ, subunit *b*, bioenergetics, tuberculosis, mycobacteria

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1 **Abstract**

2   In contrast to other prokaryotes, the *Mycobacterial* F_1F_O ATP synthase ($\alpha_3{:}\beta_3{:}\gamma{:}\delta{:}\varepsilon{:}a{:}b{:}b'{:}c_9$)

3 is essential for growth. The mycobacterial enzyme is also unique as a result of its 111 amino

4 acids extended δ subunit, whose gene is fused to the peripheral stalk subunit *b*. Recently, the

5 crystallographic structures of the mycobacterial $\alpha_3{:}\beta_3{:}\gamma{:}\varepsilon$-domain and *c* subunit ring were

6 resolved. Here, we report the first purification protocol of the intact *M. smegmatis* F_1F_O ATP

7 synthase including the F_1-domain, the entire membrane-embedded F_O sector, and the stator

8 subunits *b'* and the fused *b*-δ. This enzyme purification enabled the determination of the first

9 projected 2D- and 3D structure of the intact *M. smegmatis* F_1F_O ATP synthase by electron

10 microscopy (EM) and single particle analysis. Expression and purification of the fused

11 mycobacterial $b\text{-}\delta_{24\text{-}446}$ construct, excluding the membrane-embedded N-terminal amino acids,

12 provided insight into its secondary structure. By combining these data with homology and *ab-*

13 *initio* modeling techniques, a model of the mycobacterial peripheral stalk subunits *b*-δ and *b'* was

14 generated. Superposition of the 3D *M. smegmatis* F-ATP synthase EM-structure, the $\alpha_3{:}\beta_3{:}\gamma{:}\varepsilon$ and

15 *c*-ring, and the derived structural models of the peripheral stalk enabled a clear assignment of all

16 F-ATP synthase subunits, in particular with respect to the unique mycobacterial peripheral stalk

17 subunit *b'* and the elongated δ fused with subunit *b*. The arrangement of δ relative to the N-

18 termini of the catalytic $\alpha_3\beta_3$-headpiece and its potential as a drug target are discussed.

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1. Introduction

Tuberculosis (TB) remains one of the leading worldwide causes of infectious disease mortality globally with over one million annual deaths (World Health Organization 2018), making the bacterium *Mycobacterium tuberculosis*, which mainly causes TB, the most important bacterial pathogen in the world. The mycobacterial F_1F_O ATP synthase (F-ATP synthase), composed of nine subunits with a stoichiometry of $\alpha_3:\beta_3:\gamma:\delta:\varepsilon:a:b:b':c_9$, has been shown to be essential for growth. This is different from other prokaryotes, where the enzyme is dispensable for growth on fermentable carbon sources and where increased glycolytic flux can compensate for the loss of oxidative phosphorylation (Sassetti et al., 2003; Cook et al., 2014). The enzyme is composed of a membrane-bound F_O section (subunits $a:b:b':c_9$), and a water-soluble F_1 portion (Fig. 1A). The latter includes subunits $\alpha_3\beta_3$, which form a six-fold pseudo-symmetric ring that sits on top of a central stalk (subunits $\gamma\varepsilon$) (Zhang et al., 2019; Fig. 1A). The bottom of the central stalk sits on a ring of nine *c*-subunits (Preiss et al., 2015), which is proposed to be held against subunit *a* by the so-called peripheral stalk, which itself is composed of the two subunits *b* and *b'*. As in other F-ATP synthases (Sobti et al., 2016; Guo and Rubinstein, 2018; Colina-Tenorio et al., 2018; Hahn et al, 2016), the peripheral stalk is proposed to be attached to the top of the F_1 region by subunit δ (OSCP in mitochondria; Hahn et al, 2016; Srivastava et al. 2018) so that together the central and peripheral stalks establish two connections between the F_1 and F_O regions of the complex (Gajadeera and Weber, 2013; Lu et al., 2014). Movement of protons across the subunits *a-c* generates a proton-motive force that fuels the rotation of the *c*-ring, which interacts with both the N-terminal domain of subunit ε and the globular domain of subunit γ to transfer energy to the catalytic α- and β-subunits for ATP synthesis (Capaldi et al. 1996; Noji et al., 1997; Diez et al., 2004; Nakanishi-Matsui et al., 2016). The flexibility within the peripheral stalk is proposed to

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smoothen transmission of power between the rotary *c*-ring and the F_1 domain with significant

conformational variability of the C-terminal part of subunit *b*, which is in proximity to subunit δ

as shown by the atomic resolution structures of the *Geobacillus stearothermophilus* (formerly

Bacillus PS3) F-ATP synthase (Guo et al., 2018). The genes encoding the *b*-δ subunits of

mycobacterial F-ATP synthase are unique, in that the putative *b* subunit (*atpF*) and δ subunit

(*atpH*) genes have fused to form a single gene (*atpH*) (Gajadeera and Weber, 2013). In addition,

the *atpF* gene of mycobacteria encodes the information for subunit *b'*, which is a shorter *b*-type

subunit, without the C-terminus (Fig. 1B).

Additional special features of the mycobacterial F-ATP synthases are the unique 36 amino

acid C-terminal extension of the nucleotide-binding subunit α (*Mt*α$_{514-549}$ according to the *M.*

tuberculosis numbering; Fig. 1A) and the novel loop region γ subunit (*Mt*γ166-179; Fig. 1A),

whose deletions result in significant reduction in ATP synthesis (Hotra et al., 2016; Ragunathan

et al., 2017). Also specific for mycobacterial F-ATP synthases are the two shorter α-helices

within the C-terminal domain (CTD) of subunit ε, which is connected via a linker (amino acids

88-89 according to *M. tuberculosis*) with the N-terminal β-barrel domain (NTD, amino acids 1-

87) (Biuković et al., 2013; Joon et al., 2018). Removal of the C-terminal residue D121 of *Mt*ε

(Joon et al., 2018) was found to decrease ATP synthesis.

These unique structural differences of mycobacterial subunits α, γ, and ε have also been

described to be in part involved in the inability of mycobacterial F-ATP synthases to establish a

significant proton gradient during ATP hydrolysis, and/or its low or latent ATPase activity in the

fast- or slow-growing form (Haagsma, et al., 2010; Hotra et al., 2016; Kundu et al., 2016;

Ragunathan et al., 2017; Joon et al., 2018). Such latency of ATP hydrolysis activity has also been

observed for the α-proteobacterium *Paracoccus denitrificans* F-ATP synthase (Perez et al., 1990;

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Pacheco-Moisés et al., 2000, 2002; Zharova and Vinogradov, 2003), where the unique ζ-protein is suggested to cause the inhibition (Zarco-Zavala, et al., 2014; García-Trejo, et al., 2016).

So far, the crystallographic structures of the *M. smegmatis* α$_3$β$_3$γε complex (Zhang et al., 2019), the *c*-ring of *M. phlei* (Preiss et al., 2015) as well as the solution NMR structure of *M. tuberculosis* subunit ε (*Mt*ε) have been determined (Joon et al., 2018) (Fig. 1A). To shed more light into the overall structure of the mycobacterial F-ATP synthase, as well as the structural and mechanistic functions of the unique mycobacterial subunit stretches, a first purification protocol to isolate the entire and enzymatically active *M. smegmatis* F$_1$F$_O$ ATP synthase is described, providing a platform to determine a low-resolution structure of the enzyme complex by electron microscopy (EM). Genetic engineering enabled the production of a highly pure *M. tuberculosis* *b*-δ fusion subunit (*Mtb*-δ), whose secondary structural content is presented. Given the essential role of the mycobacterial F-ATP synthase for growth, including its unique subunit epitopes, which are potential targets for antitubercular compounds, further structural- and mechanistic features of the mycobacterial peripheral *b*-δ fusion subunit are discussed.

2. Material and Methods

2.1 Biochemicals

Pfu DNA polymerase was purchased from Thermo Scientific (Massachusetts, USA) and Ni^{2+}-NTA chromatography resin was obtained from Qiagen (Hilden, Germany). Enzymatic digestion was performed using restriction enzymes from New England BioLabs. Chemicals from Bio-Rad (California, USA) were used for SDS-PAGE. All other chemicals of analytical grade were obtained from Biomol (Hamburg, Germany), Merck (Darmstadt, Germany), Sigma, or Serva (Heidelberg, Germany), Thermo Fischer (UAS).

2.2 Preparation of the plasma membrane from M. smegmatis mc^2 155

In order to purify the plasma membrane (PM) of *M. smegmatis* mc^2 155 for isolation of the F-ATP synthase, cells were cultivated overnight at 37 °C in 7H9 supplemented with 10% ADC, 0.5% glycerol and 0.05% Tween 80 until it reached OD_{600} 0.6-0.7. The culture was expanded in 200 ml supplemented 7H9 and grown in 1-litre shake flasks (100 rpm) until OD_{600} 0.6-0.7. This culture was used to inoculate a 500 ml culture that was grown overnight in 2-litre shake flasks (100 rpm) until an OD_{600} of 0.6-0.7. About 6 g (wet weight) of *M. smegmatis* mc^2 155 were resuspended in 40 ml membrane preparation buffer (50 mM MOPS, 2 mM $MgCl_2$, pH 7.5) containing EDTA-free protease inhibitor cocktail (1 tablet in 20 ml buffer, Roche-USA) and 1.2 mg/ml lysozyme, respectively. The suspension was stirred at room temperature for 45 min and additionally supplemented with 300 μl 1 M $MgCl_2$ and 50 μl DNase I (Thermo Fischer, USA), and continued stirring for another 15 min at room temperature. All subsequent steps were performed on ice. Cells were broken by three passages through ice precooled Model M-110L Microfluidizer processor (M-110L) at 15,000 psi. The suspension containing lysed cells was centrifuged at 15,000 x g at 4 °C for 20 min. The supernatant containing membrane fraction was further subjected to ultracentrifugation at 27,000 x *g* for 40 min, and 160,000 x *g* at 4 °C for 1 h with a P50AT2 rotor using the Himac CP90WX ultracentrifuge (HITACHI) to separate the crude mycomembrane-containing cell wall elements from the PM. The supernatant was discarded while the PM fraction was resuspended in the membrane preparation buffer containing 15% glycerol, followed directly with the solubilisation of the F-ATP synthase.

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2.3 Purification of the M. smegamtis mc^2 155 F$_1$F$_O$ ATP synthase

To solubilize the *M. smegamtis* mc^2 155 F$_1$F$_O$ ATP synthase the PMs were dissolved in buffer A (50 mM Tris/HCl, 10 mM MgCl$_2$, 10% [v/v] glycerol, 2 mM Pefabloc^{SC} (4-(2-aminoethyl)benzenesulfonyl fluoride hydrochloride) (BIOMOL), 0.5% [w/v] n-dodecyl-β-maltoside (DDM; Thermo Scientific, UAS), pH 7.5) and incubated for 60 min at 4 °C. Remaining membranes were removed by ultracentrifugation (180,000 x *g*, 45 min) and the solubilisate was applied to a Ni^{2+}-NTA-chromatography. Ni^{2+}-NTA beads were equilibrated with buffer B (50 mM Tris/HCl, 10 mM MgCl$_2$, 10% [v/v] glycerol, 2 mM Pefabloc^{SC}, 0.05% [w/v] DDM, 0.8 mM dithiothreitol (DTT), pH 7.5) prior to incubation with the solubilisate for 1 h at 4 °C by mixing on a sample rotator (Neolab). The material was transferred to a column and the F-ATP synthase was eluted as an unbound fraction, while contaminants binding to the Ni-NTA material were eluted with increasing concentrations of imidazole in buffer B.

Fractions containing the F-ATP ATP synthase were pooled and applied into an ion-exchanger column (Res Q, 6 ml, GE-Healthcare). The F-ATP synthase containing fractions eluted at 250 mM NaCl and were concentrated to a volume of 500 µl (Vivaspin 20 columns, 100 kDa MWCO, Sartorius, Germany), to further purify the sample via an additional size exclusion chromatography (Superdex HR 300 column (GE Healthcare)) at room temperature. The Superdex HR 300 column was equilibrated with buffer B (50 mM Tris/HCl, 10 mM MgCl$_2$, 10% [v/v] glycerol, 0.05% [w/v] DDM, 0.8 mM DTT, pH 7.5). The protein eluted after around 10.9 ml with a flow rate of 0.5 ml/min. Only the major fractions from peak 1 were pooled and applied onto a 17% SDS-gel (Laemmli, 1970).

2.2 ATP hydrolysis activity

The ATP hydrolysis activity of *M. smegamtis* mc^2 F-ATP synthase was measured with a continuous assay. In brief, 6 µg of F_1F_O ATP synthase was added at 37 °C to 100 µl of a reaction mix, containing 25 mM Hepes/HCl (pH 7.5), 25 mM KCl, 5 mM MgCl$_2$, 5 mM KCN, 2 mM phosphoenolpyruvate, 2 mM ATP, 0.4 mM NADH, 30 U L-lactic acid dehydrogenase and 30 U pyruvate kinase. The absorbance at 340 nm was observed with a spectrometer for 5 min. The specific activity was determined from the linear slope of the graph.

The effect of trypsin on the ATP hydrolysis of the *M. smegmatis* F-ATP synthase was studied according to the protocol of Zhang et al. (2019). Hereby, purified *M. smegmatis* F-ATP synthase was incubated with bovine trypsin (1 mg/ml) at a trypsin:*M. smegmatis* F-ATP synthase ratio of 1:50 (w/w) for 2 min at 37 °C. Digestion was terminated with a 2-fold molar excess of bovine pancreatic trypsin inhibitor (5 mg/ml).

2.3 Electron microscopy, 2D- and3D image analysis of M. smegmatis F-ATP synthase

M. smegamtis mc^2 F-ATP synthase was diluted in buffer B to 80 μg/ml and a volume of 4 μl of protein sample was applied to a glow-discharged carbon coated copper transmission electron microscopy grid and stained with 2% (w/v) uranyl acetate. Electron micrographs were recorded on a Tecnai spirit T12 transmission electron microscope (FEI) equipped with a 4K CCD camera (FEI) operated at a voltage of 120 kV at a calibrated magnification of 66,350x under low dose conditions. 80 micrographs were recorded at 0° angle for the enzyme complex. A total of 8,400 particles were selected for 2D analysis. The selection criteria were clear visibility of single molecules and separation from neighboring particles. Particles were picked using EMAN2 (Tang et al., 2007) and processed using RELION v1.4. 3D classification and class refinement were

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1 performed in *RELION* v1.4 (Scheres et al., 2012). A reference density map filtered to 50 Å was

2 generated using the structural coordinates of *E. coli* F-ATP synthase (PDB code 5T4Q; Sobti et

3 al., 2016). Fitting and visualizing of the experimentally acquired surface density map of the *M.*

4 *smegmatis* F_1F_O ATP synthase complex were all achieved within UCSF Chimera.

5

6 *2.4 Cloning, production and purification of Mtb-δ*

7 In order to generate the *M. tuberculosis* b-δ_{24-446} construct (*Mtb*-δ_{24-446}), which

8 excludes the bases encoding the N-terminal, membrane-embedding amino acids, the respective

9 region of the Open Reading Frame of the *atpH* gene from *M. tuberculosis* HR37v was

10 amplified using primers engineered to contain an *Nde*I restriction site in the forward primer (5'-

11 CGATTTATC<u>CATATG</u>CTCGTAGGGCGTTTG-3') and a *Hind*III restriction site in the reverse

12 primer (5'-CTAGT<u>AAGCTT</u>TCAGTCGGGCAGTCGTGC-3'). The amplified PCR product was

13 then digested with *Nde*I/*Hind*III restriction enzymes (NEB, MA, USA). It was purified using the

14 gel extraction kit (QIAGEN) as per the manufacturer''s protocol and subsequently ligated into

15 the *Nde*I and *Hind*III restriction site of the digested and purified *E. coli*-mycobacterium shuttle

16 vector pYUB1049. The shuttle vector pYUB1049 was kindly provided by Professor Gregory M.

17 Cook (Department of Microbiology, University of Otago, New Zealand). This vector allows the

18 addition of a His-tag and a thrombin cleavage site at the N-terminus. The construct was then

19 transformed into *E. coli* TOP10 cells (Invitrogen, USA) and plated on low salt Luria-Bertani

20 (LB) agar medium containing 50 μg/ml of hygromycin B. Positive clones were selected and their

21 plasmid prepared using the QIAPrep Spin Miniprep kit (QIAGEN). Plasmids with the desired

22 insets were sent for sequencing to confirm the faithfulness and integrity of the recombination.

1   The respective plasmid was transformed into the *M. smegmatis* mc^2 4517 expression system

2   (Wang et al. 2010).

3   The expression culture was grown at 37 ^{o}C and aliquots of culture were taken at 48 hours to

4   check for protein expression. Cells were spun at 7,500 x g for 20 minutes and the cell pellets

5   were resuspended in lysis buffer (50 mM 150 mM NaCl, Tris pH 8.5). The cells were then lysed

6   by sonication on ice 4 x 2 mins using a Misonix Sonicator (U.S.A). The lysate was then spun at

7   40,000 x g to separate soluble and insoluble fractions. The filtered soluble fraction was incubated

8   with Ni^{2+}-NTA agarose beads for 1 hour at 4 °C to bind the His$_6$-tagged proteins, which were

9   later eluted with a linear imidazole gradient (0-250 mM) in Buffer A (50 mM Tris/HCl, pH 8.5,

10 10% glycerol). The eluted fractions were applied on a 17% SDS-PAGE (Laemmli, 1970) to

11 check for the presence of the desired protein. The appropriate fractions were pooled, diluted with

12 Buffer B (50 mM Tris/HCl, pH 8.5 and 10% glycerol) to reduce the salt concentration to 50 mM,

13 and subsequently applied onto an anion-exchange column (Mono Q, 6 ml, GE-Healthcare). The

14 fractions containing recombinant *Mtb*-$\delta_{24\text{-}446}$ were pooled and concentrated as required using

15 Centricon YM-30 (30 kDa molecular mass cut off) spin concentrators (Millipore).

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17 *2.5 Circular dichroism spectroscopy*

18   Steady-state Circular dichroism spectroscopy (CD) spectra were measured in 0.1 mm quartz

19 Hellma cell (60 µl volume) at 18 ºC on CHIRASCAN spectropolarimeter (Applied Photophysics)

20 instrument at a step resolution of 1 nm from 180 – 260 nm far UV range, of spectrum under

21 continuous purging of N$_2$ gas. Protein samples were buffer exchanged, reduced or oxidized by

22 appropriate protocols before measurements. The *M. tuberculosis b*-$\delta_{25\text{-}446}$ fusion protein was

23 measured in triplicates at a concentration of 1.9 mg/ml, with the buffer reading taken before and

1   after protein sample. Averaged buffer base line was subtracted from average protein values using

2   in built Chirascan software. Initial degree $cm^2 \cdot dmol^{-1}$ units were converted into mean molar

3   residue ellipticity (Θ) with the help of Chirascan software by giving appropriate cell path length,

4   molecular weight, number of amino acid residues and protein concentration values. In order to

5   analyze the CD spectrum, the programs Dicroprot (Deléage *et al.,* 1993) and Neural Net (Böhm

6   *et al.,* 1992) were used.

7

8   *2.6 Computational Details*

9   The sequence of the *b'* and fused *b*-δ subunits of *M. smegmatis* were retrieved from UniProt

10   (A0R200 and A0R203 respectively) and aligned against the sequence of *E. coli b* and δ subunits

11   derived from the PDB template 5T4Q (Sobti et al., 2016) using *mafft* (Katoh and Standley, 2013)

12   with the L-ins-I alignment strategy. Alignment resulted in a good overlap of fused *M. smegmatis*

13   *b*-δ with both F_O-*b* and F_1-δ in the N-terminal and C-terminal regions, respectively. The

14   alignment is provided as a supplementary file (Supplementary Fig. 1). A region of 111 additional

15   residues is present in fused *b*-δ for which a BLAST search was performed, but no structural

16   templates could be identified. Hence, we proceeded to use the Robetta *ab-initio* structure

17   prediction server, based on the *Rosetta* (Das & Baker, 2008) suite of modeling tools, to predict

18   the structure of this region. The resulting structures consistently show a fold containing five α

19   helices. Five structure models were obtained and attempted to fit with the geometry of F_O-*b* and

20   F_1-δ of *E. coli* structure 5T4Q (Sobti et al., 2016). The predicted fold fits well with a lightly

21   structured region at the C-terminus of F_1-δ. The model whose termini best aligned with the

22   existing template was chosen and positioned to connect with F_O-*b* and F_1-δ to create a full

23   structural template for the fused *b*-δ model. Subsequently, we used the alignment obtained

11

1 previously in conjunction with this structure as an input for homology modeling. Modeler 9.19

2 (Eswar et al., 2006) was used with default settings of the *automodeller* plugin and 100 structures

3 were generated, out of which the model with the lowest RMSD to the template was chosen. We

4 then replaced the F_O-*b* and F_1-δ segments of 5T4Q (Sobti et al., 2016) with the newly modeled

5 structure and proceeded to fit it with the electron density map described in this study. The fused

6 *b*-δ segment including the *ab initio* modeled extended *b* fit well with observed density, as shown

7 in figure 6.

8

3. Results and Discussion

10 *3.1 Isolation of a complete M. smegmatis F_1F_O ATP synthase*

11   Since disruption of the mycobacterial cells with high fluid pressure remains the best lysis

12 method for obtaining significant amounts of PM fractions from these bacteria (Rezwan et al.,

13 2007), 6 g of *M. smegmatis* mc^2 155 were resuspended in buffer (50 mM MOPS, 2 mM $MgCl_2$,

14 pH 7.5, EDTA-free protease inhibitor and 1.2 mg/ml lysozyme) and broken by three passages

15 through a Microfluidizer (see details in Material and Methods). The suspension containing lysed

16 cells was centrifuged at 15,000 x *g* as described recently (Ragunathan et al., 2017), followed by

17 subsequent ultracentrifugation steps at 27,000 x *g* and 160,000 x *g* to separate the crude

18 mycomembrane-containing cell wall elements from the PM. To solubilize the mycobacterial F-

19 ATP synthase the PM pellet was dissolved in buffer containing 0.5% [w/v]

20 n-dodecyl-β-maltoside (DDM), incubated for 1 h, and remaining membranes were removed by

21 ultracentrifugation (180,000 x *g*) and the solubilisate was applied to a Ni^{2+}-NTA-

22 chromatography, to separate contaminants binding to the affinity column. To further remove

23 impurities, we introduced an ion–exchange column (Resource[TM] Q column) and a size exclusion

12

1   chromatography step (Superdex 300 column). The elution profile showed one major peak (Fig.

2   2A). Fractions from this peak contained *M. smegmatis* F-ATP synthase with all subunits (Fig.

3   2A). The identity of major subunit α, β, γ and the mycobacterial specific fused *b-δ* was

4   established using MALDI mass spectrometry (Supplementary Tables S1A-D). These studies

5   revealed that the 59 kDa, 52 kDa, 48 kDa, and 34 kDa band corresponds to subunit α, β, *b-δ*, and

6   the rotary subunit γ (Fig. 2B; Supplementary Tables S1A-D). The band at 54 kDa was identified

7   to contain the mycobacterial Glutamine synthetase (Supplementary Table S1E).

8

9   *3.2 ATP hydrolysis traits of the M. smegmatis F_1F_O ATP synthase*

10   The isolated *M. smegmatis* F-ATP synthase was used for electron microscopy imaging (see

11   below) and enzymatic assays (Fig. 2B). The ATP hydrolysis activity of this complex was 0.4 ±

12   0.1 μmol min^{-1} (mg protein)$^{-1}$, slightly higher compared to the ATPase activity of about 0.04 ±

13   0.01 μmol min^{-1} (mg total protein)$^{-1}$ of the *M. smegmatis* F-ATP synthase within inverted

14   membrane vesicles (IMVs) determined recently (Ragunathan et al., 2017), and to the activity of

15   the recombinant *M. smegmatis* F_1 ATPase ($α_3$:$β_3$:γ:ε) of about 0.07 μmol min^{-1} (mg protein)$^{-1}$

16   (Zhang et al., 2019). In comparison, the ATP hydrolysis activity of the $α^{chi}_3$:$β_3$:γ complex was

17   determined to be 3.4 ± 0.07 μmol/min/mg protein (Fig. 2B), which is comparable to that

18   determined in previous studies (Ragunathan et al., 2017; Bogdanović et al., 2019), and reflects

19   the low ATP hydrolysis activity of the mycobacterial F-ATP synthase described previously

20   (Haagsma et al., 2010; Hotra et al., 2016). Considering the aspects of protein concentration

21   determination of soluble, detergent-solubilized and membrane-embedded complexes, the data

22   also indicate that no drastic difference can be observed between the ATP hydrolysis activity of

23   the membrane-embedded, DDM-solubilized F-ATP synthase as well as the F_1-ATPase.

1   Because of the presented low ATP hydrolase activity of the isolated *M. smegmatis* F_1F_O ATP

2   synthase as well as the described recombinant *M. smegmatis* F_1-ATPase (Zhang et al., 2019),

3   which can not be stimulated by lauryldimethylamine oxide (LDAO), but by trypsin cleavage

4   (Zhang et al., 2019), the *M. smegmatis* F_1F_O ATP synthase was pretreated with trypsin according

5   to Zhang et al., (2019) and an ATP hydrolysis activity of 0.8 ± 0.1 µmol min^{-1} (mg protein)$^{-1}$ was

6   determined (Fig. 2B). Taken together, the data reflect that an enzymatically active and entire *M.*

7   *smegmatis* F_1F_O ATP synthase was isolated.

8

9   *3.3 Electron microscopy and three-dimensional reconstruction*

10   The negatively-stained enzyme, prepared for electron microscopy, yielded dispersed single

11   particles (Fig. 3A). The negatively stained *M. smegmatis* F-ATP synthase shows a preferred

12   orientation on the electron microscope grids with its long axis lying in the plane of the carbon

13   support film (Fig. 3A). A total of 8,400 particles were subjected to image processing. After two

14   rounds of particle elimination and classification, 3,335 particles were used for 2D class averaging

15   to generate the *M. smegmatis* F-ATP synthase projections. All of the resulting projections

16   revealed a tripartite structure consisting of the F_1 headpiece, a membrane-embedded domain, F_O,

17   and the connecting central- and peripheral stalks, including the tip on the top of the F_1-domain

18   formed by the fused *b*-δ (Fig. 3B). The averaged classes were separated based on the orientation

19   of the asymmetrical central stalk, the asymmetrical F_O domain (subunit *a* and the *c*-ring) and/or

20   the visibility of the peripheral stalk connecting the F_1 and the F_O domains. The entire *M.*

21   *smegmatis* F-ATP synthase extends to a length of around 240 Å. In the second class (Fig. 3B-

22   A1), the peripheral stalk is shown to extend upward and downward to contact subunit δ of F_1 and

23   subunit *a* of F_O, respectively, whose densities are indicated with the arrows (Fig. 3B-A1, 3B-B3,

14

1 and 3B-B4). Besides the peripheral stalk, mass contributing to the central stalk is visible as well.

2 The data presented confirm that a stable and well assembled *M. smegmatis* F-ATP synthase was

3 isolated.

4   The final three-dimensional reconstruction (Fig. 4) was calculated from the two-dimensional

5 class averages (Fig. 3B). The resolution was determined to be 33.4 Å by the Fourier shell

6 correlation criterion with a threshold of 0.143 times the noise correlation value (Supplementary

7 Fig. 2). The dimensions of the F_1 headpiece, the central stalk domain, and the membrane part, F_O,

8 are approximately 120 x 134, 40 x 70, and 80 x 110 Å, respectively (Fig. 4A1-2). The final

9 reconstruction visualized the peripheral stalk connecting the membrane-embedded F_O domain

10 (Fig. 4A1, B1-2) and moving up on top of the $\alpha_3\beta_3$ crown forming the "tip-volume" (Fig. 4B1-3).

11 Superimposition of subunit δ of the chloroplast F-ATP synthase cryo-EM structure (PDB ID:

12 6FKF; Hahn et al., 2018) fills a part of this volume and brings this subunit in the vicinity to the

13 N-terminal crown of the three nucleotide-binding subunit α (Fig. 4A3).

14   The final *M. smegmatis* F-ATP synthase reconstruction accommodates the *M. smegmatis*

15 $\alpha_3\beta_3\gamma\epsilon$ complex- (PDB ID: 6FOC; Zhang et al., 2019) and *c*-ring structure of *M. phlei* (PDB ID:

16 4V1G; Preiss et al., 2015) (Fig. 4B1-3). The comparison highlights the space lacking at the

17 bottom of subunit α inside the 3D reconstruction of the entire F-ATP synthase (Fig. 4B2), which

18 may be due to the unresolved C-terminal stretch of 37 residues in subunit α of the *M. smegmatis*

19 $\alpha_3\beta_3\gamma\epsilon$ structure (Zhang et al., 2019). In *M. smegmatis*, *M. phlei* and *M. ulcerans* this C-terminal

20 region of amino acids 512-548 is predicted to be disordered, while in *M. bovis* or *M. tuberculosis*

21 it is proposed to include an α-helix (Zhang et al., 2019), as shown for the NMR structure of the α-

22 helical residue 526-539 within the C-terminal peptide $\alpha_{521-540}$ from *M. tuberculosis* ($Mt\alpha_{520-540}$)

23 (Ragunathan et al., 2017). A cross-section at the distinct C-terminal region of subunit α reflects

15

1 that the additional mass in the 3D reconstruction could be due to the presence of the additional

2 mycobacterial C-terminal stretch (Fig. 4B3). Similarly, a comparison of the top of the *M.*

3 *smegmatis* $\alpha_3\beta_3\gamma\epsilon$ structure and the 3D reconstruction of the *M. smegmatis* F-ATP synthase

4 highlights the space available to anchor the mycobacterial *b*-δ subunit (Fig. 4B3).

5

6 *3.4 Production, purification and characterization of the fused b-δ subunit*

7 Our sequence analysis of the *Actinobacteria* phylum, to which *Mycobacteria* belong,

8 highlights variations in the δ subunit (Fig. 5A). Whereas, some early branching *Actinobacteria*

9 such as the *Rubrobacter xylanophilus* (Gao et al., 2012) present a canonical δ subunit consisting

10 of 179 amino acids, which is similar in length to the *E. coli δ subunit*, the *Streptomyces* and

11 *Mycobacteria species* possess a more elongated δ subunit, due to an N-terminal 111 amino acid

12 extension as in the case of *M. smegmatis*, resulting in a 272 amino acids protein. Furthermore, in

13 the case of mycobacteria, there is a fusion between the extended δ and the *b* subunit leading to

14 the *b*-δ fusion protein (446 residues according to *M. tuberculosis*).

15 To demonstrate that a fused *b*-δ protein is encoded by the *atpH* gene and to characterize its

16 secondary structural content in solution, the *M. tuberculosis* *b*-$\delta_{25\text{-}446}$ fusion protein was

17 generated, excluding the predicted 24 amino acids of the hydrophobic transmembrane domain of

18 *b*-δ. *Mtb*-$\delta_{25\text{-}446}$ was produced in the *M. smegmatis* mc^{2}4517 strain and isolated to high quality

19 and quantity using Ni-NTA-affinity- and ion-exchange chromatography (Fig. 5B). The proper

20 secondary folding of the recombinant *Mtb*-$\delta_{25\text{-}446}$ was studied by circular dichroism spectroscopy,

21 measured between 189-260 nm (Fig. 5C). The concentration of the purified recombinant protein

22 δ was 1.9 mg/ml in buffer 50 mM Tris/HCl (pH 8.5) and 150 mM NaCl. The maximum at 192

23 nm and the minima at 210 and 222 nm indicate the presence of mainly α-helical structures in the

16

1 protein. The average secondary structure content was 69.2% α-helix, 6.6% β-sheet, and 24.2%

2 random coil. These results are consistent with secondary structure predictions based on the

3 subunit Mtb-$\delta_{25\text{-}446}$ amino-acid sequence, and the β-sheet content is reflective of the amount

4 observed in the four-stranded β-sheets of the CTD of the chloroplast δ subunit (Hahn et al.,

5 2018). The molar ellipticity values at 208 nm and at 222 nm are in a ratio of 0.93.

6

7 *3.5 The peripheral stalk within the mycobacterial F-ATP synthase*

8   With the input of the secondary structural information of the mycobacterial $\delta_{25\text{-}446}$ described

9 above and the structural models of the *E. coli* (Sobti et al., 2016) and chloroplast δ (Hahn et al.,

10 2018) an *ab-initio* structural model of the mycobacterial δ subunit with its extended N-terminal

11 111 amino acids region as well as the subunits *b* and *b'* (Fig. 6A-C) was generated (see Material

12 and Methods). Like the *E. coli*- and chloroplast subunit δ, the mycobacterial counterpart

13 displayed a similar bundle of six short α-helices (α7-α12), followed by the four-stranded mixed

14 β-sheet (β1-β4) and two α helices (α13-α14) at the C-terminal domain (Fig. 6A, -7). Interestingly,

15 the N-terminal 111-residues extension consists of six α-helices (α1-α6). The *ab-initio* model of

16 the subunit δ extension resulted in a configuration that readily accommodates connectivity to the

17 distinct *b* and δ subunits, which is consistent with the density observed in the 3D EM structure of

18 the *M. smegmatis* F-ATP synthase, by filling the tip volume of the $\alpha_3\beta_3$ crown (the correlation

19 coefficient being 0.918 as calculated using Chimera program; (Fig. 6A2-A3, 6B1-B4)), which

20 was only partially occupied by the canonical chloroplast δ (Fig. 4A3). In this configuration, the

21 helices α1 and α3 of the 111-residues extension would come in proximity to the interface of the

22 N-termini of one α-β pair (α1β1), forming the catalytic interface within the crystallographic

23 structure of the *M. smegmatis* F_1-ATPase (Zhang et al., 2019; Fig. 7A). In addition, helix α9 and

17

1 α11 are in the neighborhood to the N-termini of subunit β (β3) and α (α3) (Fig. 7B), respectively,

2 while the α-helix 14 is in proximity to subunit α (α1) (Fig. 7C-D). In comparison, the canonical

3 subunit δ within the *E. coli-* (Sobti et al., 2016) and chloroplast F-ATP synthase (Hahn et al.,

4 2018) or its mitochondrial equivalent OSCP of the yeast *Yarrowia lipolytica* (Hahn et al., 2016)

5 or *Saccharomyces cerevisiae* (Srivastava et al., 2018) interact only with the α subunits via helices

6 corresponding to the mycobacterial helix bundle (α7-α12; Hahn et al., 2016, 2018).

7   Finally, the *ab initio* model of the peripheral stalk displayed subunit *b* and *b'* to form a right-

8 handed coiled coil, whose N-termini contribute to the membrane-embedded F_O-domain (Fig.

9 6A2, B1). Together with the subunit *a*, they fill the remaining volume within the mycobacterial

10 F-ATP synthase EM map (Fig. 6B1-B3).

11

12 *3.5 An evolutionary view to the topological variations of the peripheral stalk*

13   The canonical δ, as well as OSCP, are described to be essential for the assembly of the *b-*

14 dimer with the rest of the entire engine and therefore to connect the F_1- with the F_O-rotor

15 elements (reviewed in Colina-Tenorio et al, 2018). This enables the peripheral stalk subunits δ

16 and *b* to provide transient elastic energy during the rotary catalytic cycle. This assumption has

17 been made based on the determined heterodimeric right-handed coiled-coil structure of the

18 peripheral stalk subunits E–H of the archaea-type ATP synthases (Lee, et al. 2010; Balakrishna et

19 al. 2012), which consists of the two peripheral stalk subunits E and G. The structure of subunit E

20 (equivalent to subunit *b* in F-ATP synthases) reveals an extended S-shaped N-terminal α-helix,

21 followed by a globular head group (Fig. 8A). The latter is made up of four-stranded β-sheets and

22 two α-helices, followed by a C-terminal α-helical tail (Lee, et al. 2010; Balakrishna et al. 2012), a

23 structural content similar to the C-terminal domain of the canonical subunit δ (Hahn et al., 2018;

18

1   Guo et al., 2018; Fig. 8B). Because of the essential functions of δ as an anchor of the peripheral

2   stalk at the top of F_1 and its partial contribution to the transient elastic energy during rotation,

3   evolution may have extended the mycobacterial δ to adapt to specific mechanistic and/or

4   regulatory needs (Fig. 8C). As reflected by the peripheral stalk subunit of the related V_1V_O-

5   ATPase, disruption of the α-helical subunit G (equivalent to subunit *b*) provides the stalk some

6   degree of movement to the complex, and enables the enzyme to dis- or reassemble the V_1- and

7   V_O sector (Oot et al., 2017). The mechanistic importance of the peripheral stalk and in particular

8   the subunit δ homologue, OSCP in mitochondria is revealed to be a target of the insecticide

9   dichlorodiphenyltrichloroethane (DDT) (Younis et al., 2011), the compound Bz-423, which

10   induces apoptosis (Stelzer *et al.*, 2009), as well as the estrogen 17β-estradiol (Zheng *et al.*, 1999).

11   In this context, the mycobacterial δ subunit with its unique N-terminal extension and arrangement

12   within the F-ATP synthase, promises to be an interesting drug target.

13

4.   Conclusion

15   The purification protocol developed here enabled the enzymatic characterization and

16   visualization of the entire *M. smegmatis* F-ATP synthase with its characteristic $\alpha_3\beta_3$-headpiece, a

17   central and peripheral stalk both connecting the catalytic $\alpha_3\beta_3$ with the membrane-embedded F_O

18   domain. The overexpressed peripheral stalk subunit Mtb-$\delta_{25\text{-}446}$ demonstrated that the peripheral

19   stalk subunit *b* and δ are fused via a 111-residues linker region, forming a mainly α-helical

20   protein (69.2% α-helix). Combining these structural insights with the existing structures of the

21   mycobacterial F-ATP synthase ($\alpha_3\beta_3\gamma\varepsilon$ (Zhang et al., 2018), *c*-ring (Preiss et al., 2015), and $Mt\varepsilon$

22   (Joon et al., (2018), a structural model of the $\alpha_3\beta_3\gamma\varepsilon ab$-$\delta b'c_9$ ensemble was computed, providing

23   a comprehensive insight into the arrangement of the subunit ensemble and in particular the N-

1 terminal 111-residues stretch at the tip of the catalytic $\alpha_3\beta_3$ headpiece, predicted to be an

2 additional epitope to probe as attractive drug target for TB.

3

12

13 **Author contributions**

14 K.N., W.N., R.G.H., P.J.B. and G.G. designed the experiments. K.N., W.N., R.G.H., S.B. and

15 G.G. performed the experiments. K.N., W.N., R.G.H. analyzed the data. Writing - Original Draft

16 K.N., W.N., R.G.H. and G.G.; Writing - Review and Editing: all authors

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26

1 **Figure Legends**

2 **Fig. 1.** (*A*) The structural model of the $\alpha_3\beta_3\gamma\varepsilon c$ complex of the mycobacterial F-ATP synthase.

3 Subunits α (*green*), β (*orang*e), γ (yellow), and ε (*magenta*) are from the *M. smegmatis* crystal

4 structure ((PDB ID: 6FOC; Zhang et al., 2018), whereby the missing β-sheet elements of subunit

5 γ were added by the respective subunit γ elements of the *E. coli* F-ATP synthase (PDB ID: 5T4Q;

6 Sobti et al., 2014). Subunit γ has a unique γ-loop (Hotra et al., 2016) in case of the mycobacterial

7 one which is highlighted in *red*. The solution shape of α^{chi} is displayed as *green sphere*

8 (Ragunathan et al., 2017). The *c*-ring loop residues of *M. phlei* (*wheat*; PDB ID: 4V1G; Preiss et

9 al., 2015), proposed to interact with the rotating ε and γ stalks subunits are indicated. (*B*) The F-

10 ATP synthase operon of *M. tuberculosis* showing the large size of the *atpH* gene, encoding the *b*-

11 δ fusion protein, and the smaller *atpF* gene for the shorter *b*-type subunit, *b'*.

12

13 **Fig. 2.** (*A*) Isolation of the *M. smegamatis* F-ATP synthase using size-exclusion chromatography.

14 The collected fractions at around 10.9 ml are shown in grey. *Inset*, the 17% SDS gel shows the

15 purity and subunit composition of the enzyme (*lane P*). *G.s.*, mycobacterial Glutamine

16 synthetase. (*B*) Continuous ATPase activity of the *M. smegmatis* F-ATP synthase, the *M.*

17 *smegmatis* F-ATP synthase after treatment with trypsin, and the $\alpha^{chi}_3:\beta_3:\gamma$ complex plotted against

18 the time. The graphs are an average of three determinations.

19

20 **Fig. 3.** Negative stained EM of purified *M. smegamatis* F_1F_O ATP synthase. (*A*) Electron

21 micrograph showing the selected particles consisting of two visible domains. (*B*) The *gallery*

22 shows eight 2D class averages resulting from two rounds of 2D classifications. Classes showing

23 the prominent structural features of the complex are magnified in *A1*, *B3* and *B4* below. *A1* shows

1 the lateral view of the complex where the F_1 and F_O parts are clearly distinguished. *turkis*

2 *arrowheads* indicate the mass of the peripheral stalk connecting the F_1 (tip on the top of the F_1

3 domain) and F_O part. The *white arrowhead* indicates the mass of the asymmetrical central stalk.

4 The *white arrows* indicate the membrane-embedded subunit *a* associated with the *c*-ring and the

5 peripheral stalk. *B3* and *B4* reveal the side-views of the complex with different positions as

6 discerned from the orientation of the mass of the central- and peripheral stalks, reveals the

7 superimposition of the *E. coli* F-ATP synthase (PDB ID: 5T4Q; Sobti et al., 2014) on the

8 projections of the *M. smegmatis* F_1F_O ATP synthase. *light rose arrow* points to the mass of the δ

9 subunit of the *E. coli* F-ATP synthase.

10

11 **Fig. 4.** Surface representation of the 3D reconstruction of the *M. smegmatis* F-ATP synthase

12 refined to about 33.4 Å using *RELION* v*1.4* (Tang et al. 2007) with side views (*A1-A2*) and top

13 view (*A3*). *A3*, reveals subunit δ (*purple*) of the chloroplast F-ATP synthase cryo-EM structure

14 (PDB ID: 6FKF; Hahn et al., 2018) which sits on top of the three α (*green*) subunits (*B3*). *B1-B2*

15 show that the mycobacterial $\alpha_3\beta_3\gamma\varepsilon c$ complex (PDB ID: 6FOC; Zhang et al., 2019; PDB ID:

16 4V1G; Preiss et al., 2015) fitted into the surface density map obtained from the negative stained

17 EM of the reconstituted *M. smegmatis* F-ATP synthase. The unoccupied volume of the low

18 resolution *M. smegmatis* F-ATP synthase (side-view *B1*) visualizes the volume available for the

19 F_O subunits *a*, the N-terminal and membrane-embedded parts of subunits *b*, *b'*, and the peripheral

20 stalk (*b*, *b'*), which fuses with the mycobacterial subunit δ at the crown of the F_1 domain.

21 Subunits α, β, γ, ε, and *c* are colored in *green*, *orange*, *yellow*, *red*, and *beige*, respectively. The

22 *yellow arrowhead* in *B1* indicates the missing structural elements in the crystal structure of

23 subunit γ (PDB ID: 6FOC; Zhang et al., 2019). The *green arrow* and *green arrowhead* reveal the

28

1   last residue F511 of subunit α and the available space for the unresolved residues 512-548 within

2   the subunit α structure of the *M. smegamatis* $\alpha_3\beta_3\gamma\epsilon$ complex (PDB ID: 6FOC; Zhang et al.,

3   2019), respectively. (*B4*) a cross-section at the distinct C-terminal region of subunit α (*green line*

4   *in B1*) reflects that the additional mass in the 3D reconstruction (*B1-B2*) could be due to the

5   presence of the additional mycobacterial C-terminal stretch residues 512-548.

6

7   **Fig. 5.** Amino acids sequence alignments and purification and CD spectroscopy of *Mtb*-$\delta_{25\text{-}446}$.

8   (*A*) Multiple sequence alignment of the peripheral subunit *b*-δ, extended δ and the canonical δ

9   from the bacteria domain. The amino acid sequence of the *b*-δ fusion protein of members of the

10   Corynebacteriales suborder (including the genus *Gordonia, Tsukamurella, Williamsia* and

11   *Mycobacterium*) were aligned with the extended δ subunit of the *Actinobacteria phylum* and the

12   canonical δ subunit of other bacteria species. The alignment was performed using Clustal Omega

13   software (Sievers et al., 2011) and visualized using Jalview (Waterhouse et al., 2009). The default

14   Clustal colour scheme was used accordingly to denote conservation and categories of the amino

15   acids. The predicted secondary structure using the *M. tuberculosis* sequence was generated by

16   JnetPred in the Jalview program. The Accession numbers for the selected sequence are as

17   follows; *M. tuberculosis*: WP_031698503.1, *G. effusa*: WP_007316229.1, *T. pseudospumae*:

18   WP_068575214.1, *W. marianensis*: WP_099383244.1, *P. dioxanivorans*: WP_013673849.1, *S.*

19   *rugosus*: WP_007467277.1, *S. griseus*: WP_030762241.1, *R. opacus*: WP_128641830.1, *E. coli*:

20   WP_097290843.1, *S. enterica*: WP_058106926.1, *K. pneumoniae*: WP_102009146.1, *R.*

21   *xylanophilus*: WP_011564619.1. (*B*) Elution of the recombinant *Mtb*-$\delta_{25\text{-}446}$ by a linear gradient

22   of NaCl on anion exchange column (Resource Q 6 ml) with a constant flow rate of 2 ml/min. The

1 fractions of peak 1, indicated by the grey area, where applied onto a 17% SDS-gel (*1*). (*C*) Far

2 UV Circular dichroism spectroscopy of recombinant *Mtb*-$\delta_{25\text{-}446}$.

3

4 **Fig. 6.** *Ab-intio* structure of mycobacterial subunit δ and superimposition of the 3D

5 reconstruction of the *M. smegmatis* F-ATP synthase with structural models of its individual

6 subunits. *A1* displays the derived *ab-initio* structure of mycobacterial subunit δ with its N-

7 terminal 111-residues domain (α1-α6) in *hot pink*, the α-helices (α7-α12), which form the N-

8 terminus in canonical δ's in *light pink*, and the C-terminal domain composed of β1-β4 and α13-

9 α14 (*magenta*). *A2* and *A3* show side- and top view with the superimposed *ab-inito* of the fused

10 *b*-d and subunit b' (*turkish blue*), respectively. *B1-B3* show side- and *B4* top views, respectively,

11 that the mycobacterial $\alpha_3\beta_3\gamma\varepsilon c$ complex (PDB ID: 6FOC; Zhang et al., 2019; PDB ID: 4V1G;

12 Preiss et al., 2015) fitted into the surface density map obtained from the negative stained EM of

13 the reconstituted *M. smegmatis* F-ATP synthase. The unoccupied volume of the low resolution

14 *M. smegmatis* F-ATP synthase visualized in figure 4 above becomes occupied by the volume of

15 the *ab-initio* structure of mycobacterial subunits *a* (*blue*), the N-terminal and membrane-

16 embedded parts of the mycobacterial subunits *b*, *b'* (in *turkish blue*), and the peripheral stalk (*b*,

17 *b'*), which fuses with the novel mycobacterial subunit δ (*light-* and *hot pink*). The latter occupies

18 well the tip of the F_1 domain. The crystallographic structures of subunits α, β, γ, ε, and *c* are

19 colored in *green*, *orange*, *yellow*, *red*, and *beige*, respectively.

20

21 **Fig. 7.** The relative arrangement of mycobacterial subunit δ to the $\alpha_3\beta_3$ head. (*A*) The helices α1

22 and α3 of the 111-residues extension of the *ab-initio* determined mycobacterial δ are predicted to

23 be in proximity to the interface of the N-termini of one α-β pair within the crystallographic

30

1 structure of the *M. smegmatis* F$_1$-ATPase (Zhang et al., 2019). (*B*) Helix α9 and α11 are proposed

2 to be in the neighborhood to the N-termini of subunit β (β3) and α (α3), respectively, (*C*) while α-

3 helix 14 is in proximity to subunit α (α1). The crystallographic structures of subunits α and β are

4 colored in *green* and *orange*, respectively, while the *ab-initio* determined mycobacterial subunit *b*

5 is displayed in *turkish blue*. (*D*) The top view shows the fused *b*-δ sitting on top of α$_3$:β$_3$ crown of

6 the *M. smegmatis* F-ATP synthase.

7

8 **Fig. 8.** Similarities and diversities of structural features within the evolutionary related A-ATP

9 synthase peripheral stalk subunit E, the canonical- and mycobacterial subunit δ of F-ATP

10 synthases. (*A*) The topological arrangement of the peripheral subunits E of the *Pyrococcus*

11 *horikoshii* OT3 A-ATP synthase reveals its N-terminal helix α1 which continues into the globular

12 domain (Balkrishna et al., 2012). The latter is composed of α2-α3, the β1-β4 stretch, followed by

13 the C-terminal helix α4. (*B*) Subunit *b* of the chloroplast F-ATP synthase (Hahn et al., 2018) is

14 equivalent to the N-terminal stator element α1 of subunit E of A-ATP synthases. In comparison,

15 this canonical δ subunit consists of a similar C-terminal domain with a β1-β4 and very C-terminal

16 α helix arrangement as observed for the archaeal subunit E, while its N-terminus contains a

17 bundle of α-helices. (*C*) The topological arrangement represented by the *ab-initio* structure of the

18 mycobacterial subunit δ highlights the novel N-terminal 111-residues extension, providing

19 additional contacts to the α$_3$β$_3$ headpiece essential for stability for the two rotary elements within

20 the engine and may in part contribute to an efficient transfer of elastic energy.

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