Design, Synthesis and Characterization of Novel Inhibitors Against Mycobacterial β-Ketoacyl CoA Reductase FabG4

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S1. NMR spectra of selected compounds

Compound 6: ¹H NMR (CDCl₃, 400 MHz) spectrum





Compound 8: ¹H NMR (CDCl₃, 400 MHz) spectrum

Compound 10: ¹H NMR (CDCl₃, 200 MHz) spectrum





Compound 10: ¹³C NMR (CDCl₃, 50 MHz) spectrum







Compound 11: ¹³C NMR (CDCl₃, 100 MHz) spectrum







Compound 12: ¹³C NMR (CDCl₃, 50 MHz) spectrum

Compound 13: ¹H NMR (CDCl₃, 200 MHz) spectrum



Compound 13: ¹H NMR (CDCl₃, 50 MHz) spectrum



Compound 16: ¹H NMR (CDCl₃, 200 MHz) spectrum





Compound 16: ¹³C NMR (CDCl₃, 50 MHz) spectrum

Compound 14: ¹H NMR (CDCl₃, 400 MHz) spectrum





Compound 14: ¹³C NMR (CDCl₃, 100 MHz) spectrum







Compound 15: ¹³C NMR (CDCl₃, 100 MHz) spectrum





Compound 17: ¹³C NMR (CDCl₃, 100 MHz) spectrum

Compound 19: ¹H NMR (CDCl₃, 400 MHz) spectrum



Compound 19: ¹³C NMR (CDCl₃, 100 MHz) spectrum



Compound 1: ¹H NMR (Acetone-d₆, 400 MHz) spectrum





Compound 1: ¹³C NMR (Acetone-d₆, 100 MHz) spectrum

Compound 1: DEPT-135 NMR (Acetone-d₆, 100 MHz) spectrum





Compound 2: ¹H NMR (Acetone-d₆, 400 MHz) spectrum

Compound 2: ¹³C NMR (Acetone-d₆, 100 MHz) spectrum





Compound 2: DEPT-135 NMR (Acetone-d₆, 100 MHz) spectrum

Compound 3: ¹H NMR (Acetone-d₆, 400 MHz) spectrum





Compound 3: ¹³C NMR (Acetone-d₆, 100 MHz) spectrum

Compound 4: ¹³C NMR (Acetone-d₆, 100 MHz) spectrum



0



Compound 1: LCMS mass spectrum





Compound 2: LCMS mass spectrum





Compound 4: HRMS mass spectrum

S3. HPLC traces of the synthesized final compounds



HPLC trace of c

HPLC trace of compound 4, Eluent: 100 % methanol, Flow rate: 1 ml /min, Ret. Time: 9.66 min



S5. Secondary plots of inhibition kinetics

Compound 1 (Competitive Inhibitor)



Compound 2 (Mixed Inhibitor)

S6. Images of REMA assay





Resazurin assay plate. Pink colour indicates growth and blue indicates inhibition. Row A = only media, negative control; Row B = only culture, growth control; Row C = culture + INH, positive control; Row D = culture + compound **2**; Row E = culture + compound **1**.

S7. Details interaction from docking studies with distances

Compound 1:



Compound 1 with interacting residues (distances in Å)

A-subsite of NADH	P-subsite of NADH	N-subsite of NADH	Catalytic tetrad
binding region binding region		binding region	
Val268 (H-bond, 3.7 Å)	Gly297 (H-bond, 2.5 Å)	Ser346 (H-bond, 2.8 Å)	Lys364 (H-bond, 2.9 Å)
Leu26 (H-bond, 3.7 Å)	Thr299 (H-bond, 3.3 Å)	Ser346 (H-bond, 2.6 Å)	
Gly220 (H-bond, 2.7 Å)			

Compound **1** totally competes at all three binding subsites of NADH binding region; supports that compound 1 is a competitive inhibitor.

Compound 2:



Compound 2 with interacting residues (distances in Å)

A-subsite of NADH binding region	P-subsite of NADH binding region	N-subsite of NADH binding region		Loop I	Catalytic tetrad	
Х	Х	Ser346 2.0 Å)	(H-bond,	Arg300 (H-bond, 3.3 Å)	Ser347 3.4 Å)	(H-bond,
Х	Х	Gly391 3.0 Å)	(H-bond,			

Compound **2** mainly interacts with catalytic tetrad and loop I; It can bind with free enzyme as well as enzyme-NADH complex resulting mixed inhibition.

Compound 3:



Compound 3 with interacting residues (distance in Å)

Compound 4:





Compound 4 with interacting residues (distances in Å)

A typical kinetic plot of absorbance vs time with increasing concentration of inhibitor (compound 4) in presence of substrate acetoacetyl CoA (positive control).