Supplementary Material (SM)

Natural-product-inspired Design and Synthesis of Thiolated Coenzyme Q Analogs as Promising Agents against Gram-positive Bacterial Strains: Insights into Structure-activity Relationship, Activity Profile, Mode of Action, and Molecular Docking

Hatice Yıldırım ^a, Mahmut Yıldız ^b, Nilüfer Bayrak ^a, Emel Mataracı-Kara ^c, Berna Özbek-Çelik ^c, Masami Otsuka ^{d,e}, Mikako Fujita ^d, Mohamed O. Radwan ^{d,f}, and Amaç Fatih TuYuN ^{*, g}

- ^a Department of Chemistry, Engineering Faculty, Istanbul University-Cerrahpasa, Avcilar, 34320, Istanbul, Turkey
- ^b Department of Chemistry, Gebze Technical University, Gebze, 41400, Kocaeli, Turkey
- ^c Department of Pharmaceutical Microbiology, Pharmacy Faculty, Istanbul University, Beyazit, 34116, Istanbul, Turkey
- ^d Medicinal and Biological Chemistry Science Farm Joint Research Laboratory, Faculty of Life Sciences, Kumamoto University, 5–1 Oe-honmachi, Chuo-ku, Kumamoto, Kumamoto 862–0973, Japan
- ^e Department of Drug Discovery, Science Farm Ltd., 1–7–30 Kuhonji, Chuo-ku, Kumamoto, Kumamoto 862– 0976, Japan
- f Chemistry of Natural Compounds Department, Pharmaceutical and Drug Industries Research Division, National Research Centre, Dokki, Cairo 12622, Egypt
- ^g Department of Chemistry, Faculty of Science, Istanbul University, Fatih, Istanbul, Turkey
- * Author to whom correspondence should be addressed; E-Mail: <u>aftuyun@gmail.com</u>, <u>aftuyun@istanbul.edu.tr</u> (A. F. T.).

Tel.:	+90212	440	0000.
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Isolate	Specimens	MIC values (µg/mL)	
Isolute		CoQ1	CoQ2
MRSA	Blood	39.06	39.06
MRSA	Blood	39.06	39.06
MRSA	Blood	19.53	19.53
MRSA	Blood	19.53	19.53
MRSA	Blood	19.53	19.53
MRSA	Blood	19.53	19.53
MRSA	Blood	78.12	625.00
MRSA	Blood	39.06	78.12
MRSA	Blood	39.06	39.06
MRSA	Blood	19.53	19.53
MRSA	Blood	9.76	19.53
MRSA	Blood	9.76	19.53
MRSA	Blood	78.12	78.12
MRSA	Blood	19.53	19.53
MRSA	Blood	19.53	19.53
MRSA	Blood	39.06	78.12
MRSA	Blood	39.06	78.12
MRSA	Blood	39.06	78.12
MRSA	Blood	39.06	39.06
MRSA	Blood	19.53	19.53
	Isolate MRSA MRSA MRSA MRSA MRSA MRSA MRSA MRSA	IsolateSpecimensMRSABlood	IsolateSpecimensMIC valueMRSABlood39.06MRSABlood39.06MRSABlood19.53MRSABlood19.53MRSABlood19.53MRSABlood19.53MRSABlood19.53MRSABlood19.53MRSABlood19.53MRSABlood39.06MRSABlood39.06MRSABlood19.53MRSABlood9.76MRSABlood9.76MRSABlood9.76MRSABlood19.53MRSABlood19.53MRSABlood39.06MRSABlood39.06MRSABlood39.06MRSABlood39.06MRSABlood39.06MRSABlood39.06MRSABlood39.06MRSABlood39.06MRSABlood39.06MRSABlood39.06MRSABlood39.06MRSABlood39.06MRSABlood39.06MRSABlood39.06MRSABlood39.06MRSABlood39.06

Table S1. Properties and MIC results of the 20 clinically obtained MRSA



Figure S2: ¹³C NMR (125 MHz) spectrum of the CoQ1 in CDCl₃-d1



Figure S4: ¹³C NMR (125 MHz) spectrum of the CoQ2 in CDCl₃-d1



Figure S6: ¹³C NMR (125 MHz) spectrum of the CoQ3 in CDCl₃-d1



Figure S8: ¹³C NMR (125 MHz) spectrum of the CoQ4 in CDCl₃-d1



Figure S10: ¹³C NMR (125 MHz) spectrum of the CoQ5 in CDCl₃-d1



Figure S12: ¹³C NMR (125 MHz) spectrum of the CoQ6 in CDCl₃-d1



Figure S14: ¹³C NMR (125 MHz) spectrum of the CoQ7 in CDCl₃-d1



Figure S16: ¹³C NMR (125 MHz) spectrum of the CoQ8 in CDCl₃-d1

Crystallographic data of CoQ1

Computing details

Data collection: Bruker Instrument Service v2013.12.0.0 (Bruker AXS); cell refinement: APEX2 v2014.9-0 (Bruker AXS); data reduction: SAINT V8.34A (Bruker AXS); program(s) used to solve structure: SHELXTL V6.14 (Bruker AXS); program(s) used to refine structure: SHELXTL V6.14 (Bruker AXS); molecular graphics: Mercury (Macrae et al., 2006); software used to prepare material for publication: PLATON V1.16 (Spek, 2009), SHELXTL V6.14 (Bruker AXS).

Crystal data

C12H14O6S $M_r = 286.29$ Monoclinic, P21/n a = 3.9584 (5) Å b = 23.942(3) Å c = 13.7731 (15) Å $\beta = 91.887 \ (8)^{\circ}$ V = 1304.6 (3) Å₃ Z = 4

Data collection

Bruker APEX II QUAZAR three-circle diffractometer Radiation source: microfocus sealed tube, ImuS Multilayer QUAZAR mirrors monochromator Detector resolution: 8.3333 pixels mm-1 φ and ω scans $\theta_{\text{max}} = 25.0^{\circ}, \ \theta_{\text{min}} = 1.7^{\circ}$ $h = -4 \rightarrow 4$ $k = -28 \rightarrow 28$ $1 = -16 \rightarrow 16$

Refinement

Refinement on F2 Hydrogen site location: inferred from neighbouring Least-squares matrix: full sites $R[F^2 > 2\sigma(F^2)] = 0.049$ H-atom parameters constrained $w = 1/[\sigma^2(Fo^2) + (0.0386P)^2 + 1.4745P]$ $wR(F^2) = 0.124$ S = 1.04 where $P = (F_0^2 + 2F_c^2)/3$ 2291 reflections $(\Delta/\sigma)_{\rm max} = 0.015$ 176 parameters $\Delta \rho_{max} = 0.25 \text{ e} \text{ Å}^{-3}$ 0 restraints

Special details

Geometry. All esds (except the esd in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell esds are taken into account individually in the estimation of esds in distances, angles and torsion angles; correlations between esds in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell esds is used for estimating esds involving l.s. planes.

F(000) = 600 $D_x = 1.458 \text{ Mg m}{-3}$ Mo K α radiation, $\lambda = 0.71073$ Å Cell parameters from 2473 reflections $\theta = 2.3 - 21.1^{\circ}$ $\mu = 0.27 \text{ mm}^{-1}$ T = 293 KPlate, red $0.51 \times 0.06 \times 0.05 \text{ mm}$

Absorption correction: multi-scan SADABS V2014/4 (Bruker AXS) $T_{min} = 0.87, T_{max} = 0.99$ 18184 measured reflections 2291 independent reflections 1555 reflections with $I > 2\sigma(I)$ $R_{int} = 0.078$

 $\Delta \rho_{min} = -0.21 \text{ e} \text{ Å}^{-3}$

Geometric parameters (Å, °) for CoQ1

$\begin{array}{c} S1C4\\ S1C3\\ O3C11\\ O4C10\\ O4C12\\ O1C2\\ O1C1\\ O5C8\\ O5C9\\ O6C7\\ O2C2\\ C10C8\\ C10C11\\ C11C4\\ C4C5\\ C5C7\\ C5C6\\ \end{array}$	$\begin{array}{c} 1.761 (3) \\ 1.803 (3) \\ 1.218 (4) \\ 1.365 (4) \\ 1.446 (4) \\ 1.318 (4) \\ 1.444 (4) \\ 1.344 (4) \\ 1.344 (4) \\ 1.209 (4) \\ 1.188 (4) \\ 1.337 (4) \\ 1.473 (4) \\ 1.473 (4) \\ 1.497 (4) \\ 1.343 (4) \\ 1.486 (5) \\ 1.495 (4) \end{array}$	C3—C2 C3—H3A C3—H3B C8—C7 C6—H6A C6—H6B C6—H6C C12—H12A C12—H12B C12—H12C C9—H9A C9—H9B C9—H9C C1—H1A C1—H1B C1—H1C	1.485 (4) 0.97 0.97 1.490 (5) 0.96 0.
$\begin{array}{ccccccc} C4 & S1 & -C3 \\ C10 & -O4 & -C12 \\ C2 & -O1 & -C1 \\ C8 & -O5 & -C9 \\ C8 & -C10 & -O4 \\ C8 & -C10 & -C11 \\ O4 & -C10 & -C11 \\ O3 & -C11 & -C4 \\ C10 & -C11 & -C4 \\ C5 & -C4 & -C11 \\ C5 & -C4 & -C11 \\ C5 & -C4 & -S1 \\ C11 & -C4 & -S1 \\ C4 & -C5 & -C6 \\ C7 & -C5 & -C6 \\ C2 & -C3 & -S1 \\ C2 & -C3 & -H3A \\ S1 & -C3 & -H3A \\ S1 & -C3 & -H3B \\ C10 & -C8 & -C7 \\ O5 & -C8 & -C7 \\ O2 & -C2 & -O1 \\ O2 & -C2 & -C3 \\ O1 & -C2 & -C3 \\ \end{array}$	100.42 (15) $115.5 (3)$ $118.8 (3)$ $122.5 (3)$ $122.2 (3)$ $120.4 (3)$ $116.9 (3)$ $120.3 (3)$ $121.0 (3)$ $118.7 (3)$ $119.9 (3)$ $121.4 (2)$ $118.2 (2)$ $119.7 (3)$ $124.6 (3)$ $115.7 (3)$ $110.5 (2)$ 109.5 100.5	06-C7-C5 06-C7-C8 C5-C7-C8 C5-C6-H6B H6A-C6-H6B H6A-C6-H6C H6B-C6-H6C H6B-C6-H6C 04-C12-H12A 04-C12-H12B H12A-C12-H12C H12B-C12-H12C H12B-C12-H12C H12B-C12-H12C H12B-C12-H12C D5-C9-H9A 05-C9-H9B H9A-C9-H9B D5-C9-H9C H9B-C9-H9C H9B-C9-H9C H9B-C9-H9C H9B-C9-H9C H9B-C9-H9C H1A-C1-H1B H1A-C1-H1B H1A-C1-H1C H1B-C1-H1C H1B-C1-H1C	120.5 (3) 120.0 (3) 119.4 (3) 109.5
C12O4C10C8 C12O4C10C11 C8C10C11O3 O4C10C11O3 C8C10C11C4 O4C10C11C4 O3C11C4C5 C10C11C4S1 C10C11C4S1 C3S1C4C5	124.0 (4) -64.0 (4) 165.0 (3) -7.2 (5) -13.4 (5) 174.4 (3) -162.6 (3) 15.8 (5) 9.4 (4) -172.1 (2) -136.1 (3)	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	-176.3 (4) 174.2 (3) 2.5 (5) -17.9 (6) 163.3 (3) 1.9 (6) -177.9 (3) -0.1 (5) 179.7 (2) 179.6 (4) -1.9 (5)

C3—S1—C4—C11	52.0 (3)	C4—C5—C7—C8	-4.1(5)
C11—C4—C5—C7	-7.0(5)	C6—C5—C7—C8	174.4 (3)
S1—C4—C5—C7	-178.8(3)	C10—C8—C7—O6	-177.1 (4)
C11—C4—C5—C6	174.7 (3)	O5—C8—C7—O6	1.8 (5)
S1—C4—C5—C6	2.9 (5)	C10—C8—C7—C5	6.5 (5)
C4—S1—C3—C2	175.5 (3)	O5—C8—C7—C5	-174.5 (3)
O4—C10—C8—O5	-4.5 (6)		

Hydrogen-bond geometry (Å, °) for CoQ1

D—H···A	D—H	Н…А	D····A	D—H…A
C3—H3A…O3	0.97	2.33	2.974 (4)	123
С3—Н3В⋯О3і	0.97	2.60	3.425 (4)	143
С9—Н9А…О4і	0.96	2.65	3.508 (5)	149
C1—H1A…O5ii	0.96	2.54	3.456 (5)	160

Symmetry codes: (i) x+1, y, z; (ii) -x+3/2, y+1/2, -z+1/2.

Table S2. Crystallographic data for the CoQ1.

CoOl
C ₁₂ H ₁₄ O ₆ S
286.29
273
0.71073
Monoclinic
P 1 2 ₁ /n 1, 4
a = 3.9584(5)
b = 23.942(3)
c = 13.7731(15)
$\alpha, \gamma = 90^{\circ}$
$\beta = 91.887(8)^{\circ}$
1304.6(3)
0.053 x 0.055 x 0.507
1.458
0.268
multi-scan, 0.986 and 0.876
1.70 to 25.00
1.039
-4 <u>≤</u> h <u>≤</u> 4
-28≤k≤28
-16 <u>≤</u> 1 <u>≤</u> 16
18184
2291 [R(int) = 0.0781]
1555 data
R1 = 0.0491
wR2 = 0.1037

R indices (all data)	R1 = 0.0872
	wR2 = 0.1244
Refinement method	Full-matrix least-squares on F ²
Data/restraints/parameters	2291 / 0 / 176
Largest diff. peak and hole (eÅ ⁻³)	0.253 and -0.212

Table S3. Selected bond lengths (Å) for CoQ1

S1-C4	1.761(3)	S1-C3	1.803(3)
O3-C11	1.218(4)	O4-C10	1.365(4)
O4-C12	1.446(4)	01-C2	1.318(4)
O1-C1	1.444(4)	05-C8	1.344(4)
O5-C9	1.413(4)	O6-C7	1.209(4)
O2-C2	1.188(4)	C3-C2	1.485(4)

Table S4. Selected bond angles (°) for CoQ1

C4-S1-C3	100.42(15)	C10-O4-C12	115.5(3)
C2-O1-C1	118.8(3)	C8-O5-C9	122.5(3)
O4-C10-C11	116.9(3)	O5-C8-C7	110.5(3)

Table S5. Selected torsion angles (°) for CoQ1

O3-C11-C4-S1	9.4(4)	C12-O4-C10-C11	-64.0(4)
C3-S1-C4-C5	-136.1(3)	O4-C10-C11-O3	-7.2(5)
C3-S1-C4-C11	52.0(3)	05-C8-C7-06	1.8(5)
S1-C4-C5-C7	-178.8(3)	C9-O5-C8-C7	163.3(3)
S1-C4-C5-C6	2.9(5)	C1-O1-C2-C3	-177.9(3)
C4-S1-C3-C2	175.5(3)	C1-O1-C2-O2	1.9(6)

D-H···A	Donor-H	Acceptor-H	Donor- Acceptor	Angle
СЗ-НЗА-ОЗ	0.97	2.33	2.974(4)	123.0
C3-H3B···O3 ⁱ	0.97	2.60	3.425(4)	143.3
C9-H9A···O4 ⁱ	0.96	2.65	3.508(5)	148.8
C1-H1A O5 ⁱⁱ	0.96	2.54	3.456(5)	160.4

 Table S6. Hydrogen-bond geometry (Å, °) for CoQ1

Symmetry codes: (i) x+1, y, z; (ii) -x+3/2, y+1/2, -z+1/2

ADME data for CoQ3-8

Property/rule	CoQ3	CoQ4	CoQ5	CoQ6	CoQ7	CoQ8
MW	314	300	314	342	384	384
Log P	2.80	2.62	2.31	3.47	3.69	3.62
TPSA Å ²	104.20	104.20	104.20	104.20	104.20	104.20
HBA	6	6	6	6	6	6
HBD	0	0	0	0	0	0
Lipinski	Yes, 0 violation					
Ghose	Yes	Yes	Yes	Yes	Yes	Yes
Veber	Yes	Yes	Yes	Yes	No	No
Egan	Yes	Yes	Yes	Yes	Yes	Yes
Muegge	Yes	Yes	Yes	Yes	Yes	Yes
Leadlikeness	Yes	Yes	Yes	No	No	Yes

Property	CoQ3	CoQ4	CoQ5	CoQ6	CoQ7	CoQ8
BBB permeability	No	No	No	No	No	No
GI absorption	High	High	High	High	High	High
Log S	-2.70	-2.07	-2.32	-2.9	-4.2	-4.2
Solubility	Soluble	Soluble	Soluble	Moderately Soluble	Moderately Soluble	Moderately Soluble
Bioavailability score	0.56	0.56	0.56	0.56	0.56	0.56
CYP1A2, CYP2C9, CYP2D6, CYP3A4	No	No	No	No	No	No