

***In silico* evaluation of the stability and antibacterial activity of some cobalt complexes**

Ana-Cristiane DRAGOMIR,¹ Alina Ramona BUZATU,² Oana-Raluca POP^{1,3}, Mihaiela ANDONI,³ Doru BUZATU,⁴ and Marilena MOTOC²

¹Doctoral School, Department of Biochemistry and Pharmacology, Faculty of Medicine, Victor Babeş University of Medicine and Pharmacy, 2 Eftimie Murgu Square, 300041 Timisoara, Romania

²Discipline of Biochemistry, Department of Biochemistry and Pharmacology, Faculty of Medicine, Victor Babeş University of Medicine and Pharmacy, 2 Eftimie Murgu Square, 300041 Timisoara, Romania

³Faculty of Pharmacy, University of Medicine and Pharmacy "Victor Babeş" Timisoara, Eftimie Murgu Square 2, 300041 Timișoara, Romania

⁴National Institute for Research and Development in Electrochemistry and Condensed Matter, Dr. A. Paunescu Podeanu Street 144, 300569, Timisoara, Romania

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Receptor: *S. aureus* tyrosyl-tRNA (1jjj.pdb)

Table S1. Binding affinity for cobalt complexes (M06L/TZ2P geometries) with *S. aureus* tyrosyl-tRNA (1jjj.pdb) for nine conformations (kcal/mol) (rigid ligands)

	E1	E2	E3	E4	E5	E6	E7	E8	E9	E
1a	-5.3	-5.1	-5.0	-5.0	-4.7	-4.7	-4.6	-4.6	-4.5	-4.83
1b	-6.4	-6.3	-6.0	-5.8	-5.7	-5.6	-5.6	-5.4	-5.3	-5.78
1c	-7.4	-6.9	-6.6	-6.2	-6.2	-6.2	-6.0	-6.0	-6.0	-6.38
2a	-5.5	-5.4	-5.0	-5.0	-4.8	-4.8	-4.7	-4.7	-4.7	-4.96
2b	-6.1	-6.0	-5.6	-5.4	-5.3	-5.3	-5.2	-5.2	-5.2	-5.47
2c	-6.9	-6.7	-6.6	-6.5	-6.2	-6.1	-6.1	-5.9	-5.8	-6.31
Cefazolin	-7.4	-7.4	-7.1	-6.9	-6.9	-6.7	-6.5	-6.5	-6.5	-6.87

Table S2. Binding affinity for cobalt complexes (M06L/TZ2P geometries) with *S. aureus* tyrosyl-tRNA (1jjj.pdb) for nine conformations (kcal/mol) (torsion ligands)

	E1	E2	E3	E4	E5	E6	E7	E8	E9	E
1a	-4.9	-4.8	-4.7	-4.6	-4.6	-4.5	-4.5	-4.4	-4.3	-4.58
1b	-5.7	-5.6	-5.5	-5.4	-5.3	-5.3	-5.1	-5.1	-5.1	-5.34
1c	-6.2	-6.1	-6.1	-5.9	-5.9	-5.8	-5.8	-5.7	-5.6	-5.90
2a	-5.0	-4.9	-4.9	-4.7	-4.6	-4.6	-4.5	-4.5	-4.4	-4.67
2b	-5.7	-5.6	-5.5	-5.4	-5.4	-5.3	-5.1	-5.0	-5.0	-5.33
2c	-6.0	-6.0	-6.0	-6.0	-5.9	-5.8	-5.7	-5.7	-5.6	-5.85
Cefazolin	-6.5	-6.4	-6.3	-6.3	-6.0	-6.0	-5.9	-5.9	-5.8	-6.12

Table S3. Binding affinity for cobalt complexes (B3LYP/LanL2DZ geometries) with *S. aureus* tyrosyl-tRNA (1jjj.pdb) for nine conformations (kcal/mol) (rigid ligands)

	E1	E2	E3	E4	E5	E6	E7	E8	E9	E
1a	-5.5	-5.4	-5.1	-4.9	-4.9	-4.7	-4.6	-4.5	-4.5	-4.90
1b	-6.1	-6.0	-5.9	-5.9	-5.7	-5.7	-5.6	-5.5	-5.5	-5.76
1c	-7.0	-6.4	-6.4	-6.1	-6.0	-6.0	-5.9	-5.8	-5.8	-6.15
2a	-5.6	-5.2	-5.0	-5.0	-4.9	-4.7	-4.7	-4.6	-4.5	-4.91

¹ Corresponding author. E-mail address: pop.raluca@umft.ro (Oana-Raluca Pop)

	E1	E2	E3	E4	E5	E6	E7	E8	E9	E
2b	-6.1	-5.9	-5.9	-5.9	-5.7	-5.5	-5.5	-5.4	-5.4	-5.70
2c	-7.0	-6.5	-6.4	-6.4	-6.1	-6.0	-5.8	-5.7	-5.7	-6.17
Cefazolin	-7.4	-7.4	-7.1	-6.9	-6.9	-6.7	-6.5	-6.5	-6.5	-6.87

Table S4. Binding affinity for cobalt complexes (B3LYP/LanL2DZ geometries) with *S. aureus* tyrosyl-tRNA (1jjj.pdb) for nine conformations (kcal/mol) (torsion ligands)

	E1	E2	E3	E4	E5	E6	E7	E8	E9	E
1a	-4.8	-4.7	-4.6	-4.6	-4.6	-4.5	-4.5	-4.2	-4.2	-4.52
1b	-5.3	-5.2	-5.2	-5.2	-5.1	-5.0	-4.9	-4.9	-4.9	-5.08
1c	-5.9	-5.8	-5.8	-5.7	-5.5	-5.4	-5.4	-5.4	-5.4	-5.59
2a	-4.9	-4.8	-4.7	-4.7	-4.6	-4.6	-4.6	-4.4	-4.4	-4.63
2b	-5.6	-5.3	-5.2	-5.2	-5.2	-5.2	-5.0	-5.0	-5.0	-5.19
2c	-6.1	-6.0	-5.9	-5.7	-5.6	-5.6	-5.6	-5.6	-5.5	-5.73
Cefazolin	-6.5	-6.4	-6.3	-6.3	-6.0	-6.0	-5.9	-5.9	-5.8	-6.12

Receptor: *E. coli* DNA polymerase II (1q8i.pdb)

Table S5. Binding affinity for cobalt complexes (M06L/TZ2P geometries) with *E. coli* DNA polymerase II for nine conformations (kcal/mol) (rigid ligands)

	E1	E2	E3	E4	E5	E6	E7	E8	E9	E
1a	-5.5	-5.5	-5.5	-5.3	-5.3	-5.2	-5.2	-5.1	-5.1	-5.30
1b	-6.6	-6.5	-6.4	-6.0	-5.9	-5.7	-5.7	-5.7	-5.7	-6.02
1c	-7.0	-6.8	-6.5	-6.5	-6.5	-6.4	-6.1	-6.1	-6.0	-6.43
2a	-5.5	-5.5	-5.5	-5.4	-5.4	-5.4	-5.3	-5.3	-5.2	-5.38
2b	-6.5	-6.5	-6.2	-6.2	-6.2	-6.1	-6.0	-5.9	-5.8	-6.15
2c	-7.1	-7.0	-6.9	-6.9	-6.7	-6.4	-6.3	-6.2	-6.2	-6.63
Cefazolin	-8.1	-7.5	-7.4	-7.3	-7.3	-7.1	-6.9	-6.8	-6.7	-7.23

Table S6. Binding affinity for cobalt complexes (M06L/TZ2P geometries) with *E. coli* DNA polymerase II for nine conformations (kcal/mol) (torsion ligands)

	E1	E2	E3	E4	E5	E6	E7	E8	E9	E
1a	-5.4	-5.1	-5.1	-5.1	-5.1	-5.1	-5.0	-4.9	-4.8	-5.06
1b	-5.6	-5.6	-5.5	-5.4	-5.4	-5.4	-5.3	-5.3	-5.2	-5.41
1c	-6.1	-6.1	-6.1	-6.0	-5.9	-5.8	-5.8	-5.8	-5.7	-5.92
2a	-5.1	-5.0	-5.0	-5.0	-4.9	-4.9	-4.8	-4.7	-4.7	-4.90
2b	-5.6	-5.6	-5.5	-5.3	-5.3	-5.3	-5.3	-5.3	-5.1	-5.36
2c	-6.2	-6.2	-6.1	-5.9	-5.8	-5.8	-5.7	-5.7	-5.5	-5.87
Cefazolin	-7.1	-6.5	-6.5	-6.4	-6.3	-6.3	-6.3	-6.3	-6.2	-6.43

Table S7. Binding affinity for cobalt complexes (B3LYP/LanL2DZ geometries) with *E. coli* DNA polymerase II for nine conformations (kcal/mol) (rigid ligands)

	E1	E2	E3	E4	E5	E6	E7	E8	E9	E
1a	-5.6	-5.4	-5.3	-5.3	-5.3	-5.2	-5.1	-5.1	-4.9	-5.24
1b	-6.5	-6.2	-6.2	-6.2	-6.1	-6.1	-6.0	-5.9	-5.8	-6.11
1c	-7.1	-6.8	-6.7	-6.7	-6.6	-6.5	-6.4	-6.3	-6.3	-6.60
2a	-5.6	-5.3	-5.1	-5.1	-5.1	-5.0	-5.0	-5.0	-4.8	-5.11
2b	-6.4	-6.3	-6.3	-6.2	-6.2	-6.1	-6.1	-5.8	-5.7	-6.12
2c	-7.0	-6.9	-6.8	-6.6	-6.6	-6.5	-6.3	-6.2	-6.2	-6.56
Cefazolin	-8.1	-7.5	-7.4	-7.3	-7.3	-7.1	-6.9	-6.8	-6.7	-7.23

Table S8. Binding affinity for cobalt complexes (B3LYP/LanL2DZ geometries) with *E. coli* DNA polymerase II for nine conformations (kcal/mol) (torsion ligands)

	E1	E2	E3	E4	E5	E6	E7	E8	E9	E
1a	-5.4	-5.2	-5.0	-5.0	-4.7	-4.7	-4.6	-4.6	-4.5	-4.85
1b	-5.8	-5.7	-5.7	-5.6	-5.6	-5.6	-5.5	-5.5	-5.4	-5.60
1c	-6.1	-6.0	-6.0	-5.9	-5.9	-5.8	-5.8	-5.7	-5.7	-5.88
2a	-3.8	-3.8	-3.6	-3.6	-3.5	-3.4	-3.3	-3.2	-3.2	-3.49
2b	-6.2	-6.0	-5.7	-5.6	-5.3	-5.3	-5.2	-5.2	-5.2	-5.52
2c	-6.7	-6.2	-5.9	-5.9	-5.9	-5.8	-5.8	-5.7	-5.7	-5.96
Cefazolin	-7.1	-6.5	-6.5	-6.4	-6.3	-6.3	-6.3	-6.3	-6.2	-6.43

Receptor: Methicillin-resistant *S. aureus*, a panthetonate synthetase (2x3f.pdb)

Table S9. Binding affinity for cobalt complexes (M06L/TZ2P geometries) with Methicillin-resistant *S. aureus*, a panthetonate synthetase (2x3f.pdb) for nine conformations (kcal/mol) (rigid ligands)

	E1	E2	E3	E4	E5	E6	E7	E8	E9	E
1a	-5.4	-5.3	-5.0	-5.0	-5.0	-4.8	-4.7	-4.6	-4.5	-4.92
1b	-5.7	-5.6	-5.5	-5.5	-5.5	-5.4	-5.4	-5.4	-5.3	-5.47
1c	-6.5	-6.4	-6.3	-6.3	-6.2	-6.1	-5.9	-5.9	-5.9	-6.16
2a	-5.3	-5.2	-5.0	-4.9	-4.8	-4.7	-4.6	-4.5	-4.5	-4.83
2b	-5.9	-5.9	-5.8	-5.8	-5.5	-5.4	-5.4	-5.4	-5.4	-5.38
2c	-6.4	-6.2	-6.2	-6.2	-6.1	-6.1	-6.1	-6.0	-5.9	-6.13
Cefazolin	-7.3	-7.0	-7.0	-7.0	-6.9	-6.9	-6.5	-6.5	-6.4	-6.83

Table S10. Binding affinity for cobalt complexes (M06L/TZ2P geometries) with Methicillin-resistant *S. aureus*, a panthetonate synthetase (2x3f.pdb) for nine conformations (kcal/mol) (torsion ligands)

	E1	E2	E3	E4	E5	E6	E7	E8	E9	E
1a	-4.7	-4.7	-4.6	-4.4	-4.3	-4.3	-4.2	-4.2	-4.1	-4.45
1b	-5.4	-5.4	-5.3	-5.3	-5.2	-5.1	-5.1	-5.0	-5.0	-5.20
1c	-6.1	-6.1	-5.9	-5.8	-5.8	-5.7	-5.7	-5.6	-5.6	-5.83
2a	-4.7	-4.7	-4.6	-4.5	-4.4	-4.4	-4.3	-4.3	-4.3	-4.46
2b	-5.4	-5.2	-5.1	-5.1	-5.1	-4.9	-4.9	-4.9	-4.8	-5.04
2c	-5.9	-5.7	-5.6	-5.5	-5.5	-5.4	-5.4	-5.4	-5.3	-5.52
Cefazolin	-6.0	-5.7	-5.6	-5.5	-5.5	-5.4	-5.4	-5.4	-5.4	-5.54

Table S11. Binding affinity for cobalt complexes (B3LYP/LanL2DZ geometries) with Methicillin-resistant *S. aureus*, a panthetonate synthetase (2x3f.pdb) for nine conformations (kcal/mol) (rigid ligands)

	E1	E2	E3	E4	E5	E6	E7	E8	E9	E
1a	-5.1	-5.0	-4.9	-4.8	-4.8	-4.7	-4.6	-4.5	-4.5	-4.76
1b	-6.1	-5.8	-5.6	-5.5	-5.5	-5.4	-5.4	-5.4	-5.4	-5.56
1c	-6.7	-6.5	-6.4	-6.3	-6.2	-6.2	-6.2	-6.1	-6.1	-6.30
2a	-4.9	-4.8	-4.8	-4.7	-4.6	-4.5	-4.3	-4.3	-4.3	-4.57
2b	-6.0	-5.7	-5.6	-5.6	-5.5	-5.5	-5.5	-5.4	-5.3	-5.56
2c	-6.5	-6.5	-6.4	-6.3	-6.2	-5.8	-5.7	-5.6	-5.6	-6.06
Cefazolin	-7.3	-7.0	-7.0	-7.0	-6.9	-6.9	-6.5	-6.5	-6.4	-6.83

Table S12. Binding affinity for cobalt complexes (B3LYP/LanL2DZ geometries) with Methicillin-resistant *S. aureus*, a panthetonate synthetase (2x3f.pdb) for nine conformations (kcal/mol) (torsion ligands)

	E1	E2	E3	E4	E5	E6	E7	E8	E9	E
1a	-4.8	-4.7	-4.6	-4.5	-4.5	-4.3	-4.0	-4.0	-4.0	-4.38

	E1	E2	E3	E4	E5	E6	E7	E8	E9	E
1b	-5.6	-5.6	-5.5	-5.2	-5.1	-5.0	-4.8	-4.8	-4.8	-5.16
1c	-6.5	-6.2	-5.9	-5.7	-5.6	-5.6	-5.6	-5.6	-5.6	-5.81
2a	-4.7	-4.7	-4.4	-4.4	-4.4	-4.3	-4.1	-4.1	-4.1	-4.36
2b	-5.5	-5.3	-5.2	-5.1	-5.0	-4.9	-4.8	-4.8	-4.7	-5.03
2c	-6.6	-6.3	-6.1	-6.0	-5.9	-5.5	-5.4	-5.4	-5.3	-5.83
Cefazolin	-6.0	-5.7	-5.6	-5.5	-5.5	-5.4	-5.4	-5.4	-5.4	-5.54

The interactions ligand-receptor, for the best average binding affinities, are presented in figures below.

Receptor: *S. aureus* tyrosyl-tRNA (1jjj.pdb)

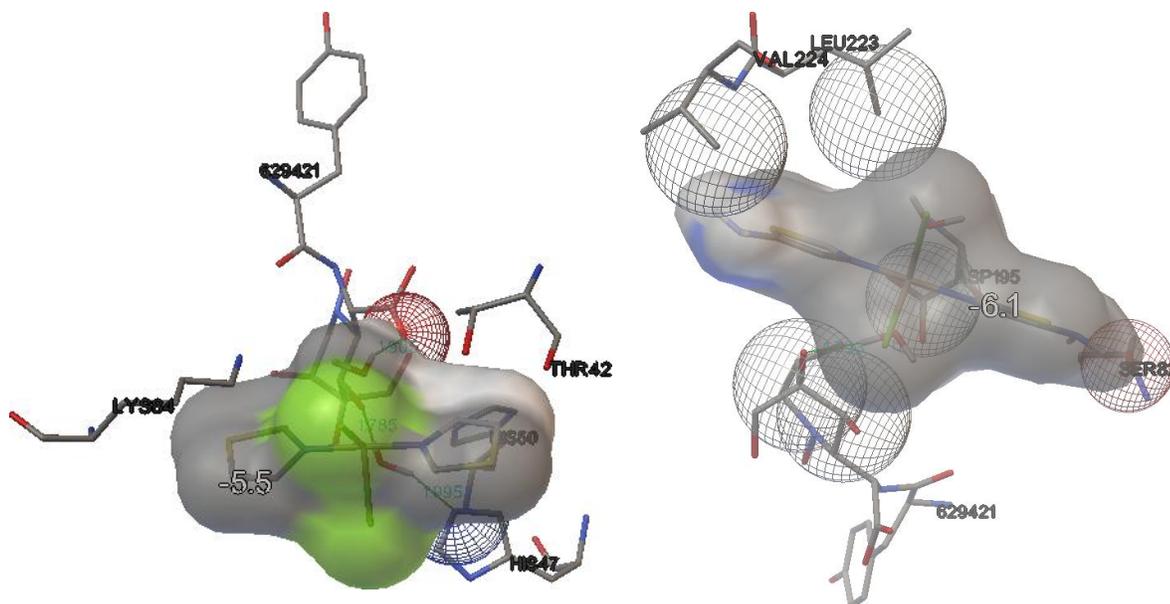


Figure S1. Ligand **1a** (B3LYP/LanL2DZ) – receptor interactions (left) and ligand **1b** (M06L/TZ2P) – receptor interactions (right)

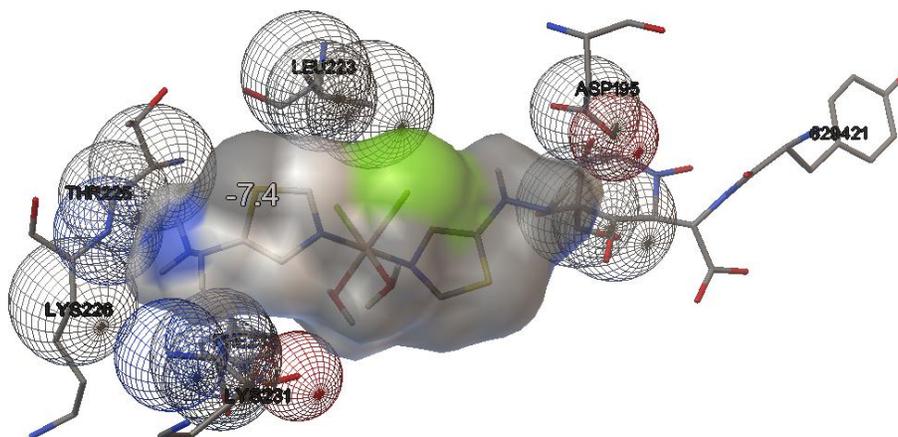


Figure S2. Ligand **1c** (M06L/TZ2P) – receptor interactions

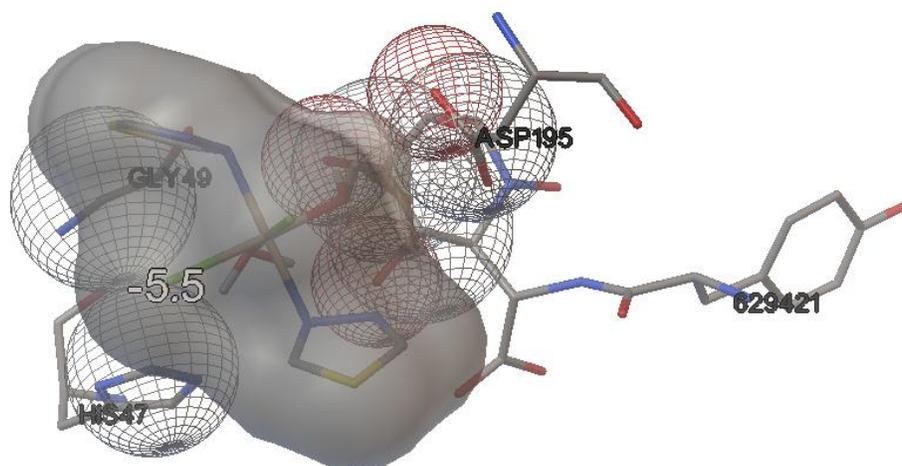


Figure S3. Ligand 2a (M06L/TZ2P) – receptor interactions

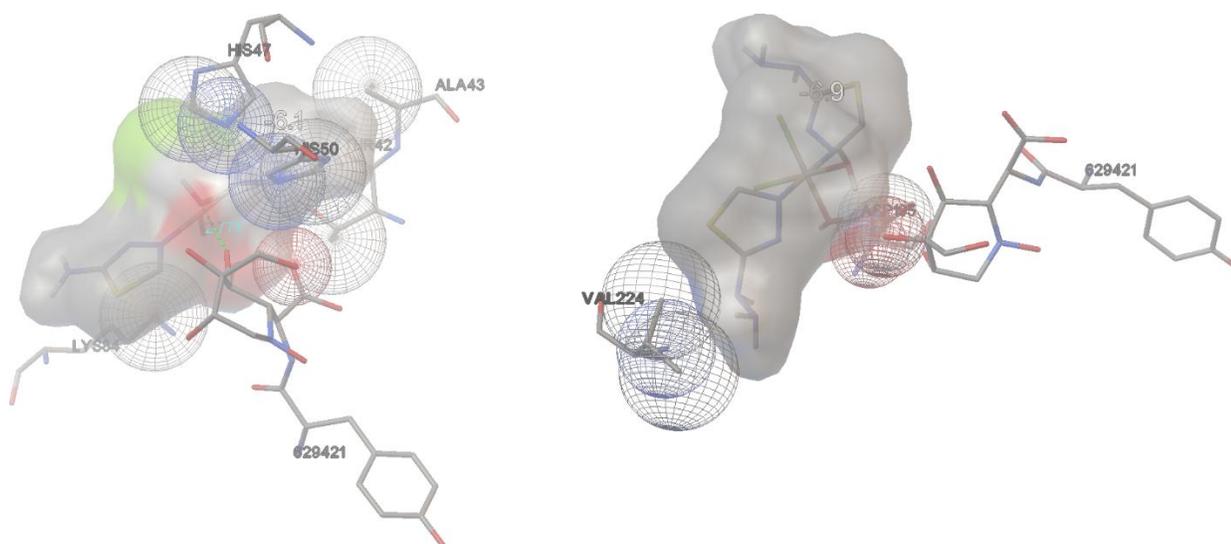


Figure S4. Ligand 2b (B3LYP/LanL2DZ) – receptor interactions (left) and ligand 2c (M06L/TZ2P) – receptor interactions (right)

Receptor: *E. coli* DNA polymerase II (1q8i.pdb)

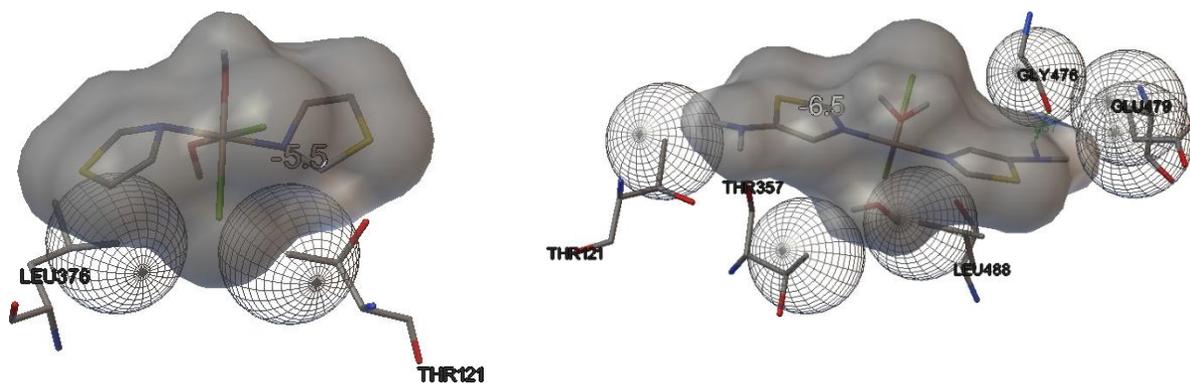


Figure S5. Ligand 1a (M06L/TZ2P) – receptor interactions (left) and ligand 1b (B3LYP/LanL2DZ) – receptor interactions (right)

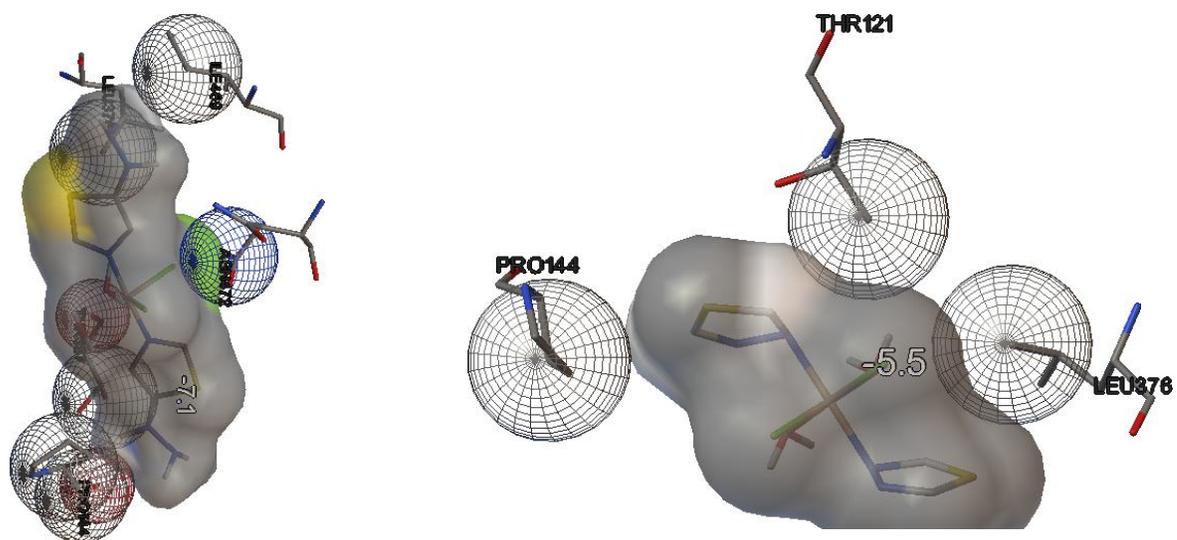


Figure S6. Ligand 1c (B3LYP/LanL2DZ) – receptor interactions (left) and ligand 2a (M06L/TZ2P) – receptor interactions (right)

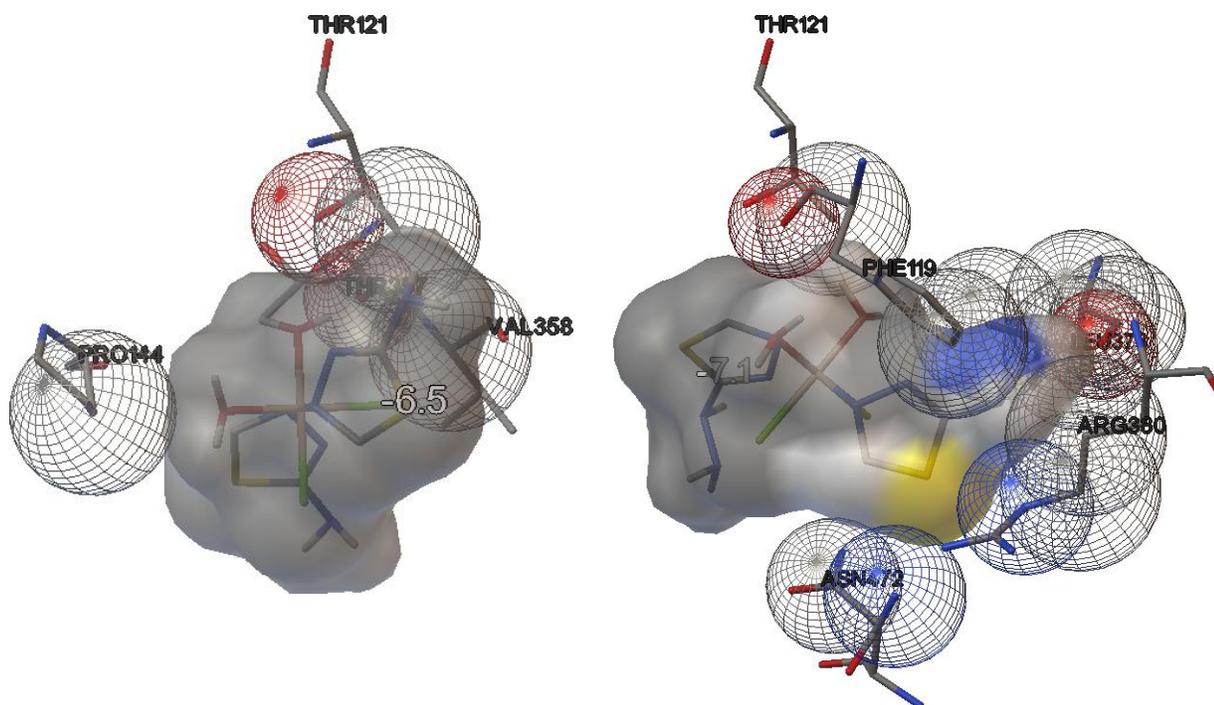


Figure S7. Ligand 2b (M06L/TZ2P) – receptor interactions (left) and ligand 2c (M06L/TZ2P) – receptor interactions (right)

Receptor: Methicillin-resistant *S. aureus*, a panthetonate synthetase (2x3f.pdb)

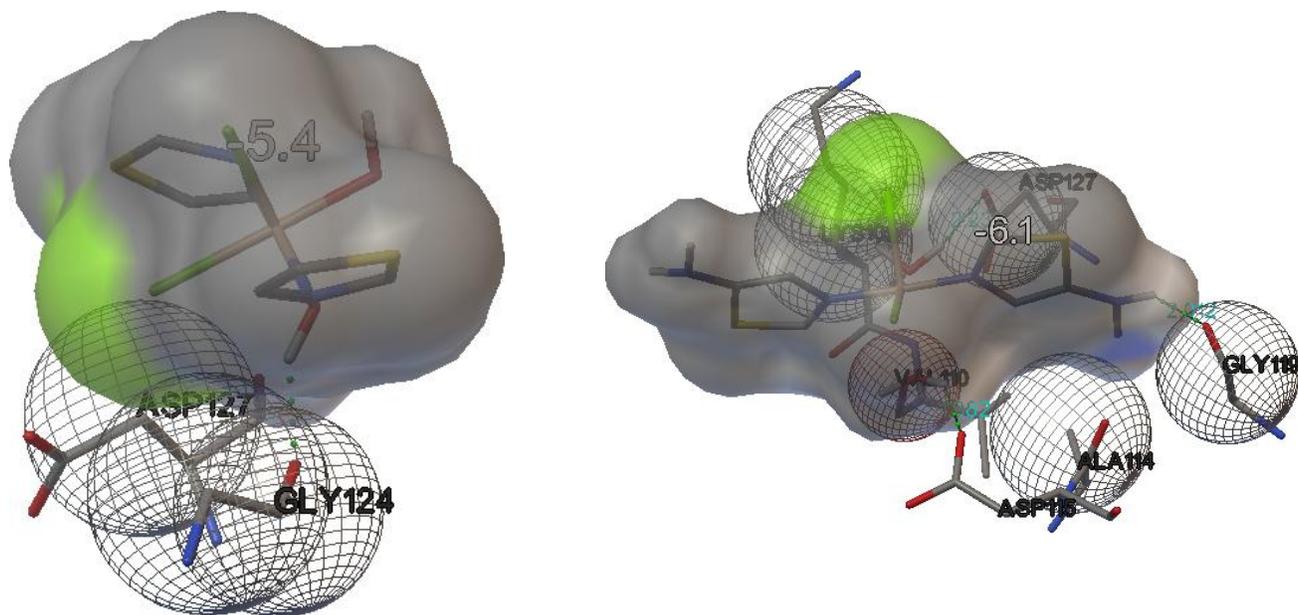


Figure S8. Ligand 1a (M06L/TZ2P) – receptor interactions (left) and ligand 1b (B3LYP/LanL2DZ) – receptor interactions (right)

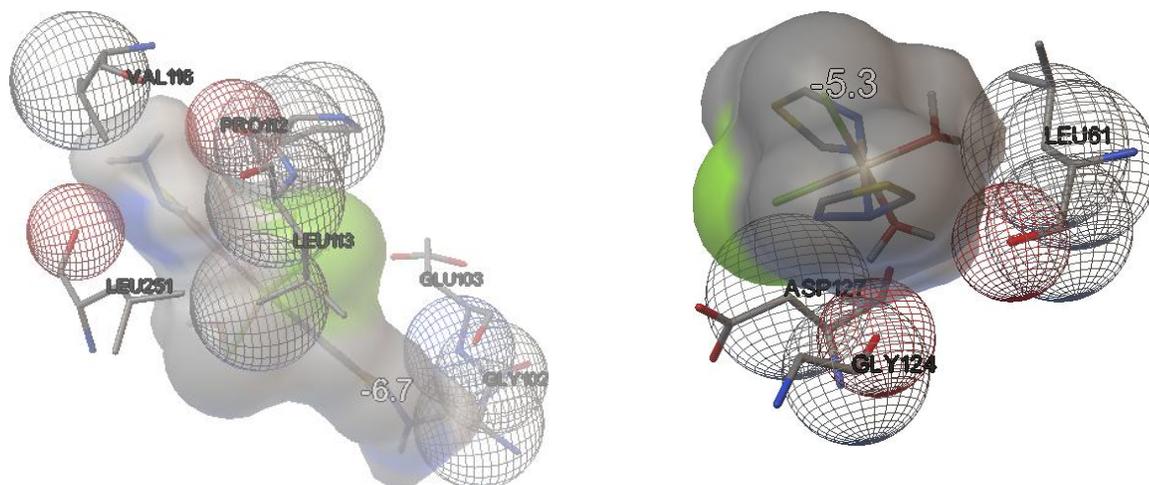


Figure S9. Ligand 1c (B3LYP/LanL2DZ) – receptor interactions (left) and ligand 2a (M06L/TZ2P) – receptor interactions (right)

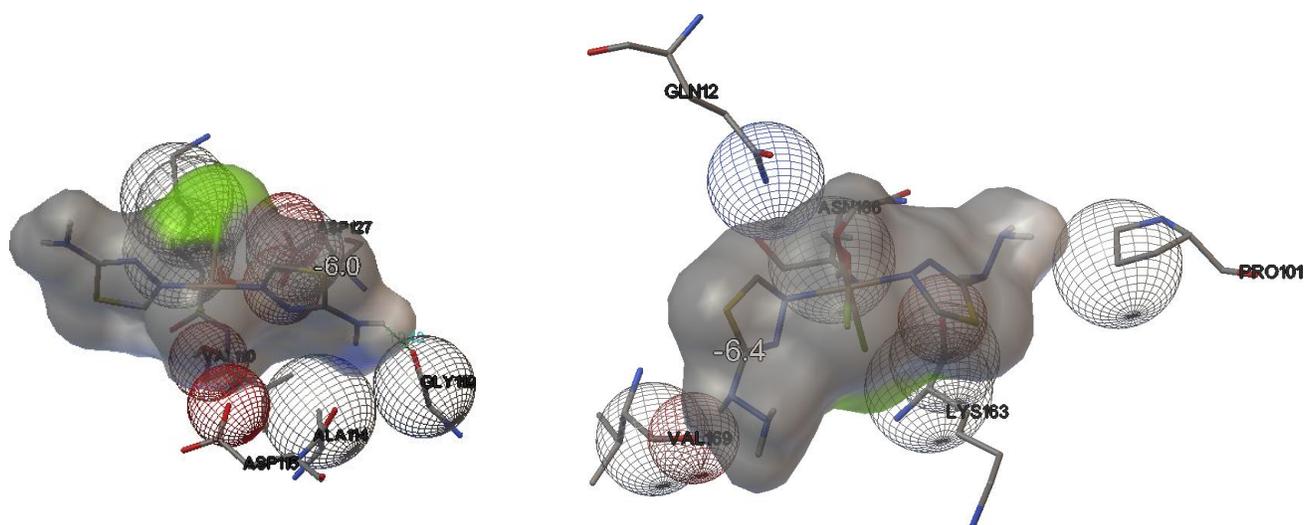


Figure S10. Ligand **2b** (B3LYP/LanL2DZ) – receptor interactions (left) and ligand **2c** (M06L/TZ2P) – receptor interactions (right)

Cefazolin interactions

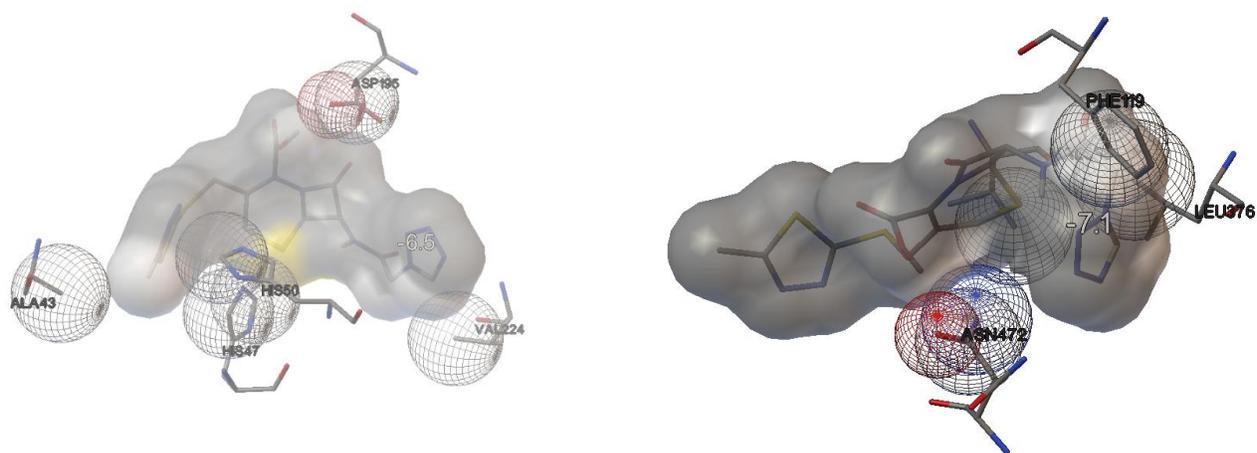


Figure S11. Cefazolin interactions (flexible docking) with *S. aureus* tyrosyl-tRNA (1jjj.pdb) (left) and *E. coli* DNA polymerase II (1q8i.pdb) (right)

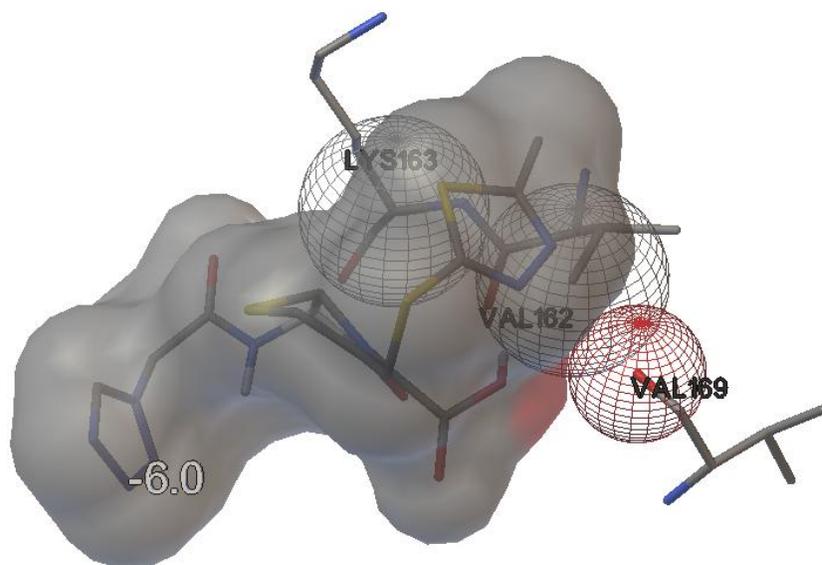


Figure S12. Cefazolin interactions (flexible docking) with **Methicillin-resistant *S. aureus***, a panthetonate synthetase (2x3f.pdb)