# **Supplementary Material**

# Convergent synthesis and biological evaluation of 3-[2-(benzylidenehydrazinyl)thiazol-4-yl]-4-hydroxycoumarins

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## 1. Bioassay and *in silico* docking protocols and data.

#### 1.1. Antimalarial and anti-trypanosomal assays

To assess antimalarial activity, percentage viability of *Plasmodium falciparum* (3D7 strain) parasites incubated for 48 hours with 20  $\mu$ M of the test compounds was determined by detecting plasmodium lactate dehydrogenase (pLDH) activity as described previously by Lunga *et al.*(*ChemMedChem* **2018**, *13*, 1352-1362). For anti-trypanosomal and cytotoxicity evaluation, percentage viability of *Trypanosoma brucei brucei* (427 strain) parasites or HeLa cells incubated with 20  $\mu$ M of the test compounds for 48 hours was determined using resazurin, as previously described by Veale and Hoppe (*Med. Chem. Commun.* **2018**, *9*, 2037).

| Table 1. Anti-bacterial and cytoto> | xicity data for compound | ls <b>14a,c-e,g</b> at a concentration of |
|-------------------------------------|--------------------------|---|
| 50 mg/mL                            |                          |   |

| Compd, | E. coli<br>Activity | %<br>growth | S. aureus<br>Activity | %<br>growth<br>ª | Cytotoxicity<br>Status |
|--------|---------------------|-------------|-----------------------|------------------|------------------------|
| 14a    | not active          | 114         | active                | 37-47            | not toxic              |
| 14c    | not active          | 97          | active                | 46               | toxic                  |
| 14d    | not active          | 120         | active                | 31               | not toxic              |
| 14e    | not active          | 106         | active                | 43               | not toxic              |
| 14g    | not active          | 109         | active                | 50               | not toxic              |

<sup>a</sup> As % metabolic activity

#### 2.2. In silico docking protocols and data.

*In silico* docking was performed using Schrödinger software (Maestro 11.4, Schrödinger 2017-4). The reported ligands were built in Maestro and prepared for docking using the LigPrep module (Schrodinger, LLC, NY, USA, 2009). The OPLS\_2005 force field was selected in LigPrep for the energy minimization of the ligands to generate low-energy ligand isomers. The protein structures were obtained from Protein Data Bank (<u>http://www.rscb.org</u>) and prepared for docking using the protein preparation wizard as implemented in Maestro. The receptor grid generations were achieved using "Glide Grid Generation" module and the active site was selected with the radius of 20 Å around the crystal ligand. Glide module (Schrodinger, LLC, NY, USA, 2009) was used for docking protocol using Standard precision (SP) approach. The results obtained were visualized using Maestro interface (Schrödinger Suite, LLC, NY).

**Table 2.** *In silico* binding affinities in Kcal/mol for the ligands **14a-g** in selected enzyme receptor sites.



| Ligand | Ar                                    | HIV-1 IN<br>5FRN | HIV-1 PR<br>1YT9 | HIV-1 PR<br>1ZP8 | <i>Рf</i><br>1Т2С | <i>Pf</i><br>1V00 | T.b.<br>brucei<br>4FWN | <i>M.tb</i><br>4BFW |
|--------|---------------------------------------|------------------|------------------|------------------|-------------------|-------------------|------------------------|---------------------|
| 14a    | но                                    | -5.981           | -6.933           | -5.935           | -7.961            | -3.219            | -4.668                 | -7.479              |
| 14b    | но он                                 | -5.666           | -7,257           | -6.306           | -8.294            | -4.460            | -5.337                 | -5.899              |
| 14c    |                                       | -7.558           | -7,341           | -6.169           | -8.849            | -3.750            | -4.906                 | -5.714              |
| 14d    |                                       | -5.531           | -7.127           | -5.666           | -7.823            | -3.439            | -3.240                 | -4.774              |
| 14e    | N N N N N N N N N N N N N N N N N N N | -6.845           | -7,191           | -5.985           | -8.118            | -4.075            | -4.325                 | -6.197              |
| 14f    |                                       | -6.138           | -6.960           | -5.183           | -6.701            | -3.554            | -4.521                 | -5.841              |
| 14g    |                                       | -6.085           | -6,092           | -5.439           | -5.226            | -3.296            | -3.630                 | -5.913              |

4FBW\_14a

4FBW\_14a



Docking and receptor-site interactions of ligand **14a** in the *M.tb* enzyme 4FBW.

#### 4FWN\_14b

4FWN\_14b



Docking and receptor-site interactions of ligand 14b in the T.b.brucei enzyme 4FWN.

### 2. NMR Spectra.



150 MHz <sup>13</sup>C NMR spectrum of compound **13g** in DMSO-*d*<sub>6</sub>











Partial HSQC NMR spectrum of compound 14d in DMSO- $d_6$ .









150 MHz  $^{13}$ C NMR spectrum of compound **14g** in DMSO- $d_{6.}$