

Supporting Information

Benzoxaboroles as efficient inhibitors of the β -carbonic anhydrases from pathogenic fungi: activity and modelling study.

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CA inhibition assay

An applied photophysics stopped-flow instrument has been used for assaying the CA catalysed CO₂ hydration activity.¹ Bromothymol blue (at a concentration of 0.2 mM) has been used as indicator, working at the absorbance maximum of 557 nm, with 10–20 mM TRIS (pH 8.3) as buffer, and 20 mM NaBF₄ for maintaining constant the ionic strength, following the initial rates of the CA-catalysed CO₂ hydration reaction for a period of 10–100 s. The CO₂ concentrations ranged from 1.7 to 17 mM for the determination of the kinetic parameters and inhibition constants. For each inhibitor at least six traces of the initial 5–10% of the reaction have been used for determining the initial velocity. The uncatalysed rates were determined in the same manner and subtracted from the total observed rates. Stock solutions of inhibitor (10 mM) were prepared in distilled-deionized water and dilutions up to 0.01 μ M were done thereafter with the assay buffer. Inhibitor and enzyme solutions were preincubated together for 15 min at room temperature prior to assay, in order to allow for the formation of the E–I complex. The inhibition constants were obtained by non-linear least-squares methods using the Cheng–Prusoff equation whereas the kinetic parameters for the uninhibited enzymes from Lineweaver–Burk plots, as reported earlier,^{2,3} and represent the mean from at least three different determinations. All CAs were recombinant proteins obtained as reported earlier by these groups.^{4,5,6,8}

Molecular modelling

The dimeric form of the homology built model of MgCA⁷ and CAN2 (PDB 2W3N)⁸ crystal structures were prepared for docking using the Schrodinger preparation wizard protocol. It consists of preliminary pre-treatment by adjusting the bond orders, metal ions and cofactors, evaluating the ionization states, adding hydrogen atoms, refining loop region and energy minimization.^{9a-d}

3D ligand structures were prepared by Maestro MM^{9a} and their atomic electrostatic charges were computed with Jaguar MM^{9e} fitting them to an electrostatic potential calculated at the B3LYP/6-31G*+ level of theory. ESP atomic charges were used in docking simulations.

Grids for docking analysis were centered in the centroid of the catalytic cavity residues. Docking studies were carried out with the program Glide.^{9f} The standard precision (SP) mode of the GlideScore function was applied to evaluate the predicted binding poses.

The pictures were generated with Maestro.

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