

Screening of heteroaromatic scaffolds against Cystathionine beta-synthase enables identification of substituted pyrazolo[3,4-c]pyridines as potent and selective orthosteric inhibitors

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SUPPLEMENTARY MATERIAL

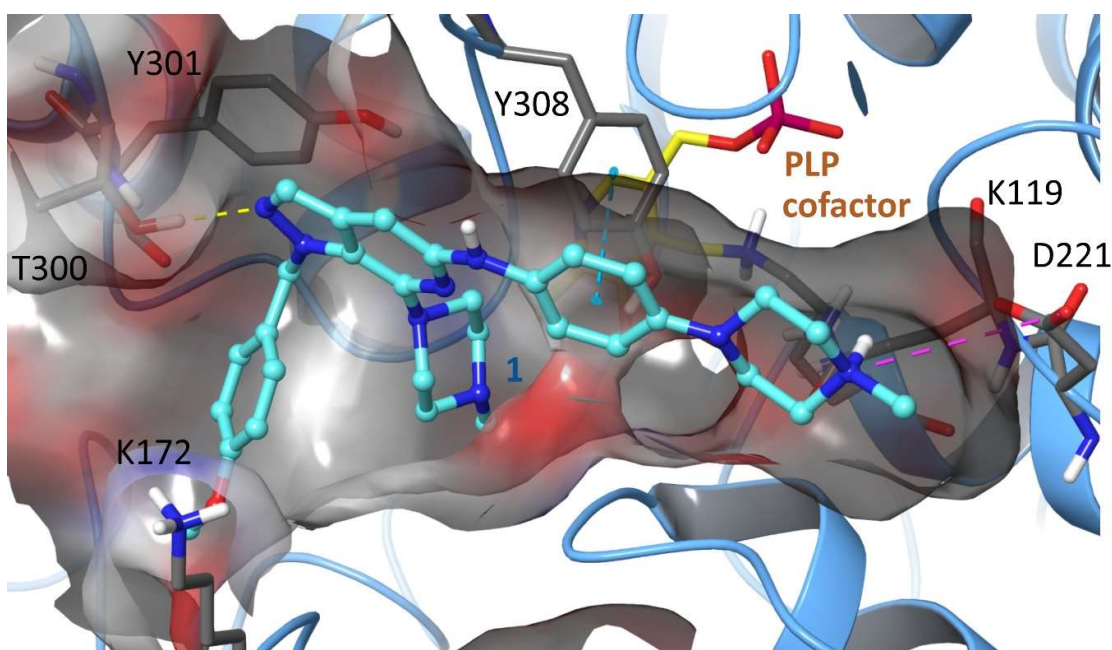


Figure S1. The dominant binding geometry of the protonated **1** inside the CBS active site as determined by the induced-fit algorithm for docking calculations. The inhibitor is mainly anchored to the enzyme by a hydrogen bond depicted as a yellow dashed line between the side chain of Thr300 and the inhibitor pyrazole ring, whereas a salt bridge (magenta dashed line) is formed between the protonated N4 of piperazine and the side chain of Asp221. A stacking interaction between the phenylamino ring of **1** and Tyr308 (shown as blue dashed line) further stabilizes the complex. The protein is depicted as a blue ribbon and molecular surface colored according to the electrostatic potential (red: negative; blue: positive).