

Supplementary Information

Evaluation of Porcine and *Aspergillus oryzae* α -Amylases as Possible Model for the Human Enzyme

Mauro Marengo ¹, Davide Pezzilli ¹, Eleonora Gianquinto ¹, Alex Fissore¹, Simonetta Oliaro-Bosso¹, Barbara Sgorbini ¹, Francesca Spyarakis ^{1,*} and Salvatore Adinolfi ^{1,*}

Department of Drug Science and Technology, University of Turin, via Giuria 9, 10125 Turin, Italy; mauro.marengo@unito.it (M.M.); davide.pezzilli@edu.unito.it (D.P.); eleonora.gianquinto@unito.it (E.G.); alex.fissore@edu.unito.it (A.F.); simona.oliaro@unito.it (S.O.); barbara.sgorbini@unito.it (B.S.); francesca.spyarakis@unito.it (F.S.); salvatore.adinolfi@unito.it (S.A.).

* Correspondence: francesca.spyarakis@unito.it (F.S.); salvatore.adinolfi@unito.it (S.A.); Tel.: +39-011-6707185 (F.S.); +39-011-6706862.

Supplementary Information Content

Figure S1: Sequence alignment of HAS, PPA and AOA.

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Figure S1. Sequence alignment of HAS, PPA and AOA. The same color identifies all conserved aminoacidic residues. The calcium binding site is highlighted in dark blue, the chloride binding site in dark red, and the catalytic triad in dark green.

