

VOLUME 292 (2017) PAGES 8412–8423

DOI 10.1074/jbc.A117.779256

The crystal structure of a multidomain protease inhibitor (HAI-1) reveals the mechanism of its auto-inhibition.

Min Liu, Cai Yuan, Jan K. Jensen, Baoyu Zhao, Yunbin Jiang, Longguang Jiang, and Mindong Huang

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The x axis unit labels in Fig. 6A were incorrect. This error has now been corrected and does not affect the results or conclusions of this work.

