Electronic supplementary information (ESI)

## Factors influencing the catalytic activity of metal-dependent histidine-rich peptides: sequence, conformation, stereochemistry, self-assembly or their interplay?

Patrizia Janković, <sup>a</sup> Marko Babić, <sup>a</sup> Marko Perčić, <sup>b,c,d</sup>, Ana S. Pina, <sup>e</sup> and Daniela Kalafatovic, <sup>\*a,d</sup>

<sup>a</sup> University of Rijeka, Department of Biotechnology, Radmile Matejčić 2, 51000 Rijeka, Croatia.

<sup>d</sup> University of Rijeka, Center for Artificial Intelligence and Cybersecurity, 51000 Rijeka, Croatia. <sup>e</sup> Instituto de Tecnologia Química e Biológica António Xavier (ITQB), Universidade Nova de Lisboa, Av. da República, 2780-157, Oeiras, Portugal.

\* Correspondence: daniela.kalafatovic@uniri.hr

<sup>&</sup>lt;sup>b</sup> University of Rijeka, Faculty of Engineering, Vukovarska 58, 51000 Rijeka, Croatia.

 $<sup>^{</sup>c}$ University of Rijeka, Centre for Micro- and Nanosciences and Technologies, 51000 Rijeka, Croatia.



Figure S1: a) LC chromatogram at 220 nm (purity of 96.79%), b) chemical structure and (c) the MS trace for Ac-IHIHINI-Am (peptide A) (m/z 900.5) .



Figure S2: a) LC chromatogram at 220 nm (purity of 98.76%), b) chemical structure and (c) the MS trace for Ac-IHINIHI-Am (peptide B) (m/z 900.5) .



Figure S3: a) LC chromatogram at 220 nm (purity of 98.67%), b) chemical structure and (c) the MS trace for [IHIHINI]-Am (cy-HH) (m/z 969.5) .



Figure S4: a) LC chromatogram at 220 nm (purity of 94.59%), b) chemical structure and (c) the MS trace for [IhIhINI]-Am (cy-hh) (m/z 969.5) .



Figure S5: **a**) Fluorescence intensities of ThT at different concentrations of cy-hh, **b**) CAC in MiliQ water, plotted as a function of ThT fluorescence emission at 480 nm.



Figure S6: Dependence of p-NPA hydrolysis rate on the concentration of the peptide B.



Figure S7: (a) Kinetic plot and (b) Michaelis-Menten graph for peptide A in 25 mM TRIS, 1 mM ZnCl<sub>2</sub> at pH 8 was employed for the determination of a  $k_{cat}/K_M$  value of 83.21 ± 26.99  $M^{-1}$   $s^{-1}$ .



Figure S8: (a) Kinetic plot and (b) Michaelis-Menten graph for Peptide A in 25 mM TRIS Buffer at pH 7.4 without ZnCl<sub>2</sub>, demonstrating minimal catalytic activity resulting in the inability to calculate kinetic parameters.



Figure S9: Kinetic plots of a) p-NPA, b) p-NPB, and c) p-NPO assayed for Peptide A at pH 7.4 in 25 mM TRIS Buffer with 1 mM ZnCl<sub>2</sub>.



Figure S10: Cluster analysis of (**a**) Ac-IHIHINI-Am; (**b**) Ac-IHINIHI-Am; (**c**) [IHIHINIE]-Am; (**d**) [IhIhINIE]-Am. Clusters 1 to 10 are overlapped, the most dominant cluster is opaque, the remaining 9 are transparent.



Figure S11: RMSD plots for (a) Ac-IHIHINI-Am; (b) Ac-IHINIHI-Am; (c) [IHIHINIE]-Am; (d) [IhIhINIE]-Am.



Figure S12: N- $\delta$ -His to N- $\delta$ -His average distance plots (reported in Table 3) for (a) Ac-IHIHINI-Am; (b) Ac-IHINIHI-Am; (c) [IHIHINIE]-Am; (d) [IHIHINIE]-Am.



Figure S13: MD simulations of linear peptides (a) Ac-IHIHINI-Am; (b) Ac-IHINIHI-Am. The images show the initial Monte-Carlo placement of 24 peptides in solution and their aggregation into  $\beta$ -sheet structures after 500 ns.



Figure S14: SASA analysis of (a) Ac-IHIHINI-Am; (b) Ac-IHINIHI-Am simulations in water and 0.08 M Tris buffer