**(Supporting Information)**

**RNA-binding peptide and edosomal escape-assisting peptide (L2) improved siRNA delivery by the** [**hexahistidine-metal assembly**](https://www.x-mol.com/paperRedirect/1456724358190759936)

Yan Zhanga,c†, Li-Miao Qina,c†, Meng-fan Fenga,c , Xianghui Yub, Yuqing Wua,c\*

\*Corresponding author: Prof. Yuqing Wu, E-mail: [yqwu@jlu.edu.cn](mailto:yqwu@jlu.edu.cn).



Fig. S1 The verification of the stability of siBCL-2+L2NTD digested by 2% agarose electrophoresis. Lane 1 is naked siBCL-2 (0.5 nmol/mL) without RNase A; Lines 2-4 for free siBCL-2, Lines 5-7 for siBCL-2+L2NTD in different molar ratios, after co-incubation with RNase A (3 mg mL-1) at 37 °C for 30 min. The results indicated that, after RNase A treatment, different amounts of siBCL-2 in Lanes 2-4 were completely digested; while the complex of siBCL-2+L2NTD with different proportions of L2-NTD in Lanes 5-7 still showed large amounts of siBCL-2. Meanwhile, the remained siBCL-2 increased with the increase of the L2-NTD proportion, indicating the well protective effects of L2-NTD the vulnerable siBCL-2.



Fig. S2. DLS histograms of HmA being assembled at pH 5.0, 7.0, 8.0, 9.0, and 10.0, respectively.





**Fig. S3.** SEM image and the corresponding EDS mapping for the element of Zn, C, N, O, and P in siGFP+L2-NTD@HmA, respectively.





**Fig. S4.** SEM image and the corresponding EDS mapping for the element of Zn, C, N, O, and P in siBCL-2+L2-NTD@HmA, respectively.



Fig. S5 Electrophoresis mobility shift assay (EMSA) of siBCL-2+L2-NTD@HmA after dis-assembled in acidic buffer of pH = 4.0, 4.5, 5.5, and 6.5 for 6 h, respectively.