Supporting Information

Fluorescent Histidine-derived Biodynamers as Biocompatible and Highly Water-Soluble Copper(II)-Sensors

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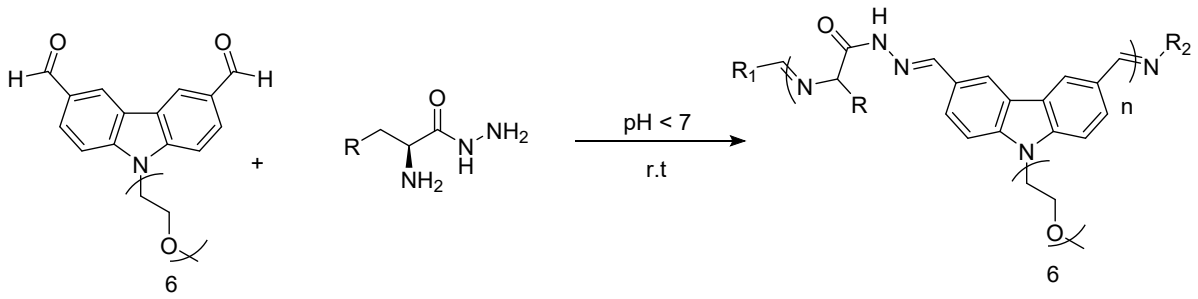


Scheme S1. Synthesis of amino acid-derived biodynamers. R_1 represents different amino acid-derived sidechains as shown in Scheme 1.[1]

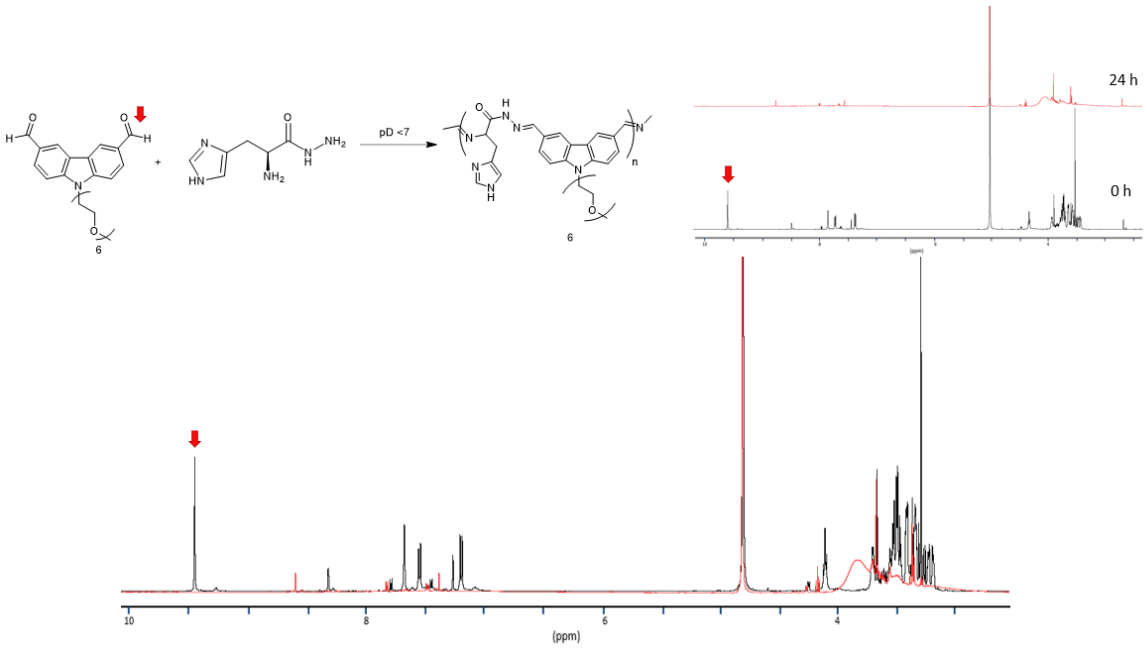


Figure S1. Scheme of HisBD synthesis and ^{1}H-NMR spectrum of 10 mM HisBD (500 MHz, 10 mM d-actetate solution). The aldehyde proton peak (marked at 9.47 ppm) was monitored at reaction time 0h (black) and 24h (red).

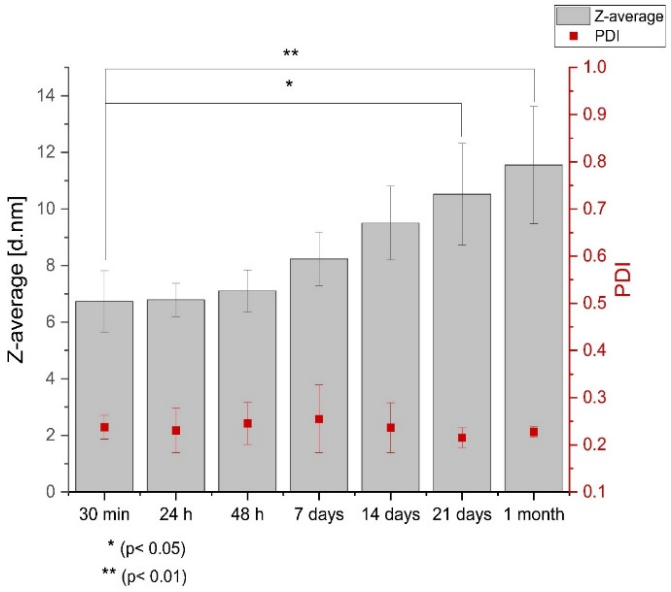


Figure S2. Dynamic light scattering (DLS) analysis of HisBD (10 mM) in pH 7.4 phosphate buffer (10 mM). The Z-Average and PDI were measured at different time points up to 1 month. All samples remained in solution under light exclusion and room temperature. Data represented as mean ± SD: (n=3)

Biodynamer	**λ_{abs} (nm)**	**λ_{em} (nm)**
HisBD	320	525
LysBD	320	495
ArgBD	315	460
AspBD	310	450
GluBD	310	455

Table S1. Absorption (λ_{abs}) and emission (λ_{em}) maxima of 0.1 mM amino acid-derived biodynamers with a concentration in 10 mM pH 7.4 phosphate buffer.

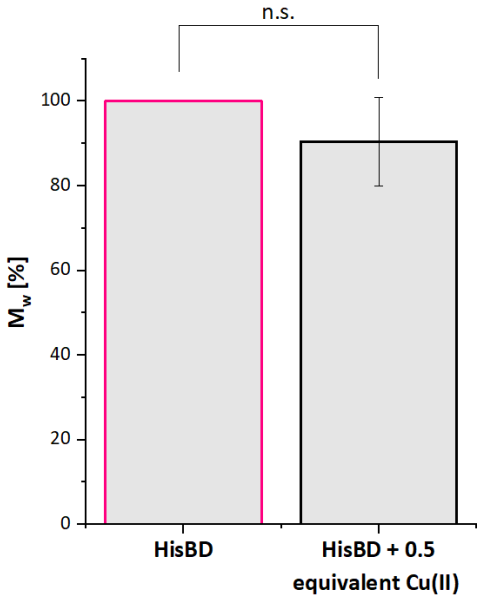


Figure S3. Static Light Scattering (SLS) Analysis of HisBD with and without Cu(II) in 10 mM pH 7.4 phosphate buffer (pH 7.4). The graph shows the relative molecular weight (M_w) of HisBD in % before (pink) and after the addition of 0.5 equivalents Cu(II) (black) (in %). ANOVA analysis confirmed that the difference in M_w (%) between the samples is not significant. Data is presented as mean ± SD: (n=3)

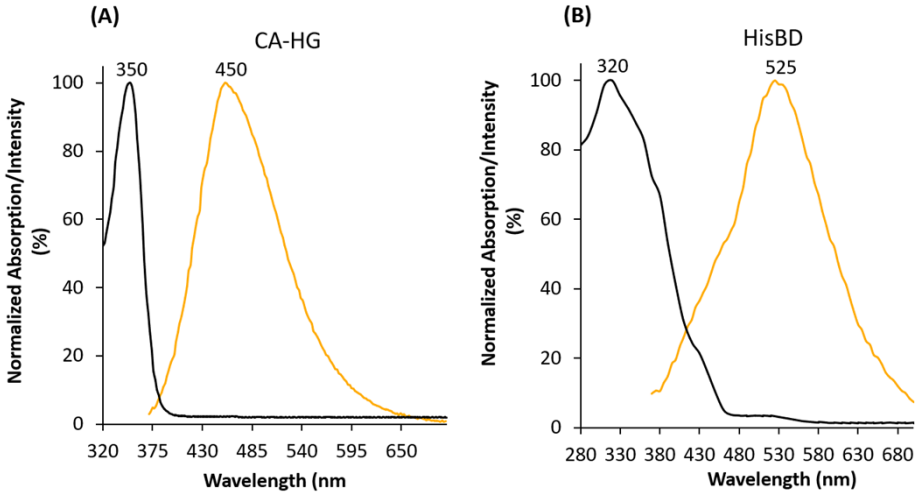


Figure S4. Normalized absorption (black) and emission spectra (orange) of carbazole hexaethylene glycol **(A)**, and histidine-biodynamer (HisBD) **(B)**.

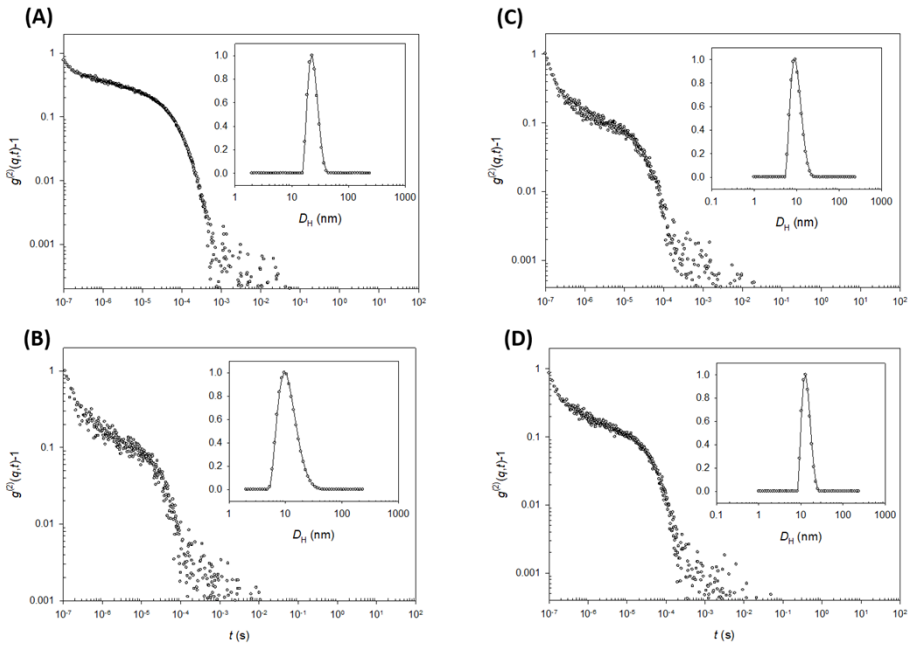
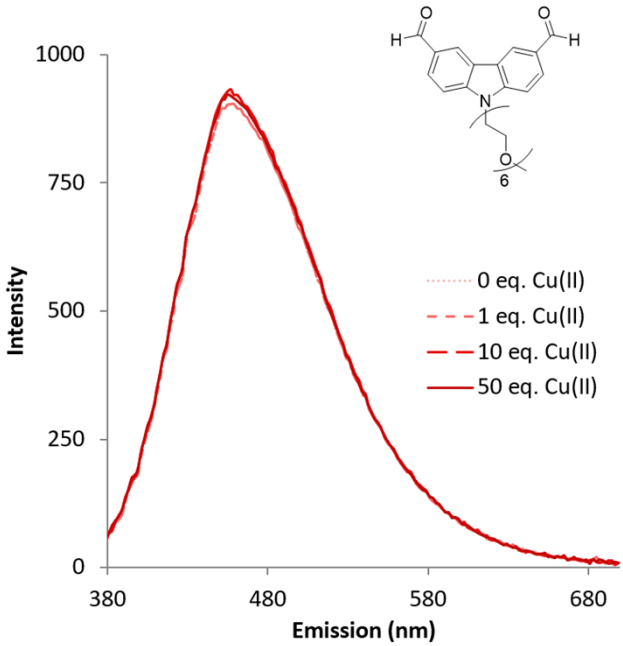


Figure S5. (A)-(D) DLS intensity autocorrelation function and hydrodynamic radius D_H (nm) of (A) LysBD, (B) ArgBD, (C) AspBD and (D) GluBD (1 mg/mL) at a scattering angle ϑ=90° and c=1 g/L in pH 5 acetic acid buffer (100 mM). The inset represents the hydrodynamic diameter (D_H) distribution obtained by applying the Contin method to the data.



Figures S6. Chemical structure of the monomer CA-HG and emission spectra of CA-HG (100 mM) upon the addition of 0-50 molar equivalents Cu(II).

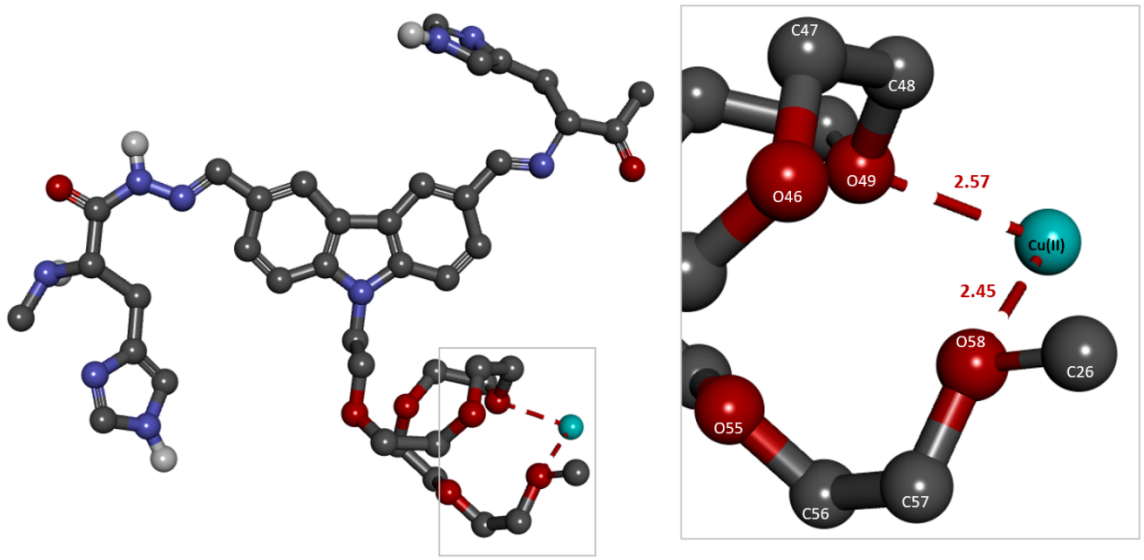


Figure S7. MD Autodock in silico simulation of HisBD as trimer, showing equivalent carbazole-hexaethylene glycol moiety and the Cu(II)-binding site with the numbered heteroatoms involved. The calculated binding-distances are displayed in Angstrom (Å): The simulation calculated a distance of one Copper (II) ion to HisBD of 2.4478 (O58) and 2.5676 (O49) Å with a binding free energy of -0.6 kcal/mol.

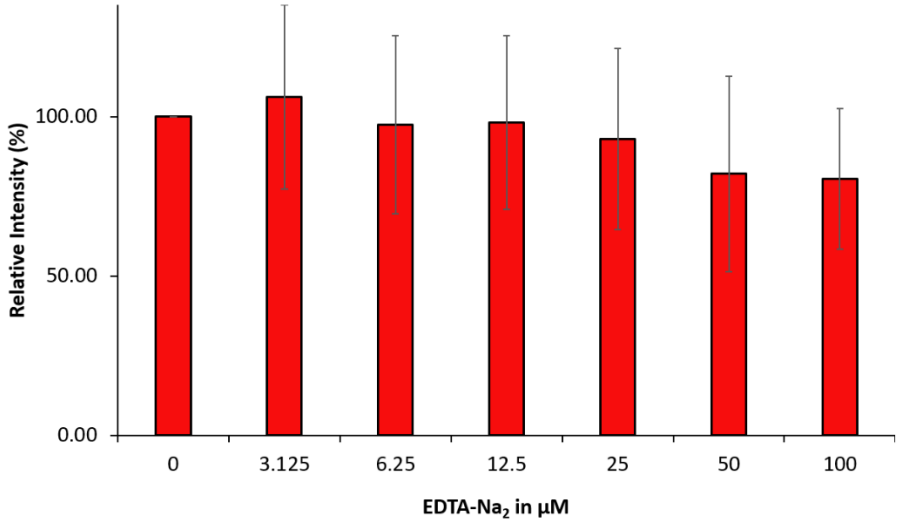


Figure S8. Effect of EDTA-Na_2 on the relative fluorescence intensity (%) of HisBD. A variety of 3.125 µM up to 100 µM ETDA-Na_2 was added to a stable concentration of 100 µM HisBD. Data represented as mean ± SD: (n=3)

References

(1) Liu, Y.; Stuart, M. C. A.; Buhler, E.; Lehn, J.-M.; Hirsch, A. K. H. Proteoid Dynamers with Tunable Properties.

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