Electronic Supplementary Material (ESI) for Dalton Transactions.

Peptides derived from histidine-proline rich glycoprotein bind copper ions and exhibit anti-angiogenic properties

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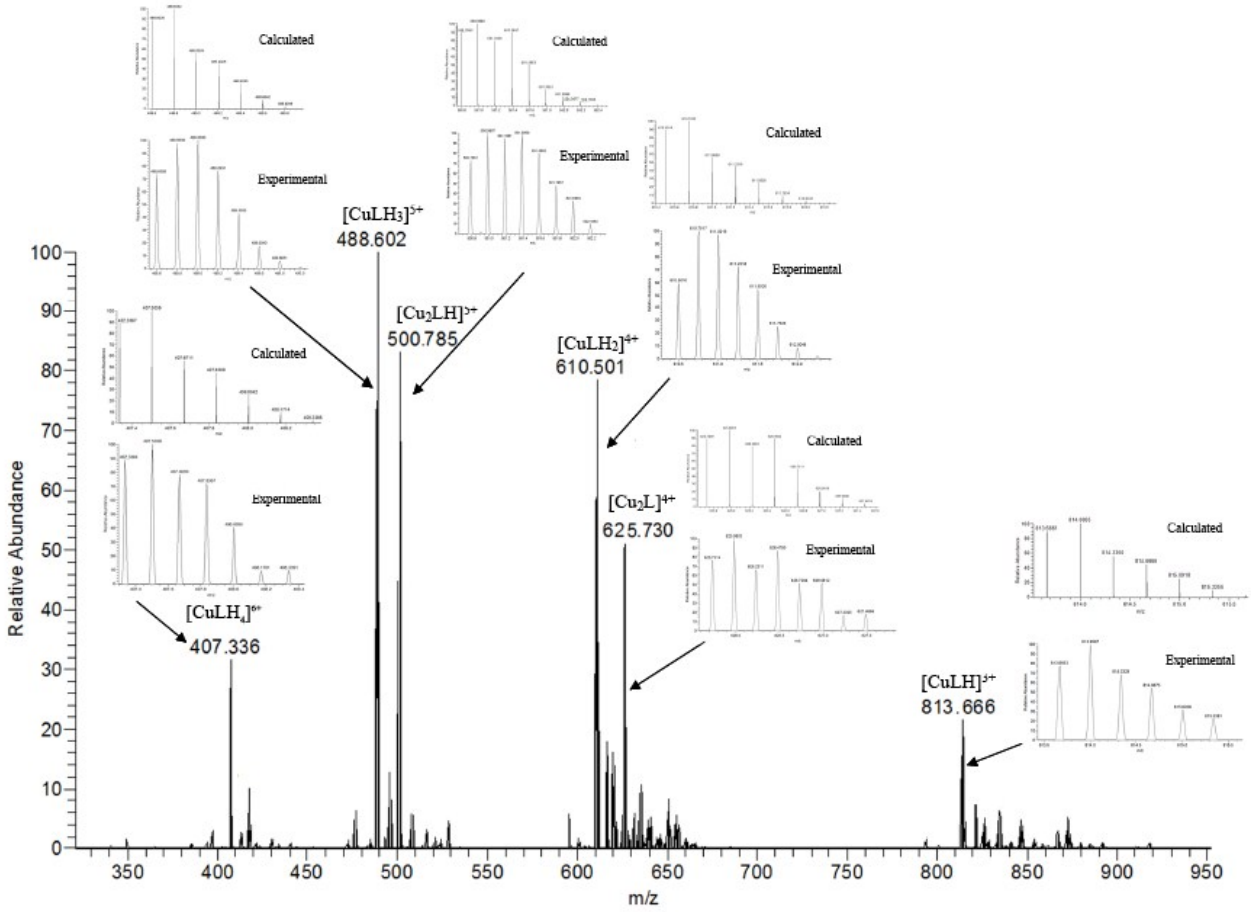

Figure S1. ESI-MS spectrum of aqueous solution of TetraHPRG/Cu(II) 1:1 ratio at pH 7 in positive ion mode. Experimental and calculated isotope patterns for the peaks at m/z=407.336, 488.602, 500.785, 610.501, 625.730 and 813.666.

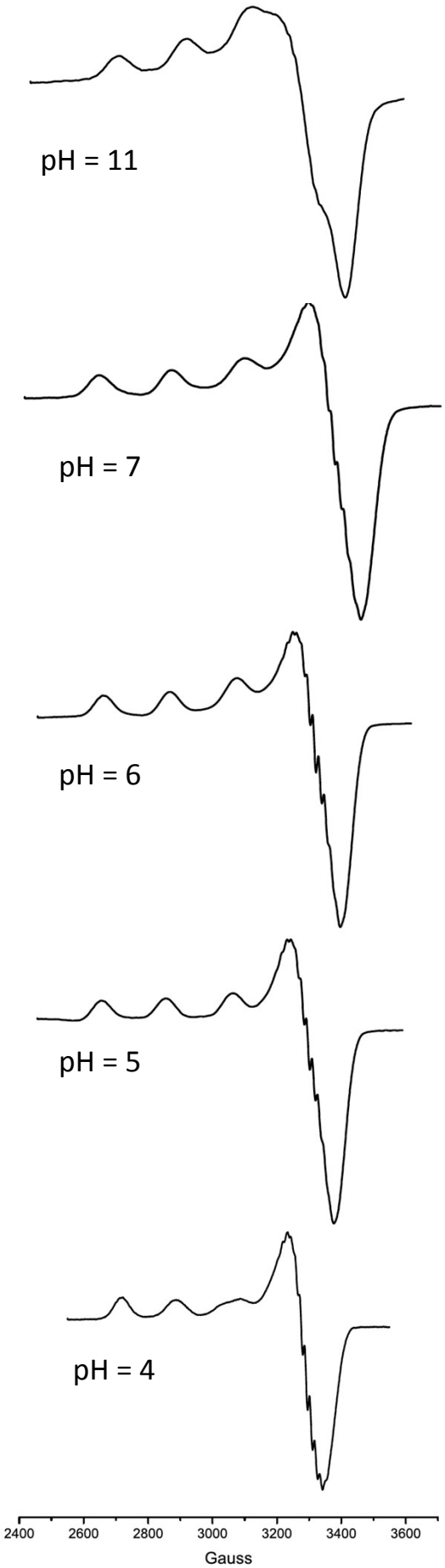

Figure S2. EPR spectra of Cu-TetraHPRG at 1:1 molar ratio. [Cu^{2+}]= 1x 10^{-3} M

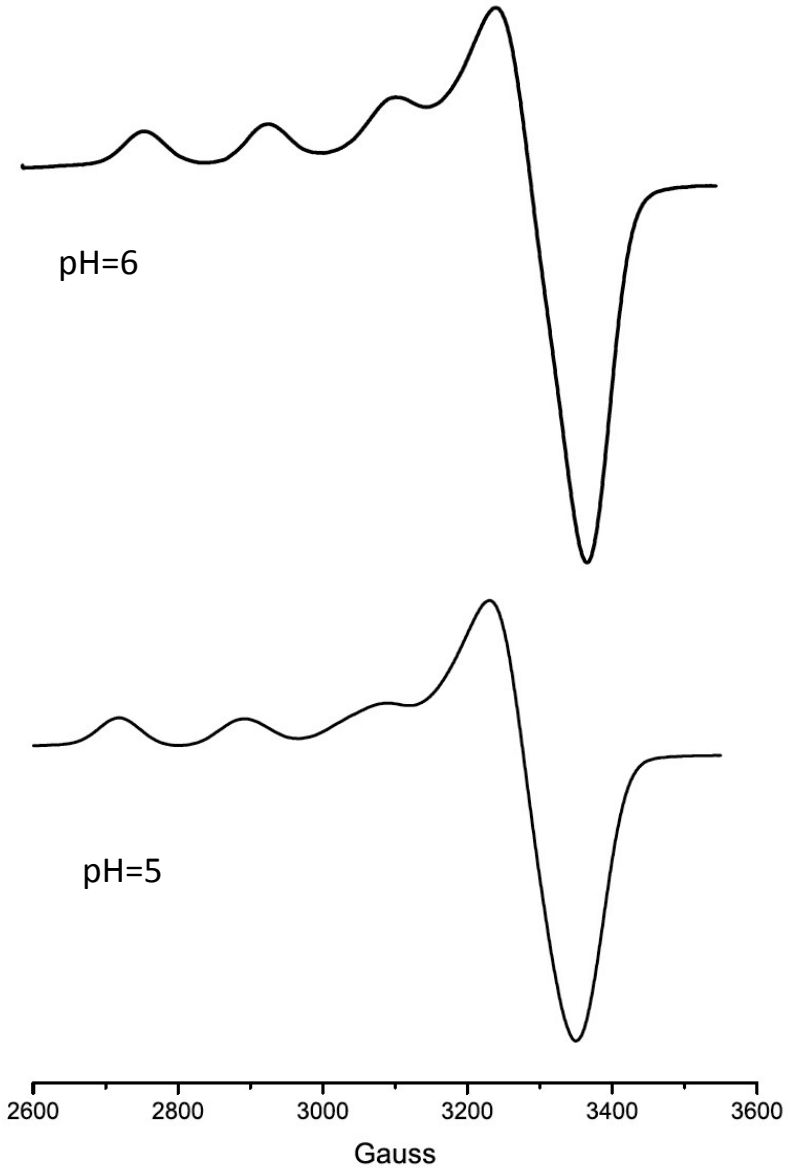

Figure S3. EPR spectra of Cu-TetraHPRG at 2:1 molar ratio. [Cu^{2+}]= 2 x 10^{-3} M

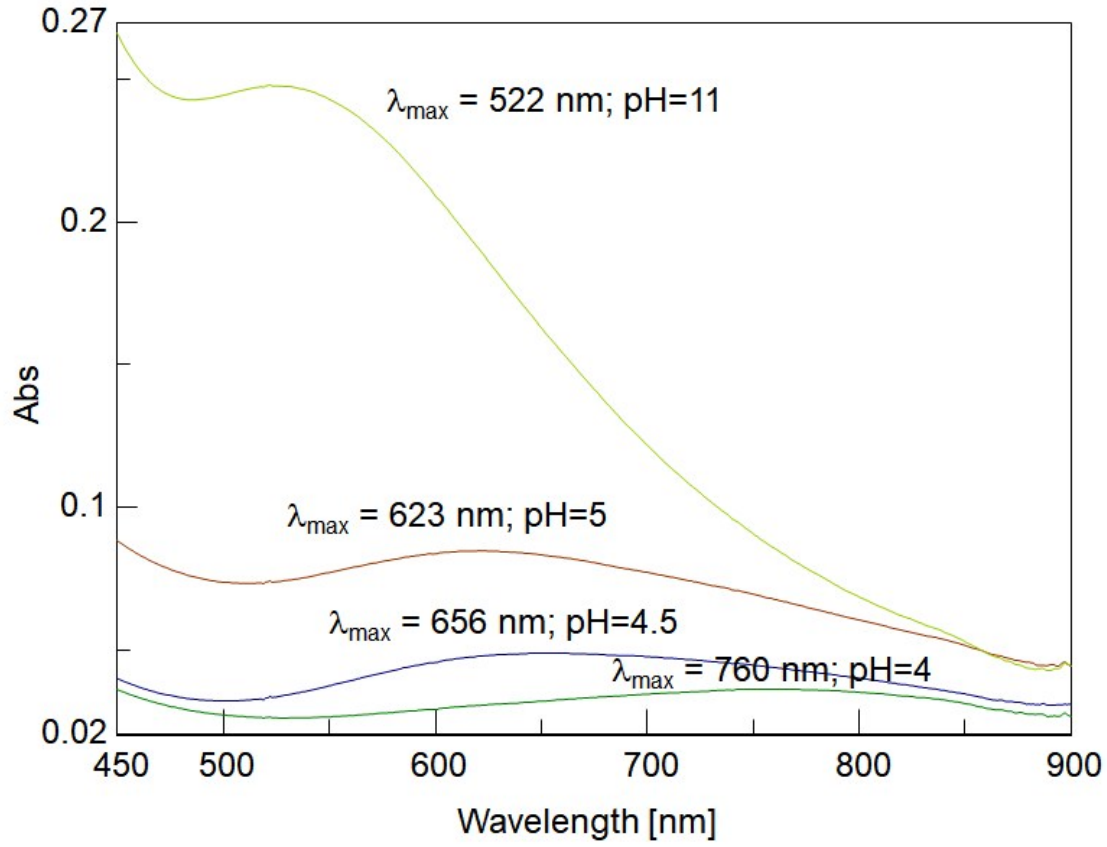

Figure S4. UV-vis spectra of Cu^{2+} complexes with TH-TetraHPRG at 1:1 M/L molar ratio. $[Cu^{2+}]$=[TH-TetraHPRG]= 1×10^{-3} M.

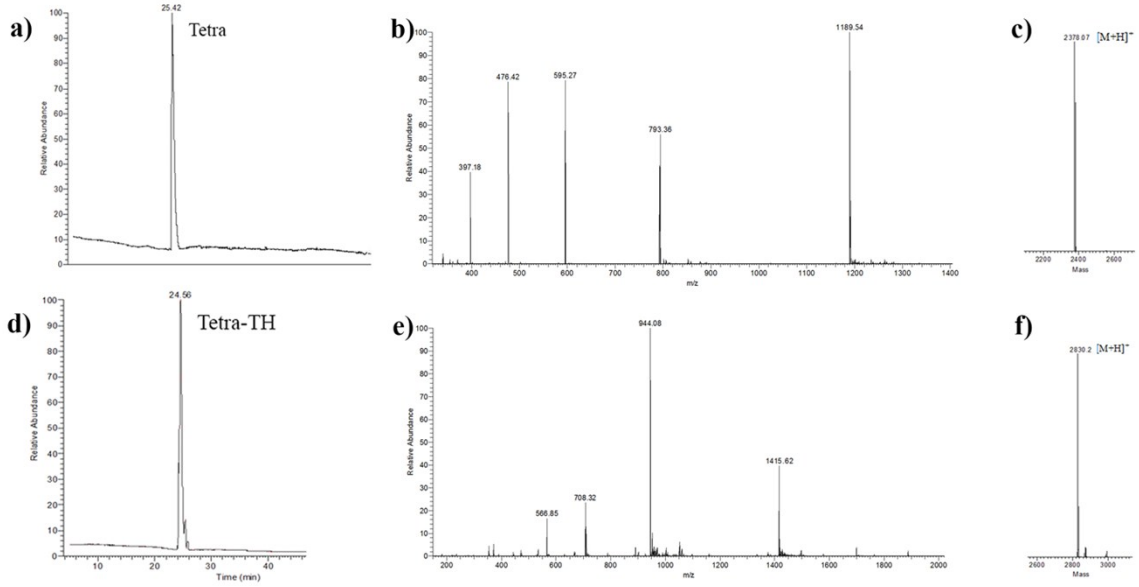

Figure S5. LC-MS (positive ions) analysis (Q-Exactive mass spectrometer Thermo coupled to a Ultimate 3000 HPLC system) of TetraHPRG and TH-TetraHPRG peptides (Easy Spray PepMap C18 Thermo column 15 cm × 75 µm i.d., 3 µm, 100 Å. HPLC method: (A) 0.1% formic acid and (B) acetonitrile/water 80:20 (v/v) containing 0.1% formic acid. The gradient was linear from 0 to 45% B over 60 min. a) Chromatogram of Tetra; b) Full mass spectrum of peak eluted at approximately 25.42 min; c) The deconvoluted ESI mass spectrum of b, using MagTran software program; d) Chromatogram of Tetra-TH; e) Full mass spectrum of peak eluted at approximately 24.56 min; f) The deconvoluted ESI mass spectrum of e, using MagTran software program.

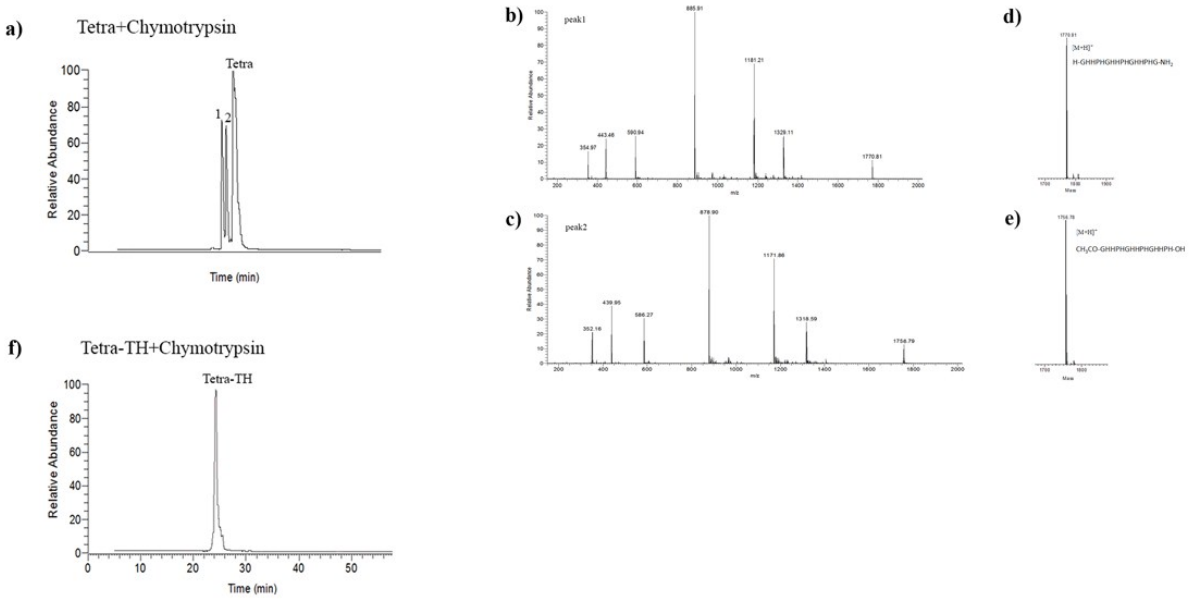

Figure S6. LC-MS (positive ions) analysis (Q-Exactive mass spectrometer Thermo coupled to a Ultimate 3000 HPLC system) of Chymotrypsin proteolytic digestion of TetraHPRG and TH-TetraHPRG peptides (Peptide/enzyme 200:1, Tris 50mM, pH 7.8 T=37°C for 2h. Easy Spray PepMap C18 Thermo column 15 cm × 75 µm i.d., 3 µm, 100 Å. HPLC method: (A) 0.1% formic acid and (B) acetonitrile/water 80:20 (v/v) containing 0.1% formic acid. The gradient was linear from 0 to 45% B over 60 min. a) Chromatogram of TetraHPRG+Chymotrypsin; b) Full mass spectrum of peak eluted at approximately 23.04 min; c) Full mass spectrum of peak eluted at approximately 23.51 min; d) The deconvoluted ESI mass spectrum of b using MagTran software program; e) The deconvoluted ESI mass spectrum of c using MagTran software program; f) Chromatogram of TH-TetraHPRG + Chymotrypsin.