Supporting Information

Amino- and chloro-8-hydroxyquinolines and their copper complexes as proteasome inhibitors and antiproliferative agents

Valentina Oliveri,^{a,b} Valeria Lanza,^c Danilo Milardi,^c Maurizio Viale,^d Irena Maric,^d Carmelo Sgarlata^a, Graziella Vecchio^{a,*}

^a Dipartimento di Scienze Chimiche, Università degli Studi di Catania, Viale A. Doria 6, 95125 Catania, Italy

^b Consorzio Interuniversitario di Ricerca in Chimica dei Metalli nei Sistemi Biologici, C.I.R.C.M.S.B., Unità di Ricerca di Catania, Viale A. Doria 6, 95125 Catania, Italy.

^c Istituto di Biostrutture e Bioimmagini, CNR, Viale P. Gaifami 18, 95126 Catania, Italy.

^d IRCCS Azienda Ospedaliera Universitaria San Martino-IST Istituto Nazionale per la Ricerca sul Cancro, U.O.C. Bioterapie, L.go R. Benzi 10, 16132, Genova, Italy



Figure S1. UV-vis spectra of 5-AHQ (4.0 × 10⁻⁵ M) in MOPS (pH 7.4, 10 mM). The spectra were collected every 180 s for 2 h.



Figure S2. Plot of the absorbance at 271 nm versus the molar ratio Cu^{2+}/L with L=2-AHQ (MOPS/dioxane 50:50 v/v).



Figure S3. Plot of the absorbance at 259 nm versus the molar ratio Cu^{2+}/L with L=AMHQ (MOPS/dioxane 50:50 v/v).



Figure S4.UV-vis competition titration of EDTA (5.49×10^{-4} M) into a Cu²⁺/AMHQ (1:1) solution in water/dioxane 50/50 v:v at pH 7.4 (MOPS 0.01 M). C_L = 4.07×10^{-5} M.



Figure S5. Hyperquad output for the Cu^{2+} – AMHQ system (blue squares: experimental points; red dotted lines: theoretical fit). The fit is reported at one wavelength only (232 nm); however, the entire 220-340 nm range was analyzed through a multi-wavelength treatment of the data. The species distribution diagram is also shown in the same window; residuals (observed/calculated values) are shown below the curves.



Figure S6. UV-vis competition titration of EDTA (5.41 × 10⁻⁴ M) into a Cu²⁺/HQ (1:1) solution in water/dioxane 50/50 v:v at pH 7.4 (MOPS 0.01 M). $C_L = 4.19 \times 10^{-5}$ M.



Figure S7. Hyperquad output for the Cu^{2+} – HQ system (blue squares: experimental points; red dotted lines: theoretical fit). The fit is reported at one wavelength only (263 nm); however, the entire 220-340 nm range was analyzed through a multi-wavelength treatment of the data. The species distribution diagram is also shown in the same window; residuals (observed/calculated values) are shown below the curves.

5-AHQ 2-AHQ AMHQ CIHQ CIMHQ 0.44 I50 (µM) 0.51 0.30 n.d n.d 95% Confidence 0.20 to 0.25 to 0.12 to n.d n.d 0.99 Intervals 1.3 0.77 R² 0.91 0.90 0.90 n.d n.d 5-AHQ 2-AHQ AMHQ CIMHQ CIHQ Cu(II) Cu(II) Cu(II) Cu(II) Cu(II) 1.22 4.5 1.3 I50 (µM) 0.34 0.85 95% Confidence 0.26 to 0.77 to 0.77 to 1.6 to 1.06 to 1.9 Intervals 0.44 0.95 12.7 1.60 R² 0.99 0.96 0.99 0.82 0.99

Table S1. Data fitting relative to the evaluation of the I_{50} values of HQ compounds and their copper complexes for ChT-L peptidase activity of the h-CP. Curve fitting was performed by using equation 1 reported in the main text.



Figure S8. Fluorescence vs time plots of 20S activity in the presence of Bortezomib (2 nM) and Cu(II), (1, 5 and 10 μ M).



Figure S9. Normalized concentration-response plot for inhibition of ChT-L residual activities of CP reported as a semilog plot fitted by equation 1 in presence of 5-AHQ, 2-AHQ and 5-AMHQ (red points and curves) and their copper complexes (blue points and curves). I₅₀ values for the distinct peptidase activities and the related fitting parameters are reported in Table S1.



Figure S9. Spectrophotometric determination of $P_2O\tau^{2-}$ anion in Lys48-linked polyubiquitination reactions in the presence of HQ compounds and their copper complexes (10 μ M).