Electronic Supplementary Information

Bioinspired nonheme iron complex that triggers mitochondrial apoptotic signalling pathway specifically for colorectal cancer cells

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Fig. S1. ESI MS spectra of (a) **1**, and (b) $[Mn(HN3O2)(Cl)_2]$ recorded in CH₃CN. The prominent ion peak at m/z of (a) 442.0, and (b) 377.1 correspond to $[Fe(HN3O2)(ClO4)]^+$ (calculated m/z of 442.1) and $[Mn(HN3O2)(Cl)]^+$ (calculated m/z of 377.1), respectively. Insets show the observed isotopic distribution patterns of **1**, and $[Mn(HN3O2)(Cl)_2]$.



Fig. S2. (a) UV-vis spectrum of **1** (0.25 mM) in CH₃CN at 20 °C. Inset shows the time course monitored at 330 nm for the stability of **1**. (b) UV-vis spectra of $[Mn(HN3O2)(Cl)_2]$ (0.25 mM, green line), $[Co(HN3O2)]^{2+}$ (0.25 mM, red line) and $[Cu(HN3O2)]^{2+}$ (0.25 mM, blue line) in CH₃CN at 20 °C. (c) Time courses monitored at 300 nm for $[Mn(HN3O2)(Cl)_2]$ (green circle), $[Co(HN3O2)]^{2+}$ (red circle) and 600 nm for $[Cu(HN3O2)]^{2+}$ (blue circle).



Fig. S3. (a) UV-vis spectrum of **1** (0.25 mM) in H₂O at 20 °C. Inset shows the time course monitored at 330 nm for the stability of **1**. (b) UV-vis spectra of $[Mn(HN3O2)(Cl)_2]$ (0.25 mM, green line), $[Co(HN3O2)]^{2+}$ (0.25 mM, red line) and $[Cu(HN3O2)]^{2+}$ (0.25 mM, blue line) in H₂O at 20 °C. (c) Time courses monitored at 300 nm for $[Mn(HN3O2)(Cl)_2]$ (green circle), $[Co(HN3O2)]^{2+}$ (red circle) and 600 nm for $[Cu(HN3O2)]^{2+}$ (blue circle).



Fig. S4. (a) UV-vis spectra of **2** (0.20 mM) obtained in the reaction of **1** (0.20 mM) with PhIO (0.40 mM, blue line) and H_2O_2 (0.60 mM, red line) in CH₃CN at 20 °C. (b) UV-vis spectrum of **2** obtained in the reaction of **1** (0.20 mM) with H_2O_2 (0.60 mM, red line) in CH₃CN:H₂O (v/v 1:1) at 5 °C.



Fig. S5. ESI MS spectra of **2** obtained (a) in the reaction between **1** (0.20 mM) and PhI^{16/18}O (0.40 mM) in CH₃CN at 20 °C and (b) in the dioxygen activation reaction of **1** in the presence of BNAH, and HClO₄ in ¹⁶O₂ and ¹⁸O₂-saturated CH₃CN at 20 °C. The prominent ion peak at m/z of 350.1, and 799.1 correspond to [Fe₂(O)(N3O2)₂]²⁺ (calculated m/z of 350.1) and [Fe₂(O)(N3O2)₂(ClO₄)]⁺ (calculated m/z of 799.1), respectively. Insets show the observed isotopic distribution patterns of [Fe₂(O)(N3O2)₂]²⁺, [Fe₂(¹⁶O)(N3O2)₂(ClO₄)]⁺ and [Fe₂(¹⁸O)(N3O2)₂(ClO₄)]⁺.



Fig. S6. (a) UV-Vis spectral changes observed in the reaction of **1** (black line, 0.10 mM) and BNAH (blue line, 0.20 mM) in the presence of HClO₄ (0.10 mM) in air-saturated CH₃CN at 20 °C. The use of hydrochloric acid instead of HClO₄ showed the identical spectrum (data not shown). Inset shows the time courses monitored at 345 nm due to the decay of BNAH. (b) UV-vis spectrum of BNAH (0.20 mM) in air-saturated CH₃CN at 20 °C.



Fig. S7. Cyclic voltammogram of (a) **1** (2.0 mM) in CH₃CN containing TBAPF₆ (0.10 M) with a glassy carbon working electrode at 20 °C with a scan rate of 0.10 V s⁻¹ and (b) **1** (4.0 mM) in H₂O containing NaClO₄ (0.10 M) with a glassy carbon working electrode at 20 °C with scan rates of 0.10 (orange line), 0.20 (yellow line), 0.50 (red line), and 1.0 (blue line) V s⁻¹.



Fig. S8. Fluorescence intensity changes obtained in the reaction between 1 and TA in DW at room temperature.



Fig. S9. Effects of treatment of negative control (NC), deionized water (DW), and $[M(HN3O2)]^{2+}$ (M(L); M = Mn, Fe, Co, and Cu) on (a) MDA-MB-231 (b) HeLa S3 (c) AU565 (d) SK-BR-3 cells by WST-8 assay with respect to total cell viability after 24h. The viability of cells without additional complexes is defined as 100%. The statistical analysis was performed using one way ANOVA-Dunnett's test (* *p* < 0.05, ** *p* < 0.01, *** *p* < 0.001 and ns = nonsignificant as compared to control).



Fig. S10. Representative images of HCT116 cells (a) negative control, (b) deionized water, and after incubation with (c) **1**, (d) $[Mn(HN3O2)]^{2+}$, (e) $[Co(HN3O2)]^{2+}$, and (f) $[Cu(HN3O2)]^{2+}$ for 24 h. Scale bar: 100 µm.

Fig. S11. Effects of treatment of deionized water (DW, green), $[M(HN3O2)]^{2+}$ (M(L); M = Mn (blue), Fe (red), Co (pink), Cu (cyan)), and ligand on HCT116 cells by WST-8 assay (a) with respect to time and (b) total cell viability after 24 h. The viability of HCT116 cells without additional complexes is defined as 100%. The statistical analysis was performed using one way ANOVA-Dunnett's test (*** = p < 0.0001; ns = nonsignificant as compared to control).

Fig. S12. Controlled confocal fluorescence images of HCT116 cells after 24 h incubation with DW followed by staining with (a) DAPI (blue), (b) antibody-COX IV (green), (c) antibody-E-cadherin (red), and (d) merged image. Scale bar: 20 μm.

Fig. S13. Confocal fluorescence images of HCT116 cells after 24 h incubation with **1** followed by staining with (a) DAPI (blue), (b) antibody-COX IV (green), (c) antibody-E-cadherin (red), and (d) merged image. Scale bar: 20 μm.

Fig. S14. The expression level of BID in HCT116 cells treated with 1.

| | [Mn(HN3O2)(Cl) ₂] | 1 | 2 |
|--|---|---|---|
| Empirical formula | $C_{16}H_{21}Cl_2MnN_3O_2$ | $C_{16}H_{25}Cl_2FeN_3O_{12}$ | $C_{32}H_{46}Cl_4Fe_2N_6O_{23}$ |
| Formula weight | 413.20 | 578.41 | 1136.25 |
| Temperature (K) | 120 | 120 | 120 |
| Wavelength (Å) | 0.71073 | 0.71073 | 0.71073 |
| Crystal system/space group | orthorhombic, P_{na21} | monoclinic, P_{21} | monoclinic, $P_{c2/c}$ |
| Unit cell dimensions | | | |
| <i>a</i> (Å) | 14.289(4) | 14.194(4) | 15.9079(12) |
| <i>b</i> (Å) | 8.933(2) | 10.712(3) | 17.3412(13) |
| <i>c</i> (Å) | 28.022(7) | 15.769(4) | 16.1343(12) |
| α(°) | 90 | 90 | 90 |
| <i>bβ</i> (°) | 90 | 102.510(4) | 90.724(1) |
| γ(°) | 90 | 90 | 90 |
| Volume (Å ³) | 3576.8(16) | 2340.8(11) | 4450.5(6) |
| Z | 8 | 4 | 4 |
| Calculated density (g/cm ⁻³) | 1.535 | 1.641 | 1.696 |
| Absorption coefficient (mm^{-1}) | 1.051 | 0.939 | 0.985 |
| Reflections collected | 6188 | 7959 | 3913 |
| Absorption correction | $\begin{array}{l} \text{multi-scan} \\ (T_{\text{min}}=0.591, \\ T_{\text{max}}=0.745) \end{array}$ | $\begin{array}{l} \text{multi-scan} \\ (\text{T}_{\text{min}} = 0.601, \\ \text{T}_{\text{max}} = 0.745) \end{array}$ | $\begin{array}{l} \text{multi-scan} \\ (\text{T}_{\text{min}} = 0.689, \\ \text{T}_{\text{max}} = 0.745) \end{array}$ |
| Independent reflections | 5717 | 6552 | 3589 |
| Goodness-of-fit on F^2 | 1.097 | 1.017 | 1.082 |
| $R [F^2 > 2 \text{sigma}(F^2)]$ | 0.0404 | 0.0359 | 0.0298 |
| wR^2 | 0.1052 | 0.0864 | 0.0817 |

Table S1. Crystallographic data and refinements for [Mn(HN3O2)(Cl)₂], 1, and 2.

| | [Mn(HN3O2)(Cl) ₂] | 1 | 2 |
|------------------------------------|-------------------------------|------------|-------------|
| Bond Distances (Å) | | | |
| M1-N1 2.255(4) | | 2.118(4) | 2.2167(18) |
| M1-N2 | 2.341(4) | 2.252(4) | 2.1813(17) |
| M1-N3 | 2.248(4) | 2.122(3) | 2.1431 (17) |
| M1-O1 | 2.358(4) | 2.158(3) | 2.1813(17) |
| M1-O2 | - | 2.068(3) | 2.0016(15) |
| M1-O3 _(H2O or bridging) | - | 2.148(3) | 1.7799(4) |
| M1-M2 | 2.4054(13) | - | 3.530(1) |
| M1-Cl1 | 2.4054(13) | - | - |
| M1-Cl2 | 2.4580(14) | - | - |
| Bond Angles (°) | | | |
| N1-M1-N2 | 72.73(13) | 77.59(14) | 77.39(6) |
| N1-M1-N3 | 146.48(14) | 150.88(14) | 154.99(7) |
| N1- M1-O1 | 82.61(13) | 95.35(14) | 88.05(6) |
| N2-M1-O2 | - | 155.06(14) | 153.37(6) |
| N1-M1-O3 | - | 85.04(14) | 96.94(6) |
| O1-M1-O3 | - | 166.26(12) | 174.52(6) |
| M1-O3-M2 | - | - | 165.08(6) |
| N2-M1-Cl1 | 163.21(11) | - | - |
| O1-M1-Cl2 | 165.23(9) | - | - |
| N1-M1-Cl1 | 108.05(11) | - | - |
| N1-M1-Cl2 | 92.31(11) | - | - |

Table S2. Selected bond distances (Å) and angles (°) for [Mn(HN3O2)(Cl)₂], 1, and 2.

Table S3. Sequences of qRT-PCR primers.

| Gene | | Sequences $(5' \rightarrow 3')$ |
|---------------|---------|---------------------------------|
| hBCL2 alpha – | Forward | ATGTGTGTGGAGAGCGTCAA |
| | Reverse | CCGTACAGTTCCACAAAGGC |
| hBCL2 beta – | Forward | ATGTGTGTGGAGAGCGTCAA |
| | Reverse | GCCCAGACTCACATCACCAA |
| hBAX - | Forward | TGGGCTGGACATTGGACTTC |
| | Reverse | AAAGTAGGAGAGGAGGCCGT |
| hBAK – | Forward | AAAGTAGGAGAGGAGGCCGT |
| | Reverse | ATGGGACCATTGCCCAAGTT |
| hBID - | Forward | AGCACAGTGCGGATTCTGT |
| | Reverse | CTCATCCCTGAGGCTGGAAC |
| h18s rRNA | Forward | GTCGGCGTCCCCCAACTTCT |
| | Reverse | CGTGCAGCCCCGGACATCTA |