Electronic Supplementary Material (ESI) for RSC Advances

The Adsorption of an Anticancer Hydrazone by Protein: An Unusual Static Quenching Mechanism

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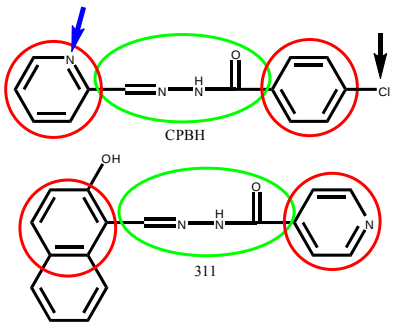
Content:



Scheme SI 1 Comparison of CPBH and 311 and the design principle of CPBH

As we desired, the target compound CPBH must share the basic structure and pharmacophore of the template molecules, meanwhile it needs to avoid the disadvantages of the template molecules such as poor solubility and binding strength to protein. As showed in scheme 2, CPBH shares the common hydrazone structure in the green ellipse and the aromatic system in the red circle. The pharmacodynamic effect has been greatly limited and weakened by its poor solubility, due to the big aromatic system in 311. So as to keep the basic aromatic system in 311, we replace the naphthalene group by some small aromatic functional group. In order to get a higher coordination efficiency according the chelating effect, we held the pyridine group and move it to the left of the molecular structure. Whereas we employ a chlorine atom in the right side of the molecule in order to obtain a better pharmacodynamic effect by heavy atom effect.

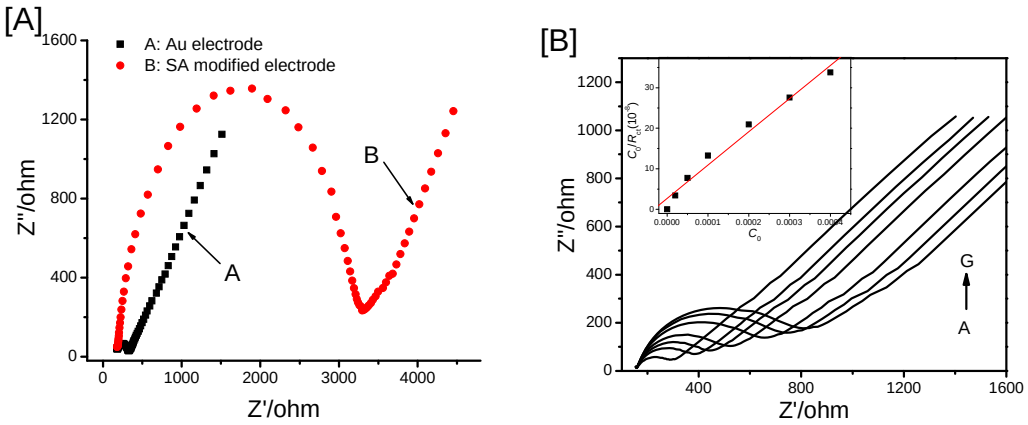


Figure SI 1. The control experiments for EIS.

[A]EIS of bare Au electrode (curve A) and modified Au electrode(Curve B).[B]The adsorption of CPBH by the barely Au electrode. The concentration of CPBH for A to G is (μM):0; 20; 50; 100; 200; 300; 400. The inset corresponds to the Langmuir isotherm plots for the adhesion.

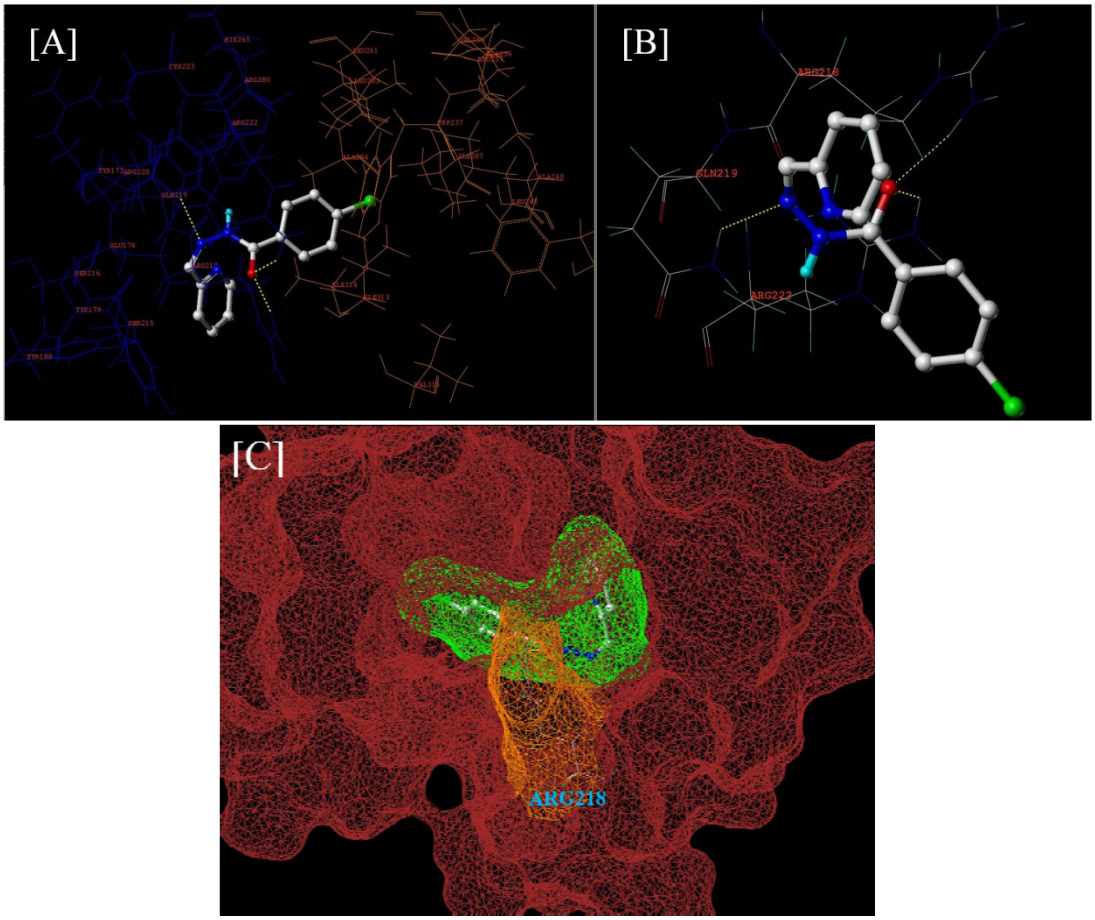


Figure SI 2. The detailed illustration of the interaction between CPBH and BSA [A] The hydrophobic amino acid residues are showed in orange, while the hydrophilic amino acid residues are showed in blue. And three hydrogen bonds between CPBH and BSA are showed as well. [B] The detailed illustration of the hydrogen bonds formation. [C] The surface mode of the CPBH in the binding site of the BSA. The surface of the BSA is showed in red, while ARG218 is showed in orange. The surface of CPBH is green.

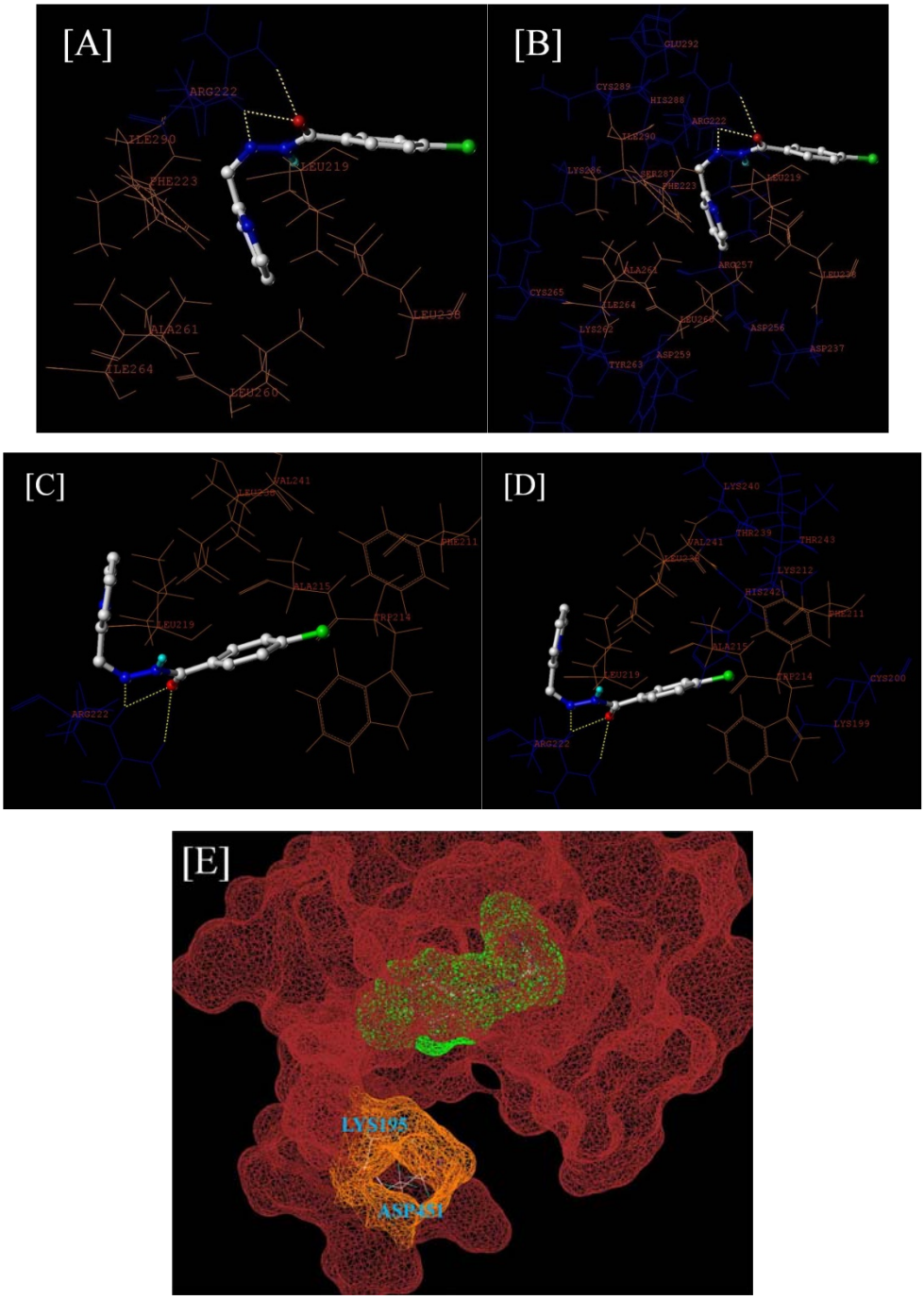


Figure SI 3. The detailed illustration of the interaction between CPBH and HSA

The hydrophobic amino acid residues are showed in orange, while the hydrophilic amino acid residues are showed in blue. And three hydrogen bonds between CPBH and Arg222 are showed as well. [A] The pyridine group in CPBH inserts into a hydrophobic loop formed by Ile290, Phe223, Ala261, Ile264, Leu260, Leu219. [B] The hydrophobic loop is buried in a pocket created by hydrophilic residues. [C] The 4-chlorophenyl group stretches to a hydrophobic pocket made by Leu238, Val241, Ala215, Trp214, Phe211. [D]Some hydrophilic residues lay around the hydrophobic pocket. [E] The surface mode of the CPBH in the binding site of the HSA. The surface of the HSA is showed in red, while LYS195 and ASP451 are showed in orange. The surface of CPBH is green.

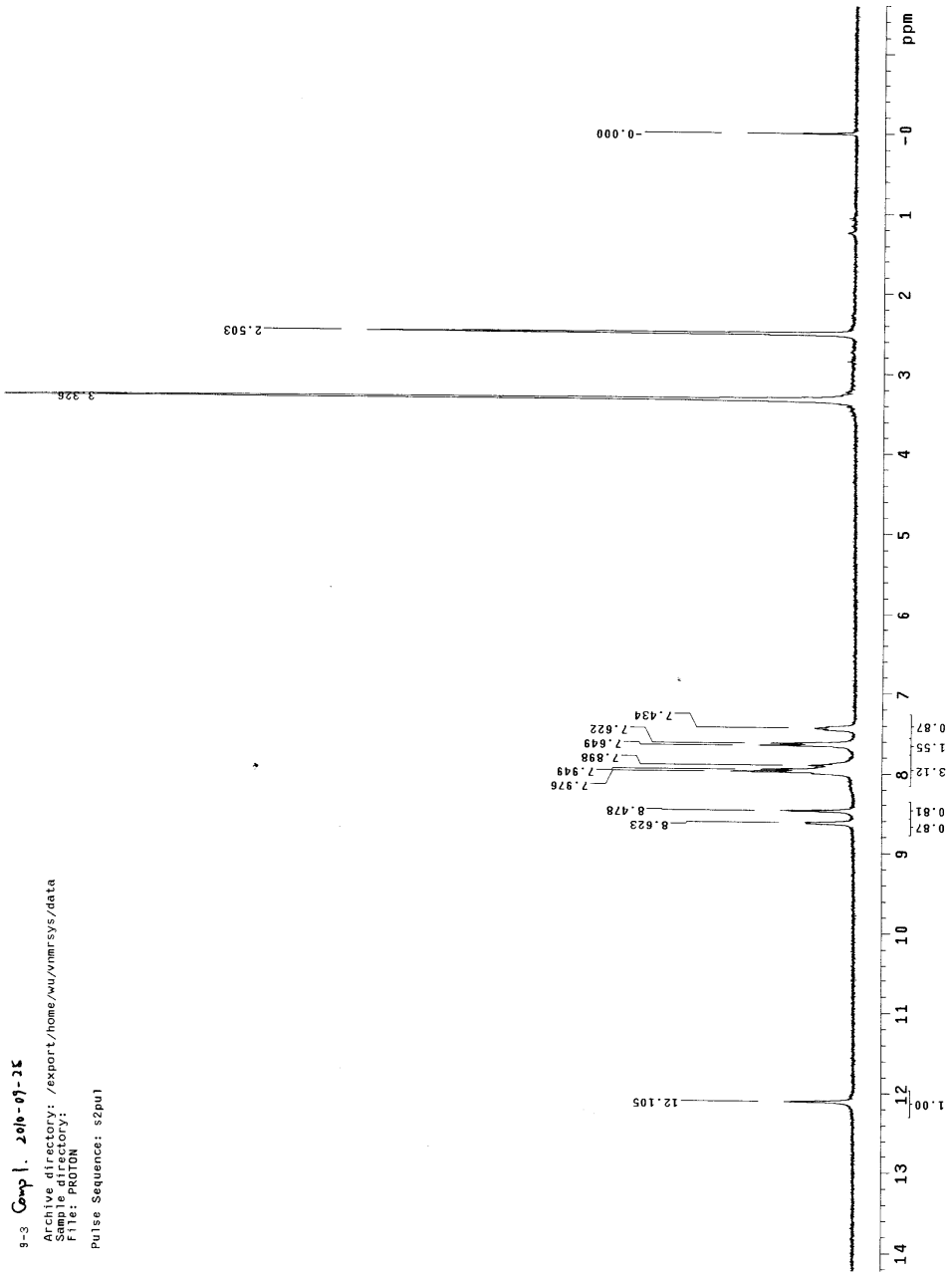


Figure SI 4. The ^{1}H NMR for CPBH

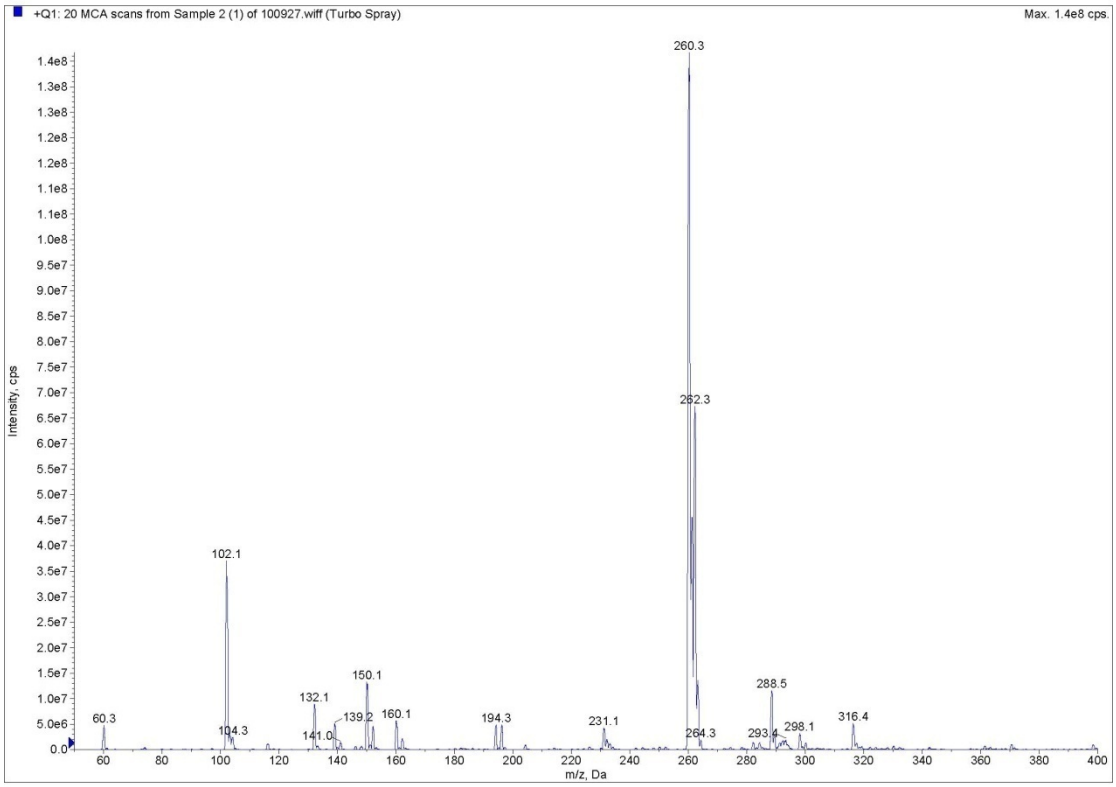


Figure SI 5. The MS of CPBH

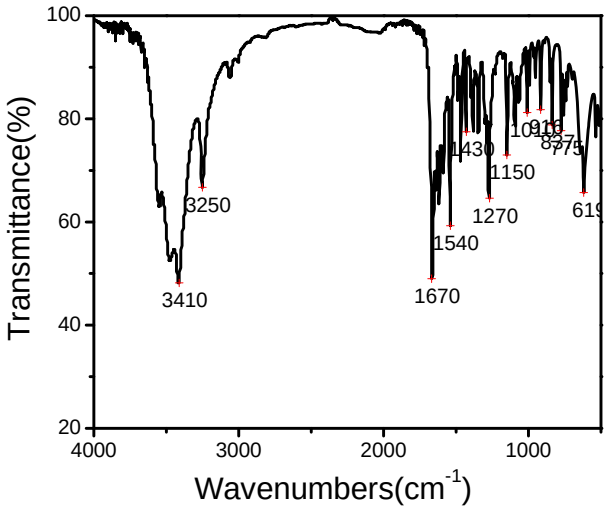


Figure SI 6. The IR spectrum of CPBH

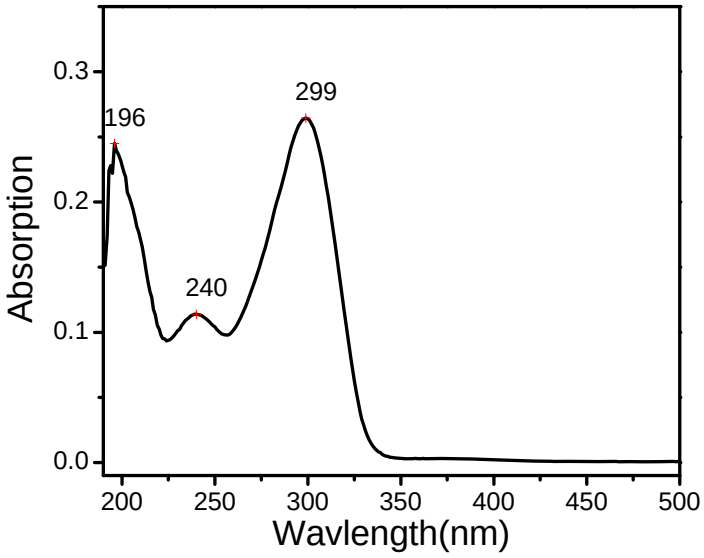


Figure SI 7. The UV-visible absorption spectrum of CPBH(5 μM in PBS)