Supporting Information

Multifaceted Interaction Studies between Carbon Dots and Proteins of Clinical Importance for Optical Sensing Signals

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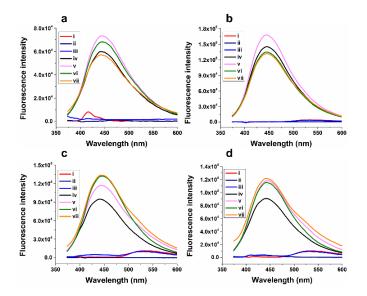


Fig. S1: (a) Fluorescence change of different reaction systems at the CD excitation wavelength ($\lambda_{354 \text{ nm}}$): (i) ChOx, (ii) Chol, (iii) ChOx+Chol, (iv) CD, (v) CD+ChOx (after 5 minutes), (vi) CD+Chol, (vii) CD+ChOx+Chol.

(b) (i) GOx, (ii) GL, (iii) GOx+GL, (iv) CD, (v) CD+GOx (after 5 minutes), (vi) CD+GL, (vii) CD+GOx+GL. (c) (i) AOx , (ii) MeOH, (iii) AOx+MeOH, (iv) CD, (v) CD+AOx (after 5 minutes), (vi) CD+MeOH, (vii) CD+AOx+MeOH. (d) (i) AOx , (ii) EtOH, (iii) AOx+EtOH, (iv) CD, (v) CD+AOx (after 5 minutes), (vi) CD+EtOH, (vii) CD+AOx+EtOH.

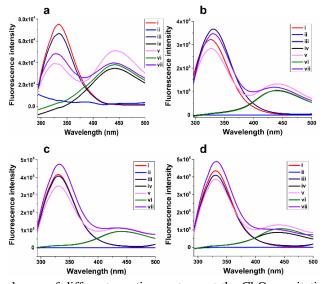


Fig. S2: (a) Fluorescence change of different reaction systems at the ChOx excitation wavelength ($\lambda_{274 \text{ nm}}$): (i) ChOx, (ii) ChOl, (iii) ChOx+Chol, (iv) CD, (v) CD+ChOx (after 5 minutes), (vi) CD+Chol, (vii) CD+ChOx+Chol. (b) Fluorescence change of different reaction systems at the GOx excitation wavelength ($\lambda_{274 \text{ nm}}$): (i) GOx, (ii) GL, (iii) GOx+GL, (iv) CD, (v) CD+GOx (after 5 minutes), (vi) CD+GL, (vii) CD+GOx+GL. (c) Fluorescence change of different reaction systems at the AOx excitation wavelength ($\lambda_{274 \text{ nm}}$): (i) AOx , (ii) MeOH, (iii) AOx+MeOH, (iv) CD, (v) CD+AOx (after 5 minutes), (vi) CD+MeOH, (vii) CD+AOx+MeOH. (d) Fluorescence change of different reaction systems at the AOx excitation wavelength ($\lambda_{274 \text{ nm}}$): (i) AOx , (ii) EtOH, (iii) AOx+EtOH, (iv) CD, (v) CD+AOx (after 5 minutes), (vi) CD+MeOH, (vii) CD+AOx+MeOH. (d)

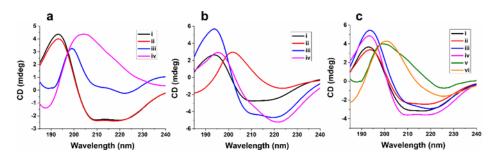


Fig. S3. (a) Circular dichroism spectra of (i) ChOx, (ii) ChOx+CD, (iii) ChOx+Chol, (iv) ChOx+Chol+CD, (b) Circular dichroism spectra of (i) GOx, (ii) GOx+CD, (iii) GOx+GL, (iv) GOx+GL+CD. (c) Circular dichroism spectra of (i) AOx, (ii) AOx+CD, (iii) AOx+EtOH, (iv) AOx+MeOH, (v) AOx+EtOH+CD, (vi) AOx+MeOH+CD.

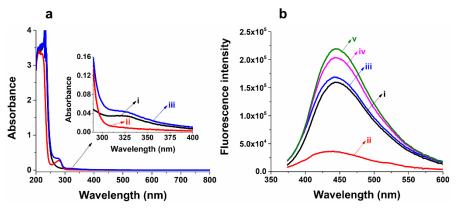


Fig. S4. (a) Absorbance of different reaction systems: (i) CD, (ii) HSA, and (iii) CD+HSA, (b) Fluorescence emission (i) CD, (ii) HSA, and CD+HSA at (iii) 2 mins, (iv) 6 mins, and (v) 10 mins at excitation of CD (at λ_{ex} ^{354 nm}) (Inset: Fluorescence intensity of CD+HSA at different time intervals. Experiment was carried out using 50 µL of stock 10.3 mg/mL HSA and 10 µL of stock CD solution (100 mg/mL).

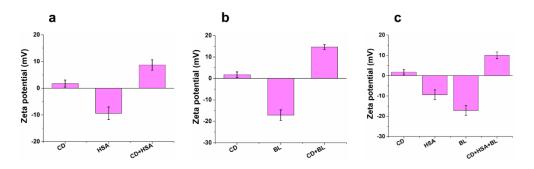


Fig. S5. Zeta potential of (a) CD, HSA, and CD+HSA, (b) CD, BL (Bilirubin), and CD+BL, and (c) CD, HSA, BL, and CD+HSA+BL. The concentration of CD (1 mg/mL), HSA (0.52 mg/mL), and BL (2 μ M) used in the reaction mixture are shown in the bracket.

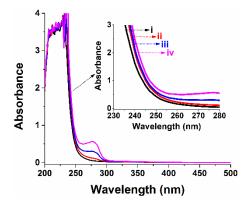


Fig. S6. UV-vis spectra of CD and increasing concentrations of HSA. (i) CD, (ii) CD+103 µg/mL HSA, (iii) CD+515 µg/mL HSA, (iv) CD+1.03 mg/mL HSA. The concentration of CD used in the experiment is 1 mg/mL.

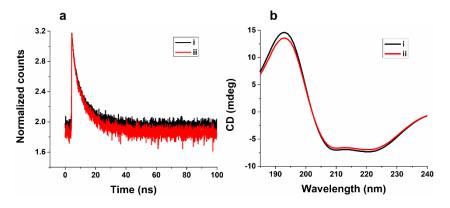


Fig. S7. (a) Time resolved fluorescence spectra of (i) CD, and (ii) CD+HSA, (b) Circular Dichroism spectra of (i) HSA, (ii) CD+HSA.

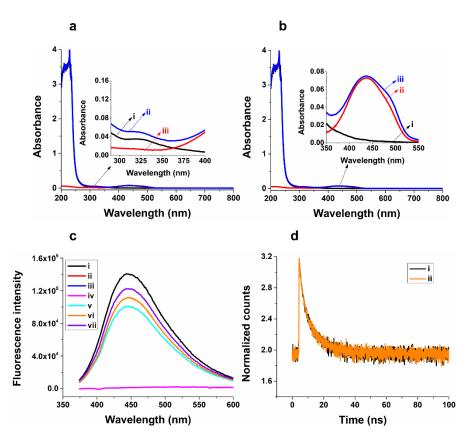


Fig. S8. (a) Effect of BL on absorbance of CD. (i) CD, (ii) BL, and (iii) CD+BL, (b) Effect of CD on the absorbance of BL. (i) CD, (ii) BL, (iii) CD+BL, (c) Fluorescence of (i) CD, (ii) 0.02 μ M BL, (iii) 0.3 μ M BL, (iv) 2.43 μ M BL, (v) CD+0.02 μ M BL, (vi) CD+0.3 μ M BL, (vii) CD+2.43 μ M BL, (d) Time resolved fluorescence spectra of (i) CD, and (ii) CD+BL. The concentration of CD used in the experiment is 1 mg/mL.

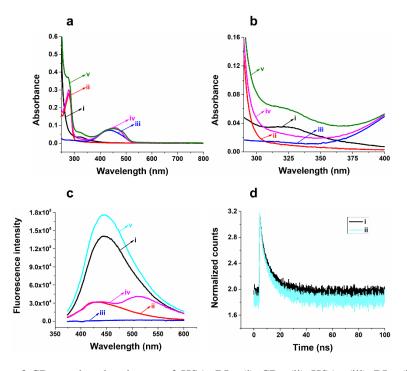


Fig. S9. (a) Effect of CD on the absorbance of HSA+BL. (i) CD, (ii) HSA, (iii) BL, (iv) HSA+BL, (v) CD+HSA+BL, (b) Effect of HSA+BL on the absorbance of CD. (i) CD, (ii) HSA, (iii) BL, (iv) HSA+BL, (v) CD+HSA+BL, (c) Effect of HSA+BL on the fluorescence of CD (CD excitation wavelength: 354 nm). (i) CD, (ii) HSA, (iii) BL, (iv) HSA+BL, (v) CD+HSA+BL, (d) Time resolved fluorescence spectra of (i) CD, and (ii) CD+HSA+BL. Experiment was carried out using 50 μ L of stock 10.3 mg/mL HSA, 10 μ L of stock CD solution (100 mg/mL), and 20 μ L of stock 100 μ M bilirubin.

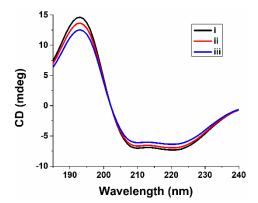


Fig. S10. Circular Dichroism spectra of (i) HSA, (ii) HSA+BL, (iii) HSA+BL+CD.

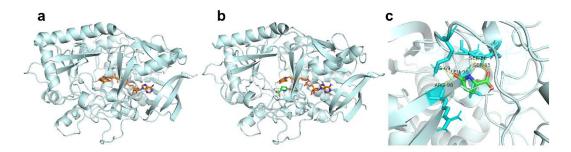


Fig. S11. (a) Crystallographic structure of ChOx with the FAD (orange), (b) Best binding pose for PGA (green) with ChOx; (c) Amino acid residues in ChOx that form hydrogen bond with PGA.

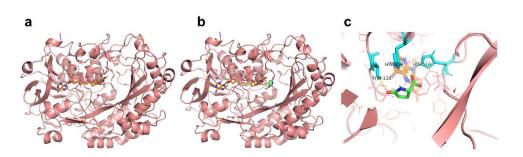


Fig. S12. (a) Crystallographic structure of GOx with the FAD (orange), (b) Best binding pose for PGA (green) with GOx; (c) Amino acid residues in GOx that form hydrogen bond with PGA.

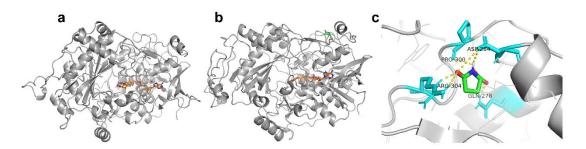


Fig. S13. (a) Crystallographic structure of AOx with the FAD (orange), (b) Best binding pose for PGA (green) with AOx; (c) Amino acid residues in AOx that form hydrogen bond with PGA.

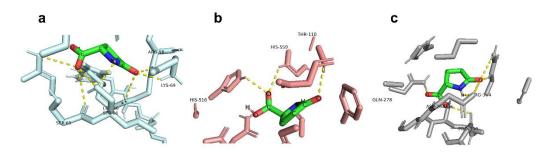


Fig. S14. Different functional groups of PGA involved in the binding with amino acids of (a) ChOx, (b) GOx, and (c) AOx.

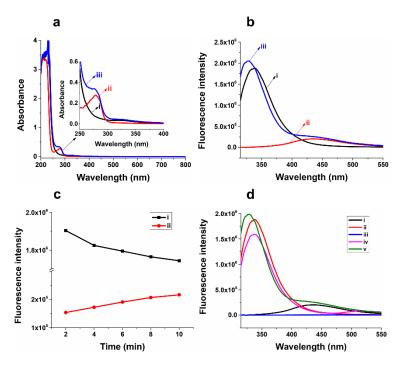


Fig. S15. (a) Absorbance of different reaction systems: (i) CD, (ii) HSA, and (iii) CD+HSA, (b) Fluorescence of (i) HSA, (ii) CD, and (iii) CD+HSA (after 5 minutes) at the HSA excitation wavelength ($\lambda_{ex 295 nm}$), (c) Fluorescence change of (i) HSA and (ii) CD at different incubation time at HSA excitation wavelength ($\lambda_{ex 295 nm}$), (d) Effect of CD on the fluorescence of HSA+BL (HSA excitation wavelength: 295 nm). (i) CD, (ii) HSA, (iii) BL, (iv) HSA+BL, (v) CD+HSA+BL. Experiment was carried out using 50 µL of stock 10.3 mg/mL HSA and 10 µL of stock CD solution (100 mg/mL).

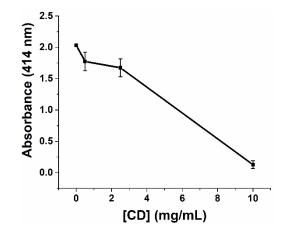


Fig. S16. Influence of interaction of CD on the catalytic activity of GOx. Experiment was performed using different concentrations (0 mg/mL, 1 mg/mL, 2.5 mg/mL, and 10 mg/mL) of stock 100 mg/mL CD solution, 10 μ L of 1 mg/mL stock GOx, 10 mM GL, and 5 mM ABTS.

Table S1. The content of different secondary structures of HSA in the absence and presence of CD

Reaction system	Helix (%)	β strand (%)	Turns (%)	Unordered (%)
HSA	48.1	10.2	17.2	25.1
HSA+CD	48.0	11.4	17.8	25

Table S2. The content of different secondary structures of HSA in different reaction systems

Reaction system	Helix (%)	β strand (%)	Turns (%)	Unordered (%)
HSA	48.1	10.2	17.2	25.1
HSA+BL	47.7	12.9	17.5	25.1
HSA+CD+BL	45.1	13.7	19.7	26.4

Table S3. Binding of the different functional groups of the PGA to the amino acid residues of the enzymes

Functional groups	ChOx	GOx	AOx
-C=O	LYS69, LEU96, ARG98	THR110	ARG304, ASP284
-COOH	SER65, SER66, 219TYR	HIS516, HIS559	GLN278, PRO300
-NH	SER66		ASP284

Table S4. Binding site of the substrates with their respective enzyme

Enzyme	Substrate	Interacting amino acids (hydrophobic bond)	Interacting amino acids (hydrogen bond)
Cholesterol oxidase	Cholesterol	70ASN, 71ARG, 72THR 73GLU, 74ALA, 75PRO, 76LEU, 78SER, 79PHE, 86ASN, 98ARG, 107TYR, 432LEU, 433PHE, 434GLY	77GLY
Glucose oxidase	Glucose	80TYR, 94ILE, 95ARG, 103SER, 289ALA, 290GLY, 293VAL, 294SER, 328ASP, 450TYR, 515TYR, 516HIS, 518VAL, 548ASP, 550SER	96SER, 291SER, 292ALA, 517GLY, 549GLY
Alcohol oxidase	Methanol	6LYS, 87ALA, 269GLY, 270THR, 271ILE, 568LYS	-