

Structure, antimicrobial activity, albumin– and DNA–binding of manganese(II)–sparfloxacinato complexes

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Supplementary material

Table S1. Hydrogen bonding parameters for 1·4MeOH.

Interaction	D–H (Å)	H···A (Å)	D···A (Å)	D–H···A (°)	Symmetry transformation for acceptors
N(3)–H(3A)···O(5)	0.86	2.32	3.076(4)	147.4	$-x + \frac{1}{2}, -y + \frac{1}{2}, z$
N(3)–H(3B)···O(3)	0.86	2.00	2.630(3)	129.5	x, y, z
N(5)–H(5A)···O(2)	0.92(3)	2.21(3)	3.126(3)	173(2)	$-x + \frac{1}{2}, y, z + \frac{1}{2}$
O(4)–H(4)···N(5)	0.82	2.03	2.830(4)	165.7	x, y, z
O(5)–H(5)···O(2)	0.82	1.93	2.739(3)	169.5	x, y, z

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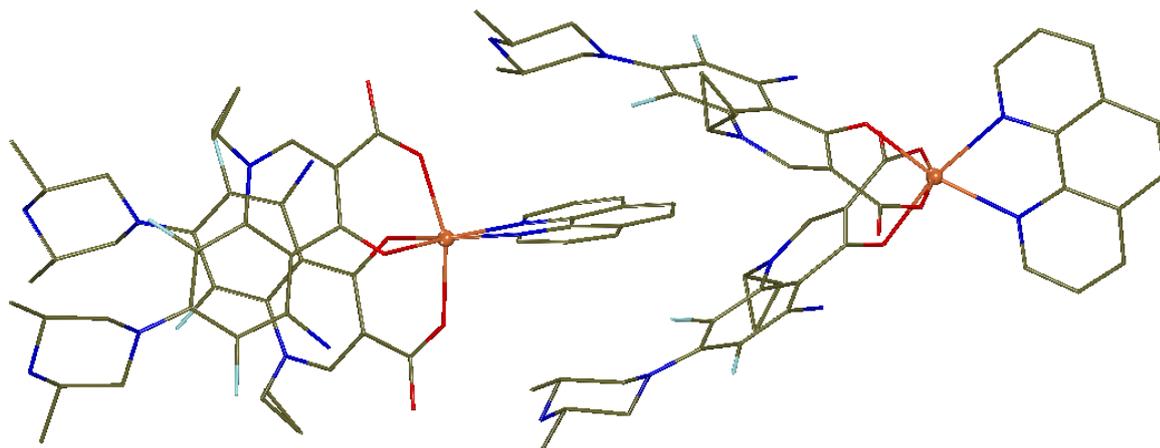
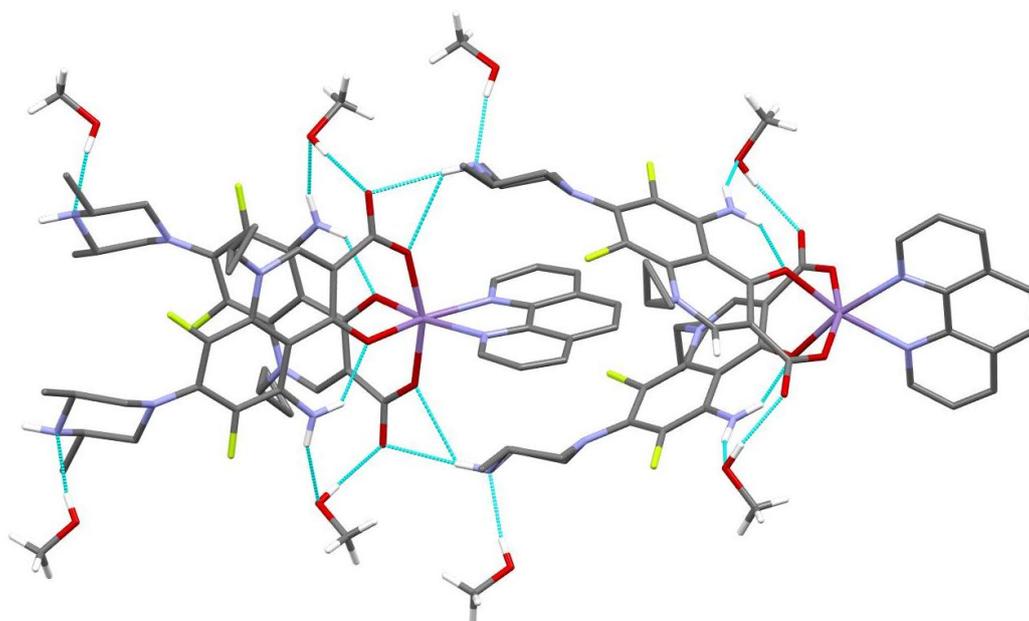
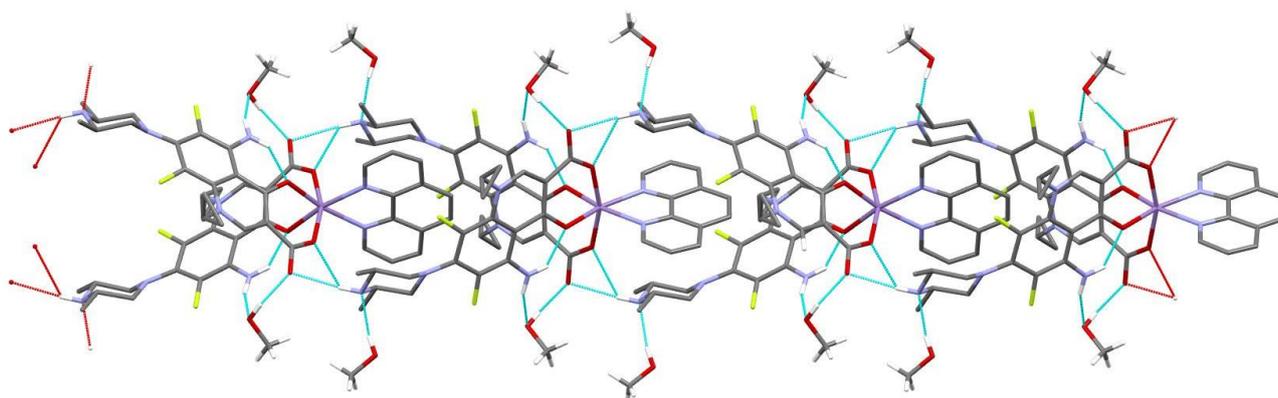


Figure S1. Interaction of guest–host molecules in **1**. Mn in orange, O in red, N in blue, C in dark yellow and F in light blue.



(A)



(B)

Figure S2. (A) Hydrogen bonding in 1:4MeOH, (B) chain formation. Hydrogen atoms not involved in the motif shown have been omitted for clarity.

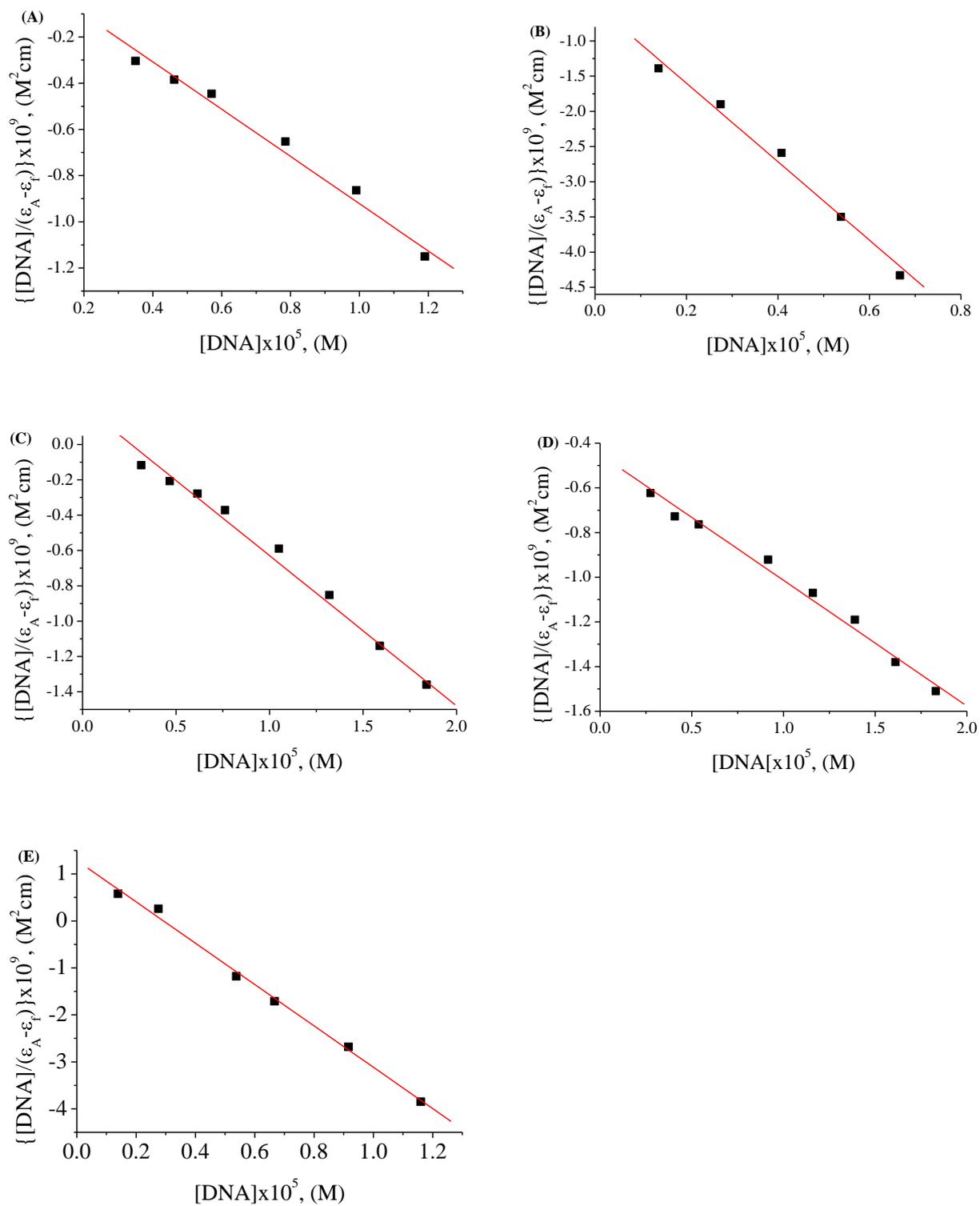


Figure S3. (A)–(E) Plot of $\frac{[DNA]}{(\epsilon_A - \epsilon_f)}$ vs $[DNA]$ for complexes 1–5, respectively.

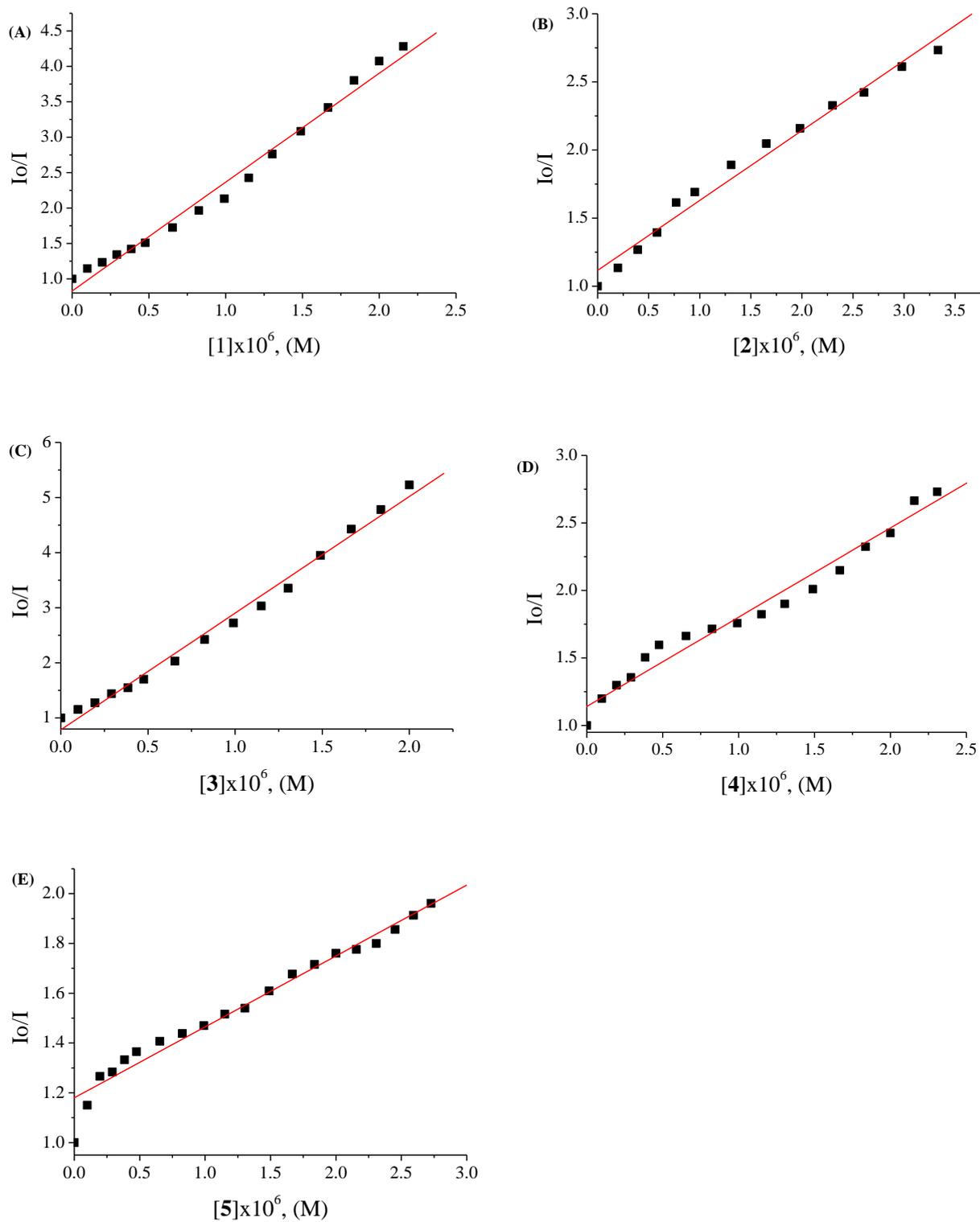


Figure S4. (A)–(E) Stern–Volmer quenching plot of EB bound to CT DNA for complexes 1–5, respectively.

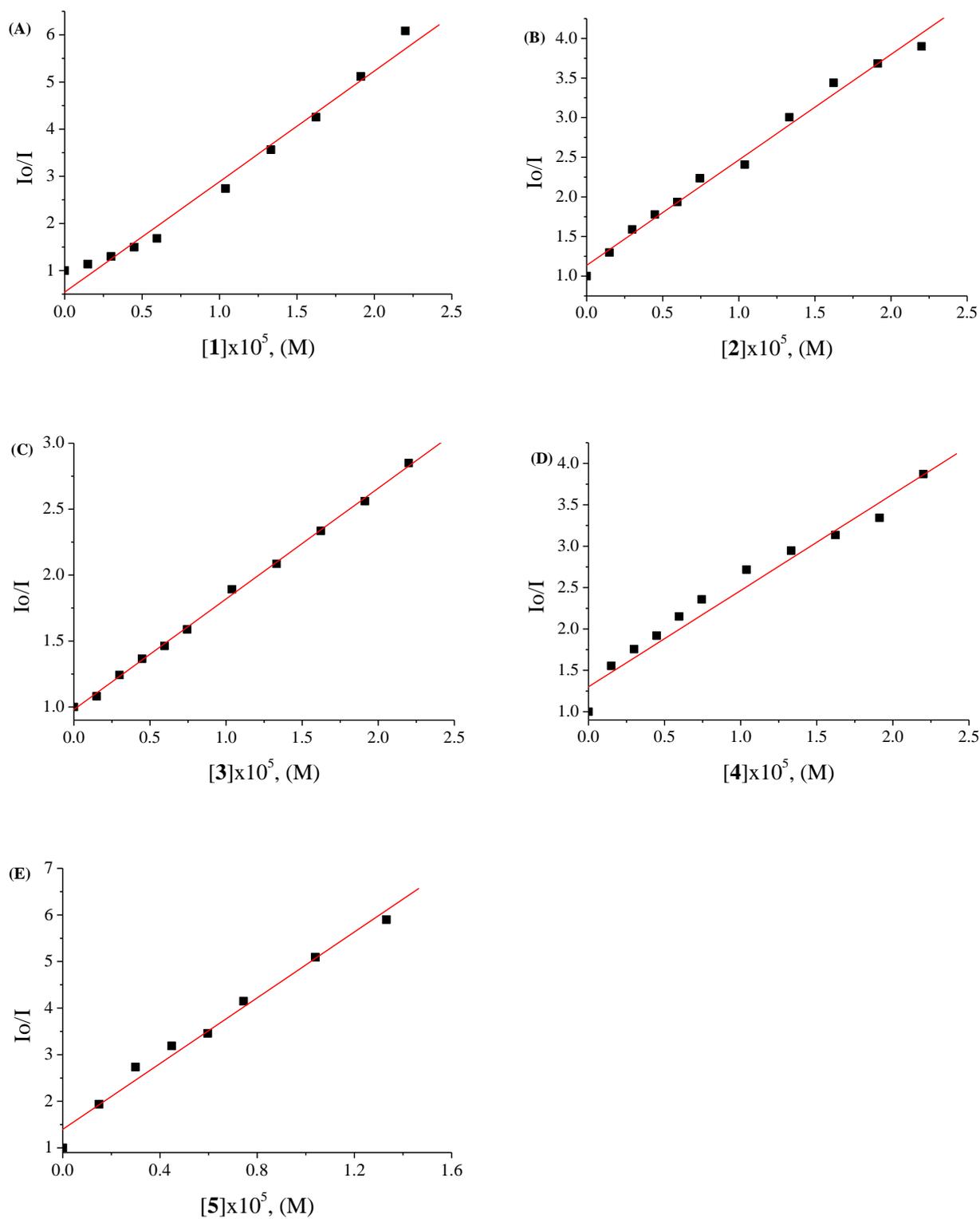


Figure S5. (A)–(E) Stern–Volmer quenching plot of HSA for complexes 1–5, respectively.

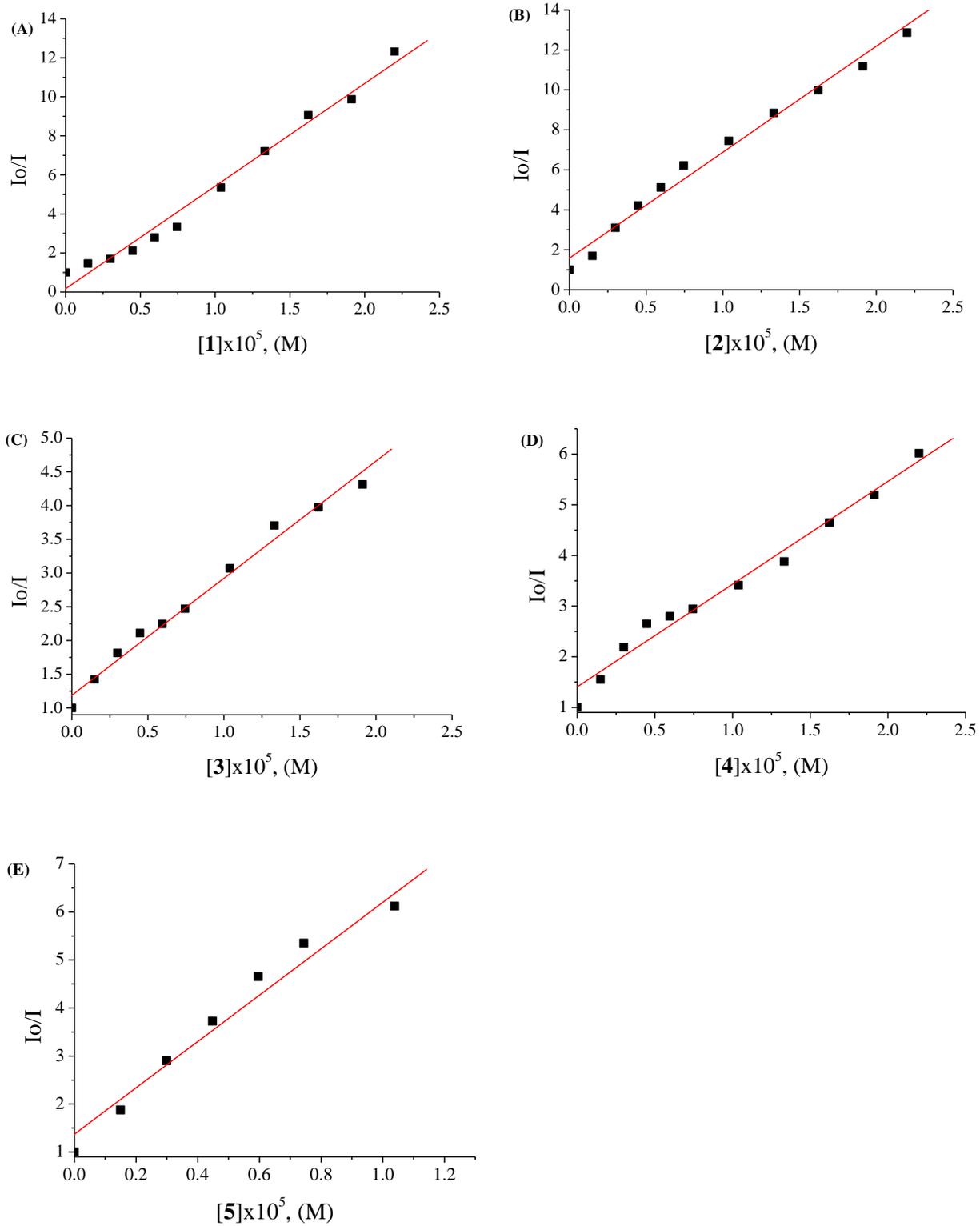


Figure S6. (A)–(E) Stern–Volmer quenching plot of BSA for complexes 1–5, respectively.

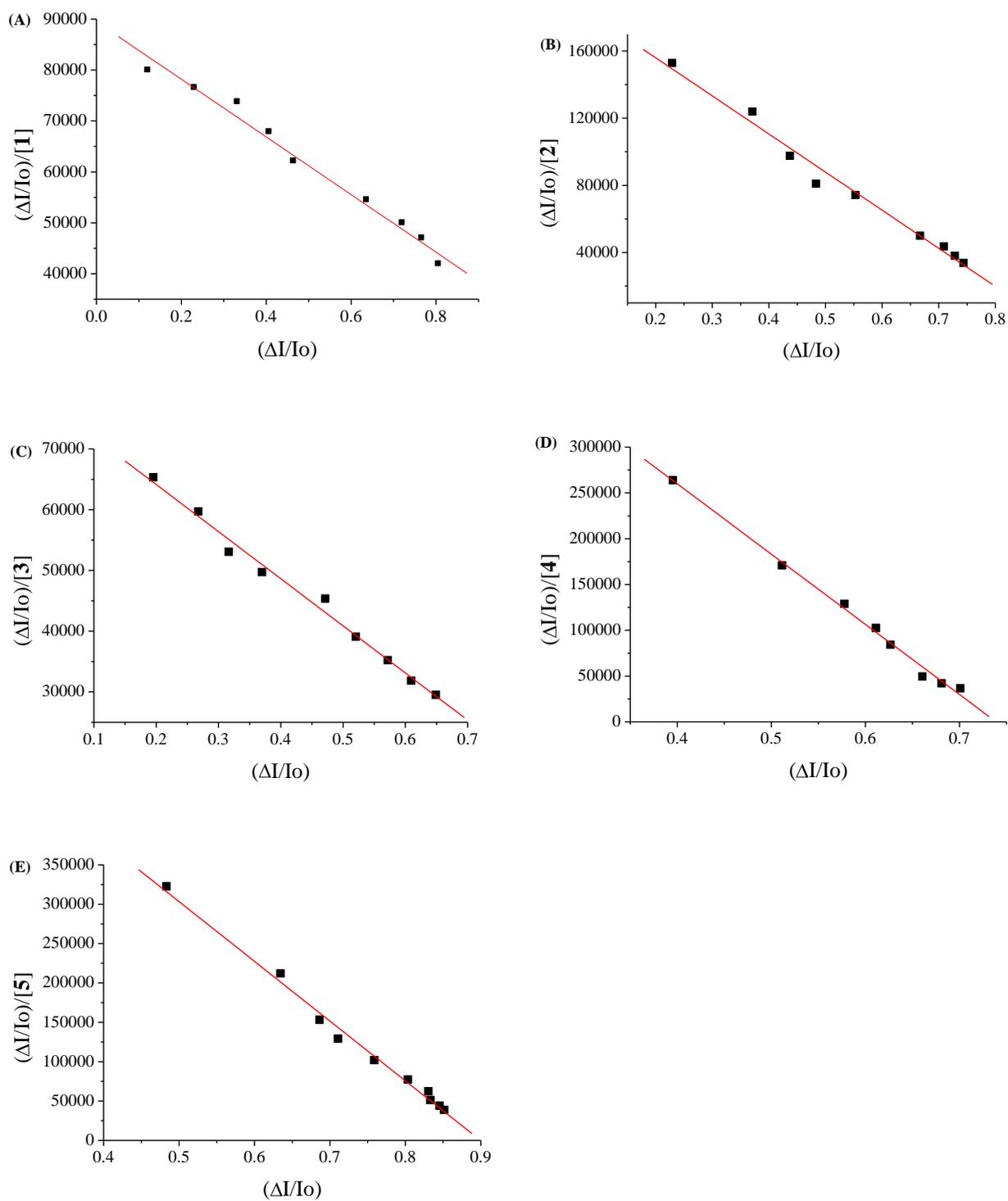


Figure S7. (A)–(E) Scatchard plot of HSA for complexes 1–5, respectively.

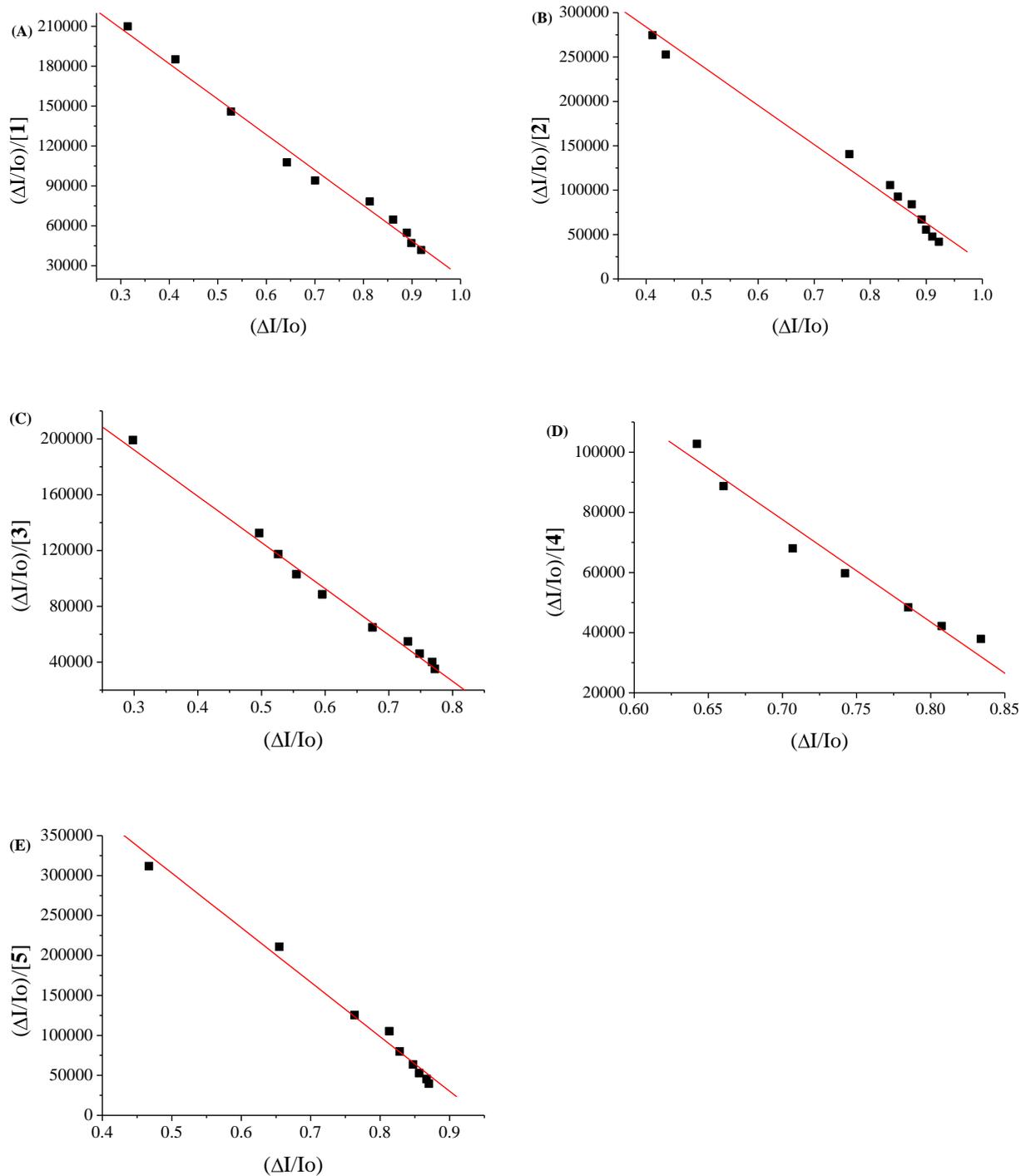


Figure S8. (A)–(E) Scatchard plot of BSA for complexes 1–5, respectively.