

# Detailed Experimental and in Silico Investigation of Indomethacin Binding with Human Serum Albumin Considering Primary and Secondary Binding Sites

## Supplementary Materials

UV–Visible spectra were recorded between the wavelength range of 200 to 400 nm on Perkin-Elmer Lambda 45 Spectrophotometer equipped with autosampler and water-bath with temperature controller. Quartz cuvettes of 1 cm path length were used for the measurements.

Fluorescence measurements were performed on Hitachi spectrofluorometer (Model F 7000) equipped with a PC and programmable temperature controller. Unless stated, the fluorescence spectra were collected at 25 °C with a cell of path length 1 cm. The excitation and emission slits were set at 5 nm. Intrinsic fluorescence was measured by exciting HSA at 280 nm and 295 nm.

The circular dichroism studies of HSA in presence of indomethacin were carried out with JASCO J-815 spectropolarimeter equipped with a Peltier-type temperature controller. The instrument was calibrated with d-10-camphorsulfonic acid. All the CD spectra were collected in a cell of 0.5 mm path-length. The scan speed was 100 nm/min and response time of 1 s for all measurements. Each spectrum was the average of 3 scans.

### Equation used for inner filter effect correction:

The observed fluorescence spectra were corrected with following equation:

$$F_{corr} = F_{obs} \times 10^{(A_{exi} + A_{emi})/2} \quad (S1)$$

where,  $F_{\text{corr}}$  and  $F_{\text{obs}}$  are the corrected and observed fluorescence emission intensities, of HSA respectively,  $A_{\text{exi}}$  and  $A_{\text{emi}}$  are the absorbances of indomethacin at the excitation and emission wavelengths, respectively.

**Equation used to calculate thermodynamic parameters:**

van 't Hoff equation is given as:

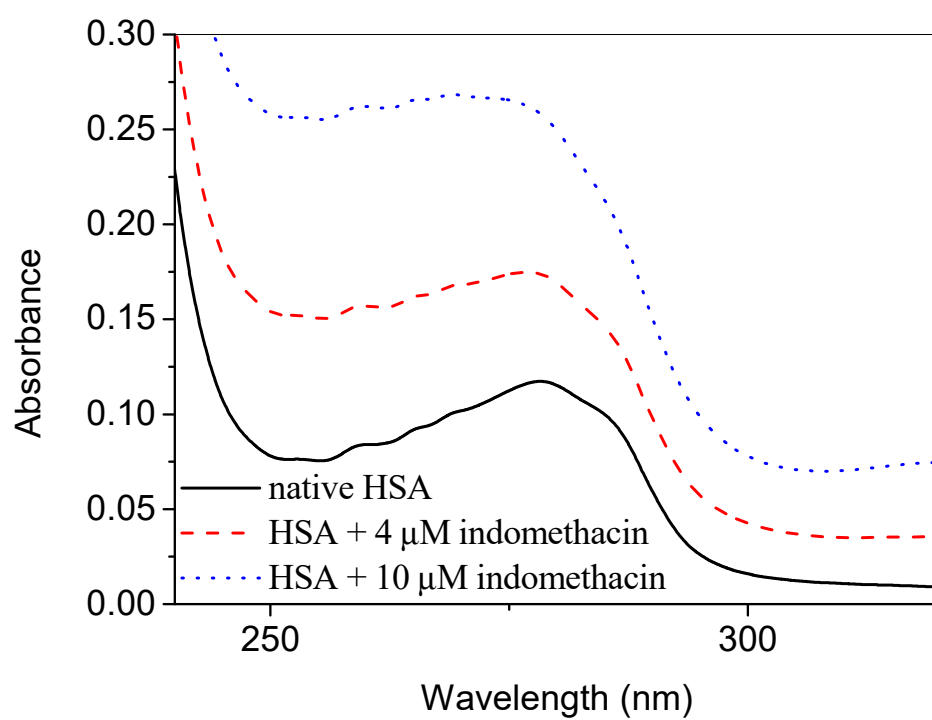
$$\ln K_b = \frac{-\Delta H}{RT} + \frac{\Delta S}{R} \quad (\text{S2})$$

$$\Delta G = \Delta H - T\Delta S \quad (\text{S3})$$

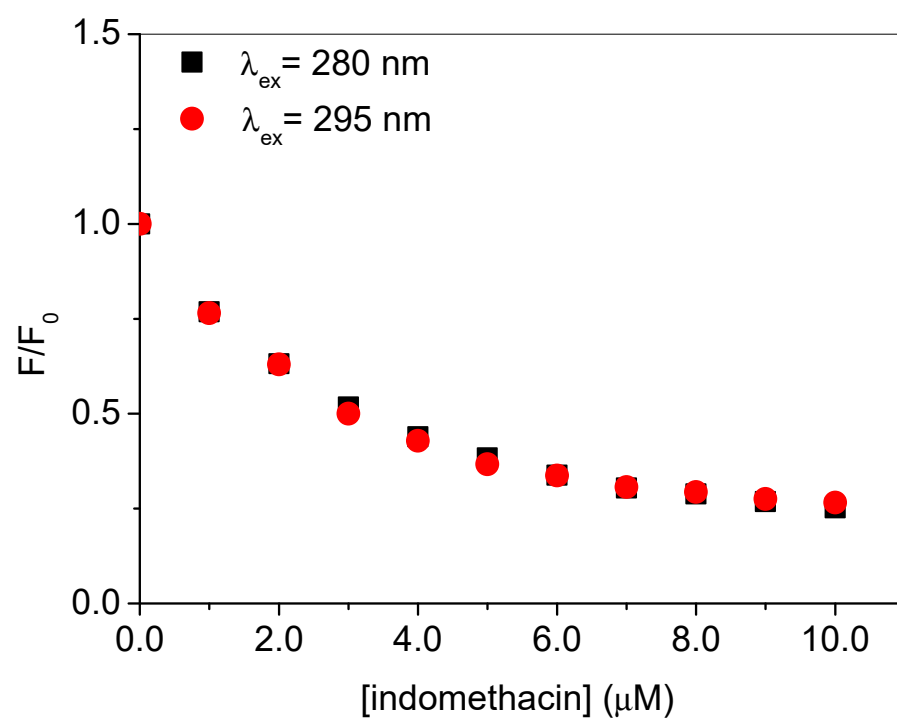
where  $\Delta H$  is enthalpy change,  $\Delta S$  is entropy change and  $\Delta G$  is free energy change.  $R$  is gas constant and  $T$  is temperature in K.

**Table S1.** Biomolecular quenching constants ( $K_{q1}$ ,  $K_{q2}$ ) of HSA-indomethacin interaction by exciting the protein at 295 nm.

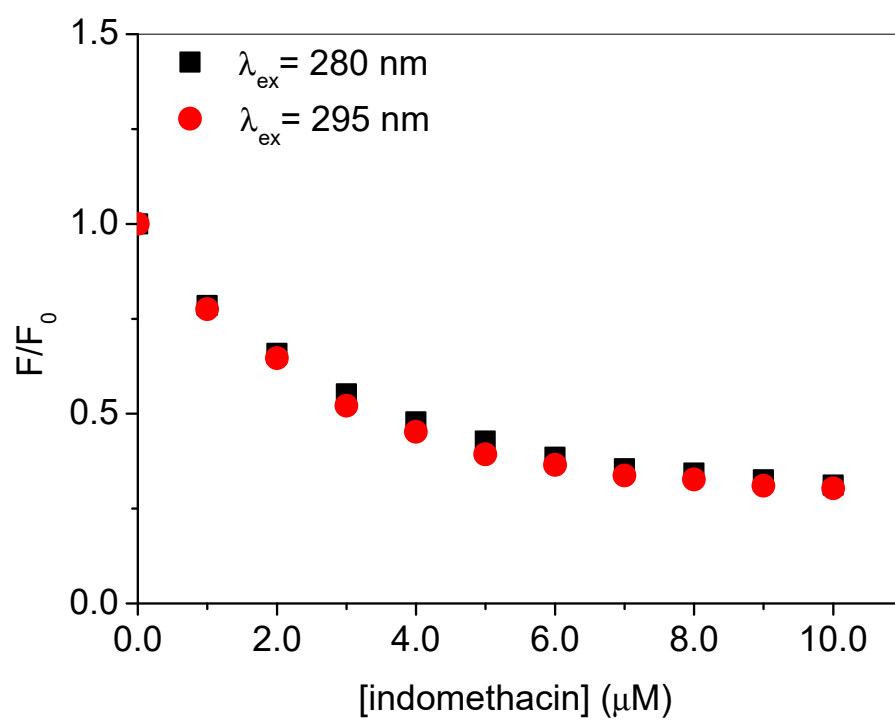
	Temperature		
	25°C	35°C	45°C
$K_{q1} (\text{mol}^{-1})$	$5.1 \times 10^{13}$	$4.1 \times 10^{13}$	$3.6 \times 10^{13}$
$K_{q2} (\text{mol}^{-1})$	$2.5 \times 10^{13}$	$2.2 \times 10^{13}$	$1.7 \times 10^{13}$



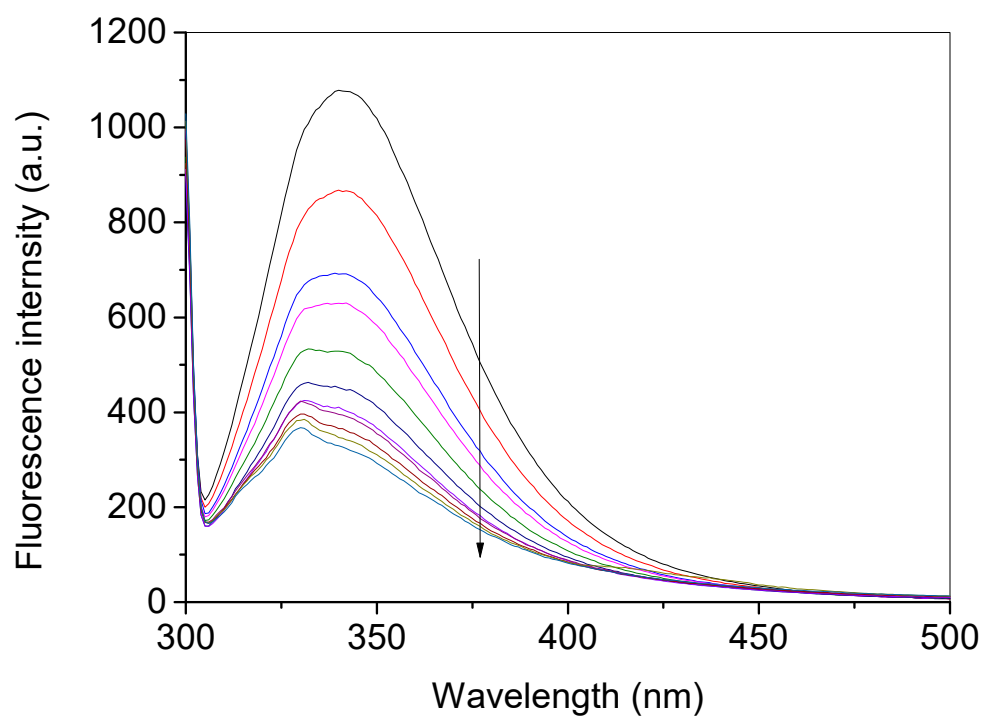
**Figure S1.** UV-visible spectra of HSA in absence and presence of indomethacin at 25 °C.



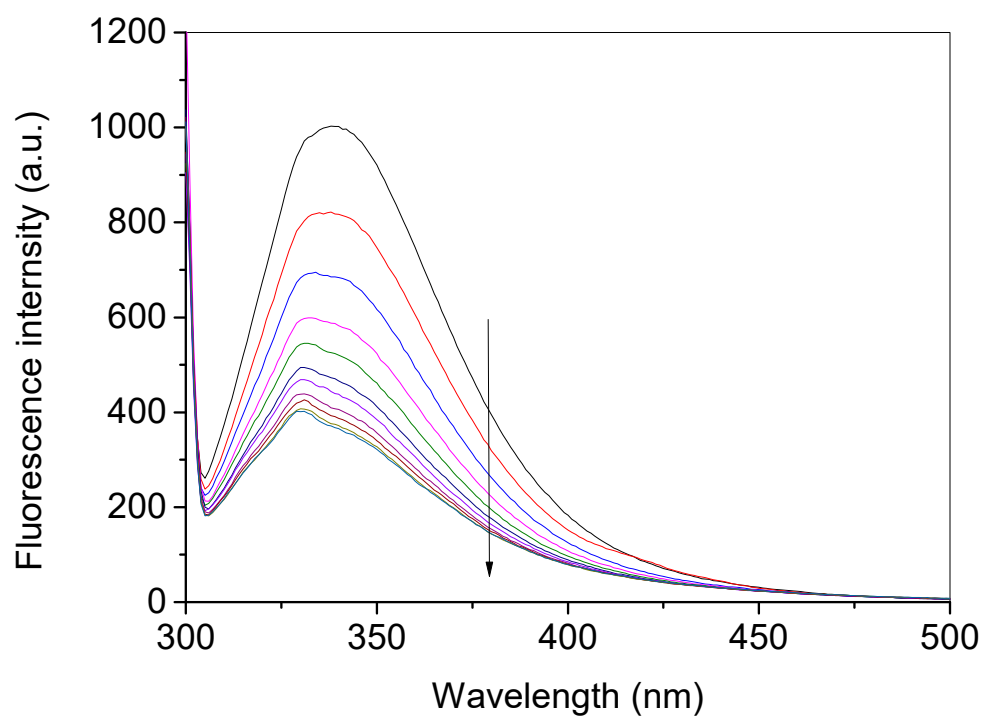
**Figure S2.** RFI of HSA fluorescence at 340 nm obtained from the observed data at 25 °C at two excitation wavelengths.



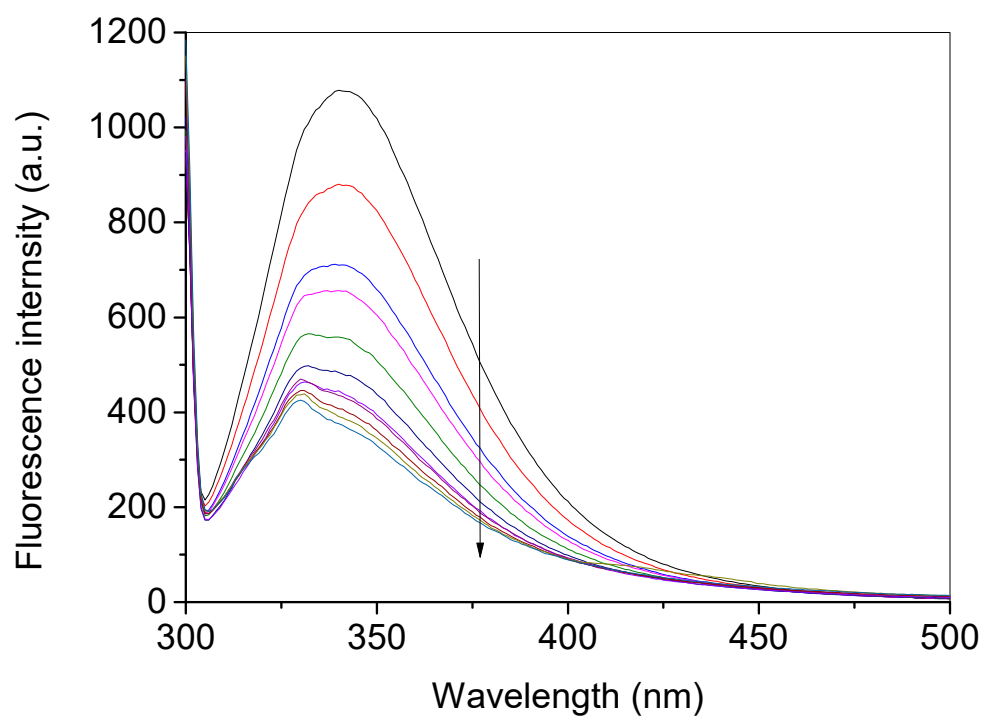
**Figure S3.** RFI of HSA fluorescence at 340 nm obtained from the corrected data at 25 °C at two excitation wavelengths.



**Figure S4.** Observed fluorescence spectra of HSA in absence and presence of indomethacin at  $\lambda_{\text{ex}}$  of 295 nm at 35 °C. [HSA] = 3  $\mu\text{M}$  and [indomethacin] = 0, 1.0, 2.0, 3.0, 4.0, 5.0, 6.0, 7.0, 8.0, 9.0 and 10.0  $\mu\text{M}$ .

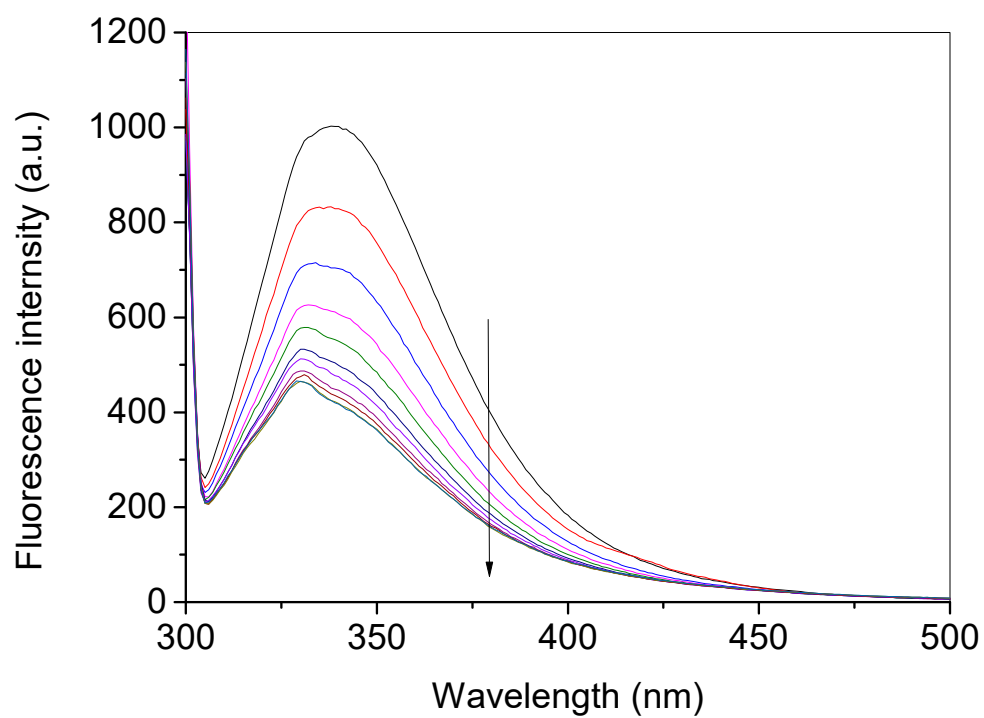


**Figure S5.** Observed fluorescence spectra of HSA in absence and presence of indomethacin at  $\lambda_{\text{ex}}$  of 295 nm at 45 °C. [HSA] = 3  $\mu\text{M}$  and [indomethacin] = 0, 1.0, 2.0, 3.0, 4.0, 5.0, 6.0, 7.0, 8.0, 9.0 and 10.0  $\mu\text{M}$ .

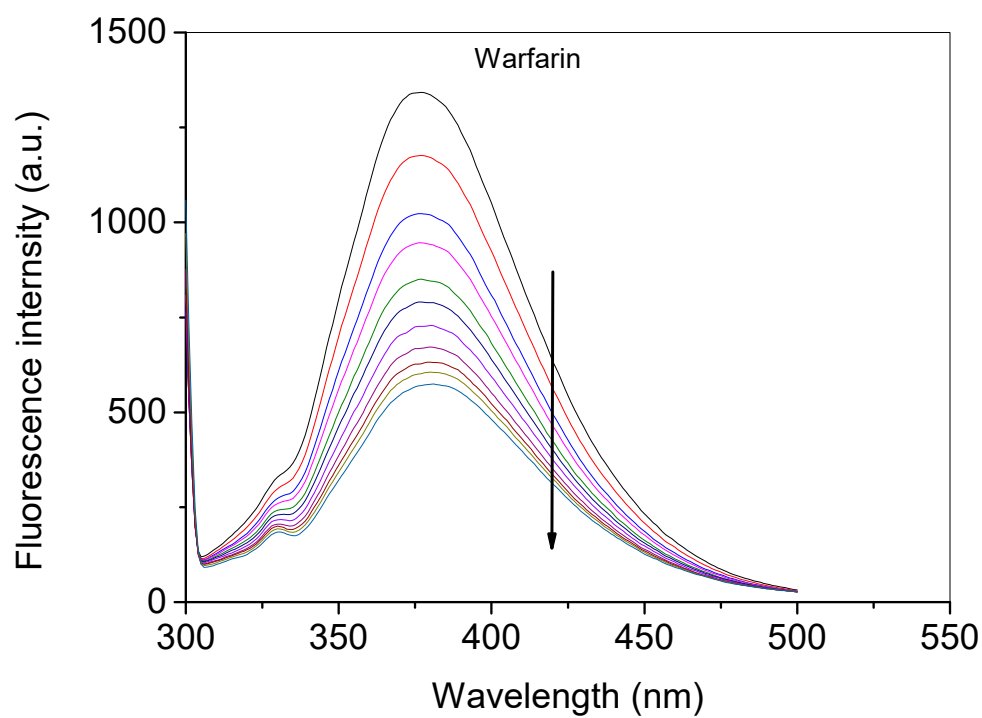


**Figure S6.** Corrected fluorescence spectra of HSA in absence and presence of indomethacin at  $\lambda_{\text{ex}}$  of 295 nm at 35  $^{\circ}\text{C}$ . [HSA] = 3  $\mu\text{M}$  and [indomethacin] = 0, 1.0, 2.0, 3.0, 4.0, 5.0, 6.0, 7.0, 8.0, 9.0 and 10.0  $\mu\text{M}$ .

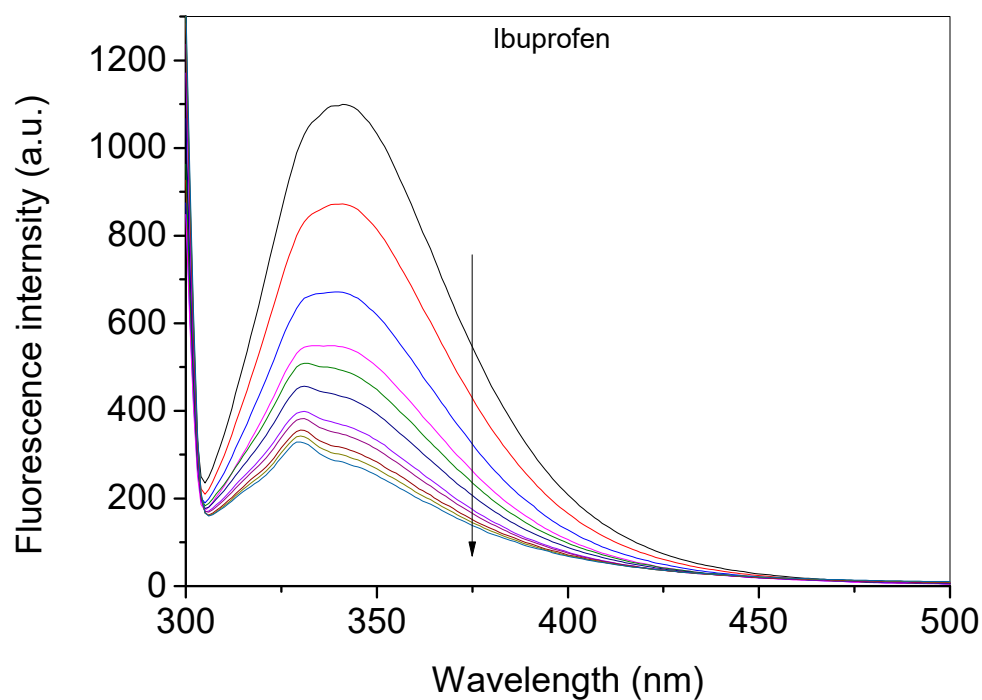




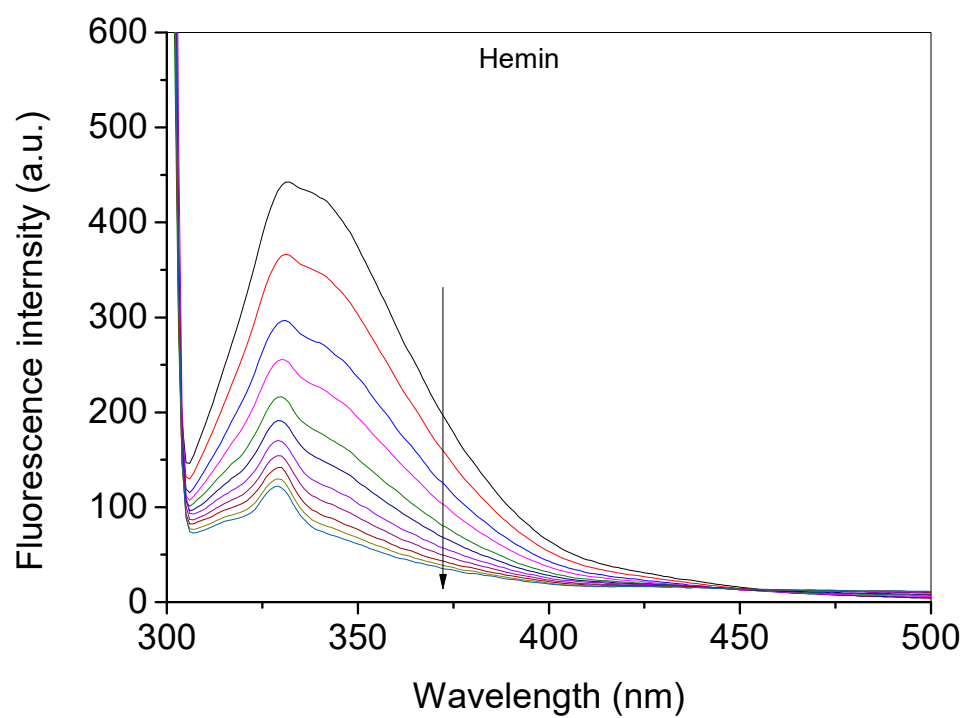
**Figure S7.** Corrected fluorescence spectra of HSA in absence and presence of indomethacin at  $\lambda_{\text{ex}}$  of 295 nm at 45 °C. [HSA] = 3  $\mu\text{M}$  and [indomethacin] = 0. 1.0, 2.0, 3.0, 4.0, 5.0, 6.0, 7.0, 8.0, 9.0 and 10.0  $\mu\text{M}$ .



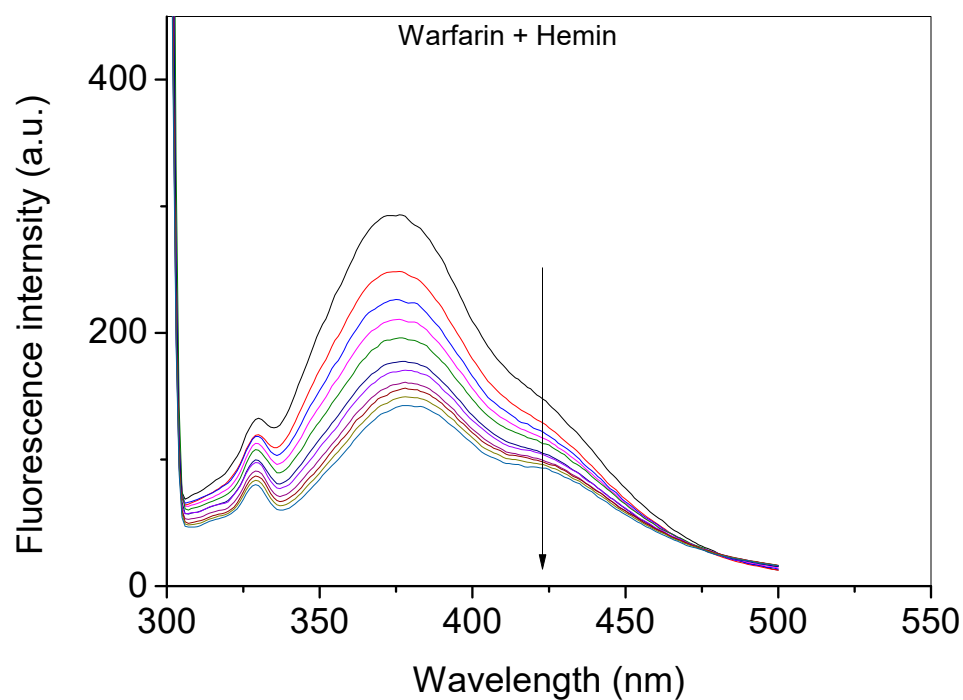
**Figure S8.** Observed fluorescence spectra of HSA-warfarin system in absence and presence of indomethacin at  $\lambda_{\text{ex}}$  of 295 nm at 25 °C. [HSA] = 3  $\mu\text{M}$  and [indomethacin] = 0.1, 2.0, 3.0, 4.0, 5.0, 6.0, 7.0, 8.0, 9.0 and 10.0  $\mu\text{M}$ .



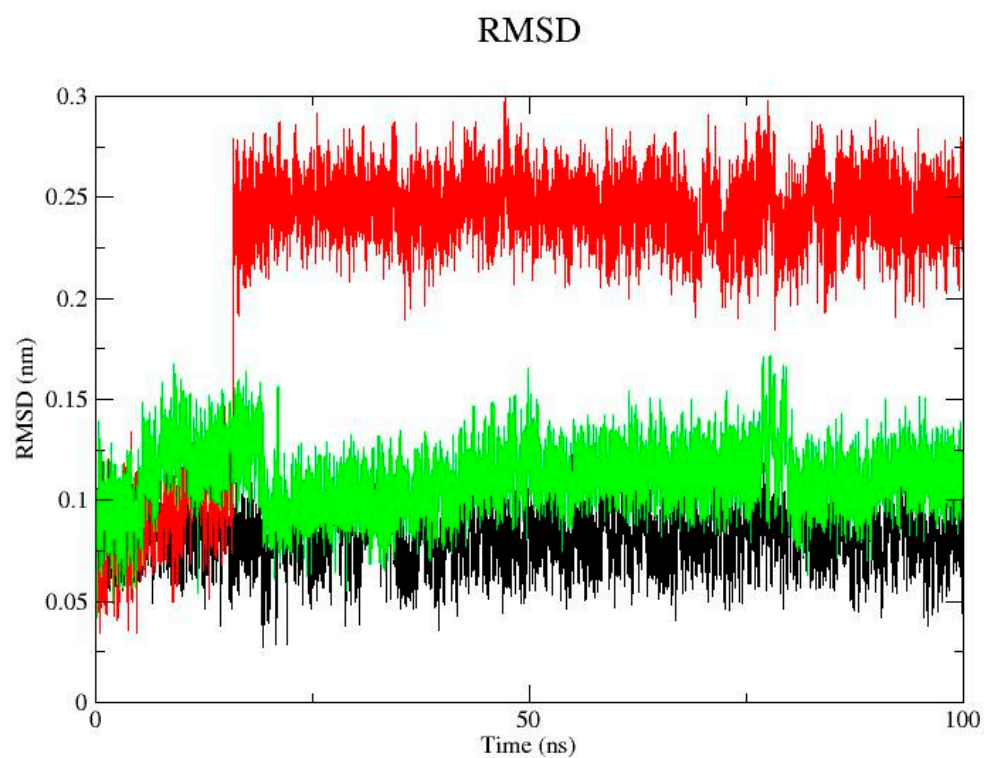
**Figure S9.** Observed fluorescence spectra of HSA-ibuprofen system in absence and presence of indomethacin at  $\lambda_{\text{ex}}$  of 295 nm at 25 °C. [HSA] = 3  $\mu\text{M}$  and [indomethacin] = 0, 1.0, 2.0, 3.0, 4.0, 5.0, 6.0, 7.0, 8.0, 9.0 and 10.0  $\mu\text{M}$ .



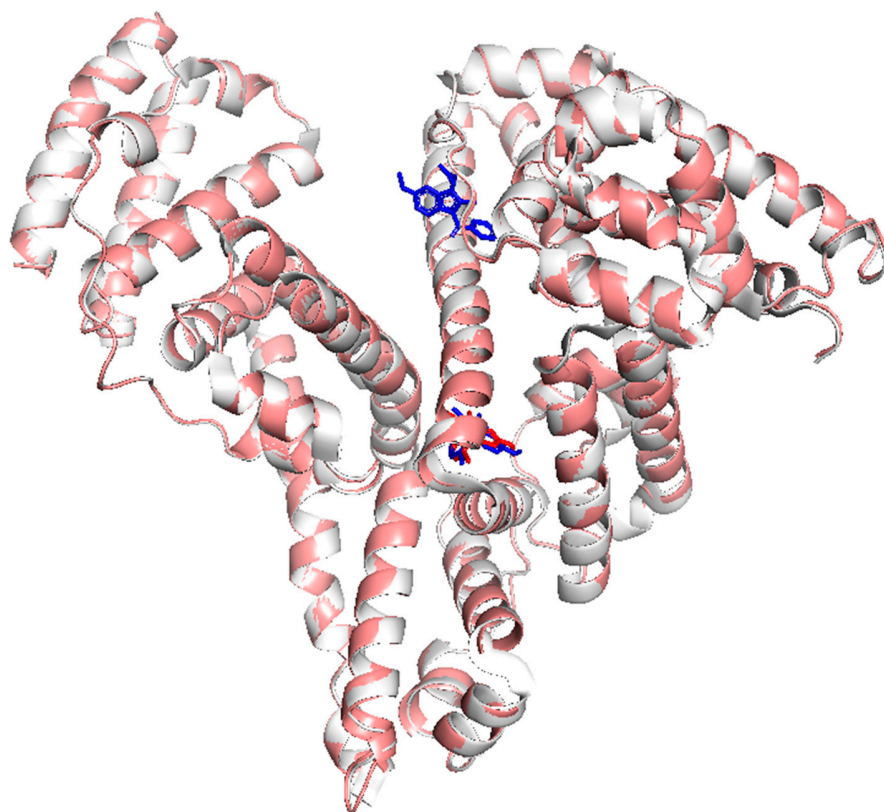
**Figure S10.** Observed fluorescence spectra of HSA-hemin system in absence and presence of indomethacin at  $\lambda_{\text{ex}}$  of 295 nm at 25 °C. [HSA] = 3  $\mu\text{M}$  and [indomethacin] 0. 1.0, 2.0, 3.0, 4.0, 5.0, 6.0, 7.0, 8.0, 9.0 and 10.0  $\mu\text{M}$ .



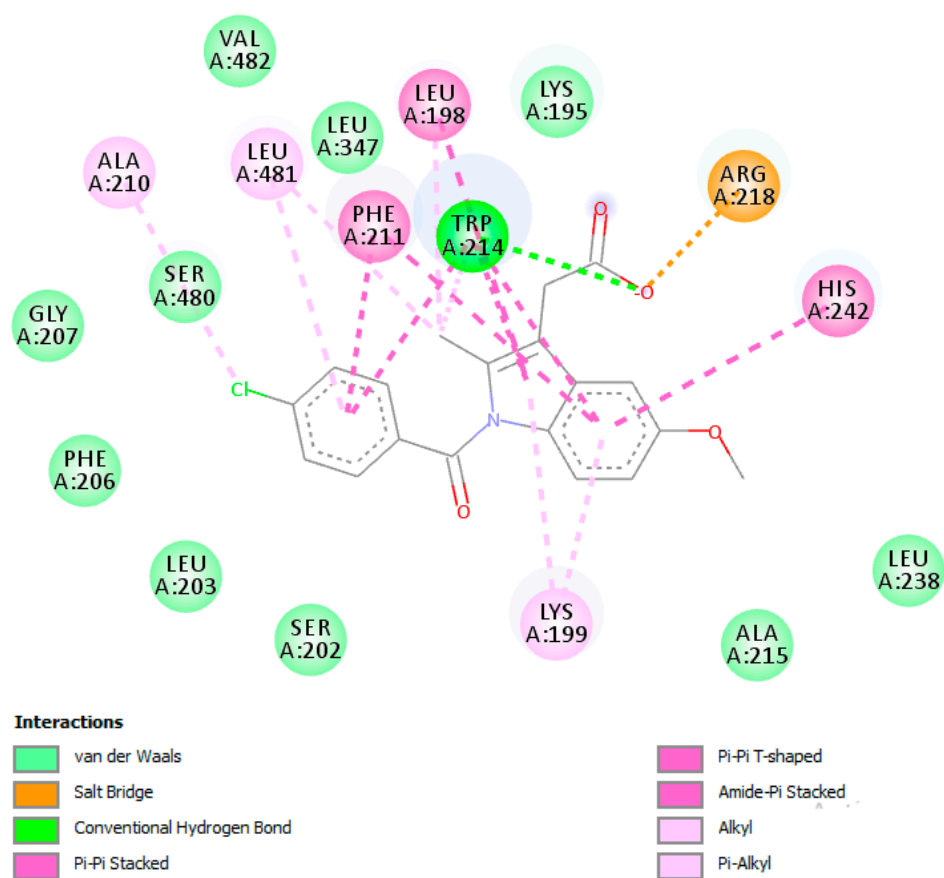
**Figure S11.** Observed fluorescence spectra of HSA-warfarin-hemin system in absence and presence of indomethacin at  $\lambda_{\text{ex}}$  of 295 nm at 25 °C. [HSA] = 3  $\mu\text{M}$  and [indomethacin] = 0. 1.0, 2.0, 3.0, 4.0, 5.0, 6.0, 7.0, 8.0, 9.0 and 10.0  $\mu\text{M}$ .



**Figure S12.** Root Mean Square Deviation of indomethacin towards three sites of HSA (Black-DS1, Red-DS2 and Green-FA1)

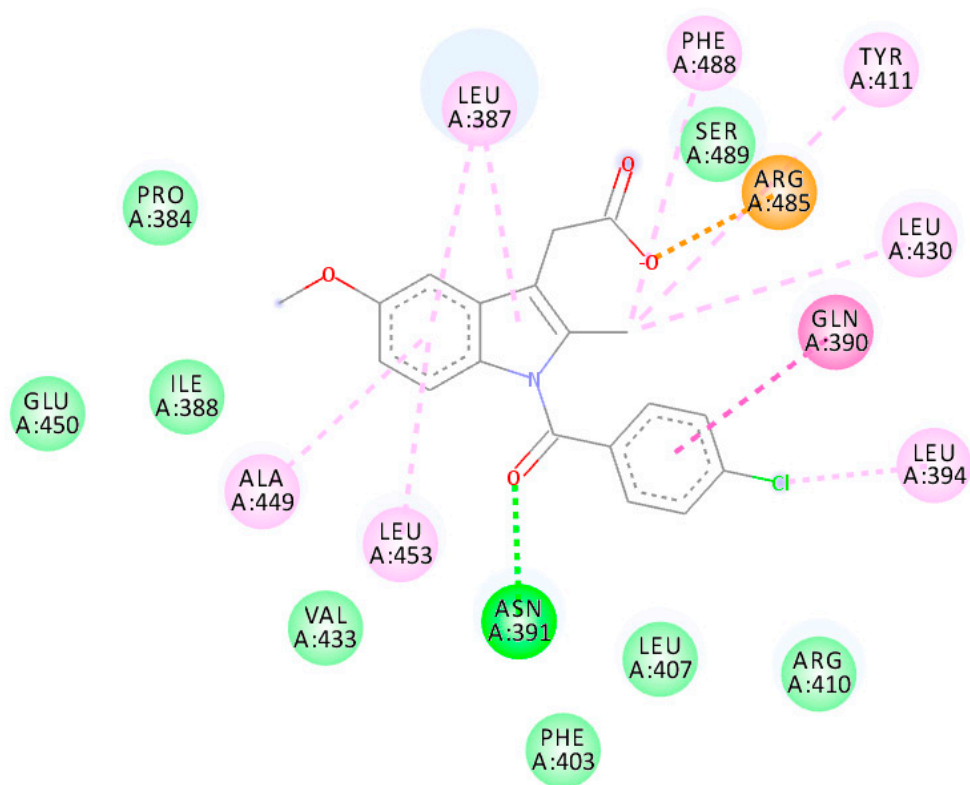


**Figure S13.** Structural superposition of docking solution of indomethacin bound HSA with crystal structure of indomethacin bound HSA (PDB ID: 2BXM) (Blue: Crystal orientation of indomethacin, Red: Docking orientation of indomethacin)



**Figure S14.** Two-dimensional protein-ligand interaction of indomethacin towards DS1 of HSA (optimized conformation from 100ns MD simulation)



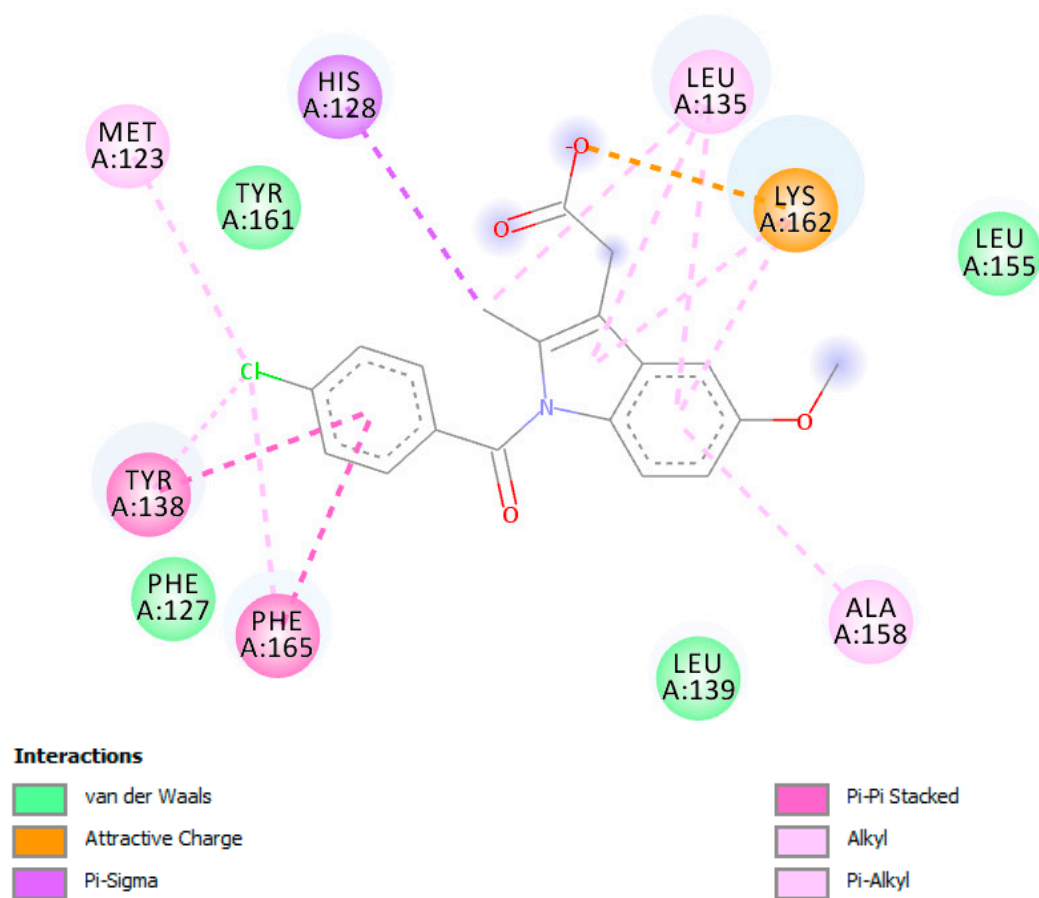


#### Interactions

- van der Waals
- Attractive Charge
- Conventional Hydrogen Bond

- Amide-Pi Stacked
- Alkyl
- Pi-Alkyl

**Figure S15.** Two-dimensional protein-ligand interaction of indomethacin towards DS2 of HSA (optimized conformation from 100ns MD simulation)



**Figure S16.** Two-dimensional protein-ligand interaction of indomethacin towards FA1 of HSA (optimized conformation from 100ns MD simulation)