Supplementary files

Folate conjugated albumin as a targeted nanocarrier for the delivery of Fisetin: *In-silico* and *in-vitro* biological studies

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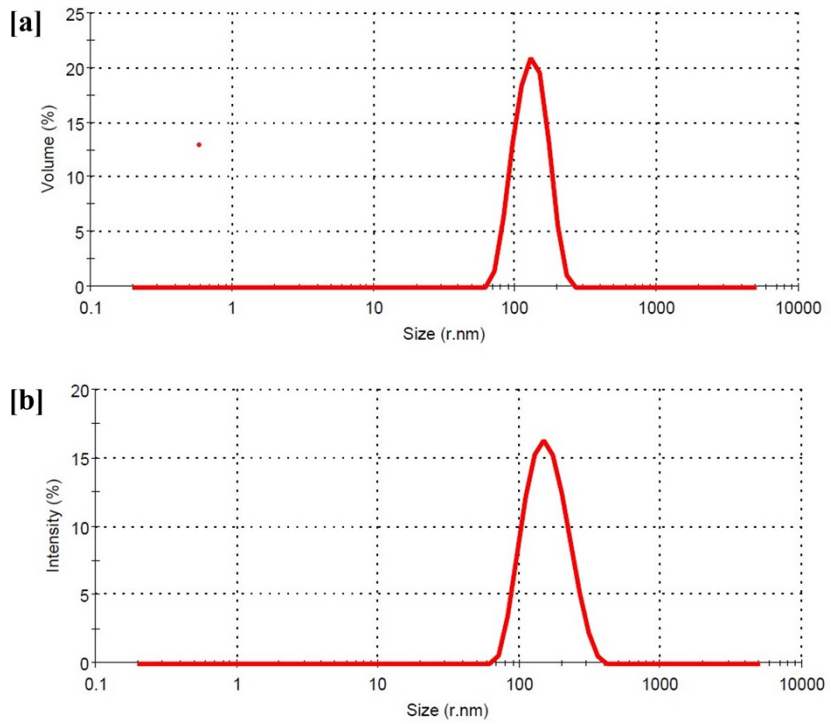

Figure S1. *Hydrodynamic size distribution of CNPs (a) and FNPs (b) determined using DLS.*

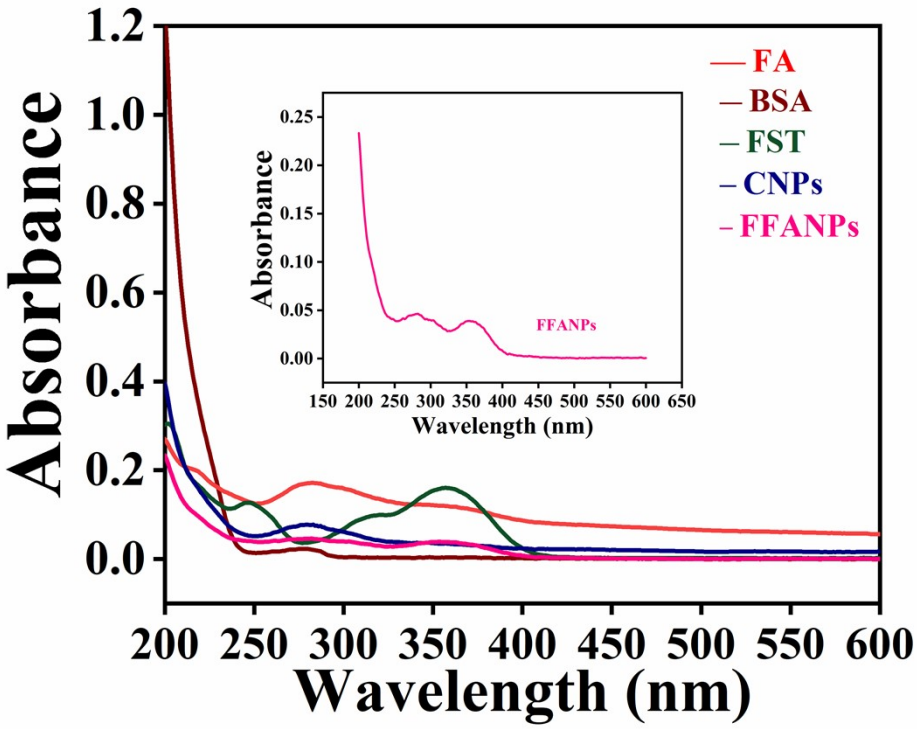

Figure S2. *UV spectrum of FA, BSA, FST, CNPs and FFANPs.*

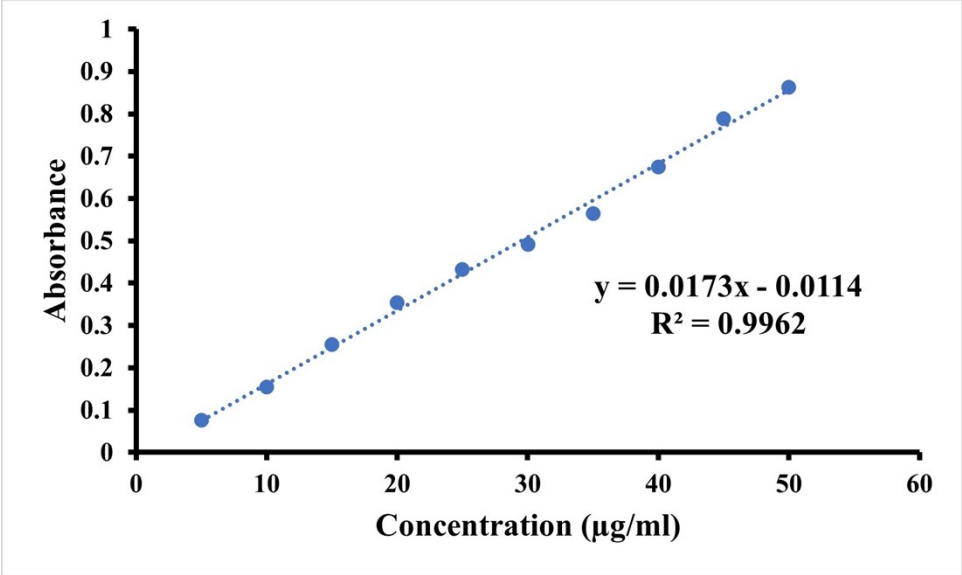

Figure S3. *Standard curve of Folic acid.*

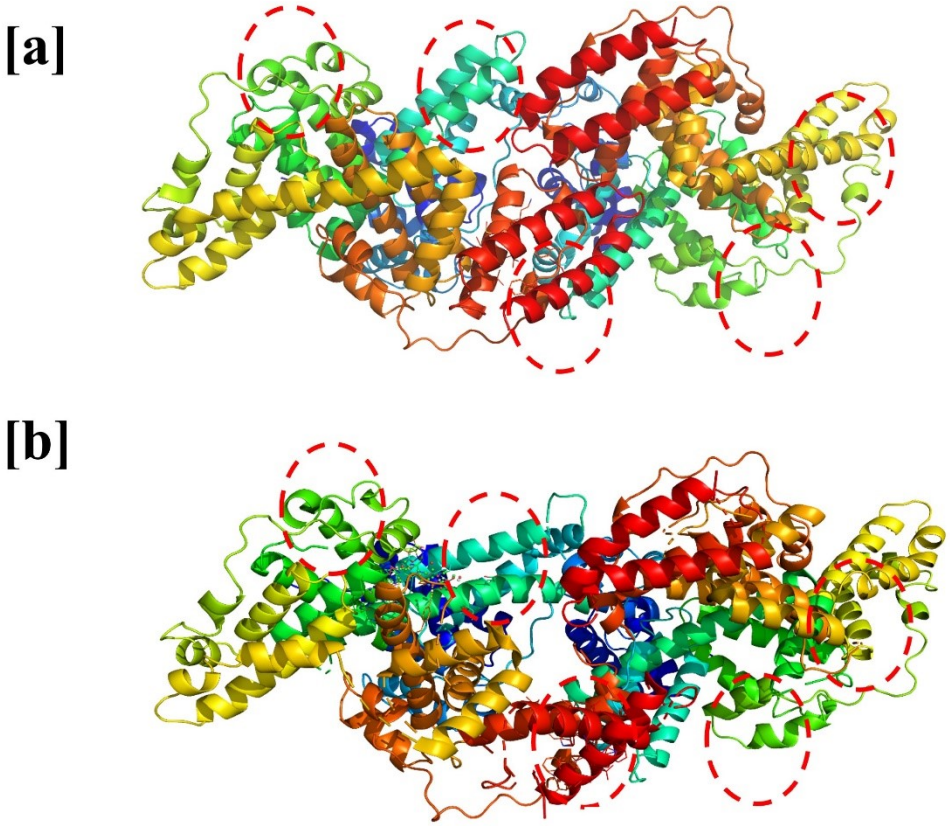

Figure S4. *3D structural comparison of BSA (a) and BSA/FST/FA complex system (b).*

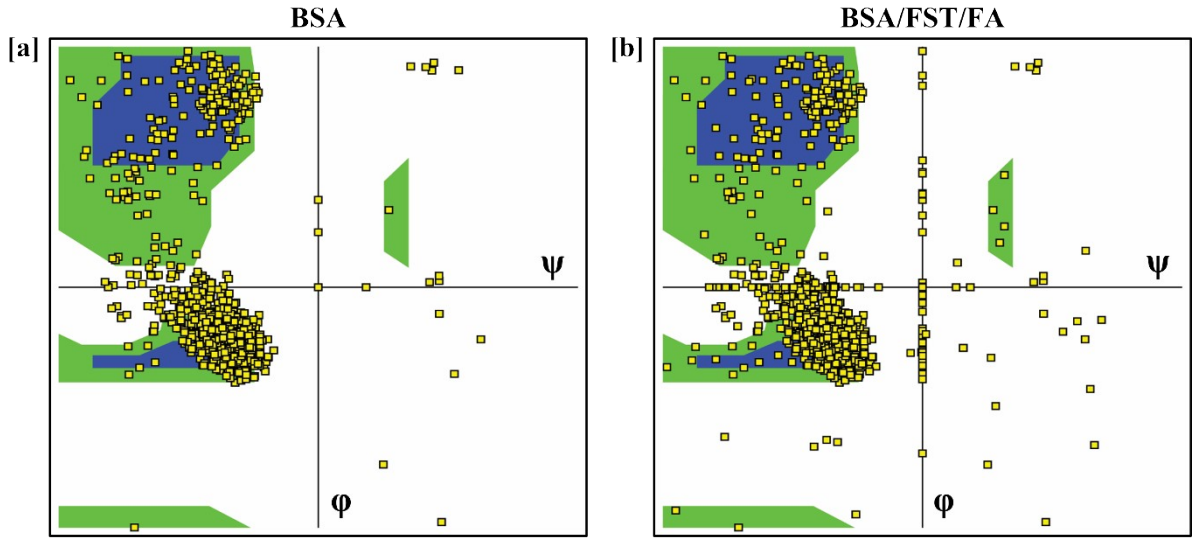

Figure S5. *Ramachandran plot of BSA (a) and BSA/FST/FA complex (b).*

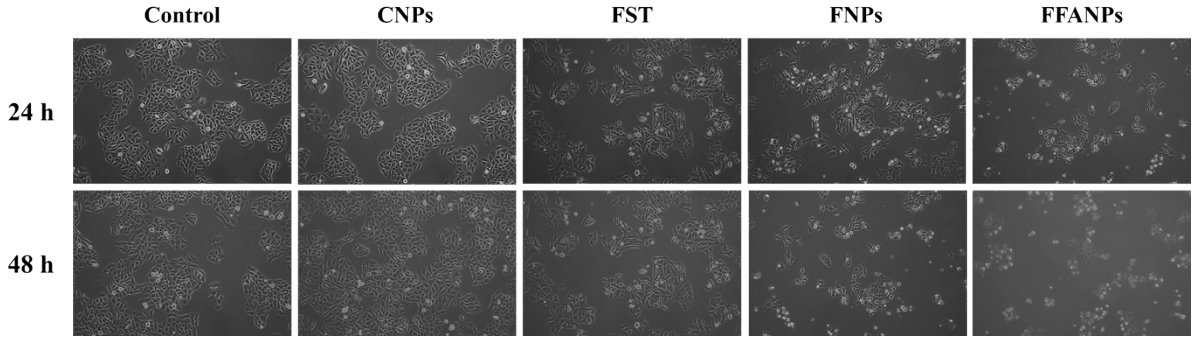

Figure S6. *Morphological analysis of HeLa cells after treatment with CNPs, FST, FNPs and FFANPs at IC_{50} concentration dose for 24 h and 48 h.*

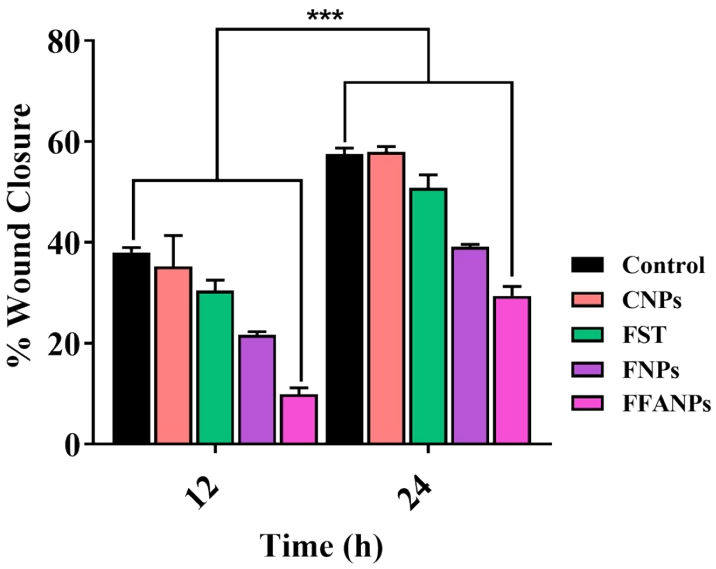

Figure S7. *Cells were treated with CNPs, FST, FNPs and FFANPs, photographed were captured and % wound closure calculated by using ImageJ software.*

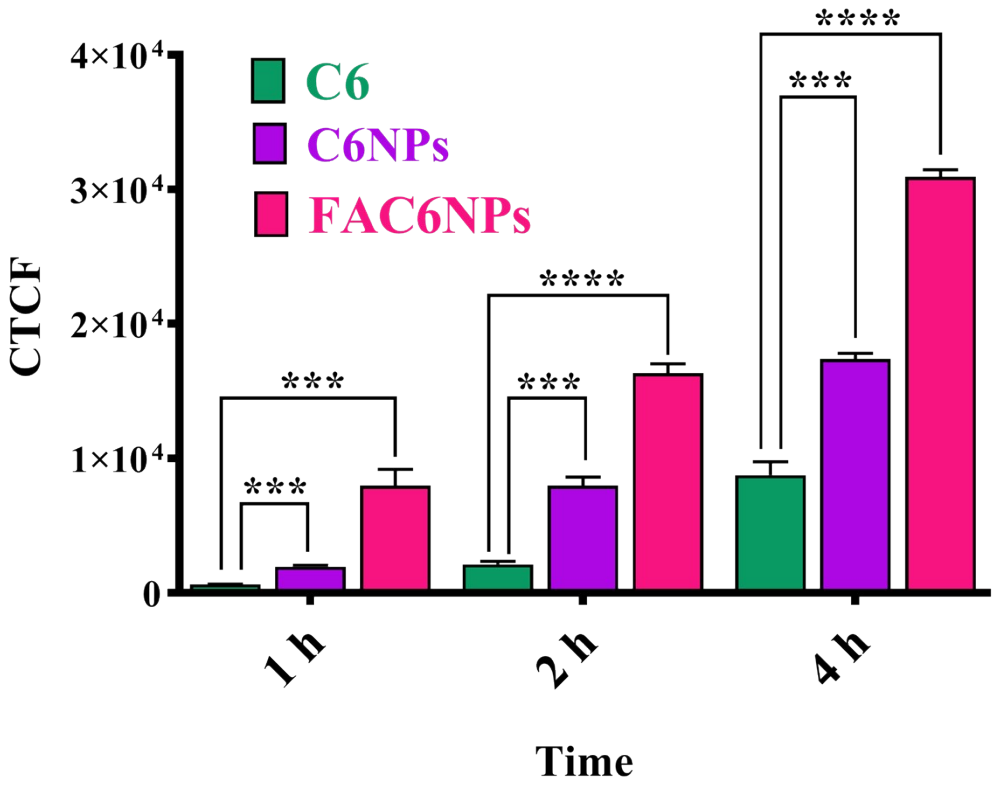

Figure S8. *Quantitative cellular uptake. CTCF values were calculated from respective fluorescence images of HeLa cells after treatment with C6, C6NPs and FAC6NPs for 1 h, 2 h and 4 h.*

Table S1. *Intermolecular docking score and analysis of BSA amino acid with FST and FA.*

Compound	Binding Energy (kcal/mol)	Amino Acid	Types of Bonding
BSA/FST	-8.1	GLU-125(A) (3.0,2.7)	Hydrophobic, π – cation
		LYS-136(A) (2.9)	H-bond
		LYS-350(B) (2.9)	H-bond
		VAL-481 (B) (3.2)	H-bond
		LEU-480(B) (3.1)	H-bond
BSA/FA	-8.8	TYR-149(A) (3.0)	H-bond
		TYR-156(A) (2.8)	Hydrophobic, π – cation
		LYS-187(A) (2.9)	Hydrophobic, π – π
		ARG-194(A) (3.0, 3.1)	π –cation, π – π, Hydrophobic
		ARG-256(A) (3.2, 3.1)	π –cation, π – π
		GLU-152(B) (2.9)	H-Bond
		GLN-220(B) (3.3)	H-Bond
		HIS-287(B) (3.2)	H-bond
		GLU-339(B) (3.0)	H-bond
		TYR-340(B) (2.8)	H-bond
		VAL-342(B) (3.3)	H-bond
BSA/FST/FA	-12.3	GLU-152(A) (2.9)	H-bond
		ARG-435(A) (3.3,3.3)	Hydrophobic, π – cation
		TYR-451(A) (2.8)	H-Bond
		GLU-186(B) (3.0)	H-Bond
		LEU-189(B) (3.3)	H-Bond
		SER-192(B) (2.8)	H-Bond
		ARG-427(B) (2.8)	H-Bond
		THR-518(B) (2.9)	H-Bond

Table S2. *Analysis of BSA/FST/FA complex structure amino acid through Ramachandran Plot.*

	Most Favoured Regions [A, B, L] (%)	Additional Allowed Regions [a, b, l, p] (%)	Generously Allowed Region (%)	Disallowed Regions (%)	G-Factor
BSA/FST/FA	91.6	5.9	1.9	0.6	-0.27

Table S3. *Analysis of BSA/FST/FA complex structure amino acid through Ramachandran Plot.*

Free Energy binding (Kcal/mol)	BSA/Fisetin/Folic Acid
ΔEelectrostatic	-39.28±0.38
ΔEvdw	-46.87±0.20
ΔG_{GB}	18.35±0.52
ΔG_{SA}	-22.82±0.87
ΔH	-35.77±0.77
-TΔS	19.5±0.33
ΔG	-71.12±0.07