Malachite nanoparticle: a new basic hydrophilic surface for pH controlled adsorption of BSA with a high loading capacity

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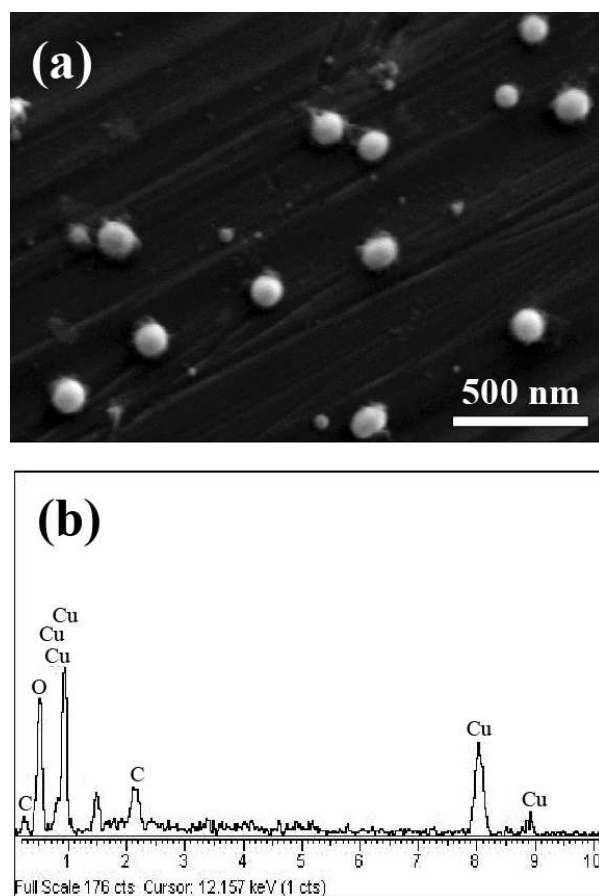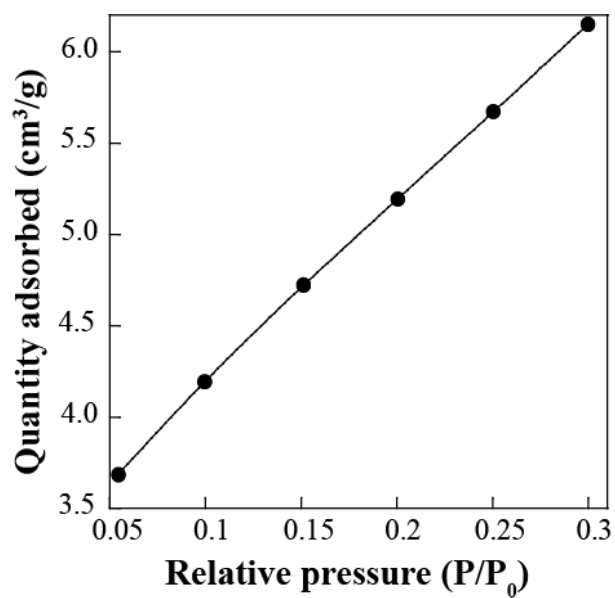
Supporting information

Figure S2. N_2 adsorption/desorption isotherms of malachite NPs measured from BET analysis.
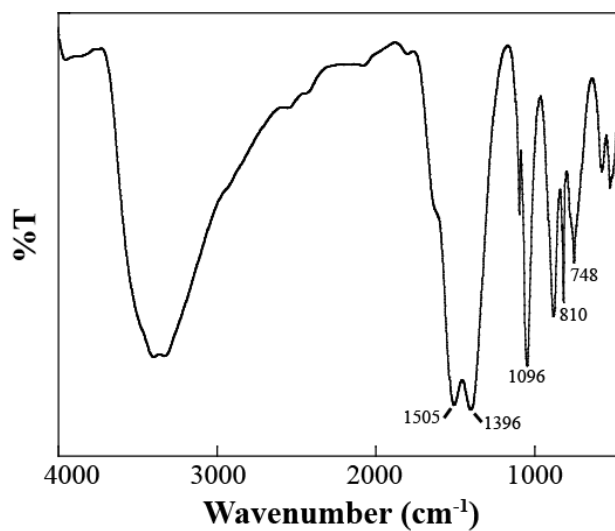
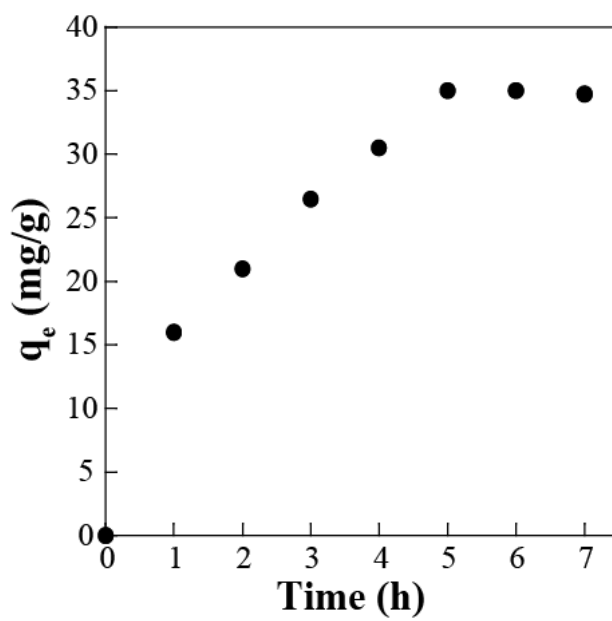**Figure S3.** FT-IR spectra of malachite NPs.

Figure S4. Adsorption kinetics with 1 mg/L BSA and 20 g/L malachite NPs at pH ~5.0. The steady state reaches within 5 h.
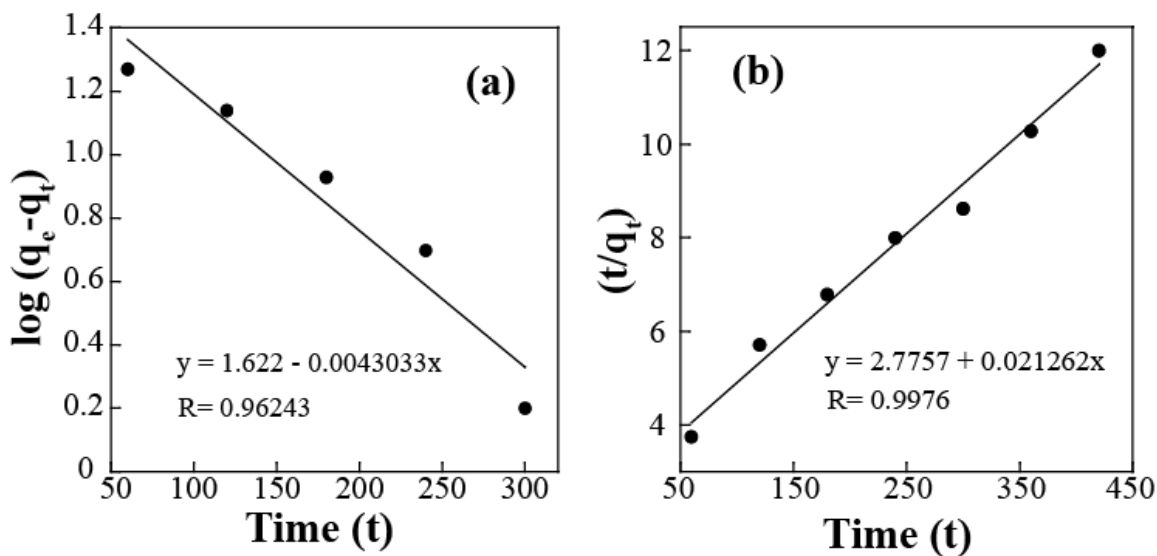
Figure S5. (a) Pseudo first order and (b) second order kinetics model of BSA adsorption studies on malachite performed with 1 mg/mL BSA and 20 g/L of malachite at pH ~5.0.
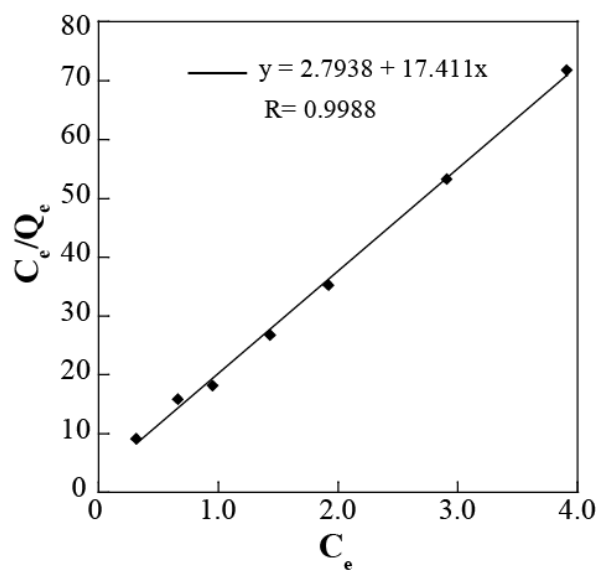

Figure S4. Scatchard plot of BSA adsorption on malachite NPs at different protein concentration. Correlation coefficient (R) value of 0.998 implies no significant co-operative effect.
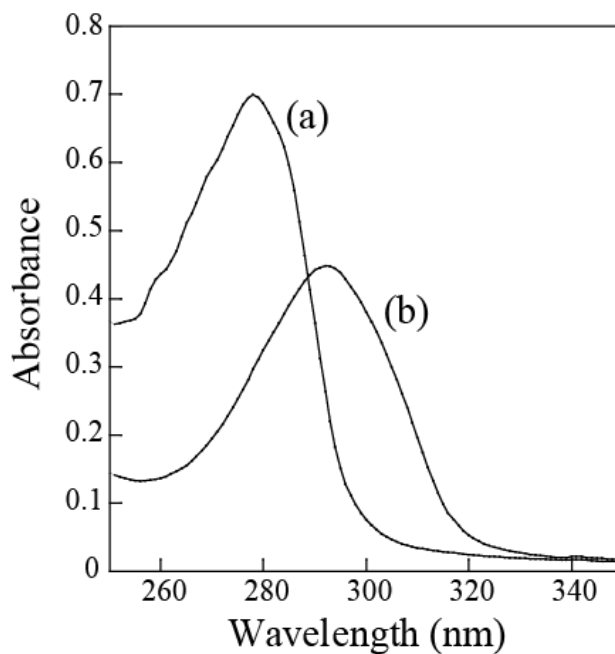
Figure S5. UV spectra of BSA in (a) native and (b) after desorption from malachite surface. Desorbed spectra shows a ~10 nm shift which is due to alteration in protein conformation upon adsorption-desorption cycle.
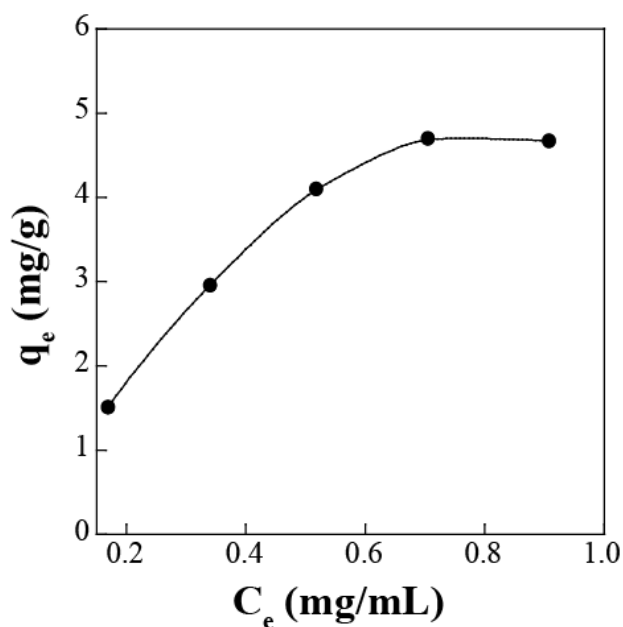

Figure S6. Steady state adsorption isotherm of BSA on stearic acid coated malachite NPs at pH ~5.0. Maximum adsorption capacity was very much lower (~5 mg/g) compared to that on bare malachite surface (~50 mg/g).
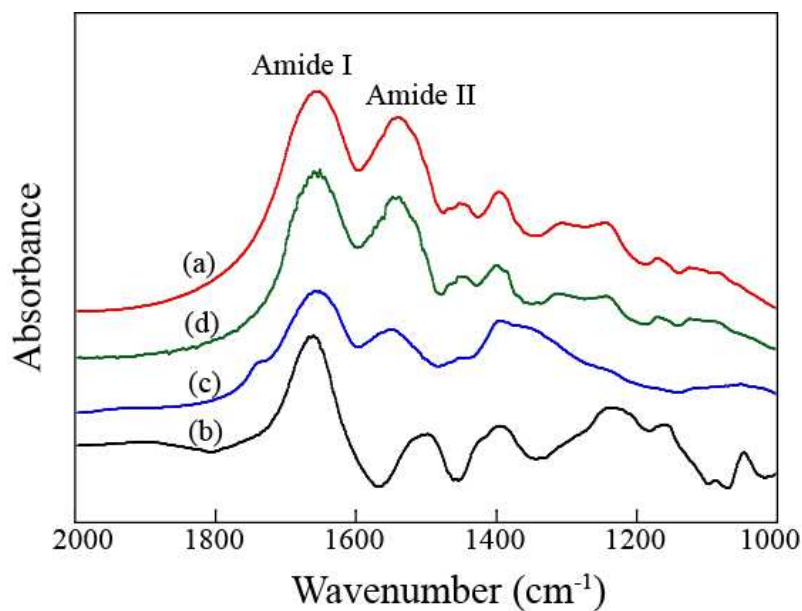
Figure S7. FTIR of lyophilized BSA in (a) native, (b) adsorbed (after subtraction of only malachite spectra), (c) desorbed and (d) after interaction with SA-malachite NPs.
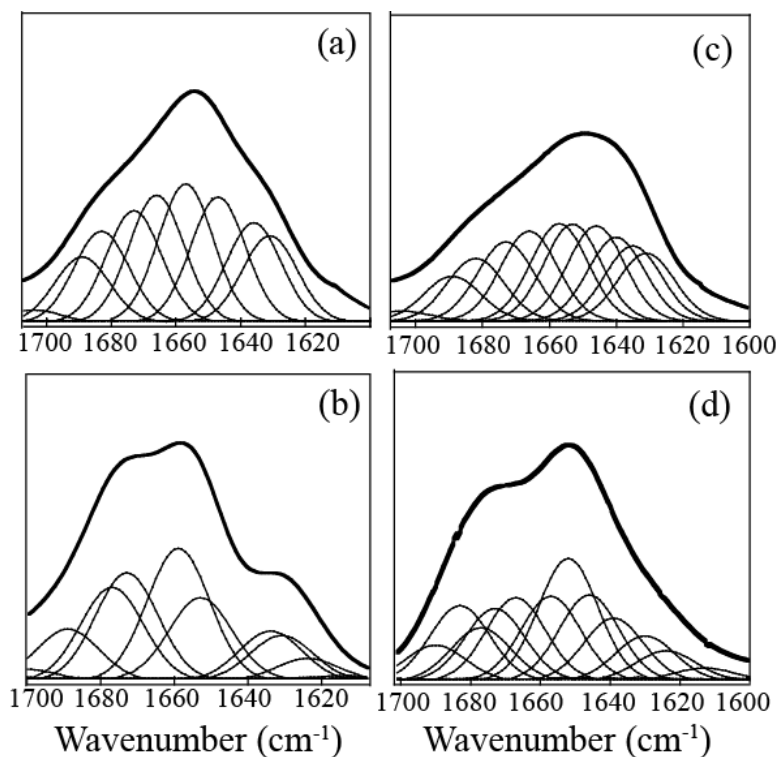
band position (cm^{-1}) Gaussian curve fit	Area (%) of Gaussian bands of BSA				assignment
	native state	adsorbed on malachite NPs	after desorption	interacted with SA-malachite NPs	
1704 ± 2	1 ± 1	2 ± 1	4 ± 1	3 ± 1	Un-ordered
1689 ± 1	6 ± 1	7 ± 2	12 ± 2	6 ± 1	β-sheet
1683 ± 2	8 ± 2	15 ± 1	4 ± 1	12 ± 2	Un-ordered
1673 ± 1	11 ± 1	17 ± 1	8 ± 2	10 ± 1	Un-ordered
1666 ± 2	8 ± 2	21 ± 2	8 ± 1	6 ± 2	Un-ordered
1656 ± 2	31 ± 2	15 ± 1	23 ± 2	30 ± 1	α-helix
1647 ± 1	7 ± 1	4 ± 1	8 ± 2	8 ± 2	Un-ordered
1640 ± 1	5 ± 1	2 ± 1	11 ± 2	6 ± 1	β-sheet
1635 ± 2	10 ± 1	8 ± 2	9 ± 1	6 ± 1	Un-ordered
1630 ± 1	8 ± 2	6 ± 1	9 ± 2	9 ± 1	β-sheet
1624 ± 2	5 ± 1	3 ± 1	4 ± 1	4 ± 1	Un-ordered

Figure S9. PDB structure of 'BSA-like' human serum albumin dimer showing the tryptophan residue (red) (PDB ID 1bm0).