Table S1. Spectral secondary structure composition of BSA in pH 2, 7.4 and 9 solutions, as obtained by CDPRO fitting (CDSSTR, SP43/SDP48).[a]

	α (%)	Distorted α (%)	β (%)	turn (%)	random (%)
pH 7.4 (native)					
	55 ± 0.76	24 ± 0.53	10 ± 0. 37	8.0 ± 0.72	3.0 ± 0.81
pH 2					
Initial Reading	37 ± 0.75	26 ± 0.72	15 ± 0.36	13 ± 0.68	10 ± 0.78
Day 1	30 ± 0.52	24 ± 0.58	17 ± 0.29	13 ± 0.57	17 ± 0.80
Day 2	31 ± 0.58	23 ± 0.50	20 ±0.25	14 ± 0.77	13 ± 0.86
Day 3	31 ± 0.53	25 ± 0.65	16 ± 0.29	15 ± 0.86	14 ± 0.82
Day 4	44 ± 0.91	28 ± 0.58	14 ±0.33	8.0 ± 0.63	7.0 ± 0.82
Day 5	29 ± 0.83	23 ± 0.40	19 ± 0.12	14 ± 0.72	15 ± 0.94
Day 6	34 ± 0.74	26 ± 0.47	16 ± 0.20	13 ± 0.82	11 ± 0.78
pH 9					
Initial Reading	50 ± 0.80	25 ± 0.84	12 ± 0.66	7.6 ± 0.51	5.8 ± 0.44
Week 1	55 ± 0.79	25 ± 0.44	8.6 ± 0.59	4.7 ± 0.51	6.2 ± 0.74
Week 2	48 ± 0.95	25 ± 0.65	13 ± 0.91	7.6 ± 0.68	6.5 ± 0.47
Week 3	46 ± 1.10	25 ± 0.62	13 ± 0.88	8.6 ± 0.78	7.1 ±.050
Week 4	52 ± 1.00	24 ± 0.71	10 ± 0.59	7.1 ± 0.47	6.7 ± 0.67
Week 5	49 ± 0.79	24 ± 0.56	13 ± 0.65	7.1 ± 0.65	6.0 ± 0.63
Week 6	48 ± 1.16	25 ± 0.46	13 ± 0.66	8.1 ± 0.93	6.9 ± 0.44
Week 7	48 ± 0.76	24 ± 0.78	12 ± 0.59	7.7 ± 0.67	7.5 ± 0.47
Week 8	50 ± 0.99	25 ± 0.32	10 ±0.66	6.9 ±0.62	7.5 ± 0.75

[a] β content has been taken as the combination of β-sheet + distorted β-sheet.

Table S2. $\frac{[\theta]_{222}}{[\theta]_{208}}$ ratios of bovine serum albumin CD MRE spectra.

	pH 2		pH 9
Initial reading	1.07± 0.01	Initial reading	1.01± 0.01
Day 1	1.01± 0.01	Week 1	0.99± 0.01
Day 2	1.06± 0.01	Week 2	0.97± 0.01
Day 3	0.95± 0.02	Week 3	0.98± 0.01
Day 4	0.87± 0.01	Week 4	0.93± 0.01
Day 5	0.84± 0.02	Week 5	0.93± 0.01
Day 6	0.98± 0.01	Week 6	0.99± 0.01
		Week 7	1.08± 0.01
		Week 8	1.04± 0.01

Figure S1A

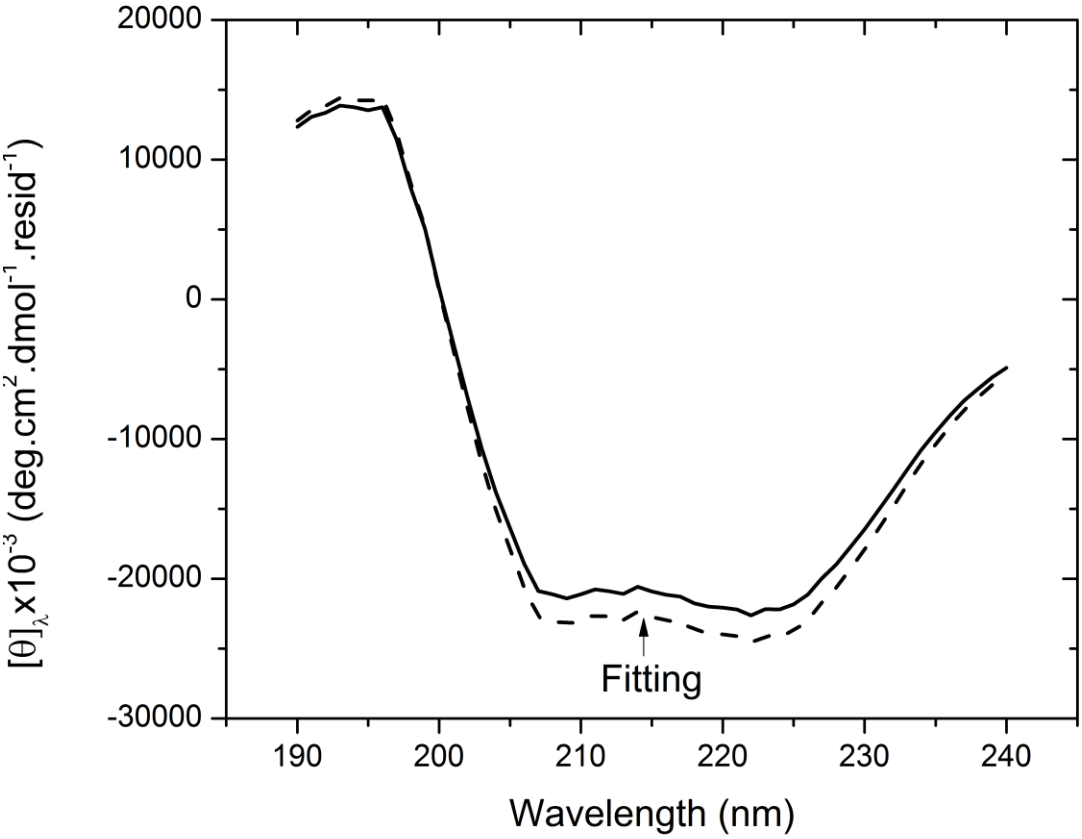
20000
10000
0
-10000
-20000
-30000
190
200
210
220
230
240
Wavelength (nm)
Fitting
[θ]λx10-3 (deg.cm2.dmol-1.resid-1)

Figure S1B

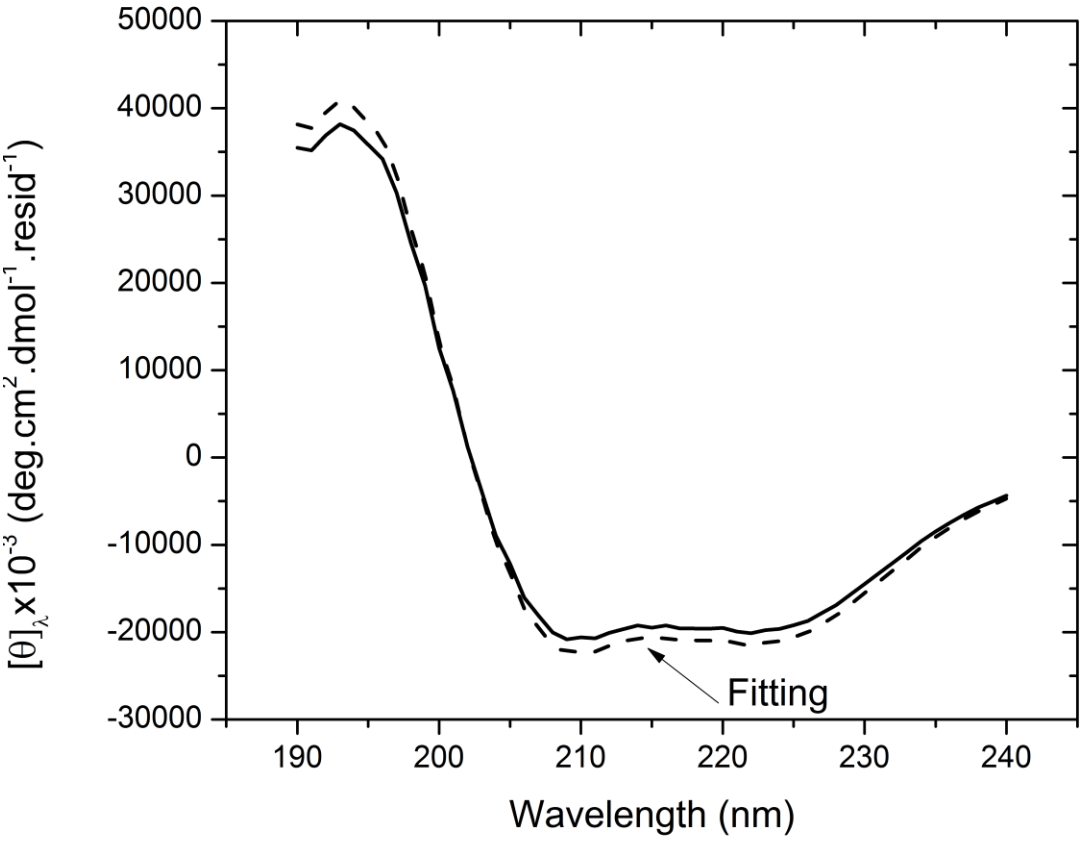

Figure S1. Representative fitting results using the CDPro CDSSTR SP43 fitting algorithm to the initial circular dichroic spectra of A) pH 2 and B) pH 9 bovine serum albumin. In both cases, the solid line represents the raw data of the initial spectra, while the dashed line represents the fitted spectral results using the aforementioned algorithm.