

## Supporting Information

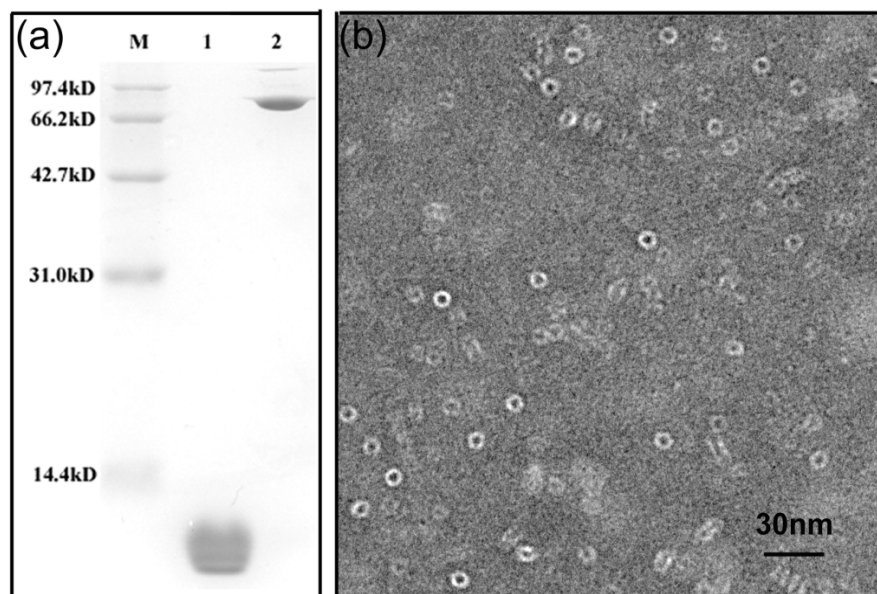
# Quantum Dot-Induced Self-Assembly of Cricoid Protein for Light-Harvesting

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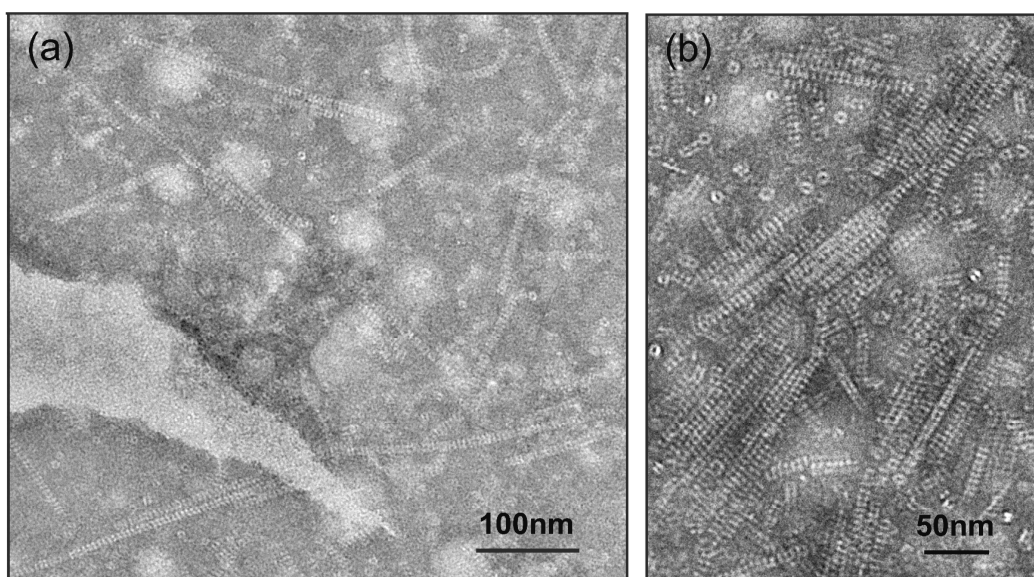
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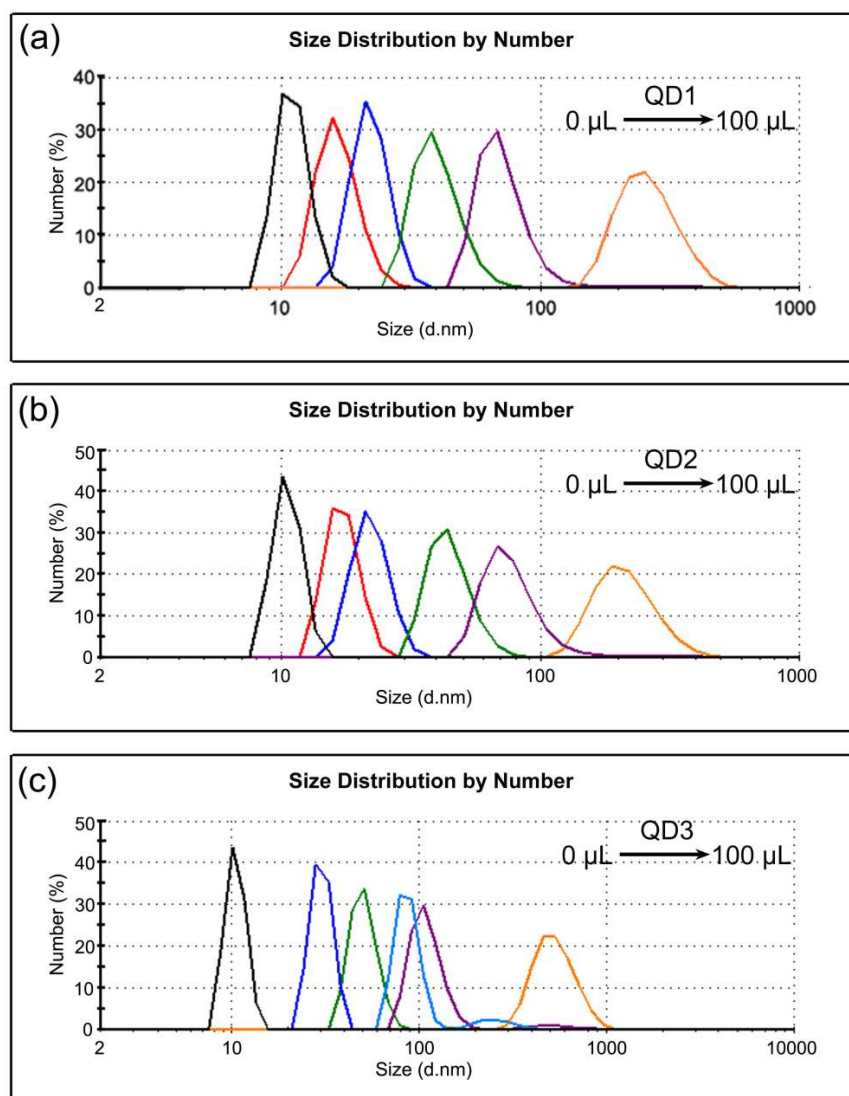
## Additional Figures



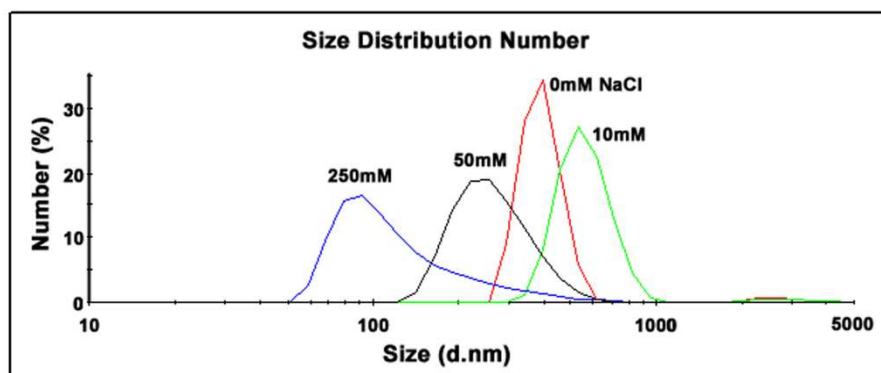
**Figure S1.** SDS-PAGE and TEM analysis of wild type SP1. (a) SDS-PAGE analysis of SP1 protein. W. T. SP1 boiled in the presence of 2% SDS with (lane 1) and without (lane 2) boiling treatment; (b) TEM image of ordered W. T. SP1 dodecamer in aqueous solution.



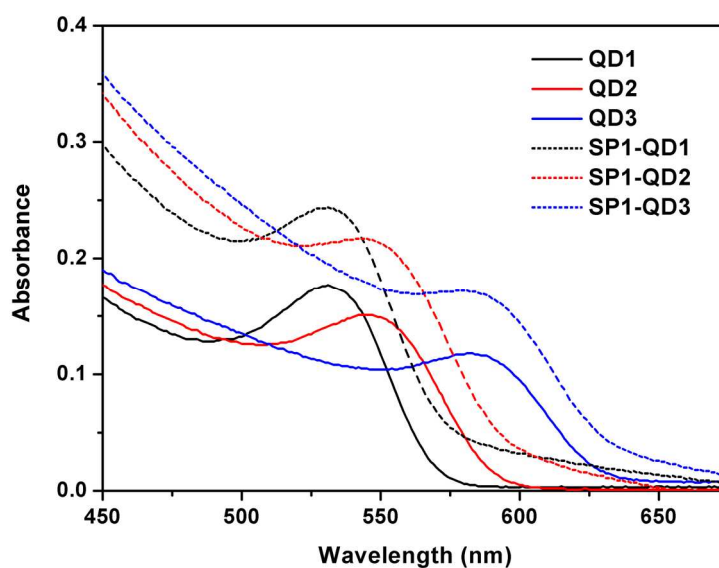
**Figure S2.** TEM images of the assemblies of SP1-QD1 (a) and SP1-QD2 (b) at high concentration. [SP1]=125 mg/L, [QD1]=2.5  $\mu$ M, and [QD3]=25  $\mu$ M.



**Figure S3.** DLS curves for the titration of SP1 solution (25 mg/L 1 mL) with the titration of QD1 (10  $\mu$ M) 0  $\mu$ L, 10  $\mu$ L, 20  $\mu$ L, 40  $\mu$ L, 60  $\mu$ L, and 100  $\mu$ L (a); QD2 (25  $\mu$ M) 0  $\mu$ L, 10  $\mu$ L, 20  $\mu$ L, 40  $\mu$ L, 60  $\mu$ L, and 100  $\mu$ L (b); and QD3 (100  $\mu$ M) 0  $\mu$ L, 20  $\mu$ L, 40  $\mu$ L, 50  $\mu$ L, 60  $\mu$ L, and 100  $\mu$ L (c) in aqueous solution.



**Figure S4.** DLS results for the effect of different NaCl concentrations in SP1-QD1 assembly. The concentrations of SP1 and QD1 were 25 mg/L and 1  $\mu$ M, and assembly with 0 mM, 10 mM, 50 mM, and 250 mM NaCl.



**Figure S5.** Absorption spectra of QDs and SP1-QDs assemblies

### Fluorescence quantum yield calculations

Rhodamine 6G, with a quantum yield of 0.95 under water was used as a standard in these experiments. Samples of increasing concentration (0.1  $\mu$ M to 1  $\mu$ M for Rhodamine 6G, and 0.1 mM to 1 mM for QDs) were excited at 488 nm and the integrated fluorescence emission (500 to

650 nm) was quantified. The integrated fluorescence intensity was plotted against the maximum absorbance of the sample as shown in Figure S6. The slope, which is proportional to the quantum yield, was calculated using the Rhodamine 6G standard as follows:

$$\Phi_{QDs} = \Phi_{Rh} \times \frac{K_{QDs}}{K_{Rh}} \times \frac{n_{QDs}^2}{n_{Rh}^2},$$

where  $\Phi_{Rh}$  represents the quantum yield of the standard,  $\Phi_{QDs}$  represents the quantum yield of QDs,  $K_{Rh}$  represents the slope of the best linear fit for the standard plot,  $K_{QDs}$  represents the slope of the best linear fit for the QDs plot, and  $n$  is the refractive index of the buffer used. Since both buffers were aqueous, the refractive index ratio was approximated to be unity.

The quantum yield of the QD1, QD2, and QD3 were calculated to be 0.147, 0.144, and 0.097, respectively. Since the fluorescent intensity of the SP1-QDs complexes increased as shown in Figure 6a, the quantum yield of the QDs assembled with SP1 would be higher as follows:

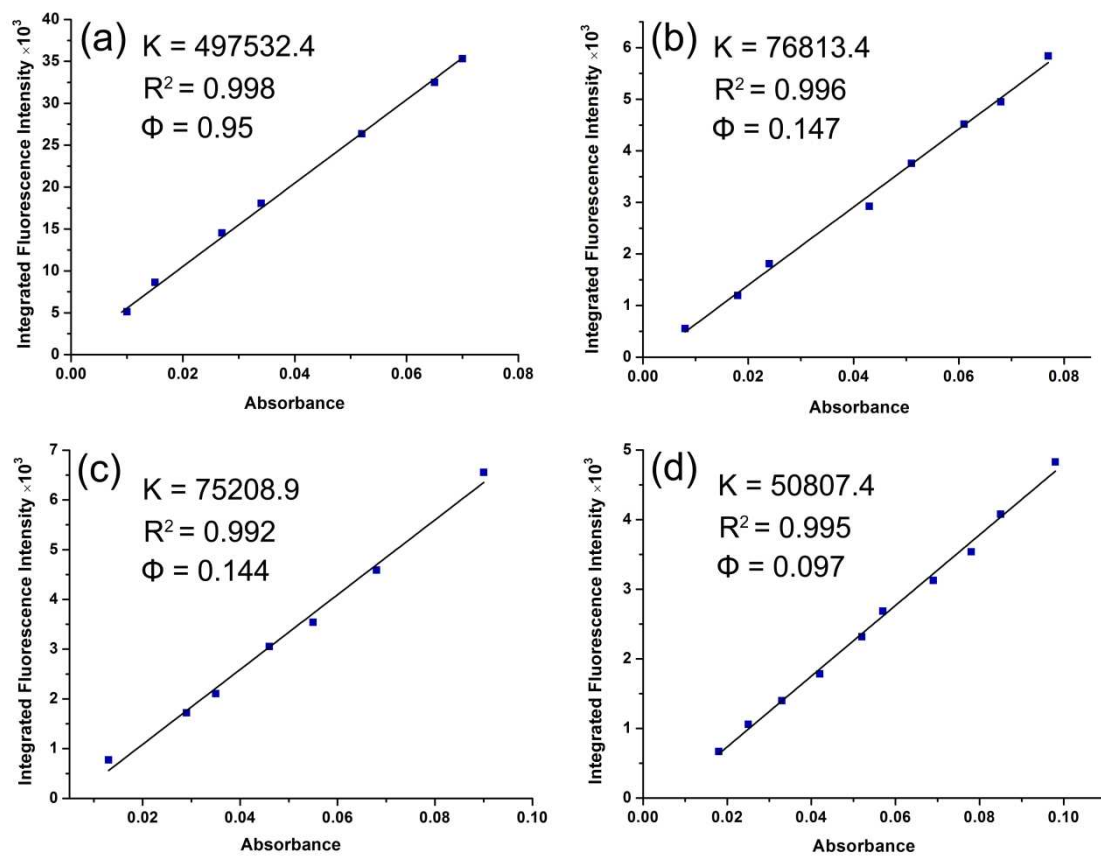
$$\Phi_{SP1-QDs} = \Phi_{QDs} \times \frac{I_{SP1-QDs}}{I_{QDs}},$$

Where  $I$  is the integrated fluorescent intensity.

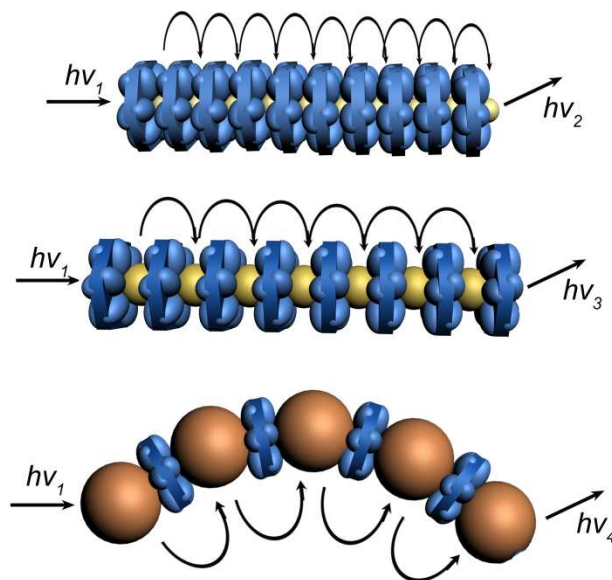
The quantum yield of SP1-QD1:  $\Phi_{SP1-QD1}=0.170$

The quantum yield of SP1-QD2:  $\Phi_{SP1-QD2}=0.176$

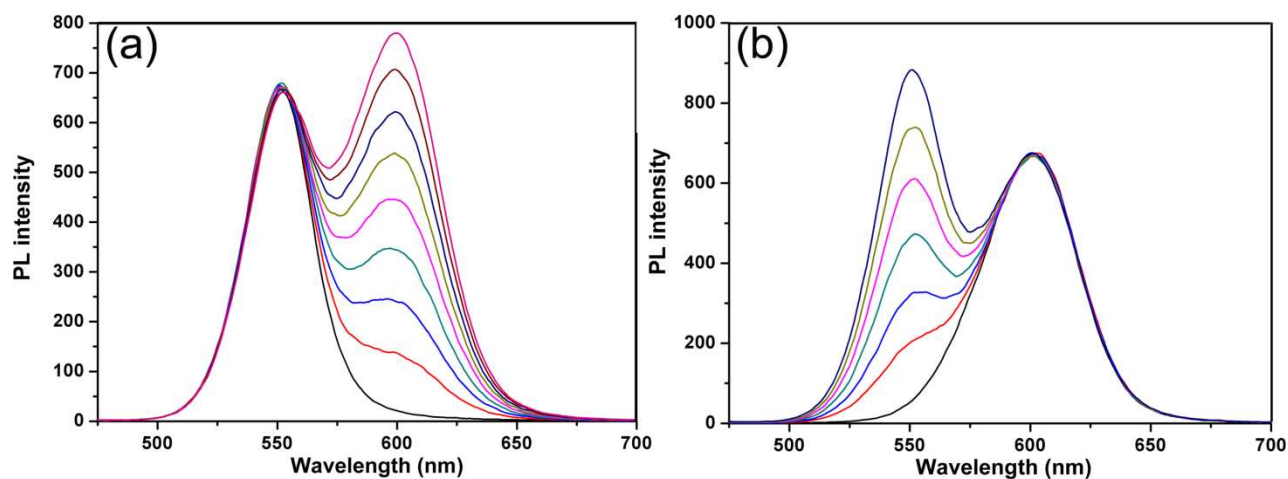
The quantum yield of SP1-QD3:  $\Phi_{SP1-QD3}=0.123$



**Figure S6.** Fluorescence quantum yield calculations for the QDs. Integrated fluorescence intensity vs. absorbance plots used to determine the relative quantum yield of (a) the reference standard, Rhodamine 6G, (b) QD1, (c) QD2, and (d) QD3.



**Figure S7.** The schematic description of the light-harvesting antenna through energy transfer from the same QDs



**Figure S8.** (a) fluorescence spectra of free QD1 (0.5 mM) in the presence of different concentrations of QD3. The [QD3] was 0 mM, 0.2 mM, 0.4 mM, 0.6 mM, 0.8 mM, 1.0 mM, 1.2 mM, 1.4 mM and 1.6 mM from bottom to top. (b) fluorescence spectra of free QD3 (0.8 mM) in the presence of different concentrations of QD1. The [QD1] was 0 mM, 0.1 mM, 0.2 mM, 0.3 mM, 0.4 mM, 0.5 mM, 0.6 mM from bottom to top ( $\lambda_{\text{ex}} = 462 \text{ nm}$ ).