A Supramolecular Assembly of Hemoproteins Formed in a Star-Shaped Structure via Heme-Heme Pocket Interactions

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ELECTRONIC SUPPLEMENTARY INFORMATION

Table of contents:

- 1. Figure S1. Image analysis of SDS-PAGE for HTHP and relationship between band density and HTHP concentration.
- 2. Figure S2. Image analysis of SDS-PAGE for 1-Cyt b_{562} ^{N80C} and relationship between band density and 1-Cyt b_{562} ^{N80C} concentration.
- 3. Figure S3. Image analysis of SDS-PAGE for assemblies.
- 4. Table S1. Peak areas of SDS-PAGE bands for various concentration of HTHP.
- 5. Table S2. Peak areas of SDS-PAGE bands for various concentration of $1-Cyt b_{562}$ ^{N80C}.
- 6. Table S3. Peak areas of SDS-PAGE bands for assemblies.



Figure S1: (**A**) Plots of peak area of the intensity derived from band density against the HTHP concentration as a monomer. (**B**) Plots of intensity derived from band density against migration distance by image analysis for lanes 3-7 of SDS-PAGE in Figure 7. Broken line shows corresponding least square fitting.



Figure S2. (**A**) Plots of peak area of the intensity derived from band density against the concentration of 1-Cyt b_{562} ^{N80C}. (**B**) Plots of intensity derived from band density against migration distance by image analysis for lanes 10-16 of SDS-PAGE in Figure 7. Broken line shows corresponding least square fitting.



Figure S3. Plots of intensity derived from band density against migration distance by image analysis for lanes 8 and 9 of SDS-PAGE in Figure 7.

Lane	Concentration as a monomer (µM)	Peak area ¹
3	10	9919 ± 674
4	8	8417 ± 897
5	6	5525 ± 103
6	4	3556 ± 99
7	2	1937 ± 65

Table S1: Peak areas of SDS-PAGE bands for various concentration of HTHP.

¹The error for each peak area was obtained from the standard deviation of three separate SDS PAGE experiments.

Lane	Concentration (µM)	Peak area ¹	
10	30	0 13176 ± 1201	
11	25	11594 ± 1292	
12	20	9436 ± 960	
13	15	7066 ± 1095	
14	10	5142 ± 698	
15	5	2238 ± 363	
16	2	970 ± 105	

Table S2. Peak areas of SDS-PAGE bands for various concentration of 1-Cyt b_{562} ^{N80C}.

¹The error for each peak area was obtained from the standard deviation of three separate SDS PAGE experiments.

Table S3. Peak areas of SDS-PAGE bands for assemblies.

Lane	Assembly	Components	Peak areas ¹	Concentration as a monomer (µM)²
9 1/1-	1/1-(1 -Cyt	1- Cyt <i>b</i> ^{562N80C}	2392 ± 214	4.7 ± 0.19
	b562 ^{N80C})n- apoHTHP assembly	apoHTHP	2312 ± 83	2.6 ± 0.44
8	8 3/1-(1-Cyt	1- Cyt <i>b</i> ₅₆₂ N80C	4125 ± 825	8.3 ± 1.2
b562 ^{N80C})n- apoHTHP assembly	b562 ^{N80C})n- apoHTHP assembly	apoHTHP	3047 ± 153	3.2 ± 0.51

¹The error for each peak area was obtained from the standard deviation of three separate SDS PAGE experiments. ²Concentrations were determined from the peak areas and calibration curve for each protein.