Electronic Supplementary Material (ESI) for Physical Chemistry Chemical Physics

Heme prevents Abeta aggregation through hydrophobic interaction

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Table S1: Calculated pKa value for titratable residues.

Residues	pKa values
N-terminus	7.9
AspNT	2.4
Glu-3	4.2
Arg-5	12.2
His-6	6.0
Asp-7	4.2
Tyr-10	11.0
Glu-11	4.6
His-13	5.5
His-14	7.6
Lys-16	9.7
Glu-22	4.5
Asp-23	4.4
Lys-28	10.3
C-terminus	4.4

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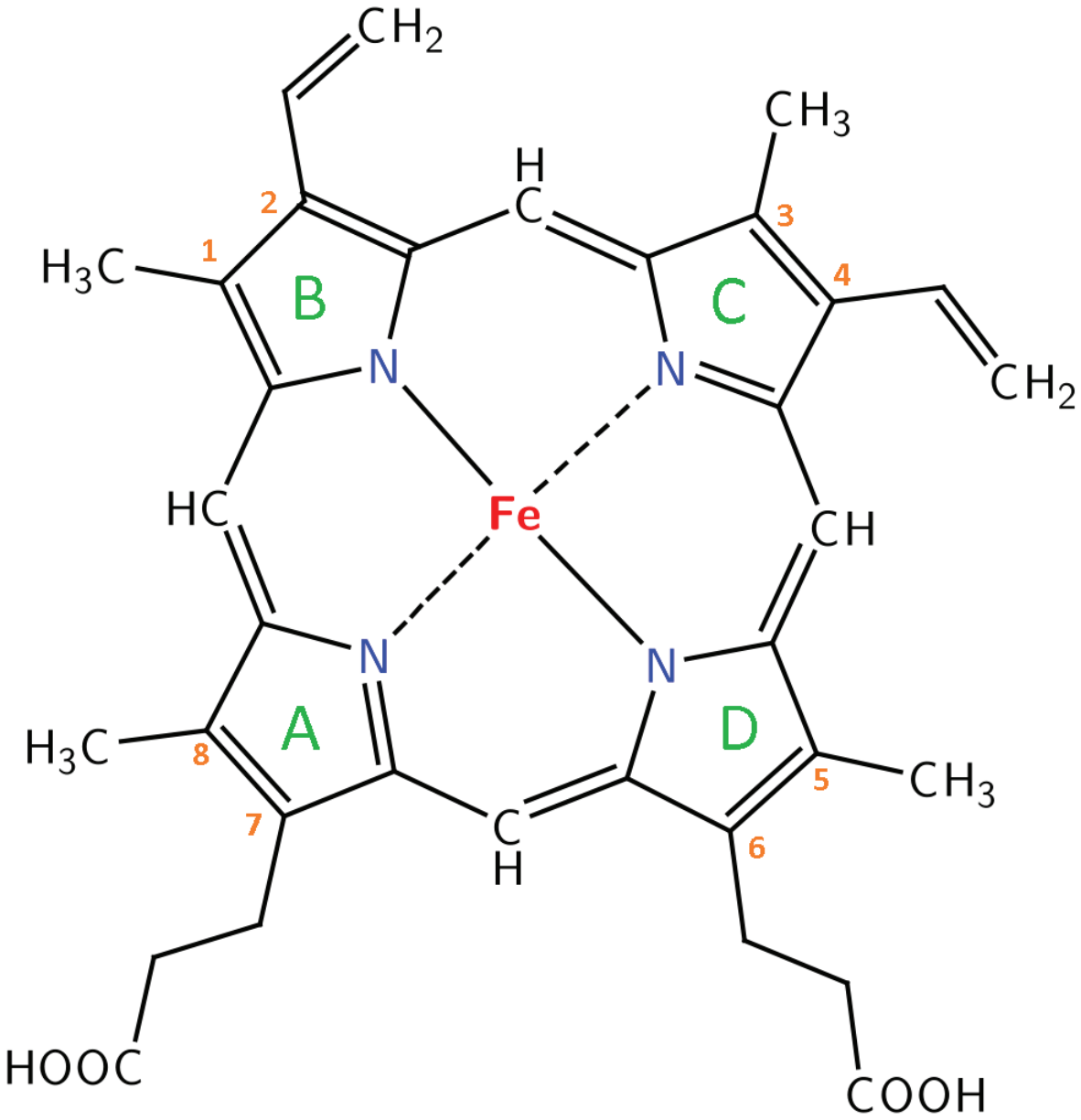

Figure S1: The chemical structure of heme.

The temperatures of the 32 replicas are as follows:

315.00 K, 317.98 K, 321.98 K, 325.01 K, 328.06 K, 331.14 K, 334.24 K, 337.36 K, 340.50 K, 343.67 K, 346.86 K, 350.08 K, 353.32 K, 356.58 K, 359.87 K, 363.19 K, 366.52 K, 369.89 K, 373.28 K, 376.69 K, 380.13 K, 383.60 K, 387.09 K, 390.61 K, 394.16 K, 397.73 K, 401.33 K, 404.96 K, 408.61 K, 412.29 K, 416.00 K, 419.74 K.

Table S2: Aβ residues vicinity affinity.

Aβ-Fe atom		$0 \sim 500\ ns$		last $100ns$	
Residues	Vicinity affinity (%)	Residues	Vicinity affinity (%)	Residues	Vicinity affinity (%)
PHE	22.86	PHE	19.99	PHE	21.56
VAL	13.93	VAL	16.11	VAL	14.00
ILE	11.77	ILE	10.69	MET	11.74
LEU	10.60	MET	10.66	ILE	11.23
MET	10.22	ARG	8.26	ARG	10.01
ARG	8.68	LEU	7.78	LEU	9.97
HIS	6.11	HIS	6.35	HIS	6.15
GLY	5.52	ALA	5.58	ALA	4.28
ALA	4.71	GLY	4.61	LYS	3.28
GLN	3.05	GLU	2.89	GLY	3.19
LYS	2.39	LYS	1.83	GLN	3.03
GLU	1.74	GLN	1.74	GLU	1.03
ASP	0.23	SER	1.58	ASP	0.30
SER	0.17	TYR	1.01	SER	0.25
ASN	0.06	ASP	0.81	ASN	0.00

Table S3: The Heme hydrogen bond forming propensity.

Atoms	hydorgen bond forming propensity (%)
NC	5.80
ND	6.36
O1A	19.01
O2A	19.09
O1D	19.09
O2D	19.09

Table S4: The Aβ residues hydrogen bond forming propensity.

Residues	hydorgen bond forming propensity (%)
ARG-5	12.89
ASP-1	8.54
HIS-14	7.01
HIS-6	6.20
LYS-16	5.96
SER-26	5.16
GLN-15	5.16
LYS-28	4.67
ASN-27	4.67
HIS-13	4.51
SER-8	4.03
TYR-10	3.55
ALA-2	2.82
PHE-19	2.66
LEU-34	2.50
ALA-30	2.01
VAL-36	1.93
GLY-37	1.61
LEU-17	1.29
PHE-4	1.21
ALA-21	1.21
VAL-40	1.13
GLY-25	1.13
GLY-38	1.05
GLY-29	0.97
ALA-42	0.89
GLU-3	0.89
GLY-33	0.81
GLY-9	0.73
VAL-39	0.64
MET-35	0.40
ILE-31	0.40
VAL-12	0.40
ASP-23	0.32
PHE-20	0.24
GLU-11	0.16
ASP-7	0.08
ILE-41	0.08
ILE-32	0.08
VAL-24	0.00
GLU-22	0.00
VAL-18	0.00

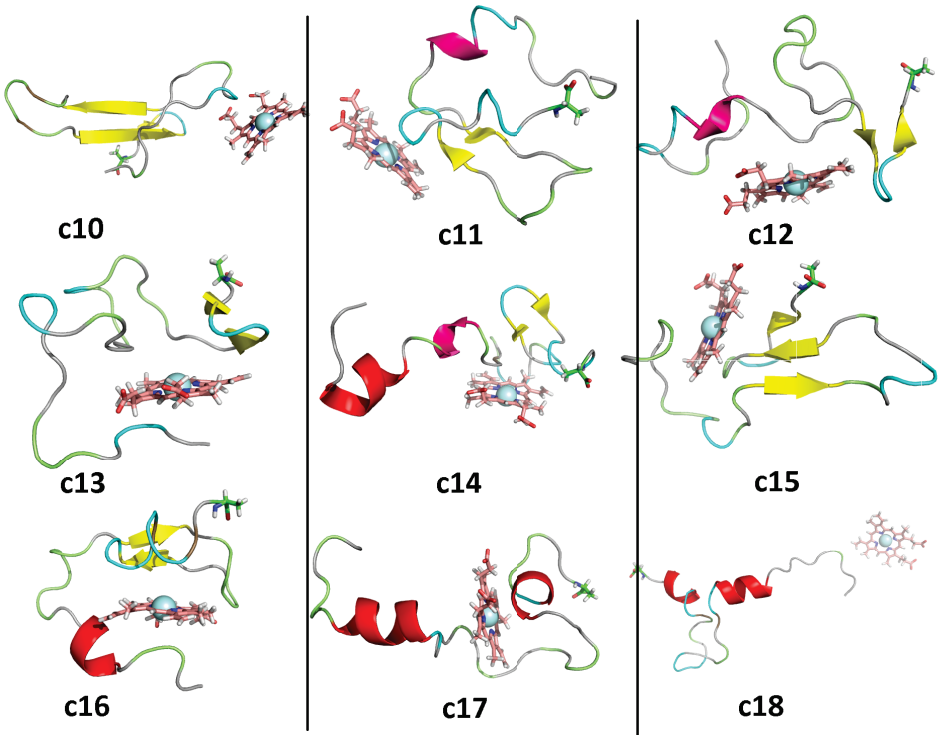

Figure S2: Cluster analysis of Aβ-heme complex. The central portion of the $10 \sim 18$ most dominant clusters of the 20 trajectories in the last 100 *ns* are shown in cartoon for protein, sticks for heme and sphere for Fe ion. The C-terminal of Aβ are distinguished by sticks.

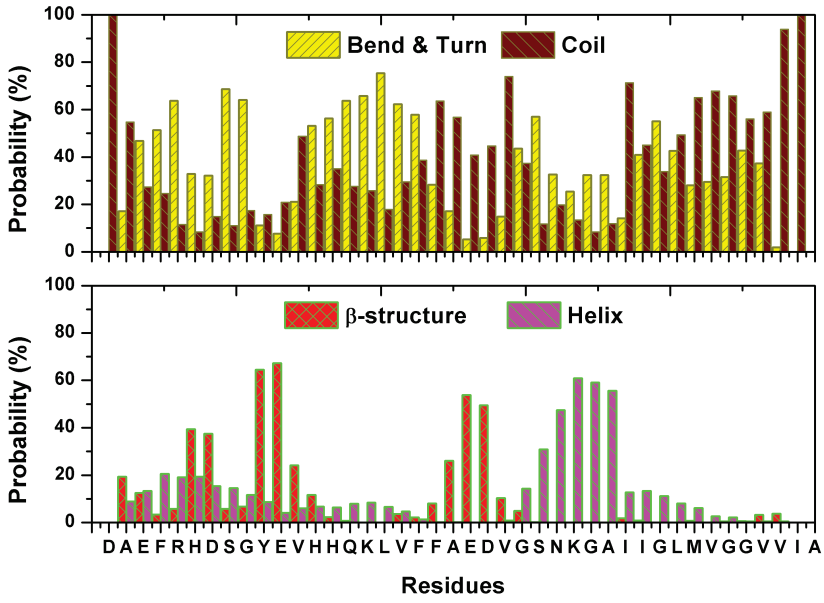

Figure S3: Aβ secondary structure propensity in the presence of heme was examined by averaging over 20 trajectories every 5 *fs*. The average statistical error is found to be 0.18.

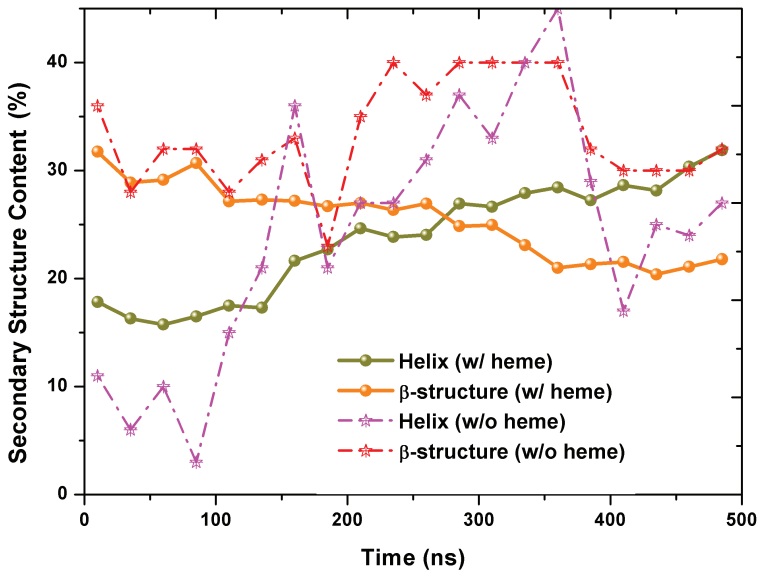

Figure S4: The number of residues adopting β-structure and helical content in the presence/absence of heme were examined by averaging over 20 trajectories every 50 *ns*. The statistical error is found to be less than 2.