

Elucidation of the key role of isomerization in the self-assembly and luminescence properties of AIEgens

Hui Wang,^a Junfang Yang^a and Xiaoyan Zheng^{*ab}

^aKey Laboratory of Cluster Science of Ministry of Education, Beijing Key laboratory of Photoelectronic/Electro-photon Conversion Materials, Key Laboratory of Medicinal Molecule Science and Pharmaceutics Engineering of Ministry of Industry and Information Technology, School of Chemistry and Chemical Engineering, Beijing Institute of Technology, Beijing, 100081, China.

^bGuangdong Provincial Key Laboratory of Luminescence from Molecular Aggregates (South China University of Technology), Guangzhou, 510640, China.

*E-mail: xiaoyanzheng@bit.edu.cn.

Contents

I. Supplementary Charts S1-S2 and Figures S1-S9

Chart S1: Schematic representation of the AP.

Chart S2: The chemical structure of QM region of QM/MM model.

Figure S1: The evolution of pair-wise UPy distance and the number of intermolecular H-bonds of (Z)-TPE-UPy and (E)-TPE-UPy as a function of simulation time during the tetramer formation process.

Figure S2: The evolution of (Z)-open-hexamer, (Z)-close-hexamer and (E)-linear-hexamer assemblies presented by the representative snapshots of extracted from MD trajectories in chloroform.

Figure S3: Typical conformations of typical chain-like tetramers and hexamers extracted from MD trajectories.

Figure S4: Schematic diagrams of $\phi_{terminal}$ and $\phi_{internal}$ of four typical tetramers and hexamers.

Figure S5: The evolution of the COM distance and two representative angles $\phi_{terminal}$ and $\phi_{internal}$ of equilibrated oligomers as a function of simulation time.

Figure S6: The evolution of (Z)-close-dimer assemblies at different concentrations and “(Z)-TPE-UPy assembly” by the representative snapshots extracted from MD trajectories in chloroform.

Figure S7: The evolution of “(E)-TPE-UPy assembly” shown by representative snapshots extracted from MD trajectories in chloroform.

Figure S8: Evolution of number of intermolecular H-bonds as a function of time in three typical aggregates.

Figure S9: The QM/MM models for the representative nanostructures, including two dimers and three typical aggregates.

II. Supplementary Tables S1-S8

Table S1-S5: Selected bond lengths, bond angles, and dihedral angles of typical dimers and aggregates at both S_0 and S_1 minimum and the difference between S_0 and S_1 .

Table S6: The extracted key dihedral angles of representative dimers and assembled aggregates.

Table S7: Calculated vertical excitation energy (ΔE_{vert}), electronic dipole moment (EDM), oscillator strength (f), the assignment for S_1 of TPE and radiative decay rate constant (k_r).

Table S8: Reorganization energy of representative dimers and assembled aggregates.

I. Supplementary Chart S1-S2 and Figures S1-S9

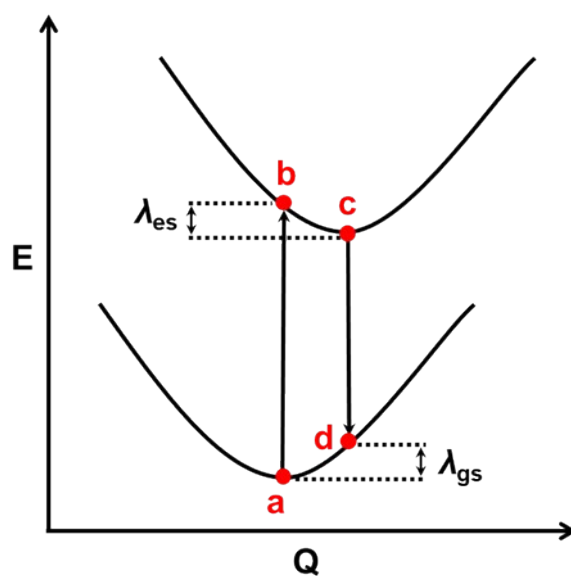


Chart S1. Schematic representation of the AP. Q refers to the nuclear configuration.

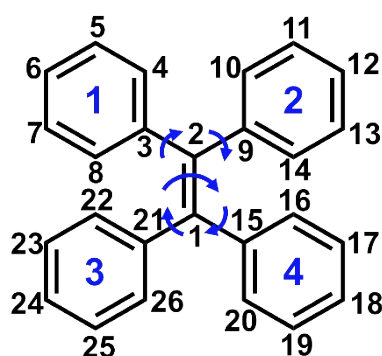


Chart S2. The chemical structure of QM region of QM/MM model in this work. The key structural parameters related to photophysical properties were also shown.

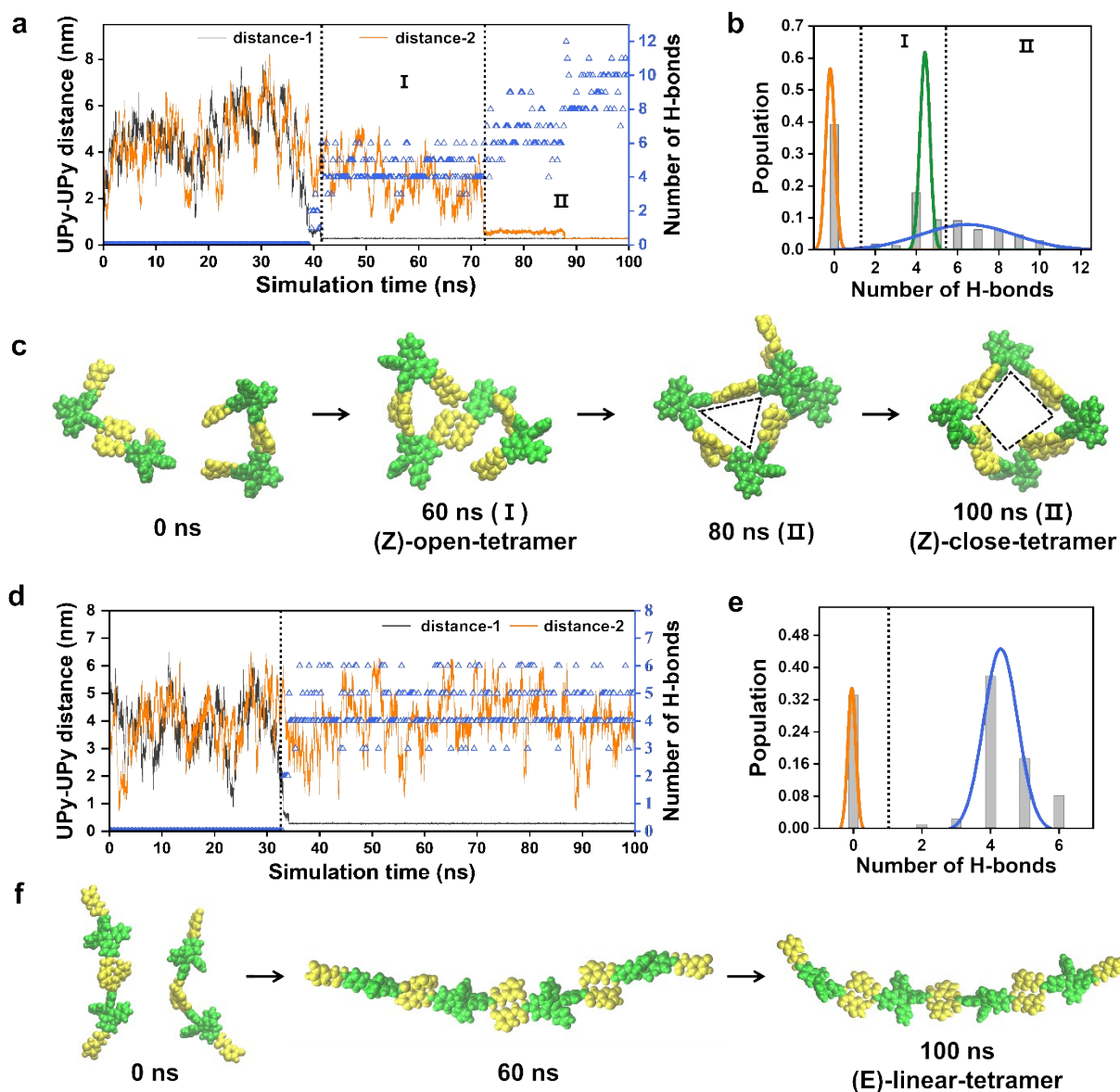


Fig. S1 (a) and (d) The distance evolution and the number of intermolecular H-bonds among unoccupied UPy moieties of (Z)-TPE-UPy and (E)-TPE-UPy at different stage of tetramer formation process. (b) and (E) Population of number of intermolecular H-bonds at different stage of (Z)- and (E)-TPE-UPy tetramer formation. (c) and (f) Representative snapshots extracted from MD trajectories of (Z)- and (E)-TPE-UPy tetramer formation. The TPE and UPy motifs are shown in green and yellow, respectively. The alkyl groups of UPy and chloroform solvents are not shown for clarity.

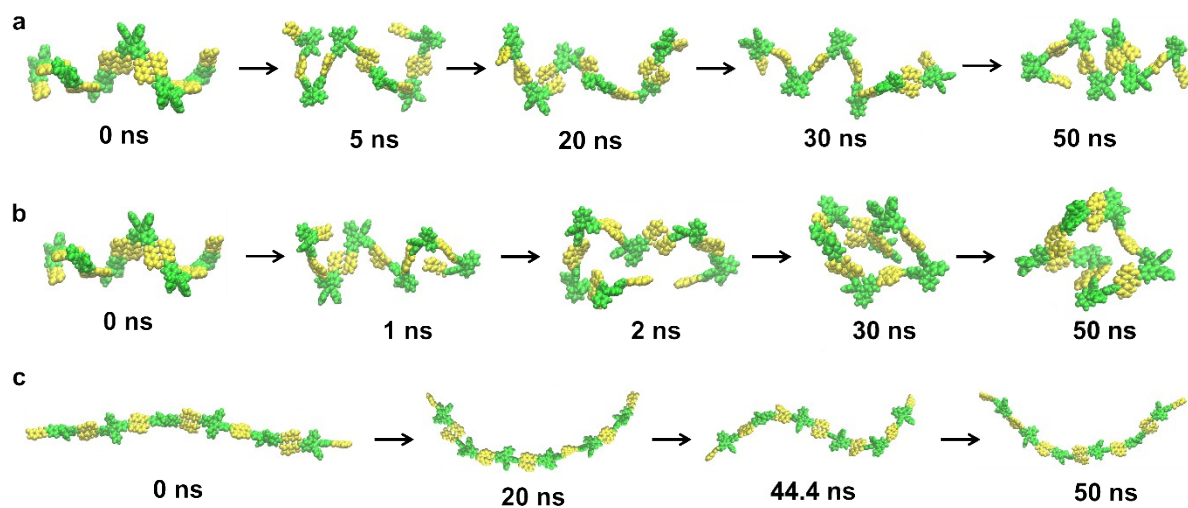


Fig. S2 The evolution of (a) (Z)-open-hexamer, (b) (Z)-close-hexamer and (c) (E)-linear-hexamer assemblies presented by the representative snapshots of extracted from MD trajectories in chloroform. The TPE and UPy motifs are shown in green and yellow, respectively. The alkyl groups of UPy and chloroform solvents are not shown for clarity.

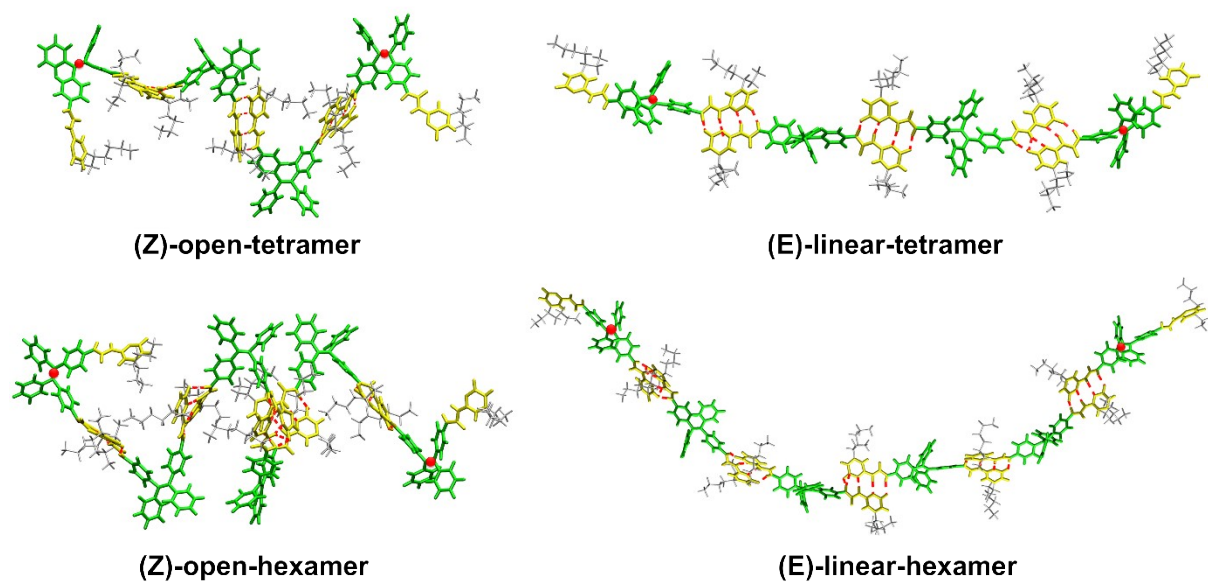


Fig. S3 Typical conformations of typical chain-like tetramers and hexamers extracted from MD trajectories. The positions of center-of-mass (COM) distance definition are marked by red dots.

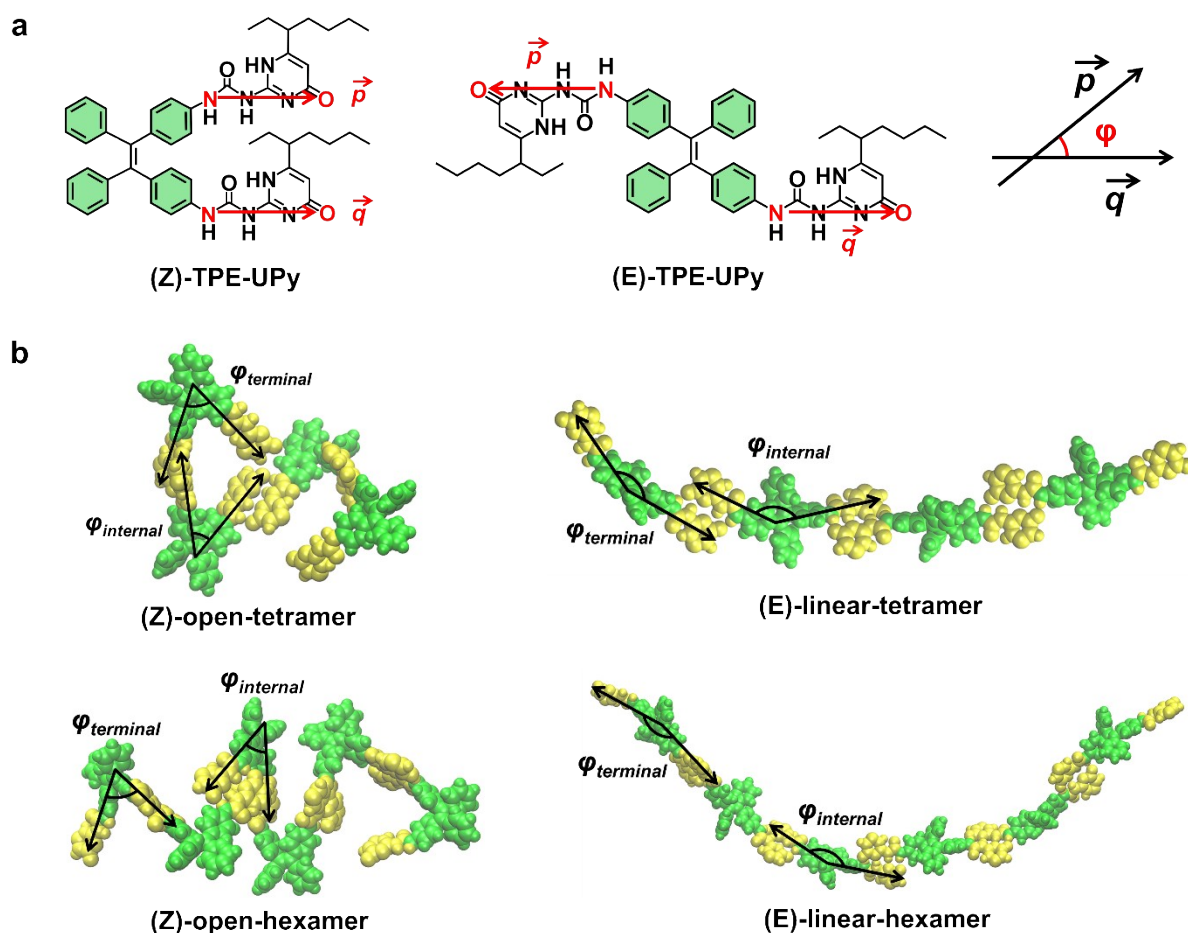


Fig. S4 (a) Definitions of two representative angles used to describe the conformational changes of both tetramers and hexamers. Two vectors \vec{p} and \vec{q} , respectively, represent vectors connecting one nitrogen and one oxygen atoms marked in red. The included angle between \vec{p} and \vec{q} is defined as φ . (b) Two representative angles ($\varphi_{terminal}$ and $\varphi_{internal}$) at the terminus and the internal part of each (Z)-open-tetramer/hexamer or (E)-linear-tetramer/hexamer, respectively.

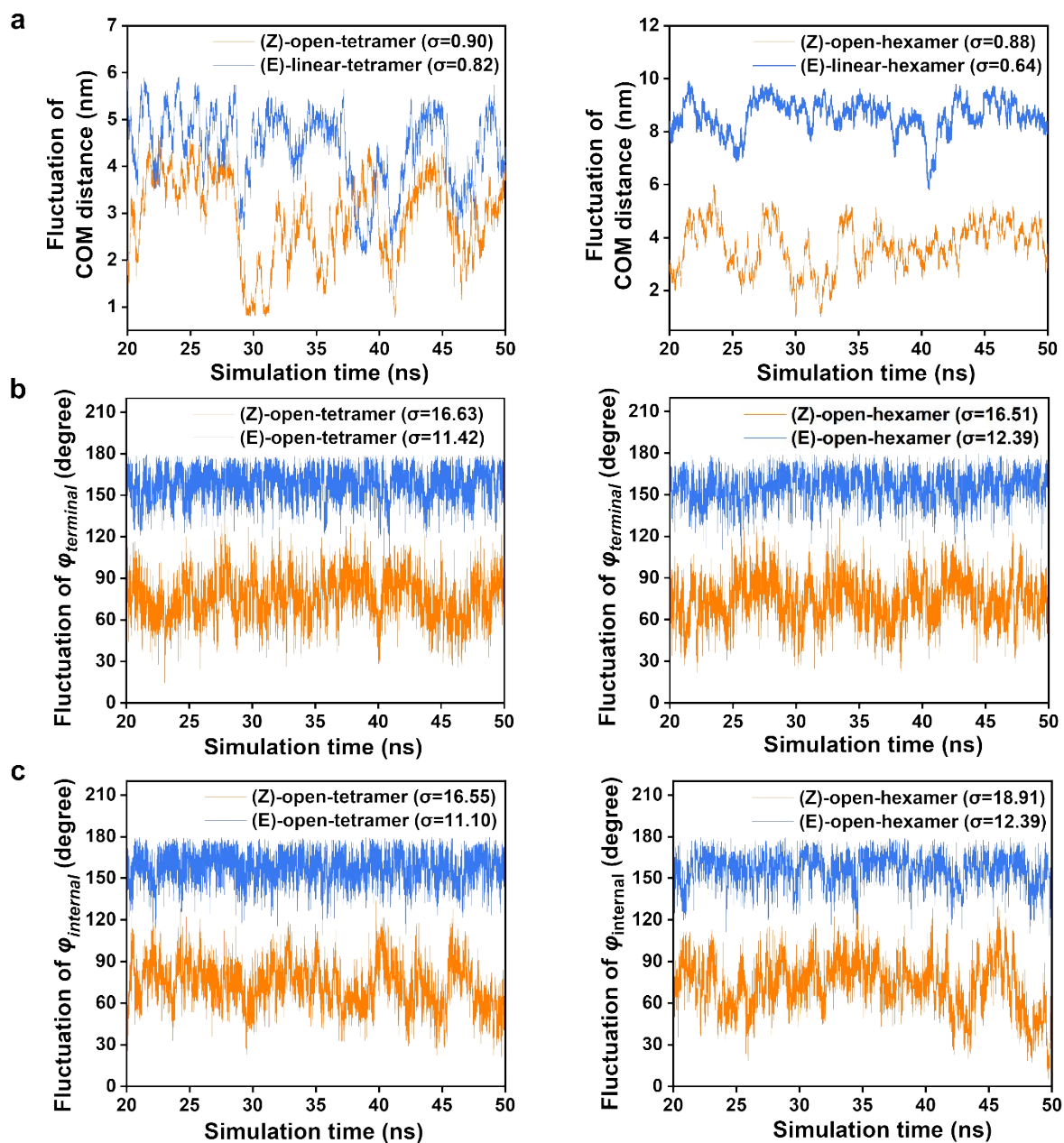


Fig. S5 The evolution of (a) COM distance and (b-c) two representative angles $\varphi_{terminal}$ and $\varphi_{internal}$ of equilibrated tetramers and hexamers as a function of simulation time. The corresponding standard deviations (σ) are shown above.

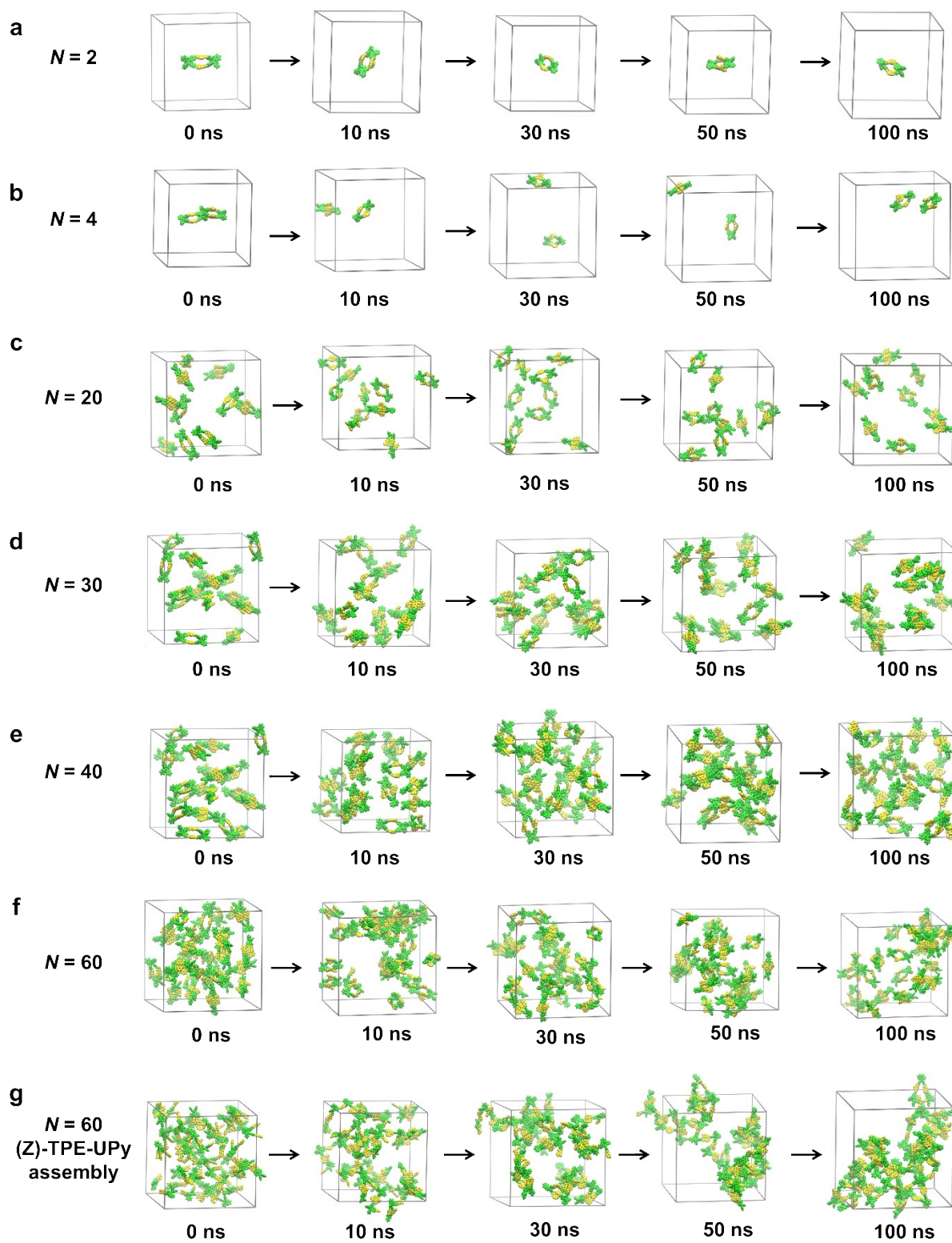


Fig. S6 The evolution of (Z)-close-dimer assemblies at different concentrations and “(Z)-TPE-UPy assembly” by the representative snapshots extracted from MD trajectories in chloroform.

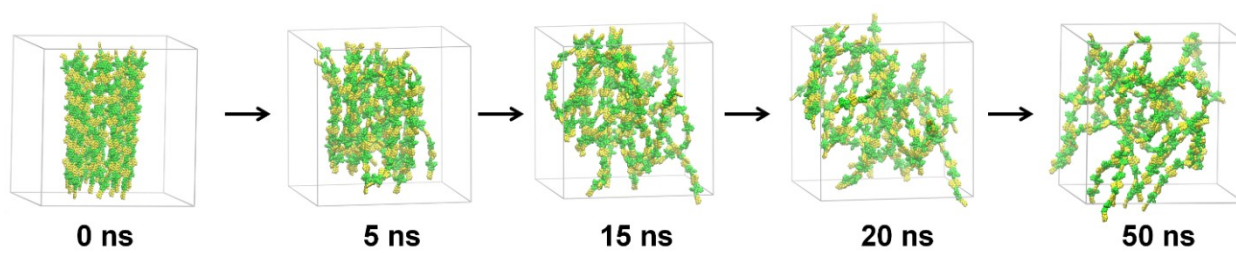


Fig. S7 The evolution of “(E)-TPE-UPy assembly” shown by representative snapshots extracted from MD trajectories in chloroform.

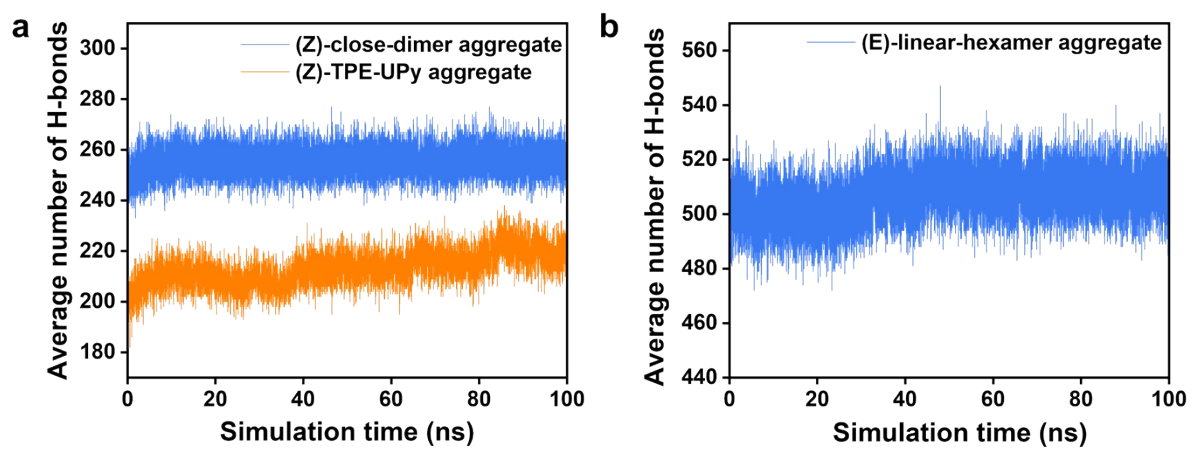


Fig. S8 Evolution of number of intermolecular H-bonds as a function of time in three typical aggregates.

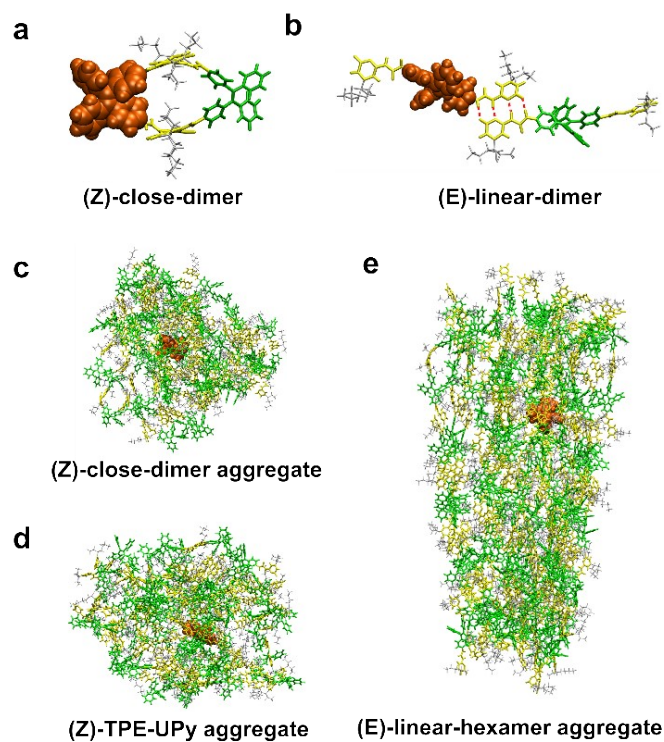


Fig. S9 The QM/MM models for the representative nanostructures, including two dimers and three typical aggregates, including (a) (Z)-close-dimer and (b) (E)-linear-dimer, (c) (Z)-close-dimer aggregate, (d) (Z)-TPE-UPy aggregate and (e) (E)-linear-hexamer aggregate. For each system, the TPE moiety in orange is selected as the high-layer QM region and treated at the M06-2X/6-311G* level.

II. Supplementary Tables S1-S8

Table S1 Selected bond lengths (in Å), bond angles (in degree), and dihedral angles (in degree) of (Z)-close-dimer at S_0 and S_1 minimum and the difference between S_0 and S_1 . The definition of structural parameters are shown in Chart S2.

structural parameters		(Z)-close-dimer		
		S_0	S_1	$ S_0-S_1 $
bond lengths				
	C ₁ -C ₂	1.354	1.465	0.102
	C ₂ -C ₃	1.490	1.442	0.048
	C ₂ -C ₉	1.491	1.444	0.047
	C ₁ -C ₁₅	1.489	1.443	0.046
	C ₁ -C ₂₁	1.490	1.444	0.046
bond angles				
	C ₁ -C ₂ -C ₃	123.2	118.9	4.3
	C ₁ -C ₂ -C ₉	122.0	118.2	3.8
	C ₂ -C ₁ -C ₁₅	121.8	117.9	3.9
	C ₂ -C ₁ -C ₂₁	122.9	118.7	4.2
dihedral angles				
D ₁	C ₁ -C ₂ -C ₃ -C ₄	136.2	155.4	19.2
D ₂	C ₁ -C ₂ -C ₉ -C ₁₀	129.9	147.6	17.7
D ₃	C ₂ -C ₁ -C ₁₅ -C ₁₆	-48.9	-22.7	26.2
D ₄	C ₂ -C ₁ -C ₂₁ -C ₂₂	-46.2	-21.0	25.2
D ₅	C ₃ -C ₂ -C ₁ -C ₁₅	168.0	124.9	43.1

Table S2 Selected bond lengths (in Å), bond angles (in degree), and dihedral angles (in degree) of (Z)-close-dimer aggregate at S₀ and S₁ minimum and the difference between S₀ and S₁.

structural parameters		(Z)-close-dimer aggregate		
		S ₀	S ₁	S ₀ -S ₁
bond lengths				
	C ₁ -C ₂	1.365	1.461	0.096
	C ₂ -C ₃	1.493	1.444	0.049
	C ₂ -C ₉	1.498	1.453	0.045
	C ₁ -C ₁₅	1.492	1.459	0.033
	C ₁ -C ₂₁	1.486	1.440	0.046
bond angles				
	C ₁ -C ₂ -C ₃	124.2	123.6	0.6
	C ₁ -C ₂ -C ₉	119.8	118.5	1.3
	C ₂ -C ₁ -C ₁₅	118.9	118.1	0.8
	C ₂ -C ₁ -C ₂₁	123.6	122.3	1.3
dihedral angles				
D ₁	C ₁ -C ₂ -C ₃ -C ₄	156.5	157.4	0.9
D ₂	C ₁ -C ₂ -C ₉ -C ₁₀	137.6	141.1	3.5
D ₃	C ₂ -C ₁ -C ₁₅ -C ₁₆	-46.4	-35.6	10.8
D ₄	C ₂ -C ₁ -C ₂₁ -C ₂₂	-44.1	-25.9	18.2
D ₅	C ₃ -C ₂ -C ₁ -C ₁₅	161.9	153.2	8.7

Table S3 Selected bond lengths (in Å), bond angles (in degree), and dihedral angles (in degree) of (Z)-TPE-UPy aggregate at S₀ and S₁ minimum and the difference between S₀ and S₁.

structural parameters		(Z)-TPE-UPy aggregate		
		S ₀	S ₁	S ₀ -S ₁
bond lengths				
	C ₁ -C ₂	1.357	1.455	0.098
	C ₂ -C ₃	1.493	1.454	0.039
	C ₂ -C ₉	1.491	1.451	0.04
	C ₁ -C ₁₅	1.487	1.450	0.037
	C ₁ -C ₂₁	1.492	1.445	0.047
bond angles				
	C ₁ -C ₂ -C ₃	118.8	117.3	1.5
	C ₁ -C ₂ -C ₉	124.1	122.4	1.7
	C ₂ -C ₁ -C ₁₅	123.4	122.5	0.9
	C ₂ -C ₁ -C ₂₁	123.9	122.1	1.8
dihedral angles				
D ₁	C ₁ -C ₂ -C ₃ -C ₄	127.4	137.7	10.3
D ₂	C ₁ -C ₂ -C ₉ -C ₁₀	156.3	160.0	3.7
D ₃	C ₂ -C ₁ -C ₁₅ -C ₁₆	-57.7	-43.4	14.3
D ₄	C ₂ -C ₁ -C ₂₁ -C ₂₂	-38.3	-26.3	12
D ₅	C ₃ -C ₂ -C ₁ -C ₁₅	161.4	148.9	12.5

Table S4 Selected bond lengths (in Å), bond angles (in degree), and dihedral angles (in degree) of (E)-linear-dimer at S₀ and S₁ minimum and the difference between S₀ and S₁.

structural parameters		(E)-linear-dimer		
		S ₀	S ₁	S ₀ -S ₁
bond lengths				
	C ₁ -C ₂	1.353	1.458	0.105
	C ₂ -C ₃	1.489	1.446	0.039
	C ₂ -C ₉	1.484	1.450	0.034
	C ₁ -C ₁₅	1.494	1.454	0.04
	C ₁ -C ₂₁	1.484	1.445	0.039
bond angles				
	C ₁ -C ₂ -C ₃	123.7	120.4	3.3
	C ₁ -C ₂ -C ₉	120.5	119.3	1.2
	C ₂ -C ₁ -C ₁₅	122.7	118.9	3.8
	C ₂ -C ₁ -C ₂₁	122.8	121.7	1.1
dihedral angles				
D ₁	C ₁ -C ₂ -C ₃ -C ₄	136.2	151.3	15.1
D ₂	C ₁ -C ₂ -C ₉ -C ₁₀	127.1	140.9	13.8
D ₃	C ₂ -C ₁ -C ₁₅ -C ₁₆	-49.5	-30.2	19.3
D ₄	C ₂ -C ₁ -C ₂₁ -C ₂₂	-47.6	-24.8	22.8
D ₅	C ₃ -C ₂ -C ₁ -C ₁₅	170.5	145.0	25.5

Table S5 Selected bond lengths (Å), bond angles (degree), and dihedral angles (degree) of (E)-linear-hexamer aggregate at S₀ and S₁ minimum and the difference between S₀ and S₁

structural parameters		(E)-linear-hexamer aggregate		
		S ₀	S ₁	S ₀ -S ₁
bond lengths				
	C ₁ -C ₂	1.354	1.454	0.1
	C ₂ -C ₃	1.498	1.463	0.035
	C ₂ -C ₉	1.491	1.442	0.049
	C ₁ -C ₁₅	1.492	1.442	0.05
	C ₁ -C ₂₁	1.487	1.456	0.031
bond angle				
	C ₁ -C ₂ -C ₃	122.1	119.9	2.2
	C ₁ -C ₂ -C ₉	124.2	123.4	0.8
	C ₂ -C ₁ -C ₁₅	125.1	123.2	1.9
	C ₂ -C ₁ -C ₂₁	123.0	121.0	2.0
dihedral angle				
D ₁	C ₁ -C ₂ -C ₃ -C ₄	128.2	134.5	6.3
D ₂	C ₁ -C ₂ -C ₉ -C ₁₀	148.9	151.4	2.5
D ₃	C ₂ -C ₁ -C ₁₅ -C ₁₆	-61.5	-30.1	31.4
D ₄	C ₂ -C ₁ -C ₂₁ -C ₂₂	-46.9	-36.4	10.5
D ₅	C ₃ -C ₂ -C ₁ -C ₁₅	174.9	165.4	9.5

Table S6 The extracted key dihedral angles (in degree) of two representative dimers: (Z)-close-dimer and (E)-linear-dimer, and three assembled aggregates: (Z)-close-dimer aggregate, (Z)-TPE-UPy aggregate, (E)-linear-hexamer aggregate, respectively. S_0 , S_1 and $|S_0-S_1|$ represent the geometric parameters extracted from the ground, excited states and the difference between them, respectively. The definition of key dihedral angles is shown in Chart 1.

	(Z)-close-dimer			(Z)-close-dimer aggregate			(Z)-TPE-UPy aggregate			(E)-linear-dimer			(E)-linear-hexamer aggregate		
	S_0	S_1	$\Delta S_0-S_1 $	S_0	S_1	$\Delta S_0-S_1 $	S_0	S_1	$\Delta S_0-S_1 $	S_0	S_1	$\Delta S_0-S_1 $	S_0	S_1	$\Delta S_0-S_1 $
D ₁	136.2	155.4	19.2	156.5	157.4	0.9	127.4	137.7	10.3	136.2	151.3	15.1	128.2	134.5	6.3
D ₂	129.9	147.6	17.7	137.6	141.1	3.5	156.3	160.0	3.7	127.1	140.9	13.8	148.9	151.4	2.5
D ₃	-48.9	-22.7	26.2	-46.4	-35.6	10.8	-57.7	-43.4	14.3	-49.5	-30.2	19.3	-61.5	-30.1	31.4
D ₄	-46.2	-21.0	25.2	-44.1	-25.9	18.2	-38.3	-26.3	12	-47.6	-24.8	22.8	-46.9	-36.4	10.5
D ₅	168.0	124.9	43.1	161.9	153.2	8.7	161.4	148.9	12.5	170.5	145.0	25.5	174.9	165.4	9.5

Table S7 Calculated vertical excitation energy (ΔE_{vert}), electronic dipole moment (EDM), oscillator strength (f), the assignment for S_1 of TPE and radiative decay rate constant (k_r).

S_1	ΔE_{vert}	EDM	f	assignment	k_r (10^7)
(Z)-close-dimer	1.94 eV/638 nm	5.23 D	0.2017	HOMO→LUMO O (100%)	3.29
(Z)-close-dimer aggregate	2.57 eV/482 nm	5.17 D	0.2604	HOMO→LUMO O (99.4%)	7.46
(Z)-TPE-UPy aggregate	2.61 eV/474 nm	5.55 D	0.3049	HOMO→LUMO O (99.3%)	9.01
(E)-linear-dimer	2.47 eV/502 nm	5.15 D	0.2485	HOMO→LUMO O (99.6%)	6.58
(E)-linear-hexamer aggregate	2.72 eV/456 nm	5.03 D	0.2604	HOMO→LUMO O (98.6%)	8.36

Table S8 Reorganization energy of each system calculated adiabatic potential method.

	λ_{gs} (eV)	λ_{es} (eV)	λ (eV)
(Z)-close-dimer	1.14	0.93	2.07
(Z)-close-dimer aggregate	0.52	0.57	1.09
(Z)-TPE-UPy aggregate	0.59	0.60	1.19
(E)-linear-dimer	0.74	0.81	1.53
(E)-linear-hexamer aggregate	0.67	0.73	1.40