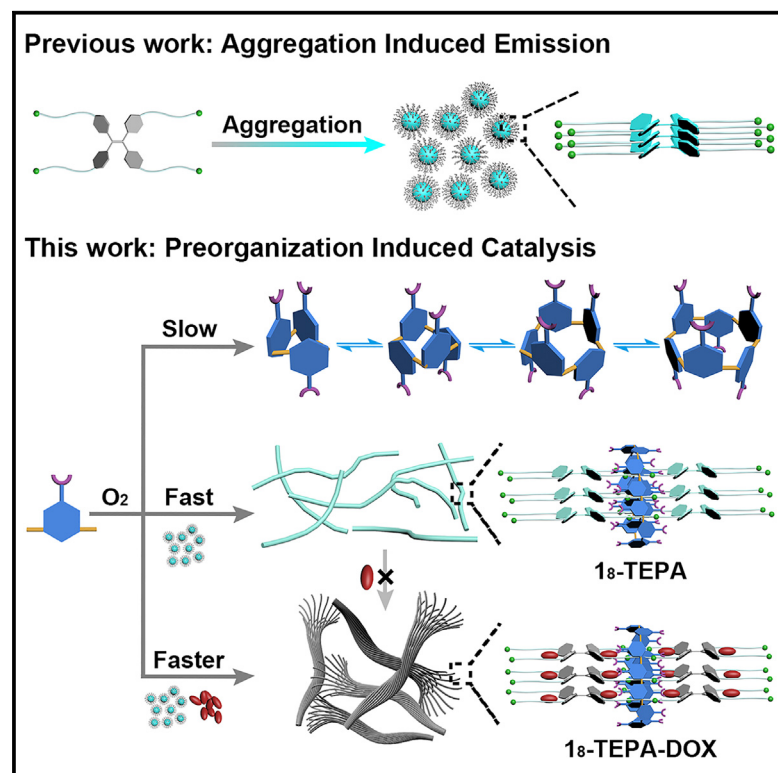


Quantitative synthesis of dynamic combinatorial macrocycles accelerated by preorganization of AIEgens for live visualization of drug release

Graphical abstract



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In brief

Jinghui et al. demonstrate that AIE preorganization catalyzes chemical reactions, with steric effects enhancing selectivity. The interplay of covalent and noncovalent interactions in the AIE-driven reaction shapes structure and optical properties, enabling a multicomponent nanosystem for real-time drug release visualization.

Highlights

- AIE-related preorganization catalyzes chemical reactions
- AIE's steric effects enhance selective production of the reaction
- The AIE-driven reaction creates nanosystems for visualizing drug release



Article

Quantitative synthesis of dynamic combinatorial macrocycles accelerated by preorganization of AIEgens for live visualization of drug release

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SUMMARY

In the aggregated state, restricted molecular movement leads to decreased entropy, a phenomenon closely associated with the release of luminescence known as aggregation-induced emission (AIE). This unique optical property is used in optoelectronic devices, biochemical sensors, and bioimaging. Complementing AIE's optical characteristics, we report that AIE-related preorganization can catalyze chemical reactions, yielding highly selective products. These products can affect aggregation states, modulating fluorescence. Incorporating an anticancer drug into this system intensified entropy reduction, accelerated reactions, and altered nanostructure. The drug's electron-donating properties quench fluorescence via energy transfer with the AIE molecule. These components engage in reversible reactions and noncovalent interactions, creating responsive nanosystems for real-time drug release visualization in drug-resistant cancer cells. This synergy between AIE and *in situ* dynamic covalent reactions offers a promising strategy for synthesizing specific molecules and exploring adaptive nanosystems with advanced optical properties for biomedical applications.

INTRODUCTION

Dynamic combinatorial chemistry (DCC) has proven to be a powerful methodology for synthesizing complex molecular architectures, offering a versatile approach to creating adaptive systems that respond to environmental stimuli.^{1–5} In DCC, a dynamic library of interconverting species is generated, where the most stable or "fittest" members, those that best interact with a given template, are selectively amplified through reversible reactions.^{6,7} This process enables the selective synthesis of specific molecular entities, such as macrocycles, which hold significant potential for various applications, including drug delivery.^{8–11}

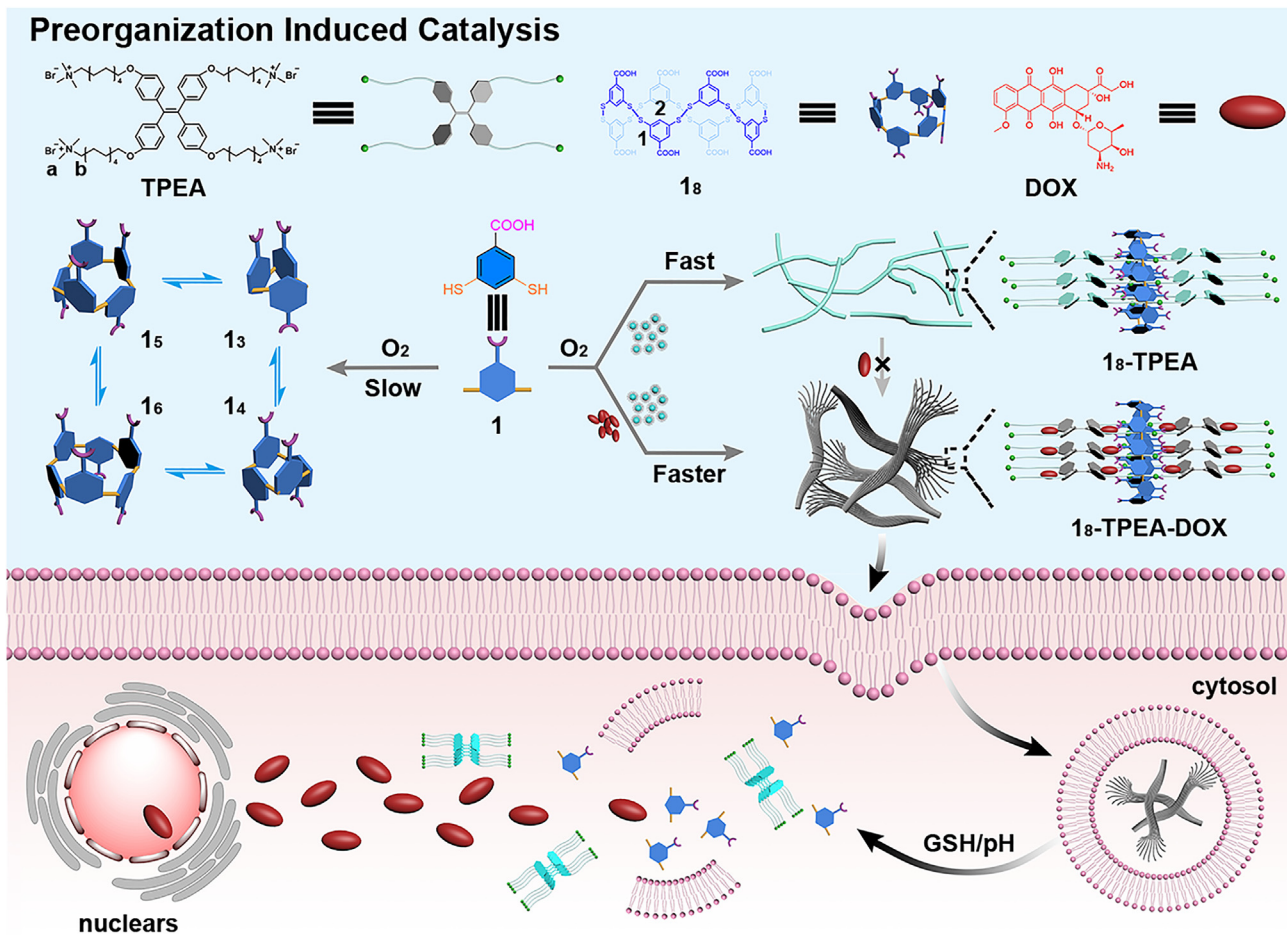
A key challenge in DCC, however, is achieving both high efficiency and selectivity in the synthesis of desired species.^{12–14} Here, we demonstrate that the preorganization of template molecules provides a solution to this challenge. By preorganizing the template molecules, the dynamic system can be directed toward the accelerated formation of specific target structures.¹⁵ This preorganization effectively lowers the energy barriers associated with macrocyclization, thereby enhancing both the rate and selectivity of the process.^{16–18}

In recent years, aggregation-induced emission luminogens (AIEgens) have gained significant attention due to their unique

property of becoming highly emissive upon aggregation, an advantage in complex and dynamic environments.^{19–25} Integrating AIEgens into DCC systems introduces an additional layer of control and functionality.^{26–28} When AIEgens are employed as template molecules within preorganized dynamic systems, their inherent propensity to aggregate can be exploited to promote the selective and rapid synthesis of specific macrocycles.^{29–32} This preorganization of AIEgen templates not only accelerates the formation of the desired structures but also endows the resulting macrocycles with intrinsic fluorescence, making them ideal for real-time monitoring.³³

In our study, we utilized the classic thiol oxidation reaction in water to generate a variety of dynamic combinatorial macrocyclic disulfides. The final distribution of these species was influenced by their relative energy levels.³⁴ The introduction of an AIE-active molecule, specifically a tetraphenylethene derivative (**TPEA**), significantly accelerated the oxidation rate. Remarkably, a specific disulfide product, which was scarcely produced in the absence of **TPEA**, became the predominant species in the presence of this AIEgen. This outcome was attributed to the thermodynamic stabilization provided by noncovalent interactions between functional units of adjacent **TPEA** derivatives.^{35,36} Additionally, the **TPEA**-induced nanostructure transitioned from





Scheme 1. Illustration of preorganizing nanosystems

This study on catalysis induced by preorganizing of templates in dynamic systems. Guided by an AIE template molecule, the thiol oxidation of a disulfide-based Dynamic Combinatorial Libraries (DCLs) was accelerated, selectively and quantitatively amplifying octameric disulfide macrocycle (1a). Introducing the anti-cancer drug DOX into the reactive system resulted in its encapsulation within the AIE aggregates, further decreasing entropy and accelerating thiol oxidation. Additionally, the morphology and fluorescence of the nanostructures adapted and responded to changes in the solution's pH and redox levels. This adaptability enabled *in situ* bioimaging for drug delivery against DOX-resistant cancer *in vitro*.

micelles to nanofibers, with a corresponding decrease in fluorescence intensity. However, when the same systems were conducted in acetonitrile, the **TPEA** templates were fully dissolved, and the fully oxidized library consisted of a mixture of multiple species. These findings suggest that the preorganization of **TPEA** facilitated thiol oxidation, while the adjacent functional groups in the aggregated state aided in the selective synthesis of the specific disulfide.

Further, by introducing the anticancer drug doxorubicin (DOX) into the system, we observed that its incorporation into the multi-component self-assembly reduced the system's entropy and further accelerated the chemical reaction.³⁷ This process resulted in a nanosystem with dual responsiveness, capable of visualizing the drug delivery process.^{38–40} These results highlight the synergy between AIE and *in situ* dynamic chemical reactions, suggesting a promising strategy for the efficient synthesis of specific molecules and the exploration of adaptive nanosystems with advanced optical properties.⁴¹

RESULTS AND DISCUSSION

Synthesis and characterization of the 1a-TPEA nanofibers

To achieve AIE in water, the **TPEA** was functionalized with positively charged quaternary ammonium salt groups linked by alkyl chains to increase its water solubility while keeping its hydrophobicity (see [Scheme 1](#)).^{30,36} Indeed, the **TPEA** molecule self-assembled into micelles with a diameter around 20 nm in a PBS buffer (pH 7.4) ([Figure 1A](#)), when its concentration was over the critical aggregation concentration (CAC) 2.1×10^{-6} M determined by fluorescence spectroscopy ([Figure S1](#)). Its AIE property was confirmed by measuring fluorescence in a mixed solution of water and acetonitrile ([Figure S2](#)). The **TPEA** exhibited non-fluorescence or weak fluorescence when dissolved in a solution with the higher percentage of acetonitrile than 40%, owing to its high solubility in this solvent. However, fluorescence emerged with an increasing water fraction in the medium

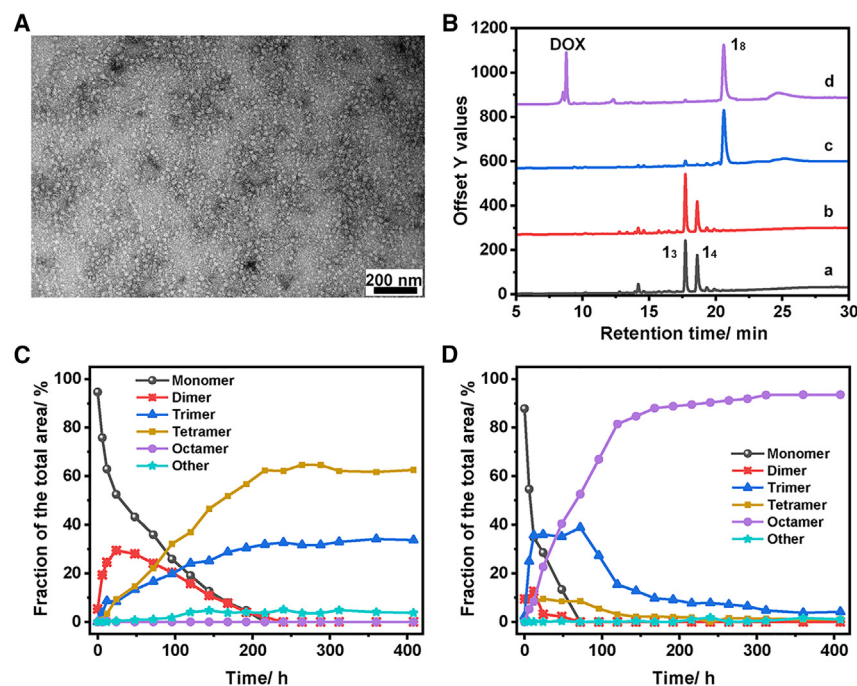


Figure 1. Characterization of 1_g-TPEA nanofiber and kinetic study

(A) TEM analysis of **TPEA** micelles. Scale bar: 200 nm.

(B) HPLC-MS analysis of fully oxidized DCLs made from (a) only building block **1** (1.0 mM), (b) building block **1** (1.0 mM) and **TPEA** (0.125 mM), (c) building block **1** (1.0 mM) and **TPEA** (0.25 mM), and (d) building block **1** (1.0 mM), **TPEA** (0.25 mM), and DOX (0.50 mM) in PBS buffers (50 mM, pH 7.4).

(C and D) Kinetic study for DCLs made from (C) only the building block **1** (1.0 mM) and (D) the building block **1** (1.0 mM) and **TPEA** (0.25 mM) in PBS buffers (50 mM, pH 7.4).

due to the lowering of the solubility of **TPEA**. Encouraged by such an excellent AIE property of **TPEA**, we proceed to verify whether the preorganization of AIE templates could serve as a catalyst for chemical reactions. A dithiol building block **1** was chosen as the starting molecule for the reaction. It (1.0 mM) could be oxidized to generate disulfide macrocyclic molecules in a PBS buffer (pH 7.4) at room temperature by the oxygen in the air. The kinetics of the oxidation reaction was monitored by high-performance liquid chromatography-mass spectrometry (HPLC-MS), suggesting that the full oxidation was reached after 9 days, and the main products were trimeric macrocycle (**1₃**) and tetrameric macrocycle (**1₄**) (see Figures 1B and 1C). In parallel, a control experiment was designed by running the same reaction but with the participation of **TPEA** molecules (0.25 mM) in the same solution. Remarkably, the oxidation process was shortened to 3 days (see Figures 1B and 1D), which revealed that the reaction was accelerated 3-fold. To show the detailed oxidation kinetics of thiols, we monitored their concentration changes over time using Ellman's method (see Figures S6 and S7). By comparing the oxidation profiles of thiols in the absence and presence of **TPEA**, we observed a significant acceleration in the oxidation rate with **TPEA**. Specifically, the overall oxidation rate in the presence of **TPEA** was three times higher than without it, confirming the results determined by HPLC peak areas (see Figures S8 and S9). To examine the relationship between the fluorescence intensity of **TPEA** and the oxidation process, we also studied the kinetics of fluorescence changes of a diluted library consisting of **1** (1.0 mM) and **TPEA** (0.25 mM) in PBS buffer (50 mM, pH 7.4). After the building block and **TPEA** are mixed, the fluorescence of **TPEA** undergoes a blue shift. With the oxidation of building block **1**, the fluorescence gradually decreased and finally stabilized, showing a similar trend to the thiol concentration decrease during the oxidation (see

Figure S10). Compared with the fluorescence intensity of **TPEA** alone, that of the **TPEA** in the end of the reaction was decreased by 41.1% (Figure 2A). We reasoned that the preorganizing of **TPEA** with dynamic systems should speed up chemical reactions.

Interestingly, the presence of **TPEA** in the reaction also resulted in the quantitative production of a specific disulfide

product octamer (**1₈**) (see Figure S4). At the same time, the morphology of **TPEA** transformed into nanofibers with a width of 3.7 nm from the micelles (see Figure 2). Since this width resembled the width of the **TPEA** molecules (see Figure S3), they probably stacked in line to form the nanofibers. The further comparison of fluorescence spectra of **TPEA** after the oxidation in water showed a blue shift, suggesting an H-aggregation (see Figure 2A).^{42,43}

We proceeded to understand the highly selective production. First, the zeta potential of the micelles self-assembled by only **TPEA** was determined as +8.4 mV, while that of the nanofiber was +6.6 mV (see Figure S5). This more negatively shifted value should result from the complexation of the negatively charged **1₈** with the positively charged surface of **TPEA** aggregation. Subsequently, we tried to investigate the molecular organization of the nanofiber by analyzing the fully oxidized reaction mixture in D₂O (pD 7.4) using ¹H-nuclear magnetic resonance (¹H-NMR) technologies. Unfortunately, no signal was observed due to the severely decreased tumbling rate in solution arising from the complete aggregation for the formation of the nanostructure. Therefore, instead of studying the fully oxidized sample, we focused on the analysis of the sample at the initial stage of oxidation to get insights into the interaction between building block **1** and **TPEA** using NMR. In the presence of **TPEA**, the H2 proton of building block **1** shifted upfield, and its spin-spin relaxation (T2 relaxation) time decreased markedly from 3,049 to 608.4 ms (see Figure S11). These results suggest that building block **1** entered the hydrophobic region of the pre-assembled AIEgens, resulting in restricted molecular motion and an enhancement in electrostatic interactions between the components, which should help the synthesis of **1₈**. Considering that the electrostatic complementarity was the main driving force for the binding between the **TPEA** and **1₈**, we used a cationic surfactant octadecyl

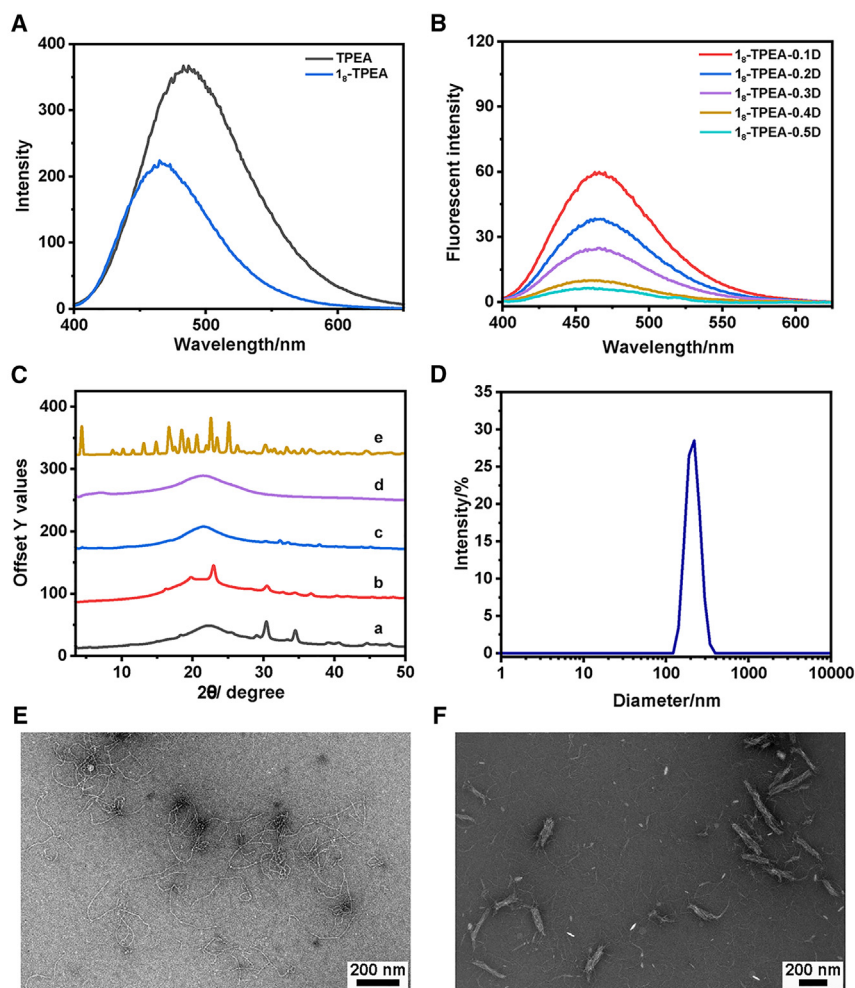


Figure 2. Characterization of 1_g -TPEA-DOX nanofiber bundles

(A) Fluorescence spectra of a **TPEA** (10 μ M) solution and a diluted library 1_g -**TPEA** consisting of 1_g (5 μ M) and **TPEA** (10 μ M) in PBS buffer (50 mM, pH 7.4). **TPEA** λ_{ex} = 330 nm.
 (B) Fluorescence analysis of diluted libraries 1_g -**TPEA**-DOX containing 1_g (5 μ M), **TPEA** (10 μ M), and DOX with various concentrations ranging from 0.1 to 0.5 equiv of building block **1** in PBS buffer (50 mM, pH 7.4).
 (C) PXRD analysis of (a) $1_3 + 1_4$, (b) **TPEA**, (c) 1_g -**TPEA**, (d) optimized ratio of 1_g -**TPEA**-DOX, and (e) DOX.
 (D) Size distribution in 1_g -**TPEA**-DOX library analyzed by DLS at room temperature.
 (E and F) TEM analysis of (E) 1_g -**TPEA** and (F) 1_g -**TPEA**-DOX libraries. Scale bar: 200 nm.

stant of $6.2 \times 10^5 \text{ M}^{-1}$ was obtained in PBS buffer (50 mM, pH 7.4) at room temperature. A slight decrease in the binding constant was noted at lower pH levels, while temperature variations had a minimal effect, indicating excellent binding stability across different temperatures. The minor reduction in binding strength at lower pH likely resulted from the protonation of the carboxyl group, which weakened the electrostatic interactions between 1_g and **TPEA**. These results revealed that one 1_g molecule was strongly associated with two quaternary ammonium salt groups from two adjacent **TPEA** molecules. To verify this hypothesis, we prepared a library with the same concentrations as

trimethyl ammonium bromide (OTAB) equipped with the same quaternary ammonium salt group to elucidate the noncovalent interactions (for structures, see Figure S12). Upon addition of the 1_g into a solution of the template OTAB in D_2O (2 mM, pD 7.4), the signals of the methyl protons of trimethyl ammonium units and the methylene protons (H_a and H_b) of the template showed remarkable upfield shifts, while the signal of the aromatic protons H_1 and H_2 of 1_g moved downfield. These complementary changes of chemical shifts should be the result of the electrostatic interaction between the deprotonated carboxylic acid groups on hosts and the positively charged ammonium salts as guests.³⁵

To further understand the spatial conformation of the inclusion complex, we also conducted two-dimensional nuclear Overhauser effect (2D NOESY) experiments. The NOE correlation signals were observed between protons on the 1_g and the H_a and H_b on the template, confirming the above threading binding mode. The complex stoichiometry between 1_g and the **TPEA** was 1:2, determined by the Job's plot method on a fluorescence spectrophotometer (see Figure S13). The binding constant was further determined using the fluorescence titration method under various experimental conditions (see Figure S14). A binding con-

stant of $6.2 \times 10^5 \text{ M}^{-1}$ was obtained in PBS buffer (50 mM, pH 7.4) at room temperature. A slight decrease in the binding constant was noted at lower pH levels, while temperature variations had a minimal effect, indicating excellent binding stability across different temperatures. The minor reduction in binding strength at lower pH likely resulted from the protonation of the carboxyl group, which weakened the electrostatic interactions between 1_g and **TPEA**. These results revealed that one 1_g molecule was strongly associated with two quaternary ammonium salt groups from two adjacent **TPEA** molecules. To verify this hypothesis, we prepared a library with the same concentrations as before, using building block **1** (1.0 mM) and **TPEA** (0.25 mM), but this time in a solution containing 70% acetonitrile by volume in water. The addition of acetonitrile, which dissolved the **TPEA** aggregates as indicated by the quenching of fluorescence, likely increased the spacing between the quaternary ammonium salt groups. As a result, the trimer (1_3) emerged as the predominant species, while the 1_g nearly vanished in this specific library setup (see Figure S15). Altogether, the quantitative yield of 1_g should be driven by the strong surface binding of the pre-assembled **TPEA**, and the molecular organization of the nanofiber consisting of **TPEA** and 1_g is shown in Figure S16.

Synthesis and characterization of the 1_g -TPEA-DOX nanofiber bundles

Furthermore, apart from the investigation of only **TPEA** molecules, we also introduced another anticancer drug, DOX, into the system. It is well known that DOX can be encapsulated into the hydrophobic domain of supramolecular nanostructures. A previous work⁴⁴ has reported that the freedom degree of drug molecules would be reduced after the encapsulation process occurred and that the entropy of the whole chemical system should decrease more. Based on this conclusion, we expected

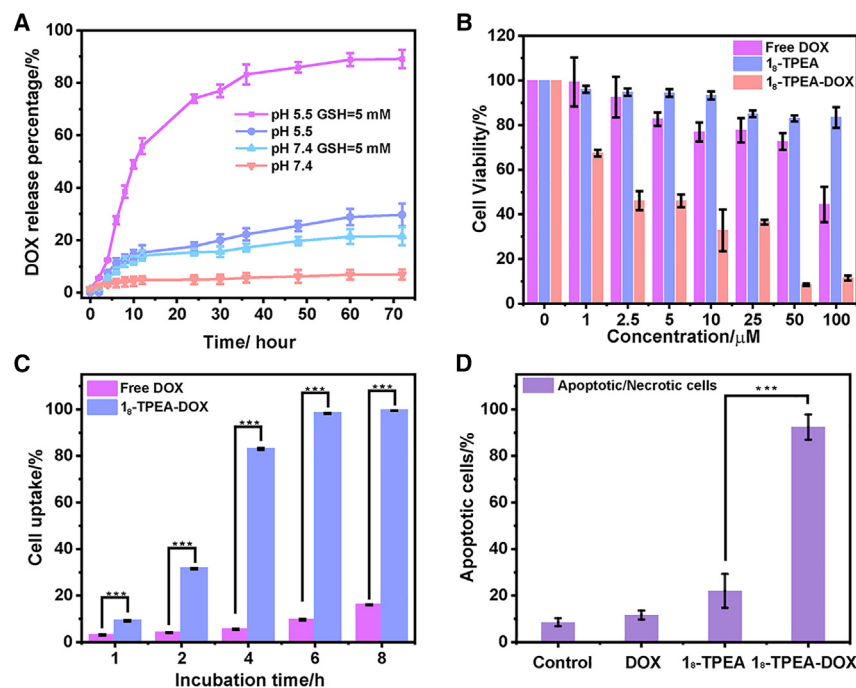


Figure 3. 1_8 -TPEA-DOX nanofiber bundles show enhanced anti-proliferation efficiency via rapid, effective drug release, cellular uptake, and drug efflux inhibition

(A) Time course of DOX released from nanobundles of the 1_8 -TPEA-DOX at pH 5.5, 7.4 and pH 5.5, 7.4 with 5 mM GSH at 37°C.

(B) The anti-proliferative activity of free DOX, 1_8 -TPEA nanofibers, and 1_8 -TPEA-DOX nanofiber bundles on drug-resistant NCI/RES-ADR cells were measured by MTT assay.

(C) The cellular uptake in drug-resistant NCI/RES-ADR cells was quantified using flow cytometry after treatment with free DOX ($C_{DOX} = 10.0 \mu\text{M}$) and 1_8 -TPEA-DOX ($C_{DOX} = 10.0 \mu\text{M}$) at 1, 2, 4, 6, and 8 h.

(D) Quantitative analysis of Annexin V-positive cells after treatment with nontreatment control, free DOX, 1_8 -TPEA, and 1_8 -TPEA-DOX after 4 h. All the measurements were performed at least in triplicate; error bars represent SDs about the mean. * $p < 0.05$, ** $p < 0.01$, and *** $p < 0.001$.

that such an entropy decrease should be compensated by releasing more energy to obey the second law of thermodynamics, and the energy release may be presented by driving the thiol oxidation more quickly. Thus, we tested the DCLs prepared from the same concentrations of building block **1** (1.0 mM) and **TPEA** (0.25 mM) with varying concentrations of DOX and observed fluorescence quenching (Figure 2B). Additionally, the octamer 1_8 remained the dominant species, but its production was 4.8 times faster in the presence of DOX (0.4 mM) compared to the library made with the same concentrations of building block **1** and **TPEA** (see Figure S17). These results further validate our concept of utilizing pre-assembly to catalyze selective synthesis in dynamic systems.

Notably, the fluorescence was quenched almost completely when the DOX concentration reached 0.50 mM (Figure 2B). This quenching phenomenon was attributed to energy transfer relay (ETR) by the overlap between the emission of **TPEA** and the absorption of DOX (Figure S18).³⁹ The maximum drug loading capacity of 1_8 -TPEA-DOX achieved was 31.8%, with a corresponding encapsulation efficiency of 93.5%. At this optimized ratio (1_8 :TPEA:DOX = 0.125:0.25:0.5 mM), the morphology of the complex chemical system had a new adaptation to fiber bundles with an approximate dimension of 50 × 220 nm determined by transmission electron microscopy (TEM), which was consistent with the Z-average size of 260 nm measured via dynamic light scattering (DLS) analysis (see Figures 2D and 2F). Additionally, the disappearance of the DOX signal in power X-ray diffraction (PXRD) analysis indicated that DOX was fully encapsulated in a non-crystalline form within the newly formed nanosystem (see Figure 2C). Given the amphiphilicity of DOX and the observed fluorescence quenching, it is suggested that DOX molecules are likely embedded in the hydrophobic region of 1_8 -TPEA-DOX, near the **TPEA** core.⁴⁵ Inter-

estingly, adding DOX into the oxidized library containing 1_8 -TPEA nanofibers failed to disperse and encapsulate effectively, suggesting that the thiol-disulfide exchange had significant kinetic control over the drug encapsulation and nanomorphological evolution process.

Considering that the optical property was highly dependent on the composition of the multicomponent nanosystem and the nanosystem was organized by noncovalent interactions and reversible chemical reactions, we reasoned that the system should be dynamic and responsive. Thus, together with the high drug loading content of the 1_8 -TPEA-DOX composite, this nanosystem held great potential as an excellent drug delivery system for cancer therapy while imaging the drug release in real time to better understand its pharmacokinetics and pharmacodynamics.

Redox- and pH-induced release of DOX and TPEA from the nanofiber bundles

Keeping these results in mind, we moved forward to first evaluate the responsiveness of the 1_8 -TPEA-DOX nanosystem. In the context of drug delivery, it is crucial to control the drug release profile at tumor sites. Tumor cells typically exhibit a more acidic environment than normal cells due to the accumulation of lactic acid and CO₂ in a hypoxic microenvironment.⁴⁶ Additionally, the concentration of glutathione (GSH) inside cancer cells, exceeding 5 mM, is significantly higher than that in the extracellular matrices at tumor sites.^{47,48} Consequently, we applied these dual stimuli to simulate the biological and endolysosomal environments and monitor the release profile of DOX and **TPEA** *in vitro* (Figure 3A). The cumulative release of DOX was <7% at pH 7.4, indicating that the 1_8 -TPEA-DOX nanofiber bundles remained stable under physiological pH conditions. However, at the endo-lysosomal pH of 5.5 in the presence of GSH, the release of DOX from the 1_8 -TPEA-DOX nanofiber bundles was significantly accelerated. Within 24 h, nearly 80% of the

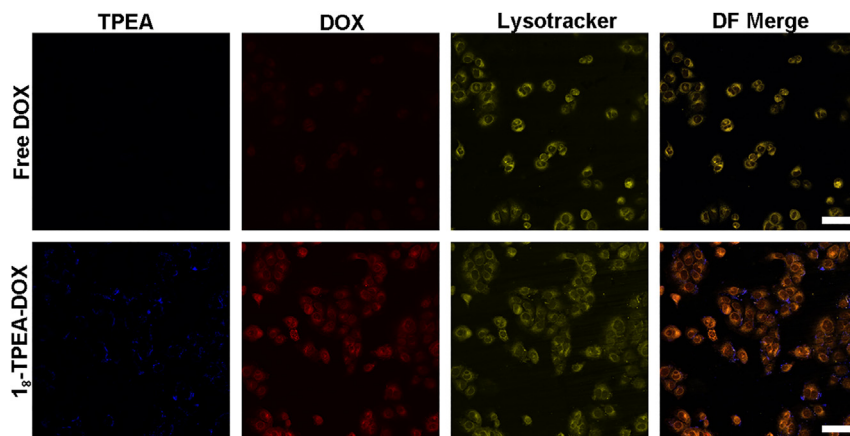


Figure 4. The cellular uptake was imaged using a confocal microscope

Images of NCI/ADR-RES cells incubated with free DOX and 1_g -TPEA-DOX nanofiber bundles at a DOX concentration of $10\ \mu\text{M}$ for 4 h. Blue, red, and yellow fluorescence indicate TPEA, DOX, and the LysoTracker, respectively. Scale bar, $50\ \mu\text{m}$.

total DOX in the nanofiber bundles was released, while the cumulative leakage was $<18\%$ over the same period at pH 5.5 without GSH. Under physiological conditions, the deprotonation of carboxylic groups of 1_g enhanced the electrostatic interaction with the positive charge of TPEA, thereby maintaining the stability of the nanostructure. However, as the pH became acidic (pH 5.5), the carboxylate anions of 1_g were protonated, as indicated by a decrease in solubility compared to that observed at pH 7.4 (see Figure S19). The protonation would weaken the electrostatic interaction and render the entire nanofiber bundle fragile, resulting in the release of DOX. Furthermore, the amine-bearing DOX loaded in the system became more positively charged at low pH, increasing the solubility of DOX (see Figure S19), further promoting drug release.^{49–51}

Following the establishment of the favorable drug release profile of 1_g -TPEA-DOX nanofiber bundles, we conducted a comprehensive evaluation of their anti-proliferative efficiency in NCI/RES-ADR DOX-resistant human breast ovarian cancer cells. As depicted in Figure 3B, the IC_{50} value of free DOX for NCI/RES-ADR cells was approximately $100\ \mu\text{M}$. The pronounced resistance to DOX observed was attributed to the overexpression of P-glycoprotein (P-gp) by NCI/RES-ADR cells. P-gp functions by pumping DOX molecules out of cancer cells. However, DOX resistance could be overcome by nanofiber bundles that inhibited P-gp efflux and depleted adenosine triphosphate (ATP). Notably, the IC_{50} value of 1_g -TPEA-DOX nanofiber bundles for NCI/RES-ADR cells was $3.2\ \mu\text{M}$, remarkably lower than that ($100\ \mu\text{M}$) of free DOX, signifying a 30-fold increase in toxicity. This outcome unequivocally demonstrated the substantial superiority of 1_g -TPEA-DOX nanofiber bundles over free DOX in enhancing cell anti-proliferation in drug-resistant cell lines.⁸

Enhanced cellular uptake of the nanofiber bundles

To gain insights into the mechanism underlying the enhanced proliferation inhibition by 1_g -TPEA-DOX nanofiber bundles, we examined their cellular uptake in NCI/RES-ADR cells using flow cytometry analysis. The drug uptake efficiencies in NCI/RES-ADR cells were approximately 3% and 5% after incubation with free DOX at $10\ \mu\text{M}$ for 1 and 4 h, respectively. In contrast, drug uptake reached nearly 90% after a 4 h incubation with 1_g -TPEA-DOX nanofiber bundles ($10\ \mu\text{M}$ DOX) (Figure 3C). This

observation strongly suggests that DOX-loaded nanofiber bundles significantly enhance the time-dependent cellular internalization and accumulation of DOX. Collectively, these results clearly demonstrated that 1_g -TPEA-DOX nanofiber bundles were much more effective than free DOX in enhancing anti-proliferation efficiency in DOX-resistant NCI/RES-ADR cells, ultimately leading to apoptosis-induced anticancer activity (Figure 3D).

We validated the augmented cellular uptake of 1_g -TPEA-DOX nanofiber bundles in NCI/RES-ADR cells using confocal laser scanning microscopy (CLSM). When free DOX was employed, the red fluorescence was barely detectable in cancer cells and did not induce cytotoxicity. Following 4 h incubation of NCI/RES-ADR cells with 1_g -TPEA-DOX nanofiber bundles, DOX fluorescence was observed in both the cytoplasm and nucleus. Simultaneously, TPEA fluorescence appeared in the cytoplasm, with no TPEA signal observed in the nucleus. This observation indicated that the carrier solely served its delivery function and did not influence the anticancer effect of DOX. Notably, each cell contained a substantial cytoplasm displaying a notably strong fluorescence signal from both TPEA and DOX. We hypothesized that this cytoplasm region corresponded to lysosomes, where the detachment of DOX from the 1_g -TPEA-DOX nanofiber bundles led to a fluorogenic response. To test this, we stained lysosomes with LysoTracker Deep Red (Figure 4, Dual Field [DF] merge) and found that the strong TPEA and DOX signals did indeed colocalize with lysosomes. These results further confirmed that the 1_g -TPEA-DOX nanofiber bundles were responsive to low pH and GSH in cancer cells, and TPEA and DOX were released in lysosomes.

Real-time visualization release of DOX and TPEA from the nanofiber bundles *in vitro*

Real-time visualization of drug release will enable us to understand this process better and will enlighten future designs of sophisticated nanocarriers. Our 1_g -TPEA-DOX bundle is well suited to this purpose. The pH and GSH induce a dual-color fluorogenic response from both TPEA and DOX once the DOX is released. To achieve real-time visualization of the drug release at the subcellular level and observe subtle changes at each time point during this process, we employed a real-time CLSM system equipped with a continuous shooting apparatus. This non-invasive method eliminates the need for cell disruption or organelle isolation. NCI/RES-ADR cells were incubated with 1_g -TPEA-DOX and monitored using real-time CLSM, capturing snapshots every 5 min over a 240 min period. A noticeable "from darkness to brightness" phenomenon was observed for

both **TPEA** and DOX. The initial dark background indicated the stability of **1_g-TPEA-DOX** in the cell culture medium, making them suitable for *in vitro* real-time visualization of intracellular stimulus-triggered drug release. Following this initial period of darkness, the areas containing lysosomes became bright, displaying orange and blue colors, signifying the awakening of both DOX and **TPEA** and the initiation of the fluorogenic process due to the disruption of **1_g-TPEA-DOX**. Subsequently, the cell nucleus became light, indicating that DOX had reached its site of action.⁴¹ Based on these results (Figure S20), we propose the following drug release process: **1_g-TPEA-DOX** was taken up by the cells and transported to lysosomes. Within the lysosomes, owing to the acidic pH and higher GSH concentration, the nanofiber bundles began to break down. This disruption interrupted the ETR between DOX and **TPEA**, causing the quenched fluorescence to "wake up" and light the lysosomes. Subsequently, the released DOX from **1_g-TPEA-DOX** entered the nucleus and exerted its anti-tumor function.

In conclusion, we have demonstrated that the energy derived from AIE's preorganization is multifaceted. It manifests not only as luminescence but can also be converted into chemical energy through catalysis for a reaction, with enhanced production selectivity resulting from AIE's steric effects. Such a complex chemical system operated by covalent reactions and noncovalent interactions also dictated the adaptation of structure and optical property to produce a multicomponent nanosystem to visualize the drug release process in real time. These findings have highlighted the energy transfer between supramolecular aggregation and *in situ* chemical reactions to evolve into functional multicomponent nanosystems for advanced applications. Our research has presented complex yet interesting molecular behaviors and functions at the systems level, orchestrating a harmonious dance of physical and chemical processes. Such advancements hint at the promising trajectory of systems chemistry, echoing nature's intricate complexities and heralding breakthroughs in realms like sensing, anti-counterfeiting, and electronics.

METHODS

Details regarding the methods can be found in the [supplemental methods](#).

RESOURCE AVAILABILITY

Lead contact

Further information and requests for resources and reagents should be directed to and will be fulfilled by the lead contact, Dr. Jianwei Li (jianwei.li@utu.fi).

Materials availability

All stable and unique materials generated in this study are available from the [lead contact](#) upon reasonable request.

Data and code availability

All of the data supporting this study have been included in the article and [supplemental information](#). Other related data are available from the corresponding authors upon reasonable request.

ACKNOWLEDGMENTS

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AUTHOR CONTRIBUTIONS

J.Y. conceived the idea, carried out the synthesis, characterization, and cell experiments, and wrote the manuscript. X. Wang and X. Wu helped with cell experiments. A.C.P. carried out the PXRD characterization. Y.L. and X. Wang carried out part of the synthesis. J.L. supervised the research and wrote the paper.

DECLARATION OF INTERESTS

The authors declare no competing interests.

SUPPLEMENTAL INFORMATION

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