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Supramolecular nanostructures with tunable donor loading for controlled H₂S release

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Abstract

Hydrogen sulfide (H₂S), an endogenously generated and regulated signaling gas, plays a vital role in a variety of (patho)physiological processes. In the past few years, different kinds of H₂S-releasing compounds (often referred to as H₂S donors) have been developed for H₂S delivery, but it is still challenging to make H₂S donors with tunable payloads in a simple and efficient manner. Herein, a series of peptide-H₂S donor conjugates (PHDCs) with tunable donor loadings are designed for controlled H₂S release. The PHDCs self-assemble into nanoribbons with different geometries in aqueous solution. Upon addition of cysteine, these nanostructures release H₂S, delivering their payload into H9C2 cells, as visualized using an H₂S-selective fluorescent probe. Beyond imaging, *in vitro* studies show that the ability of PHDCs to mitigate doxorubicin-induced cardiotoxicity in H9C2 cardiomyocytes depends on their nanostructures and H₂S release profiles. This strategy may enable the development of sophisticated H₂S-releasing biomaterials for drug delivery and regenerative medicine.

Graphical Abstract

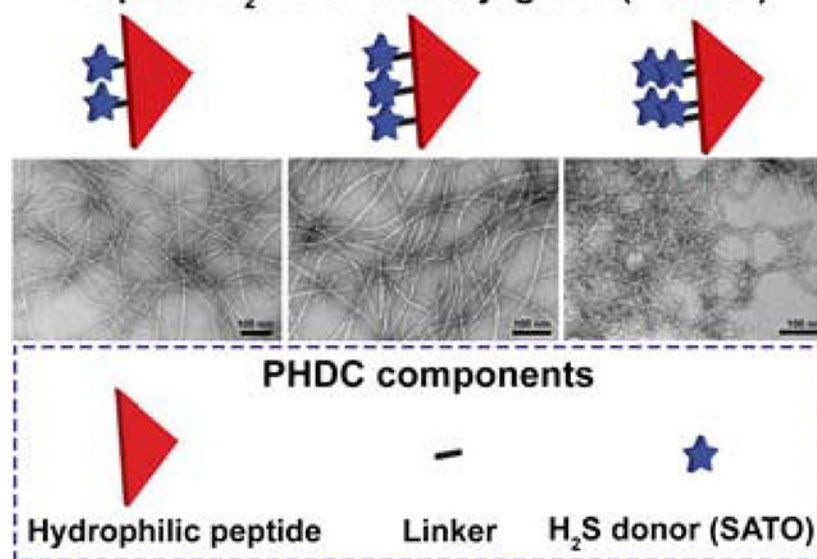
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The authors declare no competing financial interest.

ASSOCIATED CONTENT

Supporting Information. The Supporting Information is available free of charge on the ACS Publications website. Detailed experimental section, further cell studies, and additional characterization (circular dichroism, CAC measurements, ESI-MS, and UV-vis).

Payload Tunable Self-Assembling Peptide- H_2S Donor Conjugates (PHDCs)



Keywords

Hydrogen Sulfide; Self-assembly; Drug delivery; Controlled release; Peptide

INTRODUCTION

As a biological signaling molecule, hydrogen sulfide (H_2S) is involved in many physiological and/or pathological processes such as vasodilation and angiogenesis.¹⁻⁴ Although the majority of foundational reports in this area used inorganic salts such as sodium sulfide (Na_2S) or sodium hydrosulfide ($NaSH$) as H_2S sources,⁵⁻⁶ these molecules are not ideal compounds for studying H_2S biology due to their instantaneous release profiles and the transient nature of this signaling gas. In order to provide tools for studying H_2S biology with slow and sustained rates of H_2S delivery, several groups have recently developed many H_2S -releasing compounds (so-called H_2S donors).⁷⁻¹² These donors respond to specific triggers, releasing H_2S after application of a stimulus such as light, biologically-relevant thiols, changes in pH, enzymatic activity, and many others. However, despite this variety of synthetic H_2S donors, several issues still need to be addressed. Low water solubility, few methods to tune release kinetics, and in most cases no capacity for delivery to a specific biological target limit the use of many H_2S donors both as chemical tools for investigating the biological roles of H_2S and as potential therapeutics.

One promising strategy to address these limitations is to incorporate H_2S donors into materials, either through physical encapsulation¹³⁻¹⁴ or by covalent conjugation to hydrophilic polymers.¹⁵⁻¹⁸ While these methods can be effective, the short- and long-term biological activities, combined with potential toxicity arising from the synthetic polymers, may be cause for concern.¹⁹ Additionally, polydispersity must be considered, referring here both to polymer length and the amount of conjugated H_2S donor, making polymeric drug

delivery vehicles of all kinds consistently vulnerable to batch-to-batch variability. To circumvent these problems, we began designing and evaluating H₂S-releasing materials based on self-assembling peptides.^{20–24} Peptides are useful materials from which to build self-assembled nanostructures for biomedical applications due to their inherent biodegradability and biocompatibility under many circumstances.²⁵ Moreover, they can be quickly synthesized and purified with direct sequence control.^{26–27} Previously, our group showed that H₂S-donating *S*-aroylthiooximes (SATO) appended to the hexapeptide Ile-Ala-Val-Glu-Glu-Glu (IAVEEE) assembled into nanofibers in water.²⁰ The nanostructures protected the SATO groups from hydrolytic decomposition and prolonged the release time in water as compared to small molecule SATOs. Very recently, we found that conjugation of SATOs to short tetrapeptides not only extended their H₂S release profiles, but also modulated their release behaviors as a result of their different self-assembled morphologies.

Despite progress in developing peptide-based H₂S donors, a remaining downside of existing constructs is their limited tunability in terms of donor loading. A series of H₂S-donating peptides with variable numbers of SATO groups per peptide has not been explored. In this context, we report here a group of peptide-H₂S donor conjugates (PHDCs) that self-assemble in water to form stable supramolecular nanostructures with an ability to tune the SATO loading by molecular design. We aimed to evaluate how donor loading affects the self-assembled morphology, H₂S release profiles, and biological activity of these PHDCs.

To achieve this goal, we appended SATOs, a thiol-triggered H₂S donor developed in our lab,²⁸ onto peptide sequences of 2–7 amino acids. Specifically, *S*-benzoylthiohydroxylamine (SBTHA) was added to three peptides, each with the same pentapeptide, Phe-Glu-Glu-Glu-Glu (FE₄), but with different numbers of 4-formylbenzoic acid (FBA) units attached to Lys residues on the side chain ϵ -amine or the *N*-terminus. This molecular design allowed us to precisely attach two, three, or four SATOs onto the peptides, corresponding to respective SATO loadings of 24%, 28% and 31% by weight (Eq. S1–3). The structures of these three PHDCs are shown in Figure 1 and are labeled **dSATO-FE₄**, **tSATO-FE₄**, and **qSATO-FE₄** for short. Synthetic procedures and characterization details are included in the Supporting Information (Figure S1).

RESULTS AND DISCUSSION

We first probed each PHDC after dissolution in aqueous 10 mM phosphate buffer (pH 7.4) by conventional transmission electron microscopy (TEM). Images showed that all three PHDCs assembled into long, one-dimensional nanostructures (Figure 1D–F). The dominant morphology observed for PHDC **dSATO-FE₄** was twisted ribbons (Figure 1D). The widths were 7 ± 1 nm, and average lengths were a few micrometers. PHDC **tSATO-FE₄** also formed twisted ribbons 7 ± 1 nm in width and several micrometers in length (Figure 1E). In contrast, a different morphology was observed for PHDC **qSATO-FE₄**. It associated into curved ribbons with average widths of 6 ± 1 nm (Figure 1F). Although not as long as the twisted ribbons formed by **dSATO-FE₄** and **tSATO-FE₄**, the curved ribbons tended to form bundles, which we expected could be beneficial for prolonging H₂S release. These results

show how incorporating different numbers of SATOs into the PHDC structure allows for tuning of both the SATO loading content and the self-assembled morphologies.

To probe the differences among these PHDCs in their self-assembled states, we began by conducting Nile Red assays to measure their critical aggregation concentrations (CACs), followed by circular dichroism (CD) spectroscopy to study the secondary structures of the self-assembled PHDCs. The Nile Red assay showed that the CAC value for each of the three PHDCs was between 20 and 30 μM (Figure S2 and Table S1). This is consistent with previous CAC measurements on PHDCs.²¹ Despite their similar self-assembled morphologies, CD spectroscopy revealed that the secondary structures of these PHDC nanostructures were quite different. All three exhibited signals in the peptide region (190–240 nm), where amide bonds in peptides absorb, and in the SATO region (300–360 nm). Absorptions in the SATO region are consistent with UV-vis absorption peaks (Figure S3). In the peptide region, the spectra for both **dSATO-FE₄** (Figure 2A) and **qSATO-FE₄** (Figure 2C) showed primarily random coil structure with some amount of α -helix, although the intensity in the peptide region for **qSATO-FE₄** was substantially greater than that for **dSATO-FE₄**. In contrast, the CD spectrum for **tSATO-FE₄** was consistent with both a β -sheet structure, as indicated by the positive peak at 215 nm, and some random coil contribution (Figure 2B). These data indicate that secondary structures of these nanoassemblies are quite sensitive to the nature of the hydrophobic component, even though the peptide sequences are similar. The absorption of each PHDC varied in the SATO region as well. PHDCs **dSATO-FE₄** and **qSATO-FE₄** showed negative peaks near 330 nm, with **qSATO-FE₄** exhibiting a much more intense peak than **dSATO-FE₄**. Unlike the negative absorption peaks of **dSATO-FE₄** and **qSATO-FE₄** in the SATO region, **tSATO-FE₄** exhibited a positive peak in the same range, possibly due to different handedness within these nanoribbons.²⁹ The intensity of the SATO peak for **tSATO-FE₄** was between that of **dSATO-FE₄** and **qSATO-FE₄**. We speculate that the observed intensity differences in this region among the three PHDCs is a result of increased hydrophobic effects and therefore stronger molecular packing among SATO groups as more SATO groups are introduced into the molecular design.

We next examined how the H₂S release profiles of the three PHDCs was affected by their supramolecular structure. Because these PHDCs self-assemble in water, we expected that the nanostructures would shield SATO components from the aqueous environment, providing a method to control release of H₂S triggered by cysteine (Cys). We typically assess release profiles from H₂S donors by an H₂S-selective microelectrode probe. This method provides a real-time measurement of H₂S solution concentration; however, it is not capable of providing cumulative release curves because H₂S volatilizes and oxidizes as it is produced. Therefore, H₂S release profiles obtained with this electrochemical probe-based method are often compared using peaking times, which provide an approximate quantification of relative release rates among similar samples.

H₂S release from these PHDCs was triggered by Cys, which we and others use commonly to trigger release of H₂S from SATO-based materials.^{16, 20–21, 30} In order to eliminate the false response from the electrochemical probe generated by Cys, we used a specially made vial, reported previously,²¹ to evaluate PHDC release profiles. In these experiments, the releasing

solution was loaded into the inner well of the vial; next the well was sealed with a gas-permeable membrane (Figure S4). We kept PHDC concentration in the inner well at 1 mM while varying the amounts of Cys (4 mM total Cys for **dSATO- FE_4** , 6 mM for **tSATO- FE_4** , and 8 mM for **qSATO- FE_4**) to keep the molar ratio of SATO to Cys at 1:2. The concentration of H_2S as it passed from the inner well into a large volume of PBS was then monitored over time.

All three PHDCs showed steady and consistent H_2S release lasting for several hours (Figure 3A). Although all three PHDCs formed nanoribbons, the H_2S release profiles were quite different. Both **dSATO- FE_4** and **tSATO- FE_4** released H_2S immediately after addition of Cys. Compared with the steady release profile of **dSATO- FE_4** , there was a plateau for **tSATO- FE_4** after 20 min, and then the release rate accelerated. This interesting release profile may result from a morphology change during the H_2S release process. With three SATOs toward the N-terminal end of the peptide, Cys penetration into the core of the assemblies would not lead to reaction of all three SATOs at the same time, leading to a decrease in the magnitude of the hydrophobic and π - π interactions, changing the morphology. These newly formed nanostructures would therefore be expected to release H_2S faster as the packing among SATOs becomes weaker and the nanostructures loosen. Therefore, the observed release profile would be a combination from different nanostructures. Despite the different profiles, peaking times for **dSATO- FE_4** and **tSATO- FE_4** were quite similar, at 127 ± 8 and 136 ± 7 min, while the peaking time for **qSATO- FE_4** was significantly longer at 181 ± 4 min (Figure 3B). Interestingly, unlike the profiles for **dSATO- FE_4** and **tSATO- FE_4** , we observed an induction period of 50 min for **qSATO- FE_4** where H_2S was slowly released, after which the rate of release increased sharply. This induction time phenomenon was also observed in a different PHDC system reported by our group recently.²¹ We speculate that this initial period of slow release from **qSATO- FE_4** results from Cys diffusing more slowly into the short, curved nanoribbon bundles formed by **qSATO- FE_4** (Figure 1F) compared with the separated nanoribbons in the other two PHDCs. In order to investigate the concentration effect on H_2S release, we performed H_2S release experiments with PHDC concentrations of 100 μM in the inner well were carried out. As shown in Figure S5 and Table S2, shorter peaking times were observed at 100 μM than at 1 mM despite the 10-fold dilution. Additionally, no significant difference in peaking times was observed, and no induction time was noted for any of the three PHDCs. These results resemble those from other drug-releasing self-assembling peptides³¹⁻³² and our recently reported PHDC tetrapeptides,²¹ where the release rate increases upon dilution of the samples. These data collectively indicate that Cys penetrated into these nanoribbons in a similar manner regardless of the varying number of SATO groups when the concentration of PHDC was low, but that rates of Cys diffusion varied at higher PHDC concentrations.

We then turned our attention to biological studies on PHDCs **dSATO- FE_4** and **qSATO- FE_4** , which had the shortest and longest peaking times. Fluorescence microscopy was used to investigate whether **dSATO- FE_4** and **qSATO- FE_4** could be deliver H_2S into cells. We used WSP-5,³³ an H_2S -selective fluorescent probe, to monitor H_2S accumulation from these PHDCs in H9C2 cells. As expected, Cys alone provided no fluorescent signal, because WSP-5 responds to H_2S but not to Cys (Figure 4, first row).³³ Treating cells with PHDCs

without Cys provided a weak fluorescent signal, which likely resulted from a small amount of H₂S generated from hydrolysis of PHDCs (Figure 4, second and third rows). In sharp contrast, co-addition of **dSATO-Fe₄** or **qSATO-Fe₄** with Cys resulted in a significant increase in WSP-5 fluorescence (Figure 4, fourth and fifth rows), demonstrating that both **dSATO-Fe₄** and **qSATO-Fe₄** can be successfully activated to release H₂S *in vitro* and that the released H₂S can be imaged using an H₂S-responsive fluorescent probe.

Given that both PHDCs were capable of delivering H₂S into cells, we next explored their ability to protect against cardiotoxicity induced by doxorubicin (Dox), a common chemotherapeutic. Dox, an anthracycline with widespread antitumor activity, has potent therapeutic effects on a variety of cancers, including lymphomas, leukemias, soft-tissue sarcomas, and various types of solid tumors.³⁴ However, its clinical use is limited by its dose-limiting and at times life-threatening cardiotoxicity.³⁵ Previous studies showed that H₂S, delivered as instantaneously releasing Na₂S, rescues cardiomyocytes treated with Dox by mitigating stress in the endoplasmic reticulum,^{36–37} or depressing the p38 MAPK pathway,^{38–39} but this cardioprotective capacity has not been tested widely on sustained H₂S donors.²¹ More importantly, slow-releasing H₂S donors frequently lead to enhanced biological effects compared to instantaneously releasing Na₂S.^{16, 40} Thus, we envisioned that the PHDCs developed here might rescue cardiomyocytes in the presence of Cys.

First, we confirmed that both **dSATO-Fe₄** at 200 μM and **qSATO-Fe₄** at 100 μM (both 400 μM SATO) were nontoxic to H9C2 cells in the presence of Cys (left two columns in Figure 5). In treatment studies, H9C2 cells were pretreated with **dSATO-Fe₄** and **qSATO-Fe₄** in the presence of Cys for 30 min.^{21, 36, 41} Without removing the PHDC/Cys solution, Dox was added and cells were incubated for another 24 h. Compared to the Dox only treatment group (46% viability, brown column in Figure 5), cell viability increased significantly when cells were treated with **dSATO-Fe₄** (69% viability) or **qSATO-Fe₄** (84% viability) (black and blue columns on the right in Figure 5). More importantly, **qSATO-Fe₄** was significantly more effective in rescuing cells than **dSATO-Fe₄**. Because PHDCs were added in amounts to keep SATO loadings equal, this difference in bioactivity is likely due to the following two phenomena: 1) PHDC stock solutions (2 mM **dSATO-Fe₄** and 4 mM **qSATO-Fe₄**) were added to cell media immediately before adding media to the cells, preserving their original morphologies; 2) The length of **qSATO-Fe₄** curved ribbons are much shorter than that the **dSATO-Fe₄** nanoribbons (Figure 1), which may facilitate cell uptake. Finally, we also confirmed that sustained H₂S release was key for rescuing cardiomyocytes treated with Dox through comparisons to other H₂S donors and control compounds (Figure S6), including Cys alone (49% viability), GYY4137 (38% viability), and Na₂S (56% viability). Taken together, these results highlight the importance of release rate on H₂S bioactivity.

CONCLUSIONS

In summary, we discuss here the synthesis and self-assembly of discrete PHDC nanostructures with tunable H₂S donor content by controlling the number of H₂S-releasing SATO units near the peptide N-terminus. The release behaviors depended strongly on the self-assembled morphology of the PHDCs, which relied heavily on molecular design, with the peaking time prolonged as the SATO loading percentage increased. *In vitro* fluorescence

studies showed that in the presence of Cys, H₂S released from PHDCs could be delivered into cells and visualized using an H₂S-responsive fluorescent probe. In addition, the released H₂S mitigated Dox-induced toxicity in H9C2 cardiomyocytes, in which the PHDC with more SATO loading was more effective than its counterparts. These results highlight how variation in payload loading in amphiphilic peptides not only regulates the resulting self-assembled morphology, but also can modulate the bioactivity of these molecules. As the number of bioactive or drug molecules on a peptide can be easily changed by tuning the molecular design, we believe this strategy offers a general method to fabricate multiple types of nanostructures carrying a particular payload, enabling nanostructure-activity studies, such as this one, to be conducted on a wide variety of systems.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

ACKNOWLEDGMENT

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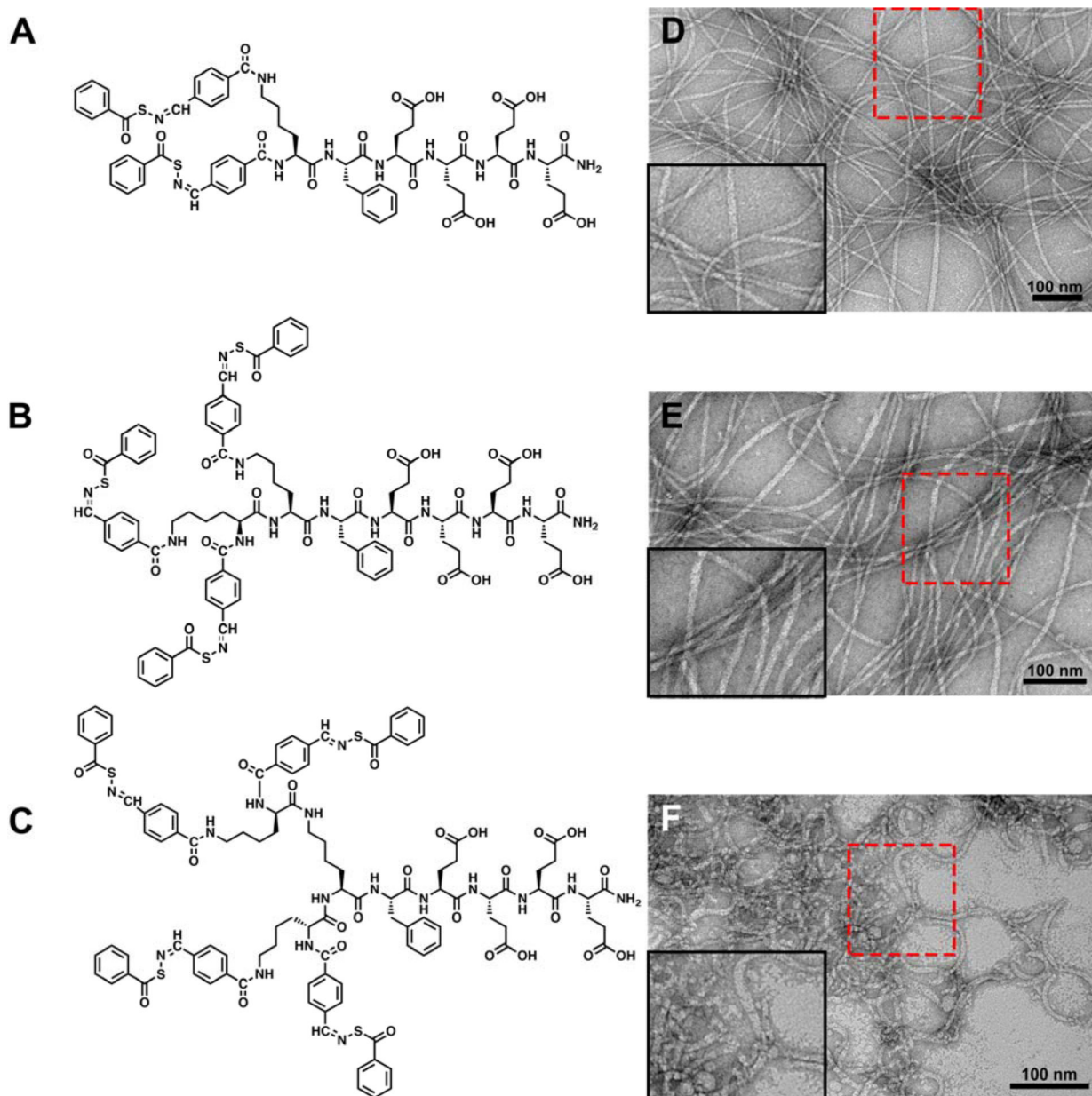


Figure 1. (A-C) Molecular structures of PHDCs studied in the present work. (A) **dsATO-FE₄**; (B) **tSATO-FE₄**; (C) **qSATO-FE₄**. (D-F) Conventional TEM images illustrate the effect of SATO numbers on the self-assembled morphologies of the PHDCs in phosphate buffer (10 mM, pH 7.4). (D) Twisted ribbons formed by **dsATO-KFE₄**; (E) Twisted ribbons formed by **tSATO-FE₄**; (F) Curved ribbons formed by **qSATO-FE₄**. Inserts in the bottom left corners of panels D-F show zoomed-in images of the areas outlined by the red rectangles. Solution concentration: 100 μ M peptides in phosphate buffer (pH 7.4). Uranyl acetate (UA) was used to stain all grids prior to imaging.

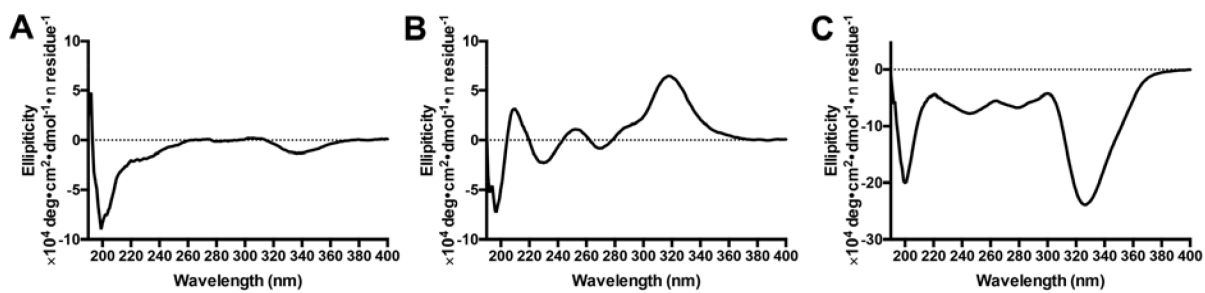


Figure 2.
CD spectra of (A) **dSATO-FE₄**, (B) **tSATO-FE₄**, and (C) **qSATO-FE₄** in phosphate buffer (75 μM , pH 7.4).

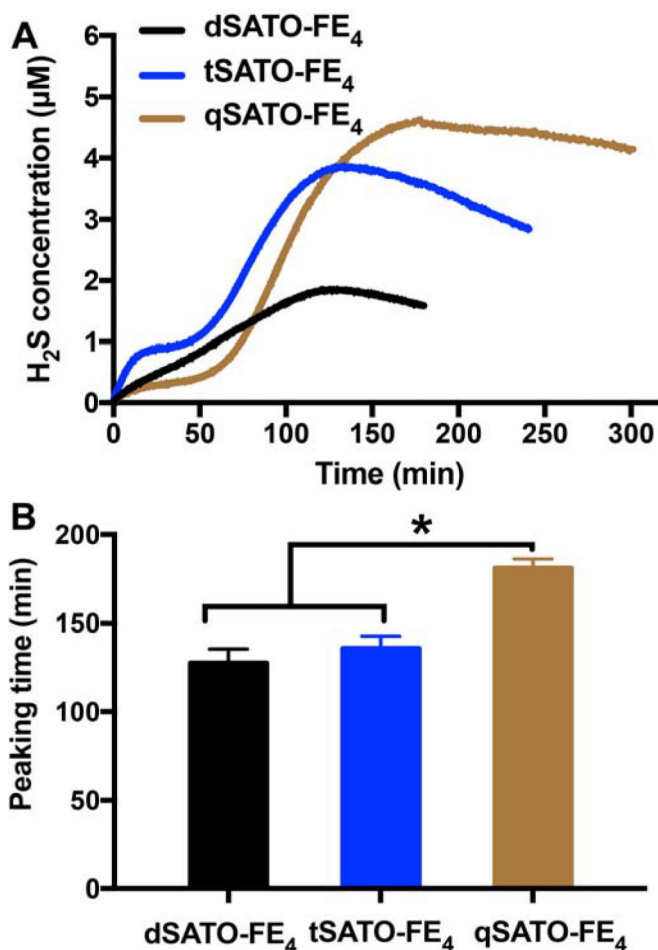


Figure 3. (A) H₂S release profiles and (B) corresponding peaking times of dSATO-Fe₄, tSATO-Fe₄, and qSATO-Fe₄ triggered by Cys at rt in PBS (pH = 7.4). Data were obtained on an H₂S-sensitive electrochemical probe from a solution of PHDC (1 mM, 110 μL total) and Cys (4 mM for dSATO-Fe₄, 6 mM for tSATO-Fe₄, 8 mM for qSATO-Fe₄) sealed in an inner well with a gas-permeable membrane inside a vial containing PBS (5 mL). Error bars indicate standard deviations of three separate experiments. * indicates p < 0.05 for a comparison of the groups indicated as determined by a one-way analysis of variance (ANOVA) with a Student-Newman-Keuls comparisons *post-hoc* test (n=3).

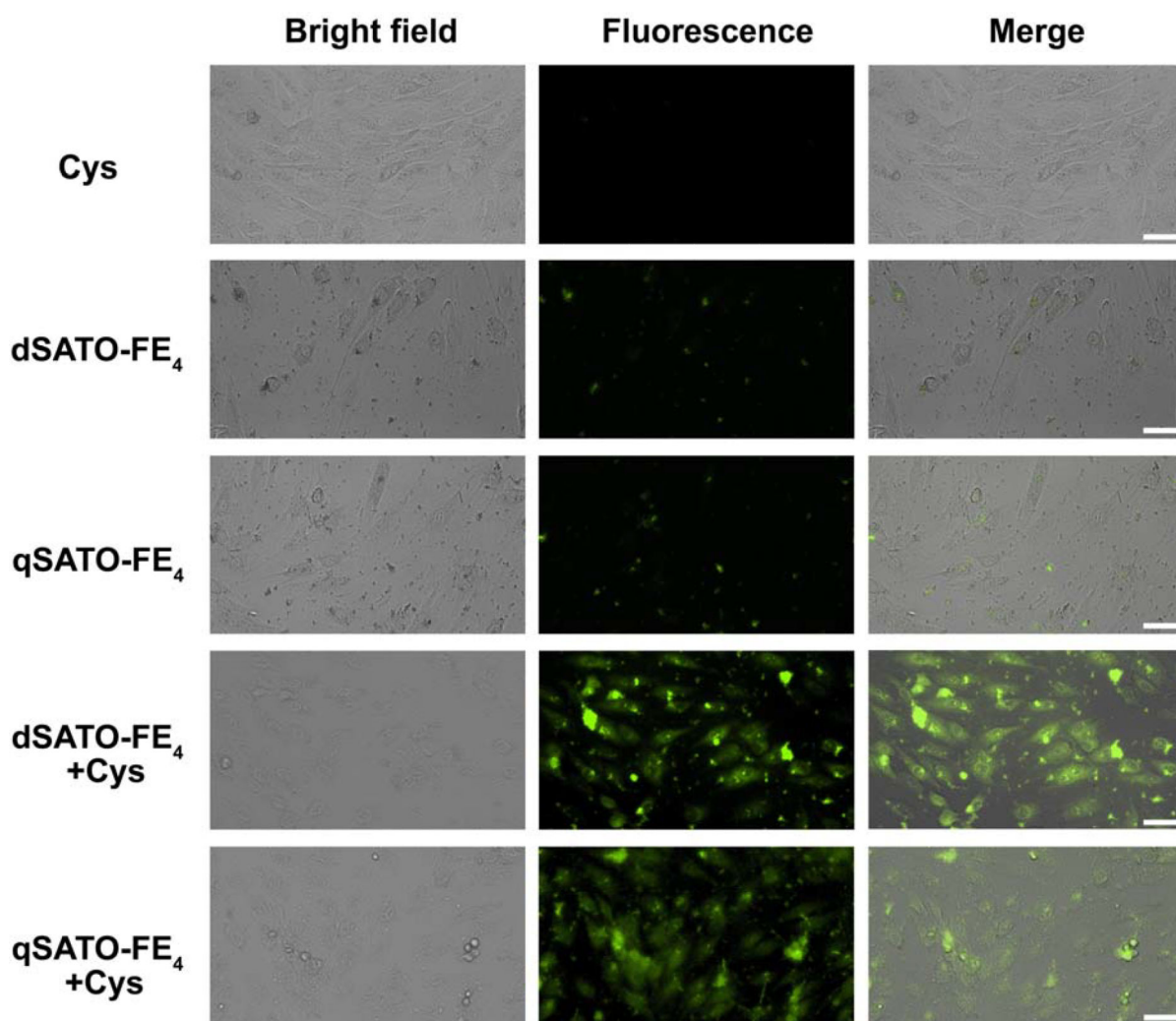


Figure 4. Bright field, fluorescence, and merged images showing fluorescence in H9C2 cells pre-incubated with H_2S probe WSP-5 ($50 \mu M$) for 30 min and then treated with the following groups: Cys ($800 \mu M$), PHDC ($200 \mu M$ for **dSATO- FE_4** ; $100 \mu M$ for **qSATO- FE_4**) or PHDC and Cys for 2 h. Cells were then washed, and fluorescence images were taken in PBS. Scale bars are $50 \mu m$.

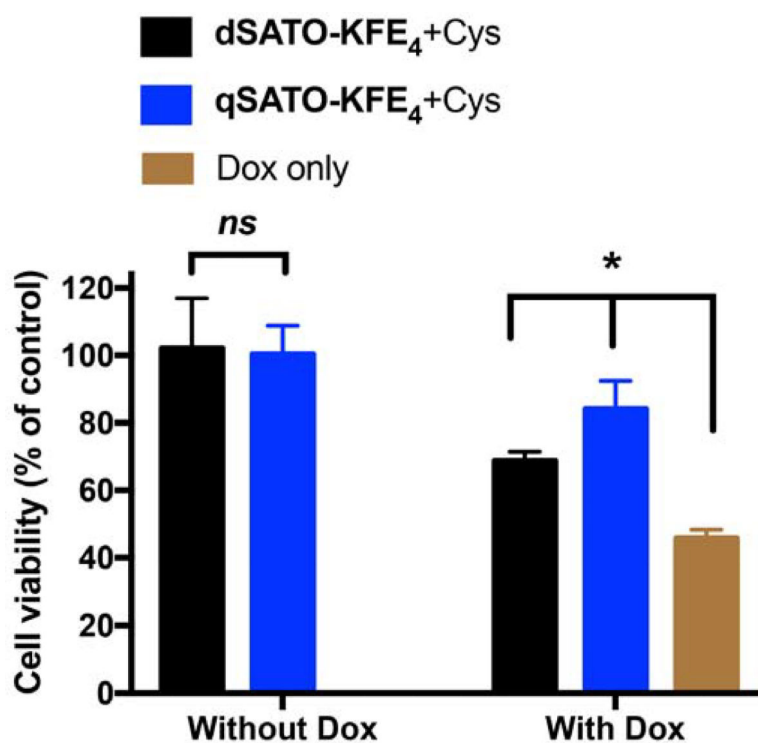


Figure 5. Cell viability of H9C2 cardiomyocytes pretreated with dSATO- FE_4 (200 μM) or qSATO- FE_4 (100 μM) in the presence of Cys (800 μM) for 30 min before Dox addition (5 μM) or not (control). * indicates $p < 0.01$. Error bars indicate standard deviations of three separate experiments with five replicates per experiment. Group comparisons are indicated as determined by a one-way ANOVA with a Student-Newman-Keuls comparisons *post-hoc* test.