

Resonance Energy Transfer Between Luminescent Quantum Dots and Diverse Fluorescent Protein Acceptors

Igor L. Medintz,^{*,†} Thomas Pons,^{‡,#} Kimihiro Susumu,[‡] Kelly Boeneman,[†] Allison M. Dennis,[∇] Dorothy Farrell,[‡] Jeffrey R. Deschamps,[§] Joseph S. Melinger,[⊥] Gang Bao,[∇] and Hedi Mattoussi^{*,‡,⊥}

Center for Bio/Molecular Science and Engineering Code 6900, U.S. Naval Research Laboratory, Washington, DC 20375, Division of Optical Sciences Code 5611, U.S. Naval Research Laboratory, Washington, DC 20375, Laboratory for the Structure of Matter Code 6030, U.S. Naval Research Laboratory, Washington, DC 20375, Electronic Science and Technology Code 6812, U.S. Naval Research Laboratory, Washington, DC 20375, and Department of Biomedical Engineering, Georgia Institute of Technology, Atlanta, Georgia 30332

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We characterized the resonance energy-transfer interactions for conjugates consisting of QD donors self-assembled with three distinct fluorescent protein acceptors, two monomeric fluorescent proteins, the dsRed derivative mCherry or yellow fluorescent protein, and the multichromophore b-phycoerythrin light-harvesting complex. Using steady-state and time-resolved fluorescence, we showed that nonradiative transfer of excitation energy in these conjugates can be described within the Förster dipole–dipole formalism, with transfer efficiencies that vary with the degree of spectral overlap, the donor–acceptor separation distance, and the number of acceptors per QD. Comparison between the quenching data and simulation of the conjugate structures indicated that while energy transfer to monomeric proteins was identical to what was measured for QD–dye pairs, interactions with b-phycoerythrin were more complex. For the latter, the overall transfer efficiency results from the cumulative contribution of individual channels between the central QD and the chromophores distributed throughout the protein structure. Due to the biocompatible nature of fluorescent proteins, these QD assemblies may have great potential for use in intracellular imaging and sensing.

Introduction

Luminescent semiconductor quantum dots (QDs) have generated intense interest for use as fluorescent probes in biological labeling and imaging.^{1–6} They are larger in size than their molecular-scale dye counterparts (typical radii of 2.5–6 nm), which implies that multiple biological molecules (i.e., proteins, peptides, or DNA) can be simultaneously conjugated to an individual QD without losing their biological functions; this can also provide added advantages such as higher local avidity. There has also been a growing interest in creating hybrid QD–protein conjugates for use in applications where the proteins provide biospecific functionality while the QD allows fluorescent tracking. These include developing assemblies with catalytic activity, as probes to detect specific protein targets in vitro, as vehicles to understand issues associated with drug delivery, and as conjugates that enable long-term in vivo tracking and sensing.^{3,5–9} Developing QDs as platforms for

immobilizing proteins and peptides with control over the number and orientation of these receptors will be key to implementing many of these applications. Fluorescent proteins provide an ideal model system for developing and testing such QD bioconjugates as they can allow concurrent monitoring of nanoparticle–biomolecule interactions. They can also permit the use of fluorescence resonance energy-transfer (FRET) interactions to gain information on conjugate structure and valence (i.e., the number of proteins attached to the nanocrystal) and the ability to monitor the fate of such hybrid assemblies inside of live cells.

A few preliminary studies characterizing FRET between QDs and fluorescent proteins or testing their mechanism of intracellular delivery have already been reported.^{10–12} Dennis and Bao examined energy transfer in assemblies of micelle-encapsulated (commercially available) CdSe–ZnS QDs self-assembled with mOrange, Tdtomato, and mCherry.¹⁰ They demonstrated that the energy-transfer efficiency strongly depended on both the degree of spectral overlap and the conjugate valence. In another elegant demonstration, Woggon and Niemeyer assembled hybrid nanoparticle–protein/DNA conjugates consisting of QDs simultaneously coupled to fluorescent proteins, oligonucleotides, and dyes and characterized the resulting two- and three-chromophore interactions. They showed that within the three-chromophore system, where a relay fluorophore plays the dual roles of an intermediary acceptor and a donor, the range of energy-transfer interactions can be extended beyond the usual 10–100 Å window.^{11,13} We recently demonstrated that the additional functionalization of similar QD–fluorescent protein conjugates with small-cell-penetrating peptides could allow their efficient intracellular delivery, which presents the opportunity for investigating and tracking these assemblies in vivo.^{12,14}

* To whom correspondence should be addressed. E-mail: igor.medintz@nrl.navy.mil (I.L.M.); mattoussi@chem.fsu.edu (H.M.).

[†] Center for Bio/Molecular Science and Engineering Code 6900, U.S. Naval Research Laboratory.

[‡] Division of Optical Sciences Code 5611, U.S. Naval Research Laboratory.

[§] Laboratory for the Structure of Matter Code 6030, U.S. Naval Research Laboratory.

[⊥] Electronic Science and Technology Code 6812, U.S. Naval Research Laboratory.

[∇] Georgia Institute of Technology.

[#] Present address: Laboratoire de Physique et Etude des Matériaux, CNRS UPR5, Ecole de Physique et Chimie Industrielle (ESPCI), 10 rue Vauquelin, 75005 Paris, France.

⁺ Present address: Department of Chemistry and Biochemistry, Florida State University, 4006 Chemical Sciences Building, Tallahassee, FL 23306.

Here, we extend the previous findings and demonstrate that QDs can function as effective self-assembly vehicles for a variety of structurally and photophysically diverse fluorescent proteins. CdSe–ZnS core–shell QDs were self-assembled with either the monomeric yellow fluorescent (YFP) or mCherry proteins via metal affinity coordination, and the multichromophore b-phycoerythrin (abbreviated as b-PE) were coupled via biotin–streptavidin interactions. We used steady-state and time-resolved fluorescence measurements to monitor the energy-transfer interactions in these conjugates. Our results showed that the transfer efficiencies for these pairs depend on the degree of spectral overlap between QD emission and protein absorption, the center-to-center separation distance, and the conjugate valence for monomer protein. For b-PE, multichannel FRET interactions with the individual chromophores in the protein structure had to be taken into account in order to properly interpret the efficiency data. Furthermore, we show that energy-transfer data can overall be interpreted within the Förster dipole–dipole formalism. Information on conjugate conformation derived from energy-transfer data together with the QD structure and the protein crystallographic coordinates provided insight into the architectures of these hybrid assemblies.

Materials and Methods

Quantum Dots. We used four sets of CdSe–ZnS core–shell QDs with emission maxima centered at ~510, 520, 540, and 550 nm. Nanocrystals were synthesized using a high-temperature reaction of organometallic precursors in hot coordinating solvents.^{15–18} They were made hydrophilic by exchanging the native capping shell with either neat dihydrolipoic acid (DHLA) or a mixture of DHLA-PEG₆₀₀ and biotin-terminated DHLA-PEG₄₀₀ (9:1 ratio of DHLA-PEG₆₀₀/DHLA-PEG₄₀₀-biotin). DHLA-PEG_{400,600} designate dihydrolipoic acid appended with polyethylene glycol segments of MW = 400 or 600.^{14,19} The chemical structures of the ligands are provided in the Supporting Information.

Fluorescent Proteins and Self-Assembly of Quantum Dot Bioconjugates. YFP and mCherry are monomeric proteins (MW ~ 27 kD) derived from the jellyfish *Aequorea* and the tetrameric mRFP red fluorescent protein, respectively; they originate from the Tsien laboratory.^{20–22} Both proteins have similar tertiary β -barrel structures formed from arranging 11 β -strands into a hollow cylinder with a centrally located chromophore. The active chromophore in each arises from the rearrangement of several key residues during the maturation process, similar to the *p*-hydroxybenzylideneimidazolinone chromophore in GFP, which originates from modification of the Ser-Tyr-Gly residues at position 65–67.^{20–22} b-PE is a member of the chromophore-bearing phycobiliproteins found in the macromolecular light-harvesting phycobilisome complexes of red algae and cyanobacteria.^{23,24} b-PE is photophysically and structurally different from YFP and mCherry. These multisubunit protein complexes have a large molecular weight (MW ~ 240 kD, ~10 times larger than those of YFP or mCherry monomers) with ~34 covalently attached bilins (open-chain tetrapyrrole chromophores) per functional moiety; this results in an extinction coefficient that is ~100 times larger than that of monomeric fluorescent proteins. This fluorescent protein has been extensively utilized as a sensitive and biocompatible fluorescent probe.²³

The yellow fluorescent protein was originally obtained on plasmid pRSET B (Invitrogen, Carlsbad, CA) within a gene encoding a blue fluorescent protein (glucose binding protein) YFP FRET-based glucose sensor.²⁵ The final YFP gene encoding a His₆ sequence after the start ATG, Asp-Gln, an Xpress

epitope (Asp-Leu-Tyr-Asp-Asp-Asp-Asp-Lys), and another His₆ sequence at the start of the YFP coding sequence was constructed, expressed, and purified over Ni-NTA resin (Qiagen, Valencia, CA) as described in refs 12 and 26. The mCherry expression plasmid and usage license was obtained from Clontech (Mountain View, CA). The protein, inserted between *Bam*H1 and *Eco*R1 of the multicloning site on plasmid pRSET B (Invitrogen, Carlsbad, CA), was expressed under the T7 promoter with a N-terminal linker of 35 residues that encodes a His₆ sequence after the start methionine, a T7 gene 10 leader sequence, an Xpress epitope, and an enterokinase domain. The plasmid was transformed into Rosetta 2 (DE3) cells (Novagen, San Diego, CA), and starter cultures were grown under 2% glucose suppression; then, cells were induced with 1 mM isopropyl-beta-D-thiogalactopyranoside overnight at 30 °C. Mature mCherry was purified over Ni-NTA resin (Qiagen, Valencia, CA). Maltose binding protein (MBP) was prepared as described in ref 27. One-to-one b-phycoerythrin–streptavidin conjugates (1 mg/mL, abbreviated as b-PE) were obtained from Invitrogen.

Self-Assembly of Quantum Dot Bioconjugates. We utilized two self-assembly approaches to form our QD–protein bioconjugates, namely, metal affinity coordination between CdSe–ZnS nanocrystals and a polyhistidine (His)_n sequence appended onto the protein termini or biotin–avidin coupling. YFP and mCherry were engineered to express N-termini bearing (His)₆ sequences, and these were separated from their respective proteins by spacer segments to allow access to the QD surface. Streptavidin-modified b-PE was coupled to QDs functionalized with DHLA-PEG₄₀₀-biotin. Both conjugation approaches provided tight coupling between QDs and protein, with reported dissociation constants K_D of ~1–10 × 10^{−9} M for QD–His₆ binding and ~10^{−15} M for biotin–avidin, respectively.^{28,29}

His-appended YFP was self-assembled on DHLA QDs together with His₅-appended MBP (mixed surface conjugates) at a constant total valence of 12 proteins per QD while varying the fraction of YFP in the conjugate. This configuration allows us to maintain a given number of proteins per nanocrystal and removes issues associated with small changes in QD PL observed when assembling varying number of His-appended proteins onto DHLA-capped nanocrystals.²⁷ The indicated molar ratios of YFP and MBP were added to 30 picomoles of 510 nm DHLA QDs in 100 μ L of 10 mM Tris-Cl pH 8 (0.3 μ M QD) and allowed to self-assemble for ~30 min at room temperature. A similar method was used for assembling mCherry onto 550 nm DHLA QDs. b-PE–streptavidin was coupled to either 520 or 540 nm emitting DHLA-PEG-biotin QDs by incubating the reagents in phosphate-buffered saline (137 mM NaCl, 10 mM phosphate, 2.7 mM KCl, pH 7.4, PBS) overnight at 4 °C. Selected QD–fluorescent protein bioconjugates were also separated and characterized on agarose gels buffered with 1×TBE (0.89 M Tris, 0.89 M boric acid and 0.02 M EDTA, pH 8.3), which provided an additional means of verifying conjugate formation. Representative gel images are provided in the Supporting Information.

FRET Data Collection and Analysis. Steady-state fluorescent spectra from solutions of QD–protein bioconjugates and proteins alone (controls) were collected on a Tecan Safire dual monochromator multifunction microtiter plate reader (Tecan, Research Triangle Park, NC) using 325 nm excitation. Following subtraction of the direct excitation contribution to the acceptor (using the control solutions), the composite spectra were deconvoluted to separate the QDs and fluorescent protein signals. This allowed us to account for the loss of QD PL together with

the increase in the protein signal due to energy transfer. The steady-state experiments were complemented (only for QD–mCherry assemblies) with fluorescence lifetime measurements performed using a time-correlated single-photon counting system with a temporal resolution of 50 ps. A brief description of the system can be found in the Supporting Information. The QD and mCherry fluorescence intensities were integrated over narrow windows centered at 537 and 620 nm, respectively, in order to isolate signals that are representative of QD and mCherry emissions. Fluorescence decay traces of the QD signal with time (collected for the indicated protein-to-QD ratio, n) were fit to a three-exponential function

$$I(t) = A_1 e^{-t/\tau_1} + A_2 e^{-t/\tau_2} + A_3 e^{-t/\tau_3} \quad (1)$$

where t is time and A_i is a weighting parameter associated with each decay time. An average amplitude-weighted lifetime defined as

$$\tau_D = (A_1 \tau_1 + A_2 \tau_2 + A_3 \tau_3) / (A_1 + A_2 + A_3) \quad (2)$$

was extracted from the fit using FluoFit (Picoquant, Berlin, Germany). The average energy-transfer efficiency E was extracted from either the steady-state or time-resolved fluorescence data for each set of QD conjugates using the expressions

$$E = \frac{(F_D - F_{DA})}{F_D} \quad \text{for steady-state data}$$

or

$$E = \frac{(\tau_D - \tau_{DA})}{\tau_D} \quad \text{for time-resolved data} \quad (3)$$

where F_D and F_{DA} are, respectively, the fluorescence intensities of the donor alone and donor in the presence of acceptor(s); similarly, τ_D and τ_{DA} designate the QD excited-state lifetimes without and with the protein acceptor.¹³ The metal–His-driven self-assembly (applied to YFP and mCherry) provides conjugates with a centrosymmetric distribution of acceptors around the QD, with a constant average center-to-center separation distance r .^{27,30} If analyzed within the Förster dipole–dipole formalism, the energy-transfer efficiency can be fit to the expression²⁷

$$E = \frac{nR_0^6}{nR_0^6 + r^6} \quad (4)$$

where n is the average number of fluorescent proteins per QD and R_0 is the Förster separation distance corresponding to 50% energy-transfer efficiency;¹³ R_0 is expressed as

$$R_0 = \left(\frac{[9000 \times (\ln 10)] \times \kappa_p^2}{128\pi^5 n_D^4 N_A} Q_D I \right)^{1/6} \quad (5)$$

where n_D is the refractive index of the medium, Q_D is the QD PL quantum yield, I designates the integral of the spectral overlap function, $J(\lambda)$, defined as

$$J(\lambda) \sim PL_{D\text{-corr}} \times \varepsilon_A(\lambda) \times \lambda^4 \quad (6)$$

with $\varepsilon_A(\lambda)$ being the acceptor extinction coefficient spectrum and $PL_{D\text{-corr}}$ the normalized donor emission spectrum. A value of $\kappa_p^2 = 2/3$ for the dipole orientation factor was used for our QD–protein assemblies in eq 5.^{27,31} For conjugates having small numbers of acceptors ($n < 5$), heterogeneity in the conjugate valence was taken into account using the Poisson distribution function, $p(N, n)$, when fitting the efficiency data³²

$$E = \sum_n p(N, n) E(n) \quad \text{and} \quad p(N, n) = N^n \frac{e^{-N}}{n!} \quad (7)$$

where n designates the exact numbers of acceptors (valence) for conjugates with a nominal average valence of N . We have previously shown that the valence of QD–protein bioconjugates formed, for example, via metal affinity self-assembly follows a statistical distribution that is well described by the Poisson function (see ref 32 for additional details).

Results and Discussion

Spectral Overlap of the Quantum Dot–Fluorescent Protein Pairs. Figure 1 shows the absorption and emission spectra for the various QD–fluorescent protein pairs used together with the corresponding spectral overlap function $J(\lambda)$. Table 1 presents the relevant QDs and fluorescent protein photophysical characteristics, the acceptor extinction coefficients at the peak absorption, together with the corresponding R_0 values for the various QD–protein pairs. Data indicate that R_0 varies from one pair to another, depending on the degree of spectral overlap and the acceptor extinction coefficient spectrum. As previously demonstrated for QD–dye pairs, R_0 and thus the rate of energy transfer can potentially be optimized by choosing a QD donor that offers the best spectral overlap with a particular fluorescent protein acceptor.²⁷ For example, by switching from 520 to 540 nm emitting QDs, R_0 was increased from 44 to 53 Å for the b-PE acceptor, which constitutes a substantial extension of the distance range allowing efficient FRET interactions. Similarly, two QD samples with distinct emissions were used with YFP or mCherry to optimize the spectral overlap for each pair. We should emphasize that for QD–b-PE pairs, the overlap integral I and thus R_0 were estimated using the extinction coefficient of an individual bilin chromophore ($\sim 71\,000 \text{ M}^{-1} \text{ cm}^{-1}$) and not the extinction coefficient spectrum for the full protein; this is reasonable since all chromophores in the protein are identical. This assumption is more appropriate than treating the whole protein as a monomeric chromophore acceptor (as was done for YFP and mCherry above) since the bilins are located at different separation distances and thus interact with the QD via distinct energy-transfer channels (and rates). YFP and mCherry in comparison each presents a single chromophore located at the center of the β -barrel and can both be treated as point acceptors.

Steady-State and Time-Resolved Fluorescence. Steady-State Fluorescence Data. Figure 2A–C shows the deconvoluted PL emission spectra for an increasing number of proteins per QD for the three sets of conjugates. Samples were excited at 325 nm, which coincides with the absorption minima for all three proteins, in order to reduce the direct excitation of the acceptor. This contribution (determined from protein-only control samples), though small, was carefully subtracted prior to deconvolution. Data clearly show that for all three sets of

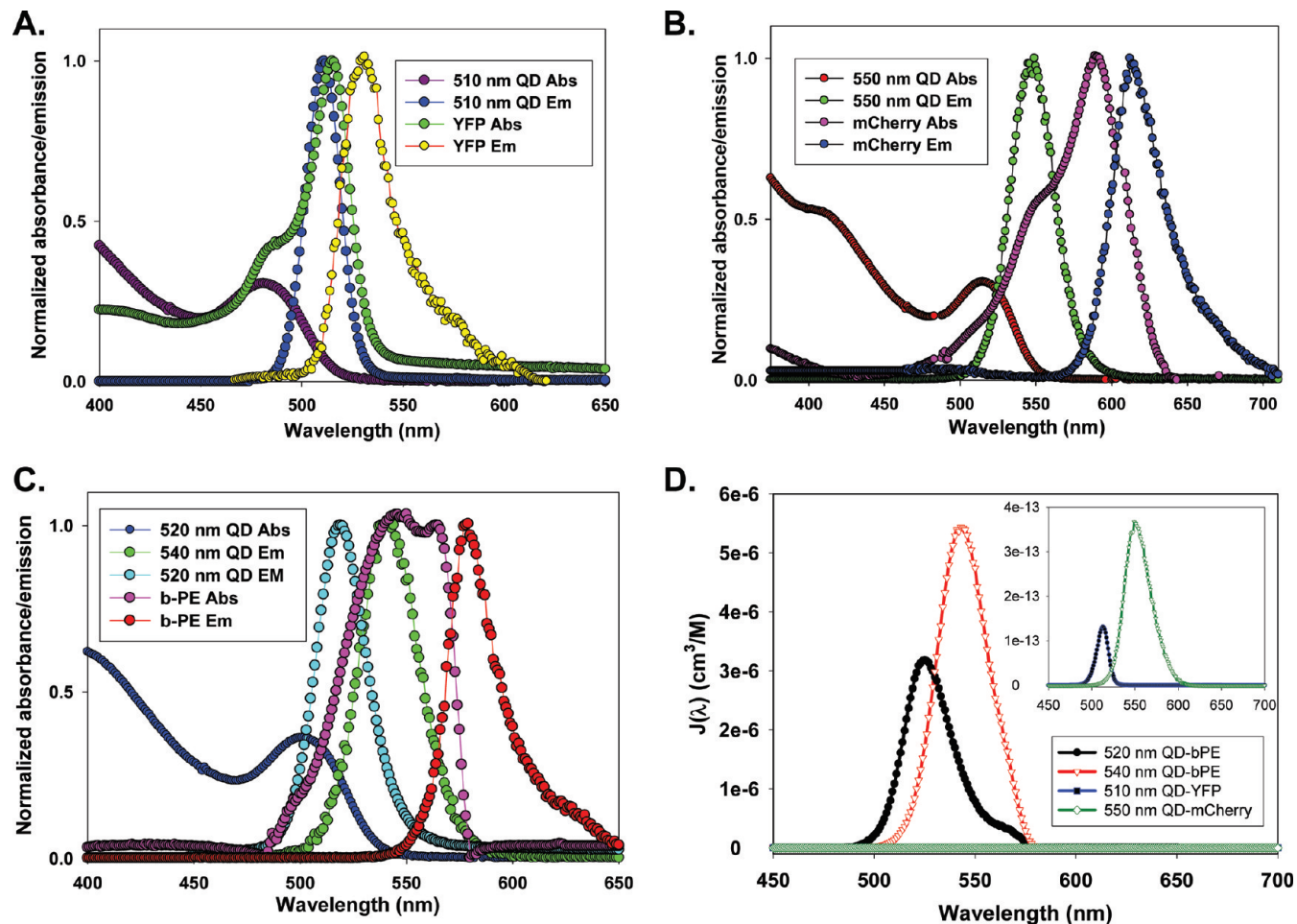


Figure 1. Photophysical characteristics of the fluorophores. Normalized absorption and PL spectra of the 510 nm QD–YFP pair (A), 550 nm QD–mCherry pair (B), and 520 nm QD–b-PE and 540 nm QD–b-PE pairs (C). Spectral overlap functions for the four pairs are shown in panel (D). The inset shows a close-up of the QD–YFP and QD–mCherry overlap functions.

TABLE 1: Selected Characteristics of the Quantum Dot–Fluorescent Protein Pairs Used in This Study^a

quantum dot donor				fluorescent protein acceptor					
QD λ_{max} emission	quantum yield	conjugation strategy	protein acceptor	λ_{max} absorption	λ_{max} emission	extinction coeff. ($\text{M}^{-1} \text{cm}^{-1}$)	quantum yield	R_0	r^c
510 nm	12%	metal affinity	YFP	516 nm	529 nm	20 200	60%	39 Å	62 Å
550 nm	20%	metal affinity	mCherry	587 nm	610 nm	71 000	22%	49 Å	56 Å
520 nm	20%	biotin/streptavidin	b-PE	545 565 nm	575 nm	2 410 000	98%	44 Å ^b	
540 nm	19%	biotin/streptavidin	b-PE	545 565 nm	575 nm	2 410 000	98%	53 Å ^b	

^a YFP: yellow fluorescent protein. b-PE: b-phycoerythrin. ^b R_0 calculated for interactions with a single bilin chromophore ^c Standard deviations associated with the experimental r values were $\sim 5\text{--}7\%$.

conjugates, there is a consistent and progressive loss of the QD PL accompanied with a gradual increase in the protein emission as the number of acceptors per QD conjugate increases. The corresponding QD PL quenching efficiencies derived from the above spectra (following deconvolution of the raw spectra for every QD–FP pair) along with the sensitized acceptor reemission as a function of conjugate valence are shown in Figure 2D–F. The acceptor reemission varied from one set to the other and did not always directly trace the QD PL loss, which can be attributed to differences in protein fluorescent yields and their sensitivity to the surrounding environment. Even though the general trend for the QD PL loss and acceptor gain are comparable, there are substantial differences in the exact values, with the most pronounced quenching efficiencies measured for the 540 nm QD–b-PE pair and the smallest measured for the 510 nm QD–YFP pair. For example, at $n = 2$, $\sim 80\%$ PL loss

was measured for the 540 nm QD–b-PE conjugates compared to less than 10% quenching for the 510 nm QD–YFP pair. This is due to a combination of differences in the spectral overlap and conjugate architecture. Similarly, the higher quenching efficiency measured for the 550 nm QD–mCherry pair compared to that for the 510 nm QD–YFP can also be primarily attributed to a larger spectral overlap integral (or higher R_0 ; see Table 1).

Time-Resolved Fluorescence Data. We focused on the 550 nm QD–mCherry pair as a representative and easier to analyze system. The other two conjugates either did not allow easy separation of the donor and acceptor signals because of a strong overlap of their emissions or a limited range of conjugate valence was explored in order to reduce the direct excitation contribution of the acceptor (case of the 540 nm QD–b-PE pair). Figure 3A,B shows plots of QDs and mCherry intensity versus

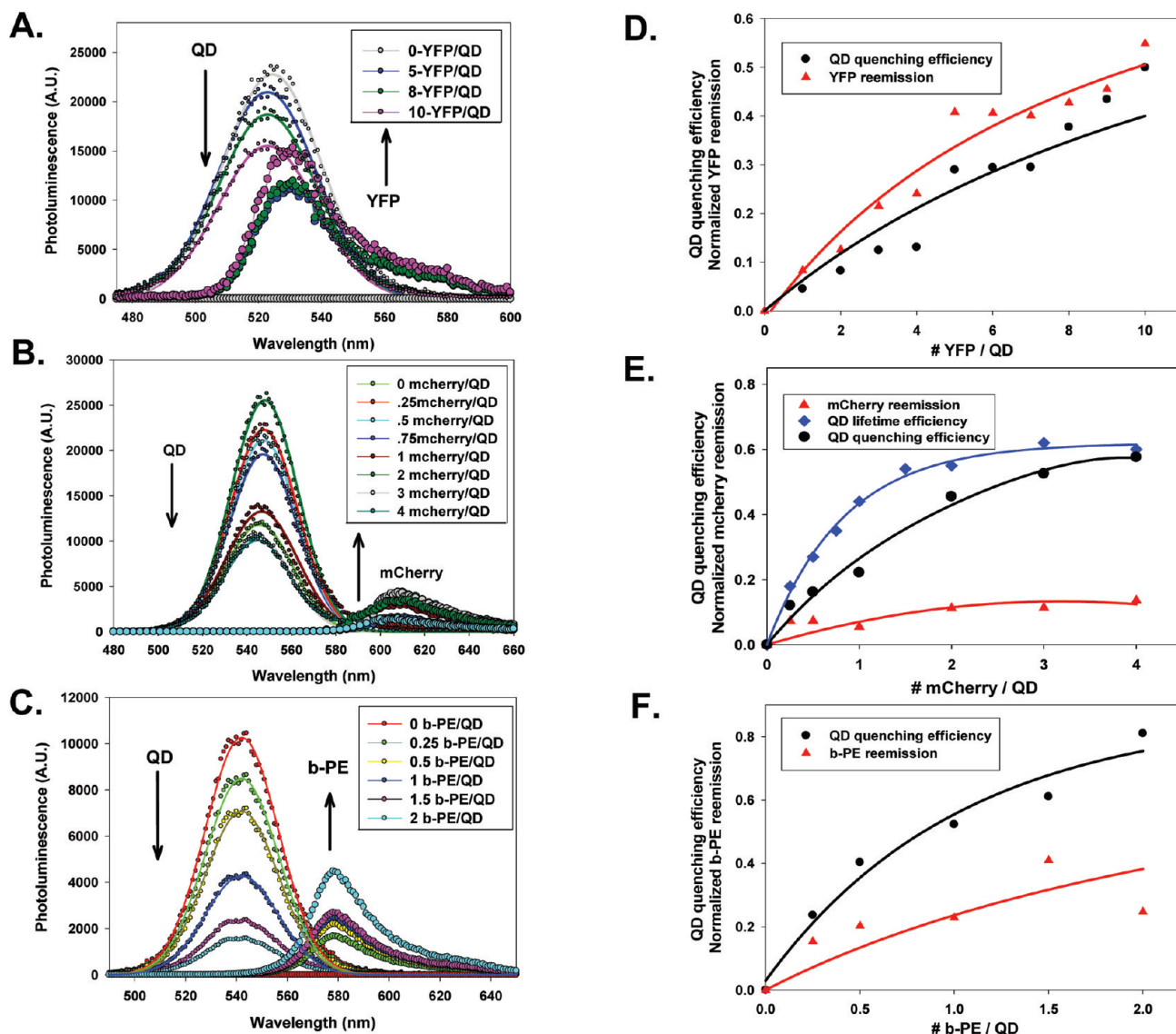


Figure 2. Fluorescence spectra and quenching efficiencies. (A–C) Representative composite and deconvoluted spectra showing individual PL contributions as a function of the protein-to-QD ratio for 510 nm QD–YFP, 550 nm QD–mCherry, and 540 nm QD–b-PE assemblies. (D–F) Plots of the corresponding quenching efficiencies along with the acceptor-sensitized emission. In panel (E), the energy transfer efficiency extracted from changes in the QD excited-state lifetime are also shown for the 550 nm QD–mCherry pair. (F) Data are corrected for the direct excitation of the b-PE. QD emission profiles were fit with a Gaussian function.

time for several protein-to-QD ratios immediately following the laser pulse. We verified that at the excitation wavelength and conjugate concentrations used, the direct excitation contribution to the protein signal was essentially negligible. Figure 3C shows the normalized intensity–time traces at a few representative ratios along with the traces collected for the control samples (QDs and protein only). For each mCherry/QD ratio, the QD trace shown in Figure 3A was analyzed and an average exciton lifetime extracted using equation 2 (see Table 2). There is a ratio-dependent reduction (shortening) of the average QD lifetime with increasing conjugate valency for $n \leq 4$, before saturation at higher values. The energy-transfer efficiencies versus n extracted from the lifetime data (using eq 3) are in reasonable agreement with those derived from steady-state PL (Figure 2E). Efficiencies were consistently higher than those extracted from steady-state measurements, though. This may be attributed to the nonexponential decay traces and the complex method used to extract the exciton lifetime (multiexponential fit) combined with a small leakage of the protein signal into the QD detection channel. Regardless, the trend clearly follows the ensemble fluorescence data.

In comparison, the mCherry intensity–time traces show a more complex behavior, with a clear rise of the signal immediately after the excitation pulse, followed by a more progressive decay at longer time. In addition, we observed acceleration of the signal rise with increasing ratio n (Table 2). This behavior is typical of a FRET acceptor intensity–time trace, where rapid transfer of energy from an excited donor to a ground-state acceptor manifests in a rapid increase of the acceptor signal with time;¹³ it also reflects the simultaneous and cumulative energy transfer to several acceptors. Decay behavior at longer times is dominated by the characteristics of the QD donor. This is not unexpected since the natural decay time of the acceptor is short (1.5 ns), and thus the signal at longer times will ultimately follow the tail of the QD excitation. Additional details showing analysis of the mCherry fluorescence rise and decay dynamics is presented in the Supporting Information.

Overall, the steady-state and time-resolved fluorescence data confirm that the signature observed for these pairs is due to energy transfer between QDs and fluorescent proteins and that the process is essentially driven by dipole–dipole coupling and can be treated within the Förster formalism. This manifests in

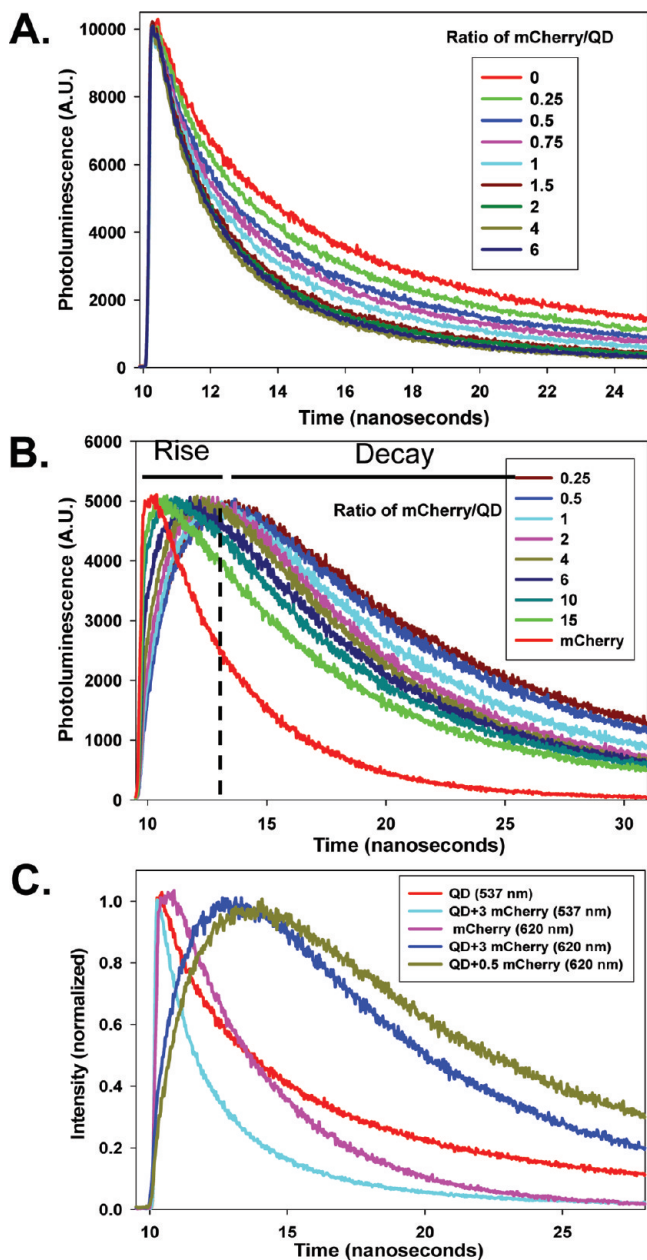


Figure 3. Time-resolved fluorescence data for 550 nm QD–mCherry conjugates. (A) Plot of 550 nm QD PL intensity (monitored at 537 nm) versus time for several mCherry-to-QD ratios. (B) Plot of the mCherry intensity (monitored at 620 nm) versus time for several mCherry-to-QD ratios. (C) Superimposed plots of the normalized QD and mCherry intensity versus time for selected ratios.

the progressive increase in the donor (QD) PL quenching with increasing protein-to-QD ratio. It also manifests in a ratio-dependent shortening of the exciton lifetime of the QD donor. Analysis of the QD PL quenching data within the framework of the Förster dipole–dipole formalism, taking into account conjugate heterogeneity where necessary (using eq 7) for the two QD–monomeric fluorescent protein assemblies, YFP and mCherry, provided estimates for the separation distances r (see Table 1). The value for the QD–YFP pair might be subject to a slightly larger uncertainty given the difficulties associated with deconvolution of the spectra shown in Figure 2A. Nevertheless, the r values for these two pairs are close, which is consistent with the overall structure of these QD–protein conjugates. We should emphasize that the separation distances measured for the present QD–mCherry assemblies are comparable to those

TABLE 2: Donor–Acceptor Excited-State Lifetimes for 550 nm DHLA QDs Assembled with Increasing mCherry Protein^a

ratio of mCherry/QD	QD donor ^b	mCherry acceptor ^c	mCherry acceptor rise time ^d
0	8.51 (QD only)	1.55 (mcherry alone)	
0.25	6.98	4.32	0.80
0.5	6.19	4.10	0.75
0.75	5.51	3.69	0.77
1	4.74	3.44	0.74
1.5	3.89	3.44	0.70
2	3.86	3.41	0.64
3	3.22	3.00	0.69
4	3.37	3.02	0.67
6	3.51	3.30	0.60
8	3.47	3.06	0.67
10	3.67	3.12	0.63
15	3.89	3.13	0.56

^a Amplitude-weighted average lifetimes (τ_{AV}) are given in nanoseconds. ^b Fitted with an average of three or four lifetime components. ^c Fitted with an average of two or three lifetime components. ^d Extracted from the data shown in Figure 3B. QD and mCherry lifetimes were monitored at 537 and 620 nm, respectively. Standard deviations were <5% for all values.

reported for the same protein assembled via metal–His affinity onto commercial carboxyl-functionalized EviTag QDs.¹⁰ In that report, the QD PL quenching similarly reached saturation at ~ 4 proteins/QD. The much higher rate of quenching measured for QD–b-PE conjugates can be primarily attributed to the nature of the protein. (Similar data were collected from 520 nm QD–b-PE conjugates.) Treating the QD–b-PE as a single donor–single acceptor (simple pair) is not appropriate for these conjugates, given the characteristics of the protein. With the large number of individual chromophores distributed across the protein structure, the QD–b-PE assembly is essentially equivalent to a system consisting of one donor interacting with an array of acceptors distributed at varying separation distances (see below).

Modeling of QD–Protein Structures. Using the dimensions of the nanocrystals, the FRET-derived center-to-center separation distances, and aided by the crystallographic structures of the proteins, we modeled the conformation of our QD–protein conjugates. To do this, we combined information on (1) the QD–ligand structure, (2) how the proteins are expected to self-assemble onto the QD surface, (3) the separation distance r for each system, and (4) the protein structure as determined by X-ray crystallography. This approach of correlating the model structure with the fluorescence data has allowed us to gain additional insights into the overall conformation of the conjugates and their potential as sensing assemblies.^{30,33} The protein structures were obtained from the Protein Data Bank (www.rcsb.org/pdb) and include entries 1B8D for b-PE, 1F0B for YFP, 1RXJ for streptavidin, and 2H5Q for mCherry. QD radii were extracted from X-ray scattering and TEM measurements.^{15,34} The conformations of DHLA, DHLA-PEG₆₀₀, and DHLA-PEG₄₀₀-biotin ligands bound to the nanocrystal were modeled using Chem3D and the MM2 module (CambridgeSoft, www.cambridgesoft.com). The hybrid conjugates were assembled from their components using MidasPlus (www.cgl.ucsf.edu), where torsion angles were adjusted to match the measured separation distances.^{35,36} Images were rendered in MidasPlus and assembled from individual composite sections (required only for the larger b-PE complex) in Photoshop (Adobe, San Jose, CA). Modeling the conformational structures of our QD–protein

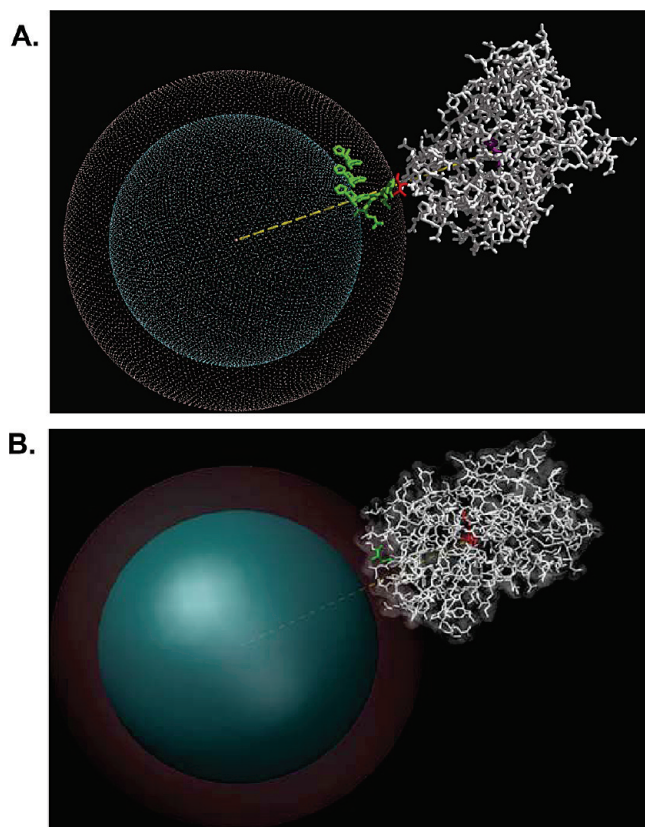


Figure 4. Model structures for QD–YFP and QD–mCherry conjugates. (A) The 510 nm QD–YFP structure. The QD with a radius of ~ 28 Å (blue) is surrounded by a DHLA shell of 10 Å (crimson). The YFP is attached to the QD via a double His₆ sequence; only the N-terminal His₆ is shown in green. The YFP residue attached to the double (His)₆ linker is shown in red. The central YFP chromophore is shown in magenta. The yellow line corresponds to the 62 Å experimental separation distance. (B) Rendition of a 550 nm QD–mCherry structure using 56 Å separation distance (yellow), with the protein chromophore shown in red. The mCherry residue attached to the (His)₆ linker sequence is shown in green, but the 35 amino acid linker and terminal His₆ sequence are not shown.

conjugates has inherent uncertainties that result from errors in the separation distance measurements, the availability of the crystal structures in the PDB, and the assumptions made in the comparison.

Figure 4A shows a representative structure for the 510 nm QD–YFP conjugates; a DHLA-capped QD with one YFP is shown for simplicity. The core–shell QD is represented by a sphere of ~ 25 Å radius and the DHLA solubilizing layer by ~ 10 – 11 Å crimson crown.^{15,27} The YFP β -barrel structure has dimensions of $\sim 41 \times 28$ Å (length \times barrel diameter). The YFP chromophore (magenta) was placed at ~ 62 Å from the QD center (distance determined from FRET). In assembling a model structure of the QD–protein conjugate, we neglected the contributions of the His tag since polyhistidine is proven to interact directly with the QD surface.²⁸ We also did not include the 23-residue linker between the terminal (His)₆ and the YFP in the simulated structure because there are no coordinates available for it in the PDB; the lack of structural data despite multiple occurrences of homologous sequences in the PDB indicates that this region is not well ordered and likely has many conformations in the solid state.^{28,30,33} This analysis suggests that by allowing for some rotational freedom around the cylinder axis (while self-assembled via the histidine tag on the QD), the optimal configuration of the protein consists of the β -barrel

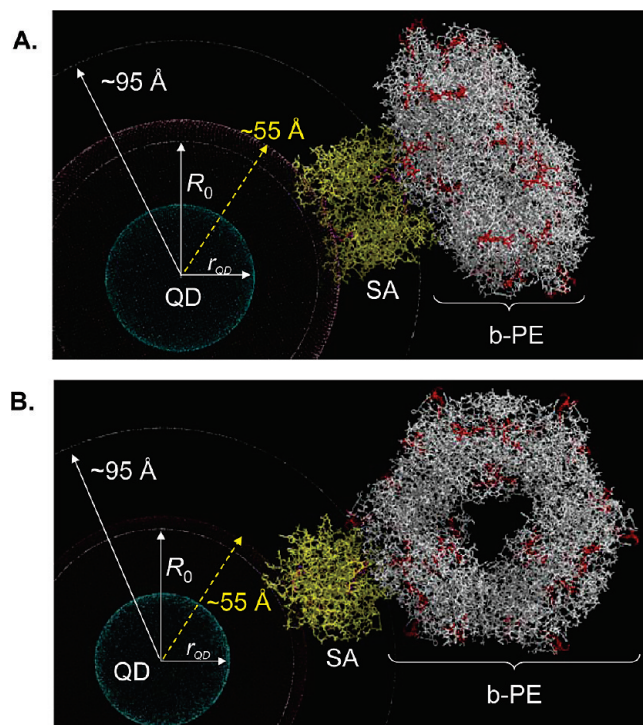


Figure 5. Models of the QD–b-PE conjugate structure/conformation. (A) b-PE is parallel to the QD surface ($\theta_{\text{QD/b-PE}} = 0^\circ$), and (B) b-PE is fully extended away from the QD ($\theta_{\text{QD/b-PE}} = 90^\circ$). The central QD with a radius of ~ 29 Å (r_{QD}) shown in blue is surrounded by a crimson shell of ~ 25 Å thickness representing the DHLA-PEG-biotin. The intermediary streptavidin (SA) protein is shown in yellow with biotin binding sites highlighted in purple. The b-PE ring structure is shown in white, with the multiple chromophores highlighted in red. The inner concentric white circle corresponds to the R_0 (53 Å) for the 540 nm QD–b-PE assembly. The second outer white circle is a visual distance marker set at ~ 95 Å from the QD center and represents the closest approach of the b-PE to the QD.

aligned with its base facing the QD surface. This analysis also suggests that up to ~ 15 YFP can be self-assembled around each 510 nm QD, in agreement with valences anticipated for similar size proteins.³⁷ To compensate for the rather weak spectral overlap ($r/R_0 \sim 1.5$), one could use an enhanced YFP variant such as “Venus”, which has a higher extinction coefficient; this could improve the measured FRET efficiency for such conjugates.^{22,38,39}

The 56 Å average separation distance measured for QD–mCherry conjugates is slightly smaller than that for the QD–YFP pair, even though the two proteins have nearly identical molecular weights and structures; 550 nm QDs have a radius of ~ 30 Å. mCherry is expressed with a slightly longer 35 amino acid N-terminal linker between the His₆ tag and the protein. A search in the PDB found more than 25 identical linker sequences present in various crystallized protein structures; as it is a commonly expressed N-terminal portion of the pRSET B plasmid but similar to the YFP linker above, no coordinates for this particular region were available. We thus assumed that it had a flexible conformation and that its contribution allows for additional freedom of lateral “rotation” of the mCherry while assembled onto the QD. This may also explain the slightly smaller r value extracted for this conjugate. For this pair, an estimated ~ 15 – 18 mCherry proteins can be immobilized on the QDs.

The QD–b-PE conjugate has a starkly different structure from that of the QD–monomeric protein conjugates. b-PE consists of α, β -paired monomers associated into a symmetrical hexam-

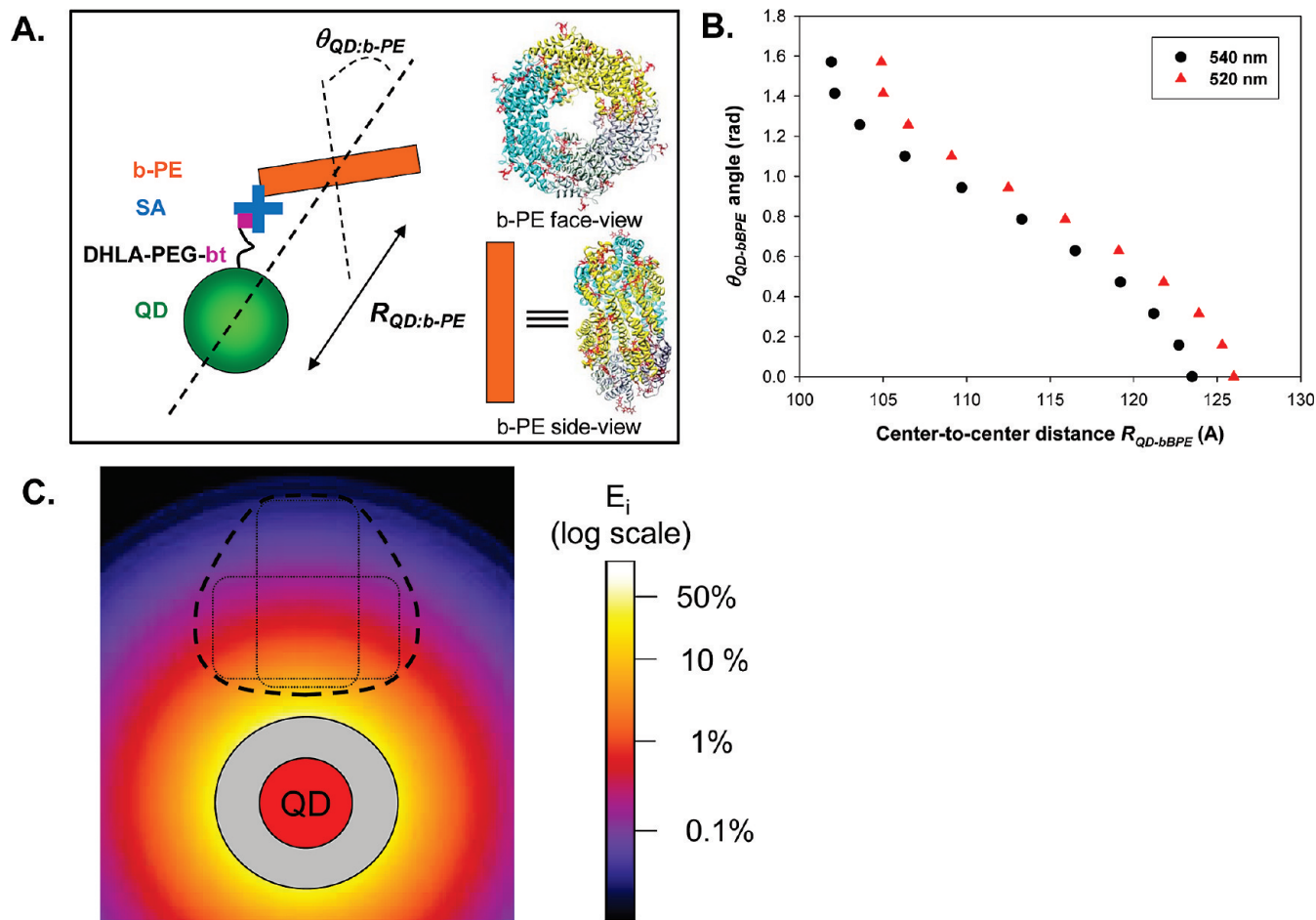


Figure 6. Correlations between b-PE structure and FRET data. (A) Schematic representation of possible conformations. The $\theta_{\text{QD:b-PE}}$ is the angle between the QD–b-PE center-to-center axis and the axis perpendicular to the b-PE structure. $R_{\text{QD:b-PE}}$ is the QD–b-PE center-to-center separation distance. (B) QD–b-PE center-to-center distances estimated from FRET efficiencies and plotted versus $R_{\text{QD:b-PE}}$ (correspond to $0^\circ \leq \theta_{\text{QD:b-PE}} \leq 90^\circ$) for 540 nm (circles) and 520 nm (triangles) QDs. (C) Schematic mapping of the FRET efficiency for the QD–b-PE conjugate showing the effects of the distance and distribution of the chromophores in the protein. Two representative b-PE conformations (dotted) along with the region explored by all possible conformations sampled by the protein on the nanocrystal (dashed). The color intensities indicate the FRET efficiencies between the QD and individual dyes in the b-PE (see bar on the right).

eric ring structure $(\alpha\beta)_6$ with a diameter of 110 Å ($\sim 2 \times$ that of the QD) and a thickness of 60 Å formed around a central channel with a diameter of 35–45 Å.^{40,41} The supplied b-PE is covalently linked to a single streptavidin (on average), but the SA–b-PE conjugate structure is heterogeneous since the coupling chemistry used does not allow for a unique attachment site. Figure 5 shows models of two representative configurations of b-PE bound to the QDs via a streptavidin bridge. The central QD is surrounded by a crimson sphere of ~ 25 Å (i.e., ~ 55 Å overall radius), representing the DHLA-PEG/DHLA-PEG-biotin solubilizing and functionalizing layer; this energy-minimized value accounts for ligand flexibility in solution. The streptavidin tetramer is shown in yellow, with the biotin-binding sites highlighted in dark purple. Interpenetration between the streptavidin and the ligands is meant to account for the fact that the biotin-binding pocket is deep inside the protein. The b-PE is shown in white, with the location of the ~ 34 individual chromophores in red. The two configurations shown in Figure 5A,B correspond to the hexamer “disk” either laying with its face parallel to the QD surface or facing away from the QD surface, respectively. Other conformers are also possible (for example, streptavidin attached in the central b-PE pocket), and these results represent a range of possible conformations rather than a set of fixed acceptor sites. The concentric white circle closest to the QD (in both panels) corresponds to the R_0 value

of ~ 53 Å. The second outer white concentric circle is a visual distance marker set at ~ 95 Å from the QD center and corresponds to the overall QD–streptavidin radius; it is the closest point of b-PE approach to the QD. In these representations, the range of distances sampled by the chromophores was set between 100 and 210 Å. To take into account the multi-chromophore nature of b-PE, we analyzed the quenching efficiency for the QD–b-PE pair using a modified expression of eq 4, where the efficiency is now a sum of the individual FRET channels between the QD and all of the chromophores distributed across the protein structure

$$E = \frac{n \sum_i 1/r_i^6}{n \sum_i 1/r_i^6 + 1/R_0^6} \quad (8)$$

where n is the number of proteins around the central QD and r_i designates the separation distance between the nanocrystal center and chromophore i in the protein ($1 \leq i \leq 34$). We assumed that the chromophores were optically identical and their positions were invariant by rotation around the axis perpendicular to the b-PE torus. The position/coordinates of each chromophore with

respect to the QD could then be described by two parameters, the QD center-to-b-PE center distance, $R_{\text{QD/b-PE}}$ and the angle between the b-PE axis and the QD/b-PE center-to-center axis, $\theta_{\text{QD/b-PE}}$ (see schematic in Figure 6A and Supporting Information). Using the b-PE crystallographic structure, we developed a geometrical expression for the distances r_i for each chromophore i in the overall protein structure, as a function of $R_{\text{QD/b-PE}}$ and $\theta_{\text{QD/b-PE}}$. Replacing each r_i by this geometrical expression in eq 8, we obtained a theoretical FRET efficiency that depended only on $R_{\text{QD/b-PE}}$ and $\theta_{\text{QD/b-PE}}$. Using this expression and the experimental FRET efficiency obtained from Figure 2C,F, we calculated the separation distance $R_{\text{QD/b-PE}}$ corresponding to different protein orientations (i.e., varying $\theta_{\text{QD/b-PE}}$ between 0 and 90°). We found that these fitted parameters corresponded to separation distances $R_{\text{QD/b-PE}}$ ranging from ~ 102 Å when the b-PE disk structure was parallel to the QD surface (closest separation) to a distance of ~ 125 Å when it was perpendicular to the QD (Figure 6B). For the 540 nm emitting QDs, a slightly larger distance of ~ 2.5 – 3 Å was measured concomitant with the larger size.

The structure shown in Figures 5 and 6 suggests that all of the chromophores are essentially located at a distance exceeding $2 \times R_0$ (~ 106 Å). Thus, individually, the rate of FRET experienced by each chromophore when it interacts with the QD center is very small ($<5\%$). The schematics in Figure 6C show the range of FRET efficiencies expected between the QD and bilin chromophores. Yet, a large FRET efficiency (~ 0.6 at a valence of 1) was measured for this QD–protein pair. This is a direct reflection of the unique property of the multichromophore b-PE protein acceptor used. The measured FRET efficiency results from multiple FRET channels between the central nanocrystal and the chromophores distributed within the protein structure, which cumulatively results in high measured quenching efficiencies. We should also emphasize that FRET experiments using commercially available streptavidin QDs (inherently large in size) required the use of a large number of dye acceptors per QD to achieve sizable energy-transfer efficiencies.⁴² Multichromophore proteins such as b-PE could provide an easy alternative to the design and assembly of targeted QD biosensors based on FRET interactions.

Conclusions

We have characterized the energy-transfer interactions between luminescent QDs and several fluorescent proteins brought in close proximity via two self-assembly approaches, metal affinity coordination and biotin–avidin coupling. This study combines aspects of two structurally and photophysically different fluorescent probes that have attracted increasing interest in the past decade, inorganic QDs and engineered fluorescent proteins. We used very dissimilar fluorescent protein acceptors, two monomeric (single chromophore) proteins, YFP and mCherry, and a large molecular weight multichromophore protein, b-PE. Steady-state and time-resolved fluorescence measurements proved that energy transfer in these systems is fully consistent with the Förster dipole–dipole interaction formalism, as demonstrated for QD–dye pairs.²⁷ Analysis also confirmed that the transfer efficiency could be easily controlled and tuned by varying the degree of spectral overlap and the number of proteins assembled on the QD surface.^{27,30} Furthermore, our study demonstrated that when using the b-PE multichromophore protein as an acceptor, limitations due to the rather large separation distances could be circumvented, as high energy transfer efficiencies were measured for overall separation distances exceeding 100 Å even at low valences. This property

results from the cumulative interactions of all of the individual chromophores arrayed within the protein structure with the same QD donor. This is a rather remarkable finding as it opens up the possibility of using QD donors to probe biological interactions and processes that occur over larger distances than those initially considered as the boundaries for FRET (10–100 Å).¹³ It also opens up new opportunities in biological sensing and tracking, where one can take advantage of the growing range of available fluorescent proteins combined with their natural biocompatibility.^{22,43,44}

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Supporting Information Available: Ligand structures, agarose gel electrophoresis, and further discussion of the lifetime collection and modeling. This material is available free of charge via the Internet at <http://pubs.acs.org>.

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