

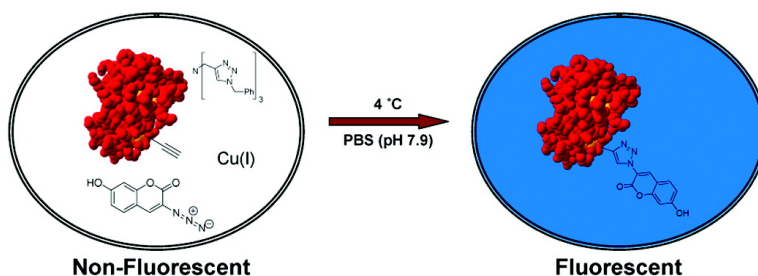
Communication

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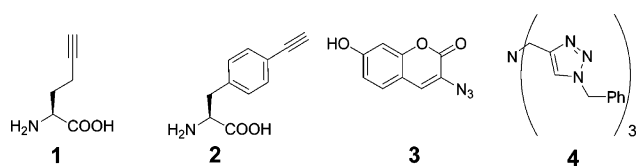
## Selective Dye-Labeling of Newly Synthesized Proteins in Bacterial Cells

Kimberly E. Beatty,<sup>†</sup> Fang Xie,<sup>‡</sup> Qian Wang,<sup>‡</sup> and David A. Tirrell\*<sup>†</sup>

Division of Chemistry and Chemical Engineering, California Institute of Technology, Pasadena, California 91125,  
and Department of Chemistry and Biochemistry, University of South Carolina, 631 Sumter Street,  
Columbia, South Carolina 29208

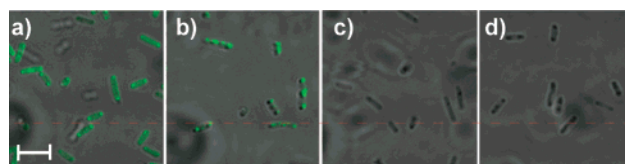
Received July 12, 2005; E-mail: tirrell@caltech.edu

Fluorescence labeling of proteins has become a central tool in the study of biological systems. Most labeling methods rely on fusion of an enzyme, fluorescent protein, or peptide tag to the protein of interest.<sup>1,2</sup> Green fluorescent protein (GFP) is the most common fusion partner for monitoring cellular interactions and protein localization.<sup>3</sup> While it is likely that GFP and its many variants will continue to find widespread use, the size of GFP and the requirement for genetic manipulation of the target protein place limits on its utility. Tsien and co-workers have reported a less invasive strategy in which a tetracysteine motif is added to the protein of interest to allow site-specific labeling by fluorogenic bisarsenical dyes.<sup>2</sup> This strategy demonstrates some of the most important traits of a useful fluorogenic label: small size, membrane permeability, low background, and selective reactivity. For some purposes, however, it would be desirable to circumvent the need for genetic introduction of fluorescent reporters or labeling sites. For example, spatially regulated protein translation is believed to contribute to synaptic plasticity, but the products of local protein synthesis have not yet been fully identified.<sup>4</sup> We describe here an approach that involves co-translational labeling of proteins by the non-natural amino acids homopropargylglycine (Hpg, **1**) or ethynylphenylalanine (Eth, **2**) to provide alkyne sites for attachment of fluorogenic dyes. The method permits fluorescence labeling of newly synthesized proteins in *Escherichia coli* cells by means of a Cu(I)-catalyzed cycloaddition between the alkyne amino acid side chains and the dye 3-azido-7-hydroxycoumarin (**3**).



The azide–alkyne cycloaddition has been used in many bioconjugation reactions, including identification of enzyme inhibitors, labeling of the *E. coli* cell surface, profiling of enzyme activities, and labeling of glycoproteins on the surface of mammalian cells.<sup>5–8</sup> Recently, the azide–alkyne cycloaddition has been used to activate weakly fluorescent coumarins to give intensely fluorescent triazole products.<sup>9</sup> Desirable features of **3**, as well as other quenched coumarin probes, include small size, membrane permeability, and intense fluorescence upon activation. The azido functionality of **3** is essentially “bioorthogonal” and allows selective *in vivo* labeling only when the alkyne coupling partner is accessible in the cell.<sup>10</sup>

Previous work has demonstrated that alkyne amino acids can be incorporated easily into recombinant proteins in a residue-specific manner. Hpg serves effectively as a methionine (Met) surrogate even without modification of the translational machinery of the host,



**Figure 1.** Fluorogenic labeling of barstar in *E. coli* cells. Cells were induced in media supplemented with 19 amino acids and one of the following amino acids: Hpg (a); Eth (b); Met (c); Phe (d). Cells were treated overnight with 100  $\mu\text{M}$  CuBr, 200  $\mu\text{M}$  **3**, and 50  $\mu\text{M}$  **4**. Scale bar is 5  $\mu\text{m}$ .

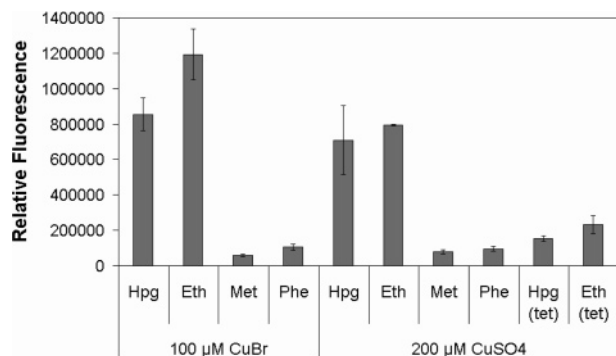
and Eth acts as a phenylalanine (Phe) analogue in strains that overexpress appropriately designed mutant phenylalanyl-tRNA synthetases.<sup>11,12</sup> We show here that these two analogues allow efficient labeling and visualization of newly synthesized proteins in bacterial cells.

Histidine-tagged barstar was used as the model protein.<sup>13</sup> Cells expressing recombinant barstar in medium containing the 20 natural amino acids, 19 amino acids plus Hpg, or 19 amino acids plus Eth were used for whole cell fluorescence studies with **3**. Barstar contains two Met sites and two Phe sites, all of which could potentially constitute targets for dye conjugation. Auxotrophic *E. coli* cells harboring a plasmid for inducible expression of barstar were grown to an OD<sub>600</sub> of 1, washed twice with 0.9% NaCl, and resuspended in medium supplemented with 19 amino acids plus 1 mM Hpg, 1.5 mM Eth, 0.75 mM Met, or 1.5 mM Phe.<sup>11</sup> Protein expression was induced by addition of isopropyl- $\beta$ -D-thiogalactopyranoside (IPTG). After 3.5 h, cells were harvested by centrifugation and washed twice with 0.9% NaCl to remove excess alkyne amino acid. The cells were resuspended in PBS (pH 7.9), and the OD<sub>600</sub> was adjusted to 1. The cultures were divided into 5 mL aliquots and supplemented with 50  $\mu\text{M}$  **3**. For copper-free reactions, there was no further supplementation. For reaction with CuSO<sub>4</sub> catalyst, the aliquots were supplemented with 200  $\mu\text{M}$  CuSO<sub>4</sub>, 200  $\mu\text{M}$  **4**, and 400  $\mu\text{M}$  TCEP.<sup>6</sup> For reaction with CuBr catalyst, the aliquots were supplemented with 100  $\mu\text{M}$  CuBr and 200  $\mu\text{M}$  **4**.<sup>7</sup> Labeling reactions were allowed to proceed for 14–15 h at 4 °C. Cells were harvested by centrifugation, washed twice, and resuspended in 5 mL of PBS (pH 7.9).

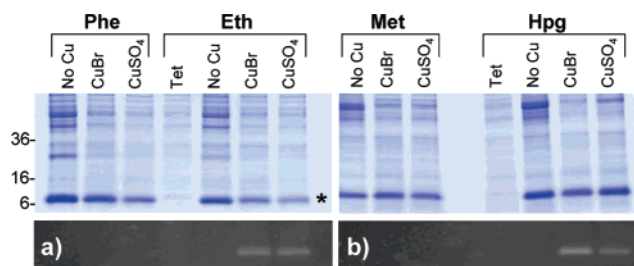
Strong fluorescence enhancement was observed only in cells containing alkyne-barstar reacted overnight with Cu(I) and **3** (Figure 1a,b). We examined the fluorescence of individual cells by confocal microscopy; images were obtained by overlaying a fluorescence image (excitation at 800 nm with a two-photon laser) and a differential interference contrast image. Cells lying out of the plane of focus did not appear fluorescent. In the plane of focus, however, punctate fluorescence was observed, presumably where barstar was localized in inclusion bodies (vide infra). No fluorescent cells were observed in experiments in which barstar was expressed in media supplemented with 19 amino acids plus Met or Phe (Figure 1c,d) or in control reactions run in the absence of Cu(I) (data not shown). Although uncatalyzed azide–alkyne reactions proceed

<sup>†</sup> California Institute of Technology.

<sup>‡</sup> University of South Carolina.



**Figure 2.** Fluorescence of induced *E. coli* cells after reaction with **3**. Fluorescence was also measured for uninduced cells in media supplemented with tetracycline (tet).



**Figure 3.** Polyacrylamide gel electrophoresis of proteins labeled with **3**. Samples were imaged under UV illumination (bottom) before staining with Coomassie blue (top). Barstar appears at ~12 kDa (\*). Bacterial lysates were from cultures supplemented with (a) Phe or Eth; (b) Met or Hpg.

favorably under selected conditions, the reaction rate is greatly enhanced by addition of a Cu(I) catalyst.<sup>5,14</sup>

Measuring the fluorescence emission from a volume of treated cells allowed us to determine the extent of fluorescence enhancement. After washing and resuspension, cells were excited at 395 nm and emission was monitored from 450 to 500 nm. Significant enhancement of the emission at 470 nm was observed only for cells treated with Hpg or Eth and labeled overnight with **3** and Cu(I) (Figure 2). To calculate the extent of enhancement, fluorescence from cells expressed in medium supplemented with 19 amino acids and an alkynyl amino acid was compared to background fluorescence from similarly treated cells grown in media supplemented with 19 amino acids and Met or Phe. Cells treated with Hpg and then ligated with **3** and CuSO<sub>4</sub> gave an 8.4-fold enhancement in emission intensity; ligation with CuBr gave a 10.1-fold enhancement. The corresponding enhancements for cells treated with Eth were 9.4- and 14.1-fold, respectively. Addition of tetracycline as an inhibitor of protein synthesis reduced the fluorescence emission to levels slightly above background.

To verify that labeling occurred selectively on newly synthesized proteins (i.e., primarily on barstar), we performed gel electrophoresis on crude bacterial lysates (Figure 3). Under UV illumination, the most intensely fluorescent band was that of barstar, although low levels of labeling were observed in other proteins, consistent with predominant, but not exclusive, expression of barstar following induction by IPTG. Fluorescence was detectable only in samples that were treated with **3** and a Cu(I) catalyst, confirming that Cu(I) was required for *in vivo* labeling. Lysates from cultures prepared in media supplemented with 19 amino acids plus Phe or Met lacked detectable fluorescence.

The punctate fluorescence shown in Figure 1 suggests that the labeled protein is localized predominantly in inclusion bodies. Cells from cultures supplemented with Eth or Hpg were labeled with **3**, and inclusion bodies were isolated and subjected to gel electrophoresis. Fluorescence imaging of the resulting gel was fully consistent with predominant dye-labeling of barstar in the insoluble fraction.

The results reported here demonstrate the utility of the Cu(I)-catalyzed azide–alkyne cycloaddition to effect selective fluorescence labeling of newly synthesized proteins in bacterial cells. The method exploits the natural scarcity of alkynes and azides in the cellular milieu, and offers a complement to current approaches that require genetic manipulation in order to ensure specific labeling. Susceptibility to labeling is determined not by the identity of the protein, but rather by the extent to which it was translated during the “pulse” of the alkynyl amino acid. The method is operationally similar to conventional pulse-labeling with <sup>35</sup>S-methionine, but avoids the technical challenges of high-resolution autoradiography.<sup>15</sup> We are currently studying the labeling of alkynyl amino acid side chains in proteins expressed in mammalian cells.

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**Supporting Information Available:** Experimental protocols. This material is available free of charge via the Internet at <http://pubs.acs.org>.

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