

Tag–probe labeling methods for live-cell imaging of membrane proteins

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Abbreviations: ACP, acyl carrier protein; eDHFR, *E. coli* dihydrofolate reductase; EDT, 1,2-ethanedithiol; FlAsh, fluorescein arsenical helix binder; FRET, Förster resonance energy transfer; GPCR, G protein-coupled receptor; NK₁, neurokinin-1; SFL', a synthetic ligand specific for FKBP12 (F36V); STIM, stromal interaction molecule; TMR, tetramethylrhodamine; hAGT, human O⁶-alkylguanine-DNA alkyltransferase

Abstract

Instead of using reconstituted proteoliposomes, in situ investigations of membrane proteins in living cell membranes are important because the heterogeneous and dynamic nature of biomembranes significantly affects their behavior. Protein-specific labeling is a key technique for the detection of a target protein by fluorescence measurements, particularly fluorescence microscopy. However, conventional genetic fusion with fluorescent proteins has several shortcomings. Post-translational labeling methods using a genetically encodable tag and synthetic probes targeting to the tag can overcome these limitations. This review summarizes emerging tag–probe techniques for labeling specific membrane proteins and their applications, including endocytotic internalization, partitioning to specific membrane domains, interprotein interactions, and conformational changes.

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1. Introduction

Integral membrane proteins are essential for vital functions across cell membranes such as signal transduction, material transport, energy conversion, and intercellular communication. These dynamic functionalities of the proteins are based on a ligand-induced shift in conformational equilibrium, which, in some cases, sequentially induces new intermolecular interactions and translocation of the protein via membrane trafficking machinery. Lipids also highly influence the folding and conformation of integral membrane proteins. For example, the lipid compositions of reconstituted proteoliposomes could dramatically alter the activity of incorporated membrane proteins [1,2]. Experimental systems using model transmembrane helices have also revealed that the thermodynamics of helix–helix interaction, the major driving force for membrane protein folding, strongly depends on lipid composition [3–5]. A biomembrane contains several hundred or more different lipid species varying in physicochemical properties such as electric charge and fluidity. The distribution of the lipids is heterogeneous among organelles [6,7] and between the extracellular and cytosolic leaflets of a bilayer [7], and even laterally within a leaflet on a nanoscale [8]. These facts suggest the structure and function of membrane proteins to be sophisticatedly regulated by lipids in cell membranes. Therefore, experimental approaches for the in situ investigation of membrane proteins in living cell membranes are essential to

observe the dynamic behavior of the proteins, in addition to reconstituted systems using isolated proteins.

Fluorescence microscopy, such as epifluorescence or confocal microscopy, has been widely used to detect proteins in living cells in combination with protein-specific labeling techniques. The visualization of membrane proteins in living cells can reveal dynamic behavior such as endocytotic internalization (Fig. 1A) and partitioning to specific membrane domains (Fig. 1B). In addition to simple observations of the intracellular dynamics of proteins, Förster resonance energy transfer (FRET) between different fluorophores having a spectral overlap detects changes in distance and/or orientation of the fluorophores in the range $<100 \text{ \AA}$ and thus is useful for monitoring interprotein interactions (Fig. 1C) and conformational changes (Fig. 1D). Other advanced applications of fluorescence techniques are reviewed in Ref. [9], including pulse-chase labeling and chromophore-assisted laser inactivation of the target protein.

Genetic fusion of fluorescent proteins to a target protein has been widely used for protein-specific labeling in living cells [9,10]. However, the large size of fluorescent proteins (e.g. $\sim 27 \text{ kDa}$ for GFP) might disrupt the normal trafficking and function of target proteins (see [11,12], for example). The large size also greatly restricts use for site-specific labeling within a protein, for example, for detection of conformational changes (Fig. 1D).

Furthermore, modern imaging techniques such as single molecule microscopy require fluorophores with better photophysical properties, such as long-term photostability and greater brightness. Precise control of the labeling ratio in multicolor labeling for FRET measurements is not easy using fluorescent proteins either. To overcome these shortcomings, post-translational labeling methods using a genetically encodable tag and synthetic probes targeting the tag have recently emerged to specifically label proteins in living cells. Diverse fluorophores with improved brightness, photostability, and spectral properties, including quantum dots, can be specifically attached to target proteins using the tag–probe techniques, although the size of quantum dots could be a major problem. Integral membrane proteins expressed on the cell surface are generally available for most tag–probe techniques because probes are accessible to the tags attached to the extracellular domains of the proteins. This review summarizes tag–probe techniques for labeling membrane proteins and their applications. Several related reviews have also been published on selective labeling techniques generally used in living cells [13–16], fluorescent probes for super-resolution imaging [17], metal-chelation labeling [18] and bioorthogonal chemistry in living cells [19].

2. Labeling principles and applications

Various labeling methods developed so far rely on protein–ligand interaction,

peptide–peptide interaction, peptide–fluorophore interaction, metal chelation, and enzymatic reactions (Fig. 2 and Table 1). A protein tag genetically fused to a target protein can be labeled with a ligand conjugated to a fluorophore (Fig. 2A). If the ligand is a peptide, it can be used as a tag that is labeled by a protein probe (Fig. 2A'). Two peptides that form a tight heterodimer are also used as a tag–probe combination (Fig. 2B). A minimalist approach is the use of a peptide tag that directly binds a fluorophore (Fig. 2C). A combination of a peptide and a chemical that cooperatively binds a metal ion is another principle for tag–probe labeling (Fig. 2D). Finally, an enzymatic reaction that covalently conjugates a substrate to a specific site of a peptide is useful for covalent labeling (Fig. 2E).

2.1 Protein–ligand interaction

Noncovalent binding of a ligand to a protein has been used for specific labeling of membrane proteins. The ligand trimethoprim has been used to label *E. coli* dihydrofolate reductase (eDHFR) at the plasma membrane by fusing the N-terminus of eDHFR to the myristoylation/palmitoylation sequence (MGCIKSKGKD) (Table 1) [20]. A labeling kit (LigandLink™) is available from Active Motif (Carlsbad, CA). Also, a mutant of the human FKBP12 protein (FKBP12 (F36V)) and a synthetic ligand specific for the protein (SFL') can label a variety of proteins (Table 1), including caveolin, rac, and rho in HeLa cells [21,22],

although only two types of fluorophores [tetramethylrhodamine (TMR) and fluorescein] are suitable for effective labeling in spite of the extensive examination of a number of fluorophores with different linkers [22]. If the ligand is a peptide, it is useful as a tag that binds to the protein probe (Fig. 2A'). A 13-amino acid peptide that binds to α -bungarotoxin has been successfully used as a tag to label extracellular domains of target proteins (Table 1) [23,24]. Membrane trafficking of AMPA receptors and a vesicle-associated protein VAMP2 has been observed.

A covalent bond can form if the ligand is metabolized by the protein. For example, a dysfunctional mutant of a bacterial haloalkane dehalogenase (HaloTagTM, Promega, Madison, WI), which forms a stable bond with the substrate chloroalkane, is useful for both cell-surface and intracellular specific labeling (Table 1) [25]. In addition to organic fluorophores such as TMR and fluorescein, quantum dots (QD₆₅₅) have been attached to the extracellular domain of platelet-derived growth factor receptors for long-term imaging [26]. This labeling method was recently used to visualize endocytotic-like structures in filopodia (diameters: 90–130 nm) of HeLa cells in combination with a super-resolution imaging, stimulated emission depletion microscopy [27]. Johnsson and colleagues reported a method involving the irreversible transfer of an alkyl group from *O*⁶-alkylguanine-DNA to human *O*⁶-alkylguanine-DNA alkyltransferase (hAGT) (Table 1) [28], which is currently

commercially available (SNAP-tagTM, New England Biolabs, Ipswich, MA). In a recent publication, this technology was used to specifically label cell-surface G protein-coupled receptors (GPCRs) with synthetic fluorophores or luminescent europium cryptate to circumvent the insufficient fluorescence intensity and unnecessary fluorescence from receptors accumulated within intracellular compartments, both of which are often problematic in the labeling of a GPCR by fluorescent proteins [29]. Time-resolved FRET measurements revealed the presence of oligomers for various GPCRs in COS-7 cell membranes [29]. An alternative approach to the covalent labeling of a target protein is the use of a suicide inhibitor, for example, *p*-nitrophenyl phosphonate which binds to the fungal protein cutinase (Table 1) [30]. The N and C termini of cutinase are close to each other (28.2 Å) and opposed to the active site, offering the possibility of insertion into the target protein. The integrin LFA-1 expressed on the surface of BAF cells was labeled with Alexa Fluor 488 or quantum dots (QD₆₅₅) [30]. The inhomogeneous distribution of the integrin during cell locomotion was observed.

2.2 Peptide–peptide interaction

A promising way to reduce the label's size is the utilization of peptide–peptide interactions. Simple labeling without cofactors such as metals or enzymes is an advantage

for universal use. The de novo designed peptide pair (EIAALKE)_n and (KIEELEK)_n (n = 3, 4) is known to form a tight heterodimer in a coiled-coil fashion (Fig. 3A) [31]. We found that the E3 tag peptide (EIAALKE)₃ and the probe peptide K3 (KIAALKE)₃ or K4 (KIAALKE)₄ are suitable pairs for specific labeling of cell-surface receptors, such as prostaglandin EP3 β , β 2-adrenergic, and EGF receptors by virtue of the membrane-impermeability of the probes (Table 1) [32]. The probes are nontoxic and the labeled receptors maintain their functionality. The K3 and K4 probes have apparent dissociation constants of 64 and 6 nM against the E3 tag, respectively. The labeling is completed within 1 min. The reversibility of the E3-K3 labeling enables a pulse–chase labeling of internalized and cell-surface receptors with TMR and fluorescein, respectively (Fig. 3B).

2.3 Peptide–fluorophore interaction

The minimal design of a tag–probe system consists of a fluorophore and a polypeptide that directly binds it. Sequence screening by phage display has been used to optimize such a dye-binding peptide (Table 1) [33]. The resulting 38-mer peptide TR512 composed of two dimerization domains and a dye-binding domain was assumed to recognize the xanthene core of Texas Red. The tag peptide targeting plasma membranes of NIH3T3

cells was stained with a calcium sensor derivative of Texas Red (X-rhod-5F) to detect local calcium responses. The affinity between the Texas Red probe and a phage that has five tag sequences is 25 pM. The stoichiometry of the tag–probe complex and the binding constant are yet to be determined.

2.4 Metal chelation

The first tag–probe labeling system in living cells, reported in 1998, was based on a reversible covalent bond formation between organoarsenicals and pairs of thiols [34]. The biarsenical derivative of FL [fluorescein arsenical helix binder (FlAsh)] was found to tightly bind to the tetracysteine tag motif (Table 1). The tetracysteines in the tag were initially positioned in a helical secondary structure, and subsequently positioned into optimized sequences for specific labeling in mammalian cells (HRWCCPGCCCKTF and FLNCCPGCCMEP) [35], which form a hairpin structure [36]. To minimize nonspecific labeling and the toxicity of arsenical compounds, 1,2-ethanedithiol (EDT) or other dithiols and/or suppression dyes are indispensable in the labeling and washing procedures [37]. An excellent property of FlAsh is that it is nonfluorescent in the EDT-form but becomes fluorescent after binding to the tag. FlAsh and longer-wavelength biarsenical fluorophore ReAsh are membrane-permeable and therefore suitable for the labeling of intracellular

domains of membrane proteins. On the other hand, the labeling of cysteines in extracellular domains requires reducing agents because of the oxidization of the cysteines to disulfides. Various biarsenical fluorophores including Ca^{2+} indicators have been synthesized [18,38]. A noticeable application of biarsenical–tetracysteine labeling for membrane proteins is the detection of conformational changes in GPCR following agonistic stimulation. Hoffman and colleagues constructed a FRET sensor mutant of adenosine $\text{A}_{2\text{A}}$ receptor in which a tetracysteine tag and cyan fluorescent protein were fused to the intracellular third loop and the C-terminus of the receptor, respectively [11]. After FIAsh labeling, the structural rearrangement induced by an agonist (e.g. 100 μM adenosine) occurred in the order of tens of milliseconds and could be read out as changes in fluorescence intensity of FIAsh and CFP, reflecting alterations in FRET efficiency from CFP to FIAsh. The intracellular third loop is important for coupling to downstream G-proteins. Nevertheless, the insertion of the biarsenical–tetracysteine label (< 2 kDa) into the third loop did not affect the receptor activity, in contrast to the insertion of yellow fluorescent protein which reduced the receptor activity. In a recent report, FIAsh labels were positioned at different sites of the third intracellular loop of $\alpha_{2\text{a}}$ -adrenergic receptor: N-terminally close to the transmembrane helix V (I3-N), in the middle of the loop (I3-M), and C-terminally close to the transmembrane helix VI (I3-C) [39] (Fig. 4). A full agonist evoked similar FRET changes in all three constructs whereas weak

partial agonists induced a change only in the construct I3-C. These results demonstrate distinct agonist-specific conformational changes of GPCR in living cells. A kit for biarsenical–tetracysteine labeling is available commercially (TC-FlAsh™ and TC-ReAsh™, Invitrogen, Carlsbad, CA).

Most other methods using metal chelation are based on coordination among a divalent metal cation, a tag peptide, and a probe molecule. An example is the membrane-impermeable HisZiFit probe that binds to a hexahistidine tag via Zn^{2+} coordination (Table 1) [40]. Surface exposure of a membrane protein, stromal interaction molecule (STIM) 1, from the endoplasmic reticulum in HEK293 cells was successfully detected using this method. Another promising approach is the use of DpaTyr probes that bind to an oligo-aspartate tag via Zn^{2+} coordination (Table 1) [41]. This technique has been used to visualize muscarinic acetylcholine receptors in CHO cells. Based on the tag–metal–probe assembly, the formation of a covalent bond between a cysteine residue optimally positioned in the tag and the *N*- α -chloroacetyl group attached to the probe is possible [42]. The combination of the NTA probe and hexahistidine tags in the presence of Ni^{2+} has also been used to label 5HT₃ serotonin receptors in HEK-293 cells (Table 1) [43]. A nonfluorescent chromophore was labeled at an intracellular or extracellular site of the receptor by the method and used as a quencher for a fluorophore conjugated to the receptor antagonist to obtain

structural information about the quencher-binding site and the ligand-binding site. This labeling system has several problems. The affinity of hexahistidine–NTA-Ni²⁺ is weak. Multimerization of the probe could improve the affinity [44,45]. The introduction of dichlorofluorescein [46], for example, circumvents partial quenching of the fluorescence by Ni²⁺. Another possible problem is the cytotoxicity of Ni²⁺ [47].

2.5 Enzymatic reactions

Enzymes that attach a substrate to a specific site of a polypeptide have been applied to tag–probe labeling in living cells. An example is the use of phosphopantetheinyl transferase which transfers part of a phosphopantetheinyl probe to an acyl carrier protein (ACP) tag consisting of ~80 amino acids (Table 1) [48,49]. The lateral organization of neurokinin-1 (NK₁) receptors in HEK293 cell membranes has been investigated by FRET between the receptors [50]. ACP-NK₁ receptors expressed on plasma membranes were simultaneously labeled with the Cy3 and Cy5 fluorophores at defined labeling ratios to correctly estimate FRET efficiency. Because of the strong dependence of FRET efficiency on the receptor concentration on the cell surface, the authors concluded that the receptors tended to be concentrated in microdomains rather than self-associated. Interestingly, the FRET signal was slightly sensitive to the depletion of cholesterol, which is an important

component of lipid raft microdomains. This ACP labeling was also used to visualize odorant receptors labeled with Cy5 down to the single molecule level [51]. After stimulation with an agonist, the receptors were confined to small domains of ~190 nm, which are likely precursors of clathrin-coated pits. Currently two orthogonal tag–enzyme pairs using the principle are available for multicolor labeling (ACP-tagTM and MCP-tagTM, New England Biolabs). Shorter peptide tag sequences substituted for ACP have also been reported to further reduce the label’s size [52]. Another example of tag–probe labeling with an enzymatic reaction is a system using *E. coli* biotin ligase (BirA) and a 15-amino-acid acceptor peptide (Table 1) [53]. The labeling of fluorophores using the method is carried out in two steps. First, a ketone analog of biotin (ketone 1) is attached to the tag, and second, the ketone group absent on the native cell surface is specifically reacted with a hydrazide group conjugated to a fluorophore. EGF receptors expressed on the surface of HeLa cells were labeled by this procedure [53]. Similar two-step labeling was performed using lipoic acid ligase and alkyl azide probes with an improved labeling time (total ~20 min) (Table 1) [54]. Recently, bacterial sortases have been applied to tag–probe labeling on living cell membranes (Table 1) [55,56]. This enzyme recognizes the LPXTG motif and cleaves the peptide bond between threonine and glycine, subsequently yielding a new peptide bond between the C-terminus of the threonine and the N-terminus of the pentaglycine probe. The tag should

be placed in a flexible region close to the C-terminus of the target protein [55]. Human CD 154 protein and osteoclast differentiation factor were successfully labeled and visualized in HEK 293 cells using the method. The unique features of the labeling system are 1) protein–protein conjugation was possible on the cell surface, as exemplified by the conjugation of externally added GGGGG-EGFP to ODF-LPETGG [56], and 2) tag and probe sequences could be exchanged. Another promising enzyme is transglutaminase, which introduces a cadaverine-conjugated fluorophore to a glutamine side chain in Q-rich tag sequences expressed on HeLa cells (Table 1) [57].

2.6 Pros and cons of various techniques

An ideal tag–probe labeling method should have several features: high specificity, a small tag, no toxicity, no perturbation of the target protein, versatility in the choice of available fluorophores, a short labeling time, and a simple labeling procedure, although these features are often incompatible with each other. In general, there is a trade-off between specificity and size. For example, tag–probe pairs based on protein–ligand interactions (Fig. 2A) enable highly specific labeling, when the tag is relatively large (typically comparable to GFP). On the other hand, labeling via metal chelation (Fig. 2D) could greatly reduce the label's size (down to 1 kDa), however nonspecific staining, insufficient affinity, or metal

toxicity might restrict applications. A satisfactory balance between size and specificity could be achieved by utilizing an intermediate-sized peptide–peptide assembly (Fig. 2B) or peptide–fluorophore complex (Fig. 2C). Alternative approaches are based on enzymatic reactions that catalyze the formation of a covalent bond between the tag and the probe (Fig. 2E). A smaller size and tight labeling are achieved with this approach, although a longer labeling time in the presence of excess probes (= substrates) is usually required for efficient labeling.

3. Outlook

Most of the principles for labeling membrane proteins in living cells described above have been reported in the last 5 years. New principles are also emerging, although they are yet to be tested in living cells. For example, the tetraserine-bisboronic acid labeling system, in which a tetraserine motif specifically binds fluorophores having bisboronic groups, was reported [58], however labeling in living cells is currently unavailable presumably because of abundant natural Ser-rich sequences that bind to the probe. An approach without using organic fluorophores or quantum dots is the use of luminescence from lanthanides. Imperiali and colleagues have reported a lanthanide-binding tag (15 amino acids) that strongly binds Tb^{3+} and becomes luminescent on excitation of Trp in the tag [59]. Although

the excitation wavelength is too short for conventional fluorescence imaging, this labeling system has potential for measuring distances between domains in membrane proteins using lanthanide-based resonance energy transfer coupled with emission lifetime measurements, as demonstrated for potassium channels expressed in *Xenopus* oocytes [60]. An important but currently challenging technology is protein- and site-specific labeling of fluorophores in transmembrane regions of membrane proteins in living cells. A promising strategy for this is the genetic incorporation of nonnatural fluorescent amino acids [61]. An alternative might be the use of native chemical ligation and related biochemical techniques ('expressed protein ligation' and 'protein *trans*-splicing') to perform protein semisynthesis [62], allowing the site-specific incorporation of fluorophores.

4. Conclusions

A variety of tag-probe techniques based on physicochemical interactions or biochemical reactions have been successfully applied to the labeling of membrane proteins in living cells. These techniques have advantages over the conventional genetic fusion of fluorescent proteins in diverse choice of fluorophores, smaller size, and rapid and surface-specific labeling at a defined time. These features are useful for the visualization of intracellular translocation, interprotein interactions, and conformational changes of membrane

proteins. An appropriate choice of technique is possible depending on the intended use, although the use of a smaller label generally accompanies a rather complicated procedure or a lower specificity. Multicolor labeling using multiple techniques orthogonal with each other particularly demands simple labeling procedures. Although the further improvement of existing principles and the development of new principles will be actively studied, current tag–probe techniques for specific labeling in living cells have greatly contributed to elucidation of the behavior of membrane proteins in situ, the activities of which are regulated by interactions with diverse molecules in biological membranes.

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Figure legends

Fig. 1 Dynamic behavior of membrane proteins in living cells detectable by fluorescence imaging. (A) Endocytotic internalization. Following stimulation with an agonist and/or spontaneously, membrane proteins translocate from the cell surface to intracellular vesicles via the endocytotic machinery. A recycling of proteins to the surface also occurs. (B) Partitioning into specific membrane domains. Following activation and/or interaction with other proteins, membrane proteins laterally redistribute among domains with a distinct lipid composition. The partitioning to a specific domain can be detected by fluorescence resonance energy transfer (FRET) from a fluorophore attached to a protein (green) to an adequate fluorescent marker for the domain (red) and/or colocalization of the two. The existence and detailed characteristics of lipid nanodomains are still under debate. (C) Interprotein interactions. Stimulation of membrane proteins facilitates or suppresses protein–protein interactions. FRET from the donor fluorophore (green) attached to one protein to the acceptor fluorophore (red) attached to the other interacting protein can detect the interactions. (D) Conformational changes. Following ligand stimulation and/or interaction with other proteins, the protein structure changes. Double labeling of a protein with a FRET donor and an acceptor enables detection of the structural change.

Fig. 2 Principles of tag–probe labeling. (A) Protein–ligand interaction. A protein tag fused to a target protein is labeled with a ligand conjugated to a fluorophore. (A') If the ligand is a peptide, it can be used as a tag that is labeled with the protein probe. (B) Peptide–peptide interaction. Two peptides that form a tight heterodimer are used as a combination of a tag fused to the target protein and a probe conjugated with a fluorophore. (C) Peptide–fluorophore interaction. A polypeptide that directly binds a fluorophore is used as a tag. (D) Metal chelation. A tag and a probe are cooperative chelators for a metal ion. The tag–metal–probe motif is often multimerized to obtain sufficient binding affinity. (E) Enzymatic reaction. A specific site of a tag sequence (substrate 1) is covalently modified with a probe (substrate 2) by an enzymatic reaction.

Fig. 3 Coiled-coil labeling. (A) Helical wheel representation of the E3/ K3 coiled-coil heterodimer. White and black arrows indicate hydrophobic and electrostatic interactions respectively. (B) Pulse-chase experiments for the internalization of β_2 -adrenergic receptors (β_2 AR) in response to receptor stimulation. CHO cells expressing E3- β_2 AR were labeled with tetramethylrhodamine-K3 (TMR-K3) (60 nM) for 2 min, and then incubated with the agonist isoproterenol (10 μ M) for 5 min. After the cells were washed with PBS, 20 nM

fluorescein-K4 (FL-K4) was added to label the receptors remaining on the cell surface and the cells were observed. The TMR (internalized receptor) and FL images are merged in the lower right panel. Reproduced from reference [32] with permission.

Fig. 4 Constructs of the α_{2A} -adrenergic receptor for the detection of conformational changes by FRET. For all constructs, the donor fluorophore CFP was positioned at the very C terminus of the amino acid sequence. The positions of the different FLAsh-binding sites in the third intracellular loop are marked in white. The numbers denote the amino acid segments that were replaced by the binding motif “FLNCCPGMEP.” Positions 246 to 257 represent the construct I3-N, positions 297 to 308, I3-M, and positions 350 to 361, I3-C. Modified from reference [39] with permission.

Table 1

Table 1 Various tag-probe labeling methods

principle	labeling system	tag	probe	probe structure	available fluorophores	approx. size	cofactor/enzyme	affinity	typical labeling condition	notes	references
Protein-ligand interaction	LigandLink™	E. coli dihydrofolate reductase (eDHFR)	trimethoprim		arbitrary	18 kDa	No	1 nM	10 nM, 15 min	commercial, intracellular labeling	20
	FKBP12	FKBP12 (F36V)	SLF ¹		arbitrary (structure-dependent [22])	12 kDa	No	0.1 nM	1 μM, 30 min	intracellular labeling	21,22
	BTX	WRYYESLEPYPD	α-bungatoroxin	-	arbitrary	8 kDa	No	14–60 nM	1 μM, 15 min		23,24
	HaloTag™	Haloalkane dehalogenase (modified)	chloroalkane		arbitrary	33 kDa	No	covalent	5 μM, 15 min	commercial, intracellular labeling	25–27
	SNAP-tag™	hAGT	benzilguanine		arbitrary	20 kDa	No	covalent	5 μM, 1 h	commercial, intracellular labeling	28,29
	Cutinase	cutinase	p-nitrophenyl phosphonate		arbitrary	22 kDa	No	covalent	1 μM, 30 min	insert is possible	30
Peptide-peptide interaction	Coiled-coil	EIAALKE EIAALKE EIAALKE	KIAALEK KIAALEK KIAALEK KIAALEK	-	arbitrary	6 kDa	No	6 nM (K4), 64 nM (K3)	20 nM, 1 min		32
Peptide-fluorophore	TR binding peptide	GGGSKVILFEGPAGRWTWPEI SEGAPGSKVILFEGGPG	xanthene core of Texas Red	-	Texas Red, X-rhodamine	3.5 kDa	No	80 pM (as phage)	1 μM, 30 min	intracellular labeling	33
Metal chelation	Biarsenical-tetracycline	FLNCCPGCCMEP	biarsenical fluorophores		various	2 kDa	EDT	covalent	0.5 μM, 1 h	commercial, intracellular labeling, toxicity of As	11, 34–39
	HisZiFit	HHHHHH	2-pyridylsulfoneamide		HisZiFit	1 kDa	Zn ²⁺	40 nM	100 nM, 1 min		40
	Oligo-Asp/Zn ²⁺ complex	DDDDGDDDDGDDDD	Dpa Tyr		arbitrary	3 kDa	Zn ²⁺ , DDDD	<55 nM	20 μM, 5 min	covalent labeling is also available	41,42
	NTA-His	HHHHHH	NTA		quenchers, dichlorofluorescein, quantum dot	1 kDa	Ni ²⁺	1–4 μM	15 μM, 1 min	quenching by Ni ²⁺ , toxicity of Ni ²⁺	43–46
Enzymatic reaction	ACP-tag™, MCP-tag™	acyl carrier protein	coenzyme A		arbitrary	9 kDa	PPTase	covalent	5 μM, 40 min	commercial, shorter tags are available	48–52
	BirA labeling	GLNDIFEAQKIEWHE	biotin		ketone reactive	2 kDa	biotin ligase, ATP	covalent	1 mM, 60 min	two-step labeling	53
	LplA labeling	DEVLVEIETDKAVLEVPGEIEE	lipoic acid		azide reactive	3 kDa	lipoic acid ligase, ATP	covalent	250 μM, 15 min	two-step labeling	54
	Sortagging	LPETG	GGGGG		arbitrary	2 kDa	sortase	covalent	100 μM, 10 min	limited to C-terminus labeling	55,56
	TGase labeling	PKPQQFM	cadaverine		arbitrary	2 kDa	transglutaminase, Ca ²⁺	covalent	400 μM, 25 min		57

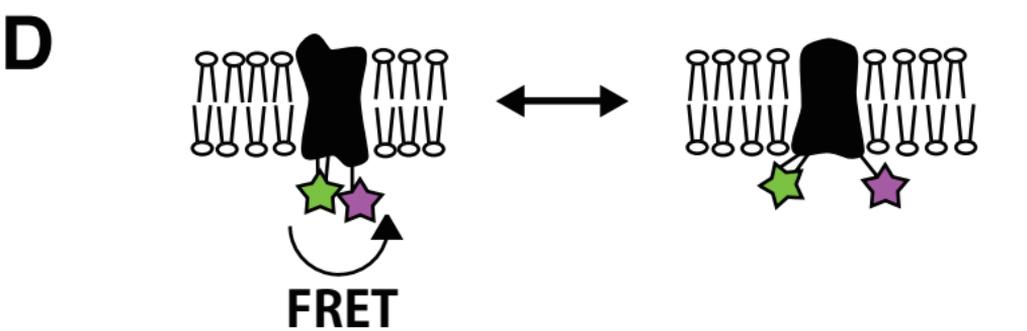
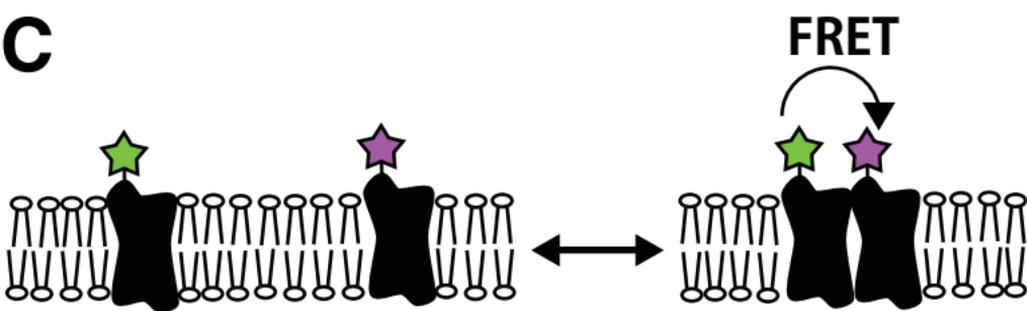
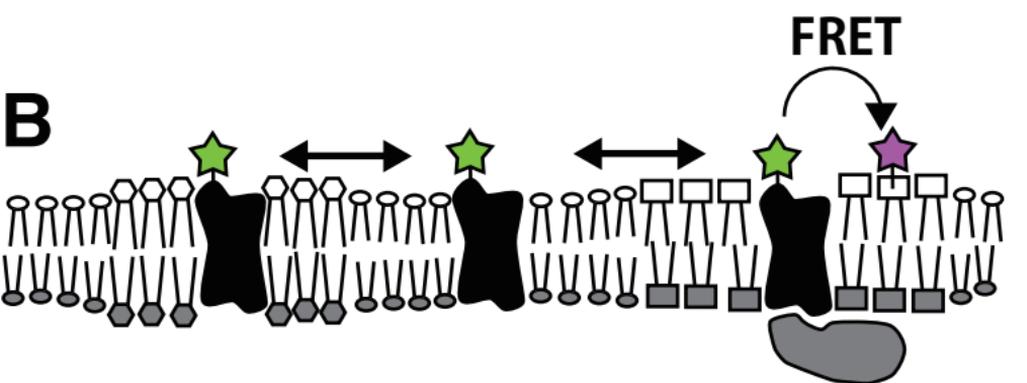
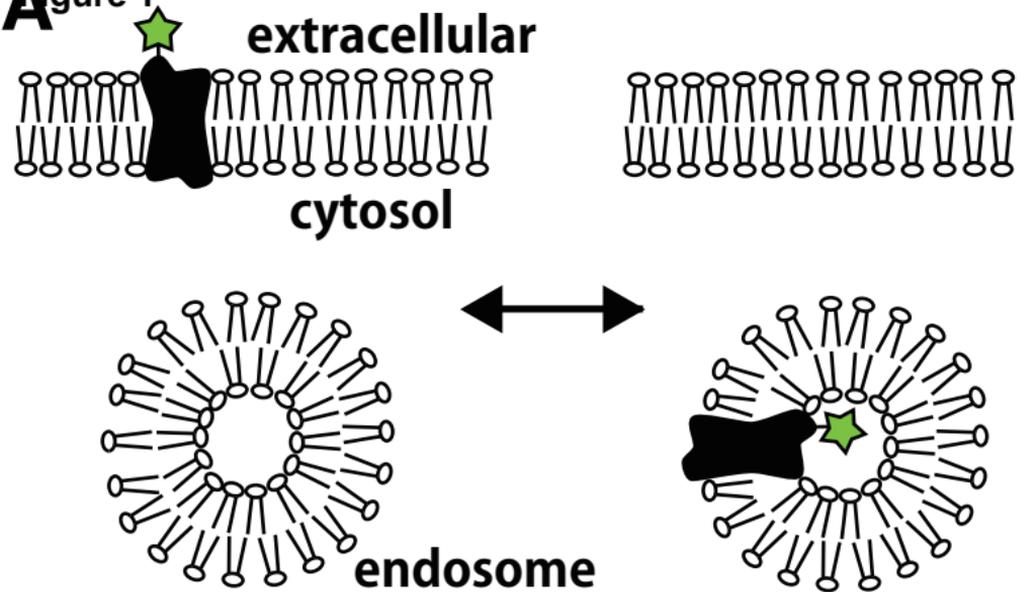
Figure 1

Figure 2

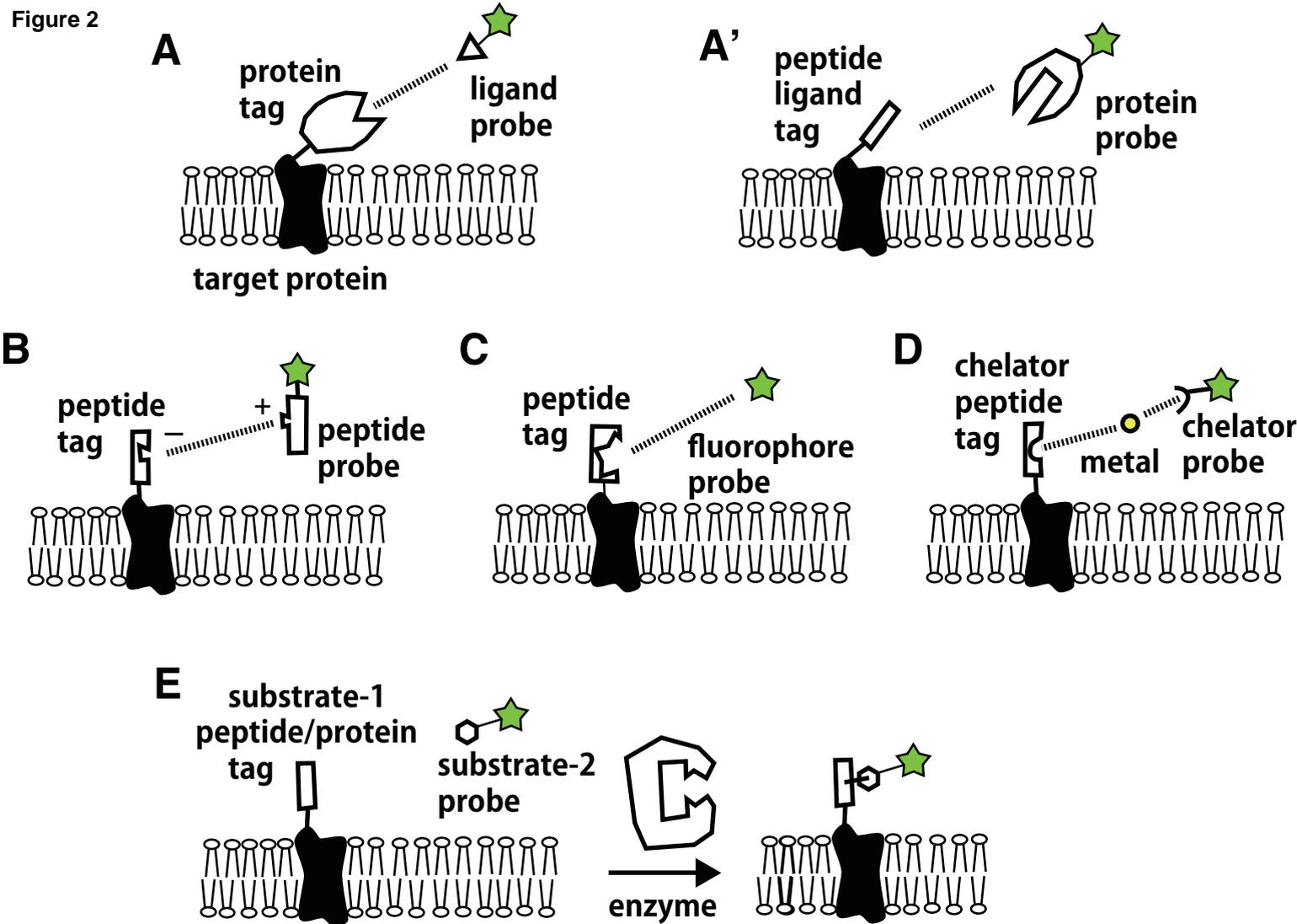


Figure 3

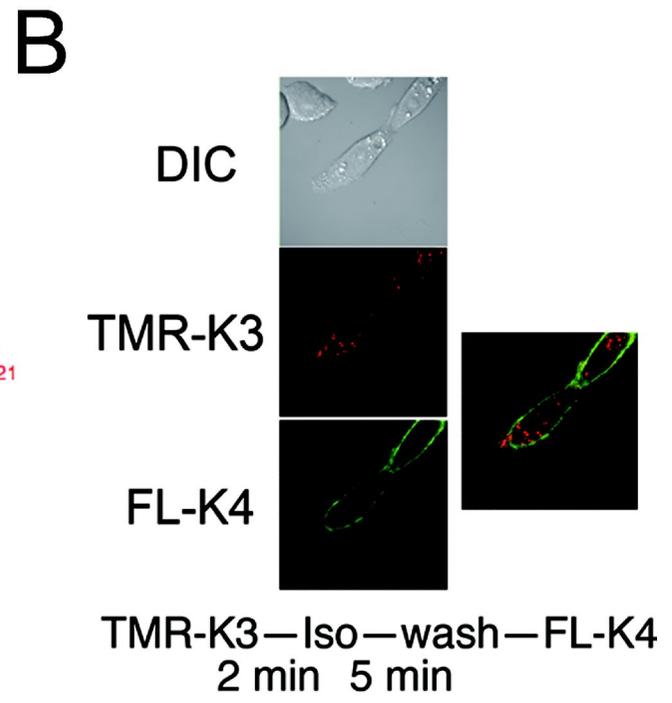
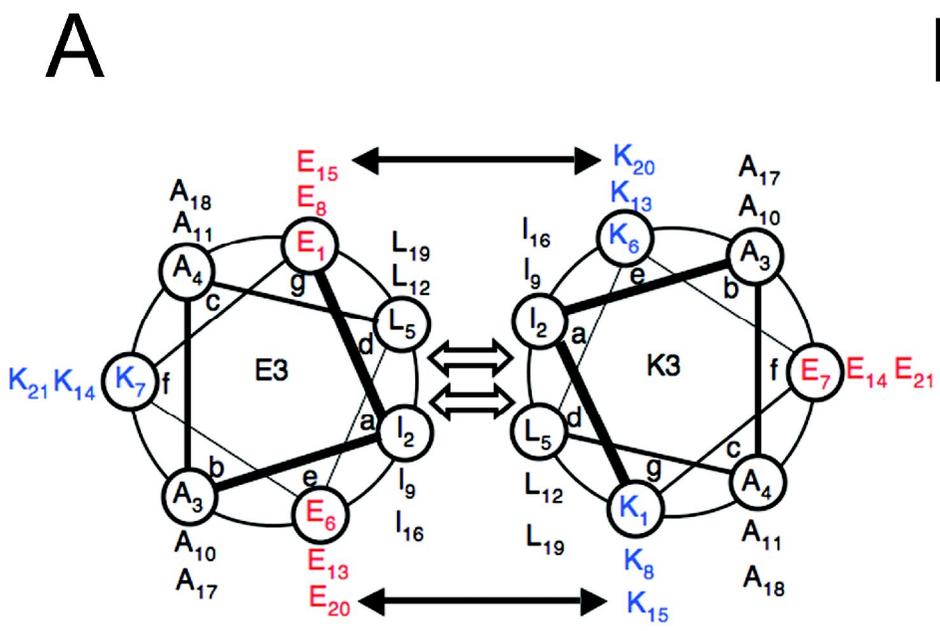


Figure 4

