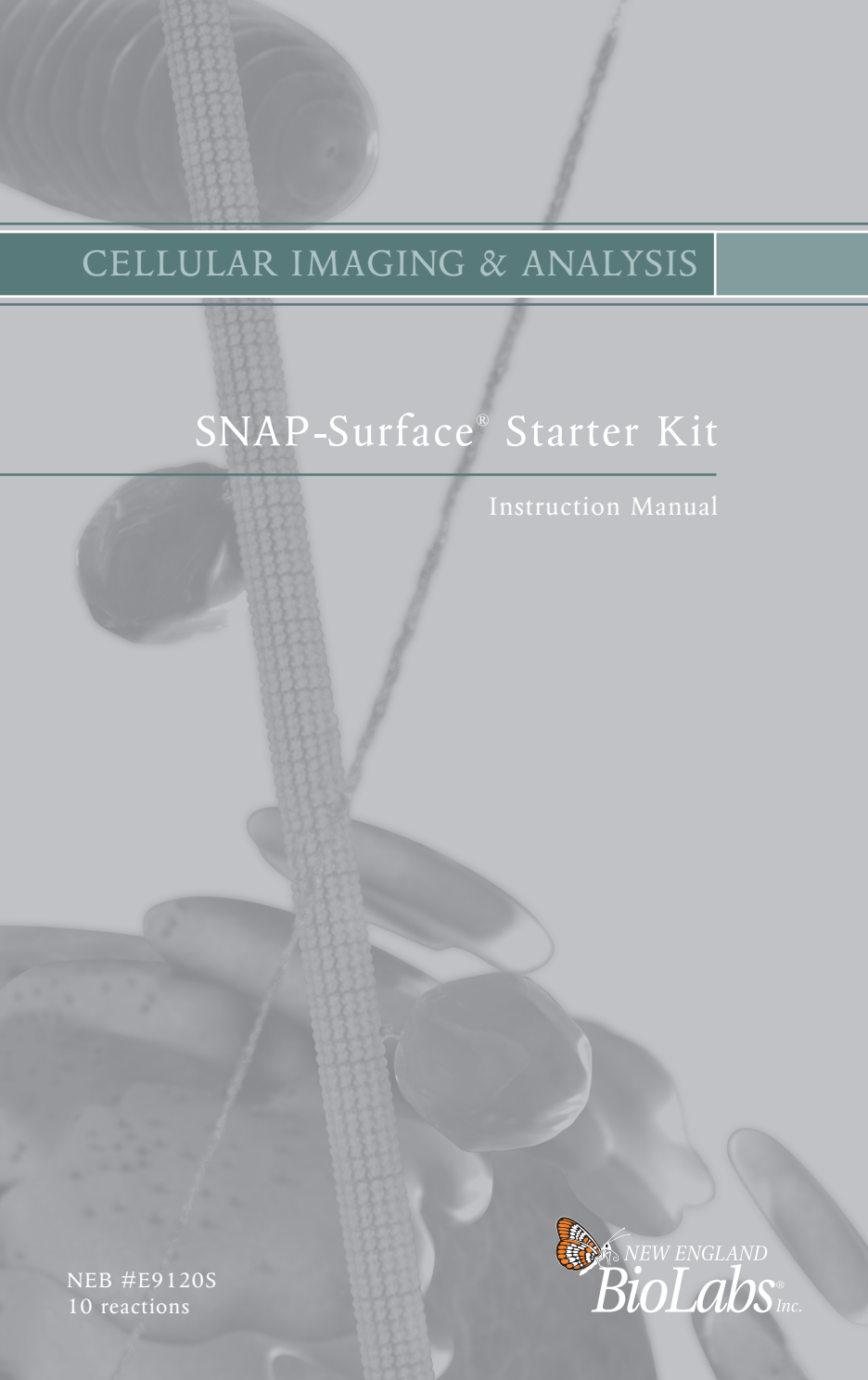


CELLULAR IMAGING & ANALYSIS

SNAP-Surface® Starter Kit

Instruction Manual

NEB #E9120S
10 reactions

NEW ENGLAND BioLabs® Inc.

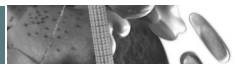


Table of Contents:

Kit Components:

All kit components should be stored at –20°C except where noted.

pSNAP$_f$ Vector ..... 20 µg
Supplied in TE buffer (10 mM Tris-HCl, pH 8.0, 1 mM EDTA), 0.5 µg/µl

pSNAP$_f$-ADRβ2 Control Plasmid ..... 20 µg
Supplied in TE buffer (10 mM Tris-HCl, pH 8.0, 1 mM EDTA), 0.5 µg/µl

SNAP-Surface 488 ..... 10 nmol
Supplied dry. Prepare a stock solution in DMSO as described on page 10.

SNAP-Surface 549 ..... 10 nmol
Supplied dry. Prepare a stock solution in DMSO as described on page 10.

SNAP-Surface Block ..... 40 nmol
Supplied dry. Prepare a stock solution in DMSO as described on page 13.

Note: For long-term storage, all kit components should be stored at –20°C. Plasmid solutions can be stored at 4°C for up to one week. Undissolved dye and blocking substrates can be stored at 4°C for up to 4 weeks protected from light and moisture. With proper storage at –20°C the substrates should be stable for at least two years dry or 3 months dissolved in DMSO.

Required Materials Not Included

Mammalian Cell Lines

DNA Transfection Reagents

Standard Tissue Culture Media and Plasticware

DMSO

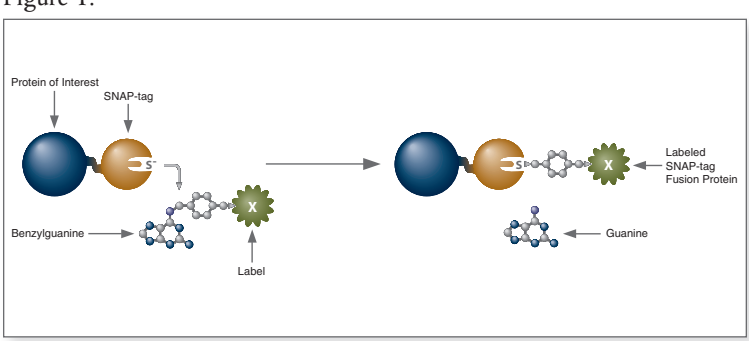
Hoechst 33342 for Nuclear Staining (optional)

Introduction:

The SNAP-tag® is a novel tool for the specific, covalent attachment of virtually any molecule to a protein of interest, providing simplicity and extraordinary versatility to the imaging of proteins in live and fixed cells, and to the study of proteins *in vitro*. The creation of a single gene construct yields a tagged fusion protein capable of forming a covalent linkage to a variety of functional groups, including fluorophores, biotin, or beads. This system provides a powerful and unique tool to study the role of proteins in a variety of highly dynamic processes, including protein trafficking, turnover and complex formation.

The SNAP-tag is a 20 kDa mutant of the human DNA repair protein O^6-alkylguanine-DNA alkyltransferase (hAGT) that reacts specifically and rapidly with benzylguanine (BG) and benzylchloropyrimidine (CP) derivatives, leading to covalent labeling of the SNAP-tag with a synthetic probe (Figure 1). The SNAP-tag has a number of features that make it ideal for a variety of protein labeling applications. The rate of the reaction of the SNAP-tag with these derivatives is largely independent of the nature of the synthetic probe attached to BG, permitting the labeling of SNAP fusion proteins with a wide variety of functional groups. Many of these SNAP-tag substrates are cell-impermeable, allowing live-cell imaging of protein expression and localization on the cell surface (Figure 2). The ability to turn on the signal at will, together with the availability of a cell-impermeable nonfluorescent blocking agent (SNAP-Surface Block), allows time-resolved pulse-chase analysis of protein trafficking to the cell surface, as well as subsequent internalization. Finally, the availability of orthogonal protein labeling systems from NEB permits simultaneous labeling of multiple proteins in a single cell (CLIP-tag™, a SNAP-tag variant that reacts exclusively with O^2-benzylcytosine substrates, and the ACP/MCP tags, small protein tags which can be enzymatically labeled on the cell surface with Coenzyme A derivatives).

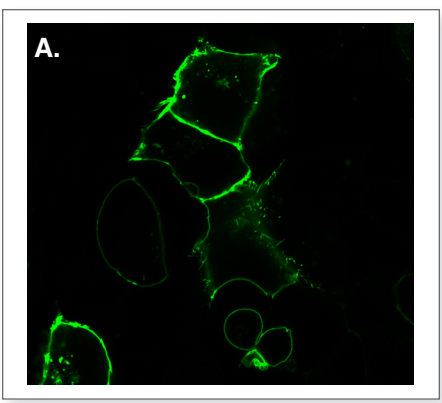
Figure 1.



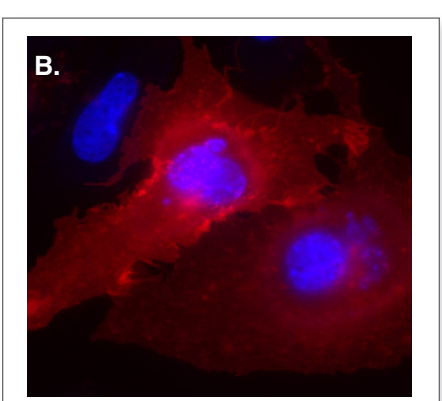
SNAP-tag reaction.

The SNAP-Surface Starter Kit contains a mammalian expression plasmid (pSNAP$_f$) encoding the SNAP-tag flanked by restriction sites for cloning a gene of interest, and two non-cell-permeable fluorescent SNAP-tag substrates. A positive control plasmid (pSNAP$_f$-ADRβ2), encoding a SNAP-tagged protein (beta-2 adrenergic receptor) with a well-characterized cell surface localization, is also included. Lastly, a negative control "blocking agent" (SNAP-Surface Block) is included that interacts with the SNAP-tag, but is not fluorescent. There are two steps to using this system: subcloning and expression of the protein of interest as a SNAP$_f$ fusion, and labeling of the fusion with the SNAP-tag substrate of choice.

Figure 2. Live cell imaging of SNAP$_f$ fusion proteins



Live HEK293 cells transiently transfected with pSNAP$_f$-ADRβ2. Cells were labeled with SNAP-Surface 488 (green) for 15 minutes.



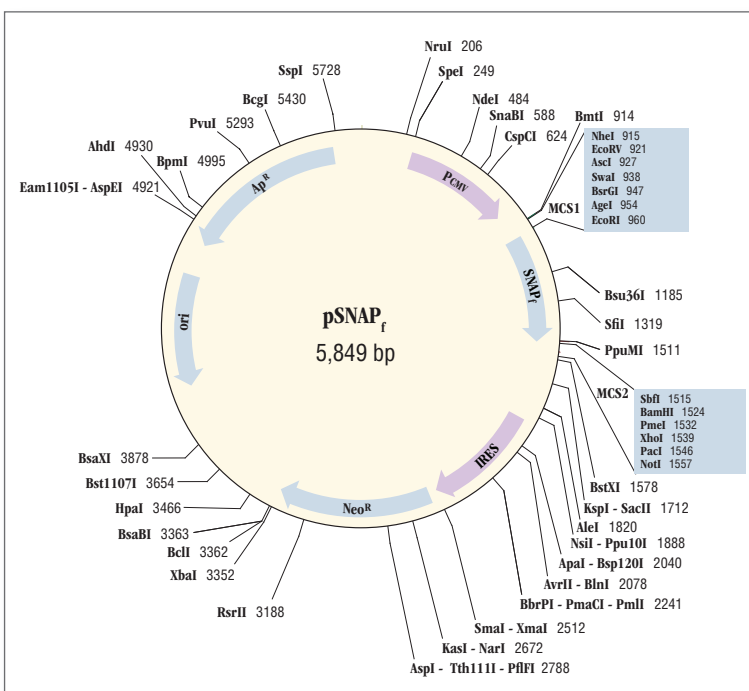
Live CHO-K1 cells transiently transfected with pSNAP$_f$-ADRβ2. Cells were labeled with SNAP-Surface 549 (red) for 15 minutes and counterstained with Hoechst 33342 (blue).

Construction and Expression of SNAP-tag Fusion Proteins:

The mammalian expression plasmid pSNAP$_f$ is intended for the cloning and stable or transient expression of SNAP-tag protein fusions in mammalian cells. This plasmid encodes the SNAP$_f$ gene, which is expressed under control of the CMV promoter. The expression vector has an IRES (internal ribosome entry site) and a neomycin resistance gene downstream of SNAP$_f$ for the efficient selection of stable transfectants. Codon usage of the gene is optimized for expression in mammalian cells. pSNAP$_f$ contains two multiple cloning sites to allow cloning of the fusion partner as a fusion to the N- or C-terminus of the SNAP-tag.

pSNAP$_f$ contains an improved version of SNAP-tag, termed SNAP$_f$. SNAP$_f$ displays faster kinetics in *in vitro* labeling and fast, specific and efficient labeling in live and fixed cell applications, thereby rendering it a desired research tool for analysis of protein dynamics.

Figure 3.



pSNAP$_f$ plasmid map.

Detailed Description of $pSNAP_f$

The sequence of the cloning region can be found in the Appendix. The complete plasmid sequence can be downloaded at www.neb.com. This plasmid encodes the gene $SNAP_f$, which is a mutant form of the gene for human O^6-alkylguanine-DNA-alkyltransferase (hAGT). The codon usage of the gene is optimized for expression in mammalian cells. In the plasmid sequence, the $SNAP_f$ gene is encoded from bp 969 to 1514.

This plasmid is intended for the cloning and stable or transient expression of SNAP-tag protein fusions in mammalian cells. It is particularly suitable for the efficient production of stable cell lines expressing SNAP-tag gene fusions. The plasmid contains the CMV promoter followed by the genes for $SNAP_f$ and neomycin resistance separated by the IRES of the encephalomyocarditis virus (ECMV), which permits the translation of two open reading frames from one messenger RNA. After selection of stable mammalian cells for neomycin resistance, nearly all surviving colonies should therefore stably express the $SNAP_f$ fusion protein. An intron is also included because this is believed to improve expression levels. Unless your expression experiments require a pure population of cells, you can simply use the pool of resistant cells. Otherwise cell clones can be isolated and characterized using standard procedures. The plasmid also contains the beta-lactamase (Ampicillin resistance) gene for maintenance in bacteria. The gene of interest can be cloned upstream or downstream of the $SNAP_f$ coding sequence, as a fusion to the N- or C-terminus of the $SNAP_f$. $pSNAP_f$ can also be used as an expression control plasmid, expressing the SNAP-tag alone, in which case the SNAP-tag protein is distributed throughout the cell. The $SNAP_f$ gene can be isolated from the plasmid using PCR or direct cloning in order to subclone it into a different vector system of choice.

Cloning of SNAP-tag Fusions in $pSNAP_f$ Vector

Cloning by PCR

1. To subclone the gene of interest into $pSNAP_f$ fused to the N-terminus of $SNAP_f$, use the available restriction sites: NheI, EcoRV (blunt), AscI, SwaI (blunt), BsrGI, AgeI or EcoRI, which are located upstream of the SNAP-tag.
2. To subclone the gene of interest into $pSNAP_f$ fused to the C-terminus of $SNAP_f$ use the available restriction sites downstream of the SNAP-tag: SbfI, BamHI, PmeI (blunt), XhoI, PacI or NotI.

Note: When fusing the gene of interest to the C-terminus of $SNAP_f$, note that there is an in-frame stop codon between the PacI and NotI sites, so SbfI, BamHI, PmeI (blunt), XhoI or PacI must be used as the 5´ cloning site for your insert.

PmeI and XhoI cannot be used together for cloning because they share a cytosine as part of their recognition sequences.

Primer Design and Cloning Considerations

1. Design your PCR primers to include a sufficient overlap with the sequence of the gene you want to amplify, adding 5–6 bases on the 5´ side of the introduced restriction site to ensure efficient cleavage prior to cloning.
2. Proteins of interest can be expressed with the SNAP-tag as either an N- or a C-terminal fusion, but note that the tag needs to be exposed to the extracellular surface of the plasma membrane for labeling with the included SNAP-Surface substrates. Note that expression of your protein of interest fused to the C-terminus of $SNAP_f$ may require addition of a surface localization signaling peptide (e.g., from the 5HT3A serotonin receptor, found on the included $pSNAP_f$-ADRβ2 control plasmid) to the free N-terminus of $SNAP_f$.
3. A stop codon can be included at the C-terminus of the fusion (in front of the downstream cloning site) in order to terminate translation at this position.
4. For fusions upstream of $SNAP_f$, ensure that a start codon is included. The addition of a Kozak sequence (e.g. GCCRCCATG, where the start codon is underlined) will increase the translation efficiency.
5. In general, any linker peptide between the proteins should be kept short to avoid degradation by proteases. If required, specific protease cleavage sites can be introduced into the linker peptide.
6. Care should be taken to design the cloning so that the fusion partners in the resulting construct are in frame.
7. Perform the PCR reaction and subsequent cloning steps according to established molecular biology protocols.
8. The ligated vector should be transformed into bacteria and the resulting plasmid isolated via a standard miniprep procedure.
9. After subcloning the gene of interest into $pSNAP_f$ as a fusion with the $SNAP_f$ gene, the resulting plasmid can be used for stable or transient expression of the $SNAP_f$ fusion proteins in a suitable cell line.

Direct Cloning

1. Direct cloning can also be used to make fusions with the SNAP-tag. This is only possible if the fusion partner has compatible sites adjacent to the gene of interest.
2. Care should be taken to design the cloning strategy so that the fusion partners in the resulting construct are in frame.

Note: When fusing the gene of interest to the C-terminus of $SNAP_f$, note that there is a stop codon between the PacI and NotI sites, so SbfI, BamHI, PmeI (blunt), XhoI or PacI must be used as the 5´ cloning site for your insert.

PmeI and XhoI cannot be used together for cloning because they share a cytosine as part of their recognition sequences.

Expression of SNAP-tag Fusions

Transient Expression

Expression of the fusion protein cloned in pSNAP$_f$ can be achieved by transiently transfecting cells in culture with standard transfection protocols. The appropriate reagent and transfection time to permit adequate expression must be empirically determined, using guidelines provided by the manufacturer of the transfection reagent as a starting point. We recommend using pSNAP$_f$ or pSNAP$_f$-ADRβ2 as expression control plasmids. Figure 2 shows that the SNAP$_f$-beta-2 adrenergic receptor fusion protein (from pSNAP$_f$-ADRβ2) gives a surface localized signal when labeled with SNAP-Surface substrates. If the empty pSNAP$_f$ plasmid is used as a control vector for transfection, a uniform distribution of the SNAP-tag between nucleus and cytoplasm should be seen (note that cell-permeable SNAP-Cell substrates must be used to visualize unfused SNAP$_f$). Both pSNAP$_f$ and the localization control plasmids have performed well in stable and transient transfection of CHO-K1, COS-7, U-2 OS and NIH 3T3 cells. Note that the intensity of the fluorescence may vary depending on cell line and labeling substrate used.

Stable Expression

pSNAP$_f$ and pSNAP$_f$-ADRβ2 can be transfected as described above for transient transfection or by other standard transfection methods. Twenty four to 48 hours after transfection begin selecting mammalian cultures in 600–1,200 µg/ml G418 (geneticin) depending on the cell line. It is recommended that you establish a kill curve for each cell line to determine optimal selection conditions. After 8–12 days of continuous selection, stable colonies will become visible. It is possible to use pools of stable cell populations for initial cell labeling to test for the presence of SNAP-tag expression. In addition, monoclonal cell lines can be isolated and characterized if desired.

Use of the SNAP$_f$ Control Plasmid pSNAP$_f$-ADRβ2:

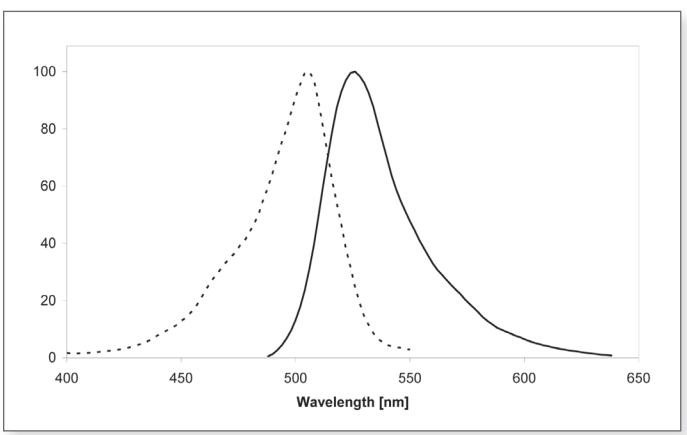
This control plasmid contains the gene encoding the Beta-2 adrenergic receptor cloned as a fusion to the C-terminus of the SNAP$_f$. The signal peptide fused to the N-terminus of SNAP$_f$ is based on the 5HT3A serotonin receptor. The Beta-2 adrenergic receptor is a member of the G protein coupled receptors and mediates the catecholamine-induced activation of adenylate cyclase through the action of G proteins. The SNAP$_f$-Beta-2 adrenergic receptor is inserted in the plasma membrane with the SNAP-tag exposed to the extracellular side of the membrane. When labeled with SNAP-tag substrates, it gives a selective cell membrane fluorescent labeling pattern. (Figure 2). The full sequence and map for pSNAP$_f$-ADRβ2 can be downloaded at www.neb.com. We strongly recommend carrying out parallel expression and labeling experiments with this plasmid as a positive control for your experiment, using the procedure described above.

Labeling SNAP-tag Fusion Proteins:

The kit includes two non-cell-permeable fluorescent SNAP-tag substrates, SNAP-Surface 488 and SNAP-Surface 549. Both can be used to label $SNAP_f$ fusion proteins localized on cell surfaces, or in solution.

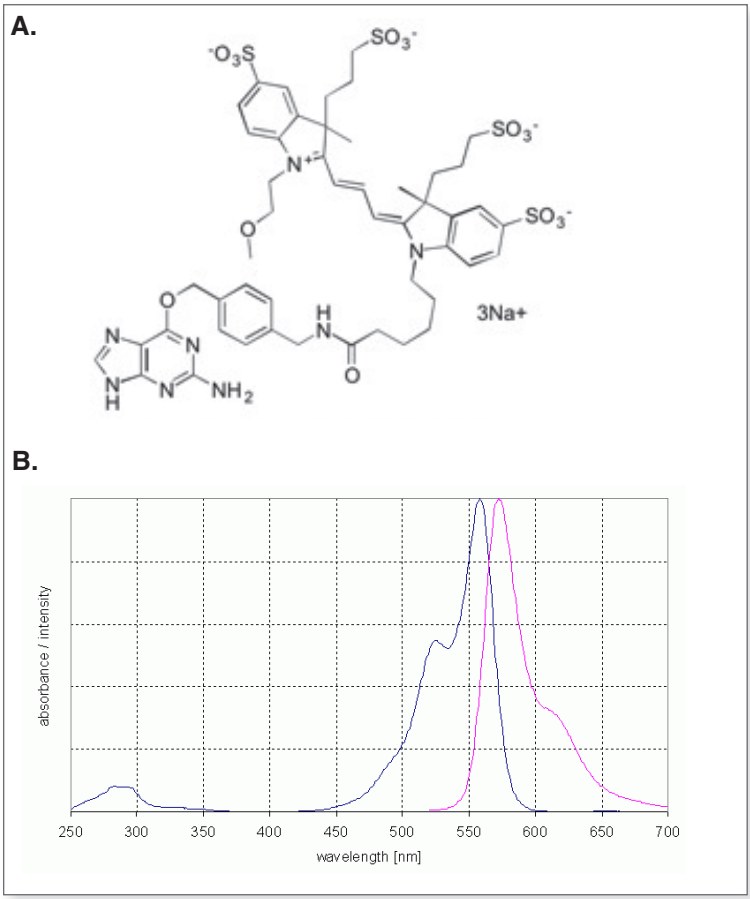
SNAP-Surface 488 (BG-488) is a non-cell-permeable photostable green fluorescent substrate that is based on the ATTO-TEC dye ATTO 488 and is suitable for standard fluorescein filter sets. It has an excitation maximum at 506 nm and an emission maximum at 526 nm (Figure 4). This kit contains 10 nmol of SNAP-Surface 488 substrate, sufficient to make 2 ml of a 5 µM $SNAP_f$ fusion protein labeling solution.

Figure 4.



Excitation (dotted line) and emission (solid line) spectra of SNAP-Surface 488 coupled to SNAP-tag in buffer at pH 7.5.

Figure 5.



(A) Structure of SNAP-Surface 549 (MW 1195.2 g/mol) (B) Excitation (blue line) and emission spectra of SNAP-Surface 549 coupled to SNAP-tag in buffer at pH 7.5.

SNAP-Surface 549 (BG-549) is a non-cell-permeable red fluorescent substrate that is based on the Dyomics dye DY-549 and is suitable for use with standard TAMRA or Cy3 filter sets. It has an excitation maximum at 560 nm and emission maximum at 575 nm. (Figure 5). This kit contains 10 nmol of SNAP-Surface 549 substrate, sufficient to make 2 ml of a 5 µM $SNAP_f$ fusion protein labeling solution.

Instructions for Cellular Labeling

Preparation of Labeling Stock Solution

Dissolve one vial of SNAP-tag substrate (10 nmol) in 10 µl of fresh DMSO to yield a labeling stock solution of 1 mM. Mix by vortexing for 10 minutes until all the SNAP-tag substrate is dissolved. Store this stock solution in the dark at 4°C, or for extended storage at –20°C. Different stock concentrations can be made, depending on your requirements. The substrates are soluble up to at least 10 mM.

Protocol for Cell Surface Labeling Reaction

1. Dilute the labeling stock solution 1:200 in medium to yield a labeling medium of 5 µM SNAP-Surface 488 or SNAP-Surface 549. Mix dye with medium thoroughly by pipetting up and down 10 times (necessary for reducing backgrounds). For best performance, add the SNAP-tag substrate to complete medium, including serum (0.5% BSA can be used for experiments carried out in serum-free media). Do not prepare more medium with SNAP-tag substrate than you will consume within one hour.

NUMBER OF WELLS IN PLATE	RECOMMENDED VOLUME FOR CELL LABELING
6	1 ml
12	500 µl
24	250 µl
48	100 µl
96	50 µl

These recommendations are for culturing cells in polystyrene plates. For confocal imaging, we recommend using chambered coverglass such as Lab-Tek II Chambered Coverglass which is available in a 1, 2, 4 or 8 well format from Nunc (www.nuncbrand.com).

2. Replace the medium on the cells expressing a $SNAP_f$ fusion protein with the SNAP-tag labeling medium and incubate at 37°C, 5% CO_2 for 10–15 minutes.
3. Wash the cells three times with tissue culture medium containing serum.
4. Image the cells using an appropriate filter set. $SNAP_f$ fusion proteins labeled with SNAP-Surface 488 should have an excitation maximum at 506 nm and an emission maximum at 526 nm, and can be imaged with standard fluorescein filter sets. $SNAP_f$ fusion proteins labeled with SNAP-Surface 549 should have an excitation maximum at 560 nm and an emission maximum at 575 nm, and can be imaged with standard TAMRA or Cy3 filter sets.
5. We recommend routinely labeling one well of non-transfected or mock-transfected cells as a negative control.

Notes for Cellular Labeling

Blocking Unreacted SNAP-tag with SNAP-Surface Block

In many cases the labeling of a non-transfected cell sample or a mock-transfected cell sample will be completely sufficient as a control. In some cases, however, it may be desirable to block the SNAP-tag activity in a cell sample expressing the $SNAP_f$ fusion protein to generate a control. This can be achieved using the included nonfluorescent non-cell-permeable SNAP-tag substrate, SNAP-Surface Block (C8-propanoic acid benzylguanine, CBG). SNAP-Surface Block may also be used in pulse-chase experiments to block the SNAP-tag reactivity during the chase between two pulse-labeling steps. A protocol for blocking with SNAP-Surface Block can be found on page 13.

Optimizing Labeling

Optimal substrate concentrations and reaction times range from 1–20 µM and 5–30 minutes, respectively, depending on experimental conditions and expression levels of the $SNAP_f$ fusion protein. Best results are usually obtained at concentrations between 1 and 5 µM substrate and 10–15 minutes reaction time. Increasing substrate concentration and reaction time usually results in a higher background without necessarily increasing the signal to background ratio.

Stability of Signal

The turnover rates of the $SNAP_f$ fusion protein under investigation may vary widely depending on the fusion partner. We have seen half-life values ranging from less than one hour to more than 12 hours. Where protein turnover is rapid, we recommend analyzing the cells under the microscope immediately after the labeling reaction or, if the application allows it, fixing the cells directly after labeling. As an alternative to visualize proteins with fast turnover rates, $SNAP_f$ fusion proteins can be labeled at lower temperatures (4 or 16°C). Labeling times may need to be optimized.

Fixation of Cells

After labeling the $SNAP_f$ fusion proteins, the cells can be fixed with standard fixation methods such as para-formaldehyde, ethanol, methanol, methanol/acetone etc., without loss of signal. We are not aware of any incompatibility of the SNAP-tag label with any fixation method.

Counterstaining

Cells can be counterstained with any live-cell dye that is compatible with the fluorescent properties of the SNAP-tag substrate for simultaneous microscopic detection. We routinely add 5 µM Hoechst 33342 to the labeling medium after the 10–15 minute incubation (Step 2 above) as a DNA counterstain for nuclear visualization. Counterstaining of cells is also possible after fixation and permeabilization.

Immunocytochemistry

Antibody labeling can be performed after SNAP-tag labeling and fixation of the cells according to standard protocols without loss of the SNAP-tag signal. The fixation conditions should be selected based on experience with the protein of interest. For example some fixation methods destroy epitopes of certain proteins and therefore do not allow antibody staining afterwards.

Instructions for Labeling of Proteins *in vitro*

1. Dissolve one vial of SNAP-Surface 488 or SNAP-Surface 549 (10 nmol) in 10 µl of fresh DMSO to yield a labeling stock solution of 1 mM SNAP-tag substrate. Mix by vortexing for 10 minutes until all the SNAP-tag substrate is dissolved. Dilute this 1 mM stock solution 1:4 in fresh DMSO to yield a 250 µM stock for labeling proteins *in vitro*.

2. Set up the reactions, in order, as follows:

COMPONENT	VOLUME	FINAL CONCENTRATION
Deionized Water	32 µl	
5X SNAP-tag Reaction Buffer	10 µl	1X
50 mM DTT	1 µl	1 mM
50 µM SNAP-tag Purified Protein	5 µl	5 µM
250 µM SNAP-tag Substrate	2 µl	10 µM
Total Volume	50 µl	

3. Incubate in the dark for 15 minutes at 37°C.

4. Run sample on an SDS-PAGE gel and detect using a fluorescent gel scanner or store samples at –20°C or –80°C in the dark.

Removal of Unreacted Substrate (optional)

After the labeling reaction you may wish to separate the nonreacted substrate from the labeled $SNAP_f$ fusion protein. You can use gel filtration or dialysis. Please refer to the vendor's instructions for the separation tools you are using.

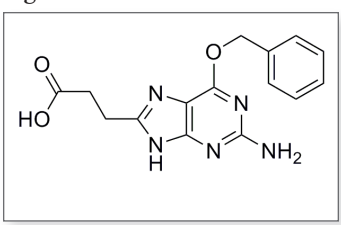
Note for Labeling in vitro

We recommend the routine addition of 1 mM DTT to all buffers used for handling, labeling and storage of the SNAP-tag. The stability of the SNAP-tag is improved in the presence of reducing agents; however it can also be labeled in their absence (e.g. for a redox-sensitive protein) if handling at temperatures above 4°C is minimized. $SNAP_f$ fusion proteins can be purified before labeling, but the labeling reaction also works in non-purified protein solutions (including cell lysates).

Use of SNAP-Surface Block to Block Reactivity of SNAP$_f$ Fusion Proteins:

SNAP-Surface Block (C8-propanoic acid benzylguanine, CBG) is a nonfluorescent non-cell-permeable compound that blocks the reactivity of the SNAP-tag on the surface of live cells (Figure 6). It can be used to generate inactive controls in live and fixed cell labeling experiments performed with SNAP$_f$ fusion proteins. SNAP-Surface Block reacts with the SNAP-tag irreversibly, inactivating it for subsequent labeling steps. This blocker is largely membrane impermeable essentially limiting blocking to cell surface-exposed SNAP-tags.

Figure 6:



Structure of SNAP-Surface Block (MW 313.31 g/mol).

Instructions for Use with SNAP-Surface Substrates

In many cases the labeling of a non-transfected cell sample or a mock-transfected cell sample will be completely sufficient as a negative control for cell labeling. In some cases, however, it may be desirable to block the SNAP-tag activity on the cell surface in a cell sample expressing the SNAP$_f$ fusion protein to generate a control. This is done by a pre-incubation of the cells with SNAP-Surface Block, followed by the incubation with the labeling solution. SNAP-Surface Block may also be used in pulse-chase experiments to block the SNAP-tag reactivity during the chase between two pulse-labeling steps.

SNAP-Surface Block should block > 90% of active SNAP-tag on the cell surface under the conditions given below, however complete blocking is difficult to achieve. SNAP-Surface Block is slightly cell permeable so use of it may slightly reduce signal from intracellular tagged proteins in later labeling steps. This effect is increased when SNAP-Surface Block is used at higher concentrations and for longer incubation times.

Note that SNAP-Surface Block is a potent blocker of the SNAP-tag! Always take care to avoid carryover of SNAP-Surface Block to samples that you do not wish to block.

Preparation of Stock Solution

Dissolve one tube of SNAP-Surface Block (40 nmol) in 10 µl of fresh DMSO to give a stock solution of 4 mM. Mix by vortexing for 10 minutes, until all the SNAP-Surface Block is dissolved. Store this stock solution in the dark at 4°C or for extended storage at –20°C. We recommend using a final concentration of 20 µM, which is a 1:200 dilution of this stock solution.

Blocking SNAP-tag Activity with SNAP-Surface Block

The following steps describe the use of SNAP-Surface Block in a typical control labeling experiment:

1. Prepare two cell samples suitable for labeling, each expressing a surface-localized $SNAP_f$ fusion protein of interest.
2. Mix an appropriate amount of medium with SNAP-Surface Block stock solution in a ratio of 1:200 to give a blocking medium of 20 µM SNAP-Surface Block. For best performance, add the dissolved SNAP-Surface Block to complete medium, including serum. Do not prepare more medium with SNAP-Surface Block than you will consume within one hour.
3. Mix an appropriate amount of medium with DMSO in a ratio of 1:200, to give a final concentration of 0.5% v/v DMSO.
4. Replace the medium on one sample of cells with the blocking medium. These are your blocked cells. Replace the medium on the other sample of cells with the medium containing DMSO. These are your test cells. Incubate both cell samples at 37°C, 5% CO_2 for 10–15 minutes.
5. Remove SNAP-Surface Block or DMSO-containing medium by washing both samples of cells twice with complete medium.
6. Label both cell samples with a SNAP-Surface substrate using the protocol on page 10.
7. Inspect both samples under the fluorescence microscope. The blocked cells should show no fluorescence, whereas the test cells should show fluorescence localized to the cell surface where the $SNAP_f$ fusion protein is present.

Note that there is a constant turnover and resynthesis of proteins in the cell. Protein transport to the membrane and internalization followed by degradation or recycling, are constantly ongoing processes. After having blocked all existing $SNAP_f$ fusion proteins on the cell membrane, newly synthesized protein may be transported to the cell surface and may get labeled during incubation with a fluorescent SNAP-tag substrate. This will give the impression that the blocking was ineffective. In order to minimize these effects of protein synthesis and protein transport, cells may have to be treated with cycloheximide and incubation with the fluorescent SNAP-tag substrate may have to be performed at 4°C.

Troubleshooting:

Cloning of the Gene of Interest

If subcloning of the gene of interest into the pSNAP$_f$ vector does not work, reconfirm all the cloning steps (primer design, choice of restriction site, etc.). If all steps are confirmed as being correct, then try the cloning using different restriction sites. Be sure to include a positive and negative control for the ligation reaction. Alternatively try to subclone the SNAP$_f$ gene into an expression vector already containing your gene of interest.

Expression

In general we have not experienced problems expressing SNAP$_f$ protein fusions. However if your fusion protein does not appear to be expressed, try expressing the SNAP$_f$-ADRβ2 protein fusion as a positive control using cells transiently transfected with the included pSNAP$_f$-ADRβ2 control plasmid. Labeling of such cells with a fluorescent SNAP-Surface substrate should show strong surface-localized fluorescence. The empty pSNAP$_f$ plasmid can also be used as a control (uniform cytosolic and nuclear fluorescence when using cell-permeable SNAP-Cell substrates). Note that the intensity of this fluorescence may vary depending on cell line and substrate used. Expression of localization controls but not your fusion protein can be due to a variety of causes. It is possible that this fusion protein may be toxic for your cell line. It is difficult to troubleshoot such instances, but the use of a different expression plasmid or cell line or tagging the opposite end of the protein may help. Signs of host cell toxicity could include slow proliferation or apoptosis. Counterstaining live cells with Hoechst 33342 or fixed cells with DAPI can be used to determine whether nuclei are healthy if toxicity is suspected.

Problems with Cellular Labeling

No Labeling

If no labeling is seen, the most likely explanation is that the fusion protein is not expressed. Verify your transfection method to confirm that the cells contain the fusion gene of interest. If this is confirmed, check for expression of the SNAP$_f$ fusion protein. If no antibody against the fusion partner is available, Anti-SNAP-tag Antibody (NEB #P9310) can be used. Alternatively, SNAP-Vista® Green (NEB #S9147) can be used to confirm presence of SNAP$_f$ fusion in cell extracts following SDS-PAGE, without the need for Western blotting. An alternate explanation is that the SNAP$_f$ is fused to the end of the protein that is not localized on the extracellular surface of the cell membrane; reversing the orientation of the fusion protein may solve this problem.

Weak Labeling

Weak labeling may be caused by insufficient exposure of the fusion protein to the substrate. Try increasing the concentration of SNAP-tag substrate and/or the incubation time within the range of 1– 20 µM and 5–30 minutes, respectively. Alternatively the protein may be poorly expressed and/or turn over rapidly. If the protein has limited stability in the cell, it may help to analyze the samples immediately after labeling.

High Background

Background fluorescence may be controlled by reducing the concentration of SNAP-tag substrate used, and by shortening the incubation time. The presence of fetal calf serum or BSA during the labeling incubation should reduce non-specific binding of substrate to surfaces.

Signal Strongly Reduced after Short Time

If the fluorescence signal decreases rapidly, it may be due to instability of the fusion protein. The signal may be stabilized by fixing the cells. Alternatively try switching the SNAP-tag from the N- to the C-terminus or vice versa. Photobleaching is generally not a problem as both SNAP-Surface 488 and SNAP-Surface 549 are very photostable. However, if you experience problems with photobleaching, addition of a commercially available anti-fade reagent may be helpful.

Problems with Labeling *in vitro*

Solubility

If solubility problems occur with your $SNAP_f$ fusion protein, we recommend testing a range of pH (pH 5.0–pH 10.0). The salt concentration may also need to be optimized for your particular fusion protein (50–250 mM).

Loss of Protein due to Aggregation or Sticking to Tube

If stickiness of the fusion protein is a problem we recommend adding Tween 20 at a final concentration of 0.05% to 0.1%. The SNAP-tag activity is not affected by this concentration of Tween 20.

Incomplete Labeling

If exhaustive labeling of a protein sample is not achieved using the recommended conditions, try the following protocol modifications: Increase the incubation time to two hours total at 25°C or to 24 hours at 4°C; or halve the volume of protein solution labeled. Both approaches may be combined. If you still have poor labeling results, we recommend checking the activity of the SNAP-tag using SNAP-Vista Green (NEB #S9147).

If the $SNAP_f$ fusion has been stored in the absence of DTT or other reducing agent, or has been stored at 4°C for a prolonged period, its activity may be compromised. Include 1 mM DTT in all solutions of the $SNAP_f$ fusion protein, and store the fusion protein at –20°C.

Using less than the recommended amount of substrate stock solution (1%) can significantly slow down the reaction rate.

Loss of Activity of Protein of Interest

If your fusion protein is particularly sensitive to degradation or to loss of activity, you can try reducing the labeling time or decreasing the labeling temperature. If you label at 4°C we recommend overnight incubation.

Appendix:
Sequence of SNAP-tag Region of pSNAP$_f$ Vector

Unique restriction sites in the regions flanking the SNAP$_f$ gene are displayed above the coding strand. The complete sequence of pSNAP$_f$ and pSNAP$_f$-ADRβ2 can be downloaded at www.neb.com.

```
    NheI  EcoRV  AscI      SwaI   BsrGI  AgeI  EcoRI
...GCTAGC GATATCGGCG CGCCAGCATT TAAATCTGTA CAGACCGGTG AATTC
   CGATCG CTATAGCCGC GCGGTCGTAA ATTTAGACAT GTCTGGCCAC TTAAG...

                                XhoI
    SbfI   BamHI    PmeI        PacI      NotI
...CCTGCA GGCGGATCCG CGTTTAAACT CGAGGTTAAT TAATGAGCGG CCGC
   GGACGT CCGCCTAGGC GCAAATTTGA GCTCCAATTA ATTACTCGCC GGCG...
```

Note

NEB 10-beta Competent *E. coli* (High Efficiency) (NEB #C3019) is recommended for propagating and subcloning of the vector and control plasmid. If using the ClaI site for subcloning, *dam-/dcm-* Competent *E. coli* (NEB #C2925) is recommended. The restriction endonuclease ClaI (NEB #R0197) is methylation sensitive.

Ordering Information

PRODUCT	NEB #	SIZE
SNAP-Surface Starter Kit	E9120S	10 reactions
COMPANION PRODUCTS		
SNAP-Vista Green	S9147S	50 nmol
SNAP-Vista Blue	S9146S	50 nmol
SNAP-Biotin®	S9110S	50 nmol
pSNAP-tag(T7)-2 Vector	N9181S	20 µg
$pSNAP_f$-ADRβ2 Control Plasmid	N9184S	20 µg
$pSNAP_f$-H2B Control Plasmid	N9186S	20 µg
$pSNAP_f$-Cox8A Control Plasmid	N9185S	20 µg
SNAP-Surface 425	S9126S	50 nmol
SNAP-Surface Alexa Fluor® 488	S9129S	50 nmol
SNAP-Surface 488	S9124S	50 nmol
SNAP-Surface 532	S9131S	50 nmol
SNAP-Surface Alexa Fluor 546	S9132S	50 nmol
SNAP-Surface 549	S9112S	50 nmol
SNAP-Surface 594	S9134S	50 nmol
SNAP-Surface Alexa Fluor 647	S9136S	50 nmol
SNAP-Surface 647	S9137S	50 nmol
SNAP-Surface 682	S9139S	50 nmol
SNAP-Surface 782	S9142S	50 nmol
SNAP-Surface Block	S9143S	200 nmol
Anti-SNAP-tag Antibody (Polyclonal)	P9310S	100 µl
SNAP-tag Purified Protein	P9312S	100 µg

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