MSD® TAG-NHS-Ester

INTRODUCTION

This note describes how to label proteins of MW > 10,000 using MSD TAG-NHS-Ester. The procedure involves a 1 hour incubation step followed by a simple column separation to isolate the labeled protein.

MSD TAG-NHS-Ester, or Ruthenium (II) tris-bipyridine, N-hydroxysuccinimide is an amine-reactive label often used for detection in assays formatted with MSD technology (Figure 1). N-hydroxysuccinimide esters readily couple to primary amine groups of proteins to form a stable amide bond. The reaction is favored at slightly alkaline pH in which a nucleophilic attack by an unprotonated amine on an ester results in amide bond formation. The reaction is rapid and occurs under mild conditions.

MSD TAG-labeled conjugates are stable and may be used at low concentrations. These features minimize time, costs, and labor since large, stable batches of conjugate can be prepared, validated, and used for long periods of time. MSD TAG-NHS-Ester is a popular conjugate for labeling molecules that contain primary amines (e.g., lysines in proteins) since the method is fast and easy.

PREPARATION OF MSD TAG-PROTEIN CONJUGATES

General Considerations

To minimize the competition of water (hydrolysis of the NHS ester) with the protein, dissolve the MSD TAG-NHS-Ester in an anhydrous solvent such as dimethyl sulfoxide (DMSO) just prior to addition of the NHS ester to the reaction mixture. The reconstituted solution is unstable and any unused material should be discarded. Consider labeling more than one protein at the same time to maximize the use of the MSD TAG-NHS-Ester.

The optimal MSD TAG:protein labeling ratio should be determined empirically. For immunoassay applications, typical MSD TAG:antibody (IgG) molar challenge ratios

MSD Technology

MSD's products are based on

MULTI-ARRAY™ technology, a proprietary combination of patterned
arrays and electrochemiluminescence detection. Patterned arrays
enable large numbers of measurements through miniaturization,
organization and parallel processing of biological assays.

Electrochemiluminescence detection offers a unique combination
of sensitivity, dynamic range and
convenience.

FIGURE 1

Ruthenium (II) tris-bipyridine, N-hydroxysuccinimide

are 4:1, 8:1, and 12:1. If reagents are limited, an 8:1 molar challenge ratio is recommended. The best challenge ratio to use with other proteins may differ and will depend on various factors including the size of the protein and the number of lysines available for coupling. Under typical labeling conditions using a 1 mg/ml lgG solution, approximately 30-40% of MSD TAG label is incorporated into the protein. Optimal assay performance is often obtained with MSD TAG:protein molar incorporation ratios between 2:1 and 6:1. Excessively high labeling ratios can increase non-specific binding and/or cause precipitation of the protein. In general, labeling with high protein concentrations (\geq 1 mg/ml) and slightly alkaline (i.e., pH 7.8) PBS solutions containing no preservatives yields the best labeling efficiency. When preparing multiple batches of labeled protein, it is important to maintain conditions (protein concentration, buffer type, label concentration, incubation time, shaking or not, temperature, etc.) to achieve consistent assay results.

This method describes the labeling procedure for proteins of MW \geq 10,000. If the protein/polypeptide to be labeled has a lysine and a MW <10,000, you may still be able to use this conjugate but conditions for labeling and separation must be modified. For example, a gel filtration resin with a smaller MW cutoff or an alternative separation method independent of molecular size may be needed. MSD offers a variety of services for the custom labeling of proteins, peptides and non-proteinaceous molecules.

This labeling method uses the following materials:

- 1. Phosphate buffered saline (PBS), pH 7.8, without preservatives
- 2. PBS Buffer, pH 7.2, containing 0.05-1% (w/v) NaN₃
- 3. 2 M glycine
- 4. Polypropylene microcentrifuge tubes
- 5. Shaker (optional)
- 6. Sephadex® G-25 size exclusion columns, such as PD-10 or NAP®-5 (Amersham Biosciences)
- 7. Spectrophotometer capable of an OD₄₅₅ measurement
- 8. A protein quantitation assay, such as BCA, Bradford or Lowry

RECOMMENDED PROCEDURE

- 1. Prepare a 1 mg/ml solution of a *purified* protein in PBS, pH 7.8. Other buffers can be used, but they should be free of amines (tris- and glycine-containing buffers cannot be used) and preservatives. Affinity-purified IgG's are often eluted using high molarity glycine solutions so it is very important that they are properly desalted prior to labeling. Samples containing sodium azide or EDTA should be desalted or dialyzed prior to labeling. Dilute proteins should be concentrated to >0.2 mg/ml. Ultra-filtration concentrating devices can be used to achieve both buffer exchange and concentration of the protein. Protein concentrations should be confirmed prior to labeling. To calculate protein recovery following labeling and purification, MSD recommends a colorimetric protein assay kit (e.g., Bradford or BCA method) for both the pre- and post-labeling determinations. The MSD TAG label will affect OD₂₈₀ absorbance readings so this method cannot be used for calculation of the labeled protein.
- 2. Use the formulas on the worksheet provided (also shown below) to calculate the amount of MSD TAG-NHS-Ester stock solution needed for the labeling reaction. An example calculation for the labeling of 1000 µl of a 1 mg/ml solution of IgG (MW 150,000) with an 8:1 molar excess of MSD TAG-NHS-Ester (MW 1057) is also shown.

FORMULA

First, determine the mass of MSD TAG label required for labeling:

<u>Protein Conc. (mg/ml)</u> x (MW of MSD TAG) x (Challenge ratio) x (Vol. to label in μ l) = μg MSD TAG MW protein

then, using this value, determine the volume of MSD TAG stock solution required:

μg MSD TAG ÷ Conc. MSD TAG stock solution (μg/μl) = μl MSD TAG stock solution required

FOR EXAMPLE

(1 mg/ml Prot. Conc.) x (1057 MW MSD TAG) x (8 ratio) x (1000 µl IgG solution) = **56.4 µg MSD TAG** (150,000 MW IgG)

then

56.4 μ g MSD TAG \div 1.5 (μ g/ μ l) Conc. MSD TAG stock solution = 37.6 μ l MSD TAG stock solution required



Note that the % (v/v) of DMSO in the reaction should never exceed 15% (v/v) or the reaction will be progressively inhibited. If high concentrations are needed, a more concentrated labeling stock should be prepared so that less organic solvent is added to the protein solution.

- 3. Immediately before use, prepare the MSD TAG-NHS-Ester stock solution by adding 50 μ l of DMSO to the vial. Twirl the vial gently to wet the bottom and lower sides of the vial with the DMSO. This volume of DMSO easily dissolves the available sizes of MSD TAG-NHS-Ester (0.075 mg, 0.150 mg, and 0.500 mg) yielding stocks of 1.5, 3, and 10 μ g/ μ l, respectively.
- 4. Add the calculated volume of MSD TAG-NHS-Ester solution to the protein solution and vortex the tube. Discard the remaining MSD TAG-NHS-Ester.
- 5. Incubate the tube contents at room temperature for 60 minutes, with or without shaking. Shaking the solution will improve the incorporation efficiency.
- 6. Stop the reaction by adding 20 µl of 2 M glycine and incubate at room temperature for 10 minutes.
- 7. To remove the uncoupled MSD TAG label, load the mixture onto a size exclusion purification column that is equilibrated with PBS containing 0.05-0.1% (w/v) sodium azide. Prepacked Sephadex G-25 columns such as PD-10 columns for 1 ml volumes or NAP-5 columns for volumes up to 0.5 ml (Amersham Biosciences) are very convenient to use. MSD does not recommend dialysis of MSD TAG conjugates or the use of membrane-based spin columns to separate labeled protein from free MSD TAG. For larger sample volumes, a longer column with a larger bed volume may be needed. Two yellow bands will be formed as the separation of bound from free MSD TAG proceeds. The labeled protein will elute first, the second yellow band corresponds to the unreacted MSD TAG. When using a PD-10 column to purify the conjugate, eight 0.5 ml fractions are typically collected after the sample volume has entered the PD-10 resin bed. A protein such as IgG is usually in the fourth fraction.
- 8. Determine the protein concentration using a standard protein assay (e.g., Bradford, Lowry, or a Pierce BCA Protein Assay kit). As mentioned above, an absorbance reading at OD₂₈₀ is not recommended since MSD TAG will absorb light at this wavelength. Collect and pool the appropriate protein-containing fractions and determine the final pooled protein concentration and molarity. The percent protein recovered is dependent upon the separation technique but typically ranges from 70-90%.
- 9. Measure the absorbance of the MSD TAG-IgG conjugate at 455 nm using a 1 cm path cuvette. Divide the value by 13,700 to obtain the MSD TAG concentration in moles per liter.
- 10. To calculate the MSD TAG:IgG ratio, divide the value obtained in step 9 by the value determined for step 8. The formula is also provided on the attached worksheet
- 11. Stabilize dilute protein solutions (<0.1 mg/ml) by adding additional proteins such as 1-3% (w/v) bovine serum albumin or other appropriate serum proteins. Antibody conjugates are usually stable for at least 12 months at 4 °C, but the stability of other proteins should be assessed. Many proteins require storage at < -20 °C. For long term storage, labeled conjugates should be stored in amber or opaque vials. Aliquots of the conjugate can usually be stored frozen as long as the protein is stable to freeze-thaw cycles.

STORAGE, STABILITY & HANDLING

MSD TAG-NHS-Ester is supplied as a dry orange to dark red solid (appears as a film on the vial) which is stable for at least 18 months from date of manufacture when stored frozen (-10 to -30° C) and desiccated. After reconstitution of the reagent with anhydrous solvent any unused material should be discarded.

Note: MSD TAG-NHS-Ester is light sensitive, therefore, MSD TAG-protein conjugates should be stored in light shielded containers such as amber polypropylene vials.

Labeling Worksheet for MSD TAG-NHS-Ester:

This worksheet is intended to be used as a guide while following the MSD Labeling Method. Refer to the MSD Labeling Method text for instructions and examples.

Protein to be Labeled:	Concentration:				
Vendor:	Catalog No				
Lot No.	Date:				
Labeling Buffer:	Vendor:				
Lot No.					
Storage Buffer:	Vendor:				
Lot No.					
2 M Glycine Lot No					
DMSO Source:	Lot No Date				
SD TAG-NHS-Ester reconstitution and use					
Vial Size:					
Lot No.					
Volume of DMSO Added:					
Concentration of MSD TAG Solution:					

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	($\underline{\text{mg/ml Protein Conc.}}$) x (1057 MW MSD TAG) x ($\underline{\text{mg/ml Protein Conc.}}$) x ($\underline{\text{1057 MW MSD TAG}}$) x ($\underline{\text{mg/ml Protein Conc.}}$)	μl) = μg MSD TAG-NHS-Ester			
	Next, divide the micrograms of label determined above by the concentration This will give you the volume of MSD TAG-NHS-Ester stock solution to be a				
	μg MSD TAG ÷ μg/μl MSD TAG stock solution = μl	MSD TAG stock solution required			
	μl of MSD TAG Solution Added and Incubation Started at:				
	With or Without Shaking:				
	Time of Addition of 20 μl of 2 M Glycine:				
	Calculation and Work Performed By:	_ Date:			
	Desalting Method:	_Date:			
	Protein Concentration Post-Labeling:	_ Assay Method:			
	OD ₄₅₅ Reading:				
Form	ula for Calculation of MSD TAG Incorporation				
10111	Concentration of Protein (mg/ml), ÷ Molecular Weight Prot	ein (lgG=150,000) = (A)M			
	OD ₄₅₅ Results				
	Ratio of MSD TAG to PROTEIN = (B), ÷ (A)	=			
ĺ	Protein Added to Storage Buffer? Yes (type)	_ No			
	Storage Temperature and Location:	_ Date			
	Work Performed by:	_ Reviewed By/Date:			

Ordering Information

Product	Size	Catalog Number
MSD TAG-NHS-Ester	150 nmol	R91BN-1
	500 nmol	R91BN-2
	Larger sizes	Please Inquire

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