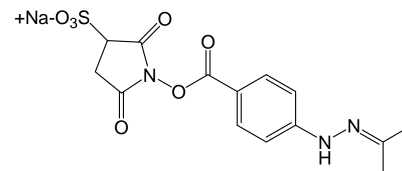
sulfo-S-HyNic

$C_{14}H_{14}N_3NaO_7S$ MW 391.33
S-1011-105; S-1011-010



Introduction to SoluLinK Bioconjugation Technology

SoluLinK's core technology is based on the formation of a stable aromatic bond that has a UV-traceable signal to indicate the real-time formation of the conjugate. This bond is a bis-arylhydrazone formed from an aromatic hydrazine and an aromatic aldehyde. S-HyNic **1** (succinimidyl 6-hydrazinonicotinate acetone hydrazone, SANH) is used to incorporate aromatic hydrazine moieties on biomolecules. S-HyNic is an amino-reactive reagent that directly converts amino groups on biomolecules and surfaces to HyNic groups. S-4FB **2** (succinimidyl 4-formylbenzoate, SFB) is used to convert amino groups to aromatic aldehydes (4-formylbenzamide (4FB) groups). Addition of a HyNic-modified biomolecule to a 4FB-modified biomolecule or surface directly leads to the formation of the conjugate (Figure 1). The bis-arylhydrazone bond is stable to 92°C and pH 2.0-10.0. The recommended pH for antibody conjugation is 6.0. Unlike thiol-based conjugation protocols where reducing reagents are required that that can compromise the activity of proteins by cleaving disulfide bonds, the HyNic-4FB conjugation couple leaves disulfide bonds intact. No oxidants, reductants or metals are required in the preparation of conjugate.

Dirksen *et al.*[1] show that aniline catalyzes the formation of this Schiff's base. This is especially effective for large biomolecule conjugations. In the case of antibody-protein conjugations the addition of 10 mM aniline to the reaction mixture converts >95% of the antibody to conjugate in ~2 hours using 1-2 mole equivalents of second protein.

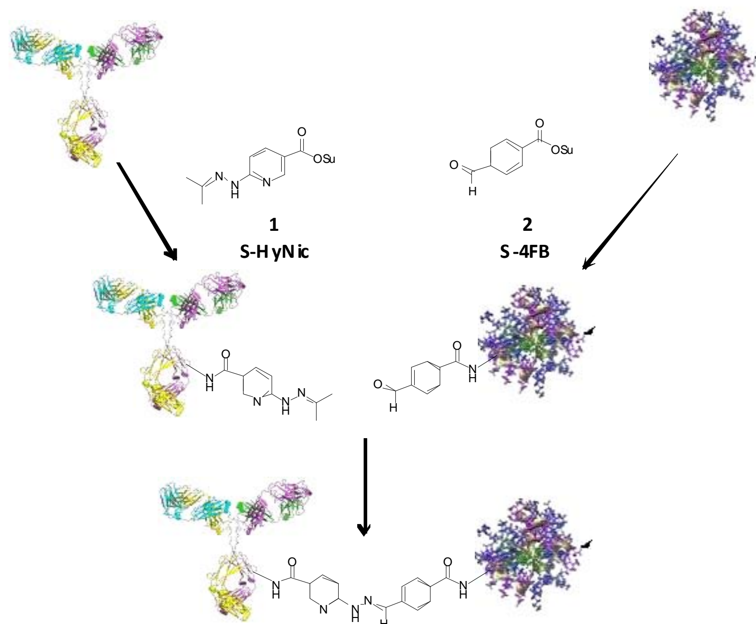


Figure 1: Schematic representation of SoluLinK Bioconjugation chemistry where an antibody is modified with S-HyNic to incorporate HyNic groups and a second protein is modified with S-4FB to incorporate 4FB groups. Conjugate is formed directly by simply mixing the HyNic-modified antibody with the 4FB-modified proteins.

The HyNic-4FB conjugation couple is chromophoric- the conjugate bond absorbs at 354 nm and has a molar extinction coefficient of 29000. This allows (1) real time spectrophotometric monitoring of a conjugate reaction, (2) ability to 'visualize' the conjugate during chromatographic purification using a UV or photodiode array detector and (3) quantification of conjugation. Furthermore, the level of incorporation of 4FB groups can be quantified colorimetrically as reaction with 2-sulfo-benzaldehyde (SoluLinK catalog# # S-2005-100). This reaction yields a chromophoric product that absorbs at A360 with a molar extinction coefficient of 20000 (Figure 2). Links to procedures and calculators to guide users through this process are given in the procedures below.

sulfo-S-HyNic (Solulink catalog: S-1011-105 (5 X 1.0 mg) and S-1011-010 (10 mg)) is a sulfo-NHS ester that converts amines on biomolecules and surfaces to HyNic groups. sulfo-S-HyNic is recommended for modification of any amino surfaces such as beads and quantum dots.

Methods

Note: This Protocol and all links below can be downloaded at http://www.SoluLinK.com/protocols.php

Additional Materials Required

Reagents	**Equipment**
Desalting spin columns (cat # S-4004-025)	Variable-speed bench-top microcentrifuge
Modification Buffer (cat # S-4003-005)	Spectrophotometer or Plate Reader
Conjugation Buffer (cat # S-4002-005)	1.5 mL microcentrifuge tubes
DMF (anhydrous) (cat # S-4001-005)	2-sulfo-benzaldehyde (S-2005-100)

Modification Procedure

A. Desalting procedure (More detailed protocols at LINK)

1. Desalt/buffer exchange the protein into Modification Buffer (100 mM sodium phosphate, 150 mM sodium chloride, pH 7.4).

Notes:

a) It is necessary to remove all free amine-containing contaminants, *e.g.* tris, glycine, from the protein solution before modification.

b) High-level buffering capacity, *i.e.* 100 mM phosphate, is necessary for successful modification.

c) For desalting proteins SoluLinK recommends Pierce Zeba Desalt Spin columns (# 89882); for oligonucleotides, Sartorius Vivaspin diafiltration units (#VS0112). Refer to desalting protocol for either apparatus.

B. Determine the concentration of the protein (More detailed protocols at LINK)

1. Determine the concentration of the protein to be modified using the BCA assay (ThermoScientific, #23223) or spectrophotometrically if the extinction coefficient of the protein is known.
2. Bring the concentration to 1-5 mg/mL in Modification Buffer pH 7.4

C. Prepare a sulfo-S-HyNic/DMF stock solution

1. Prepare a stock solution of sulfo-S-HyNic in anhydrous DMF (or DMSO) or aqueous buffer by dissolving 2-4 mg of sulfo-S-4FB in 100 µL anhydrous DMF or in aqueous buffer.

Note:

a) The sulfo-S-HyNic/DMF stock solution is stable for 2 weeks if prepared with anhydrous DMF (SoluLinK catalog# S-4001-010) and stored desiccated.

b) Stock solution prepared in buffer must be used immediately.

IgG concentration	sulfo-S-HyNic mole equivalents added	Determined ratio of HyNic/protein
1.0	20	5.5
	30	8.2
4.0	15	4.7
	20	6.4
	25	7.8

Table 1: The number of HyNic groups incorporated on an antibody is dependent on the number of mole equivalents sulfo-S-HyNic added and the protein concentration. This table can be used as a general guide for modification of any protein with a succinimidyl-based modification reagent.

D. Modification of protein (More detailed protocols at LINK) and of oligonucleotides (LINK)

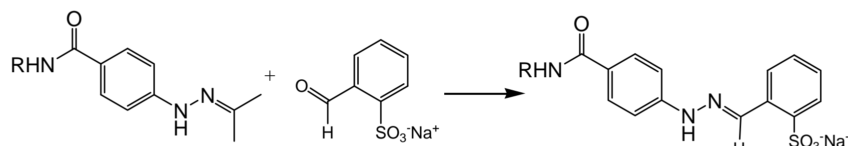
1. Using Table 1 as a guide, add the requisite volume of sulfo-S-HyNic stock solution to the protein solution.
2. Allow reaction to incubate at room temperature for 2.0 hours.

E. Desalting procedure (detailed protocols at LINK)

1. Desalt/buffer exchange the protein into Conjugation Buffer (0.1M sodium phosphate, 0.15M sodium chloride, pH 6.0). For proteins SoluLinK recommends Pierce Zeba Desalt Spin columns (# 89882) or for oligonucleotides SoluLinK recommends Sartorius Vivaspin diafiltration units (#VS0112). Refer to desalting protocol for either apparatus.

F. Quantifying modification level (detailed protocols at LINK)

1. The molar substitution ratio (MSR) can be determined using a colorimetric reaction outlined in Figure 2. Addition of 2-sulfobenzaldehyde to a HyNic-modified biomolecule yields a bis-arylhydrazone that absorbs at 350 nm. Calculator/protocols can be downloaded from: LINK



2. The biomolecule is now 4FB-modified and ready for conjugation to HyNic-modified biomolecules and surfaces.

Troubleshooting

Problem	Possible Cause	Solution
Protein was not modified or poorly modified.	Protein has been contaminated with amine containing compounds	Desalt the protein more thoroughly with a new Zeba Spin column or VivaSpin diafiltration device
	The concentration of the protein was too low	Increase the concentration of the protein to >2.0 mg/mL
sulfo-S-HyNic was hydrolyzed	Wet or poor quality DMF/DMSO hydrolyzed the NHS ester	Use a good quality anhydrous DMF/DMSO to solubilize sulfo-S-HyNic.

Stability

The stability of HyNic groups on proteins and other biomolecules varies. **It is recommended to conjugate HyNic-modified biomolecules immediately.**

Related SoluLinK Products

S-9002-2 S-HyNic Kit
S-1010-037 SS-S-4FB Linker
S-4003-005 Modification Buffer
S-4004-025 VivaSpin diafiltration device
S-4001-005 DMF anhydrous
S-4002-005 Conjugation Buffer
S-2005-100 2-sulfo-benzaldehyde
S-4011-005 Aniline
S-4012-005 Aniline conjugation buffer

References

1. Dirksen, A., et al., Nucleophilic catalysis of hydrazone formation and transimination: implications for dynamic covalent chemistry. J Am Chem Soc, 2006. 128(49): p. 15602-3.
2. Igor A. Kozlov, Peter C. Melnyk, Katie E. Stromsborg, Mark S. Chee, David L. Barker, Chanfeng Zhao, Efficient strategies for the conjugation of oligonucleotides to antibodies enabling highly sensitive protein detection, Biopolymers 2004, ***73***, 621.
3. Ryan C. Bailey, Gabriel A. Kwong, Caius G. Radu, Owen N. Witte, and James R. Heath, DNA-Encoded Antibody Libraries: A Unified Platform for Multiplexed Cell Sorting and Detection of Genes and Proteins, J. Amer. Chem. Soc. 2007, **129**, 1959-1967.