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# **Product Information**

SILu™Prot Insulin, human recombinant, expressed in *P. pastoris* SIL MS Protein Standard, <sup>15</sup>N-labeled

Catalog Number **MSST0064** Storage Temperature –20 °C

## **Product Description**

SILu<sup>™</sup>Prot Insulin is a recombinant, <sup>15</sup>N stable isotopelabeled, human insulin (INS), expressed in *P. pastoris*. Insulin is a small protein consisting of two polypeptide chains (A chain and B Chain) interconnected by two disulfide bonds.<sup>1</sup>

	<sup>15</sup> N labeled Insulin (**)	Native Insulin (***)	Measured/ Theoretical Mass shift (****)
A chain (*)	2408.5	2383.7	24.8/25.0
B chain (*)	3468.7	3429.9	38.8/39.0
Whole molecule	5871.2	5807.6	63.6/64.0

<sup>\*</sup> Reduced form

Each vial contains 10–13 μg of SILu™Prot Insulin standard, lyophilized from a solution of 1% acetic acid. Vial content was determined by HPLC using unlabeled insulin as a calibrator. Quantitation by Amino Acid Analysis is 90% for this protein.

<u>Purity</u>: ≥95% (HPLC)

Heavy nitrogen incorporation efficiency: ≥97% (MS)

UniProt: P01308

Sequence Information:

A chain:

**GIVEQCCTSICSLYQLENYCN** 

B chain:(\*\*\*\*\*)

FVNQHLCGSHLVEALYLVCGERGFFYTPKT (\*\*\*\*\*\*) All amino acids are labeled with <sup>15</sup>N except Thr<sup>30</sup> (B Chain)

#### **Precautions and Disclaimer**

This product is for R&D use only, not for drug, household, or other uses. Please consult the Safety Data Sheet for information regarding hazards and safe handling practices.

#### **Preparation Instructions**

Briefly centrifuge the vial before opening. It is recommended to reconstitute the protein with 2% acetic acid to the final concentration of 100 µg/ml.

## Storage/Stability

Store the lyophilized product at -20 °C. The product is stable for at least 2 years as supplied.

After reconstitution, it is recommended to store the protein in working aliquots at –20 °C.

#### Reference

 Nikol, D.S., and Smith, L.F., Amino Acid sequence of human insulin. Nature, 187, 483–485 (1960).

# **Legal Information**

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<sup>\*\*</sup> Average mass measured on qTOF mass spectrometer

<sup>\*\*\*</sup> Theoretical average mass

<sup>\*\*\*\*</sup> Theoretical mass shift assuming 100% <sup>15</sup>N incorporation