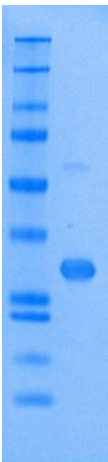


SIL-TNNI protein standard – Uniform ¹⁵ N labelling	
Human Troponin I (Uniprot accession number P19429)	
Product Description	<p>Troponin I is one subunit of the Troponin complex. It is the inhibitory subunit of troponin, the thin filament regulatory complex which confers calcium-sensitivity to striated muscle actomyosin ATPase activity. It consists of 210 amino acids.</p> <p>Recombinant human Troponin I was expressed in <i>E. coli</i> with purification tag and purified using proprietary method including ion exchange and size exclusion chromatography.</p>
Protein sequence	MSGSHHHHHHSSGIEGRADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKSKISA SRKLQLKTLILLQIAKQELEREAEERRGEKGRALSTRCQPLELAGLGFALQDLCRQLHAR VDKVDEERYDIEAKVTKNITEIADLTQKIFDLRGKFKRPTLRRVRISADAMMQALLGARAK ESLDRALHLKQVKKEDTEKENREVGDWRKNIDALSGMEGRKKKFFES
Predicted Molecular Mass	25.75 kDa
Expression system	<i>E. coli</i>
Purity	Greater than 95% as determined by SDS-PAGE analysis
Labelling	Uniform labelling on all amino acids with ¹⁵ N. U-15N incorporation >99% as determined by LC-MS/MS analysis of trypsin digested SIL-protein
Tag information	polyHis-tag at the N-terminus
Protein Content	Quantitation is carried out by Bradford protein assay
Formulation	Lyophilized from 20 mM Tris pH8.0 buffer. Centrifuge the vial prior to opening. Reconstitute by adding 20 mM Tris pH8, 5 mM DTT buffer.
Shipping and storage	The product is supplied as a lyophilized powder and shipped at room temperature. Store at -20°C upon receipt. After reconstitution, protein can be kept at 4°C for a few weeks.
Usage	The product is for research use only. Not for diagnostic or therapeutic use.



150 kDa _
100 kDa _
75 kDa _
50 kDa _
37 kDa _
25 kDa _
20 kDa _
15 kDa _
10 kDa _

SIL-TNNI protein standard – Uniform ¹⁵N labelling

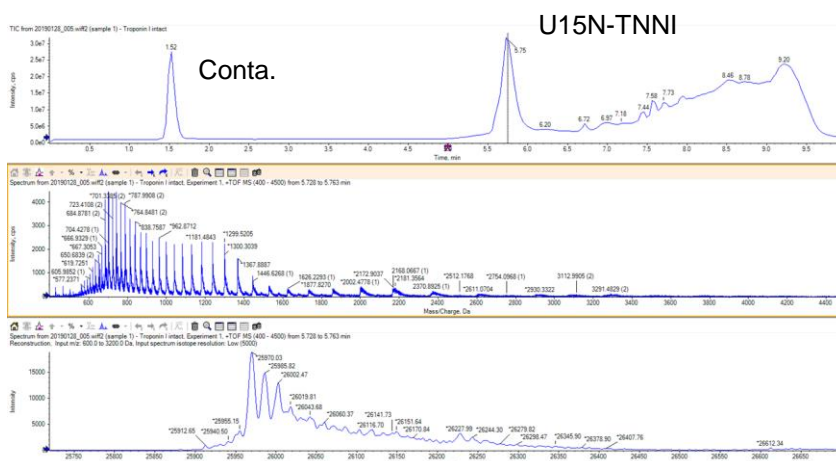
Human Troponin I (Uniprot accession number P19429)

Peptide mapping using LC-MS analysis (SCIEX X500B instrument)

MSGSHHHHHSSGIEGRADGSSDAAREPRPAPAPIRRRSSNYRAYAT
EPHAKKSKISASRKLQLKTLQLQIAKQELEREAEERRGEKGRALSTRC
QPLELAGLGFALQDLQRQLHARVDKVDEERYDIEAKVTKNITEIADLTQ
KIFDLRGKFKRPTLRVRISADAMMQALLGARAKESLDLRAHLKQVKKE
DTEKENREVDWRKNIDALSGMMEGRKKKFES

Peptide in blue detected → Coverage = 56%
Residues highlighted in yellow are present in a non-oxidized and oxidized form

Intact Mass analysis (SCIEX X500B instrument)



Mass detected

Mass	Attribution	Modification
25970.03	cTNI U15N -2	
25985.82	cTNI U15N - 2- 15.79	oxidation
26002.47	cTNI U15N - 2- 32.44	oxidation

3 major forms of TNNI are present in the batch : one form non oxidized, 1 form with a Met oxidized and probably 1 form with 2 Met oxidized.