

## PRODUCT DATA SHEET

**Pierce Intact Protein Standard Mix****Product Number: A33526, A33527**

Pub. No. MAN0016725 Rev C.00 Rev Date 08Feb2018

**Summary:**

The Thermo Scientific™ Pierce™ Intact Protein Standard Mix is a lyophilized mixture of 6 recombinant proteins for qualitative liquid chromatography (LC), direct-infusion mass spectrometry (MS), or LC/MS experiments. The mixture does not contain salts or detergents and is specifically formulated for direct-infusion MS experiments.

**Applications:**

- Qualitative LC
- LC/MS standardization and method development
- LC/MS intact protein mass measurement and top-down method development

**Stability:**

Lyophilized product is stable for >2 years at -20°C. Solubilized product can be aliquoted and stored for up to 7 days at 4°C.

**Material Preparation:**

Warm vial to room temperature before reconstitution. For LC/MS experiments, dissolve product in 100 µL of LC/MS-grade water to a final concentration of 0.76 µg/µL. For direct infusion experiments, dissolve product in 200 µL of 50% LC/MS-grade water/acetonitrile with 0.1% formic acid to a final concentration of 0.38 µg/µL. Let sample dissolve for 15 minutes at room temperature. Trifluoroacetic acid (0.1%) and 5-10% acetonitrile may also be used to solubilize proteins.

**Source:**

Recombinant proteins expressed in *E.coli* or *B.subtilis*

**Visual:**

White powder

**Formulation:**

76 µg of lyophilized protein mixture per vial

**Storage:**

Shipped on cold packs. Store at -20°C.

**Related Thermo Scientific Products**

**88321** Pierce™ Peptide Retention Time Calibration Mixture

**88341** Pierce™ BSA Protein Digest, MS grade

**88342** Pierce™ 6 Protein Digest, equimolar, LC-MS grade

**88329** Pierce™ HeLa Protein Digest Standard

**Additional Information:**

MSDS and lot-specific CofA with FASTA-formatted protein sequence file can be downloaded from the product web page. Please visit: [thermofisher.com](http://thermofisher.com) Default methods for intact and top-down analysis can be found in Thermo Scientific™ BioPharma Finder™ 3.0 and ProSight™ PC 4.0 software.

**Technical Support:**

Hardware-related: 1-800-532-4752

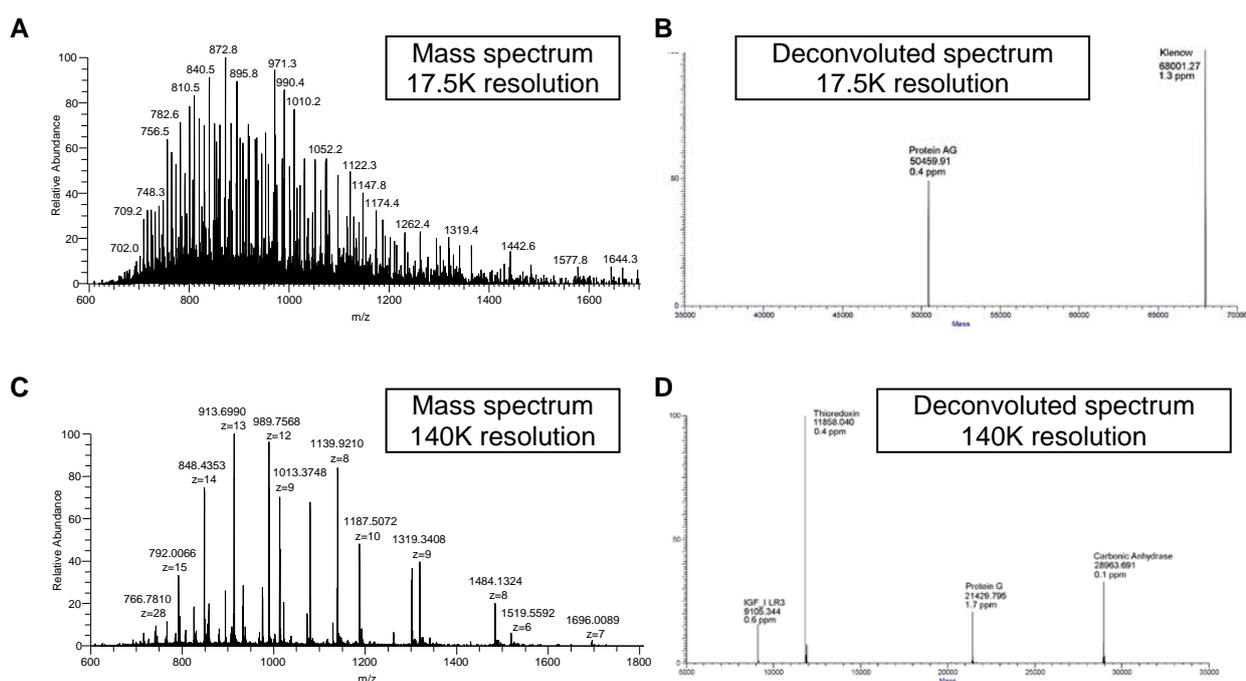
Reagent support: 1-800-874-3723

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**TABLE 1. Thermo Scientific Pierce Intact Protein Standard Mix.** The theoretical masses include known sequence variants and disulfide bonds. Uniprot accession numbers correspond to the original protein sequences.

Protein Name	Protein Accession	Theo. Average Mass (Da)	Theo. Mono Mass (Da)
Human IGF-I LR3*	P05019 (40-118)	9111.47	9105.34872
Human Thioredoxin	Q99757(60-166)	11865.52	11858.04393
<i>Streptococcus dysgalactiae</i> Protein G	P06654(223-413)	21442.61	21429.75915
Bovine Carbonic Anhydrase II*	P00921	28981.29	28963.6881
<i>Streptococcus</i> Protein AG ( <i>chimeric</i> )	P02976, P19909	50459.74	50429.84641
<i>Escherichia coli</i> Exo Klenow	P00582(324-928)	68001.15	67959.42515

\*Proteins may undergo partial deamidation in acidic conditions.



**Figure 1. Representative ESI-MS spectra of Pierce Intact Protein Standard Mix (0.38 µg/µL) reconstituted in a 50%/50%(v/v) mixture of 0.1% formic acid in 50% acetonitrile and LC/MS-grade water.** Sample was analyzed with a Thermo Scientific™ Q Exactive™ Plus mass spectrometer at 17.5K @ *m/z* 200 (A,B) and 140K @ *m/z* 200 (C,D) resolution in protein mode. Deconvoluted spectra at each resolution were obtained with Thermo Scientific™ BioPharma Finder™ 3.0 Software.

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**Protein sequences for components of Pierce Intact Protein Standard Mix in FASTA format**

**>IGF-I LR3, Sequence fragment is 89% identical to Human IGF-I LR3 (P05019) sequence fragment 40-118.**

MFPAMPLSSL FVNGPRTL CG AELVDALQFV CGDRGFYFNK PTGYGSSRR APQTGIVDEC  
CFRSCDLRRL EMYCAPLKPA KSA

**>Thioredoxin, Sequence is 100% identical to Human Thioredoxin (Q99757) sequence fragment 60-166.**

TTFNIQDGPDFQDRVVNSETPVVVDFHAQWCGPCKILGPRLEKMKVAKQHKGKVVMAKVDIDDHTDLAIE  
YEVSAPPTVLAMKNGDVVDKFKVGIKDEDEQLEAFLKLLIG

**>Protein G, Sequence fragment is 100% identical to *Streptococcus dysgalactiae* Protein G (P06654) sequence fragment 223-413.**

MDPYPLPKTDYKLIILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWYDDATKTFTVTEKPE  
VIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETA EKAFKQYANDNGVDGVWVWYDDATKTFTVTEM  
VTEVPGDAPTEPEKPEASIPVPLTPATPIAKDDAKKDDTKKEDAKKPEAKKDDAKKAETAG

**>Carbonic Anhydrase, Sequence is 99% identical to Bovine Carbonic Anhydrase II (P00921).**

SHHWGYGKHNHNGPEHWHKDFPIANGERQSPVDIDTKAVVQDPALKPLALVYGEATSRRMVNNGHSFN  
VEYDDSQDKAVLKDGPLTGTYRLVQFHFWGSSDDQGEHTVDRKKYAAELHLVHWNTKYGDFGTA  
AQQPDGLAVVGVFLKVG DANPALQKVL DALDSIKTKGKSTDFPNFDPGSLLPVNLNYWVWYDDATKTFTVTEM  
LLESVTWIVLKEPISVSSQQMLKFRTLNFNAEGEPPELLMLANWRPAQPLKNRQVRGFPK

**>Protein AG Recombinant chimera of Protein A from *Staphylococcus aureus* (Accession P02976) and Protein G from *Streptococcus dysgalactiae* (Accession P19909).**

AQHDEAQQNAFYQVLNMPNLNADQRNGFIQSLKDDPSQSANVLGEAQLNDSQAPKADAQQNNFNK  
DQSSAFYEILNMPNLNEAQRNGFIQSLKDDPSQSTNVLGEAKKLNESQAPKADNNFNKEQQNAFYEIL  
NMPNLNEEQRNGFIQSLKDDPSQSANLLSEAKKLNESQAPKADNKFNKEQQNAFYEILHLPNLNEEQR  
NGFIQSLKDDPSQSANLLAEAKKLNDAQAPKADNKFNKEQQNAFYEILHLPNLTEEQRNGFIQSLKDD  
PSVSKEILAEAKKLNDAQAPKEEDNKNKPIEGRNSRGSVDASELTPAVTTYKLVINGKTLKGETTTEAVD  
AATAEKVFKQYANDNGVDGEWYDDATKTFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAV  
DAETA EKAFKQYANDNGVDGVWVWYDDATKTFTVTEMVTEVPLESTA

**>Klenow Fragment exo-, Sequence is 99% identical to *E.coli* DNA polymerase I (P00582) sequence fragment 324-928.**

MISYDNYVTILDEETLKAWIAKLEKAPVFATATDSDLNANLVLGSLFAIEPGVAAYIPVAHDYLDAPD  
QISRERALELLKPLLEDEKALKVGNLKYDRGILANYGIELRGIAFDTMLESYILNSVAGRHDMSLAER  
WLKHKITTFEEIAGKGNQLTFNQIALEEAGRYAEDADVTLQLHLKMWPDQKHKGPLNVFENIEMPL  
VPVLSRIERNGVKIDPKVLHNSSEELTLRLAELEKKAHEIAGEEFNLSSTKQLQTLFEKQGIKPLKKTGP  
GAPSTSEEVLEELALDYPLPKVILEYRGLAKLKSTYTDKPLMINPKTRVHTSYHQAVTATGRSSTD  
PNLQNIPIVRNEEGRRIRQAFIAPEDYVIVSADYSQIELRIMAHLSRDKGLLTAFAGKDIHRATAAEVFG  
PLETVTSEQRSAKAINFGLIYGMSAFGLARQLNIPRKEAQKYMPLYFERYPGVLEYMERTRAQAKEQ  
GYVETLDGRRLYLPDIKSSNGARRAAAERAINAPMQGTAADIKRAMIAVDLQAEQPRVRMIMQV  
HDELVEVHKDDVDAVAKQIHLQMLNCTRLDVPVLLVEVSGGENWDQAH

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