

Peptide Standard Set Product Information Sheet and General Protocol

Product Category: Mass Spectrometry Standards
Catalog Number(s): s6104-10ug, s6104-3x10ug

Product Name: Particle Calibration Standard S

Product Name: Peptide Calibration Standard Set

Alternative Name(s): Peptide Standard Mixture

Contains (10 µg of each): Leu-Enkephalin, Gonadoliberin, Angiotensin I, and Neurotensin

CAS Number: Combination of Compounds Molecular Weight: 555.6, 1181.6, 1295.7, 1691.0

Monoisotopic Masses [M + H]⁺: 556.277, 1182.581, 1296.685, 1690.928*

*(-H₂O is 1672.917)

Storage: -20°C or below

Peptide standards are very useful for calibrating and verifying MALDI-MS and LCMS instrumentation. These standards are generally used to confirm that instrumentation is properly calibrated and to perform regular check-ups and validation of instrumentation. These standards are soluble in water, as well as acetonitrile/water co-solvents.

The procedure below is intended to be a general protocol or a starting point, not necessarily the best for your particular application.

Standard Preparation (for MALDI-MS)

- 1. Dissolve the contents of the tube in 1.0 mL of Proteomics Grade water or equivalent. Allow the standard(s) to sit for 2-5 minutes, then vortex moderately. This gives 10 μ g/mL solution of each peptide standard.
- 2. Prepare a 5 mg/mL CHCA stock solution in 50% Acetonitrile:Water with 0.1% TFA.
- 3. Combine 5 μL of the peptide standard stock solution (prepared in step 1) with 95 μL CHCA solution (prepared in step 2). Vortex standard:matrix solution moderately. *Other matrices and/or solvent compositions can be used.*
- 4. Apply 0.2 to 1.0 µL of this solution onto the MALDI sample plate.
- 5. Allow the matrix:sample to co-crystallize through evaporation at room temperature.
- 6. Place MALDI plate in MALDI-MS Ion Source and analyze samples.

Thin Layer Method is also a good option, although this is not covered in this product sheet.

^{*}The masses listed are the expected masses, instrument settings, solvent purity, and other conditions can affect the abundance of the $[M+H]^+$ ion abundance. Other common ions include the $[M+Na]^+$, $[M+H_3O]^+$, $[M+K]^+$, etc. In these cases add the appropriate mass to theoretical monoisotopic mass to identify peptide: 22, 18, 38 respectively. Loss of water (-18) is also a common occurrence (especially if ionization energy is elevated).