

# Standards for Protein and Peptide Analysis by Mass Spectrometry





# Standards for Mass Spectrometry

Sigma-Aldrich provides a wide range of standards designed specifically for mass spectrometry applications. Highly characterized protein and peptide mixtures are available for applications ranging from MS instrument performance to specific post-translational analysis. All standards are produced with the highest levels of quality under ISO 9001:2008 standards and are designed specifically for your MS applications.

The following table provides a general overview of our MS standards.

Detailed information on each standard can be found in the specific product description in this brochure or on our website [sigma.com/ms\\_standards](http://sigma.com/ms_standards)

	UPS 1	UPS 2	PhosphoMix	MSQC1	MSRT1	MSCAL1	MSCAL2	MSCAL3	MSCAL4	MSCAL5	MSCAL6	
Injection Ready			●	●	●					●	●	Physical Attributes
Peptide Based			●	●	●	●	●		●			
Protein Based	●	●				●		●				
Defined Composition	●	●	●	●	●	●	●	●	●	●	●	
Heavy & Light Versions			●									
MRM Quantitation				★								Performance Attributes
Protein ID	★	●		●								
Depth of Protein ID		★										
Top Down MS	●	●										
Digestion Evaluation	●	●										
Enrichment Evaluation			●									Application
Protein Fractionation	●	●										
PTM Analysis			★									
Daily System Quality m/z, RT, linearity"				●	★							
Method Development	●	●	●									
Calibration, tuning, sensitivity testing						★	★	★	★	★	★	System
MALDI			●			●	●	●	●			
LC-MS	●	●	●	●	●							
Developed specifically for LTQ XL & LTQ Hybrids									●			
Developed specifically for LTQ FT/Orbitrap ESI Positive Mode										●		
Developed specifically for LTQ FT/FT-Hybrid ESI Negative Mode											●	

● well-suited      ★ top-rate

# Universal Proteomics Standards

## Are you detecting all proteins important to you?

### Universal Proteomics Standard Set (UPS1)

UPS is intended to standardize and/or evaluate mass spectrometric (e.g., LC-MS/MS, MALDI-TOF-MS, etc.) and electrophoretic analysis conditions prior to the analysis of complex protein samples.

UPS1 contains 48 human proteins ranging in molecular mass from 6,000 to 83,000 Daltons. Each constituent protein has been HPLC-purified and AAA-quantitated prior to formulation.

#### Uses include:

- Troubleshoot and optimize your analytical protocol
- Confirm system suitability before analyzing critical samples
- Normalize analytical results day-to-day or lab-to-lab

UPS1 was developed in collaboration with the Association of Biomolecular Resource Facilities (ABRF) Proteomics Standards Research Group (sPRG).

This protein mixture was extensively evaluated and reported under the direction of ABRF's sPRG during a comprehensive 2005/2006 study.

### Components

- Universal Proteomics Standard 1 vial
- Trypsin (Sigma T6567) 20 µg

Cat-No:	Product Description
UPS1-1KT	Universal Proteomics Standard Set, Protein Mass Spectrometry Calibration Standard

For more information on UPS, visit [sigma.com/ups\\_standards](http://sigma.com/ups_standards)

## Go to the limits and challenge your MS System

### Proteomics Dynamic Range Standard Set (UPS2)

The Proteomics Dynamic Range Standard Set can be used to standardize and/or evaluate mass spectrometric and electrophoretic analysis conditions prior to the analysis of complex protein samples.

The Proteomics Dynamic Range Standard Set is produced from a mixture of 48 individual human source or human sequence recombinant proteins (the same proteins as in UPS1), each of which has been selected to limit heterogeneous post-translational modifications (PTMs).

The protein standard is formulated from 6 mixtures of 8 proteins to present a dynamic range of 5 orders of magnitude, ranging from 50 pmoles to 500 amoles.

Each protein has been AAA-quantitated prior to formulation.

Concentration : 10.6 µg/ampule protein

### Components

- Proteomics Dynamic Range Standard 1 vial
- Trypsin (Sigma T6567) 20 µg

Cat-No:	Product Description
UPS2-1SET	Proteomics Dynamic Range Standard Set, Protein Mass Spectrometry Calibration Standard

List of UPS Proteins

UniProt Accession Number	UPS1 Amount (fmol)	UPS2 Amount (fmol)	UniProt Protein Name [Synonym]	MW (Da) (calculated)	Source or recombinant	Host	Tag	Potential PTMs
P00915	5	50	Carbonic anhydrase 1	28.738	Erythrocytes			Acetylation
P00918	5	50	Carbonic anhydrase 2	29.115	Erythrocytes			Acetylation
P01031	5	50	Complement C5 [Complement C5a]	8.536	Recombinant	E. coli		
P69905	5	50	Hemoglobin alpha chain	15.126	Erythrocytes			
P68871	5	50	Hemoglobin beta chain	15.867	Erythrocytes			Acetylation, nitrosylation, glycosylation
P41159	5	50	Leptin	16.158	Recombinant	E. coli		
P02768	5	50	Serum Albumin	66.357	Recombinant	Pichia pastoris		
P62988	5	50	Ubiquitin	10.597	Recombinant	E. coli	6-His	
P04040	5	5	Catalase	59.625	Erythrocytes			
P00167	5	5	Cytochrome b5	16.022	Recombinant	E. coli	6-His	
P01133	5	5	Epidermal Growth Factor	6.353	Recombinant	E. coli		
P02144	5	5	Myoglobin C	17.053	Heart			
P15559	5	5	NAD(P)H dehydrogenase [quinone] 1 [DT Diaphorase] C	30.736	Recombinant	E. coli		
P62937	5	5	Peptidyl-prolyl cis-trans isomerase A [Cyclophilin A]	20.176	Recombinant	E. coli		
Q06830	5	5	Peroxiredoxin 1	21.979	Recombinant	E. coli		
P63165	5	5	Small ubiquitin-related modifier 1 [SUMO-1]	38.815	Recombinant	E. coli	GST	
P00709	5	500	Alpha-lactalbumin	14.078	Milk			Glycosylation
P06732	5	500	Creatine kinase M-type [CK-MM]	43.101	Heart			
P12081	5	500	Histidyl-tRNA synthetase [Jo-1]	58.233	Recombinant	E. coli		
P61626	5	500	Lysozyme C	14.701	Milk			
Q15843	5	500	Neddylin [Nedd8]	9.072	Recombinant	E. coli		
P02753	5	500	Retinol-binding protein	21.071	Urine			
P16083	5	500	Ribosyl-dihydro-nicotinamide dehydrogenase [quinone] [Quinone oxidoreductase 2] [NQO2]	25.821	Recombinant	E. coli		
P63279	5	500	Ubiquitin-conjugating enzyme E2 I [UbcH9]	18.007	Recombinant	E. coli		
P01008	5	50	Antithrombin-III	49.039	Plasma			Glycosylation
P61769	5	50	Beta-2-microglobulin	11.731	Urine			
P55957	5	50	BH3 Interacting domain death agonist [BID]	21.995	Recombinant	E. coli		
O76070	5	50	Gamma-synuclein	15.363	Recombinant	E. coli	6-His	
P08263	5	50	Glutathione S-transferase A1 [GST A1-1]	25.5	Recombinant	E. coli		
P01344	5	50	Insulin-like growth factor II	7.475	Recombinant	E. coli		
P01127	5	50	Platelet-derived growth factor B chain	12.294	Recombinant	E. coli		
P10599	5	50	Thioredoxin	12.429	Recombinant	E. coli	6-His	
P99999	5	5	Cytochrome c[Apocytochrome c]	11.618	Recombinant	E. coli		
P06396	5	5	Gelsolin	82.959	Plasma			Phosphorylation
P09211	5	5	Glutathione S-transferase P [GST]	23.225	Placenta			
P01112	5	5	GTPase HRas [Ras protein]	21.298	Recombinant	E. coli		
P01579	5	5	Interferon gamma (IFN-gamma)	16.879	Recombinant	E. coli		
P02787	5	5	Serotransferrin [Apo-transferrin]	75.181	Plasma			Glycosylation
O00762	5	5	Ubiquitin-conjugating enzyme E2 C [UbcH10]	20.475	Recombinant	E. coli	6-His	
P51965	5	5	Ubiquitin-conjugating enzyme E2 E1 [UbcH6]	22.227	Recombinant	E. coli	6-His	
P08758	5	0.5	Annexin A 5	35.806	Placenta			Acetylation
P02741	5	0.5	C-reactive protein	23.047	Plasma			
P05413	5	0.5	Fatty acid-binding protein	14.727	Plasma			Acetylation, phosphorylation
P10145	5	0.5	Interleukin-8	8.386	Recombinant	E. coli		
P02788	5	0.5	Lactotransferrin	76.165	Milk			Glycosylation
P10636	5	0.5	Microtubule-associated protein tau [Tau protein]	45.719	Recombinant	E. coli	6-His	
P00441	5	0.5	Superoxide dismutase [Cu-Zn]	15.805	Erythrocytes			Acetylation
P01343	5	0.5	Insulin-like growth factor IA	7.643	Recombinant	E. coli		
P01375	5	0.5	Tumor necrosis factor [TNF-alpha]	17.353	Recombinant	E. coli		

# MALDI Calibration Kits

## ProteoMass™ Peptide and Protein MALDI-MS Calibration Kit

This kit features a convenient selection of pre-qualified standard peptides, proteins, matrices, and solvents for calibrating and testing matrix assisted laser desorption ionization (MALDI) mass spectrometers. Configured for analyzing complex mixtures of proteins and peptides (700 to 66,000 Da), MSCAL1 is ideal for evaluating unknown samples or samples with a broad range of molecular masses. MSCAL1 can also be used for tuning and sensitivity testing of MALDI instruments from all manufacturers.

### Components

- ProteoMass™ Bradykinin Fragment 1-7 MALDI-MS Standard (Sigma B4181) 1×10 nmol
- ProteoMass™ P14R MALDI-MS Standard (Sigma P2613) 1×10 nmol
- ProteoMass™ ACTH Fragment 18-39 MALDI-MS Standard (Sigma A8346) 1×10 nmol
- ProteoMass™ Insulin chain B oxidized MALDI-MS Standard (Sigma I6154) 1×10 nmol
- ProteoMass™ Insulin MALDI-MS Standard (Sigma I6279) 1×10 nmol
- ProteoMass™ Cytochrome c MALDI-MS Standard (Sigma C8857) 1×10 nmol
- ProteoMass™ Apomyoglobin MALDI-MS Standard (Sigma A8971) 1×10 nmol
- ProteoMass™ Albumin MALDI-MS Standard (Sigma A8471) 1×10 nmol
- ProteoMass™ Aldolase MALDI-MS Standard (Sigma A9096) 1×10 nmol
- ProteoMass™ Angiotensin II MALDI-MS Standard (Sigma A8846) 1×10 nmol
- α-Cyano-4-hydroxycinnamic acid (Sigma C8982) 4×10 mg
- Sinapinic acid (Sigma S8313) 4×10 mg
- Trifluoroacetic acid 30 mL
- Acetonitrile 30 mL
- Trifluoroacetic acid solution 1% 4 mL

Cat-No:	Product Description
MSCAL1-1KT	ProteoMass™ Peptide and Protein MALDI-MS Calibration Kit, Peptide and Protein MALDI MS Calibration Standard

## ProteoMass™ Peptide MALDI-MS Calibration Kit

This kit contains a selection of pre-qualified standard peptides, matrices, and solvents for calibrating and testing matrix assisted laser desorption ionization (MALDI) mass spectrometers. Configured specifically for peptide applications (in the mass range of 700 to 3500 Da), MSCAL2 is ideal for analysis of tryptic fragments or post-source decay studies. MSCAL2 can also be used for tuning, and sensitivity testing of MALDI instruments from all manufacturers.

### Components

- ProteoMass™ Bradykinin Fragment 1-7 MALDI-MS Standard (Sigma B4181) 2×10 nmole
- ProteoMass™ Angiotensin II MALDI-MS Standard (Sigma A8846) 2×10 nmole
- ProteoMass™ P14R MALDI-MS Standard (Sigma P2613) 2×10 nmole
- ProteoMass™ ACTH Fragment 18-39 MALDI-MS Standard (Sigma A8346) 2×10 nmole
- ProteoMass™ Insulin chain B oxidized MALDI-MS Standard (Sigma I6154) 2×10 nmole
- Trifluoroacetic acid 30 mL
- Acetonitrile 30 mL
- Trifluoroacetic acid solution 1% 4 mL
- α-Cyano-4-hydroxycinnamic acid (Sigma C8982) 8×10 mg

Cat-No:	Product Description
MSCAL2-1KT	ProteoMass™ Peptide MALDI-MS Calibration Kit Peptide MALDI MS Calibration Standard

# MALDI Calibration Kits

## ProteoMass™ Protein MALDI-MS Calibration Kit

This kit features a convenient selection of pre-qualified standard proteins, matrices, and solvents for calibrating and testing matrix assisted laser desorption ionization (MALDI) mass spectrometers. Configured specifically for the mass range of 5 to 66 kDa, MSCAL3 is ideal for most protein studies. Applications include calibration, tuning, and sensitivity testing of MALDI instruments from all manufacturers.

### Components

- ProteoMass™ Insulin MALDI-MS Standard (Sigma I6279) 2 × 10 nmol
- ProteoMass™ Cytochrome c MALDI-MS Standard (Sigma C8857) 2 × 10 nmol
- ProteoMass™ Apomyoglobin MALDI-MS Standard (Sigma A8971) 2 × 10 nmol
- ProteoMass™ Aldolase MALDI-MS Standard (Sigma A9096) 2 × 10 nmol
- ProteoMass™ Albumin MALDI-MS Standard (Sigma A8471) 2 × 10 nmol
- Sinapinic acid (Sigma S8313) 8 × 10 mg
- Trifluoroacetic acid 30 mL
- Acetonitrile 30 mL
- Trifluoroacetic acid solution 1% 4 mL

Cat-No:	Product Description
MSCAL3-1KT	ProteoMass™ Protein MALDI-MS Calibration Kit, Protein MALDI MS Calibration Standard

## ProteoMass MALDI Calibration Kit for LTQ XL and LTQ Hybrids

The ProteoMass MALDI Calibration Kit for LTQ XL™ and LTQ hybrids enables calibration of Thermo Scientific ion trap and ion trap-based hybrid mass analyzers equipped with MALDI sources in positive and negative ion mode. It covers a mass range from m/z 144 to m/z 3,657, and is therefore usable for calibrations between m/z 50 and 4000.

### Features and Benefits

- Developed and qualified specifically for use with the Thermo Scientific LTQ XL and LTQ hybrid mass spectrometers with MALDI source
- Contains high purity, low alkali metal solvents and recrystallized matrix
- Conveniently packaged, freeing you from time-consuming purification and weigh-up steps, allowing you to focus on acquisition of quality data

### Components

- α-Cyano-4-hydroxycinnamic acid 5 × 5 mg
- ProteoMass™ Calibrant Mix, Normal Range 5 vials
- ProteoMass™ Calibrant Mix, High Range 5 vials
- ProteoMass™ Angiotensin II, Sensitivity Standard 2 × 500 pmols
- Trifluoroacetic acid 4 mL
- Acetonitrile 30 mL
- Ethanol (Sigma E7023) 10 mL

Cat-No:	Product Description
MSCAL4-1KT	ProteoMass™ MALDI Calibration Kit for LTQ XL and LTQ Hybrids MALDI MS Calibration Standard

# ESI Standards Kits

For Positive or Negative Mode Calibration

## Proteo Mass LTQ/FT-Hybrid ESI Positive Mode CalMix

The ProteoMass ESI Calibration Kit for LTQ based Hybrids, Positive Ion Mode Calibration Solution, enables calibration of Thermo Scientific hybrid instruments equipped with an ESI source in the positive ion mode. It covers a mass range from m/z 138 to m/z 1822, and is therefore usable for calibrations between m/z 50 and 2000.

### Features and Benefits

- Ready-to-use
- Developed and qualified specifically for use with LTQ-based Thermo Scientific hybrid instruments (LTQ FT®, LTQ FT Ultra®, and LTQ Orbitrap™ series) with ESI source and Thermo Scientific Exactive
- Conveniently packaged, freeing you from time-consuming mixing and dilution steps, allowing you to focus on acquisition of quality data

### Components

- Met-Arg-Phe-Ala Acetate
- Caffeine
- Ultramark 1621

Cat-No:	Size	Product Description
<a href="#">MSCAL5-1EA</a>	1×10 mL	ProteoMass™ LTQ/FT-Hybrid ESI Pos. Mode CalMix
<a href="#">MSCAL5-10EA</a>	10×10 mL	

## Proteo Mass LTQ/FT-Hybrid ESI Negative Mode CalMix

The ProteoMass ESI Calibration Kit for LTQ based Hybrids, Negative Ion Mode Calibration Solution, enables calibration of Thermo Scientific hybrid instruments equipped with an ESI source in the negative ion mode. It covers a mass range of m/z 265 to m/z 1880, and is therefore usable for calibrations between m/z 50 and 2000.

### Features and Benefits

- Ready-to-use
- Developed and qualified specifically for use with LTQ-based Thermo Scientific hybrid instruments (LTQ FT®, LTQ FT Ultra®, and LTQ Orbitrap™ series) with ESI source and Thermo Scientific Exactive
- Conveniently packaged, freeing you from time-consuming mixing and dilution steps, allowing you to focus on acquisition of quality data

### Components

- Ultramark 1621
- Sodium dodecyl stearate
- Taurocholic acid sodium salt

Cat-No:	Size	Product Description
<a href="#">MSCAL6-1EA</a>	1×10 mL	ProteoMass™ LTQ/FT-Hybrid ESI Neg. Mode CalMix
<a href="#">MSCAL6-10EA</a>	10×10 mL	

## MRM Peptide Mixture

For Qualitative and Quantitative Analysis and System Calibration

### MS Qual/Quant QC Mix

The MS Qual/Quant QC Mix is a LC-MS standard designed to benchmark and monitor daily performance of both qualitative and quantitative proteomic platforms. MS Qual/Quant QC Mix is an injection-ready standard, designed with multiple reaction monitoring/selected reaction monitoring (MRM / SRM) methodology in mind.

This product is optimized to assess platform characteristics, including:

- Reproducibility between runs
- System stability (drift, chromatography, signal intensity, sensitivity, etc.)
- Inter- and intra- platform and lab comparisons

### Features and Benefits

#### Qualitative

##### Mixture of 6 tryptically digested human proteins

- Low complexity, defined mixture
- 25-fold concentration range
- C18 purified

##### 14 Stable Isotope Labeled (SIL) peptides

- SIL peptides span a concentration range greater than three orders of magnitude
- 2 - 3 peptides per protein

#### Quantitative

- MRM settings provided (Skyline, xls, csv)
- MRM transitions provided (files above)
- Light : Heavy ratios from 50:1 to 1

#### Components

Each vial contains 6 pre-digested (trypsin) human proteins plus 14 corresponding stable isotope labeled (SIL) peptides (7-8 µg total dried in a 0.5 mL vial).

Up to 100 uses based upon the recommended reconstitution method.

Cat-No:	Product Description
MSQC1-1VL	MS Qual/Quant QC Mix, Proteomics LC-MS Calibration Standard

## LC-MS Calibration Mix

For Testing of LC Gradients and Columns and Retention Time Calibration

### MS RT Calibration Mix

The MS RT Calibration Mix is a LC-MS platform standard intended to test properties such as LC resolution, peptide elution profiles, and retention time prediction. The MSRT1 peptides are designed to span the normal elution profile of complex proteomic samples. The peptides have been added in various amounts, based on electrospray response, to have relatively similar response and to be readily observed.

MSRT1 is an injection-ready standard, and can serve for quick tests of LC-MS platform performance, comparison of LC gradients and columns, and monitoring column and system changes. MSRT1 can be used to predict retention times of peptides across LC-MS platforms. MSRT1 is also applicable to multiple reaction monitoring / selected reaction monitoring (MRM / SRM) analysis.

### Features and Benefits

#### General

##### Complexity

- Defined mixture gives confidence in your instrument's analysis

##### Easily visualized

- Distinct LC-MS peak profile of peptides, readily separated with similar responses

##### Injection-ready

- Decreases preparation time

#### Qualitative

- Defined mixture of 14 stable isotope labeled (SIL) peptides

#### Quantitative

- MRM settings provided ((Skyline, xls)

#### Components

Each vial contains various amounts of 14 isotopically labeled synthetic peptides dried via vacuum centrifugation. Each peptide is labeled with either a [<sup>13</sup>C,<sup>15</sup>N] Lysine (+ 8 Da), a [<sup>13</sup>C,<sup>15</sup>N] Arginine (+10 Da), or a [<sup>13</sup>C] Leucine (+6 Da).

Cat-No:	Product Description
MSRT1-1VL	MS RT Calibration Mix, Proteomics Retention Time Standard



# PhosphoMix Phosphopeptide MS Standards

## For Phosphopeptide Analysis and Workflow Verification

The MS PhosphoMix products are used to test the strengths and weaknesses of phosphopeptide enrichment techniques, sample processing, and MS-based phosphoproteomics workflows.

The MS PhosphoMix products consist of 25 mono-, di-, tri-, and tetraphosphorylated synthetic peptides formulated into 3 uniquely designed mixtures (MS PhosphoMix 1, 2, and 3).

Each mixture is available in natural (light) and isotopically labeled (heavy) versions. This makes these products highly amenable to quantitative analyses and allows comparison of recovery between workflows or enrichment techniques.

Each mixture includes phosphopeptides with a broad range of characteristics, including peptide ionizability (both ESI and MALDI), molecular weight, chromatographic retention time, charge state, and isoelectric point.

The mixtures were designed to include complimentary peptides with identical or similar amino acid sequences, but where the number of phosphorylated residues and the site-specific locations of phosphorylation vary.

MS PhosphoMix products are ideal for use as internal reference materials to gauge overall platform performance (e.g. recovery, sensitivity, repeatability) during routine phosphopeptide analysis.

Visit [sigma.com/phosphomix](http://sigma.com/phosphomix) to download the MS PhosphoMix FASTA file of all phosphopeptide sequences and to access composition, phosphorylation site, and monoisotopic mass data for each standard mixture.

### Features & Benefits

- Naturally occurring peptide sequences
- Broad range of peptide characteristics
- Complimentary produce designs
- Available in light and heavy versions

### MS PhosphoMix Product Design



Name	Cat. No.	Number of Peptide	Amount/Vial	Amount/Peptide	Volume/Vial
MS Phosphomix 1 Heavy	MSP1H-1VL	10	200 pmol	20pmol/peptide	0,5ml
MS Phosphomix 1 Light	MSP1L-1VL	10	200 pmol	20pmol/peptide	0,5ml
MS Phosphomix 2 Heavy	MSP2H-1VL	10	200 pmol	20pmol/peptide	0,5ml
MS Phosphomix 2 Light	MSP2L-1VL	10	200 pmol	20pmol/peptide	0,5ml
MS Phosphomix 3 Heavy	MSP3H-1VL	5	200 pmol	40pmol/peptide	0,5ml
MS Phosphomix 3 Light	MSP3L-1VL	5	200 pmol	40pmol/peptide	0,5ml

## Composition of PhosphoMix Products

Peptide1	FASTA Abbreviation <sup>2</sup>	Complementary Peptide	Total No. of Phosphates	Light MW (Monoisotopic)	Heavy MW (Monoisotopic)	Relative Signal Intensity <sup>3</sup>	No. of Phosphates per amino acid		
							S	T	Y
<b>PhosphoMix-1</b>									
VLHSGpS[R]	1.1		1	834.37	844.38	Weak	1		
RSpYpSRs[R]	1.2	2.2	2	1070.41	1080.41	Weak	1		1
RDSLGPtYSS[R]	1.3		1	1220.52	1230.53	Medium		1	
pTKLlpTQLRDA[K]	1.4		2	1445.70	1453.72	Strong		2	
EVQAEQPSSpSSP[R]	1.5		1	1480.62	1490.63	Medium	1		
ADEPpSSEESDLEID[K]	1.6	1.7, 2.6, 3.5	1	1742.68	1750.69	Strong	1		
ADEPpSSEEpSDLEID[K]	1.7	1.6, 2.6, 3.5	2	1822.64	1830.66	Medium	2		
FEDEGAGFEESpSETGDYEE[K]	1.8		1	2333.84	2341.85	Strong	1		
ELSNpSPLRENSFGpSPLEF[R]	1.9	1.9	2	2338.00	2348.01	Medium	2		
SPTEYHEPVpYANPFYRPTpTPQ[R]	1.10		2	2809.19	2819.20	Strong		1	1
<b>PhosphoMix-2</b>									
LPQEpTA[R]	2.1		1	893.40	903.40	Weak		1	
RSYpSpSRs[R]	2.2	1-Feb	2	1070.41	1080.41	Weak	2		
EpTQSPEQV[K]	2.3		1	1124.48	1132.49	Weak		1	
VIEDNEpYTA[R]	2.4		1	1288.53	1298.54	Medium			1
pSRSPpSPELNN[K]	2.5		2	1474.59	1482.60	Medium	2		
ADEPSSEEpSDLEID[K]	2.6	1.6, 1.7, 3.5	1	1742.68	1750.69	Strong	1		
HQYSDYDpYHSSpSE[K]	2.7		2	1904.63	1912.64	Medium	1		1
NTPpSQHSHpSIQHSPE[R]	2.8		2	2000.79	2010.80	Medium	2		
ELpSNpSPLRENSFGpSPLEF[R]	2.9	1.9	2	2338.00	2348.01	Medium	2		
LGGRPLPTFPpTSE(CAM) TSDVEPDT[R]	2.10		1	2708.22	2718.22	Strong		1	
<b>PhosphoMix-3</b>									
SLpSpYpSP[V]ER	3.1		3	1276.42	1282.43	Weak	2		1
LQGpSGVpS[L]ApSK	3.2		3	1285.48	1292.49	Medium	3		
PPpYpSRV[I]pTQR	3.3		3	1455.57	1462.59	Strong	1	1	1
pSRs[R]pSYpTPEpYR	3.4		4	1720.54	1730.55	Weak	2	1	1
ADEPpSpSEEpSDLE[I]DK	3.5	1.6, 1.7, 2.6	3	1902.61	1909.63	Medium	3		

1. A FASTA file with all of the phosphopeptide sequences in the PhosphoMix product line is available for free download on the product display page at [sigma.com/phosphomix](http://sigma.com/phosphomix).

2. This is as determined using electrospray ionization (ESI) following standard reverse phase chromatography.

For detailed information on the Phosphomix Standards please visit

[sigma.com/phosphomix\\_standards](http://sigma.com/phosphomix_standards)

# Individual Protein & Peptide Calibration Standards

The ProteoMass™ MALDI-MS Standards are peptide calibration standards designed for MALDI-MS instruments. Each vial contains 10 nmole of peptide or protein.

<b>Proteo Mass™ Bradykinin Fragment 1-7 MALDI-MS Standard</b> Bradykinin fragment 1-7, mass spec standard <b>vial = 10 nmol, monoisotopic mol wt 756.3997 Da</b>	
<b>B4181-5X1VL</b>	5 × 1 vial
<b>Proteo Mass™ Angiotensin II MALDI-MS Standard</b> Angiotensin II, mass spec standard <b>vial = 10 nmol, monoisotopic mol wt 1,045.5423 Da</b>	
<b>A8846-5X1VL</b>	5 × 1 vial
<b>Proteo Mass™ P14R MALDI-MS Standard</b> P14R P14R P14R P14R P14R P14R P14R P14R P14R P14R <b>vial = 10 nmol, monoisotopic mol wt 1,532.8582 Da</b>	
<b>P2613-5X1VL</b>	5 × 1 vial
<b>Proteo Mass™ ACTH Fragment 18-39 MALDI-MS Standard</b> Adrenocortico trop ic hormone fragment 18-39 Arg-Pro-Val-Lys-Val-Tyr-Pro-Asn-Gly-Ala-Glu-Asp-Glu-Ser-Ala-Glu-Ala-Phe-Pro-Leu-Glu-Phe [53917-42-3] <b>vial = 10 nmol, monoisotopic mol wt 2,464.1989 Da</b>	
<b>A8346-5X1VL</b>	5 × 1 vial
<b>Proteo Mass™ Insulin chain B oxidized MALDI-MS Standard</b> Insulin Chain B Oxidized from bovine pancreas FVNQHLCGSHLVEALYLVC-GERGFFYPKA [30003-72-6] C157H232N40O47S2 FW 3495.89 <b>vial = 10 nmol, monoisotopic mol wt 3,493.6513 Da</b>	
<b>I6154-5X1VL</b>	5 × 1 vial
<b>Proteo Mass™ Insulin MALDI-MS Standard</b> Insulin from bovine pancreas [11070-73-8] C254H377N65O75S6 FW 5733.49 <b>vial = 10 nmol, monoisotopic mol wt 5,729.6087 Da</b>	
<b>Proteo Mass™ Cytochrome c MALDI-MS Standard</b> Cytochrome c from equine heart; Cytochrome c from horse heart [9007-43-6] <b>vial = 10 nmol, (M+H+) 12,361.96 Da, calculation</b>	
<b>C8857-5X1VL</b>	5 × 1 vial
<b>Proteo Mass™ Apomyoglobin MALDI-MS Standard</b> Apomyoglobin, mass spec standard <b>vial = 10 nmol, (M+H+) 16,952.27 Da, calculation</b>	
<b>A8971-5X1VL</b>	5 × 1 vial
<b>Proteo Mass™ Aldolase MALDI-MS Standard</b> <b>vial = 10 nmol, average mol wt 39,211.28 Da, calculation</b>	
<b>A9096-5X1VL</b>	5 × 1 vial
<b>Proteo Mass™ Albumin MALDI-MS Standard</b> Albumin, bovine, mass spec standard <b>vial = 10 nmol, average mol wt 66,429.09 Da, calculation</b>	
<b>A8471-5X1VL</b>	5 × 1 vial
<b>Met-Arg-Phe-Ala acetate salt</b> MRFA [67368-29-0] C23H37N7O5S FW 523.65 ≥90% (HPLC) A marker in an unambiguous method for sequencing tetrapeptides using FAB, MI, and collisional activation spectra in combination.	
<b>M1170-1MG</b>	1 mg
<b>M1170-5MG</b>	5 mg

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