



Tip:

1. To search the note, press CTRL-F keys in combination
2. To navigate the note, use the [links](#).

Unstained Protein Markers (Mark12™, HiMark™, BenchMark™)

TABLE OF CONTENTS

PRODUCT DESCRIPTION

[Protein Origins](#)

[Molecular Weights](#)

SHIPPING CONDITIONS

STORAGE CONDITIONS

STABILITY

QC SPECIFICATIONS

PROTOCOL & APPLICATION NOTES

[General Notes](#)

[Application Notes](#)

[Troubleshooting](#)

ALTERNATE PRODUCTS & COMPATIBILITY

PRODUCT DOCUMENTATION

REFERENCES

PRODUCT NAME & CATALOG NUMBER

COMPONENTS

ASSOCIATED PRODUCTS

PRODUCT DESCRIPTION

[\(back to Table of Content\)](#)

[Protein Origins](#)

[Molecular Weights](#)

| Name | Product Description |
|--|--|
| Mark12™ Unstained Standard | The Mark12™ Unstained Standard is an unstained protein standard that allows the closest estimation of molecular weight of your sample protein over a wide molecular weight range. It is supplied ready-to-use for either Tris-Glycine, Tricine or NuPage Gels. Coomassie, silver or other protein staining methods are required to visualize this standard. Mark12™ has 12 bands with molecular weights ranging from 2.5 kDa to 200 kDa. |
| HiMark™ Unstained High Molecular Weight Protein Standard | The HiMark™ Unstained High Molecular Weight (HMW) Protein Standard allows accurate molecular weight estimation of high molecular weight proteins on Tris-Acetate Gels with Tris-Acetate SDS buffer system. HiMark™ Consists of 9 protein bands in the range of 40-500 kDa and is designed for use with NuPAGE® Novex 3-8% and 7% Tris-Acetate Gels under denaturing conditions. HiMark™ is Supplied in a ready-to-use format; do not heat or add reducing agent. Visualize HiMark™ using Coomassie, silver or other protein staining method. |
| BenchMark™ Protein Ladder | The BenchMark™ Protein Ladder consists of 15 engineered proteins ranging in molecular weight from 10 to 220 kDa. The proteins have been affinity purified for sharp bands and clear backgrounds, and are suitable for Coomassie or silver staining. The 20 and 50 kDa proteins are more prominent for easy orientation and to ensure proper identification of each protein. The ladder is in a ready-to-use format; do not heat or add reducing agent. This ladder can be used with Tris-Glycine, NuPAGE, or Tricine Gels. |

Note: The HiMark™ Unstained HMW Protein Standard is designed for use with NuPAGE® Novex Tris-Acetate Gels under denaturing conditions. Using the standards with NuPAGE® Novex Bis-Tris Gels or Tris-Glycine Gels may result in inaccurate molecular weight estimation.

Protein Origins

[\(back to Table of Content\)](#)

[\(back to Product Description\)](#)

Mark12™

| Protein | Origin |
|------------------------|-----------------|
| Myosin | Rabbit muscle |
| B-galactosidase | E. coli |
| Phosphorylase B | Rabbit muscle |
| Bovine serum albumin | Bovine serum |
| Glutamic dehydrogenase | Bovine liver |
| Lactate dehydrogenase | Porcine |
| Carbonic anhydrase | Bovine |
| Trypsin inhibitor | Soybean |
| Lysozyme | Egg white |
| Aprotinin | Bovine lung |
| Insulin B chain | Bovine pancreas |
| Insulin A chain | Bovine pancreas |
| Alcohol dehydrogenase | Baker's yeast |
| Myoglobin | Horse heart |

BenchMark™ Standard

The ladder consists of a series of affinity purified, recombinant proteins. The exact protein make up of each band is proprietary.

Molecular Weights

[\(back to Table of Content\)](#)

[\(back to Product Description\)](#)

Mark12™ Unstained Standard

| Protein | kDa |
|------------------------|------------|
| Myosin | 200 |
| B-Galactosidase | 116.3 |
| Phosphorylase b | 97.4 |
| BSA | 66.3 |
| Glutamic dehydrogenase | 55.4 |
| Lactate dehydrogenase | 36.5 |
| Carbonic anhydrase | 31 |
| Trypsin Inhibitor | 21.5 |
| Lysozyme | 14.4 |
| Aprotinin | 6 |
| Insulin B chain | 3.5 |
| Insulin A chain | 2.5 |

HiMark™ Unstained High Molecular Weight Protein Standard

| Band | kDa |
|-------------|------------|
| 1 | 500 |
| 2 | 290 |
| 3 | 240 |
| 4 | 160 |
| 5 | 116 |
| 6 | 97 |
| 7 | 66 |
| 8 | 55 |
| 9 | 40 |

HiMark™ Calculator - HiMark™ Calculator allows you to easily and accurately calculate the molecular weight of your proteins on NuPAGE® Novex 3-8% and 7% Tris-Acetate Gels and to extrapolate the molecular weight of proteins beyond the standard curve.

HiMark™ Calculator can be found on Invitrogen Website -

http://www.invitrogen.com/content/sfs/manuals/HiMark™_Calculator_V1.xls.

BenchMark™ Protein Ladder

| Band | kDa |
|-------------|------------|
| 1 | 220 |
| 2 | 160 |
| 3 | 120 |
| 4 | 100 |
| 5 | 90 |
| 6 | 80 |
| 7 | 70 |
| 8 | 60 |
| 9* | 50 |
| 10 | 40 |
| 11 | 30 |
| 12 | 25 |
| 13* | 20 |

| | |
|----|----|
| 14 | 15 |
| 15 | 10 |

Note: 50 & 20 kDa bands are darker intensity to serve as orientation bands.

Isoelectric Point

BenchMark™ Protein ladder:

| Band | Isoelectric Point |
|---------|-------------------|
| 220 kDa | 6.87 |
| 160 kDa | 6.74 |
| 120 kDa | 6.61 |
| 100 kDa | 6.53 |
| 90 kDa | 4.45 |
| 80 kDa | 4.46 |
| 70 kDa | 6.37 |
| 60 kDa | 4.49 |
| 50 kDa | 4.53 |
| 40 kDa | 6.24 |
| 30 kDa | 4.64 |
| 25 kDa | 4.98 |
| 20 kDa | 5.56 |
| 15 kDa | 5.51 |
| 10 kDa | 5.42 |

SHIPPING CONDITIONS

[\(back to Table of Content\)](#)

| Name | Primary | Secondary |
|--|---------|-----------|
| Mark12™ Unstained Standard | RT | Wet Ice |
| HiMark™ Unstained High Molecular Weight Protein Standard | Dry Ice | Dry Ice |
| BenchMark™ Protein Ladder | Dry Ice | Wet Ice |

STORAGE CONDITIONS

[\(back to Table of Content\)](#)

| Name | Storage |
|--|---|
| Mark12™ Unstained Standard | +4°C |
| HiMark™ Unstained High Molecular Weight Protein Standard | -20°C (Avoid repeated freezing and thawing) |
| BenchMark™ Protein Ladder | -20°C (can also be stored at +4°C) |

STABILITY

[\(back to Table of Content\)](#)

| Name | Stability |
|--|--|
| Mark12™ Unstained Standard | Guaranteed stable for 6 months when properly stored. |
| HiMark™ Unstained High Molecular Weight Protein Standard | Guaranteed stable for 6 months when properly stored. |
| BenchMark™ Protein Ladder | Guaranteed stable for 1 year when properly stored. [Stable 2.5 Years at -20°C, 4 months at 4°C, 1 month only at RT, 2 weeks only at 37°C. Stable for 50 freeze/thaws.] |

QC SPECIFICATIONS

[\(back to Table of Content\)](#)

| Name | QC Specifications |
|--|---|
| Mark12™ Unstained Standard | *Gel Testing: 8% Tris-Glycine, 10–20% Tricine, and 10% Bis-Tris. *Twelve bands must be present on the 10–20% TR and the 10% BT. *Gel test performance must be comparable to 2 previously released lots. *Band intensity must not differ more than 20% from 2 previously released lots. *Migration: Bands must be straight and sharp. *Contaminant bands must be less than 20% of the intensity of the major bands. |
| HiMark™ Unstained High Molecular Weight Protein Standard | *Gel Testing: 3–8% and 7% Tris–Acetate gels. *Nine bands must be present on both gels. *Gel test performance must be comparable to 2 previously released lots. *Band intensity when stained must not differ more than 20% from 2 previously released lots. *Bands must be straight and sharp, and must migrate in distances comparable to the 2 previously released lots. *Contaminant bands must be less than 20% of the intensity of the major bands. |
| BenchMark™ Protein Ladder | *Fifteen major sharp bands must be present on a 4–20% Tris-Glycine gel. *Gel test performance must be comparable to a previously released lot. *Band intensity when stained with Coomassie Blue R–250 must not differ more than 20% from a previously released lot. The 20 kDa and the 50 kDa bands have greater intensity than the other bands. *Bands migrate comparable to a previously released lot *There is a faint contaminant band between the 80 and 90 kDa bands. All other contaminant bands must be less than 20% of the intensity of the major bands. |

PROTOCOL AND APPLICATION NOTES

[\(back to Table of Content\)](#)

[General Notes](#)

[Application Notes](#)

[Troubleshooting](#)

General Notes

[\(back to Table of Content\)](#)

[\(back to Protocol and Application Notes\)](#)

- These protein standards are for SDS-PAGE and should not be used for native electrophoresis. These markers are denatured and have SDS in the storage buffer.
- These standards are ready to load. There is no need to heat or add reducing agents. Do not boil - boiling may cause band degradation.
- Mark12™ is modified to make re-oxidation impossible and to make this protein marker ready-to-use.
- Unstained markers like Mark12™, BenchMark™, and HiMark™ can be used for accurate molecular weight estimation of proteins. HiMark™ has a calculator to help in making a standard curve to estimate the molecular weight of an unknown protein. This calculator can be found on the Invitrogen website:
http://www.invitrogen.com/content/sfs/manuals/HiMark™_Calculator_V1.xls
- Pre-stained standards are ideal for monitoring an electrophoresis run, estimating the efficiency of transfer onto a membrane, and determining the *approximate* molecular weight of proteins. Note that the migration of a pre-stained standard is affected by factors such as pH and buffer system so in some cases the bands of a pre-stained standard may not match up exactly to the bands of an unstained standard. Note: Unstained standard is a more accurate determination of molecular weight.
- Blotting with HiMark™: To obtain higher transfer efficiency during the transfer of high molecular weight proteins, avoid using methanol in the transfer buffer. After transfer, you may stain the standard proteins on the membrane with Ponceau S, or any membrane stain of choice.

- Recommended transfer conditions: 1x NuPage transfer buffer; NO Methanol in the buffer; Add 0.1% SDS to the transfer buffer; 30V for 1 hour

Application Notes

[\(back to Table of Content\)](#)

[\(back to Protocol and Application Notes\)](#)

Quantitation/Determining Protein Concentration:

These markers are not designed for the quantitation and it is not recommended that these markers be used in the determination of protein concentration. Estimations of the protein concentration for Mark12™ are given below but these values are an approximation and should not be used to quantify samples.

Mark12™

| Band | per 5 µl |
|-----------------------|--------------------------------------|
| Myosin | 0.38 µg |
| B-Galactosidase | 0.20 µg |
| Phosphorylase-b | 0.35 µg |
| BSA | 0.20 µg |
| GDH | 0.60 µg |
| Lactate Dehydrogenase | 0.40 µg |
| Carbonic Anhydrase | 0.22 µg |
| Trypsin Inhibitor | 0.32 µg |
| Lysozyme | 0.25 µg |
| Aprotinin | 0.38 µg |
| Insulin | 1.12 µg (approx. 64% B, 35% A chain) |

HiMark™ – No Quantitation Information

BenchMark™ Standard - Protein/Band is ~0.1 µg/µl

Troubleshooting

[\(back to Table of Content\)](#)

[\(back to Protocol and Application Notes\)](#)

Missing bands

- Check % gel that is being used. Depending on gel type and/or percentage, you may not see all the bands. For example, one would not see the smallest bands of the standard on a very low % gel. A high % gel may not resolve the higher MW bands.
- Check age of ladder – expired lots may see faded or missing bands.
- Check storage of ladder – adverse storage conditions will affect the stability of the ladder.
- Boiling of ladder may contribute to degradation/missing bands.

Smeary bands

- Don't load too much protein. See recommended load volumes in the manual.
- Bands will not be as well resolved on low % gels. Try using higher gel %.

Extra Bands

- Too much protein was loaded per lane. This is especially a problem with silver stained gels.
- Cross contamination in the lane from adjacent samples.

Marker has wrong MW on gel/blot

- Pre-Stained Standards show an apparent MW that is affected by pH of the gels and buffers used. Use Unstained standards for accurate molecular weight determination.
- Don't use these markers on a native gel. These markers are only for SDS-PAGE.
- For more information on factors affecting protein migration:
Tung, Jwu-Sheng and Knight, C.A. (1972) *Analytical Biochemistry* 48, 153-163
Matagne, A., Joris, B., Frere, J. (1991) *Biochem J.* 280, 553-556

Cross Reactivity on Western Blots

- See protein origins above in 'Components' section.

Poor Transfer

- Increase voltage, current or length of time for transfer.
- For transfer to PVDF, omit the SDS from the transfer buffer. SDS will cause the proteins to bind less efficiently to membranes because it disrupts the hydrophobic interaction between the membrane and the protein. If SDS is present in transfer buffer (i.e. to facilitate transfer of large proteins), make sure that there is no more than 0.02% SDS present in buffer.
- Methanol helps to enhance the hydrophobic "stick" of the proteins to the membrane. Too much methanol however, can be a problem as the proteins can become fixed in the gel. The methanol concentration in a western blot should be between 10 – 20%.

Marker goes through membrane during transfer

- Decrease voltage, transfer time.
- Ensure proper SDS, methanol concentration. Too much SDS can prevent binding to membrane. Alcohol enhances hydrophobic binding to membrane; not enough alcohol may prevent binding.
- Check pore size of membrane and size of proteins of interest. Proteins smaller than 10kDa will more easily transfer through a 0.45um pore size membrane. If smaller proteins are the target, 0.2um pore size will better capture those proteins smaller than 10kDa.

PRODUCT DOCUMENTATION

[\(back to Table of Content\)](#)

[Brochures](#)

[Citations](#)

[Cell lines](#)

[COA](#)

[FAQ](#)

[Licensing](#)

[Manuals](#)

[MSDS](#)

[Newsletters](#)

[Vector Data](#)

REFERENCES

[\(back to Table of Content\)](#)

Factors affecting migration/apparent molecular weight

- Tung, Jwu-Sheng and Knight, C.A. (1972) *Analytical Biochemistry* 48, 153-163
- Matagne,A., Joris,B., Frere, J. (1991) *Biochem J.* 280, 553-556

PRODUCT NAME AND CATALOG NUMBERS

[\(back to Table of Content\)](#)

| Name | Size | Catalog Number |
|--|--|----------------|
| Mark12™ Unstained Standard | 1 ml (200 applications of 5ul each) | LC5677 |
| HiMark™ Unstained High Molecular Weight Protein Standard | 250 µl (50 applications of 5 µl each) | LC5688 |
| BenchMark™ Protein Ladder | 2 x 250 µl (100 applications of 5 µl each) | 10747012 |

COMPONENTS

[\(back to Table of Content\)](#)

| Name | Components |
|--|--|
| Mark12™ Unstained Standard | 1 ml supplied in loading buffer containing Tris-HCl, Glycerol, SDS, Phenol red, Coomassie Blue G-250. |
| HiMark™ Unstained High Molecular Weight Protein Standard | 250 mM Tris-HCl, pH 8.5; 0.5 mM EDTA; 50 mM DTT; 10% glycerol; 2% LDS; 0.2 mM Coomassie® G-250; 0.175 mM |

| | |
|---------------------------|---|
| | Phenol red. |
| BenchMark™ Protein Ladder | Two vials of 250 µl each are provided in loading buffer consisting of 50 mM Tris-HCl (pH 6.8); 2 mM EDTA; 10 mM DTT; 2% (w/v) SDS; 10% (w/v) Glycerol; 0.01%(w/v) Bromophenol blue. |

ASSOCIATED PRODUCTS

[\(back to Table of Content\)](#)

Novex Tris-Glycine Gels
NuPAGE Bis-Tris Gels
NuPAGE Tris-Acetate Gels

Need more help? Please email us by clicking [here](#).