Glycoproteomics

UNDERSTANDING PROTEIN MODIFICATIONS

Now includes α-Lytic Protease
Glycoproteomics Products

New England Biolabs (NEB) offers a selection of endoglycosidases and exoglycosidases for glycobiology research. Many of these reagents are recombinant, and all undergo several quality control assays, enabling us to provide products with lower unit cost, high purity and reduced lot-to-lot variation. All of our glycosidases are tested for contaminants. Since p-nitrophenyl-glycosides are not hydrolyzed by some exoglycosidases, we use only fluorescently-labeled oligosaccharides to screen for contaminating glycosidases.

GlycoBuffer Compositions

**Glycoproteomics**

Glycobiology is the study of the structure, function and biology of carbohydrates, also called glycans, which are widely distributed in nature. It is a small but rapidly growing field in biology, with relevance to biomedicine, biotechnology and basic research. Proteomics, the systematic study of proteins in biological systems, has expanded the knowledge of protein expression, modification, interaction and function. However, in eukaryotic cells the majority of proteins are post-translationally modified (1). A common post-translational modification, essential for cell viability, is the attachment of glycans, shown in Figure 1. Glycosylation defines the adhesive properties of glycoconjugates and it is largely through glycan–protein interactions that cell–cell and cell–pathogen contacts occur, a fact that accentuates the importance of glycobiology. Glycomics, the study of glycan expression in biological systems, relies on effective enzymatic and analytical techniques for correlation of glycan structure with function.

NEB offers a suite of endoglycosidases and exoglycosidases to study glycosylation modifications. Visit [www.NEBglycosidase.com](http://www.NEBglycosidase.com) for the latest list of enzymes and reagents available from NEB.

Figure 1: N- and O-Glycosylation

N-linked glycosylation occurs through the asparagine residues of the protein, while O-linked glycosylation occurs through serine or threonine.

**DOWNLOAD THE NEB AR APP**

*see back cover for details
Deglycosylation Enzymes

Several classes of glycans exist, including N-linked glycans, O-linked glycans, glycolipids, O-GlcNAc, and glycosaminoglycans. N-linked glycosylation occurs when glycans are attached to asparagine residues on the protein. O-linked glycans are most commonly attached to serine or threonine residues through the N-Acetylgalactosamine residue. Removal of oligosaccharides from glycoproteins, termed deglycosylation, is often used to simplify analysis of the peptide and/or glycan portion of a glycoprotein. Detailed knowledge of the glycan structures helps to correlate them to their respective function.

To do this, tools are required for highly sensitive analysis of glycan chains. Both chemical and enzymatic methods exist for removing oligosaccharides from glycoproteins. However, chemical methods such as β-elimination with mild alkali (1) or mild hydrazinolysis (2) can be harsh and result in the degradation of the protein; whereas enzymatic methods are much gentler and can provide complete sugar removal with no protein degradation.

### Endoglycosidase Selection Chart

<table>
<thead>
<tr>
<th>PROTEIN DEGLYCOSYLATION MIX II (P05044)</th>
<th>O-GLYcosidase (P0733 &amp; P0640)</th>
<th>PNGASE A (P0787)</th>
<th>PNGASE F (P0704 &amp; P0703)</th>
<th>REMOVE-IT PNGASE F (P0706)</th>
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<th>ENDO S (P0741)</th>
<th>ENDO D (P0742)</th>
<th>ENDO F2 (P0772)</th>
<th>ENDO F3 (P0771)</th>
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**References**


**ADVANTAGES**

- Low cost
- Easy Reaction Setup
- Digestion with a combination of enzymes can yield structural information
- Can be used under native and denaturing conditions

GF = Glycerol Free
Protein Deglycosylation Mix II

Deglycosylation of a glycoprotein often requires more than one enzyme to completely remove all carbohydrate residues. PNGase F removes almost all \( N \)-linked oligosaccharides, while monosaccharides on \( O \)-linked glycans must be removed by a series of exoglycosidases, such as \( \beta \)-1-4 Galactosidase S and \( \beta \)-N-Acetylhexosaminidase\(_f\), until only the GlcNAc\(\beta\)-1-3GalNAc (core 1) and/or the GlcNAc\(\beta\)-1-3GalNAc (core 3) cores remain attached to the core protein. \( O \)-Glycosidase can then remove these core structures leaving serine or threonine residues intact. Sialic acid residues, which will block the action of the \( O \)-Glycosidase, are easily removed by NEB’s general \( \alpha \)2,3,6,8,9 Neuraminidase A.

The Protein Deglycosylation Mix II contains all of the enzymes, reagents, and controls needed to remove all \( N \)-linked and simple \( O \)-linked glycans as well as some complex \( O \)-linked glycans. This mix contains enzyme sufficient for 20 reactions or the cleavage of as much as 2 mg of glycoprotein. The Protein Deglycosylation Enzyme Mix II (100 µl) is a single mix made up of five recombinant enzymes: PNGase F Glycerol Free Recombinant, \( O \)-Glycosidase, \( \alpha \)2–3,6,8,9 Neuraminidase A, \( \beta \)-1-4 Galactosidase S, and \( \beta \)-N-Acetylhexosaminidase\(_f\). The mix is supplied with all of the reagents and controls required to complete the experiment under either non-denaturing (native) or reducing conditions. Components include 10X Deglycosylation Mix Buffer 1, 10X Deglycosylation Mix Buffer 2, and a Fetuin control containing sialylated \( N \)-linked and \( O \)-linked glycans. All of the enzymes and reagents included in the Protein Deglycosylation Mix II are Mass Spectrometry compatible. Following the deglycosylation reaction, samples are ready to be prepared for mass spectrometry analysis.

Protein Deglycosylation Mix II ................................................................. P6044S

Enzymatic Deglycosylation of Bovine Fetuin

Enzymatic Deglycosylation of Bovine Fetuin under both native (10X Deglycosylation Mix Buffer 1) and reducing (10X Deglycosylation Mix Buffer 2) conditions. 20 µg reactions were loaded onto a 10-20% Tris-glycine SDS-PAGE gel.

Lane 1: Color Prestained Protein Standard, Broad Range (11-245 kDa) (NEB #P7712)
Lane 2: 20 µg untreated Fetuin control
Lane 3: 20 µg Fetuin deglycosylated under native conditions with Deglycosylation Mix Buffer 1
Lane 4: 20 µg Fetuin deglycosylated under reducing conditions with Deglycosylation Mix Buffer 2
Lane 5: 5 µl Protein Deglycosylation Mix II
**N-Linked Deglycosylation Enzymes**

For structural analysis of asparagine-linked carbohydrates (N-linked glycans), sugars are released from the protein backbone by enzymes such as PNGase F, PNGase A, Endoglycosidase S, Endoglycosidase D and Endoglycosidase H.

**PNGase F (native and recombinant)**

Peptide-N-Glycosidase F, also known as PNGase F, is an amidase which cleaves between the innermost GlcNAc and asparagine residues of high mannose, hybrid and complex oligosaccharides from N-linked glycoproteins. PNGase F from NEB is purified from Flavobacterium meningosepticum. A glycerol-free version of PNGase F is also offered for HPLC methods.

**Detailed Specificity:**

PNGase F hydrolyzes nearly all types of N-glycan chains from glycopeptides/proteins. PNGase F can cleave when an $\alpha_{1-6}$ Fucose is on the core GlcNAc. PNGase F cannot cleave when an $\alpha_{1-3}$ Fucose is on the core GlcNAc.

PNGase F .......................................................... P0704S/L
PNGase F, Recombinant ........................................... P0708S/L
PNGase F (Glycerol-free) ........................................ P0705S/L
PNGase F (Glycerol-free), Recombinant .................. P0709S/L

References
A growing number of antibodies and antibody fusions are currently used as therapeutic agents. A conserved N-glycan at Asn297 of the Fc region of IgG is critical for functional activity. Moreover, some antibodies have additional N-glycans that, together with the conserved site, affect recognition, half-life, and immune reactions. Antibody glycosylation is heterogeneous, and variables in cell culture can increase glycan diversity. Monitoring glycosylation during production is essential to obtain the correct glycoprotein forms.

Obtaining an accurate N-glycan profile in the shortest time possible is essential for effective process control. Typically, enzymatic release of antibody N-glycans using PNGase F requires an incubation time of several hours, followed by glycan derivatization and analysis by liquid chromatography and/or mass spectrometry. In addition, incomplete deglycosylation can lead to biased results. Some glycans are easier to remove than others and unless deglycosylation is extensive, the profile obtained will not represent the correct composition of the therapeutic antibody.

**Rapid PNGase F**

Deglycosylation in minutes for N-glycan analysis

Rapid PNGase F is an improved reagent that allows the complete and rapid deglycosylation of antibodies and immunoglobulin-fusion proteins in minutes. All N-glycans are released rapidly and without bias, and are ready to be prepared for downstream chromatography or mass spectrometry analysis. Rapid PNGase F creates an optimized workflow which reduces processing time without compromising sensitivity or reproducibility.

ESI-TOF analysis of an antibody before and after treatment with Rapid PNGase F

**Rapid PNGase F (non-reducing format)**

Deglycosylation in minutes for intact antibody analysis

Developed for proteomic applications, Rapid PNGase F (non-reducing format) is a reformulated version of Rapid PNGase F that allows the complete and rapid deglycosylation of antibodies and fusion proteins in minutes, while preserving disulfide bonds. All N-glycans are released rapidly and without bias, facilitating high throughput proteomics applications and methods for antibody characterization by mass spectrometry such as intact mass analysis. Rapid PNGase F (non-reducing format) combines the advantages of Rapid PNGase F (fast processing time), with the non-reducing conditions preserving quaternary structure.
Detailed Specificity:
Rapid PNGase F & Rapid PNGase F (non-reducing format) cleave all complex, hybrid and high-mannose type glycans from antibodies and related proteins. Core α1-3 fucosylation (found in immunoglobulins expressed in plant or insect cells) is resistant to all forms of PNGase F.

PNGase A
PNGase A is a recombinant amidase, which cleaves between the innermost GlcNAc and asparagine residues of high mannose, hybrid, and short complex oligosaccharides such as those found in plant and insect cells from N-linked glycoproteins and glycopeptides. PNGase A differs from PNGase F in that it cleaves N-linked glycans with or without α(1,3)-linked core fucose residues.

Detailed Specificity:
PNGase A hydrolyzes N-glycan chains from glycoproteins/peptides regardless of the presence of xylose or fucose. [x = H or Man or GlcNAc]
Endo S

Endo S is an endoglycosidase with a uniquely high specificity for removing N-linked glycans from the chitobiose core of the heavy chain of native IgG. Endo S is tagged with a chitin binding domain (CBD) for easy removal from a reaction and is supplied glycerol free for optimal performance in HPLC and MS intensive methods.

Endo S does not have a strict peptide requirement for activity, thus the “X” can be a protein, peptide, Asparagine, or free glycan. Endo S is active on a substrate with or without core α(1-6) fucosylation as well as with or without a bisecting N-acetylglucosamine. Triantennary and tetraantennary sialyted or asialo glycans are not a substrate for Endo S.

Endo S .......................................................................................................................... P0741S/L

Remove-iT PNGase F

Remove-iT PNGase F is an amidase which cleaves between the innermost GlcNAc and asparagine residues of high mannose, hybrid, and complex oligosaccharides from N-linked glycoproteins. Remove-iT PNGase F is purified from Flavobacterium meningosepticum and is tagged with a chitin binding domain (CBD) for easy removal from a reaction. It is supplied glycerol free for optimal performance in HPLC and MS intensive methods.

Remove-iT PNGase F .................................................................................................. P0706S/L

Remove-iT PNGase F hydrolyzes nearly all types of N-glycan chains from glycopeptides/proteins. [x = H or oligosaccharide]. Remove-iT PNGase F can cleave when an α1-6 Fucose is on the core GlcNAc

Remove-iT PNGase F cannot cleave when an α1-3 Fucose is on the core GlcNAc

ADVANTAGES

- Chitin Binding Domain (CBD) tag ensures easy removal from a reaction
- Fast reaction setup
- Compatible with protease inhibitor cocktails
- Glycerol-free formulation for optimal performance in HPLC and mass spec analysis
Endo D

Endo D also known as Endoglycosidase D is a recombinant glycosidase, which cleaves within the chitobiose core of paucimannose N-linked glycans, with or without extensions in the antennae. Endo D is active on both linear and branched upper arm extensions, and is useful for determining N-glycosylation sites. Endo D is tagged with a chitin binding domain (CBD) for easy removal from a reaction, and is supplied glycerol-free for optimal performance in HPLC and MS intensive methods.

Endo D .......................................................... P0742S/L

Endo D does not have a strict peptide requirement for activity, thus the “X” can be a protein, peptide or Asparagine. The upper branch, “Z”, can be a “H”, monosaccharide or oligosaccharide.

Endo F2

Endo F2 is a highly specific recombinant endoglycosidase which cleaves within the chitobiose core of asparagine-linked complex biantennary and high mannose oligosaccharides from glycoproteins and glycopeptides. Endo F2 cleaves biantennary glycans at a rate approximately 20 times greater than high mannose glycans. The activity of Endo F2 is identical on biantennary structures with and without core fucosylation. However, Endo F2 is not active on hybrid or tri- and tetra-antennary oligosaccharides. Endo F2 is tagged with a chitin binding domain (CBD) for easy removal from a reaction and is supplied glycerol free for optimal performance in HPLC and MS intensive methods.

Endo F2 .......................................................... P0772S/L
Endo F3

Endo F3 is a highly specific recombinant endoglycosidase which cleaves within the chitobiose core of asparagine-linked fucosylated-biantennary and triantennary complex oligosaccharides from glycoproteins. Endo F3 is tagged with a chitin binding domain (CBD) for easy removal from a reaction and is supplied glycerol free for optimal performance in HPLC and MS intensive methods.

Endoglycosidase H

Endoglycosidase H (Endo H) is a recombinant glycosidase which cleaves within the chitobiose core of high mannose and some hybrid oligosaccharides from N-linked glycoproteins. Endo H is a recombinant protein fusion of Endoglycosidase H and maltose binding protein. It has identical activity to Endo H. Endo H and Endo H\textsubscript{f} from NEB are cloned from Streptomyces plicatus and overexpressed in E. coli.

Endo H and Endo H\textsubscript{f} cleave only high mannose structures (n = 2–150, x = (Man)\textsubscript{1–2}, y = H) and hybrid structures (n = 2, x and/or y = AcMan-4GlcNAc) "X" can be a protein, peptide or Asparagine.
O-Linked Deglycosylation Enzymes

For structural analysis of serine or threonine-linked carbohydrates (O-linked glycans), sugars are released from the protein backbone by either chemical or enzymatic methods. Removing O-linked glycan chains while rendering a protein intact for further examination can be a difficult task. Chemical methods, such as β-elimination, may result in incomplete sugar removal and degradation of the protein. On the other hand, enzymatic removal of O-linked glycans must be performed as a series of exoglycosidase digestions until only the Galβ1-3GalNAc (core 1) and/or the GlcNAc β1-3GalNAc (core 3) cores remains attached to the serine or threonine residue. NEB’s *Enterococcus faecalis* O-Glycosidase, also known as Endo-α-N-Acetylgalactosaminidase, catalyzes the removal of core 1 and core 3 disaccharide structures with no modification of the serine or threonine residues (1). Any modification of the core structures, including sialylation, will block the action of the O-Glycosidase. Sialic acid residues are easily removed by a general Neuraminidase. In addition, exoglycosidases such as β1-4 Galactosidase and β-N-Acetylglucosaminidase can be included in deglycosylation reactions to remove other complex modifications often known to be present on the core structures.

O-Glycosidase

O-Glycosidase, also known as Endo-α-N-Acetylgalactosaminidase, catalyzes the removal of Core 1 and Core 3 O-linked disaccharides from glycoproteins. O-Glycosidase from NEB is cloned from *Enterococcus faecalis* and expressed in *E. coli*.

O-Glycosidase (Endo-α-N-Acetylgalactosaminidase) ................................................. P0733S/L
α2-3,6,8 Neuraminidase .......................................................... P0720S/L
O-Glycosidase & Neuraminidase Bundle ............................................. E0540S

Reference

Companion Products

Endoglycosidase Reaction Buffer Pack
The Endoglycosidase Reaction Buffer Pack contains 1 ml of every buffer necessary for optimal activity of a deglycosylation reaction including 10X GlycoBuffer 2, 10X GlycoBuffer 3, 10X Glycoprotein Denaturing Buffer and 10% NP-40.
Endoglycosidase Buffer Pack .................. B0701S

RNase B
RNase B is a high mannose glycoprotein that can be used as a positive control for endoglycosidases that cleave N-linked carbohydrates. RNase B has a single N-linked glycosylation site which makes it ideal for SDS-PAGE gel shift assays. It has an intact molecular weight of 17,000 daltons, and a molecular weight of 13,683 daltons after deglycosylation.
RNase B .................................................. P7817S

Fetuin
Fetuin is a glycoprotein containing sialylated N-linked and O-linked glycans that can be used as a positive control for endoglycosidase enzymes.
Fetuin ................................................ P6042S

Rapid PNGase F Antibody Standard
Rapid PNGase F Antibody Standard is a murine anti-MBP monoclonal antibody, isotype IgG2a. It is comprised of two heavy chains which are each approximately 49 kDa, as well as two light chains which are each approximately 24.4 kDa. This antibody standard can be used as a positive control for Rapid PNGase F.
Rapid PNGase F Antibody Standard ............... P6043S
Exoglycosidase Enzymes

NEB offers a wide selection of exoglycosidases for glycobiology research. Exoglycosidases cleave a monosaccharide from the non-reducing end of an internal glycosidic linkage in an oligosaccharide or polysaccharide. Many of these reagents are recombinant, and all undergo several quality control assays, enabling us to provide products with lower unit cost, high purity, and reduced lot-to-lot variation. All of our glycosidases are tested for contaminants. Since p-nitrophenyl-glycosides are not hydrolyzed by some exoglycosidases, we use only flourescently-labeled oligosaccharides to assay activity and screen for contaminating glycosidases.

**α2-3,6,8,9 Neuraminidase A**

Neuraminidase is the common name for Acetyl-neuraminy hydrolase (Sialidase). α2-3,6,8,9 Neuraminidase A, cloned from *Arthrhotobacter ureafaciens*, catalyzes the hydrolysis of all linear and branched non-reducing terminal sialic acid residues from glycoproteins and oligosaccharides. The enzyme releases α2-3 and α2-6 linkages at a slightly higher rate than α2-8 and α2-9 linkages.

α2-3,6,8,9 Neuraminidase A ................................................................. P0722S/L

**α2-3,6,8 Neuraminidase**

α2-3,6,8 Neuraminidase, cloned from *Clostridium perfringens*, catalyzes the hydrolysis of α2-3, α2-6 and α2-8 linked N-acetylneuraminic acid residues from glycoproteins and oligosaccharides.

α2-3,6,8 Neuraminidase ................................................................. P0720S/L

**α2-3 Neuraminidase S**

α2-3 Neuraminidase S is a highly specific exoglycosidase that catalyzes the hydrolysis of α2-3 linked N-acetylneuraminic acid residues from glycoproteins and oligosaccharides. α2-3 Neuraminidase S is cloned from *Streptococcus pneumoniae* and expressed in *E. coli*.

α2-3 Neuraminidase S ................................................................. P0743S/L

**β-N-Acetylgalactosaminidase f**

β-N-Acetylgalactosaminidase f, cloned from *Streptomyces plicatus*, is a recombinant protein fusion of β-N-Acetylgalactosaminidase and maltose binding protein with identical activity to β-N-Acetylgalactosaminidase. It catalyzes the hydrolysis of terminal β-N-Acetylgalactosamine and glucosamine residues from linear oligosaccharides.

β-N-Acetylgalactosaminidase f ................................................................. P0721S/L

References

**β-N-Acetylglucosaminidase S**

β-N-Acetylglucosaminidase S, cloned from *Streptococcus pneumoniae*, is a highly specific exoglycosidase that catalyzes the hydrolysis of terminal, non-reducing β-N-Acetylglucosamine residues from oligosaccharides. β-N-Acetylglucosaminidase S is able to efficiently cleave bisecting β-N-Acetylglucosamine residues.

β-N-Acetylglucosaminidase S ............................................................... P0744S/L

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**α1-2 Fucosidase**

α1-2 Fucosidase, cloned from *Xanthomonas manihotis*, is a highly specific exoglycosidase that catalyzes the hydrolysis of linear α1-2 linked fucose residues from oligosaccharides. A linear substrate is defined as having no branching on the adjacent residue.

α1-2 Fucosidase ............................................................... P0724S/L

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**α1-2,3,4,6 Fucosidase**

α1-2,3,4,6 Fucosidase, cloned from bovine kidney, is a broad specificity exoglycosidase that catalyzes the hydrolysis of α1-2, α1-3, α1-4 and α1-6 linked fucose residues from oligosaccharides. α1-2,3,4,6 Fucosidase cleaves α1-2 and α1-6 fucose residues more efficiently than other linkages, and has slight activity towards α1-3 fucose residues.

α1-2,3,4,6 Fucosidase ............................................................... P0748S/L

---

**α1-2,4,6 Fucosidase O**

α1-2,4,6 Fucosidase O, cloned from *Omnitrophica*, is a broad specificity exoglycosidase that catalyzes the hydrolysis of terminal α1-2, α1-4 and α1-6 linked fucose residues from oligosaccharides and glycoproteins. α1-2,4,6 Fucosidase O cleaves α1-6 fucose residue more efficiently than other linkages.

α1-2,4,6 Fucosidase O ............................................................... P0749S/L

---

**α1-3,4 Fucosidase**

α1-3,4 Fucosidase, (also known as AMF) is a broad specificity exoglycosidase that catalyzes the hydrolysis of α1-3 and α1-4 linked fucose residues from oligosaccharides and glycoproteins.

α1-3,4 Fucosidase ............................................................... P0769S/L
**β1-3 Galactosidase**

β1-3 Galactosidase, cloned from *Xanthomonas manihotis*, is a highly specific exoglycosidase that catalyzes the hydrolysis of β1-3 and, at a much lower rate, β1-6 linked galactose residues from oligosaccharides. The approximate kinetic data show >100-fold preference for β1-3 over β1-6 linkages and >500-fold preference for β1-3 over β1-4 linkages.

β1-3 Galactosidase ................................................................. P0726S/L

**β1-4 Galactosidase S**

β1-4 Galactosidase S, cloned from *Streptococcus pneumoniae*, is a highly specific exoglycosidase that catalyzes the hydrolysis of β1-4 linked galactose residues from oligosaccharides.

β1-4 Galactosidase S ............................................................... P0745S/L

**β1-3,4 Galactosidase**

β1-3,4 Galactosidase, cloned from bovine testis and also known as BTG, is a highly specific exoglycosidase that catalyzes the hydrolysis of terminal β1-3 and β1-4 linked galactose residues from oligosaccharides.

β1-3,4 Galactosidase ................................................................. P0746S/L

**α1-6 Mannosidase**

α1-6 Mannosidase, cloned from *Xanthomonas manihotis*, is a highly specific exoglycosidase that removes unbranched α1-6 linked mannose residues from oligosaccharides. When used in conjunction with α1-2,3 Mannosidase, the α1-6 Mannosidase will cleave α1-6 mannose residues from branched carbohydrate substrates.

α1-6 Mannosidase ................................................................. P0727S/L

**α1-2,3 Mannosidase**

α1-2,3 Mannosidase, cloned from *Xanthomonas manihotis*, is a highly specific exoglycosidase that catalyzes the hydrolysis of α1-2 and α1-3 linked mannose residues from oligosaccharides.

α1-2,3 Mannosidase ................................................................. P0729S/L
**α1-2,3,6 Mannosidase**

α1-2,3,6 Mannosidase, cloned from Jack Bean, and also known as JBM, is a broad specificity exoglycosidase that catalyzes the hydrolysis of terminal α1-2, α1-3 and α1-6 linked mannose residues from oligosaccharides. α1-2,3,6 Mannosidase has a slight preference for α1-2 mannose residues over α1-3 and α1-6 mannose residues.

α1-2,3,6 Mannosidase ................................................................. P0768S/L

**α1-3,6 Galactosidase**

α1-3,6 Galactosidase, cloned from *Xanthomonas manihotis*, is a highly specific exoglycosidase that catalyzes the hydrolysis of α1-3 and α1-6 linked galactose residues from oligosaccharides.

α1-3,6 Galactosidase ................................................................. P0731S/L

**α1-3,4,6 Galactosidase**

α1-3,4,6 Galactosidase, cloned from green coffee bean, is a highly specific exoglycosidase that catalyzes the hydrolysis of α1-3, α1-4 and α1-6 linked galactose residues from oligosaccharides.

α1-3,4,6 Galactosidase ................................................................. P0747S/L

**α-N-Acetylgalactosaminidase**

α-N-Acetylgalactosaminidase, cloned from *Chryseobacterium meningosepticum*, is a highly specific exoglycosidase that catalyzes the hydrolysis of α-N-acetylgalactosamine residues from oligosaccharides and N-linked glycans attached to proteins.

α-N-Acetylgalactosaminidase ................................................................. P0734S/L

**GlycoBuffer Compositions**

1X GlycoBuffer 1:
50 mM sodium acetate (pH 5.5 @ 25°C), 5 mM CaCl₂

1X GlycoBuffer 2:
50 mM sodium phosphate (pH 7.5 @ 25°C)

1X GlycoBuffer 3:
50 mM sodium acetate (pH 6.0 @ 25°C)

1X GlycoBuffer 4:
50 mM sodium acetate (pH 4.5 @ 25°C)
Heparin Lyase Enzymes

Heparin Lyase enzymes, also called Heparinases, are enzymes that cleave the glycosidic linkage between hexosamines and uronic acids and are known to cleave heparin and heparin sulfate (HS) chains selectively, via an elimination mechanism. Heparinase enzymes create a double bond on the non-reducing end of the uronic acid that absorbs at 232 nm and can be used for the detection of oligosaccharide and disaccharide products. Three Heparinase enzymes are available: Bacteroides Heparinase I, Heparinase II and Heparinase III. Heparinase I cleaves highly sulfated heparin/HS chains, Heparinase III cleaves less sulfated HS chains, while Heparinase II cleaves domains of both high and low sulfation on both heparin and HS. Heparinase I, II and III used in combination can produce a near-complete depolymerization of heparin/HS polysaccharide chains to disaccharides.

**Bacteroides Heparinase I**

*Bacteroides* Heparinase I cloned from *Bacteroides eggerthii*, also called Heparin Lyase I, is active on heparin and the highly sulfated domains of heparan sulfate. The reaction yields oligosaccharide products containing unsaturated uronic acids which can be detected by UV spectroscopy at 232 nm.

**Detailed Specificity:**

*Bacteroides* Heparinase I cleaves between N-sulfated hexosamines and 2-O-sulfated iduronic acid residues as well as the 2-O-sulfated glucuronic acid residue. The 2-O-sulfated uronic acid residue is essential for the activity of *Bacteroides* Heparinase I and 6-O-sulfation of GlcNSO does not hinder enzyme activity. Limited digest of porcine mucosal heparin with the *Bacteroides* Heparinase I results in heparin oligosaccharides with a lower extent of sulfation as reported (1).

*Bacteroides* Heparinase I ................................................................. P0735S/L

**Bacteroides Heparinase II**

*Bacteroides* Heparinase II cloned from *Bacteroides eggerthii*, also called Heparin Lyase II, is a low specificity enzyme that is active on both heparin and heparan sulfate. The reaction yields oligosaccharide products containing unsaturated uronic acids which can be detected by UV spectroscopy at 232 nm.

**Detailed Specificity:**

*Bacteroides* Heparinase II cleaves the glycosidic bond between N-sulfated glucuronic or iduronic acid residues. When used alone this enzyme rarely yields complete depolymerization of a polysaccharide chain, however disaccharide analysis is enhanced when used in combination with Heparinase I and III.

*Bacteroides* Heparinase II ................................................................. P0736S/L

**Bacteroides Heparinase III**

*Bacteroides* Heparinase III cloned from *Bacteroides eggerthii*, also called Heparin Lyase III, is active on both heparin and heparan sulfate. The reaction yields oligosaccharide products containing unsaturated uronic acids which can be detected by UV spectroscopy at 232 nm.

**Detailed Specificity:**

*Bacteroides* Heparinase III can cleave the glycosidic bond between hexosamines and either iduronic acid or glucuronic acid residues, and is active in the presence of 6-sulfation.

*Bacteroides* Heparinase III ................................................................. P0737S/L

**Note:** Heparin Hexasaccharide MS Standard 6 (NEB #P0738S) and Heparin Hexasaccharide MS Standard 7 (NEB #P0739S) are available by special order. Contact info@neb.com for details.

References

IdeZ Protease (IgG-specific) is a recombinant antibody specific protease cloned from *Streptococcus equi* subspecies *zooepidemicus* that recognizes all human, sheep, monkey, and rabbit IgG subclasses, specifically cleaving at a single recognition site below the hinge region, yielding a homogenous pool of F(ab’)2 and Fc fragments. IdeZ Protease has significantly improved activity against murine IgG2a and IgG3 subclasses compared to IdeS Protease.

**Detailed Specificity:**

- Human IgG1, IgG3, IgG4: CPAPELLG\(\beta\)GPSVF
- Human IgG2: CPAPPVA\(\beta\)GPSVF
- Murine IgG2a: CPAPNLLG\(\beta\)GPSVF
- Murine IgG3: CPPGNILG\(\beta\)GPSVF

**Notes:** IdeZ Protease efficiently cleaves human, humanized, chimeric, sheet, rabbit and monkey IgG as well as mouse IgG2a and IgG3. IdeZ Protease will also cleave Fc-fusion proteins, such as Enbrel.

IdeZ Protease does not cleave mouse IgG1 or IgG2b, rat, porcine, bovine or goat IgG. It also does not cleave non-IgG isotypes including IgA, IgM, IgD and IgE.

**Digestion of IgG with IdeZ Protease (IgG-specific), followed by denaturation.**
Trypsin-digested BSA MS Standard (CAM-modified)

A complex mixture of peptides produced by the tryptic digest of Bovine Serum Albumin (BSA) that has been reduced and alkylated with iodacetamide (CAM modified). This peptide mixture is free of salts, glycerol and detergents and can therefore be used to standardize Matrix-Assisted Laser Desorption/Ionization Time-Of-Flight (MALDI-TOF) or Electrospray Ionization (ESI) mass spectrometers (TOF, Q-TOF, Ion Trap, or Orbitrap) using a standardization range of 500-2400 Da.

Trypsin-digested BSA MS Standard (CAM-modified) .......................................................... P8108S

Trypsin-ultra,™ Mass Spectrometry Grade

Trypsin-ultra, Mass Spectrometry Grade is a serine endopeptidase isolated from Bovine pancreas. Trypsin is the most widely used enzyme in proteomics. It selectively cleaves peptide bonds C-terminal to lysine and arginine residues. Trypsin-ultra is treated with L-(tosylamido-2-phenyl) ethyl chloromethyl ketone (TPCK) to inactivate any remaining chymotryptic activity. It is modified by acetylation of the ε-amino groups of lysine residues to prevent autolysis. Trypsin-ultra cleaves at Lys-Pro and Arg-Pro bonds at a much slower rate than when Lys and Arg are N-terminal to other residues.

Trypsin-ultra, Mass Spectrometry Grade .......................................................... P8101S

α-Lytic Protease

α-Lytic Protease (aLP) cleaves after Threonine (T), Alanine (A), Serine (S) and Valine (V) residues. Its specificity makes it an orthogonal and alternative protease to others commonly used in proteomics applications, including trypsin and chymotrypsin. Peptides generated by aLP are of similar average length to those of Trypsin.

α-Lytic Protease .......................................................... P8113S/L

Endoproteinase LysC

LysC is a serine endoproteinase, isolated from Lysobacter enzymogenes, that cleaves peptide bonds at the carboxyl side of lysine. LysC is a sequencing grade enzyme and is suitable for proteomics and glyco-biology applications.

Endoproteinase LysC .......................................................... P8109S

Endoproteinase AspN

Endoproteinase AspN (flavastacin) is a zinc metalloendopeptidase which selectively cleaves peptide bonds N-terminal to aspartic acid residues.

Endoproteinase AspN .......................................................... P8104S

Endoproteinase GluC

Endoproteinase GluC (Staphylococcus aureus Protease V8) is a serine proteinase which preferentially cleaves peptide bonds C-terminal to glutamic acid residues. Endoproteinase GluC also cleaves at aspartic acid residues at a rate 100-300 times slower than at glutamic acid residues. Staphylococcus aureus Protease V8 gene was cloned and expressed in Bacillus subtilis. Endoproteinase GluC is observed as a single band on SDS-PAGE and TOF-MS and is intended for use in mass spectrometry and protein sequencing.

Endoproteinase GluC .......................................................... P8100S
### Deglycosylation Enzymes

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<th>SIZE</th>
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<tr>
<td>Protein Deglycosylation Mix II</td>
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<td>20 reactions</td>
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<td>PNGase A</td>
<td>P0707S/L</td>
<td>150/750 units (5,000 units/ml)</td>
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<td>Rapid PNGase F</td>
<td>P0710S</td>
<td>50 reactions</td>
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<td>Rapid PNGase F (non-reducing format)</td>
<td>P0711S</td>
<td>50 reactions</td>
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<td>PNGase F</td>
<td>P0704S/L</td>
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<td>PNGase F, Recombinant</td>
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<td>PNGase F (Glycerol-free)</td>
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<td>PNGase F (Glycerol-free), Recombinant</td>
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<td>Endo F2</td>
<td>P0772S</td>
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<td>Endo F3</td>
<td>P0771S</td>
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<td>Endo S</td>
<td>P0741S/L</td>
<td>6,000/30,000 units (200,000 units/ml)</td>
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<td>Endo D</td>
<td>P0742S/L</td>
<td>1,500/7,500 units (50,000 units/ml)</td>
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<td>Endo H</td>
<td>P0702S/L</td>
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<td>Endo H₁</td>
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<tr>
<td>O-Glycosidase</td>
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<tr>
<td>O-Glycosidase &amp; Neuraminidase Bundle</td>
<td>E0540S</td>
<td>2,000,000 units O-Glycosidase &amp; 2,000 units Neuraminidase</td>
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### Exoglycosidase Enzymes

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<tr>
<td>α-N-Acylgalactosaminidase</td>
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<td>β-N-Acylglucosaminidase S</td>
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<td>100/500 units (4,000 units/ml)</td>
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<td>β-N-Acetylhexosaminidase</td>
<td>P0721S/L</td>
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<td>α1-2 Fucosidase</td>
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<td>α1-3,4 Fucosidase</td>
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<td>β1-3 Galactosidase</td>
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<td>β1-4 Galactosidase S</td>
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<td>α2-3 Neuraminidase S</td>
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### Heparin Lyases

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<tr>
<td>Bacteroides Heparinase I</td>
<td>P0735S/L</td>
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<td>Bacteroides Heparinase II</td>
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<td>Bacteroides Heparinase III</td>
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### Glycoproteomics

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<td>Trypsin-digested BSA MS Standards (CAM Modified)</td>
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<td>500 pmol</td>
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<td>Trypsin-ultra, Mass Spectrometry Grade</td>
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<td>α-Lytic Protease</td>
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<td>Endoproteinase LysC</td>
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<td>Endoproteinase GluC</td>
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### Companion Products

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<td>Fetuin</td>
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<td>RNase B</td>
<td>P7817S</td>
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<td>Rapid PNGase F Antibody Standard</td>
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<td>Chitin Magnetic Beads</td>
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<td>6-Tube Magnetic Separation Rack</td>
<td>S1506S</td>
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<td>50 ml Magnetic Separation Rack</td>
<td>S1507S</td>
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<td>2-Tube Magnetic Separation Rack</td>
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<tr>
<td>96-Well Microtiter Plate Magnetic Separation Rack</td>
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