Hamster FUT8 Protein (aa 68-575, His Tag)

Catalog Number: **51166-M08B**

Sino Biological Inc.
Biological Solution Specialist

General Information

Gene Name Synonym:

FUT8; MGC26465

Protein Construction:

A DNA sequence encoding the hamster FUT8 (G3HCE4) (Arg68-Lys575) was fused with a polyhistidine tag at the C-terminus.

Source: Hamster

Expression Host: Baculovirus-Insect Cells

QC Testing

Purity: > 95 % as determined by SDS-PAGE

Endotoxin:

< 1.0 EU per μg of the protein as determined by the LAL method

Stability:

Samples are stable for up to twelve months from date of receipt at -70 ℃

Predicted N terminal: Arg 575

Molecular Mass:

The recombinant hamster FUT8 consists of 518 amino acids and has a calculated molecular mass of 60.1 kDa. The recombinant protein migrates as an approximately 55 kDa band in SDS-PAGE under reducing conditions.

Formulation:

Lyophilized from sterile 20mM Tris, 500mM NaCl, 3mM DTT, 10% glycerol, pH 7.0.

Normally 5 % - 8 % trehalose, mannitol and 0.01% Tween80 are added as protectants before lyophilization. Specific concentrations are included in the hardcopy of COA. Please contact us for any concerns or special requirements.

Usage Guide

Storage:

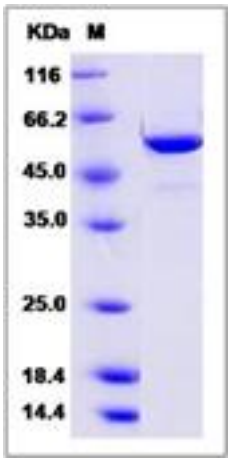
Store it under sterile conditions at -20℃ to -80℃ upon receiving. Recommend to aliquot the protein into smaller quantities for optimal storage.

Avoid repeated freeze-thaw cycles.

Reconstitution:

Detailed reconstitution instructions are sent along with the products.

SDS-PAGE:



Protein Description

Human alpha (1,6) fucosyltransferase 8, also known as FUT8, is a member of the glycosyltransferase family. Fucosyltransferases are the enzymes transferring fucose from GDP-Fuc to Gal in an alpha1,2-linkage and to GlcNAc in alpha1,3-linkage, alpha1,4-linkage, or alpha1,6-linkage. All fucosyltransferases utilize the same nucleotide sugar, their specificity reside in the recognition of the acceptor and in the type of linkage formed. Fucosyltransferases share some common structural and catalytic features. On the basis of protein sequence similarities, these enzymes can be classified into four distinct families: (1) the alpha-2-fucosyltransferases, (2) the alpha-3-fucosyltransferases, (3) the mammalian alpha-6-fucosyltransferases, and (4) the bacterial alpha-6-fucosyltransferases. The alpha-3-fucosyltransferases constitute a distinct family as they lack the consensus peptide, but some regions display similarities with the alpha-2 and alpha-6-fucosyltranferases.

References

1.Breton C, *et al.* (1998) Conserved structural features in eukaryotic and prokaryotic fucosyltransferases. Glycobiology. 8(1): 87-94.
2.Oriol R, *et al.* (1999) Divergent evolution of fucosyltransferase genes from vertebrates, invertebrates, and bacteria. Glycobiology. 9(4): 323-34.
3.de Vries T, *et al.* (2001) Fucosyltransferases: structure / function studies. Glycobiology. 11(10): 119-128.