Data Sheet (Cat.No.TMPY-02546)

FUT8 Protein, Human, Recombinant (aa 68-575, His)

General Information

Synonyms:	MGC26465;fucosyltransferase 8 (alpha (1,6) fucosyltransferase);fucosyltransferase 8 (α (1,6) fucosyltransferase)
Protein Construction:	A DNA sequence encoding the human FUT8 isoform 1 (Q9BYC5-1) (Arg 68-Lys 575) was fused with a polyhistidine tag at the carboxy-terminus. Predicted N terminal: Arg 68
Species:	Human
Expression Host:	Baculovirus Insect Cells
Accession:	Q9BYC5-1
Molecular Weight:	60 kDa (predicted); 55 kDa (reducing conditions)

QC Testing

Biological Activity:	Measured by its ability to hydrolyze the donor substrate GDP fucose. The specific activity is >0. 75 pmoles/min/μg.
Purity:	> 95 % as determined by SDS-PAGE
Endotoxin:	< 1.0 EU/μg of the protein as determined by the LAL method.
Formulation:	Supplied as sterile 20 mM Tris, 500 mM NaCl, pH 8.0, 10% gly.

Preparation and Storage

Reconstitution:

A Certificate of Analysis (CoA) containing reconstitution instructions is included with the products. Please refer to the CoA for detailed information.

Stability & Storage:

It is recommended to store the product under sterile conditions at -20°C to -80°C. Samples are stable for up to 12 months. Please avoid multiple freeze-thaw cycles and store products in aliquots.

Actual storage temperature shall be subject to the COA.

Shipping:

Proteins are shipped with blue ice.

Protein Background

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.

Reference

Breton C, et al. (1998) Conserved structural features in eukaryotic and prokaryotic fucosyltransferases. Glycobiology. 8(1): 87-94.

Oriol R, et al. (1999) Divergent evolution of fucosyltransferase genes from vertebrates, invertebrates, and bacteria. Glycobiology. 9(4): 323-34.

de Vries T, et al. (2001) Fucosyltransferases: structure / function studies. Glycobiology. 11(10): 119-128.

Baboval T, et al. (2002) Comparison of human and mouse Fuc-TX and Fuc-TXI genes, and expression studies in the mouse. Mamm Genome. 13(9): 538-41.