Recombinant OFUT2 protein (His tag)

Catalog Number	531189
Synonyms	Patterning defective protein 2; Peptide-O-fucosyltransferase 2; O-FucT-2
Species	Caenorhabditis elegans
Expression System	E. coli
Accession	Q8WR51
Gene ID	259529
Molecular Weight	Predictes a molecular mass of 47.32 kDa. In SDS-PAGE under reducing conditions, it migrates as an approximately 52 kDa band.

Product Information

Sequence Region	40-424
Form	Lyophilized powder
Formulation	Lyophilized from sterile PBS, pH 7.4
Purity	>85%, by SDS-PAGE with Coomassie Brilliant Blue staining.
Endotoxin	Not tested.
Activity	Not tested.
Stability	Samples are stable for up to twelve months from date of receipt at -70℃
Protein Construction	DNA encoding 40-424 aa (Q8WR51) were fused with 6His tag.

Storage & Handling

Reconstitution	Reconstitute at 0.25 μg/μl in sterile water for short-term storage. Reconstitution with 50% glycerol solution is recommended for longer term storage (see Stability and Storage for more details). If a different concentration is needed for your purposes please adjust the reconstitution volume as required (please note: the ion concentration of the final solution will vary according to the volume used). Note: Centrifuge vial before opening. When reconstituting, gently pipet and wash down the sides of the vial to ensure full recovery of the protein into solution.
Storage	Store it under sterile conditions at -20℃ to -80℃. It is recommended that the protein be aliquoted for optimal storage. Avoid repeated freeze-thaw cycles.
Shipping	In general, recombinant proteins are provided as lyophilized powder which are shipped at ambient temperature. Bulk packages of recombinant proteins are provided as frozen liquid. They are shipped out with blue ice unless customers require otherwise.

Description

Description	This recombinant protein product features a stable and soluble fragment (residues 40-424) of GDP-fucose protein O-fucosyltransferase 2 (Patterning defective protein 2) from Caenorhabditis elegans. This 385-amino acid fragment retains key functional properties and is ideal for structural studies, enzymatic assays, and biochemical characterization of O-fucosylation mechanisms. GDP-fucose protein O-fucosyltransferase 2 (EC 2.4.1.221), also known as Patterning defective protein 2 or Peptide-O-fucosyltransferase 2, catalyzes the attachment of fucose through O-glycosidic linkages to conserved serine or threonine residues within thrombospondin type I repeats (TSRs). This enzymatic activity is critical for modifying proteins in the ADAMTS superfamily and thrombospondin/spondin families, playing essential roles in protein function and cellular signaling. The full-length protein is primarily localized to the endoplasmic reticulum with additional presence in the Golgi apparatus, where it facilitates post-translational modifications important for protein stability and interaction networks.