Human Tubulin folding cofactor A / TBCA Protein

Catalog Number: 13918-HNAE

General Information

Gene Name Synonym:

TBCA

Protein Construction:

A DNA sequence encoding the mature form of human TBCA (O75347) (Met1-Ala108) was expressed, with a N-terminal Met.

Source: Human

Expression Host: E. coli

QC Testing

Purity: > 95 % as determined by SDS-PAGE

Endotoxin:

Please contact us for more information.

Stability:

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

Predicted N terminal: Met

Molecular Mass:

The recombinant human TBCA consists of 109 amino acids and predicts a molecular mass of 13 KDa. It migrates as an approximately 16 KDa band in SDS-PAGE under reducing conditions.

Formulation:

Lyophilized from sterile PBS, pH 7.5

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:

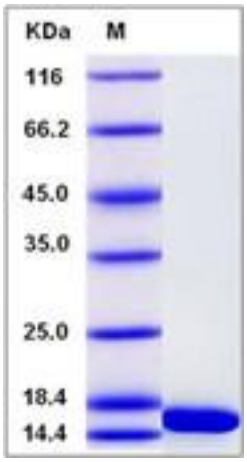
Store it under sterile conditions at -20℃ to -80℃ upon receiving. Recommend to aliquot the protein into smaller quantities for optimal storage.

Avoid repeated freeze-thaw cycles.

Reconstitution:

Detailed reconstitution instructions are sent along with the products.

SDS-PAGE:



Protein Description

Tubulin folding cofactor A belongs to the TBCA family. It is one of four proteins (cofactors A, D, E, and C) involved in the early step of the tubulin folding pathway. These proteins can fold intermediates and finally lead to correctly folded beta-tubulin. It is believed that tubulin folding cofactors A and D play a role in capturing and stabilizing beta-tubulin intermediates in a quasi-native confirmation. Tubulin folding cofactor E binds to the cofactor D/beta-tubulin complex; interaction with tubulin folding cofactor C then causes the release of beta-tubulin polypeptides that are committed to the native state.

References

1.Strausberg RL, *et al.* (2002) Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. Proc Natl Acad Sci. 99(26):16899-903. 2.Irwin DM, *et al.* (2003) Molecular evolution of vertebrate goose-type lysozyme genes. J Mol Evol. 56(2):234-42. 3.Sklar P, *et al.* (2011) Large-scale genome-wide association analysis of bipolar disorder identifies a new susceptibility locus near ODZ4. Nat Genet. 43(10):977-83.