Human DNAJC30 Protein (His Tag)

Catalog Number: 13796-H07E

Sino Biological Biological Solution Specialist

General Information

Gene Name Synonym:

WBSCR18

Protein Construction:

A DNA sequence encoding the mature form of human DNAJC30 (Q96LL9) (Ser39-Gly124) was expressed with a polyhistide tag at the N-terminus.

Source:

Expression Host: E. coli

QC Testing

Purity: > 95 % as determined by SDS-PAGE

Human

Endotoxin:

Please contact us for more information.

Stability:

Samples are stable for up to twelve months from date of receipt at -70 $^\circ\!\!\!\mathrm{C}$

Predicted N terminal: His

Molecular Mass:

The recombinant human DNAJC30 consists of 101 amino acids and predicts a molecular mass of 11.4 KDa. It migrates as an approximately 14 KDa band in SDS-PAGE under reducing conditions.

Formulation:

Lyophilized from sterile PBS, pH7.4.

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 $^\circ\!C$ to -80 $^\circ\!C$ 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.





Protein Description

NAJC30 is a member of the DNAJ molecular chaperone homology domaincontaining protein family. DNAJC30 gene is deleted in williams syndrome, a multisystem developmental disorder caused by the deletion of contiguous genes at 7q11.23. DNAJC30 is expressed in brain, heart, kidney, liver, lung, spleen, stomach and testis. It contains 1 J domain. DNAJC30 is located in the Williams-Beuren syndrome (WBS) critical region. WBS results from a hemizygous deletion of several genes on chromosome 7q11.23, thought to arise as a consequence of unequal crossing over between highly homologous low-copy repeat sequences flanking the deleted region.

References

1.Hillier L W, *et al.* (2003) The DNA sequence of human chromosome 7. Nature. 424:157-164. 2.Ota T, *et al.* (2004) Complete sequencing and characterization of 21,243 full-length human cDNAs. Nat Genet. 36:40-5. 3.Merla G, *et al.* (2002) Identification of additional transcripts in the Williams-Beuren syndrome critical region. Hum Genet. 110:429-38.

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