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Product datasheet for PH317676

WTIP (NM_001080436) Human Mass Spec Standard

Product data:

Product Type:	Mass Spec Standards
Description:	WTIP MS Standard C13 and N15-labeled recombinant protein (NP_001073905)
Species:	Human
Expression Host:	HEK293
Expression cDNA Clone or AA Sequence:	RC217676
Predicted MW:	44.9 kDa
Protein Sequence:	>RC217676 representing NM_001080436 Red=Cloning site Green=Tags(s) MQRSRAGADEAALLLAGLALRELEPGCGSPGRGRRGPRPGPGDEAAPALGRRGKGSGGPEAGADGLSRGE RGPRRAAVPELSAQPAGSPRASLAGSDGGGGGGSARSSGISLGYDQRHGSPRSGRSDPRPGPGPPSVGSA RSSVSSLGSRGSAGAYADFLPPGACPAPARSPEPAGPAPFPLPALPLPPGREGGPSAAERRLEALTRELE RALEARTARDYFGICIKCGLGIYGAQQACQAMGSLYHTDCFTCDSCGRRLRGKAFYNVGEKVYCQEDFLY SGFQQTADKCSVCGHLIMEMILQALGKSYHPGCFRCSVCNECLDGVPFTVDVENNIYCVRDYHTVFAPKC ASCARPILPAQGCETTIRVVSMDRDYHVACYHCEDCGLQLSGEEGRRCYPLAGHLLCRRCHLRRLQPGPL PSPTVHVTEL TRTRPLEQKLISEEDLAANDILDYKDDDDKV
Tag:	C-Myc/DDK
Purity:	> 80% as determined by SDS-PAGE and Coomassie blue staining
Concentration:	>0.05 µg/µL as determined by microplate BCA method
Labeling Method:	Labeled with [U- 13C6, 15N4]-L-Arginine and [U- 13C6, 15N2]-L-Lysine
Buffer:	25 mM Tris-HCl, 100 mM glycine, pH 7.3
Storage:	Store at -80°C. Avoid repeated freeze-thaw cycles.
Stability:	Stable for 3 months from receipt of products under proper storage and handling conditions.
RefSeq:	NP_001073905
RefSeq Size:	2204
RefSeq ORF:	1290
Locus ID:	126374

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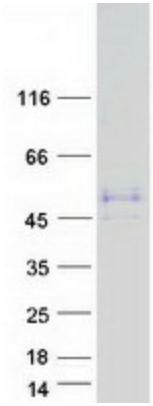
UniProt ID: A6NIX2

Cytogenetics: 19q13.11

Summary: Adapter or scaffold protein which participates in the assembly of numerous protein complexes and is involved in several cellular processes such as cell fate determination, cytoskeletal organization, repression of gene transcription, cell-cell adhesion, cell differentiation, proliferation and migration. Positively regulates microRNA (miRNA)-mediated gene silencing. Negatively regulates Hippo signaling pathway and antagonizes phosphorylation of YAP1. Acts as a transcriptional corepressor for SNAI1 and SNAI2/SLUG-dependent repression of E-cadherin transcription. Acts as a hypoxic regulator by bridging an association between the prolyl hydroxylases and VHL enabling efficient degradation of HIF1A. In podocytes, may play a role in the regulation of actin dynamics and/or foot process cytoarchitecture (By similarity). In the course of podocyte injury, shuttles into the nucleus and acts as a transcription regulator that represses WT1-dependent transcription regulation, thereby translating changes in slit diaphragm structure into altered gene expression and a less differentiated phenotype. Involved in the organization of the basal body (By similarity). Involved in cilia growth and positioning (By similarity).[UniProtKB/Swiss-Prot Function]

Product images:



Coomassie blue staining of purified WTIP protein (Cat# [TP317676]). The protein was produced from HEK293T cells transfected with WTIP cDNA clone (Cat# [RC217676]) using MegaTran 2.0 (Cat# [TT210002]).