UBE2G1 (Ubc7) [GST-tagged]

E2 – Ubiquitin Conjugating Enzyme

Alternate Names: E217K, UBC7, UBE2G

Cat. No. **62-0027-100**
Lot. No. **1394**

Quantity: 100 µg
Storage: -70˚C

FOR RESEARCH USE ONLY

NOT FOR USE IN HUMANS

CERTIFICATE OF ANALYSIS

Background

The enzymes of the ubiquitylation pathway play a pivotal role in a number of cellular processes including regulated and targeted proteasomal degradation of substrate proteins. Three classes of enzymes are involved in the process of ubiquitylation; activating enzymes (E1s), conjugating enzymes (E2s) and protein ligases (E3s). UBE2G1 is a member of the E2 conjugating enzyme family and cloning of the human gene was first described by Watanabe *et al*. (1996). UBE2G1 shares 74% sequence identity with UBC7 from *C. elegans* and a high degree of homology with UBC7 from other species. Expression of UBE2G1 and a helix-loop-helix transcription factor and member of the MYC/MAX superfamily (ROX/MNT) is decreased in medullablastoma tumours. Haploinsufficiency of the human 17p13.3 region is associated with 35% to 50% of medullablastomas, indicating the presence of one or more tumour suppressor genes which have not yet been identified (Cvekl *et al*., 2004).

References:

Cvekl A, Jr., Zavadil J, Birshtein BK, Grotzer MA, Cvekl A (2004) Analysis of transcripts from 17p13.3 in medulloblastoma suggests ROX/MNT as a potential tumour suppressor gene. *Eur J Cancer* **40**, 2525-32.

Watanabe TK, Kawai A, Fujiwara T, Maekawa H, Hirai Y, Nakamura Y, Takahashi E (1996) Molecular cloning of UBE2G, encoding a human skeletal muscle-specific ubiquitin-conjugating enzyme homologous to UBC7 of C. elegans. *Cytogenet Cell Genet* **74**, 146-8.

Physical Characteristics

Species: human

Source: *E. coli* expression

Quantity: 100 µg

Concentration: 1 mg/ml

Formulation: 50 mM HEPES pH 7.5, 150 mM sodium chloride, 2 mM dithiothreitol, 10% glycerol

Molecular Weight: ~46 kDa

Purity: >98% by InstantBlue™ SDS-PAGE

Stability/Storage: 12 months at -70˚C; aliquot as required

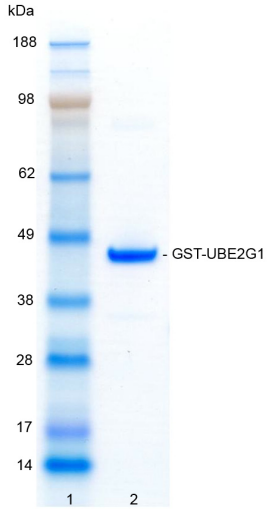
Protein Sequence:

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEH
LYERDEGDKWRNKKFELGLEFPNLPYYIDGD
VKLTQSMAIIRYIADKHNMLGGCPKERAEISM
LEGAVLDIRYGVSRIAYSKDFETLKVDFL
SKLPEMLKMFEDRLCHKTYLNGDHVTHPD
FMLYDALDVVLYMDPMCLDAFPKLVCFK
KRIEAIPQIDKYLKSSKYIAWPLQGWQATFG
GGDHPPKSDLEVLFQGPLGS***M***TELQSALLLR**
RQLAELNKNPVEGFSAGLIDDNDLYRWEVLI
IGPPDTLYEGGVFKAHLTFPKDYPLRPPKM
KFITEIWHPNVDKNGDVCISILHEPGEDKY
GYEKPEERWLPIHTVETIMISVISMLADPNGD
SPANVDAAKEWREDRNGEFKRKVARCVRK
SQETAFE

Tag (**bold text**): N-terminal GST
Protease cleavage site: PreScission™ (LEVLFQ▼GP)
UBE2G1 (regular text): Start ***bold italics*** (amino acid residues 1-170)
Accession number: NP_003333

Quality Assurance

Purity:
4-12% gradient SDS-PAGE
InstantBlue™ staining
Lane 1: MW markers
Lane 2: 1 µg GST-UBE2G1



Protein Identification:
Confirmed by mass spectrometry.

E2-Ubiquitin Thioester Loading Assay:
The activity of GST-UBE2G1 was validated by loading E1 UBE1 activated ubiquitin onto the active cysteine of the GST-UBE2G1 E2 enzyme via a transthiolation reaction. Incubation of the UBE1 and GST-UBE2G1 enzymes in the presence of ubiquitin and ATP at 30°C was compared at two time points, T_0 and T_{10} minutes. The sensitivity of this ubiquitin/GST-UBE2G1 thioester bond to the reducing agent DTT was confirmed.

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Lot-specific COA version tracker: v1.0.0