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# Recombinant human p62/SQSTM1 protein

Catalog Number: ATGP0532

# **PRODUCT INFORMATION**

# **Expression system**

E.coli

#### **Domain**

1-356aa

#### **UniProt No.**

013501

#### **NCBI Accession No.**

NP 001135771

#### **Alternative Names**

Sequestosome 1, A170, OSIL, p60, p62, p62B, PDB3, ZIP3, Sequestosome 1 EBI 3 associated protein of 60 kDa, ZIP, ZIP 3, EBI3 associated protein of 60 kDa, EBIAP, MGC127197, ORCA.M530, OSF-6, Osi, Oxidative stress induced like, Paget disease of bone 3, PDB 3, Phosphotyrosine independent ligand for the Lck SH2 domain of 62 kDa, Phosphotyrosine independent ligand for the Lck SH2 domain p62, PKC-zeta-interacting protein, Protein kinase C-zeta-interacting protein, SQSTM 1, STAP, STONE14, ubiquitin binding protein p62,

# PRODUCT SPECIFICATION

# **Molecular Weight**

39.7 kDa (364aa) confirmed by MALDI-TOF (Molecular weight on SDS-PAGE will appear higher)

#### Concentration

0.5mg/ml (determined by Bradford assay)

#### **Formulation**

Liquid in. 20mM Tris-HCl buffer (pH 8.0) containing 10% glycerol 1mM DTT

#### **Purity**

> 85% by SDS-PAGE

#### Tag

His-Tag

### **Application**

SDS-PAGE

# **Storage Condition**

Can be stored at +2C to +8C for 1 week. For long term storage, aliquot and store at -20C to -80C. Avoid repeated freezing and thawing cycles.

# **BACKGROUND**

#### **Description**

SQSTM1 is an adapter protein which binds ubiquitin and regulates signaling cascades through ubiquitination. It may regulate the activation of NFKB1 by TNF-alpha, nerve growth factor (NGF) and interleukin-1 and play a role



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in titin/TTN downstream signaling in muscle cells. This protein also may be involved in cell differentiation, apoptosis, immune response and regulation of K+ channels. Mutations in the ubiquitin-associated (uBA) domain of the sequestosome 1 protein commonly cause Paget's disease since the uBA is necessary for aggregate sequestration and cell survival. Recombinant SQSTM1 protein, fused to His-tag at C-terminus, was expressed in E. coli and purified by using conventional chromatography techniques.

# **Amino acid Sequence**

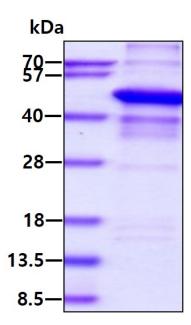
MAMSYVKDDI FRIYIKEKKE CRRDHRPPCA QEAPRNMVHP NVICDGCNGP VVGTRYKCSV CPDYDLCSVC EGKGLHRGHT KLAFPSPFGH LSEGFSHSRW LRKVKHGHFG WPGWEMGPPG NWSPRPPRAG EARPGPTAES ASGPSEDPSV NFLKNVGESV AAALSPLGIE VDIDVEHGGK RSRLTPVSPE SSSTEEKSSS QPSSCCSDPS KPGGNVEGAT QSLAEQMRKI ALESEGRPEE QMESDNCSGG DDDWTHLSSK EVDPSTGELQ SLQMPESEGP SSLDPSQEGP TGLKEAALYP HLPPEADPRL IESLSQMLSM GFSDEGGWLT RLLQTKNYDI GAALDTIQYS KHPPPL<LEHH HHHH>

#### **General References**

Falchetti A., et al. (2004) J Bone Miner Res. 19(6):1013-7.

#### **DATA**

#### **SDS-PAGE**



3ug by SDS-PAGE under reducing condition and visualized by coomassie blue stain.

