SAE1 [GST-tagged] / SAE2 [6His-tagged]

E1 Activating Enzyme

Alternate Names: SAE1 = Activator of SUMO1, AOS1; SAE2 = Ubiquitin-Like Modifier-Activating Enzyme 2, UBA2

Cat. No. 61-0005-010 Lot. No. 30078 Quantity: 10 µg Storage: -70°C

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CERTIFICATE OF ANALYSIS Page 1 of 2

Protein Sequences: Please see page 2

Background

The enzymes of the SUMOylation pathway play a pivotal role in a number of cellular processes including nuclear transport, signal transduction, stress responses and cell cycle progression. The covalent modification of proteins by small ubiquitin-related modifiers (SUMOs) may modulate their stability and subcellular compartmentalisation. Three classes of enzymes are involved in the process of SUMOylation; an activating enzyme (E1), conjugating enzyme (E2) and protein ligases (E3s). SAE1/SAE2 is a SUMO1, 2 and 3 E1 activating enzyme and functions as a heterodimer. Cloning of the human SAE1 and SAE2 genes was first described by Desterro et al. (1999). SAE1 and SAE2 share sequence similarity to the N-terminus and C-terminus of ubiguitin E1 activating enzymes respectively (Desterro et al. 1999). SAE2 harbours the E1-like active cysteine site while SUMO1 transfer to the E2 conjugating enzyme UBE2I requires both of the SAE subunits (Desterro et al. 1999). A crystal structure of the SAE1/SAE2 dimer together with the SUMO1 adenylate has been solved at 2.45 Ångström resolution (Olsen et al. 2010). Western blot analysis of cell-cycle synchronised HeLa cells demonstrated increased SAE1 expression in S phase followed by a decrease in G2 phase. Immunofluorescence showed that SAE1 and SAE2 were distributed throughout the nuclei but were excluded from the nucleoli (Azuma et al. 2001). A short hairpin RNA (shRNA) screen was carried out

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Physical Characteristics

Species: human

Source: E. coli

Quantity: 10 µg

Concentration: 0.5 mg/ml

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

Molecular Weight: SAE1 = 64.8 kDa SAE2 = 73.4 kDa

Purity: >98% by InstantBlue™ SDS-PAGE

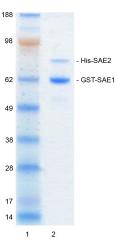
Stability/Storage: 12 months at -70°C; aliquot as required

Quality Assurance

Purity:

4-12% gradient SDS-PAGE InstantBlue™ staining Lane 1: MW markers Lane 2: 1 μg SAE1/SAE2





Protein Identification:

Confirmed by mass spectrometry.

E1 Thioester SUMO Loading Assay:

The activity of GST-SAE1/His-SAE2 was validated by loading SUMO1 onto the active cysteine of GST-SAE1/ His-SAE2. Incubation of the GST-SAE1/His-SAE2 enzyme in the presence of SUMO1 and ATP at 30°C was compared at two time points, T_0 and T_{10} minutes. Sensitivity of the SUMO / GST-SAE1/His-SAE2 thioester bond to the reducing agent DTT was confirmed.



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SAE1 [GST-tagged] / SAE2 [6His-tagged]

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CERTIFICATE OF ANALYSIS Page 2 of 2

Background

Continued from page 1

Physical Characteristics

Continued from page 1

in the presence of aberrant MYC signalling to identify genes that altered the fitness of mammary epithelial cells. In this screen SAE1 and SAE2 were identified as MYC synthetic lethal genes. Upon MYC hyperactivation inactivation of SAE2 led to mitotic catastrophe and cell death and it is thought that SAE2 inactivation could be a therapeutic strategy in MYC driven cancers (Kessler *et al.* 2012).

References:

Azuma Y, Tan SH, Cavenagh MM, Ainsztein AM, Saitoh H, et al. (2001) Expression and regulation of the mammalian SUMO-1 E1 enzyme. *FASEB J* **15**, 1825-1827.

Desterro JM, Rodriguez MS, Kemp GD, Hay RT (1999) Identification of the enzyme required for activation of the small ubiquitin-like protein SUMO-1. *J Biol Chem* **274**, 10618-10624.

Kessler JD, Kahle KT, Sun T, Meerbrey KL, Schlabach MR, et al. (2012) A SUMOylation-dependent transcriptional subprogram is required for Myc-driven tumorigenesis. *Science* **335**, 348-353.

Olsen SK, Capili AD, Lu X, Tan DS, Lima CD (2010) Active site remodelling accompanies thioester bond formation in the SUMO E1. *Nature* **463**, 906-912. **SAE1 Protein Sequence: MSPILGYWKIKGLVQPTRLLLEYLEEKYEEH** LYERDEGDKWRNKKFELGLEFPNLPYYIDGD VKLTOSMAIIRYIADKHNMLGGCPKERAEISM LEGAVLDIRYGVSRIAYSKDFETLKVDFL SKLPEMLKMFEDRLCHKTYLNGDHVTHPD FMLYDALDVVLYMDPMCLDAFPKLVCFK KRIEAIPQIDKYLKSSKYIAWPLQGWQATFG GGDHPPKSDLVPRGSMVEKEEAGGGISEEE AAQYDRQIRLWGLEAQKRLRASRVLLVGLK GLGAEIAKNLILAGVKGLTMLDHEQVTPEDP GAQFLIRTGSVGRNRAEASLERAQNLNPMVD VKVDTEDIEKKPESFFTQFDAVCLTCCSRD VIVKVDQICHKNSIKFFTGDVFGYHGYTFAN LGEHEFVEEKTKVAKVSQGVEDGPDTKRAK LDSSETTMVKKKVVFCPVKEALEVDWSSEKA KAALKRTTSDYFLLQVLLKFRTDKGRDPSSD TYEEDSELLLQIRNDVLDSLGISPDLLPED FVRYCFSEMAPVCAVVGGILAQEIVKALSQRD PPHNNFFFFDGMKGNGIVECLGPK

SAE2 Protein Sequence:

MPWHHHHHHLEVLFQGPMALSRGLPRELAE AVAGGRVLVVGAGGIGCELLKNLVLTGF SHIDLIDLDTIDVSNLNRQFLFQKKHVGR SKAQVAKESVLQFYPKANIVAYHDSIMNPDYN VEFFRQFILVMNALDNRAARNHVNRMCLAADV PLIESGTAGYLGQVTTIKKGVTECYECHP **KPTORTFPGCTIRNTPSEPIHCIVWAKYLF** NQLFGEEDADQEVSPDRADPEAAWEPTEAEA RARASNEDGDIKRISTKEWAKSTGYDPVKLFT K L F K D D I R Y L L T M D K L W R K R K P P V P L D WAEVQSQGEETNASDQQNEPQLGLKDQQVLD VKSYARLFSKSIETLRVHLAEKGDGAELIWDKD **DPSAMDFVTSAANLRMHIFSMNMKSRFDIKS** MAGNIIPAIATTNAVIAGLIVLEGLKILS GKIDQCRTIFLNKQPNPRKKLLVPCALDPPNPN CYVCASKPEVTVRLNVHKVTVLTLQDKIVKEK FAMVAPDVOIEDGKGTILISSEEGETEANNH **KKLSEFGIRNGSRLQADDFLQDYTLLINILH** SEDLGKDVEFEVVGDAPEKVGPKOAEDAAKSIT NGSDDGAOPSTSTAOEODDVLIVDSDEEDSSN NADVSEEERSRKRKLDEKENLSAKRSRIEQ KEELDDVIALD

Tag **(bold text)**: N-terminal GST Protease cleavage site: Thrombin (LVPR▼GS) SAE1 (regular text): Start **bold italics** (amino acid residues 1-346) Accession number: NP_005491.1

Tag (**bold text**): N-terminal His Protease cleavage site: PreScission™ (<u>LEVLFQ▼GP</u>) SAE2 (regular text): Start **bold italics** (amino acid residues 1-640) Accession number: NP_005490.1

To purify the SAE1 [GST-tagged] / SAE2 [6His-tagged] heterodimer the genes for these two proteins were co-expressed using a prokaryotic expression vector. Nickel resin capture was performed on cell lysate derived from the lysed *E. coli* expressing the two proteins. Glutathione resin capture was then performed on the eluate from the Nickel capture step to capture SAE1 [GST-tagged] / SAE2 [6His-tagged] heterodimer which was then eluted and dialysed into the storage buffer



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