

FACT complex subunit SPT16 (SPT16) Recombinant Protein | SPT16 recombinant protein

Recombinant Arabidopsis thaliana FACT complex subunit SPT16

CATALOG # AAA114598	HOST E Coli or Yeast or Baculovirus or Mammalian Cell
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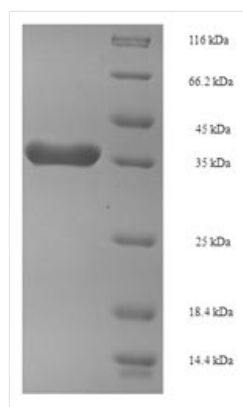
PRODUCT SYNONYMS

FACT complex subunit SPT16 (SPT16); Recombinant Arabidopsis thaliana FACT complex subunit SPT16; Facilitates chromatin transcription complex subunit SPT16; SPT16 recombinant protein

PRODUCT SPECIFICATIONS

Host	E Coli or Yeast or Baculovirus or Mammalian Cell
Purity/Purification	Greater or equal to 85% purity as determined by SDS-PAGE.
Form/Format	Lyophilized or liquid (Format to be determined during the manufacturing process)
Sequence Positions	890-1074. Fragment at the C-terminal
Sequence	DFKKDVLRLVD SVPTSSLEGI KEWLDTTDIK YYESKLNLNW RQILKTITDD PQSFIDGGW EFLNLDGSDS ESGGSEESDK GYEPSDVEVE SESEDEASES ESLVESDDDE EEDSEQESEE EKGKTWDELE REATNADREH GVESDSEER KRRKMKAFGK SRPGTSGGGG SSMKNMPPS KRKHR
Sequence Length	1074
Preparation and Storage	Store at -20 degree C, for extended storage, conserve at -20 degree C or -80 degree C.

IMAGES



SDS-PAGE

ADDITIONAL INFORMATION

Related Product Information for SPT16 recombinant protein	Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the reestablishment of the nucleosome following the passage of RNA polymerase II (Probable).
Product Categories/Family for SPT16 recombinant protein	Developmental Biology

References

Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*. Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G., Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N., Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M., Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T., Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P., Langham S.-A., McCullagh B., Bilham L., Robben J., van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F., Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E., Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H., De Keyser A., Buysschaert C., Gielen J., Villarroel R., De Clercq R., van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S., Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S., Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H., Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A., Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E., Massenet O., Quigley F., Clabaud G., Muendlein A., Felber R., Schnabl S., Hiller R., Schmidt W., Lechamy A., Aubourg S., Chedfor F., Cooke R., Berger C., Monfort A., Casacuberta E., Gibbons T., Weber N., Vandenbol M., Bagues M., Terol J., Torres A., Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T., Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C., Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K., Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L., Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J., Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J., Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D., Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K., Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W., Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D., Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshu C., Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R., Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S., Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A., Chen E., Marra M.A., Martienssen R., McCombie W.R. *Nature* 402:769-777(1999) The *Arabidopsis* Information Resource (TAIR) ORF cloning and analysis of *Arabidopsis* transcription factor genes. Fujita M., Mizukado S., Seki M., Shinozaki K., Mitsuda N., Takiguchi Y., Takagi M. The chromatin remodelling complex FACT associates with actively transcribed regions of the *Arabidopsis* genome. Duroux M., Houben A., Ruzicka K., Friml J., Grasser K.D. *Plant J.* 40:660-671(2004)

NCBI AND UNIPROT INFORMATION

NCBI GI #	15236899
NCBI GeneID	826665
NCBI Accession #	NP_192809.1
NCBI GenBank Nucleotide #	NM_117139.2
UniProt Accession #	O82491; C0SVH5
Molecular Weight	22.9 kDa
NCBI Official Full Name	FACT complex subunit SPT16
UniProt Protein Name	FACT complex subunit SPT16
UniProt Gene Name	SPT16
UniProt Entry Name	SPT16_ARATH

For Research Use Only. Not for use in diagnostic or therapeutic procedures. Small volumes of product may become entrapped in the seal of the vial during shipment and storage; if necessary, briefly centrifuge the vial on a tabletop centrifuge to dislodge any liquid in the cap.

AAA Biotech | Tel: +1 (619) 604-9440 | Fax: +1 (619) 604-9441 | contact@aaabiotech.com
Online datasheet: <https://stage.aaabiotech.com/spt16-recombinant-protein-e-coli-or-yeast-or-baculovirus-or-mammalian-cell/114598>