abcam

Product datasheet

Recombinant Human SF2 protein ab82611

Description

Product name	Recombinant Human SF2 protein
Biological activity	1 unit equals 1 nanogram of purified protein.
Purity	> 95 % SDS-PAGE. ab82611 is purified by affinity and FPLC chromatography.
Expression system	Baculovirus infected insect cells
Protein length	Full length protein
Animal free	No
Nature	Recombinant
Species	Human

Specifications

Our **Abpromise guarantee** covers the use of **ab82611** in the following tested applications.

The application notes include recommended starting dilutions; optimal dilutions/concentrations should be determined by the end user.

Applications	EMSA SDS-PAGE Functional Studies Gel Supershift Assays
Form	Liquid
Additional notes	1 unit equals 1 nanogram of purified protein.

Preparation and Storage

Stability and Storage	Shipped on dry ice. Upon delivery aliquot and store at -80ºC. Avoid freeze / thaw cycles. pH: 7.9 Constituents: 20% Glycerol (glycerin, glycerine), 0.00584% EDTA, 0.476% HEPES, 0.0077% DTT, 0.55% Ammonium sulphate

General Info

Function	Plays a role in preventing exon skipping, ensuring the accuracy of splicing and regulating alternative splicing. Interacts with other spliceosomal components, via the RS domains, to form a bridge between the 5'- and 3'-splice site binding components, U1 snRNP and U2AF. Can stimulate binding of U1 snRNP to a 5'-splice site-containing pre-mRNA. Binds to purine-rich RNA sequences, either the octamer, 5'-RGAAGAAC-3' (r=A or G) or the decamers, AGGACAGAGC/AGGACGAAGC. Binds preferentially to the 5'-CGAGGCG-3' motif in vitro. Three copies of the octamer constitute a powerful splicing enhancer in vitro, the ASF/SF2 splicing enhancer (ASE) which can specifically activate ASE-dependent splicing. Isoform ASF-2 and isoform ASF-3 act as splicing repressors.
Sequence similarities	Belongs to the splicing factor SR family. Contains 2 RRM (RNA recognition motif) domains.
Domain	The RRM 2 domain plays an important role in governing both the binding mode and the phosphorylation mechanism of the RS domain by SRPK1. RS domain and RRM 2 are uniquely positioned to initiate a highly directional (C-terminus to N-terminus) phosphorylation reaction in which the RS domain slides through an extended electronegative channel separating the docking groove of SRPK1 and the active site. RRM 2 binds toward the periphery of the active site and guides the directional phosphorylation mechanism. Both the RS domain and an RRM domain are required for nucleocytoplasmic shuttling.
Post-translational modifications	Phosphorylated by CLK1, CLK2, CLK3 and CLK4. Phosphorylated by SRPK1 at multiple serines in its RS domain via a directional (C-terminal to N-terminal) and a dual-track mechanism incorporating both processive phosphorylation (in which the kinase stays attached to the substrate after each round of phosphorylation) and distributive phosphorylation steps (in which the kinase and substrate dissociate after each phosphorylation event). The RS domain of SRSF1 binds to a docking groove in the large lobe of the kinase domain of SRPK1 and this induces certain structural changes in SRPK1 and/or RRM 2 domain of SRSF1, allowing RRM 2 to bind the kinase and initiate phosphorylation. The cycles continue for several phosphorylation steps in a processive manner (steps 1-8) until the last few phosphorylation steps (approximately steps 9-12). During that time, a mechanical stress induces the unfolding of the beta-4 motif in RRM 2, which then docks at the docking groove of SRPK1. This also signals RRM 2 to begin to dissociate, which facilitates SRSF1 dissociation after phosphorylation is completed. Arg-97 is dimethylated, probably to asymmetric dimethylarginine.
Cellular localization	Cytoplasm. Nucleus speckle. In nuclear speckles. Shuttles between the nucleus and the cytoplasm.

Terms and conditions

- Guarantee only valid for products bought direct from Abcam or one of our authorized distributors