

SUPPLEMENTARY INFORMATION

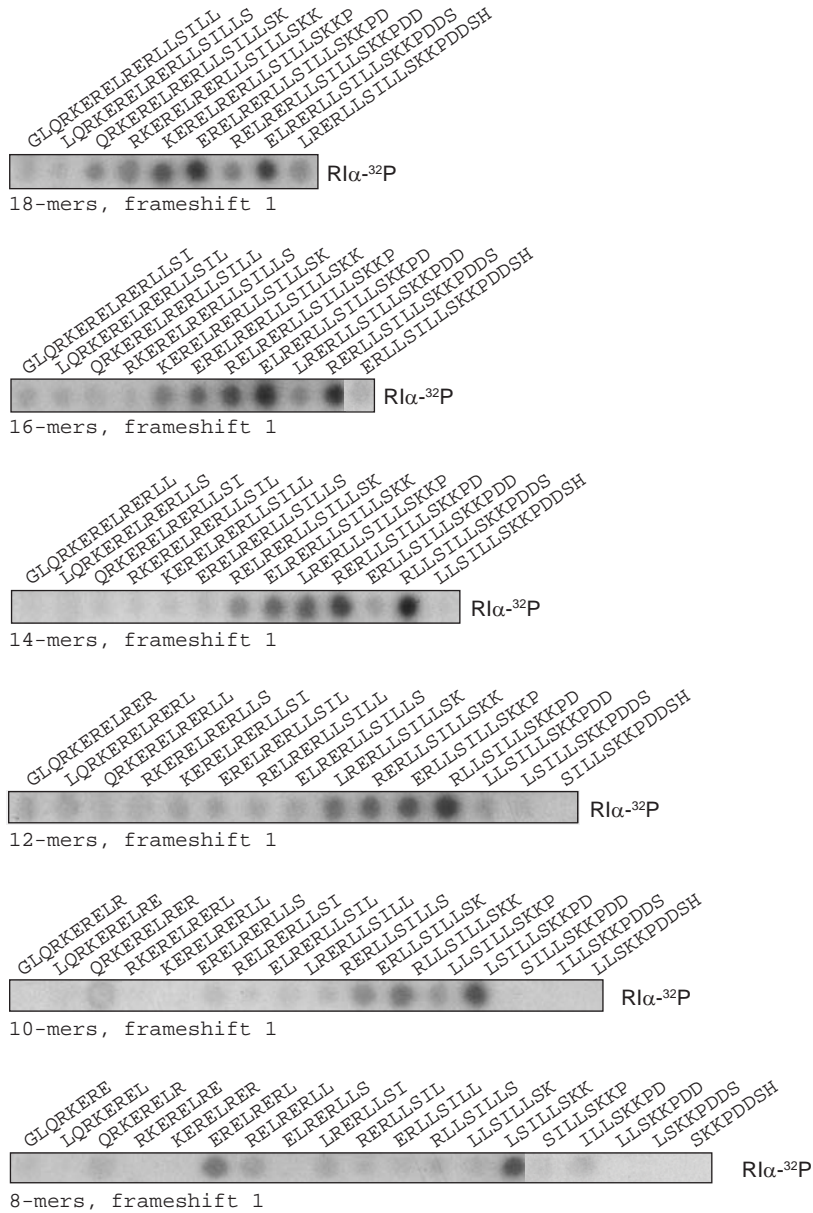
to

Jarnæss et al. “Splicing factor arginine serine rich 17A (SFRS17A) is an A-kinase anchoring protein that targets protein kinase A to splicing factor compartments”

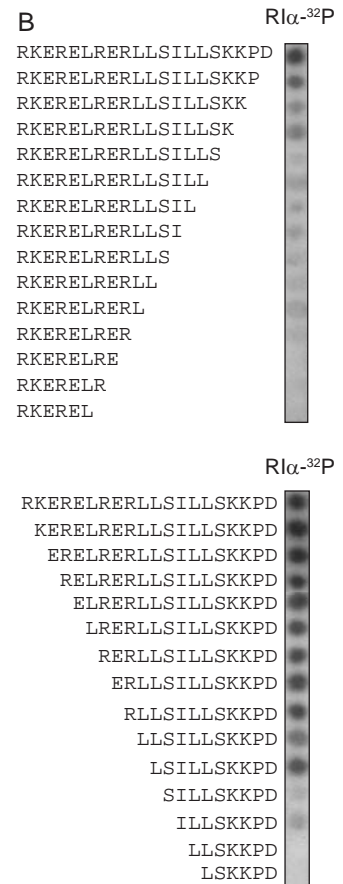
Supplement table 1. Search result from search in the International Protein Index (IPI) database. A RISR consensus sequence (L(x)₃(E)₂(x)₆E) was used to perform a search for potential AKAPs containing the RISR in the International Protein Index (IPI) database. The table shows the search result.

Protein name
SFRS17A
Espin
Pericentrin
Intersectin
EG5
Enall
INCENP
Complexin
Pap7

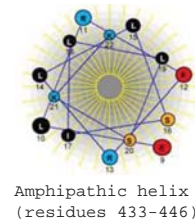
A



B

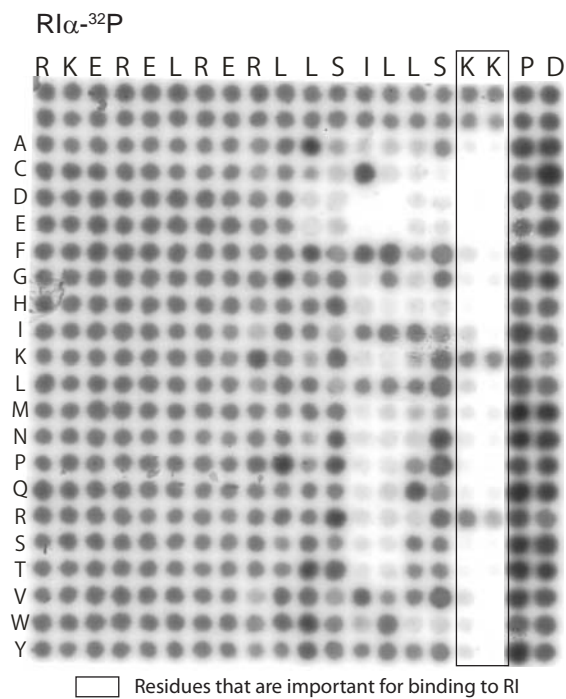


C

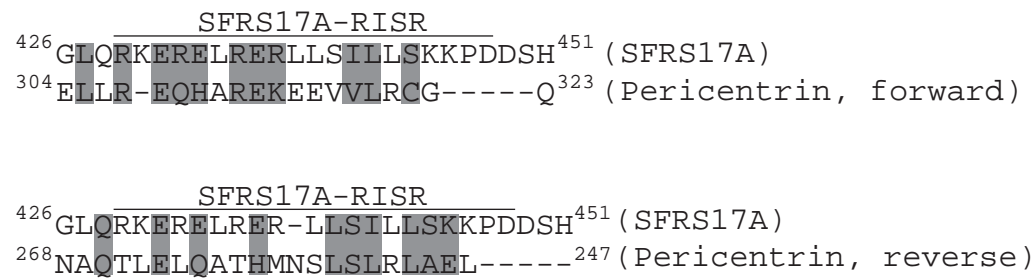


Supplement figure S1. Detailed mapping of R-binding region 2. A, R-binding region 2 was examined using overlapping peptides with one residue offset and different peptide lengths (18, 16, 14, 12, 10 and 8 residues). Binding of ³²P-labeled RI α was detected by autoradiography. B, N- and C-terminal truncated peptides from the R-binding region 2 were made on solid phase, and binding of ³²P-labeled RI α was detected by autoradiography. C, α -helical wheel representation of residues 433-446 in SFRS17A. A and B are representative of three independent experiments.

A



B



Supplement figure S2. Analysis of the SFRS17A-RISR sequence. *A*, A two-dimensional array of 440 SFRS17A-RISR-derivatives (as 20-mers) was synthesized where each residue in the native peptide (given by their single-letter codes above each array) was replaced with all the 20 amino acids (given by their single-letter codes to the left of each array). The first two rows in the array correspond to the SFRS17A-RISR. Binding of ³²P-labeled RI α was detected by autoradiography. The positions of amino acids in SFRS17A-RISR important for binding are boxed. *B*, The SFRS17A-RISR sequence was aligned with the RII-binding region of pericentrin in both forward and reverse orientation. Grey boxes indicate aligned amino acids.