MOTIF	POSITION	SEQUENCE	ELM ACCESSION
D-site MAPK docking motif	22-32	KKKCWQSNLRL	(similar to ELME000233)
Protein phosphatase-1 (PP1) docking motif RVXF	29-35	NLRLSFS	ELME000137
Pro-directed kinase (MAP kinase) Phosphorylation Site	43-49 46-52 51-57	GFFSPHS SPHSPVP VPPSPLV	ELME000159
Casein kinase (CK) 1 Phosphorylation site	46-52	SPHSPVP	ELME000063
GSK3 phosphorylation recognition site	30-37	LRLSFSDT	ELME000053
Never in mitosis A (NimA)-related kinase (NEK) 2 phosphorylation site	12-17 30-35 34-39	MAATTM LRLSFS FSDTRR	ELME000336
protein kinase A (PKA) Phosphorylation site	30-36	LRLSFSD	ELME000062

Additional File 1 Table S1

Putative kinase and phosphatase interaction (docking) and phosphorylation motifs in the C-terminal domain (pos. 435-495) of ACS6 (1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID (ACC) SYNTHASE 6). Linear motif search was carried out using the Eukaryotic Linear Motif (ELM) Resource. Putative phosphorylated residues are indicated with red font. Furthermore, the sequence contains a putative D-site MAPK docking motif. This motif contains five spacer residues between the basic cluster and the bulky hydrophobic amino acids, thus falling short of the ELM definition of 2-4 spacers. It is nonetheless commonly accepted that the D-site consensus consists of 1-6 spacer amino acids.