MOTIF	POSITION	SEQUENCE	ELM ACCESSION
MAPK docking motif	315-323 245-252*	KHKSQDMRL KKYVYLGL	ELME000233
Protein phosphatase-1 (PP1) docking motif	131-138*	QYRGVTFY	ELME000137
Phospho-dependent motif that mediates docking of CDK substrates and regulators to cyclin-CDK-bound Cks1.	296-301	PTTPQD	ELME000358
Pro-directed kinase (MAP kinase) Phosphorylation Site	21-27 295-301 347-353 397-403 410-416	CYSSPSK NPTTPQD LNHTPNS SGFSPHH STSTPHQ	ELME000159
Cyclin dependent protein kinase (CDK) Phosphorylation Site	21-27	CYSSPSK	ELME000153
CK1 phosphorylation site	23-29 33-39 35-41 311-317 332-338 397-403 410-416 127-133*	SSPSKRV SNSSSSA SSSSAVV SANSKHK SLHSNEV SGFSPHH STSTPHQ SRSSQYR	ELME000063
CK2 Phosphorylation site	8-14 199-205 252-258*	PHQTQRE TNLTKEE LFDTEVE	ELME000064
GSK3 phosphorylation recognition site	28-35 30-37 90-97 290-297 304-311 311-318 358-365 393-400	RVGSFSNS GSFSNSSS FCQSDLAT AESSGNPT LDLSLGNS SANSKHKS PGSSNIGS AAASSGFS	ELME000053
NEK2 phosphorylation site	20-25 32-37 118-123 304-309 308-313 341-346 408-413	FCYSSP FSNSSS LKKSRR LDLSLG LGNSAN LGQTGM FNSTST	ELME000336
NEK2 phosphorylation site	367-372	GGFSLF	ELME000337
phosphoinositide-3-OH-kinase related kinase (PIKK) phosphorylation site	8-14 315-321 127-133*	PHQTQRE KHKSQDM SRSSQYR	ELME000202
PKA Phosphorylation site	211-217	RRQSTGF	ELME000008

PKA Phosphorylation site	211-217 382-388 127-133* 138-144* 218-224*	RRQSTGF GRASTNQ SRSSQYR YRRTGRW PRGSSKY	ELME000062
Polo-like kinase phosphorylation site	304-310 279-285*	LDLSLGN FDPSIYD	ELME000147

Additional File 9 Table S4

Putative kinase and phosphatase interaction (docking) and phosphorylation motifs in the APETALA 2 (At4g36920.1) protein sequence (432 amino acids). Linear motif search was carried out using ELM. Motifs falling inside SMART/Pfam domains or scoring poorly with the structural filter of ELM are indicated with asterisks. Putative phosphorylated residues are indicated with red font.