

SUPPLEMENTAL DATA:

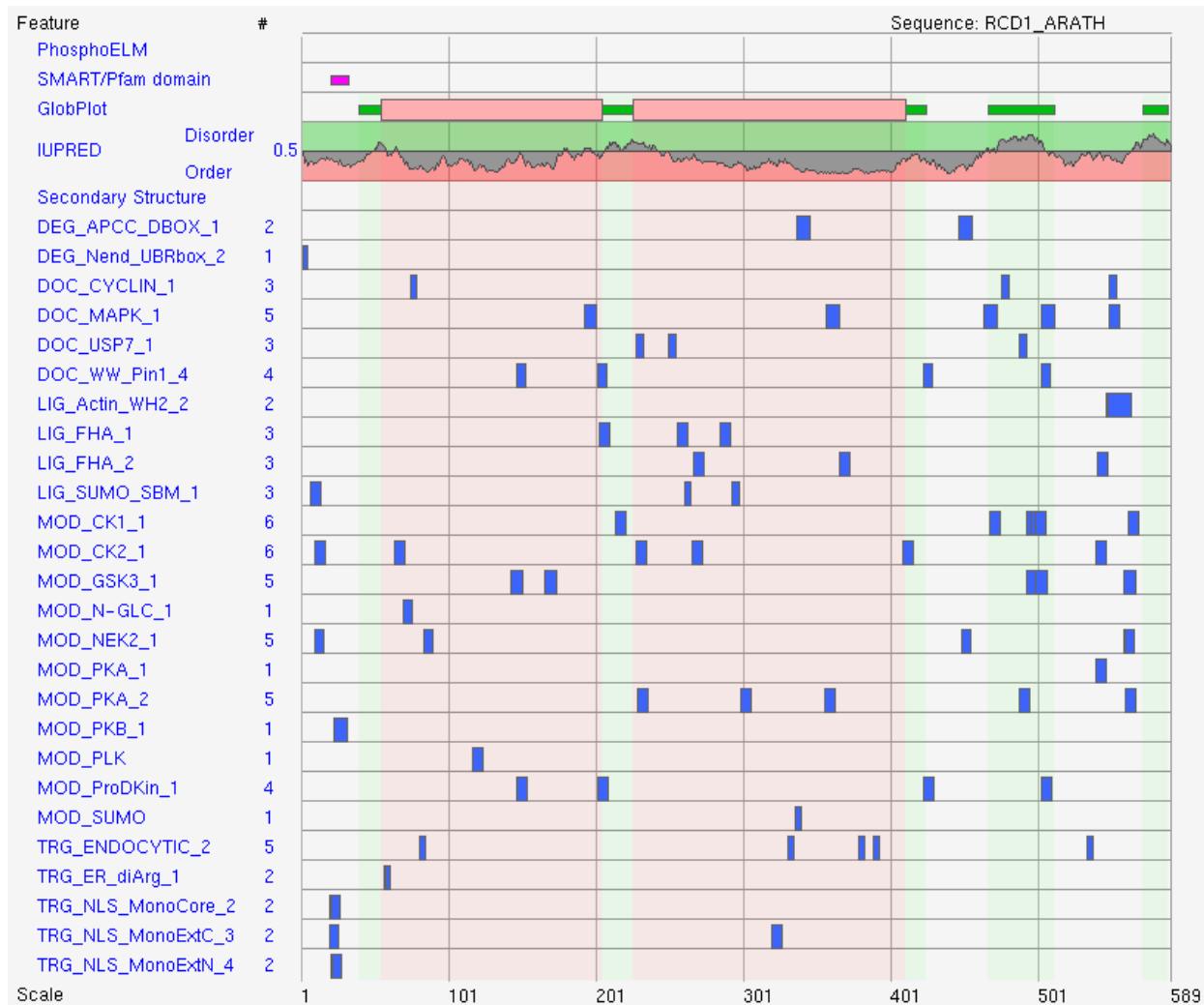


Fig. 1. Diagrammatic representation of motifs in AtRCD1 as predicted by ELM. Blue boxes showing position of motifs in the protein stretch.



Fig. 2 . Diagrammatic representation of motifs in BnSRO1 as predicted by ELM. Blue boxes showing position of motifs in the protein stretch.

Table 1. PROSITE Patterns detected in AtRCD1.

S.N O.	PATTERN	POSITION	PATTERN SEQUENCE	PATTERN ID
1	cAMP- and cGMP-dependent protein kinase phosphorylation site(PKA) [RK]{2}.[ST]	70	NRSG	PS00004 PDOC00004
2	Protein kinase C phosphorylation site [ST].[RK]	11	SRR	PS00005 PDOC00005
		72	SGK	
		204	TPR	
		244	SRK	
		319	TKK	
		375	SAR	
		425	SPK	
		500	TTR	
		518	SHK	
		578	SIR	
3	Casein kinase II phosphorylation site[ST].{2}[DE]	12	SRCE	PS00006 PDOC00006
		66	SAYE	
		230	SSNE	
		252	SKWD	
		268	TGSE	
		367	TAAD	
		411	SGGE	
		542	TRAЕ	
		578	SIRD	
4	N-glycosylation site N[^P][ST][^P]	70	NRSG	PS00001 PDOC00001
5	N-myristoylation site G[^EDRKHPFYW].{2}[STAGCN][^P]	34	GVSCAK	PS00008 PDOC00008
		264	GAKLTG	
		347	GLGVGG	
		363	GIHLTA	
		458	GNLIAK	
		486	GARGSG	
		497	GSSTTR	
6	Amidation site .G[RK][RK]	18	FGKK	PS00009 PDOC00009
7	Cell attachment sequence RGD	323	RGD	PS00016 PDOC00016
		403	RGD	

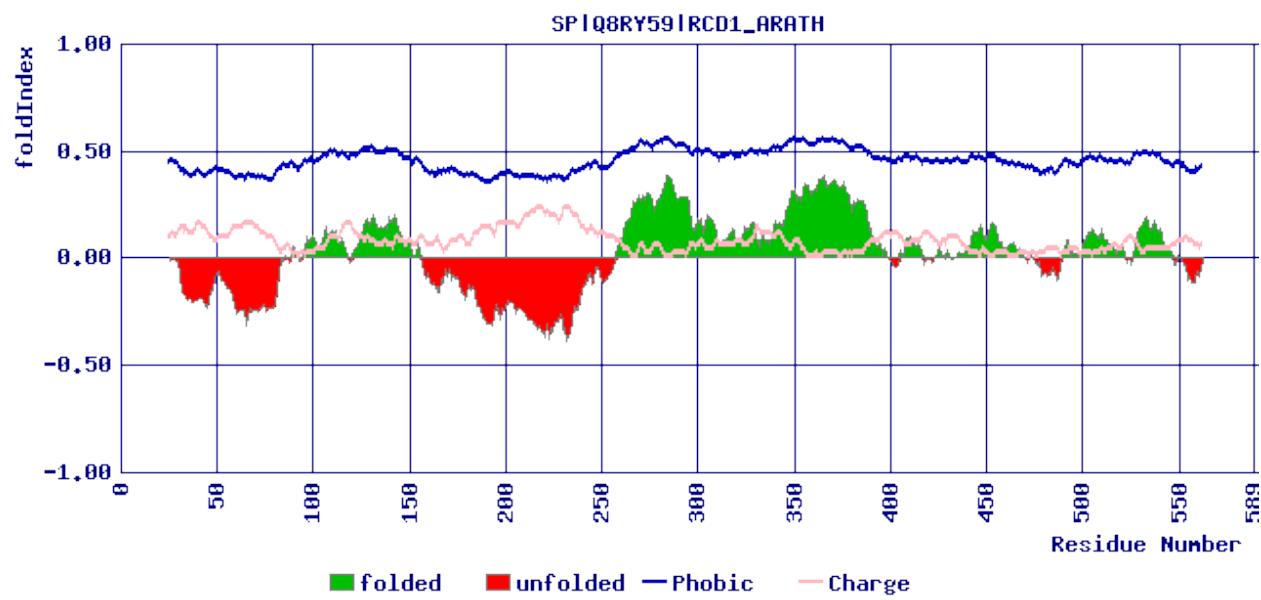


Fig. 3. FoldIndex[©]. Graphical pattern of folded and unfolded regions in AtRCD1 protein sequence.