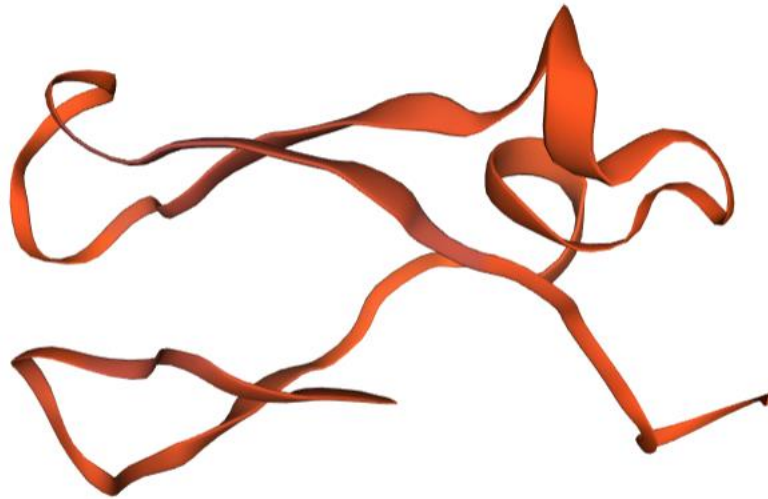


In silico characterization of the proteins from the overcount prevention system

PSP3 (BBa_I746351)

Structure prediction:



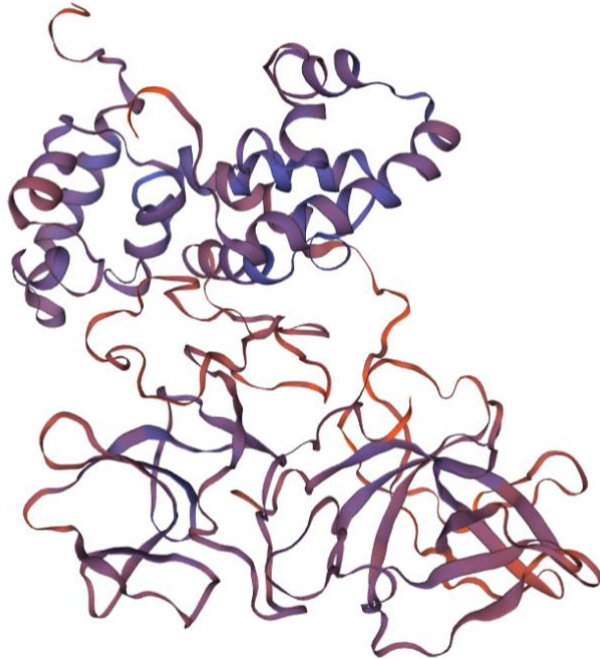
Motifs Results based on frequent pattern hits:

- 1 PKC Phosphorylation site

List of matches	FT	MYHIT	15	17	freq_pat:PKC_PHOSPHO_SITE [?]
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CI Lambda repressor (BBa_K105004)

Structure prediction:



Motifs Results based on frequent pattern hits:

- 1 N-Glycosylation sites (ASN_GLYCOSYLATION)
- 1cAMP Phosphorylation site
- 5 CK2 Phosphorylation sites
- 4 Myristoylation
- 4 PKC Phosphorylation sites

List of matches	FT	MYHIT	217	220	freq_pat:ASN_GLYCOSYLATION [?]
	FT	MYHIT	135	138	freq_pat:CAMP_PHOSPHO_SITE [?]
	FT	MYHIT	36	39	freq_pat:CK2_PHOSPHO_SITE [?]
	FT	MYHIT	73	76	freq_pat:CK2_PHOSPHO_SITE [?]
	FT	MYHIT	100	103	freq_pat:CK2_PHOSPHO_SITE [?]
	FT	MYHIT	123	126	freq_pat:CK2_PHOSPHO_SITE [?]
	FT	MYHIT	160	163	freq_pat:CK2_PHOSPHO_SITE [?]
	FT	MYHIT	42	47	freq_pat:MYRISTYL [?]
	FT	MYHIT	49	54	freq_pat:MYRISTYL [?]
	FT	MYHIT	148	153	freq_pat:MYRISTYL [?]
	FT	MYHIT	156	161	freq_pat:MYRISTYL [?]
	FT	MYHIT	2	4	freq_pat:PKC_PHOSPHO_SITE [?]
	FT	MYHIT	97	99	freq_pat:PKC_PHOSPHO_SITE [?]
	FT	MYHIT	133	135	freq_pat:PKC_PHOSPHO_SITE [?]
FT	MYHIT	191	193	freq_pat:PKC_PHOSPHO_SITE [?]	