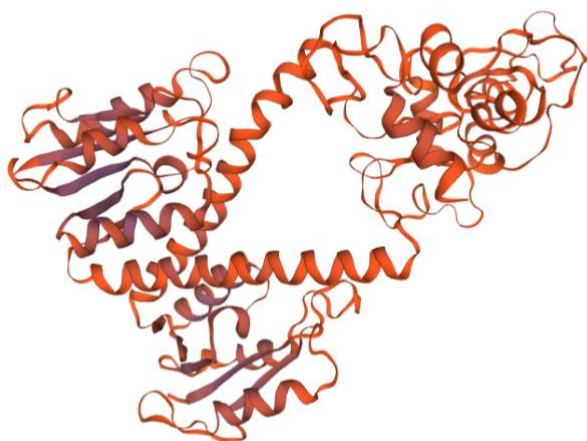


## *In silico* characterization of the proteins from the count system

### Mycobacterium BXB1 Reoptimized (BBa\_K907000)

Structure prediction:



### Motifs Results based on frequent pattern hits:

- 1 Amidation site
- 2 Glycosylation sites
- 8 CK2 Phosphorylation sites
- 4 PKC Phosphorylation sites
- 3 Myristoylation sites

	FT	MYHIT	317	320	freq_pat:AMIDATION [?]
	FT	MYHIT	141	144	freq_pat:ASN_GLYCOSYLATION [?]
	FT	MYHIT	337	340	freq_pat:ASN_GLYCOSYLATION [?]
	FT	MYHIT	17	20	freq_pat:CK2_PHOSPHO_SITE [?]
	FT	MYHIT	106	109	freq_pat:CK2_PHOSPHO_SITE [?]
	FT	MYHIT	166	169	freq_pat:CK2_PHOSPHO_SITE [?]
	FT	MYHIT	212	215	freq_pat:CK2_PHOSPHO_SITE [?]
	FT	MYHIT	254	257	freq_pat:CK2_PHOSPHO_SITE [?]
	FT	MYHIT	373	376	freq_pat:CK2_PHOSPHO_SITE [?]
List of matches	FT	MYHIT	428	431	freq_pat:CK2_PHOSPHO_SITE [?]
	FT	MYHIT	490	493	freq_pat:CK2_PHOSPHO_SITE [?]
	FT	MYHIT	370	375	freq_pat:MYRISTYL [?]
	FT	MYHIT	436	441	freq_pat:MYRISTYL [?]
	FT	MYHIT	469	474	freq_pat:MYRISTYL [?]
	FT	MYHIT	86	88	freq_pat:PKC_PHOSPHO_SITE [?]
	FT	MYHIT	212	214	freq_pat:PKC_PHOSPHO_SITE [?]
	FT	MYHIT	254	256	freq_pat:PKC_PHOSPHO_SITE [?]
	FT	MYHIT	285	287	freq_pat:PKC_PHOSPHO_SITE [?]

## BXB1 RDF Reverse (BBa\_K1039006)

Structure prediction:



**Motifs Results based on frequent pattern hits:**

- 1 ATP/GTP Binding site
- 2 CK2 Phosphorylation sites
- 4 Myristoylation
- 3 PKC Phosphorylation sites
- 2 Tyrosine Kinase phosphorylation sites

<b>List of matches</b>	FT	MYHIT	163	170	freq_pat:ATP_GTP_A [?]
	FT	MYHIT	55	58	freq_pat:CK2_PHOSPHO_SITE [?]
	FT	MYHIT	197	200	freq_pat:CK2_PHOSPHO_SITE [?]
	FT	MYHIT	87	92	freq_pat:MYRISTYL [?]
	FT	MYHIT	198	203	freq_pat:MYRISTYL [?]
	FT	MYHIT	215	220	freq_pat:MYRISTYL [?]
	FT	MYHIT	243	248	freq_pat:MYRISTYL [?]
	FT	MYHIT	2	4	freq_pat:PKC_PHOSPHO_SITE [?]
	FT	MYHIT	176	178	freq_pat:PKC_PHOSPHO_SITE [?]
	FT	MYHIT	191	193	freq_pat:PKC_PHOSPHO_SITE [?]
	FT	MYHIT	26	34	freq_pat:TYR_PHOSPHO_SITE [?]
	FT	MYHIT	56	64	freq_pat:TYR_PHOSPHO_SITE [?]

## TP901 (BBa\_K2116035)

### Structure prediction:



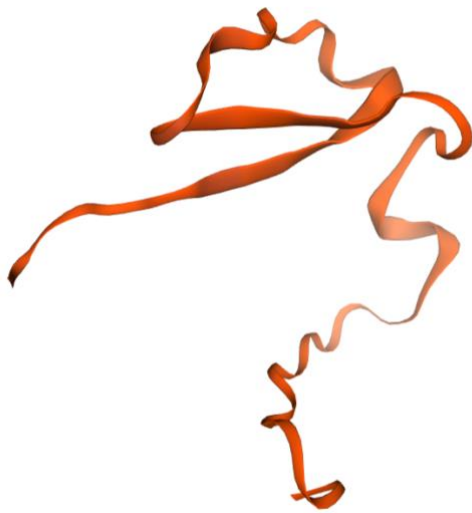
### Motifs Results based on frequent pattern hits:

- 4 N-Glycosylation sites (ASN\_GLYCOSYLATION)
- 1 ATP/GTP Binding site
- 11 CK2 Phosphorylation sites
- 2 Myristoylation
- 7 PKC Phosphorylation sites
- 3 Tyrosine Kinase phosphorylation sites

List of matches				
FT	MYHIT	119	122	freq_pat:ASN_GLYCOSYLATION [?]
FT	MYHIT	214	217	freq_pat:ASN_GLYCOSYLATION [?]
FT	MYHIT	370	373	freq_pat:ASN_GLYCOSYLATION [?]
FT	MYHIT	442	445	freq_pat:ASN_GLYCOSYLATION [?]
FT	MYHIT	157	164	freq_pat:ATP_GTP_A [?]
FT	MYHIT	32	35	freq_pat:CK2_PHOSPHO_SITE [?]
FT	MYHIT	54	57	freq_pat:CK2_PHOSPHO_SITE [?]
FT	MYHIT	96	99	freq_pat:CK2_PHOSPHO_SITE [?]
FT	MYHIT	117	120	freq_pat:CK2_PHOSPHO_SITE [?]
FT	MYHIT	191	194	freq_pat:CK2_PHOSPHO_SITE [?]
FT	MYHIT	248	251	freq_pat:CK2_PHOSPHO_SITE [?]
FT	MYHIT	353	356	freq_pat:CK2_PHOSPHO_SITE [?]
FT	MYHIT	358	361	freq_pat:CK2_PHOSPHO_SITE [?]
FT	MYHIT	395	398	freq_pat:CK2_PHOSPHO_SITE [?]
FT	MYHIT	414	417	freq_pat:CK2_PHOSPHO_SITE [?]
FT	MYHIT	477	480	freq_pat:CK2_PHOSPHO_SITE [?]
FT	MYHIT	203	208	freq_pat:MYRISTYL [?]
FT	MYHIT	295	300	freq_pat:MYRISTYL [?]
FT	MYHIT	12	14	freq_pat:PKC_PHOSPHO_SITE [?]
FT	MYHIT	96	98	freq_pat:PKC_PHOSPHO_SITE [?]
FT	MYHIT	161	163	freq_pat:PKC_PHOSPHO_SITE [?]
FT	MYHIT	226	228	freq_pat:PKC_PHOSPHO_SITE [?]
FT	MYHIT	229	231	freq_pat:PKC_PHOSPHO_SITE [?]
FT	MYHIT	320	322	freq_pat:PKC_PHOSPHO_SITE [?]
FT	MYHIT	389	391	freq_pat:PKC_PHOSPHO_SITE [?]
FT	MYHIT	95	102	freq_pat:TYR_PHOSPHO_SITE [?]
FT	MYHIT	231	239	freq_pat:TYR_PHOSPHO_SITE [?]
FT	MYHIT	343	350	freq_pat:TYR_PHOSPHO_SITE [?]

**TP901 RDF Reverse (BBa\_I20287)**

**Structure prediction:**



**Motifs Results based on frequent pattern hits:**

- 1 N-Glycosylation sites (ASN\_GLYCOSYLATION)
- 1 CK2 Phosphorylation sites

<b>List of matches</b>	FT	MYHIT	18	21	freq_pat:ASN_GLYCOSYLATION [?]
	FT	MYHIT	59	62	freq_pat:CK2_PHOSPHO_SITE [?]