

>tr|Q55136|Q55136_SYNY3 Carbonic anhydrase EcaB OS=Synechocystis sp. (strain PCC 6803 / Kazusa) OX=1111708 GN=icfA PE=3 SV=1

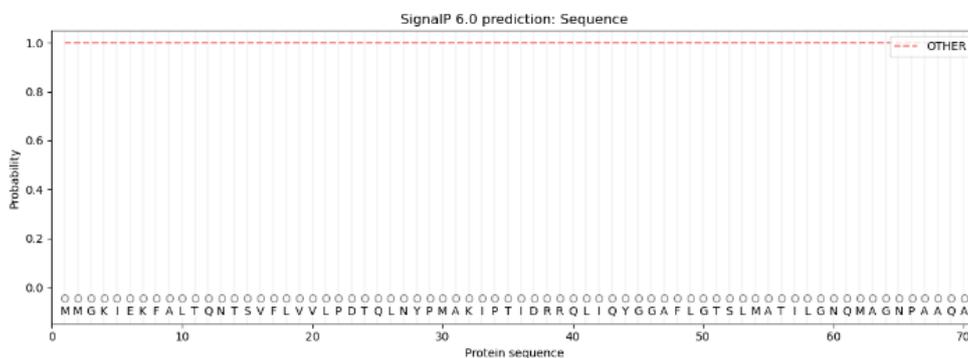
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 HQGCGAVKAAMDGGDLPGQIGSVIKKIDIGSVTDDSSNAASVVMATKANVEHQMAVLIQSPVLSQLIAEERLLIMGAYYNLESGIVTL
 L

Sequence

Prediction: Other

Protein type	Other	Signal Peptide (Sec/SPI)	Lipoprotein signal peptide (Sec/SPII)	TAT signal peptide (Tat/SPI)	TAT Lipoprotein signal peptide (Tat/SPII)	Pilin-like signal peptide (Sec/SPIII)
Likelihood	1	0	0	0	0	0

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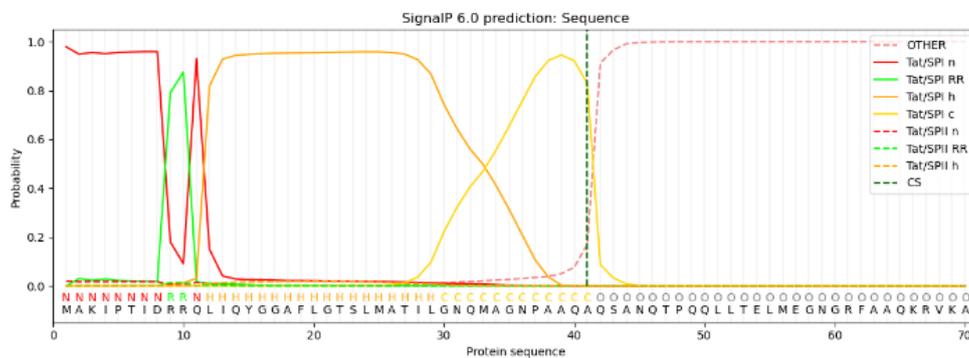
Sequence

Prediction: TAT signal peptide (Tat/SPI)

Cleavage site between pos. 41 and 42. Probability 0.828795

Protein type	Other	Signal Peptide (Sec/SPI)	Lipoprotein signal peptide (Sec/SPII)	TAT signal peptide (Tat/SPI)	TAT Lipoprotein signal peptide (Tat/SPII)	Pilin-like signal peptide (Sec/SPIII)
Likelihood	0	0	0	0.9795	0.0204	0

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Concerning Figure 1 b:

CcaA homologues N-terminal protein alignment (aa 1-50)

<i>Synechocystis</i> sp. PCC6803 CcaA	1	M	R	L	I	E	G	L	R	K	F	R	E	G	V	F	S	S	H	R	D	L	F	E	Q	L	S	H	G	H	P	R	I	L	F	I	C	S	D	S	R	V	D	P	N	I	L	T	50		
<i>S.gerasimenkoeae</i> IPPAS B-353 CahB1	1	M	K	K	L	L	R	G	L	R	Q	E	K	S	N	F	S	T	H	Q	E	L	F	E	Q	L	S	H	G	K	P	R	V	L	F	I	T	C	S	D	S	R	V	D	P	N	I	L	T	50	
<i>N. punctiforme</i> sp. PCC73102	1	M	K	K	L	I	R	G	L	R	E	E	K	S	S	F	S	A	N	E	E	L	F	E	Q	L	S	H	G	K	P	R	V	L	F	I	T	C	S	D	S	R	V	D	P	N	I	L	T	50	
<i>Synechococcus</i> sp. PCC7002	1	M	K	K	L	I	R	G	L	D	K	E	K	S	S	V	V	A	S	H	Q	D	L	F	E	Q	L	S	H	G	K	P	R	V	L	F	I	C	S	D	S	R	V	D	P	A	I	L	T	50	
<i>A. marina</i> MBIC10699	1	M	K	K	L	V	R	G	L	Q	E	E	K	S	S	V	V	A	Q	N	Q	E	L	L	E	E	L	S	H	G	K	P	R	V	L	F	I	S	C	S	D	S	R	V	D	P	N	I	L	T	50
<i>Synechococcus</i> sp. PCC7942	1	M	R	K	L	I	E	G	L	R	H	F	R	T	S	Y	Y	P	S	H	R	D	L	F	E	Q	F	A	K	G	H	P	R	V	L	F	I	T	C	S	D	S	R	V	D	P	N	I	L	T	50