

CcaA/CahB1/EcaB N-terminal Secretion Signal Prediction Software Outputs

Top: Protein sequence as extracted from NCBI Genbank
Middle: SignalP v. 6.0 graphic output (<https://services.healthtech.dtu.dk/service.php?SignalP>)
Bottom: DeepTMHMM graphic output (<https://dtu.biolib.com/DeepTMHMM>)

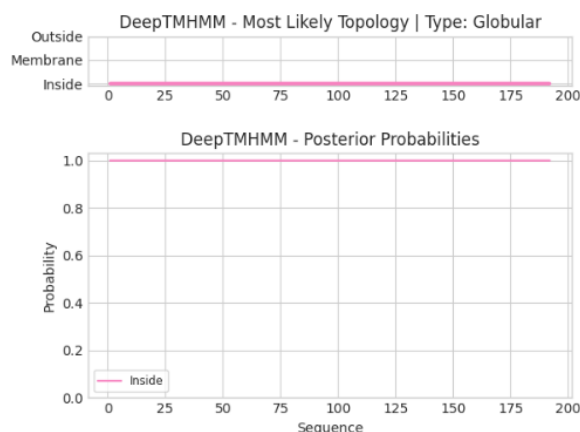
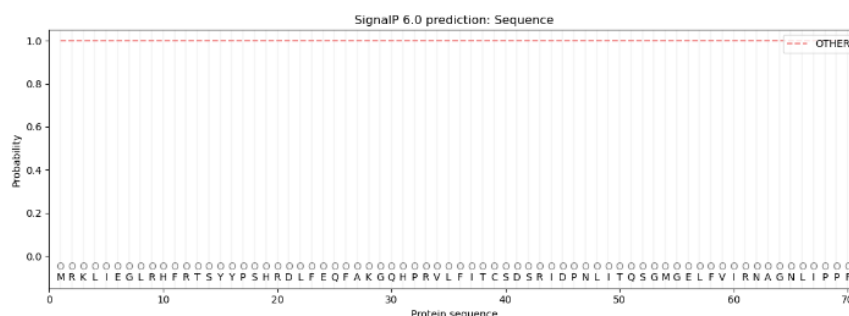
>WP_011055160.1 carbonic anhydrase [Synechococcus elongatus PCC7942]

MTVLTEVLEANQAYAAAFGEKGSALPPARQFAILTCMDARLDPAQYAGLKEGDAHVIRNAGGRASDDAIRSLVISYKLLGTKEWFEVIH
HTDCGMEFFTNSVIGSLLANSLETAVLRSDGFTDIGEGPGSEEGKYIHWLTIENTQTSVVEDVQRIRRHPLVPSNIPIYGYLYDVRSGRLL
EVPEATTAGVAR

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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MTVLTEVLEAANQAYAAAFGEKGSALPPARQFAILTCDARLDPAQYAGLKEGDAHVIRNAGGRASDDAIRSLVISYKLLGTKEWFVIHHTDCGMEFFTNISVIGSLLANSLETAVLRS DGF TDI
GEGPGSEEGKYIHWLTIENOTOSVVEDVORIRRHPLVPSNIPYGYLDVRSGR LIEVPEATTAGVAR

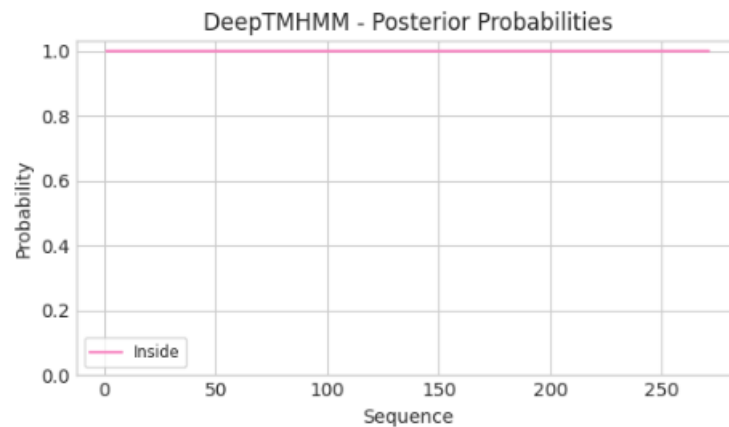
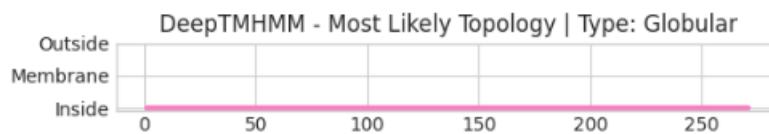
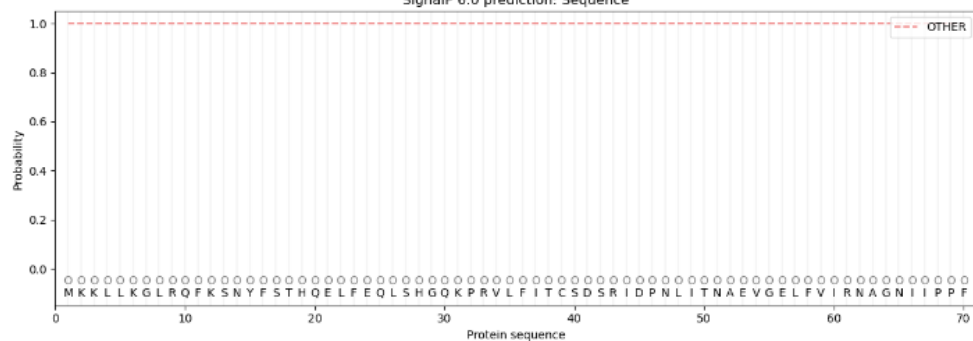
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IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
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MKKLLKGLRQFKSNYFSTHQELFEQLSHGQKPRVLFITCSDSRIDPNLITNAEVLGELFVIRNAGNIIPPGAANGGEGAAVEYAVQALGV
EHIIVCGHSHCGAMKGLLKRSSLEDEMPVYEWLRHAEATRQLLKENYSHLEGETLLEVAVAENVLTQIENLRTPVIHSLYRNKLHLH
AWIYHIETGEVLEYDSIRHDFVTPDENAMLEAYPVQCVLSLPEDVEELVPGHRQSSAPAQTEVAAADRDAKMPWLSSEQVARIHGG
NGRR

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	1.0001	0	0	0	0	0

SignalP 6.0 prediction: Sequence



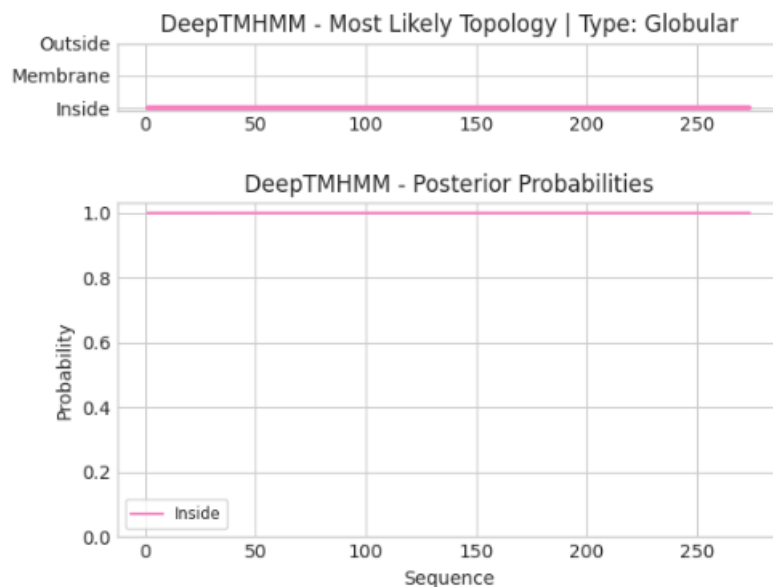
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 RHABATRLKLENYHGETTLLVAVAEVLTQIENLRTPVISHKLRNKLHLAWIYHIETGEVLEYDSIRHDFVTPDENAMLEAYPVQCVLSLPEDVEELVPGHRQSSAPAQTEVAAADR
 DAKMPFLSSEQVARIHGSGNGRR

[illegible]

MQRLEGLQKFREGYFSSHRDLFEQLSHGQHPRILFICCCSDSRVDPNLITQSEVGDLFVIRNAGNIIPPYGAANGGEGAAMEYALVALEI
 NQIIVCGSHSHCGAMKGLLKLNSLQEKLPLVYDWLKHTEATRRLVDNYSHLEGEDLIEVAVAENILTQLKNLQTPAIHSRLHRGDLSLH
 GWIYRIEEGEVLAYDGVLDHDFVAPQSRINALEPEDEYAPHPNSPLISYDAFKVPGKERPGREKATESPAPQLSPLPGFGLHPREQAERIY
 RGSR

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

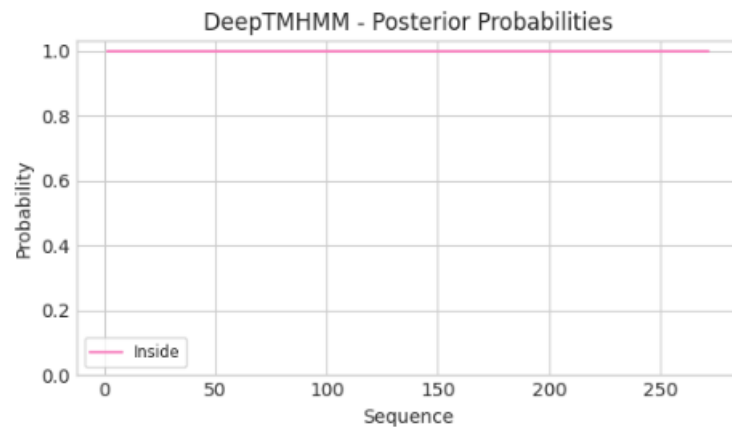
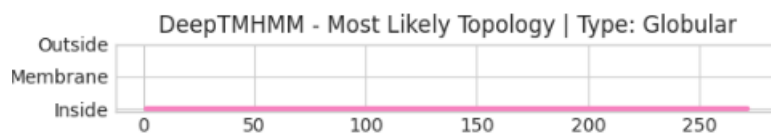
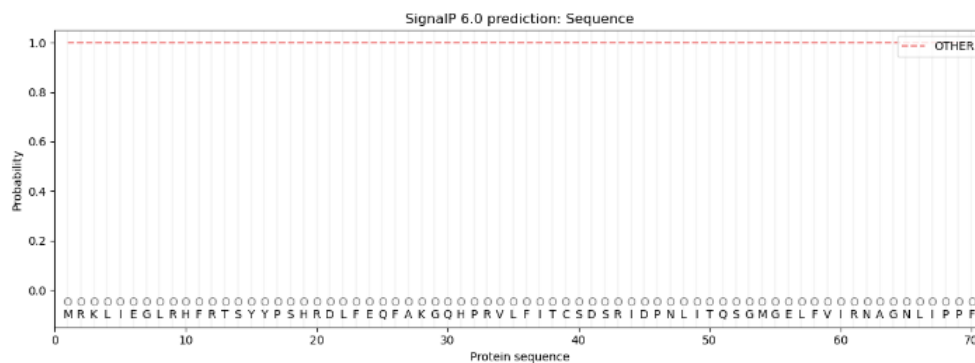
[illegible]

MRKLTIEGLRHFRTSYPPSHRDLFEQFAKGQHPRVLFITCSDSRIDPNLITQSGMGELFVIRNAGNLIPPGAANGGEGASIEYAIAALNIE
HVVVCGHSHCGAMKGLLNQLQEDMPLVYDWLQHAQATRRLVDNYSGYETDDLVEILVAENVLTQIENLKTYPIVRSRLFQGKLQI
FGWIYEVESEGEVLQISRTSSDDTGIDECVPRLPGSQEKAILGRCVPLTEEVAVAPPEPEPVIAAVAAPPANYSSRGWLAPEQQQRIYRG
NAS

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

SignalP 6.0 prediction: Sequence



MRKLI EGRHFRSTSYPPSHRDLFEQFAKGQHPRVLFITCSDSRIDPNLITQSGMGE L FVRNAGNLIPFGAANGGEGASIEY AIAALNIEHV VVCGSHSGAMG L LKLNQLQEDMPLVYDWL
QHAQATRRLLVDNYSGYETDDLVEILVAENVLTQIENLKTYPIVRSRLFQGKLQIFGWIYEVESGEVLQISRTSSDDTGIDECPVRLPGSQEKAILGRCVVPLTEEVAVAPPEPEPVIAA VAP
PANYSSRGWL APEQQORIYRGNAS

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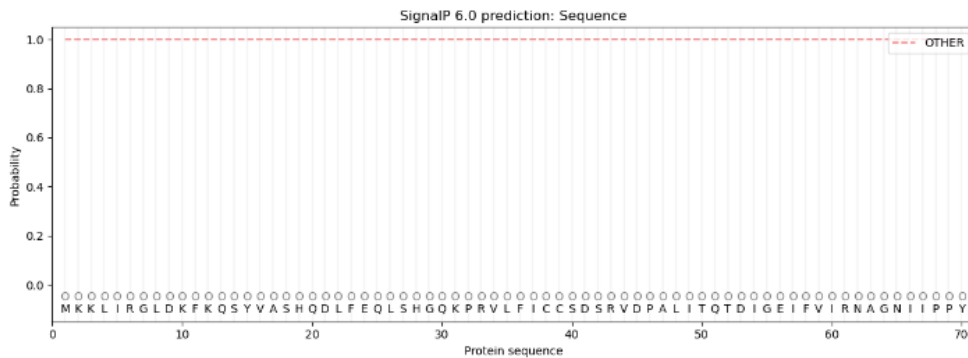
>WP_012307606.1 carbonic anhydrase CcaA [Synechococcus PCC7002]

MKKILIRGLDKFKQSYVASHQDLFEQLSHGQKPRVLFICCSDSRVDPALITQTDIGEIVIRNAGNIIPPYGAANGGEGGTLEYALQGLDIR
 QIIVCGHSHCGAMKGLLKNLQADMPLVYDWLKHAEATRRLVRDTPHCEGEELVETLVAENVLVQIDNLKTPVVRSLHQGKLKI
 YGWIYNIENGEVLAYDETKHAYVKPDYSLIDETPLTEREALGECPLPYTVASGQSLAGWYGETDTFSVSG

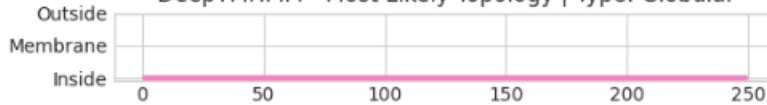
Sequence

Prediction: Other

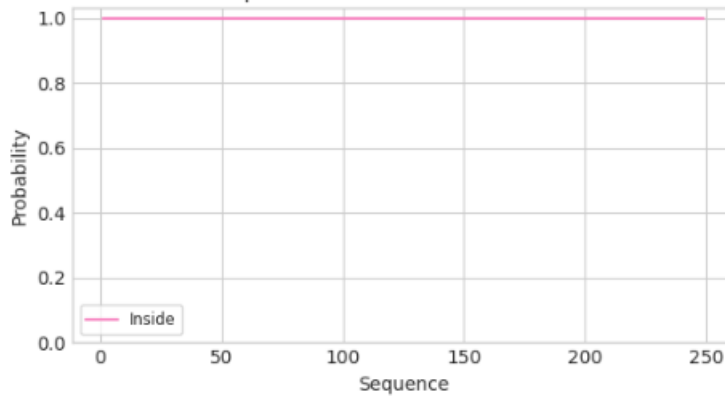
Protein type	Other	Signal Peptide (Sec/SPI)	Lipoprotein signal peptide (Sec/SPII)	TAT signal peptide (Tat/SPI)	TAT Lipoprotein signal peptide (Tat/SPII)	Pilin-like signal peptide (Sec/SPIII)
Likelihood	1	0	0	0	0	0

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DeepTMHMM - Most Likely Topology | Type: Globular



DeepTMHMM - Posterior Probabilities



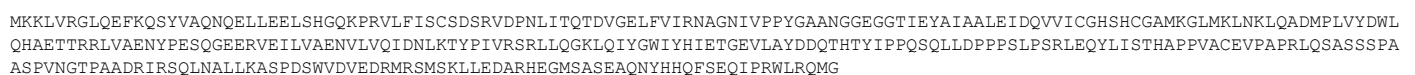
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 KHAETARRLRDTPHCEGEELVETLVAENVLVQIDNLKTPVVRSLHQGKLIYGIWYNIENGEVLAYDETKHAYVKPDYSIIDETPLTEREALGCPLPYTVASGQSLAGWYGETDTSFVS
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MKKLVRLQEFKQSYVAQNQELLEELSHGQKPRVLFISCSDSRVDPNLITQTDVGELFVIRNAGNIVPPYGAANGGEGGTIEYAIAALEI
 DQVVICGSHSHCGAMKGLMKNLQADMPVLDWLQHAETTRRLVAENYPESQGEERVEILVAENVLVQIDNLKTYPIVRSRLQGKL
 QIYGWIYHIETGEVLAYDDQTHYIPPSQLLDPPLPSRLEQYLISTHAPPVACEVPAPRLQSASSSPAASPVNGTPAADRIRSQLNAL
 LKASPDWVDVEDRMRSMSKLLDARHEGMSASEAQNYHHQFSEQIPRWLRQMG

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

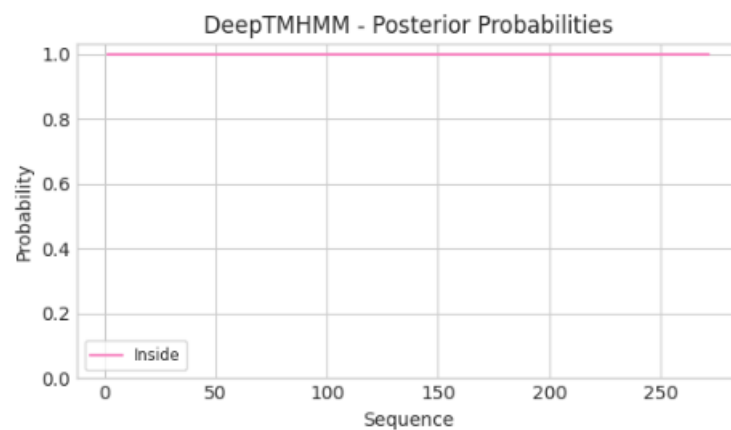
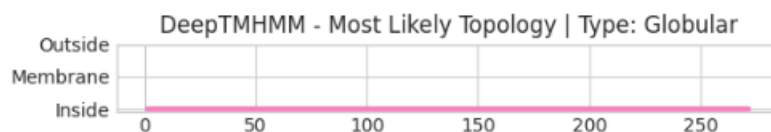
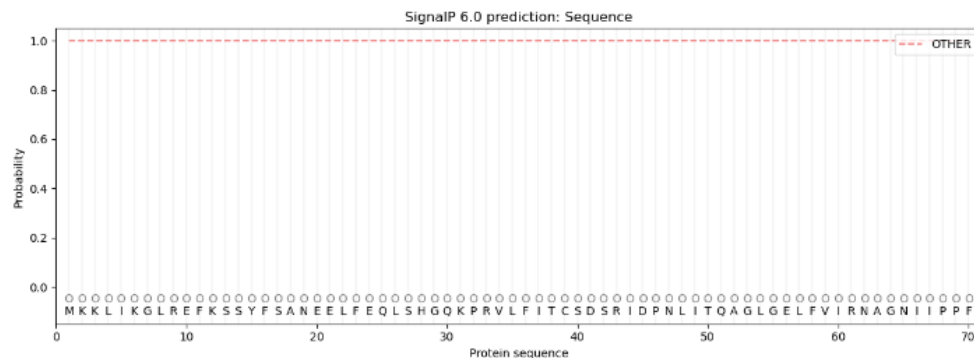
[illegible]

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VCGHSHCGAMKGLMKLDSLVRVEMPLVHDWLKYAEATRRLVKDNYSHYEGEELLEIIIAENVLTQIENLRTPVIRSKLHQGQLSIYAWIY
QIETGEILAYDPQKHAYVLPQNQLLSSEIDETLLSPPLNSNVEIHFTKTQQRPFQSSGELPIPTHEWFPMTVLSPEQMERIYRGSATK

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	1.0001	0	0	0	0	0

SignalP 6.0 prediction: Sequence



MKKLIKGLREFKSSYFSANEELFEQLSHGQKPRVLFITCSDSRIDPNLITQAGLGELFVIRNAGNIIPFGATNGEGATIEYAIQALDIQIIVCGHSHCGAMKGLMKLDSLVRVEMPLVHVDL
 KYAEATRRLVKDNYSHYEGEELLEIIIAENVLTQIENLRTPVIRSKLHQGLSIYAWIYQIETGEILAYDPQKHAYVLPQNQLLSSEIDETLLSPPLNSNVEIHFTTKTQQRPFQSSGELPIPT
 HEWFPMTVLSPEQMERIYRGSATK

[illegible]

MMGKIEKFALTQNTSVFLVLPDTQLNYPMAKIPTIDRRQLIQYGGAFGLTSLMATILGNQMAGNPAAQAQSANQTPQQLLTELME
GNGRFAAQKRVKANQDLYRLAEVAQGQNPFAAILSCADSRVPPEIIFDQGLGDLFICRIAGNVATPQEVGSLEFGTLVLGAKVLMVLG
HQGCGAVKAAMDGGDLPGQIGSVIKKIDIGSVTDDSSNAASVVMATKANVEHQMAVLIQSPVLSQLIAEERLLIMGAYYNLESGIVTL
L

Prediction: Other

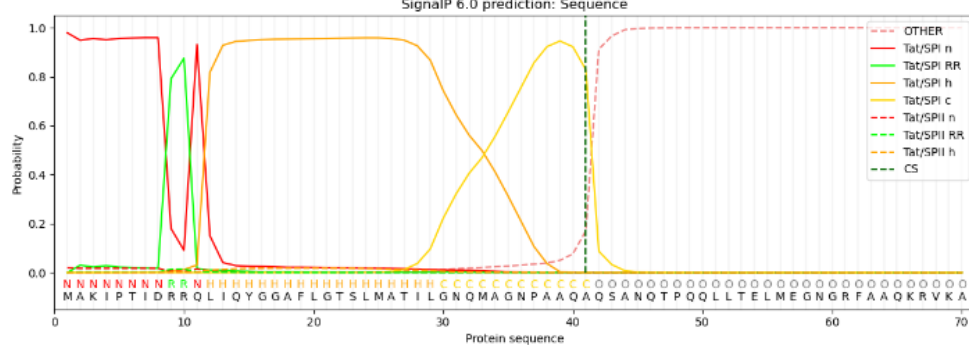
Protein type	Other	Signal Peptide (Sec/SPI)	Lipoprotein signal peptide (Sec/SPII)	TAT signal peptide (Tat/SPI)	TAT Lipoprotein signal peptide (Tat/SPII)	Pilin-like signal peptide (Sec/SPIII)
Likelihood	1	0	0	0	0	0

SignalP 6.0 prediction: Sequence

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

SignalP 6.0 prediction: Sequence



>RUR88685.1 carbonic anhydrase EcaB [Anabaena PCC 7120 = FACHB-418]

MLGKEMSRINGFIGRRNFLGLAGAGSLVVAANACAGSLTVGKEEPAIADVKSINLNPVNPQKALKLLLDG NQRFV KR K PKYPNQSRQK
LQSIAKAQYPFAAILGCADSRVPAEIVFDQGLGDLFVVVRVAGNIASDMAIASLEYATSVLDTRLIVVLGHTKCGAVAASVKDEPLPGRIG
YLAESIRPALSKLPSKSKDVNKA AVIANIQYQAEKLQQKSTILAQLVNKGTVQIIGAAYDIDTGT VSVIS

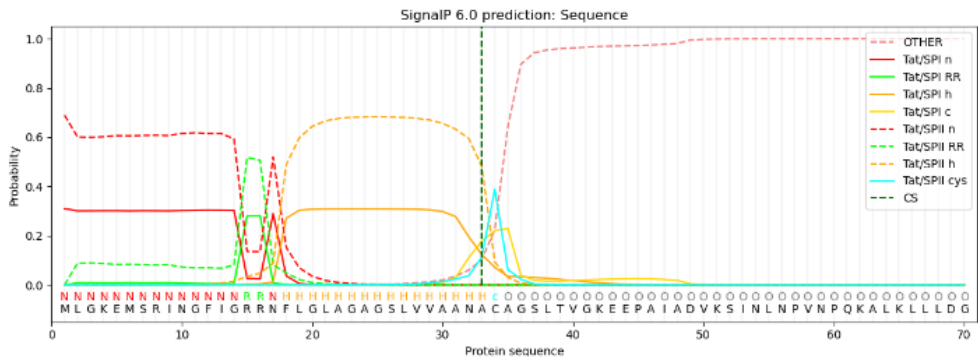
Sequence

Prediction: TAT Lipoprotein signal peptide (Tat/SPII)

Cleavage site between pos. 33 and 34. Probability 0.482341

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	0.0001	0.3101	0.6898	0

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MKHFME~~RR~~DFLKLGMTGAFGMILSASDLLWRVEQAKAADIPSTSAESLSPDAALQKLI~~EG~~NQRFVDHHPQYPDQSELRLHEVAQAQ
HPFATILSCADSRVPAEIVFDQGI~~GD~~IFDVRIAGNIATHEAIGSIEYAVVLLGSPLLMVMGHERCGAVTAAVQKESLPGDISTFVKAIKPAL
KKVKDQPGDAVENAVVANVQYQIERLQKSKLLSEQVQSGKLKIVGGRYDLDTGRVTIIT

Cleavage site between pos. 37 and 38. Probability 0.863430

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	0.9999	0.0001	0

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	C	L	Q	K	F	R	E	G	Y	F	S	S	H	R	D	L	F	E	Q	L	S	H	G	Q	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	K	G	L	R	F	K	S	N	Y	F	S	T	H	Q	E	L	F	E	Q	L	S	H	G	Q	K	P	R	V	L	F	I	T	C	S	D	S	R	E	D	P	N	I	L	T	50	
<i>N. punctiforme</i> sp. PCC73102		1	M	K	K	L	I	K	G	L	R	E	F	K	S	S	Y	F	S	A	N	E	E	L	F	E	Q	L	S	H	G	Q	K	P	R	V	L	F	I	T	C	S	D	S	R	E	D	P	N	I	L	T	50
<i>Synechococcus</i> sp. PCC7002		1	M	K	K	L	I	R	G	L	D	K	F	K	S	Y	V	A	S	H	Q	D	L	F	E	Q	L	S	H	G	Q	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	F	K	S	Y	V	A	Q	N	Q	E	E	L	E	E	L	S	H	G	Q	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	Q	H	P	R	V	L	F	I	T	C	S	D	S	R	E	D	P	N	I	L	T	50