

## A Targeting predictions

	Gene Model	Signal P	Cleavage	ASAFIND	Mitroprot	TMHMM	Verdict
NAGS1	Phatr3_J10902.t1 (+108aa)	v3.0: N (0.025)* v4.1: N (D = 0.254)	--	--	0.9489	Yes 44-63	TM domain /plastid
	Phatr3_J10902.t1 (+72aa)	v3.0: Y (0.814) v4.1: N (D = 0.384)	TLA-TL	Y – low conf.	0.2666	No	
	Phatr3_J10902.t1	v3.0: N (0.025) v4.1: N (D = 0.098)	--	--	0.0029	No	
NAGS2	Phatr3_J44492.t1	v3.0: Y (0.977) v4.1: Y (D = 0.705)	SYT-GI AKS-YT	N N	0.6859	No	Signal peptide

\*Signal anchor probability = 0.916

## B Sequences

### NAGS1

#### >Phatr3\_J10902.t1\_ESTextended

MNTAIVVYRQQLRLLQLLTVSSRSPPLRSWRGLSSKMKTSTHKVFGSLSTWVATLATLPIHWITESFVPSALPLNQKSPSLRRPPLASFPVFPNPLPITTASSS  
 SPLHMAATDKEQQLDAAANTKHAATAPKGNESHNVGHSSLSNVGGKAPKDFHVDHEAGLRVDGRSSPQRHLSSTTKESTLSFQNVTFEAQKPKGYSTFDASS  
 LLAVDPSCINIDTVPPEEEFPGPTEEALKRLEPFVSMFRGSANYIANHRNTLAVYHIPGGLLDQPGNNVFRDLMNNDIALTWLLGMKIVLVVGCRRHQIAKRVAQH  
 QSDSSLEENLQSRHGLRVTDEKTLRIVKKEEAGYVRFEVERQLARSLRMQGGMGNAPGVGSGTQGYYDGNVVSNGNFYSAQPFGLIDGVDFKYTGFRVREVEWI  
 RQKHNNRDI CLMTTLGVSFSGEVFNVNSEALASVAGALEASKVIYFTEQEMELRHTQHKKIQSLRMSDANNLLEYSGVTIHKKGFVQLDDELHEMDKAALDM  
 LLKIGWSVQALEMGVKRAHII SPKHGALLQELYTRDGSGLLISGDLYDGIRANVHDVAIHDLISPLIQMGTIDRPKSVLEKDVESYVYVTRDNHIVASGQL  
 KIFENGFAEIGCLLVNQYRSRGRGDAMLGYLERLCLVNSCSSIFVLSTQTMWFVVERGFDEVGVDRPLPPSRQATYNYKRNSKIYMKKIESDRDLDASELWWRN

Transmembrane Domain  
 EST extended model  
 PRK05279 Domain

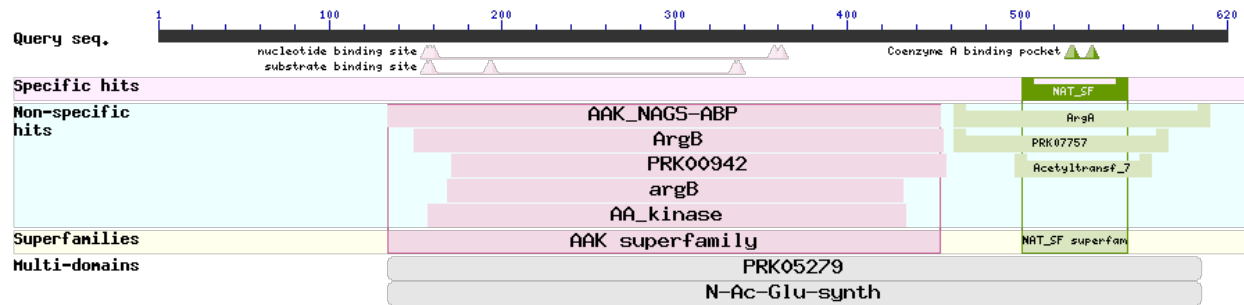
### NAGS2

#### >Phatr3\_J44492.t1

MVMSLTAIFVISTWVAKSYTGIPKASVRHPHTGPRATGSFTVNVKRKSSIAVQFSASTESSDFSTWDGSAPLSVDDSYDELVTGALQISPLSVNDPALVEFTES  
 TFRKSVRNGKVL PAMGSSHYPFAMMLQGSAPYIAAHAGKTAVIHIPGDVLDGTPNADALLADISLRLLGMKIVIVIGCRFDLDRCDMDFAENAHECHNALKI  
 TNAETLRYVEEEVGFRLRTEMERKLNRCRLRMTGGVSGTKDAPVPDGNVVSNGNFYTAQQFGIIQGEDFEYTGFTPTGQVHAENIQRVLNNDVLLTTVGLSTLGE  
 LVNVNGYHLAASVAAALKAYKVIYMSNEGSVLQKKGENISIQELPLSFAKAVLDYHHVEVHKTFGATFERARQSLEPHAVELLLHLGWASWALDHGVKRAHVVN  
 PGDGALLEELFTSKNGANTCLYHDEENTKVEEIEIGQDDWDSFFASAKQGGQKEIYIKKQQSSKRF

## C Domain architecture

### NAGS1



### NAGS2

