```
5724 multiple located sequences are accepted
ProtComp Version 9.0. Identifying sub-cellular location (Plant)
Seq name: Potri.002G128900.1, Length=238
Significant similarity in Potential Location DB - Nuclear
Database sequence: AC=Q9S7L2 Location: Nuclear DE Transcription factor MYB98; | | 93
Score=52, Sequence length=428, Alignment length=124
Predicted by Neural Nets - Extracellular (Secreted) with score
Integral Prediction of protein location: Nuclear with score
Location weights: LocDB / PotLocDB / Neural Nets / Pentamers / Integral
Location weights: LocDB / PotLocDB / Neural Nets / Pentamers / I:

Nuclear 5.0 / 5.0 / 0.00 / 0.08 /

Plasma membrane 0.0 / 0.0 / 1.00 / 0.06 /
Extracellular 0.0 / 0.0 / 1.00 / 1.60 /

Cytoplasmic 0.0 / 0.0 / 0.00 / 1.43 /

Mitochondrial 0.0 / 0.0 / 0.00 / 1.60 /
Endoplasm. retic. 0.0 / 0.0 / 0.00 / 0.23 /
Peroxisomal 0.0 / 0.0 / 1.00 / 0.00 /

Golgi 0.0 / 0.0 / 1.00 / 0.22 /

Chloroplast 0.0 / 0.0 / 0.00 / 0.13 /

Vacuolar 0.0 / 0.0 / 0.00 / 0.05 /
                                                                                                                0.93
                                                                                                               0.00
                                                                                                                 0.00
                                                                                                                0.00
                                                                                                                0.00
                                                                                                                0.11
                                                                                                               0.00
                                                                                                               0.08
```

(b)

Potri.002G128900.1 WoLFPSORT prediction nucl: 12, cyto: 1, pero: 1

PSORT features and traditional PSORTII prediction

14 Nearest Neighbors

id	site	distance	identity	comments
TFB2_ARATH	nucl	260.418	13.141%	[Uniprot] SWISS-PROT45:Nuclear.
TF2B_SOYBN	nucl	275.216	11.8211%	[Uniprot] SWISS-PROT45:Nuclear.
HX1A_MAIZE	nucl	275.242	9.3185%	[Uniprot] SWISS-PROT45:Nuclear.
TF2B_ORYSA	nucl	288.716	14.7436%	[Uniprot] SWISS-PROT45:Nuclear.
At1g68480.1	nucl	294.434	12.9921%	[Arath]
SUP_ARATH	nucl	313.349	13.0252%	[Uniprot] SWISS-PROT45:Nuclear.
At1g79810.1	pero	324.012	15.3153%	[Arath]
HAT4_ARATH	nucl	334.52	12.6761%	[Uniprot] SWISS-PROT45:Nuclear.
PRH_PETCR	nucl	341.443	7.07721%	[Uniprot] SWISS-PROT45:Nuclear.
OP2_MAIZE	nucl	370.485	11.9205%	[Uniprot] SWISS-PROT45:Nuclear.
At5g53810.1	cyto	381.431	12.1693%	[Arath]
PIF4_ARATH	nucl	382.212	11.1628%	[Arath] [Uniprot] SWISS-PROT45:Nuclear. Evidence:IDA Pubmed:12006496
TT1_ARATH	nucl	385.017	13.8158%	[Uniprot] SWISS-PROT45:Nuclear.
CPR2_PETCR	nucl	386.57	13.7157%	[Uniprot] SWISS-PROT45:Nuclear.

Supplementary Fig.S2

- (a) Subcellular localization of PagMYB73A in ProtComp
- (b) Subcellular localization of PagMYB73A in WOLF PSORT