

**Text S2.** Predicted subcellular localizations, signal peptides, and transmembrane domains for the *S. macrospora* proteins. Localization was predicted with WoLFPSORT (Proceedings of the 4th Annual Asia Pacific Bioinformatics Conference APBC06, 2006, Taipei, Taiwan: pp. 39-48), signal peptides were predicted with SignalP 3.0 (J. Mol. Biol. 2004, 340: 783-795), transmembrane domains were predicted with HMMTOP (J. Mol. Biol. 1998, 283: 489-506) and TMHMM (J. Mol. Biol. 2001, 305: 567-580). S, signal peptide; A, signal anchor; Q, no signal peptide.

### A. Localization and signal peptide predictions summary

Localization	no. of peptides	S	A	Q
cytoskeleton	264	3	0	261
cytosol	2370	78	32	2260
endoplasmic reticulum	8	3	2	3
extracellular	1239	986	59	194
Golgi apparatus	6	0	6	0
mitochondria	2112	330	63	1719
nuclear	3588	58	14	3516
peroxisome	25	0	0	25
plasma membrane	1177	197	241	739
total	10789	1655	417	8717

### B. Summary of transmembrane domain (TM) predictions

no TM domains with both programs	6467
TM domains only with HMMTOP	2390 <sup>1</sup>
TM domains only with TMHMM	28
at least one TM domain with both programs	1904

<sup>1</sup>of these, 437 are predicted to have a signal peptide with SignalP, this might be falsely predicted as TM domain.

### C. Predictions of TM domains within putative plasma membrane proteins (as predicted by WolfPSORT)

no. of TM domains	HMMTOP predictions	TMHMM predictions
0	29	73
≥ 1	1148	1104