



FIGURE S2 Protein sequence alignment of *C. orbiculare* Fam1 with *S. cerevisiae* Pex22 and Pex22-like proteins from filamentous ascomycetes. Amino acid sequence of *C. orbiculare* Fam1(N4VS^Y8) was aligned with Pex22-like proteins of *M. oryzae* (A4R2Z0), *N. crassa* (Q8WZV7), *A. oryzae* (Q2UQZ8), and *S. cerevisiae* Pex22 (PEX22 YAL055W) using the Clustal W program. Identical and similar amino acids are indicated. Residues involved in interface formation between Pex22 and Pex4 in *S. cerevisiae* (19) are underlined in red line. Residues comprising a putative N-terminal transmembrane domain are underlined in blue. Positively charged residues (PC) immediately upstream of the transmembrane domain (29) are highlighted in green.