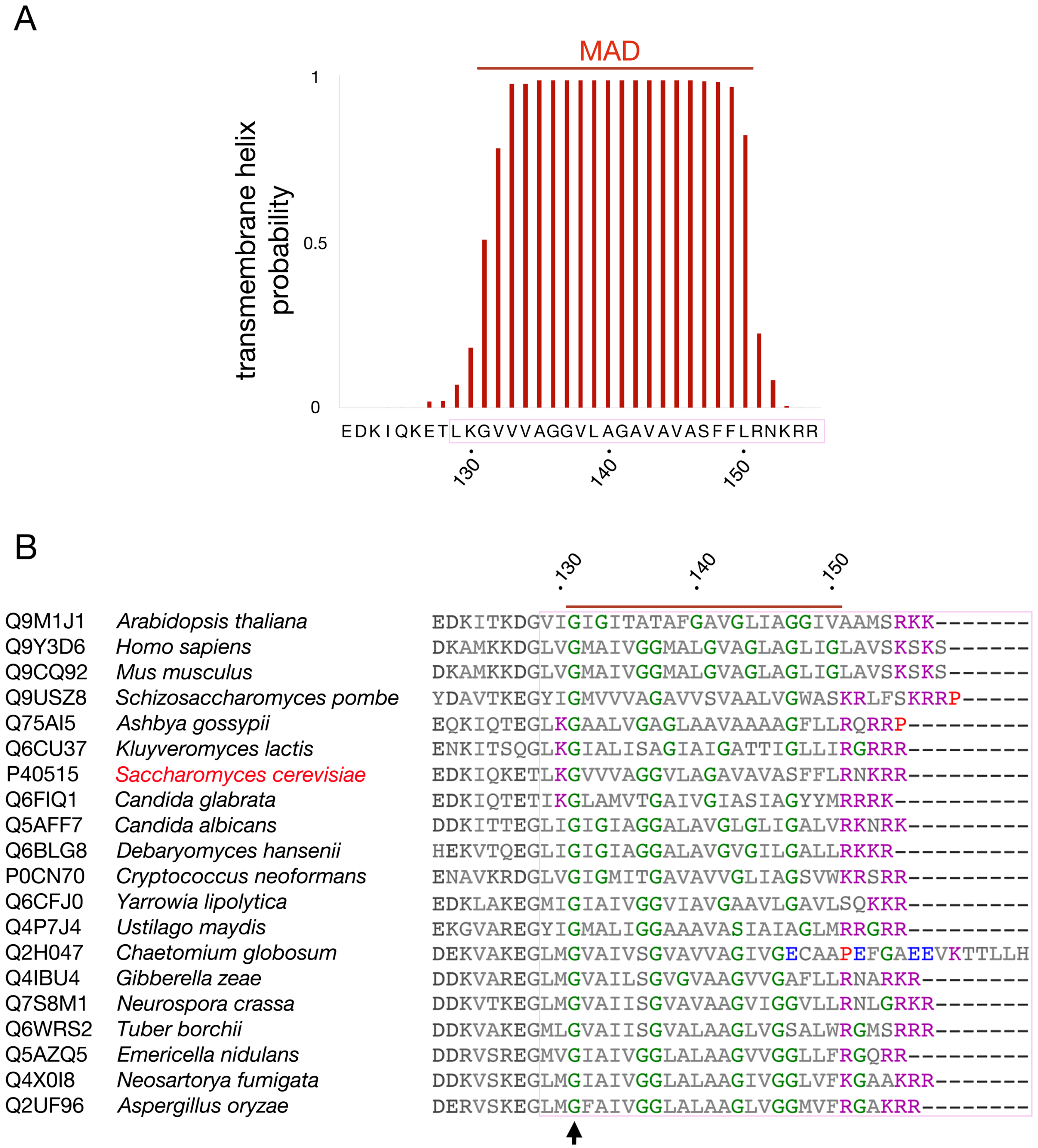

Q9M1J1	*Arabidopsis thaliana*	EDKITKDGVIGIGITATAFGAVGLIAGGIVAAMSRKK-------
Q9Y3D6	*Homo sapiens*	DKAMKKDGLVGMAIVGGMALGVAGLAGLIGLAVSKSKS------
Q9CQ92	*Mus musculus*	DKAMKKDGLVGMAIVGGMALGVAGLAGLIGLAVSKSKS------
Q9USZ8	*Schizosaccharomyces pombe*	YDAVTKEGYIGMVVVAGAVVSVAALVGWASKRLFSKRRP-----
Q75AI5	*Ashbya gossypii*	EQKIQTEGLKGAALVGAGLAAVAAAAGFLLRQRRP---------
Q6CU37	*Kluyveromyces lactis*	ENKITSQGLKGIALISAGIAIGATTIGLLIRGRRR---------
P40515	*Saccharomyces cerevisiae*	EDKIQKETLKGVVVAGGVLAGAVAVASFFLRNKRR---------
Q6FIQ1	*Candida glabrata*	EDKIQTETIKGLAMVTGAIVGIASIAGYYMRRRK----------
Q5AFF7	*Candida albicans*	DDKITTEGLIGIGIAGGALAVGLGLIGALVRKNRK---------
Q6BLG8	*Debaryomyces hansenii*	HEKVTQEGLIGIGIAGGALAVGVGILGALLRKKR----------
P0CN70	*Cryptococcus neoformans*	ENAVKRDGLVGIGMITGAVAVVGLIAGSVWKRSRR---------
Q6CFJ0	*Yarrowia lipolytica*	EDKLAKEGMIGIAIVGGVIAVGAAVLGAVLSQKKR---------
Q4P7J4	*Ustilago maydis*	EKGVAREGYIGMALIGGAAAVASIAIAGLMRRGRR---------
Q2H047	*Chaetomium globosum*	DEKVAKEGLMGVAIVSGVAVVAGIVGECAAPEFGAEEVKTTLLH
Q4IBU4	*Gibberella zeae*	DDKVAREGLMGVAILSGVGVAAGVVGAFLLRNARKR--------
Q7S8M1	*Neurospora crassa*	DDKVTKEGLMGVAIISGVAVAAGVIGGVLLRNLGRKR-------
Q6WRS2	*Tuber borchii*	DDKVAKEGMLGVAIISGVALAAGLVGSALWRGMSRRR-------
Q5AZQ5	*Emericella nidulans*	DDRVSREGMVGIAIVGGLALAAGVVGGLLFRGQRR---------
Q4X0I8	*Neosartorya fumigata*	DDKVSKEGLMGIAIVGGLALAAGIVGGLVFKGAAKRR-------
Q2UF96	*Aspergillus oryzae*	DERVSKEGLMGFAIVGGLALAAGLVGGMVFRGAKRR--------

Figure S1. Structural and sequence characteristics of the Fis1p TA. (A) The Fis1p TA is predicted to be a transmembrane helix. The indicated amino acid sequence was tested using the TMHMM Server version 2.0 (Krogh et al. 2001), and individual amino acid scores were plotted. The predicted MAD is indicated. (B) Glycines are abundant among Fis1p orthologs. Fis1 proteins from the listed species (Uniprot access numbers listed) were aligned using Clustal Omega (Soding 2005). Glycines are colored green, positively charged amino acids are colored purple, negatively charged amino acids are colored blue, and proteins are colored red. A red bar over the alignment indicates the predicted MAD, and a black arrow denotes a potentially conserved glycine. The region necessary and sufficient for Fis1p insertion is bracketed in pink.