Expanded View Figures

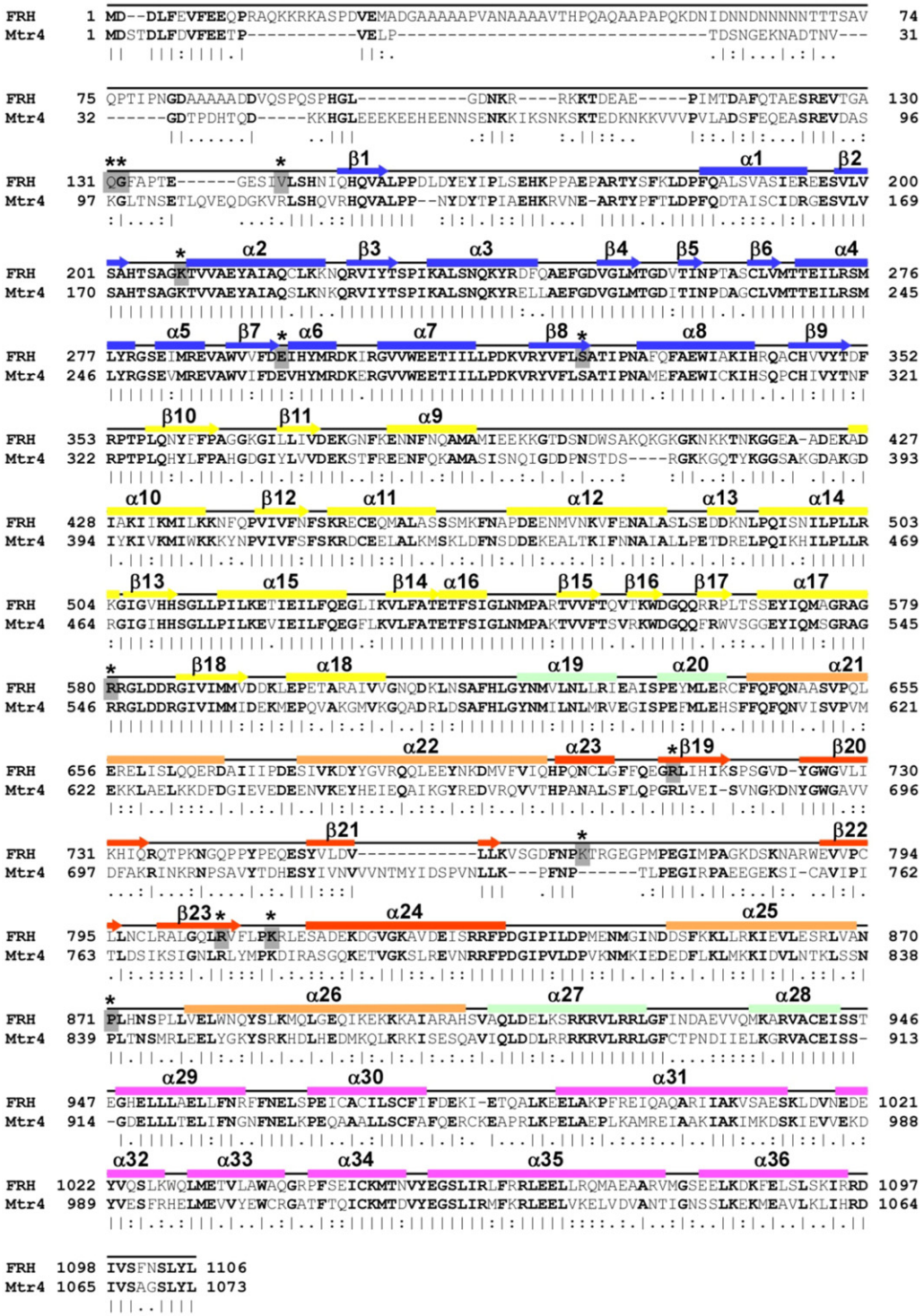

Figure EV1. Primary sequence comparison of FRH and Mtr4.
Sequence alignment of FRH and Mtr4 with secondary structure and corresponding domain identifiers colored in accordance with Fig 1. Relevant mutation sites are boxed in gray and starred.

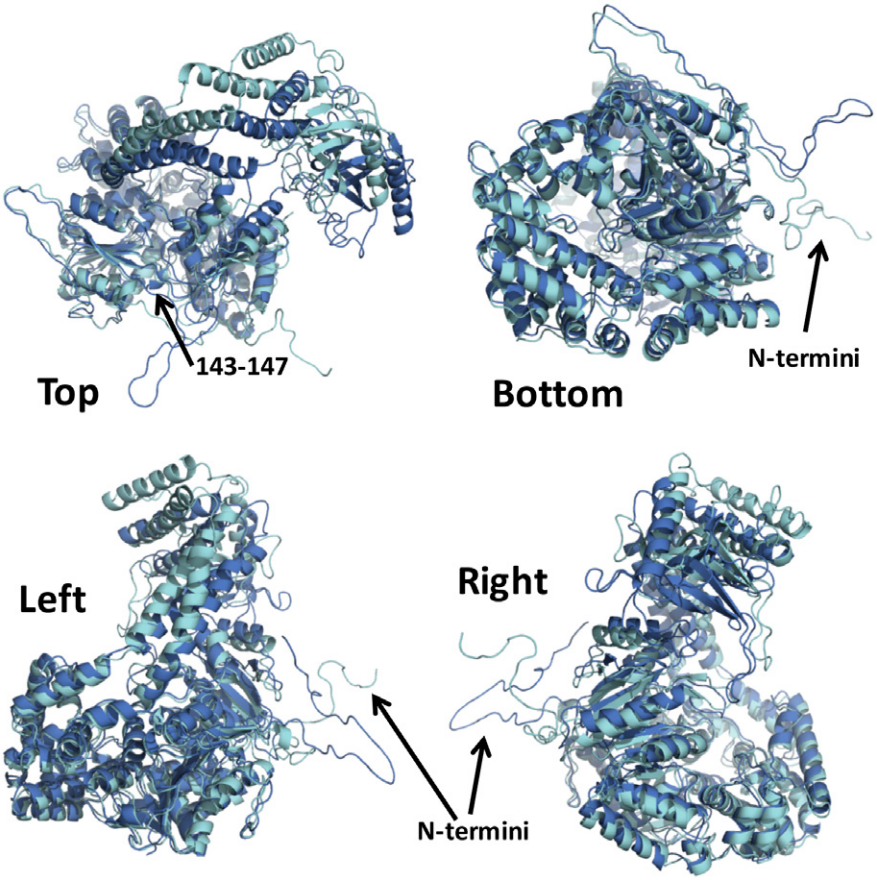

Figure EV2. Conformational variability of FRH.
Structural overlays of large (cyan) and small (marine) cell FRH structures shown from different perspectives and emphasizing the differences in the conformations of the N-terminus and the KOW modules.

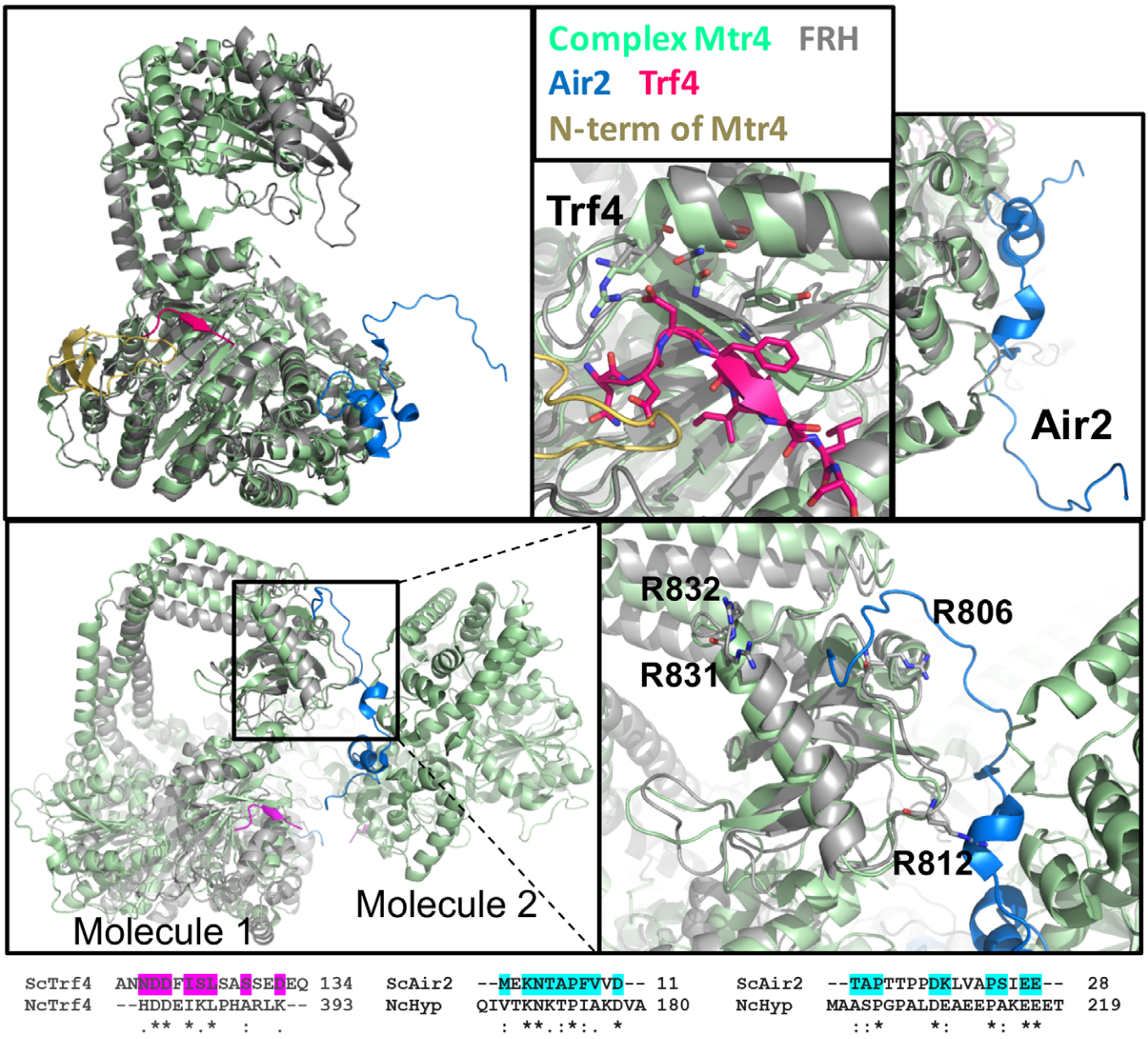

Figure EV3. Putative TRAMP complex interactions sites.
Structural comparison of the Mtr4 TRAMP complex (pdb 4U4C) with FRH (FRH in gray, Mtr4 in green with N-terminus (added from pdb 2XGJ) in gold, Air2 in blue, Trf4 in magenta). Trf4 lies along RecA-2, Air2 contacts the DSHCT, RecA-2, and the KOW domain of a symmetry-related molecule. The Trf4 and Air2 interfaces with Mtr4 are in regions well conserved by FRH. Although there is currently no data on an *N.c.* TRAMP complex, a *Neurospora* homolog of Trf4 (GenBank: EAA31314.2; NCU05588, 38% sequence identity) conserves residues that could potentially interact with α9 of FRH. A direct homolog of Air2 is even less obvious in the genome of *N.c.*, although the hypothetical protein NcHyp (GenBank: CAD37057; NCU04617) has modest sequence similarity (33%) to yeast Air2. This putative Air2 homolog also maintains some residues that could interact with conserved residues in the FRH DSHCT domain (K1048, M1049, and E1054). Segments of Trf4 and Air2 that contact Mtr4 are aligned below with the related regions of the respective *N.c.* homologs; residues that make contacts are highlighted.