

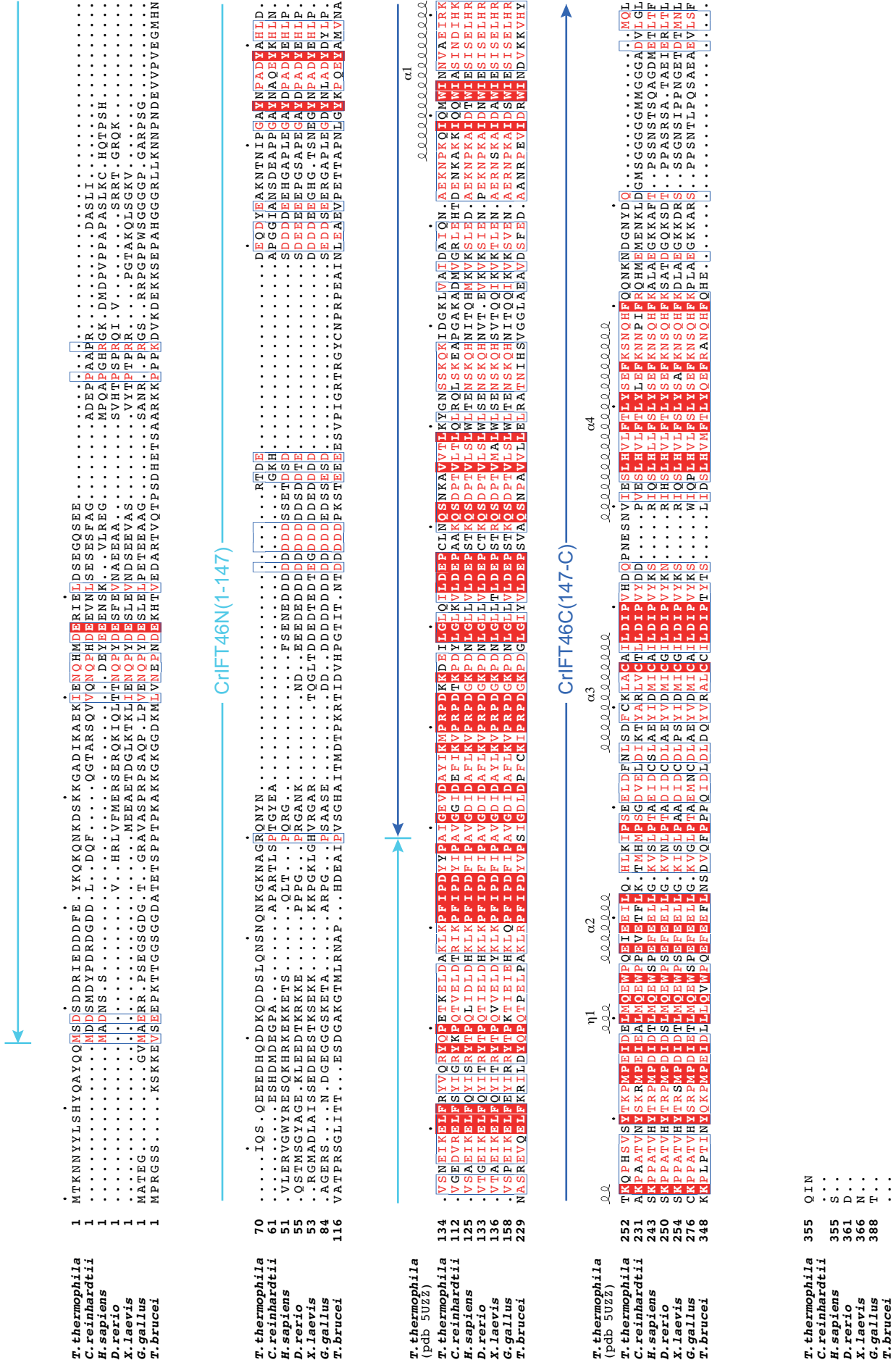
Supplemental Figure legends

FIGURE S1. Multiple sequence alignment of IFT46 homologs from various species. Known secondary structure elements as observed in the crystal structure for *Tetrahymena thermophila* IFT46 (pdb 5UZZ) are shown above the corresponding regions of the alignment. Furthermore, the two fragments of the *Chlamydomonas reinhardtii* IFT46 protein used in this study (IFT46N and IFT46C) are shown

FIGURE S2. Multiple sequence alignment of ODA16 homologs from various species. Known secondary structure elements determined in the crystal structure of *Chlamydomonas reinhardtii* ODA16 described in this work (pdb 5MZH) are shown above the alignment. The individual regions (N-terminal domain, linker, β -propeller, and C-terminal tail) are labeled.

FIGURE S3. Proteomic analysis of a pulldown from a *Chlamydomonas reinhardtii* flagellar axoneme fractions using GST-IFT46/ODA16 complex as bait. The volcano plot on the left shows the position of key proteins identified by mass spectrometry, the list on the right summarizes main interactors organised by their respective multi-subunit complexes. The Coomassie stained SDS-gel inside the volcano plot (top), as well as the Western Blot for IC2 (bottom) proves that the ODA subunit IC2 is efficiently pulled down by GST-IFT46/ODA16, but not by GST alone.

Figure S1



355 QIN
 355 S..
 361 D..
 366 N..
 388 T..
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Figure S2

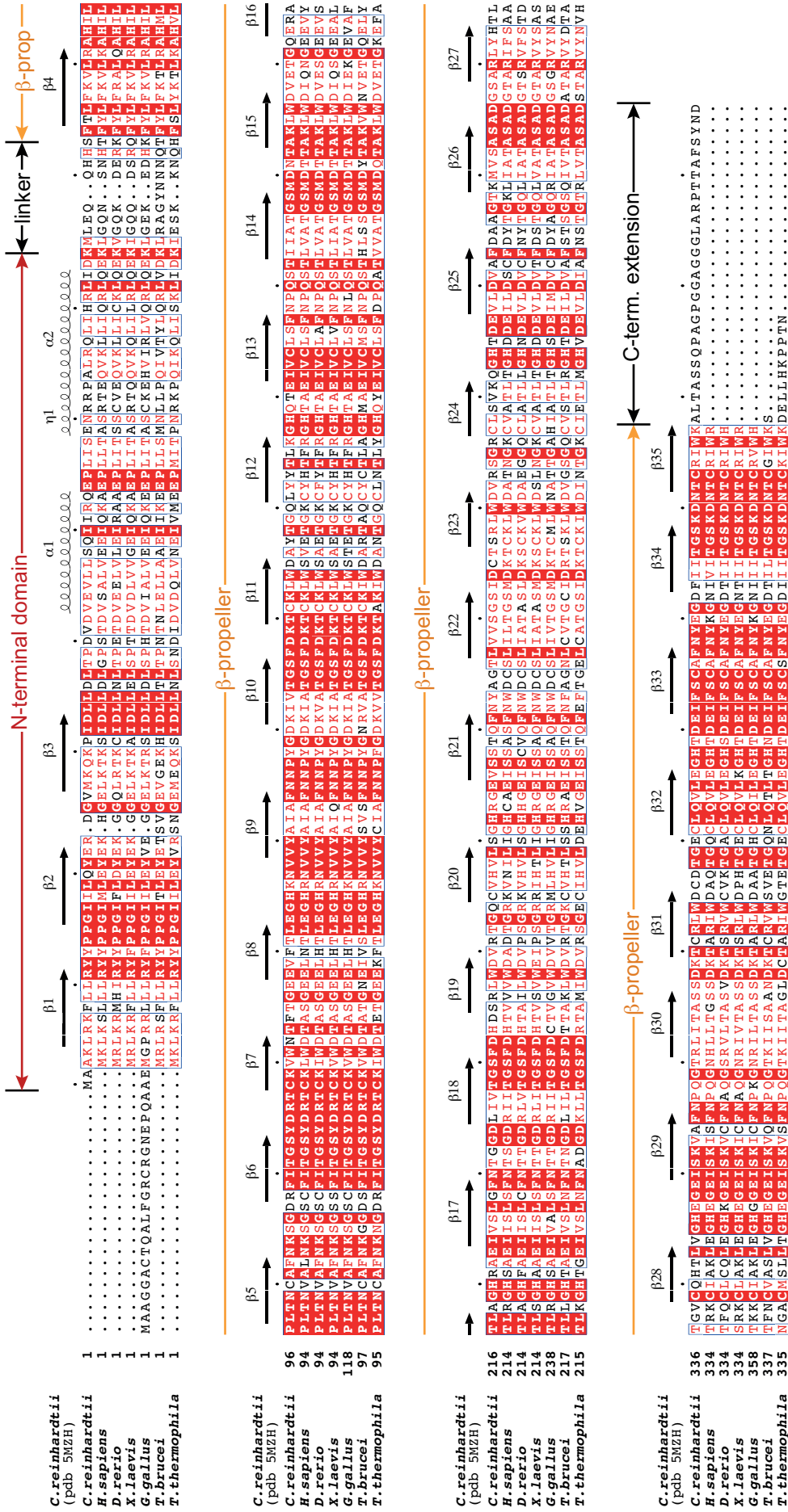


Figure S3

