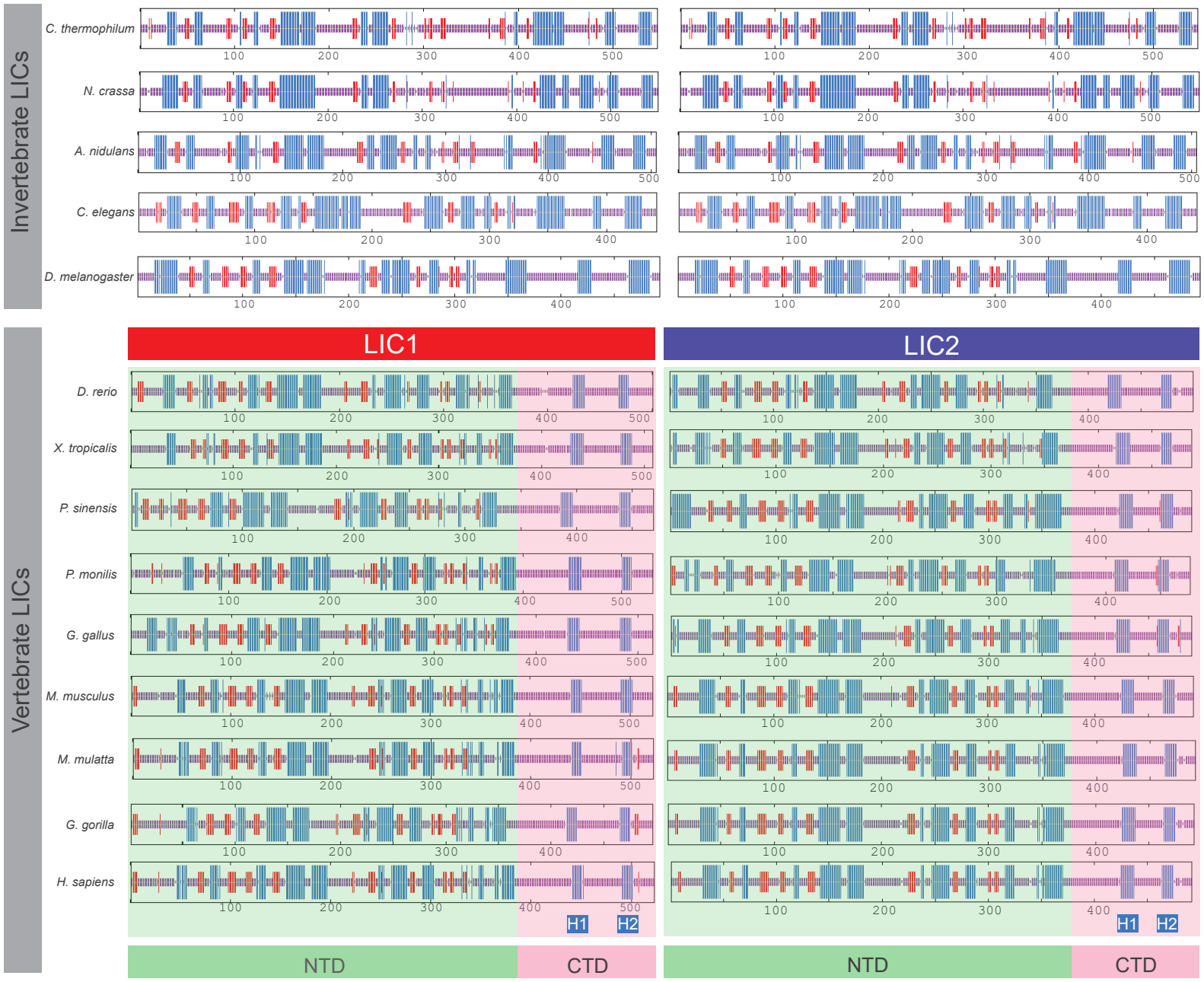
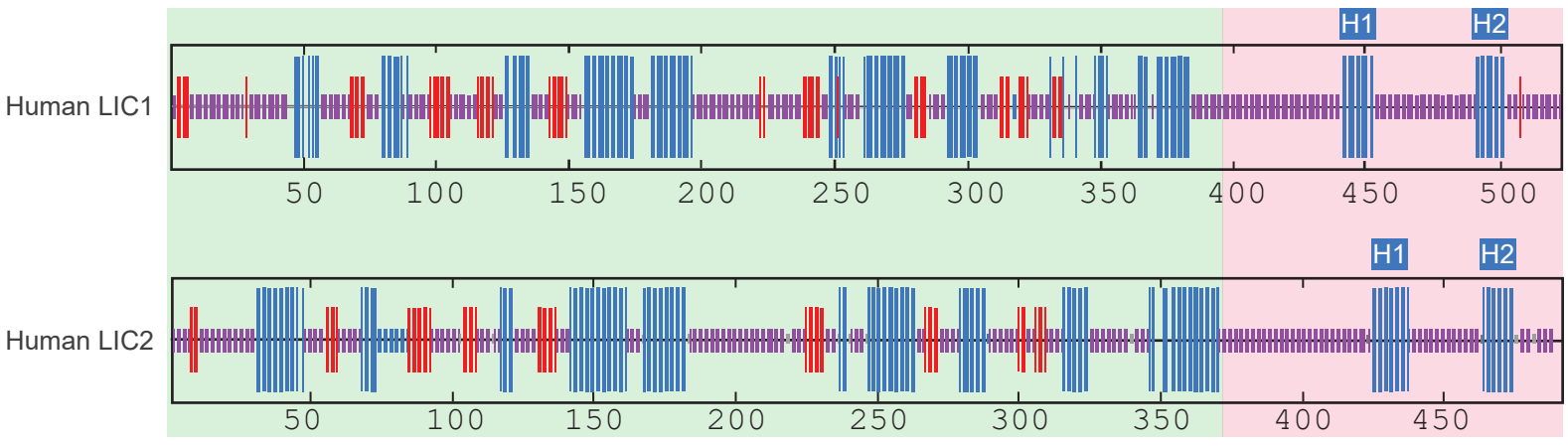
A



B



	NTD	CTD
Primary sequence identity	67%	51%
Primary sequence similarity	80%	57%

	Full length
Primary sequence identity	63%
Primary sequence similarity	74%

Fig. S1: The conserved structural features of the dynein LICs. (A) Schematic secondary structure alignment of the indicated LIC subunit primary sequences (obtained from NCBI) from both invertebrates and vertebrates. Predicted helices (blue), β-turns (red) and unstructured random coil (purple) regions are based on consensus secondary structure prediction on the NPSA server (https://npsa-prabi.ibcp.fr/cgi-bin/npsa_automat.pl?page=/NPSA/npsa_seccons.html), performed using the algorithms HNN, MLRC, DPM, DSC, PHD and PREDATOR here and in Fig. 3B. (B) Despite showing similar overall structures, including the two conserved CTD helices H1 and H2, human LIC1 and LIC2 have a higher primary sequence divergence in their largely unstructured, cargo-binding CTDs.

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