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# Structure of the human KMN complex and implications for regulation of its assembly

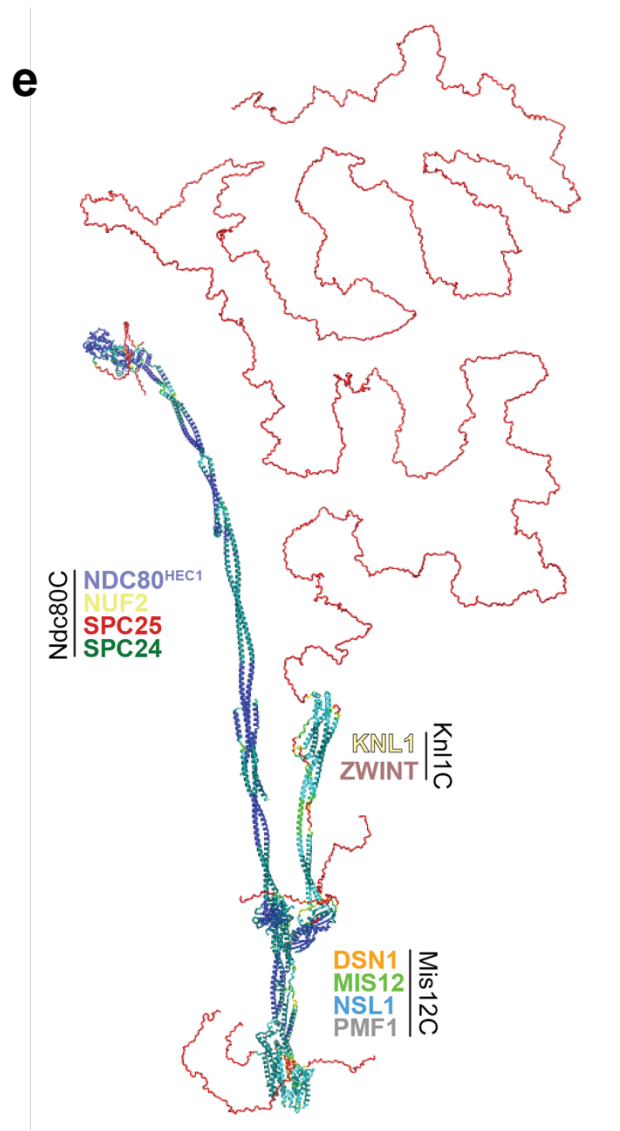
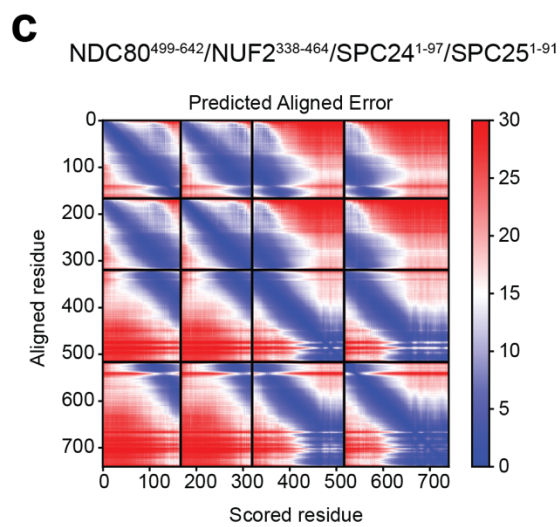
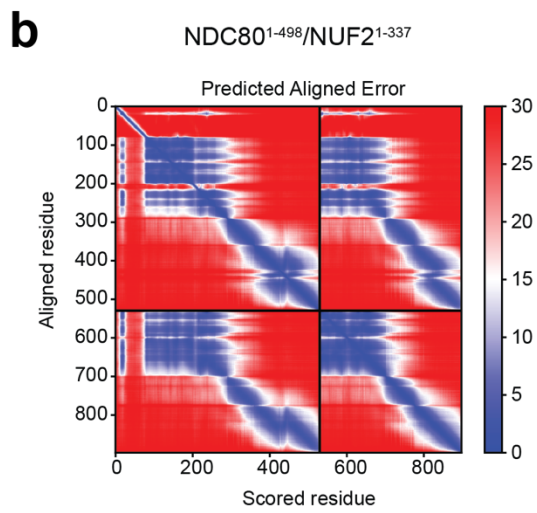
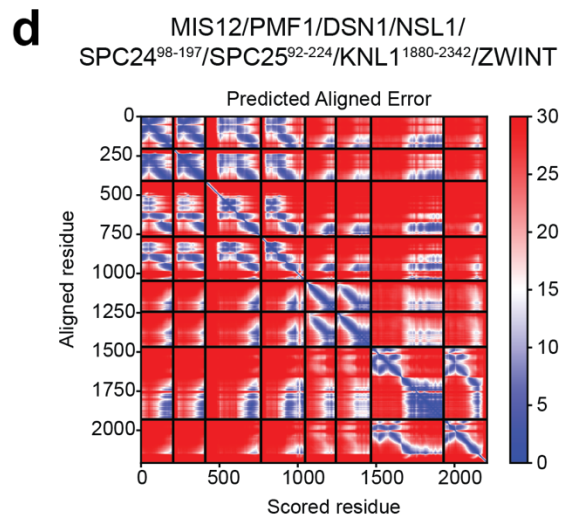
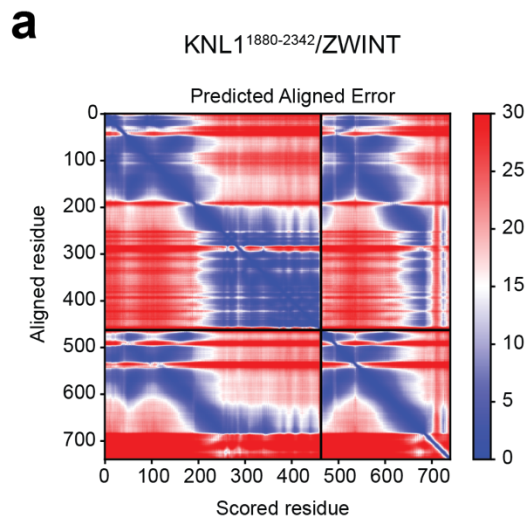
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**Structure of the human KMN complex and implications for regulation of  
its assembly**

By Soumitra Polley, Tobias Raisch *et al.*

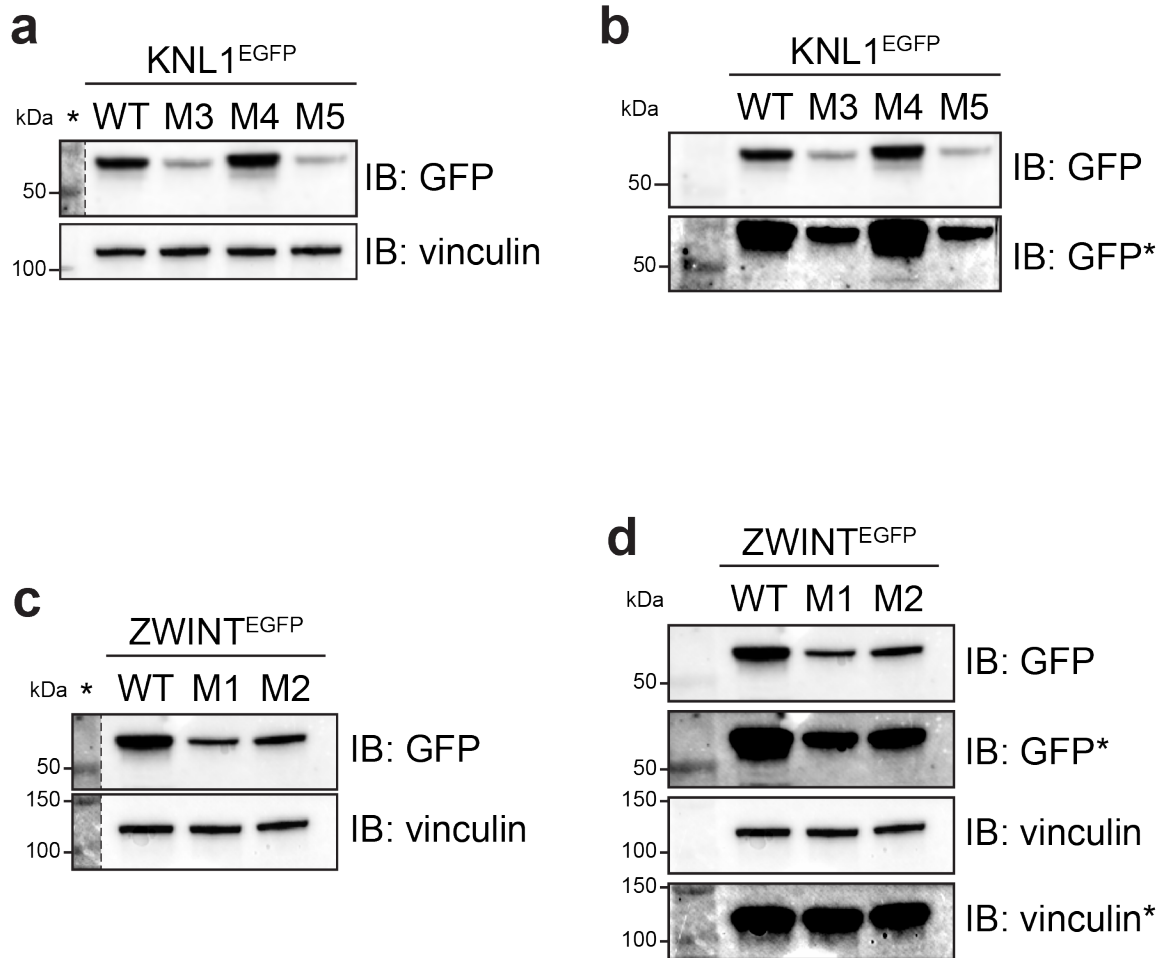
**Supplementary Information**



### **Supplementary Figure 1 *AF2 predictions***

(a-d) AF2 predicted aligned error (PAE) plots for predictions of the indicated constructs in the indicated succession (each chain is delimited by a / sign) and with the indicated residue boundaries. The human KNL1<sub>1880-2342</sub>/ZWINT prediction is depicted in Figure 6a. (e) Per-residue confidence scores (pLDDT) mapped on the model displayed in Figure 7. Dark blue indicates highest confidence, red lowest confidence/disordered segments.

\*adjusted intensity



Supplementary Figure 2

**Supplementary Figure 2 *Western blots at normal and adjusted intensities***

(a,c) Western blots with markers as shown in Extended Data Figure 4g and Extended Data Figure 10h, respectively. (b,d) Comparison of Western blots shown at normal or adjusted intensity (the latter indicated by an asterisk). To demonstrate the position of the molecular weight markers, we merged the marker from the adjusted intensity image with the normal intensity image, as in the latter the signal for the marker was very weak. The vertical line in panels a,c signals the merger from the same blot displayed at different intensities.