Supplemental material

JCB

Pamula et al., http://www.jcb.org/cgi/content/full/jcb.201603050/DC1

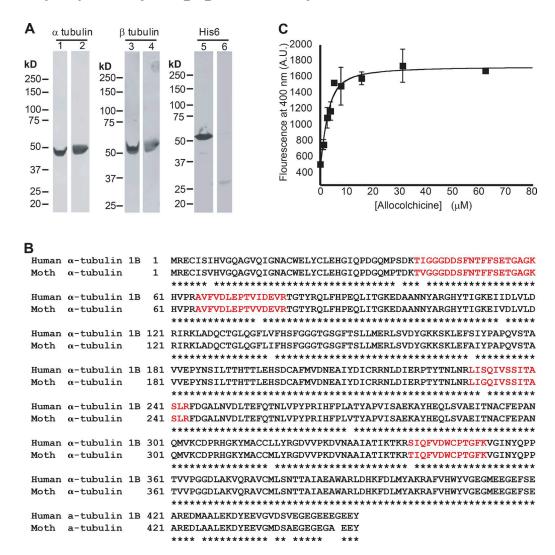


Figure S1. **Purification of recombinant** α/β **IIB tubulin heterodimers.** (A) Full blots corresponding to those shown in Fig. 1 C, showing western blot analyses of proteins eluted from nickel-affinity (lanes 1, 3, and 5) and TOG-affinity (lanes 2, 4, and 6) chromatography. Antibodies against α tubulin, β tubulin, and C-terminal hexahistidine tag are indicated. (B) Alignment of protein sequences from human α tubulin 1B (NP_006073.2) and α tubulin from insect cells (ABU94679.1). Peptide fragments that were used to estimate the relative amounts of human and insect α tubulin are labeled in red. (C) Equilibrium binding curve for α/β IIB with allocolchicine. The data from three independent experiments were averaged and fitted to a curve, weighed by the SD. $K_d = 1.8 \pm 0.42 \ \mu M$ (n = 3, mean \pm SD). A.U., arbitrary units.

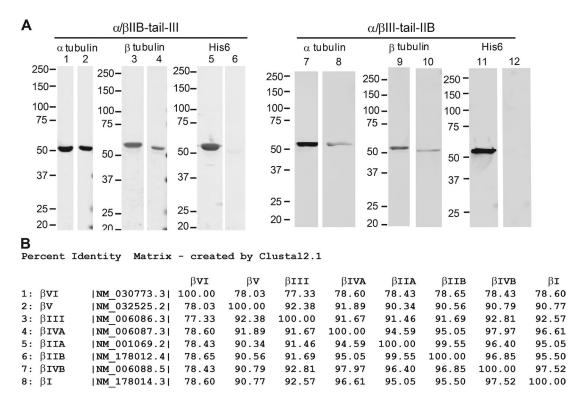


Figure S2. **Purification of chimeric** β **tubulin heterodimers and tubulin isotype identity matrix.** (A) Full blots corresponding to those shown in Fig. 4 D showing western blot analyses of proteins eluted from nickel-affinity (lanes 1, 3, 5, 7, 9, and 11) and TOG-affinity (lanes 2, 4, 6, 8, 10, and 12) chromatography. (B) Percent identity matrix for human β tubulin isotypes.

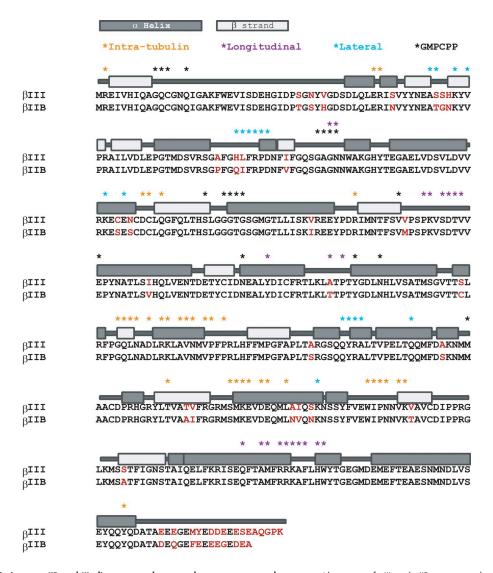


Figure S3. β tubulin isotypes IIB and III alignment and a secondary structure topology map. Alignment of β III and β IIB amino acid sequence. Secondary structure topology map corresponds to features derived from PDB listing 3J6E. Residues on β tubulin within 3 Å of intra-tubulin (orange stars), longitudinal (purple stars), or lateral (blue stars) contacts or the GMPCPP binding site (black stars) are indicated. Residues that differ between isotypes β III and β IIB are labeled in red.