

Table S4. Contact points of tubulin dimers in the microtubule lattice that overlap with predicted pockets or fragment sites.

β1α2-Tubulin

pID/sID ¹	ResID ²	Secondary structural elements involved ³
sID βαII ^α	αCys 4 αGln 133 αGly 134 αPhe 135 αLeu 136 αSer 165 αLeu 167 αAsp 199 αCys 200 αPhe 202 αLeu 242 αLeu 252 αThr 253 αGln 256 αThr 257 αLeu 259	βT3 and βH3' (longitudinal inter-tubulin dimer contact in microtubules)
----- sID βαII ^β	----- βGly 100 βAsn 101 βAsn 102 βLys 105 βVal 182 βTrp 407 βTyr 408 βGlu 411	----- αH8 (longitudinal inter-tubulin dimer contact in microtubules)
sID βαIII ^α	αLeu 248 αVal 250 αAsn 258 αPro 325 αVal 328 αAsn 329 αIle 332 αPro 348 αGly 350 αPhe 351 αLys 352 αVal 353 αGly 354 αIle 355	βT5 (longitudinal inter-tubulin dimer contact in microtubules)
----- sID βαIII ^β	----- βPro 173 βSer 174 βPro 175 βLys 176 βVal 177	----- αH10, αH10-αS9 loop, and αS9 (longitudinal inter-tubulin dimer contact in microtubules)

	βSer 178 βAsp 179 βThr 180 βVal 181 βGlu 183 βPro 184 βTyr 210 βThr 221 βPro 222 βThr 223 βTyr 224 βLeu 227 βGln 394	
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α-Tubulin

pID/sID ¹	ResID ²	Secondary structural elements involved ³
pID αI	αTyr 172 αPro 173 αAla 174 αPro 175 αSer 178 αAla 180 αVal 181 αGlu 183 αPro 184 αSer 187 αAsp 205 αGlu 207 αLys 304 αCys 305 αAla 387 αArg 390 αLeu 391 αLys 394 αLeu 397 αMet 398	βH10-βS9 loop (longitudinal intra-tubulin dimer contact)
pID αVII	αSer 54 αGlu 55 αThr 56 αVal 62 αPro 63 αArg 64 αHis 88 αGlu 90 αGln 91 αArg 121 αLys 124 αLeu 125	Adjacent αM-loop (lateral inter-tubulin dimer contact in microtubules)

	αGln 128	
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¹Pocket and site identifiers. Fragment sites that are located at the β Tub1- α Tub2 inter-dimer interface in the T₂R-TTL complex and thus represent composite sites are considered separately as half sites; they are indicated with “ α ” and “ β ” superscripts to denote whether they belong to α - or β -tubulin, respectively.

²Tubulin residues that are involved in pocket or site formation (taken from Table S1 and Table S3). Residues that are shared between a pocket or a site and an adjacent tubulin chain within the tubulin dimer or in the microtubule lattice (maximal distance of 4 Å) are shown in italic for unassembled “curved” tubulin and in bold for assembled “straight” tubulin. Residues that are shared between a pocket or a site an adjacent tubulin chain, independent on the conformational tubulin state are shown in both bold and italics.

³Secondary structural elements of the contacting tubulin monomer involved in interaction with residues forming a pocket or a site.

The Protein Data Bank ID of the microtubule structure that was used for the analysis is PDB ID 3JAR.