

**Table S5. Contact points of protein partners that overlap with predicted pockets or fragment sites in tubulin.**

**β-Tubulin**

sID/pID <sup>1</sup>	ResID <sup>2</sup>	Protein <sup>3</sup>	Structural element involved <sup>4</sup>
sID βI	βAsp 211 βIle 212 <b>βArg 215</b> βThr 216 <b>βSer 298</b> <b>βLys 299</b>	Targeting protein for Xklp2 (TPX2)  PDB ID: 6BJC	C-terminal unstructured part of the wedge domain  Binds also to sID βαI
sID βV	<b>αHis 406</b> <b>αVal 409</b> <b>αGly 410</b> <b>αGlu 411</b> βPhe 135 βIle 154 βIle 157 <b>βArg 158</b> βTyr 161 <b>βPro 162</b> <b>βAsp 163</b> βArg 164 βIle 165 βMet 166 <b>βVal 195</b> <b>βGlu 196</b> <b>βAsn 197</b> βThr 198 <b>βAsp 199</b> βArg 253 <b>βPro 263</b> <b>βArg 264</b> <b>βHis 266</b>	Cytoplasmic dynein 1 heavy chain  PDB ID: 3J1U, 3J1T, 6RZA, 6RZB	Helix 1 of the microtubule-binding domain
sID βV	<i>αHis 406</i> <i>αVal 409</i> <i>αGly 410</i> <i>αGlu 411</i> βPhe 135 βIle 154 βIle 157 <i>βArg 158</i> βTyr 161 βPro 162 βAsp 163 βArg 164 βIle 165 βMet 166 βVal 195 <i>βGlu 196</i> βAsn 197	Centrosomal P4.1-associated protein (CPAP/SAS-4)  PDB ID: 5ITZ, 5EIB	Helical SAC region of the N-terminal PN2-3 domain

	βThr 198 βAsp 199 βArg 253 βPro 263 βArg 264 βHis 266		
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### β1α2-Tubulin

sID/pID <sup>1</sup>	ResID <sup>2</sup>	Protein <sup>3</sup>	Structural element involved <sup>4</sup>
sID βαI	αTyr 262 αPro 263 αArg 264 αIle 265 αAsp 431 αGlu 434 αVal 435 βArg 400 βArg 401 βLys 402	Kinesin-13  PDB ID: 5MIO, 6BBN, 6B0I	L2 hairpin specific to the motor domain of kinesin-13 family members
sID βαI	αTyr 262 αPro 263 αArg 264 αIle 265 αAsp 431 αGlu 434 αVal 435 βArg 400 βArg 401 βLys 402	Kinesin-5  PDB ID: 5MM7	Loop L2 of the motor domain of <i>Ustilago maydis</i> kinesin-5
sID βαI	<b>αTyr 262</b> <b>αPro 263</b> αArg 264 αIle 265 <b>αAsp 431</b> <b>αGlu 434</b> αVal 435 <b>βArg 400</b> <b>βArg 401</b> <b>βLys 402</b>	Targeting protein for Xklp2 (TPX2)  PDB ID: 6BJC	N-terminal unstructured part of the ridge domain  Binds also to sID βI
sID βαI	αTyr 262 αPro 263 <b>αArg 264</b> αIle 265 <b>αAsp 431</b> <b>αGlu 434</b> <b>αVal 435</b> <b>βArg 400</b> <b>βArg 401</b> <b>βLys 402</b>	Tau  PDB ID: 6CVN, 6CVJ	R1 and R2 repeats

sID $\beta\alpha^{\alpha}$	<i><math>\alpha</math>Tyr 262</i> <i><math>\alpha</math>Pro 263</i> <i><math>\alpha</math>Arg 264</i> <i><math>\alpha</math>lle 265</i> <i><math>\alpha</math>Asp 431</i> <i><math>\alpha</math>Glu 434</i> <i><math>\alpha</math>Val 435</i>	iE5 alphaRep  PDB ID: 6GWC	Helix 2 of the N-cap
sID $\beta\alpha_{III}^{\alpha}$	<i><math>\alpha</math>Leu 248</i> <i><math>\alpha</math>Val 250</i> <i><math>\alpha</math>Asn 258</i> <i><math>\alpha</math>Pro 325</i> <i><math>\alpha</math>Val 328</i> <i><math>\alpha</math>Asn 329</i> <i><math>\alpha</math>lle 332</i> <i><math>\alpha</math>Pro 348</i> <i><math>\alpha</math>Gly 350</i> <i><math>\alpha</math>Phe 351</i> <i><math>\alpha</math>Lys 352</i> <i><math>\alpha</math>Val 353</i> <i><math>\alpha</math>Gly 354</i> <i><math>\alpha</math>lle 355</i>	Stathmin like domain of RB3  PDB ID: 1FFX, 6GVM	N-terminal $\beta$ -hairpin
sID $\beta\alpha_{III}^{\beta}$	<i><math>\beta</math>Pro 173</i> <i><math>\beta</math>Ser 174</i> <i><math>\beta</math>Pro 175</i> <i><math>\beta</math>Lys 176</i> <i><math>\beta</math>Val 177</i> <i><math>\beta</math>Ser 178</i> <i><math>\beta</math>Asp 179</i> <i><math>\beta</math>Thr 180</i> <i><math>\beta</math>Val 181</i> <i><math>\beta</math>Glu 183</i> <i><math>\beta</math>Pro 184</i> <i><math>\beta</math>Tyr 210</i> <i><math>\beta</math>Thr 221</i> <i><math>\beta</math>Pro 222</i> <i><math>\beta</math>Thr 223</i> <i><math>\beta</math>Tyr 224</i> <i><math>\beta</math>Leu 227</i> <i><math>\beta</math>Gln 394</i>	Designed Ankyrin Repeat Protein (DARPin)  PDB ID: 4DRX, 5EYP	Repeat 4

### **$\alpha$ -Tubulin**

sID/pID <sup>1</sup>	ResID <sup>2</sup>	Protein <sup>3</sup>	Structural element involved <sup>4</sup>
pID $\alpha$ 1 ( $\alpha$ 1)	<i><math>\alpha</math>Phe 141</i> <i><math>\alpha</math>Tyr 172</i> <i><math>\alpha</math>Met 203</i> <i><math>\alpha</math>Val 204</i> <i><math>\alpha</math>Asp 205</i> <i><math>\alpha</math>Glu 207</i> <i><math>\alpha</math>Phe 267</i>	Tubulin Tyrosine Ligase (TTL)  PDB ID: 4IHJ	Loops $\beta$ 3- $\beta$ 4 and $\alpha$ 9- $\beta$ 13

	<p> <i>α</i>Pro 268  <i>α</i>Leu 269  <i>α</i>Ala 270  <i>α</i>Val 303  <i>α</i>Lys 304  <i>α</i>Cys 305  <i>α</i>Asp 306  <i>α</i>Pro 307  <i>α</i>His 309  <i>α</i>Ala 383  <i>α</i>lle 384  <i>α</i>Glu 386  <i>α</i>Ala 387  <i>α</i>Trp 388  <i>α</i>Arg 390  <i>α</i>Leu 391  <i>α</i>Lys 394 </p>		
pID <i>α</i> V	<p> <i>α</i>Pro 274  <i>α</i>lle 276  <i>α</i>Lys 280  <i>α</i>Ala 281  <i>α</i>Tyr 282  <i>α</i>His 283  <i>α</i>Glu 284  <i>α</i>Gln 285  <i>α</i>Leu 286  <i>α</i>Ala 369  <i>α</i>Lys 370  <i>α</i>Val 371  <i>α</i>Gln 372  <i>α</i>Arg 373 </p>	<p> Stu2p/Alp14p    PDB ID: 6MZG </p>	<p> Helix HRA4 of the tumor overexpressed gene 1 (TOG1) domain </p>
pID <i>α</i> VI	<p> <i>α</i>Asn 258  <i>α</i>Pro 261  <i>α</i>Met 313  <i>α</i>Ala 314  <i>α</i>Cys 315  <i>α</i>Phe 343  <i>α</i>Cys 347  <i>α</i>Pro 348  <i>α</i>Gly 350  <i>α</i>Phe 351  <i>α</i>Lys 352 </p>	<p> Stathmin like domain of RB3    PDB ID: 1FFX, 6GVM </p>	<p> N-terminal <math>\beta</math>-hairpin </p>
pID <i>α</i> VII	<p> <i>α</i>Ser 54  <i>α</i>Glu 55  <i>α</i>Thr 56  <i>α</i>Val 62  <i>α</i>Pro 63  <i>α</i>Arg 64  <i>α</i>His 88  <i>α</i>Glu 90  <i>α</i>Gln 91  <i>α</i>Arg 121  <i>α</i>Lys 124 </p>	<p> iiiA5 alphaRep    PDB ID: 6GX7 </p>	<p> Helices 2 and 4 </p>

	$\alpha$ Leu 125 $\alpha$ Gln 128		
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<sup>1</sup>Pocket and site identifiers. Fragment sites that are located at the  $\beta$ Tub1- $\alpha$ Tub2 inter-dimer interface in the T<sub>2</sub>R-TTL complex and thus represent composite sites are considered separately as half sites; they are indicated with “ $\alpha$ ” and “ $\beta$ ” superscripts to denote whether they belong to  $\alpha$ - or  $\beta$ -tubulin, respectively.

<sup>2</sup>Tubulin 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 the tubulin-binding region of a protein partner (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.

<sup>3</sup>Protein partners that target a pocket or a site. The Protein Data Bank IDs of the structures that were used for the analysis are indicated. For some proteins, the composite fragment sites located at the  $\beta$ Tub1- $\alpha$ Tub2 inter-dimer interface were split and considered separately as sub  $\beta$ -tubulin and sub  $\alpha$ -tubulin sites (indicated with superscripts).

<sup>4</sup>Structural elements of the protein partner that is involved in the interaction with a pocket or a site.