Supplementary Table 1 | Measurements of different MT lattice reconstructions

	GMPCPP-	GDP.Pi-DCX-	GDP-DCX-MT	GTPyS-DCX-	GDP-DCX-
	DCX-MT	MT		MT	Taxol [®] -MT
Number of asymmetric units ^a	38,928	79,092	365,208	72,444	211,512
Lattice spacing ^b (Å)	83.74 ± 0.20	81.74 ± 0.06	81.90 ± 0.06	82.10 ± 0.07	81.91 ± 0.09
Intra-dimer distance ^c (Å)	40.52 ± 0.04	40.20 ± 0.15	40.37 ± 0.07	40.31 ± 0.04	40.37 ± 0.11
Inter-dimer distance ^c (Å)	43.22 ± 0.07	41.93 ± 0.10	41.66 ± 0.08	41.78 ± 0.01	41.68 ± 0.08
Lattice skew ^d	0.16 ± 0.08 °	0.00 ± 0.08 °	0.08 ± 0.07 °	-0.02 ± 0.08 °	0.07 ± 0.06 °

^aNumber of particles multiplied by 12 due to symmetrisation of all PFs except that at the seam, which is not decorated by DCX. ^bComputed by Chuff (see Methods) from the reconstructions: datasets were divided in 3 approximately equal subsets; the calculations were done on them and then averaged to obtain standard deviation of the measurement. Differences between GDP.Pi-, GDP- and GTPyS-DCX-MTs are insignificant according to one-way analysis of statistical variance (ANOVA) computed with Prism 6 (graphpad.com). ^cDistance between centres of mass of the N domains calculated in 6-dimer models (see Methods) using CALCOM program (Costantini, S. *et al., Bioinformation* **2**, 271–272, 2008): 3 inter-dimer and 6 intra-dimer distances produced averages and standard deviations. ^dDifferences in all pairwise comparisons are statistically significant, except: GDP-DCX-MT:GDP-DCX-Taxol®-MT and GDP.Pi-DCX-MT:GTPyS-DCX-MT pairs (Supplementary Fig. 6).