Self protein-protein interactions are involved in TPPP/p25 mediated microtubule bundling

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Supplementary Figures Legends

Figure S1 (a) Folding predictions of human TPPP/p25 according to the FOLDINDEX software, which predicts whether a given protein sequence is intrinsically unfolded. The N-and C-terminal domains are estimated to have a high probability of being intrinsically unfolded (red) in contrast to the central core domain (green) ³³. **(b)** Charge distribution plot of TPPP/p25 showing that the N-terminus and C-terminus are positively charged. The core domain has alternating charges favoring a proposed "electrostatic zipper" of protein-protein interaction mode.

Figure S2 (a) Coomasie blue staining of full length TPPP/p25 and the supernatant after centrifugation following long term incubation (longer than 24h) with taxol stabilized MTs. **(b)** The proteolytic fragments were analyzed by N-terminal sequencing and the molecular masses were determined by MALDI mass spectrometry. **(c)** The corresponding N-terminal sequences are depicted in red in the amino acid sequence of full length TPPP/p25.

Figure S3 MT binding properties of tag-free TPPP/p25. **(a)** Light scattering assays (OD₃₅₀ nm) of tubulin solutions (15 μ M) in the presence of His-tagged full length (FL) and tag cleaved full length (FL^{HISFree}) and core^{HISFree} domain of TPPP/p25 (ratios of tubulin to TPPP/p25 are shown in parentheses). **(b)** EM images of microtubules assembled from tubulin solutions (15 μ M) in the presence of FL and tag-cleaved FL and tag-cleaved core domain of TPPP/p25 (ratios of tubulin to TPPP/p25 are shown in parentheses). Scale bars in the left column of images correspond to 0,5 μ m; in the right column to 0,2 μ m). **(c)** Taxol stabilized microtubules (2 μ M tubulin) were incubated in the presence of 12 μ M of either tag-cleaved FL or core domain of TPPP/p25 for 15 min

before centrifugation. Coomassie-stained gel of microtubule bound and unbound TPPP/ p25 fragments present in the pellets and in the supernatants, respectively. **(d)** EM images of taxol stabilized microtubules incubated with bacterially expressed and purified tag-cleaved TPPP/p25 fragments (ratios of tubulin to TPPP/25 are shown in parentheses) Scale bars correspond to 0,2µm.

Figure S4 Tag-cleaved TPPP/p25 competes with GFP-tagged TPPP/p25 for MT binding. Taxol stabilized MTs were first co-incubated with 2 μ M of tag-cleaved FL and 2 μ M GFP-FL-TPPP/p25 and then with increasing concentrations of tag-cleaved FL. Each data point represents the mean ± SD from three independent experiments.

Figure S5 Cells were transfected with either HA-full length **(a)**, $\Delta C(158)$ **(b)**, $\Delta N(49)$ **(c)** or core -TPPP/p25-VC173 **(d)**. Cells were then fixed and stained for indirect immunofluorescence microscopy using a monoclonal antibody recognizing the HA-tag. Perinuclear bundles are detected in cells transfected with the full length, $\Delta N(49)$ and $\Delta C(158)$ whereas a diffuse cytoplasmic staining is observed in cells expressing the core.



b

а



SDS-PAGE	N-term	Peptide Mass
hTPPP/25	sequence	(Da)
рерпае		
FL	ADKAKP	23 694
1	ADKAKP	18580
2	SLESEGAG	15476
3	AVHGDARA	8078
4	SKIKGKSX(72%)	5904
	ΔΠΚΔΚΡΔΚ (22%)	
	EQFQEALE (6%)	

C 2 32 MADKAKPAKAANRTPPKSPGDPSKDRAAKRLSLESEGAGEGAAASPELSALEEAFRRF 59 101 AVHGDARATGREMHGKNWSKLCKDCQVIDGRNVTVTDVDIVFSKIKGKSCRTITF 114 EQFQEALEELAKKRFKDKSSEEAVREVHRLIEGKAPIISGVTKAISSPTVSRLTDTTKF

TGSHKERFDPSGKGKGKAGRVDLVDESGYVSGYKHAGTYDQKVQGGK

b



С

TXL MTs TPPP/p25

+ FL^{HISFree}

core^{HISFree}

+

no



d





TXL-MTs + FL^{HISFree} (1:1) TXL-MTs + core^{HISFree} (1:1)







а

HA / DNA

С

HA / DNA



HA-(AN49)-TPPP-VC173

HA-(∆C158)-TPPP-VC173

b

d



HA-(△N49-△C158)-TPPP-VC173

