Electronic Supplementary information

Figure S-1: Elucidates the changes in αβTub-γSyn complex during the molecular dynamic studies.

Changes observed in interface occurred due to the intertwining of helix N in γSyn with tail region of βTub was deciphered. As the intertwining occurred, hydrogen bond was formed between the residues K45 in loop L of Syn and R757 of H9-S8 Loop in βTub. The figure also displays hydrogen bonds formed between residues S9, T22, V26, E28 andV37in helix N of γSyn with D894, D882, Q884, T880 and N867 in tail region of βTub.

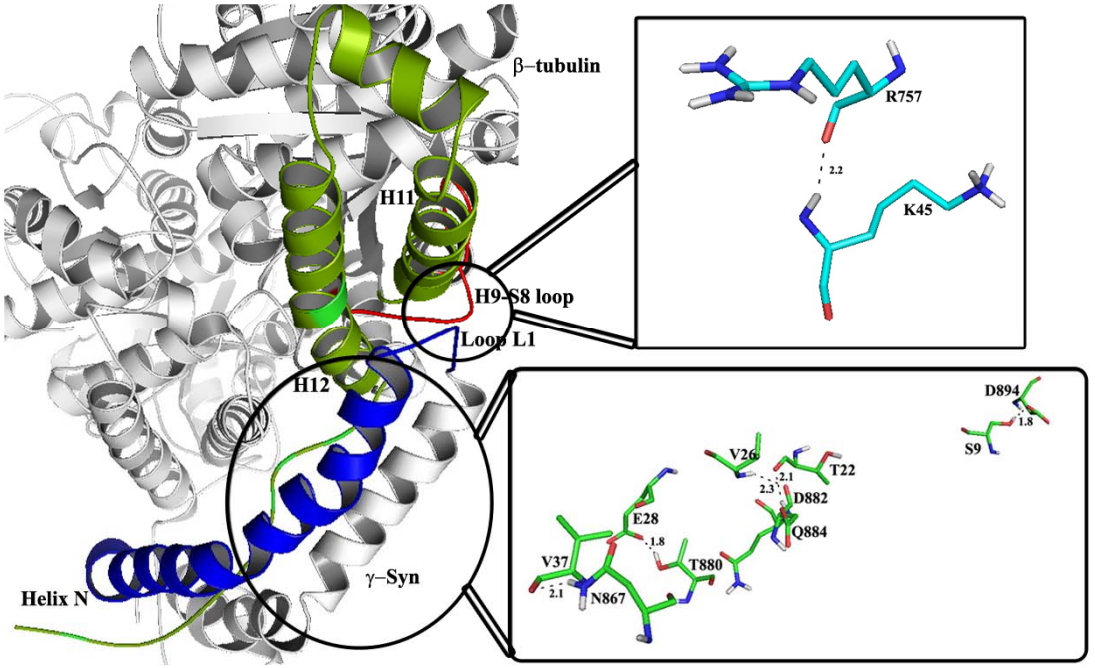

Figure S-2: Deciphers the Interactions observed in the native αβTub-γSyn complex:

S-32A Shows the presence of hydrogen bonds observed between P694 and Q696 of T7 and D896 of S-Loop in native form of βTub, while S-2B shows hydrogen bonds observed between H9-S8 Loop [M751 and N749] with H6 [D654 and T665] and S7 [P719 and F721].

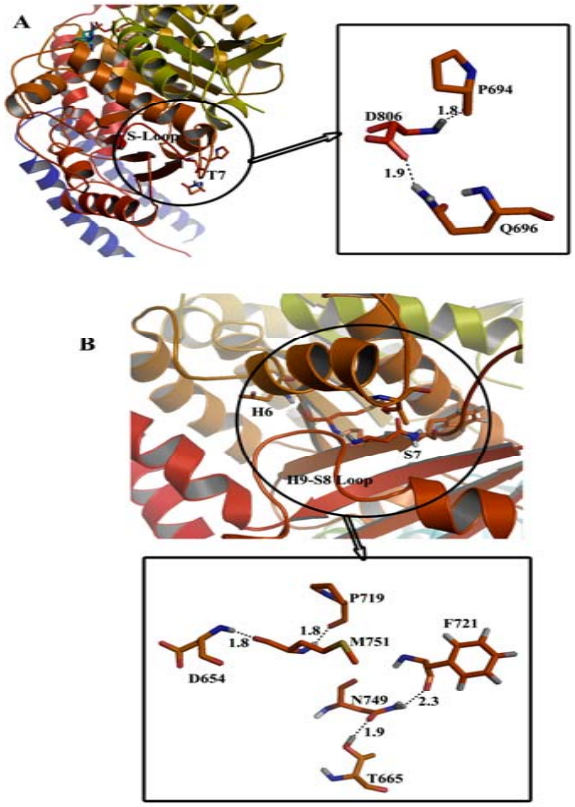

Table S-1: Details regarding the interface properties of γSyn -αTub complex:

Details of interface residues and their accessible surface area [ASA], buried surface area [BSA] and their free energy of solvation observed in the complex of γSyn associated with αβTub. γSyn is represented by Chain A and αTub by Chain B.

Residues Chain A				Residues Chain B			
Resdiue	ASA	BSA	ΔG	Resdiue	ASA	BSA	ΔG
A85	52.19	28.64	0.41	V 440	118.21	50.68	0.81
E86	120.29	11.01	0.17	E443	165.55	5.02	0.08
A89	61.64	39.34	0.57	G444	82.05	49.01	-0.23
V90	93.07	41.11	0.59	E445	157.13	39.00	0.25
G93	59.12	37.63	-0.01	E446	165.57	150.36	-0.40
V94	95.97	10.73	0.09	E447	164.58	7.12	-0.08
V95	94.31	66.06	0.92	G448	66.13	42.14	0.36
R96	249.63	90.25	-0.19	E449	171.48	96.09	-0.73
K97	68.60	16.70	-0.09	E450	155.69	92.92	-0.11
E98	138.10	45.10	0.53	Y451	281.25	100.01	0.85
D99	147.79	12.03	0.04				
Q106	119.16	22.39	0.02				
E108	70.75	2.48 |	-0.00				
S124	101.55	1.23	-0.01				
G125	43.33	40.04	0.45				
G126	54.38	33.94	0.25				
D127	156.22	42.23	-0.04				

Table S-2: Elucidates the interface properties of γSyn -βTub complex:

Here, the interface residues, accessible surface area [ASA], buried surface area [BSA] and their free energy of solvation observed in the complex of γSyn –βTub is presented. γSyn is represented by Chain A, and βTub is represented by Chain C.

Residues Chain A				Residues Chain C			
Resdiue	ASA	BSA	ΔG	Resdiue	ASA	BSA	ΔG
G36	59.88	16.45	-0.17	D755	40.61	10.17	-0.07
V37	127.74	15.06	0.24	R757	158.54	20.65	-0.14
Y39	215.68	62.69	-0.01	H758	112.03	38.41	-0.04
K45	164.16	99.20	-0.34	G759	2.70	0.50	0.01
V48	96.64	54.41	0.83	R760	70.81	63.44	0.00
V49	94.80	29.36	0.47	S790	90.56	23.33	0.25
S51	53.66	4.84	0.07	E794	93.83	8.02	0.06
V52	94.30	55.75	0.89	K830	70.48	27.77	0.39
V55	95.68	30.04	0.48	R831	166.59	1.84	0.03
T59	54.88	14.27	0.12	E834	106.37	20.36	-0.00
Q62	132.61	95.83	-0.02	N867	120.33	16.14	-0.00
A63	48.90	28.32	0.42	Q874	74.47	16.32	0.00
V66	88.68	50.28	0.80	Q877	55.26	16.16	0.01
S67	51.12	11.66	-0.06	D878	76.24	5.61	-0.02
V70	85.06	50.82	0.81	A879	62.32	43.71	0.25
S73	63.12	30.33	0.26	A881	69.80	18.19	0.27

T76	77.03	16.70	0.27	E883	115.82	25.29	-0.11
V77	92.51	27.90	0.44	Q884	173.76	21.40	-0.10
K80	138.98	57.87	-0.35	G885	68.02	44.87	0.02
				E886	149.28	80.74	0.35
				F887	183.23	45.04	0.23
				E888	138.20	12.53	0.20
				E889	108.74	34.08	0.49
				E893	168.72	100.93	-0.02
				D894	141.01	23.00	-0.17
				E895	160.76	1.11	0.02
				A896	168.62	9.72	0.10

Table S-3: *In silico* alanine scanning mutagenesis on γSyn-αβTub complex

Results of *in silico* alanine scanning mutagenesis to identify potential hot spot residues involved in harboring interactions between γSyn-αβTub. Residues with $\Delta\Delta G_{bind}$ values that are equal to or more than 1 kcal/mol are considered to be the hot spot residues. Chain A indicates γSyn, Chain B – αTub and Chain C – βTub. Column 3, *int* indicates the measure of whether the residue is buried (0) or in direct contact with the partner (1).

pdb#	chain	int	ΔΔG (bind)	ΔΔG(complex,obs)	ΔG(partner)
37	A	0	0.02	0.00	0.15
39	A	1	0.48	0.00	-1.03
45	A	1	2.35	0.00	-0.70
48	A	1	0.44	0.00	0.19
49	A	0	0.15	0.00	0.27
52	A	1	0.38	0.00	0.27
55	A	0	0.24	0.00	0.34
59	A	1	0.08	0.00	-0.05
62	A	1	2.42	0.00	-0.53
66	A	1	0.92	0.00	0.54
67	A	1	0.37	0.00	-0.66
70	A	1	0.78	0.00	0.57
73	A	0	-0.04	0.00	-0.74
76	A	1	-0.25	0.00	-0.11
77	A	1	0.12	0.00	0.21
80	A	1	1.14	0.00	-0.35
81	A	0	0.01	0.00	-0.10
82	A	0	0.04	0.00	-0.01

90	A	1	0.74	0.00	-0.04
92	A	0	0.00	0.00	-0.55
94	A	1	0.09	0.00	0.31
95	A	1	0.86	0.00	-0.15
96	A	1	2.71	0.00	-0.59
97	A	1	0.51	0.00	-0.46
106	A	1	0.52	0.00	-0.83
108	A	0	-0.10	0.00	2.07
124	A	0	-0.01	0.00	-0.18
127	A	1	-0.01	0.00	-1.03
755	C	1	0.96	0.00	0.56
758	C	1	0.50	0.00	0.16
760	C	1	-0.03	0.00	2.17
790	C	0	-0.03	0.00	-0.43
791	C	0	0.01	0.00	3.36
794	C	0	0.39	0.00	0.36
830	C	1	0.11	0.00	0.73
878	C	0	0.09	0.00	-1.02
883	C	1	0.62	0.00	-0.33
884	C	1	0.60	0.00	-0.86
886	C	1	1.30	0.00	-0.64
887	C	1	0.55	0.00	-0.62
888	C	0	-0.04	0.00	-0.19
889	C	0	1.79	0.00	-0.22
892	C	0	0.00	0.00	-0.38
893	C	1	0.11	0.00	-0.64
894	C	0	-0.03	0.00	-0.79
439	B	0	0.00	0.00	0.04
440	B	1	0.48	0.00	-0.13

443	B	0	-0.04	0.00	-0.31
445	B	1	0.08	0.00	-0.32
446	B	1	1.59	0.00	-0.30
447	B	0	0.00	0.00	-0.37
449	B	1	2.13	0.00	-0.27
450	B	1	2.44	0.00	-0.42
451	B	1	1.46	0.00	-0.86