Supporting Information

Dima and Joshi 10.1073/pnas.0806113105

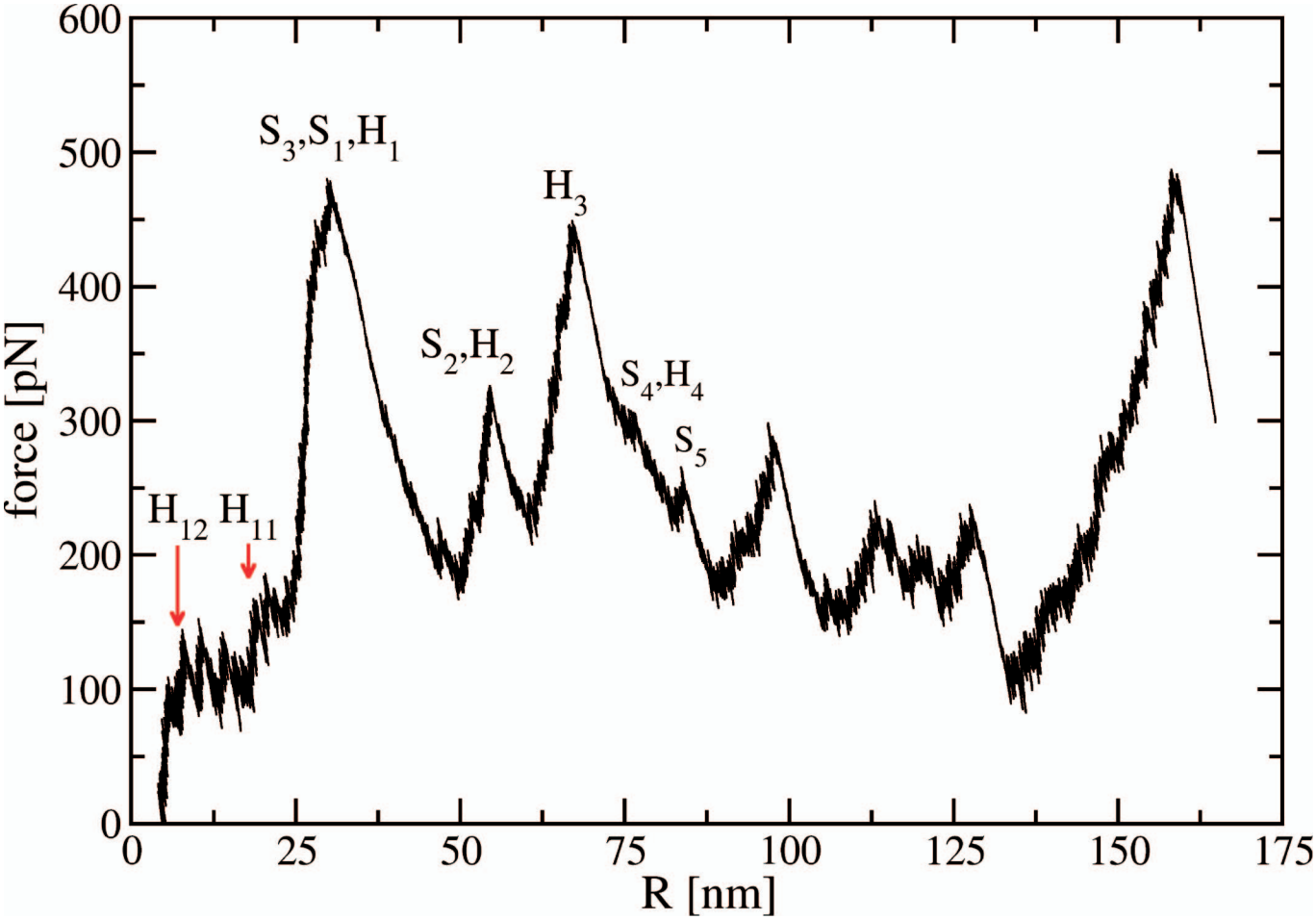

Fig. S1. FEC for the minor pathway in α-tub unfolding.

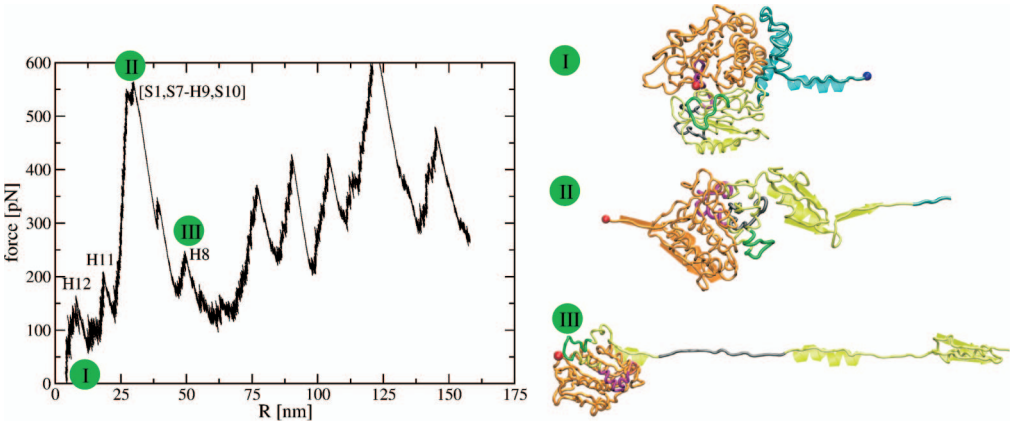

Fig. S2. The minor unfolding pathway in β-tub. On the left, we present the FEC. *Right panel* depicts conformations of the molecule at three stages (marked with green circles on the FEC). Elements that unravel at these stages are shown in cartoon representation following the convention in Fig. 1.

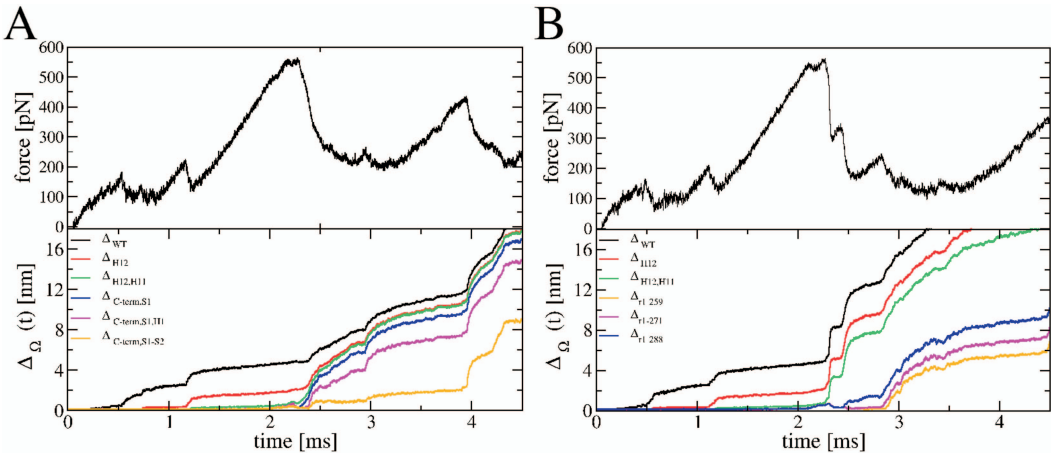

Fig. S3. Time evolution of the two β-tub pathways. (*A*) Time-dependent changes in the force (upper graph) and partial root-mean-square deviations [$\Delta\Omega(t)$] (lower graphs) for major pathway for β-tubulin unfolding. [$\Delta\Omega(t)$] indicates changes in structural elements. Ω in the black, red, green, blue, magenta and orange curves correspond to WT, H12, C-term domain (both H12, H11), S1, H1, S2, respectively. (*B*) Time-dependent changes in the force (upper graph) and [$\Delta\Omega(t)$] (lower graphs) for the minor pathway in β-tub unfolding. Ω in the black, red, green, blue, magenta and orange curves corresponds to WT, H12, C-term domain (both H12, H11), H9-S10, M-loop, and S7, respectively.

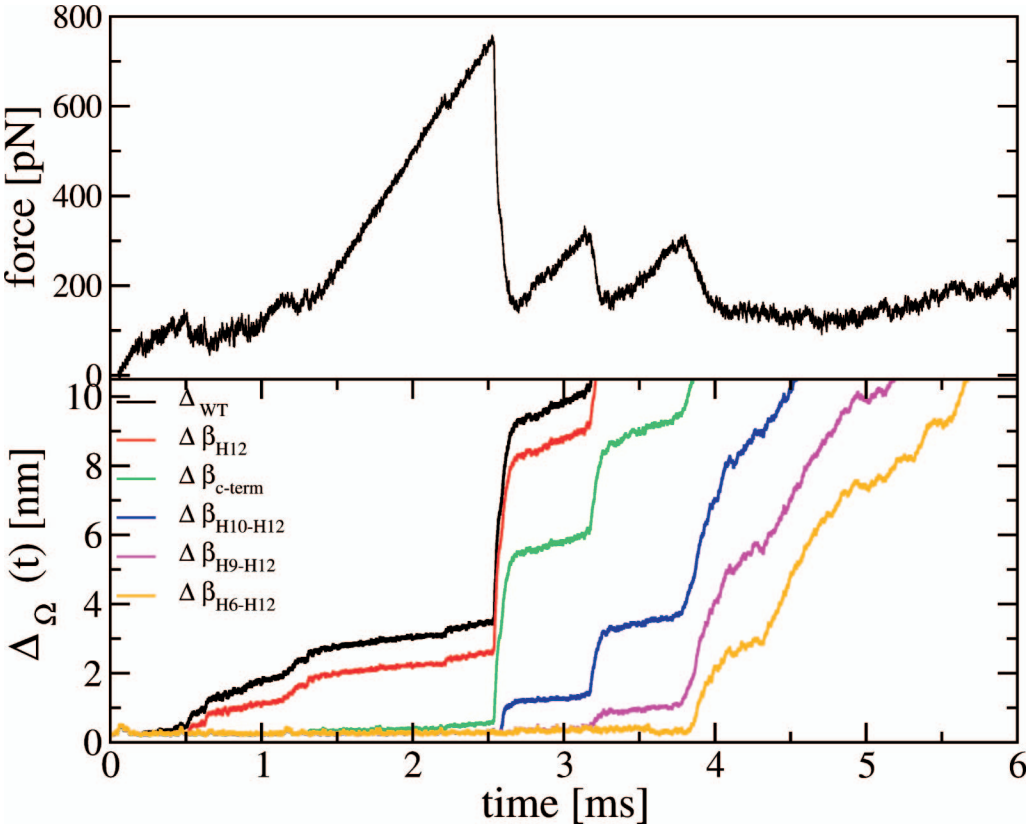

Fig. S4. Time evolution of the dimer unfolding pathway. *Upper* shows time-dependent changes in the force and *Lower* shows $[\Delta\Omega(t)]$. Ω in the black, red, green, blue, magenta and orange curves corresponds to WT, β-H12, β-C-term domain (both H12, H11), β-(H10, S9, S10), β-(H9, S8), and β-(H6, H7, H8, S7), respectively.

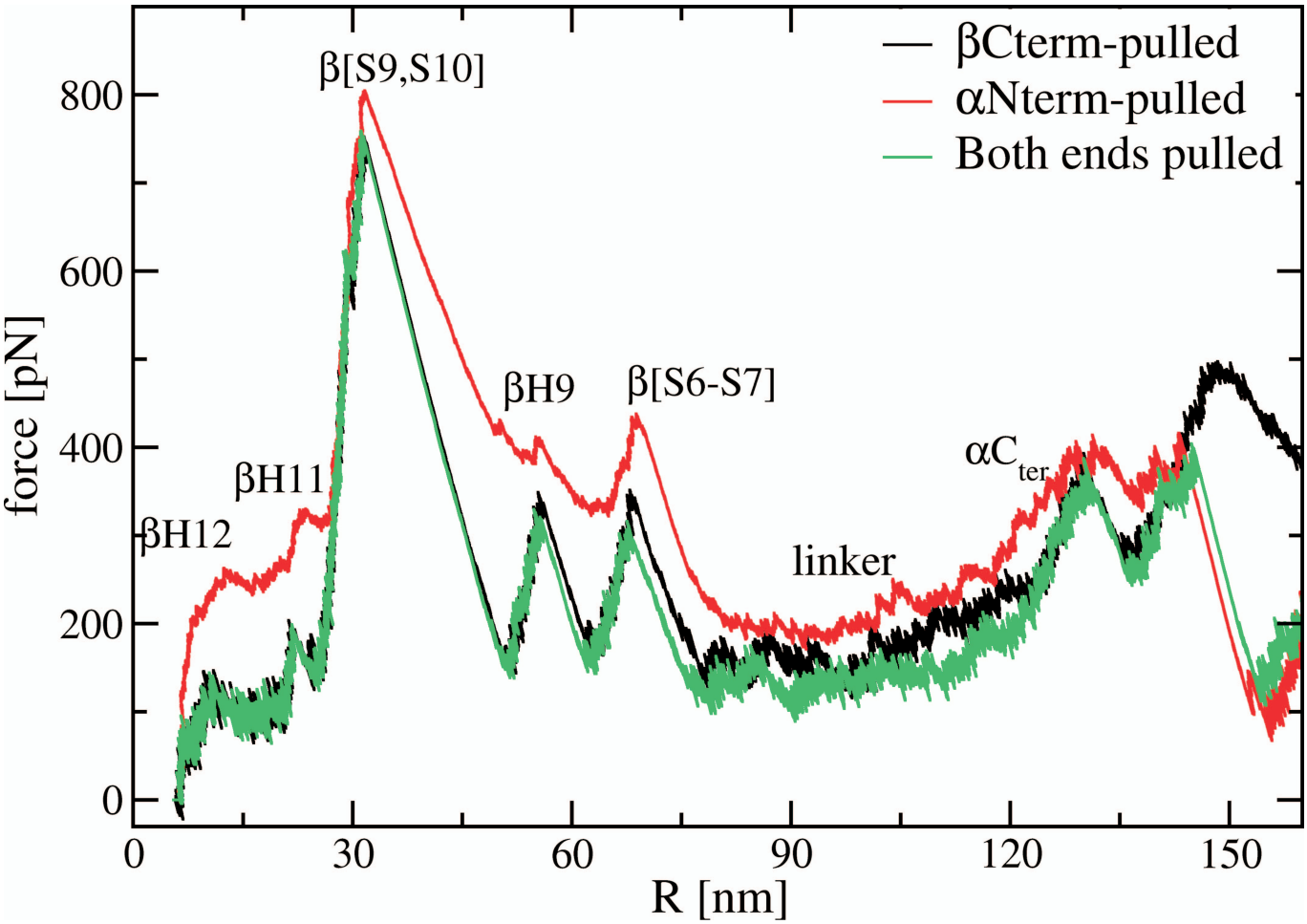

Fig. S5. FECs for the unfolding pathway of the heterodimer for each of the three pulling setups (see text for details). The black, red, and green curves represent, in order, pulling simulations performed according to setups *i*, *ii*, *iii* from *Methods*.

Table S1. Simulations performed in this work

Abbreviation	Simulation	Speed, μm/s	Time, ms	No. of simulations
α-fast	alpha-tubulin	19	9.5	10
α-slow	alpha-tubulin	1.9	85	18
β-fast	beta-tubulin	19	9.5	20
β-slow	beta-tubulin	1.9	85	16
dimer-fast	dimer-tubulin	19	19	20
dimer-slow	dimer-tubulin	1.9	90	8
dimer-fastC2N	dimer-tubulin	19	19	7
dimer-fast-both	dimer-tubulin	19	19	4

Starting structure for all simulations is 1tub. For simulations α-fast, α-slow, β-fast, β-slow, the C terminus end of the chain is being pulled, whereas the N terminus is kept fixed. For the dimer simulations, dimer-fast and dimer-slow refer to the first pulling setup (see *Methods*) where the C terminus of β-tubulin is pulled while N terminus of α-tubulin is kept fixed. The dimer-fast C2N corresponds to the second pulling setup with the N terminus of α-tubulin pulled while the C terminus of β-tubulin is kept fixed. The last entry, dimer-fast-both, corresponds to the third pulling setup, i.e., when both the C terminus of β-tubulin and the N terminus of α-tubulin are pulled in opposite directions.

Table S2. Parameters of SOP model for proteins

R_0	2 Å
k	20 kcal/(mol ·Å^2)
R_C	8 Å
ε_h	2 *k*cal/mol
ε_l	1 *k*cal/mol
σ	3.8 Å
ζ	50 τ_L^{-1}
τ_L	2 ps