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Supporting Material

Probing a Structural Model of the Nuclear Pore Complex Channel Through Molecular Dynamics

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Supplementary Materials

RMSD analysis. RMSD values of the NTF2/exonuclease molecules added to each nsp1 brush were calculated. As shown in Fig. S1, the NTF2 dimers added into the wildtype brushes experienced similar RMSD values as the ones added into the mutant brush either when all atoms are considered or when only β-sheet/α-helix atoms are considered. When all atoms are considered, NTF2 dimers exhibit a higher RMSD value than exonuclease; exonuclease experienced an average RMSD of 1.9 Å, while the NTF2 dimers experienced an average RMSD of 3.5 Å. However, NTF2's flexibility is mainly due to the loops connecting β-sheets and α-helices. When only β-sheets and α-helices are considered, the RMSD values of NTF2 dimers are reduced by more than 1 Å while those of the exonuclease molecules remain the same.

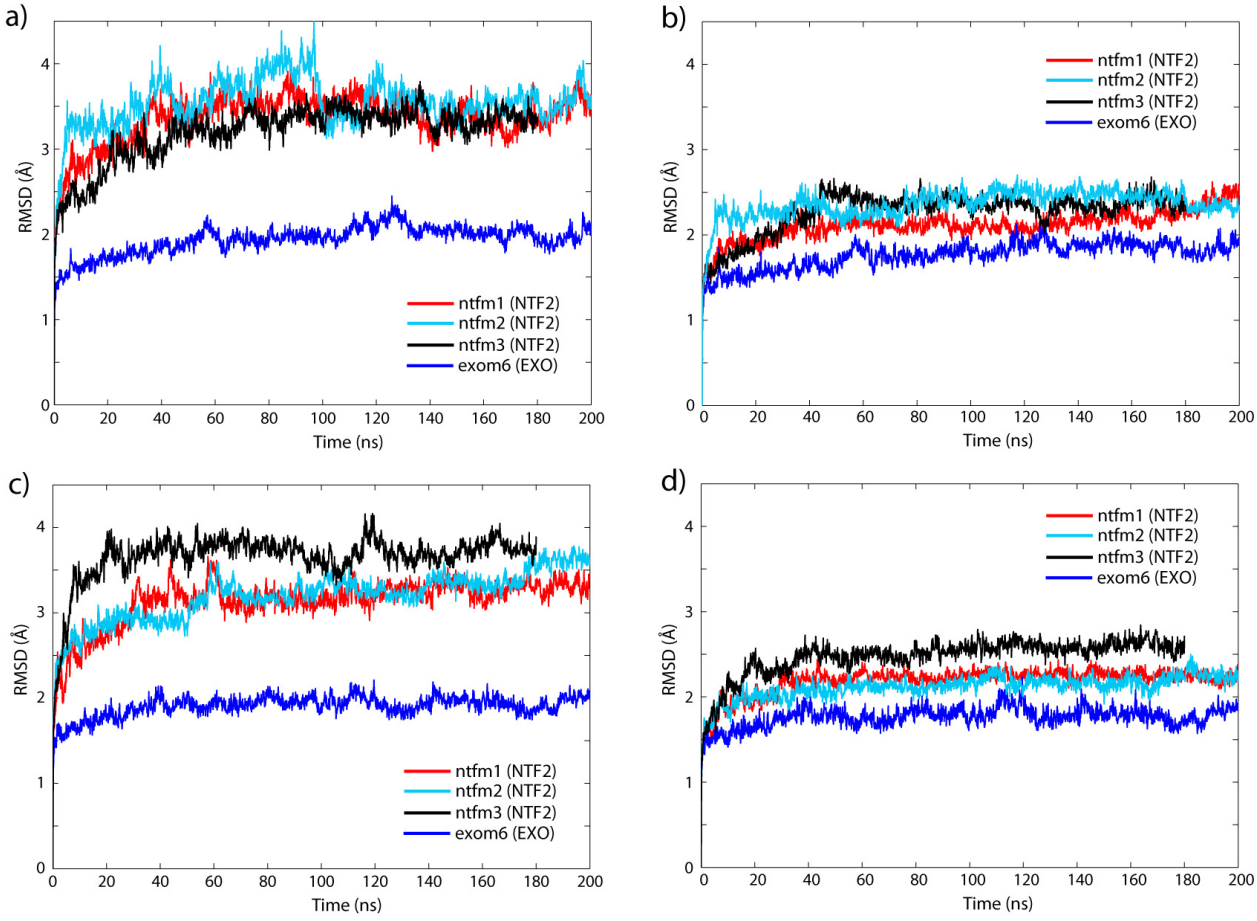

Figure S1: RMSD for NTF2 and exonuclease. a) RMSD for all atoms of the top-placed molecules. b) RMSD for only β-sheet and α-helix atoms of the top-placed molecules. c) RMSD for all atoms of the embedded molecules. d) RMSD for only β-sheet and α-helix atoms of the embedded molecules.

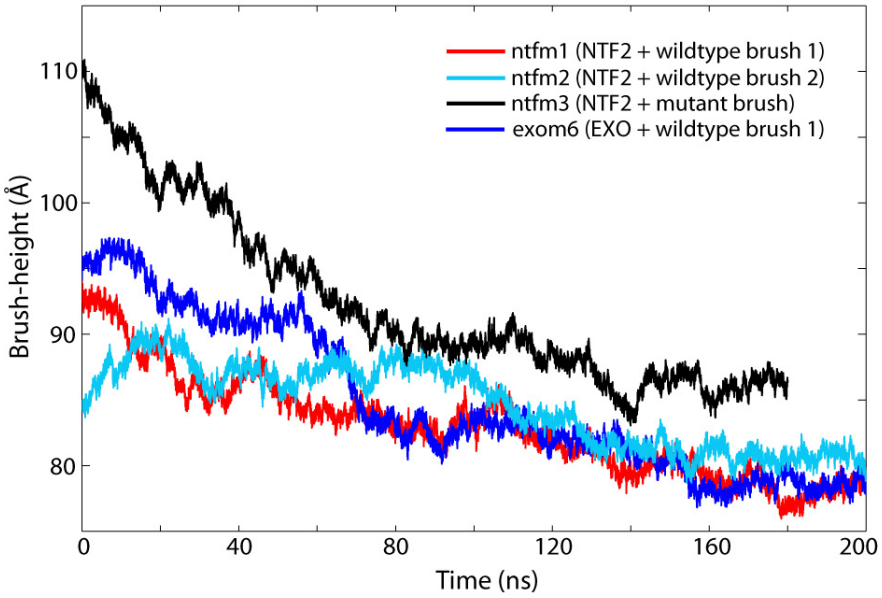

Figure S2: Time evolution of brush-height. Changes in brush-height are shown for simulation ntfm1 (NTF2 + wildtype nsp1 brush 1, red line), ntfm2 (NTF2 + wildtype nsp1 brush 2, cyan line), ntfm3 (NTF2 + mutant nsp1 brush, black line), and exom6 (exonuclease + wildtype nsp1 brush 1, blue line).

Time evolution of brush-height. During each simulation, the brush segments rearranged themselves, resulting in a decrease in brush-height as shown in Fig. S2.

Movement of NTF2 and exonuclease. Trajectories of all NTF2/exonuclease molecules (center of mass) are shown in Fig. S3.

Snapshots of steady binding events. The observed steady binding events of FG-repeats to NTF2 are shown in Fig. S4 a-d; steady binding to exonuclease is shown in Fig. S4e.

Supplemental movies. The following four movies show the results of simulation ntfm1, i.e., of NTF2 interacting with a native brush (see text, Table 2).

- **Movie S1a: Simulation ntfm1 (mmc6.mpg; initial position of NTF2).** The initial position of the top-placed NTF2 is shown. The coloring is the same as in Fig. 3a, i.e., NTF2 is colored ice blue and the brush segments orange; phenylalanines that ever bound to the molecule during the course of the simulation are shown in green.

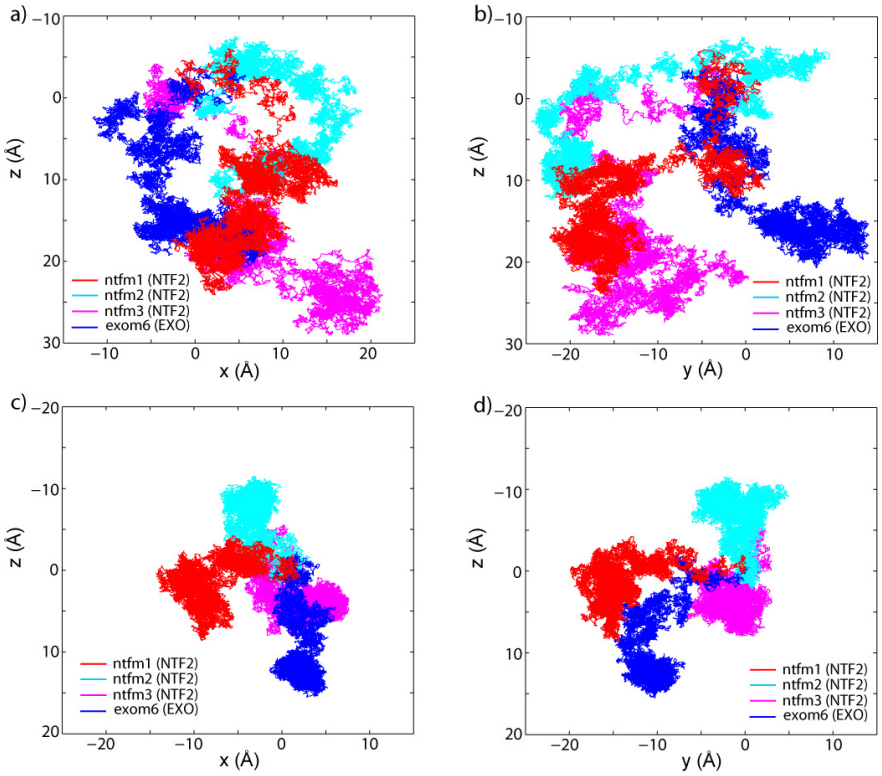

Figure S3: Center-of-mass movement of NTF2 and exonuclease. a), b) Trajectories of the center of mass of the top-placed molecules are shown in the x-z plane (a) and y-z plane (b), repectively. c), d) Trajectories of the center of mass of the embedded molecules are shown in the x-z plane (c) and y-z plane (d), repectively. The origin is set to the initial position of each molecule; the z-axis is chosen perpendicular to the brush's top surface and the x-y plane is parallel to that surface; the positive direction of the z-axis is defined from the brush's top surface to its bottom surface, i.e., a positive movement along the z-axis corresponds to movement toward the brush's bottom surface.

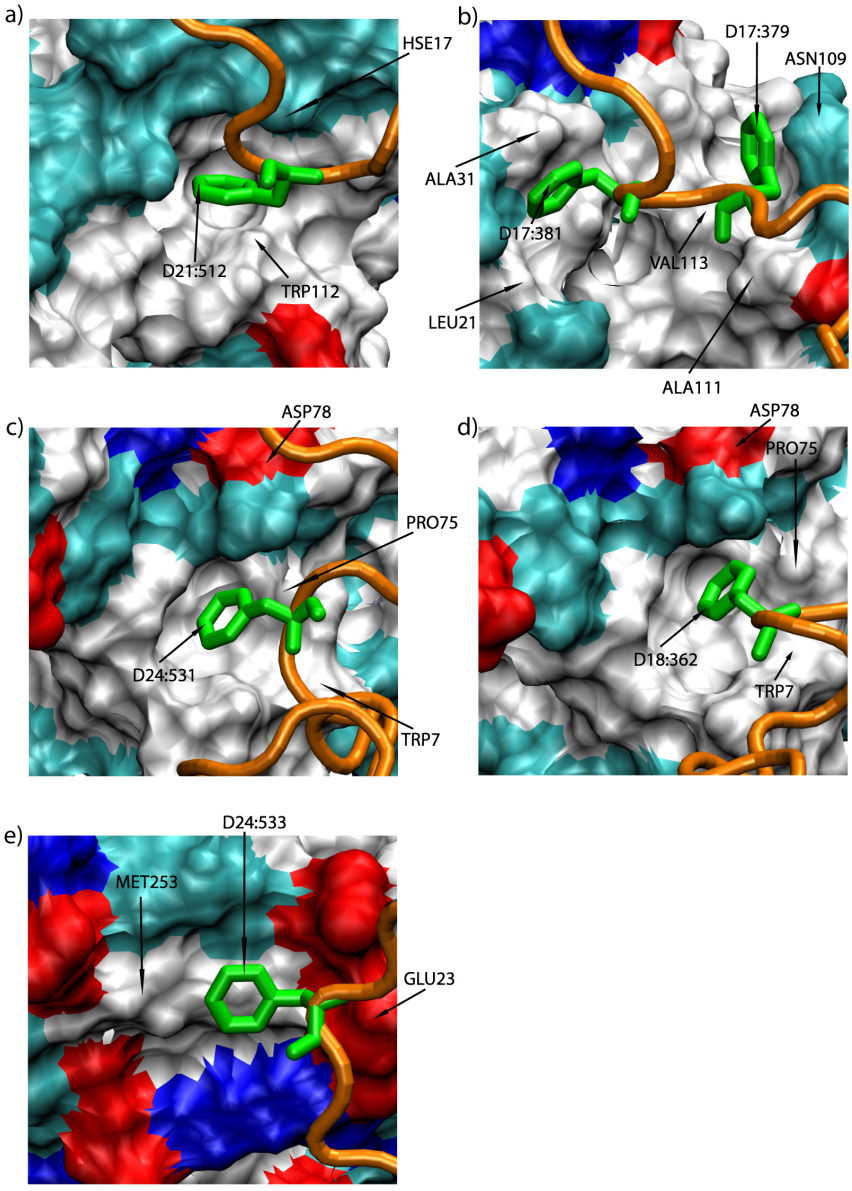

Figure S4: Snapshots of all steady binding events. a) PHE D21:512 (for notation see Table 1 in main text) binding to the top-placed NTF2 dimer in simulation ntfm1 (*c.f.* Fig. 4 a1). b) PHEs D17:379 and D17:381 binding to the embedded NTF2 dimer in simulation ntfm1 (*c.f.* Figs. 4 b1, 4 b3). c) PHE D24:531 binding to the top-placed NTF2 dimer in simulation ntfm2 (*c.f.* Fig. 5 a1). d) PHE D18:362 binding to the embedded NTF2 dimer in simulation ntfm2 (*c.f.* Fig. 5 b1). e) PHE D24:533 binding to the embedded exonuclease molecule in simulation exom6 (*c.f.* Fig. 6 b1). Phenylalanines are shown in green and the nsp1 segments containing them in orange; the NTF2 surface is colored according to residue type with polar basic residues in blue, polar acidic residues in red, polar neutral residues in cyan, and non-polar residues in white.

- **Movie S1b: Simulation ntfm1 (mmc12.mpg; motion of NTF2).** The top-placed NTF2 is shown to gradually enter the wildtype brush. The coloring is the same as in Fig. 3a, i.e., NTF2 is colored ice blue and the brush segments orange; phenylalanines that ever bound to the molecule during the course of the simulation are shown in green.

- **Movie S1c: Simulation ntfm1 (mmc4.mpg; final position of NTF2).** The final position of the top-placed NTF2 is shown. The coloring is the same as in Fig. 3a, i.e., NTF2 is colored ice blue and the brush segments orange; phenylalanines that ever bound to the molecule during the course of the simulation are shown in green.

- **Movie S1d: Simulation ntfm1 (mmc10.mpg; water residence time).** Water residence times averaged over the last 20 ns of the simulation are shown. NTF2 dimers and nsp1 segments are colored according to the water residence time τ, blue representing $\tau \geq 250$ ps, white representing $\tau \simeq 125$ ps, and red representing $\tau < 10$ ps.

The following three movies show the results of simulation ntfm2, i.e., of NTF2 interacting with a native brush (see text, Table 2).

- **Movie S2a: Simulation ntfm2 (mmc16.mpg; initial position of NTF2).** The initial position of the top-placed NTF2 is shown. NTF2 is colored ice blue and the brush segments orange; phenylalanines that ever bound to the molecule during the course of the simulation are shown in green.

- **Movie S2b: Simulation ntfm2 (mmc8.mpg; motion of NTF2).** The top-placed NTF2 is shown to gradually enter the wildtype brush. NTF2 is colored ice blue and the brush segments orange; phenylalanines that ever bound to the molecule during the course of the simulation are shown in green.

- **Movie S2c: Simulation ntfm2 (mmc11.mpg; final position of NTF2).** The final position of the top-placed NTF2 is shown. NTF2 is colored ice blue and the brush segments orange; phenylalanines that ever bound to the molecule during the course of the simulation are shown in green.

The following four movies show the results of simulation ntfm3, i.e., of NTF2 interacting with a mutant brush (see text, Table 2).

- **Movie S3a: Simulation ntfm3 (mmc3.mpg; initial position of NTF2).** The initial position of the top-placed NTF2 is shown. NTF2 is colored ice blue and the brush segments orange.

- **Movie S3b: Simulation ntfm3 (mmc9.mpg; motion of NTF2).** Movement of the top-placed NTF2 is shown. It did not enter the mutant brush during the course of the simulation. NTF2 is colored ice blue and the brush segments orange.

- **Movie S3c: Simulation ntfm3 (mmc15.mpg; final position of NTF2).** The final position of the top-placed NTF2 is shown. NTF2 is colored ice blue and the brush segments orange.

- **Movie S3d: Simulation ntfm3 (mmc7.mpg; water residence time).** Water residence times averaged over the last 20 ns of the simulation are shown. NTF2 dimers and nsp1 segments are colored according to the water residence time τ, blue representing $\tau \geq 250$ ps, white representing $\tau \simeq 125$ ps, and red representing $\tau < 10$ ps.

The following four movies show the results of simulation exom6, i.e., of exonuclease interacting with a native brush (see text, Table 2).

- **Movie S4a: Simulation exom6 (mmc13.mpg; initial position of exonuclease).** The initial position of the top-placed exonuclease is shown. The coloring is the same as in Fig. 3b, i.e., exonuclease is colored ice blue and the brush segments orange; phenylalanines that ever bound to the molecule during the course of the simulation are shown in green.

- **Movie S4b: Simulation exom6 (mmc2.mpg; motion of exonuclease).** Movement of the top-placed exonuclease is shown. It barely entered the wildtype brush during the course of the simulation. The coloring is the same as in Fig. 3b, i.e., exonuclease is colored ice blue and the brush segments orange; phenylalanines that ever bound to the molecule during the course of the simulation are shown in green.

- **Movie S4c: Simulation exom6 (mmc14.mpg; final position of exonuclease).** The final position of the top-placed exonuclease is shown. The coloring is the same as in Fig. 3b, i.e., exonuclease is colored ice blue and the brush segments orange; phenylalanines that ever bound to the molecule during the course of the simulation are shown in green.

- **Movie S4d: Simulation exom6 (mmc5.mpg; water residence time).** Water residence times averaged over the last 20 ns of the simulation are shown. Exonuclease molecules and nsp1 segments are colored according to the water residence time τ, blue representing $\tau \geq 250$ ps, white representing $\tau \simeq 125$ ps, and red representing $\tau < 10$ ps.