Supplemental material belonging to

SIMULATING THE MOTION UNDERLYING THE MECHANISM OF THIOREDOXIN REDUCTASE

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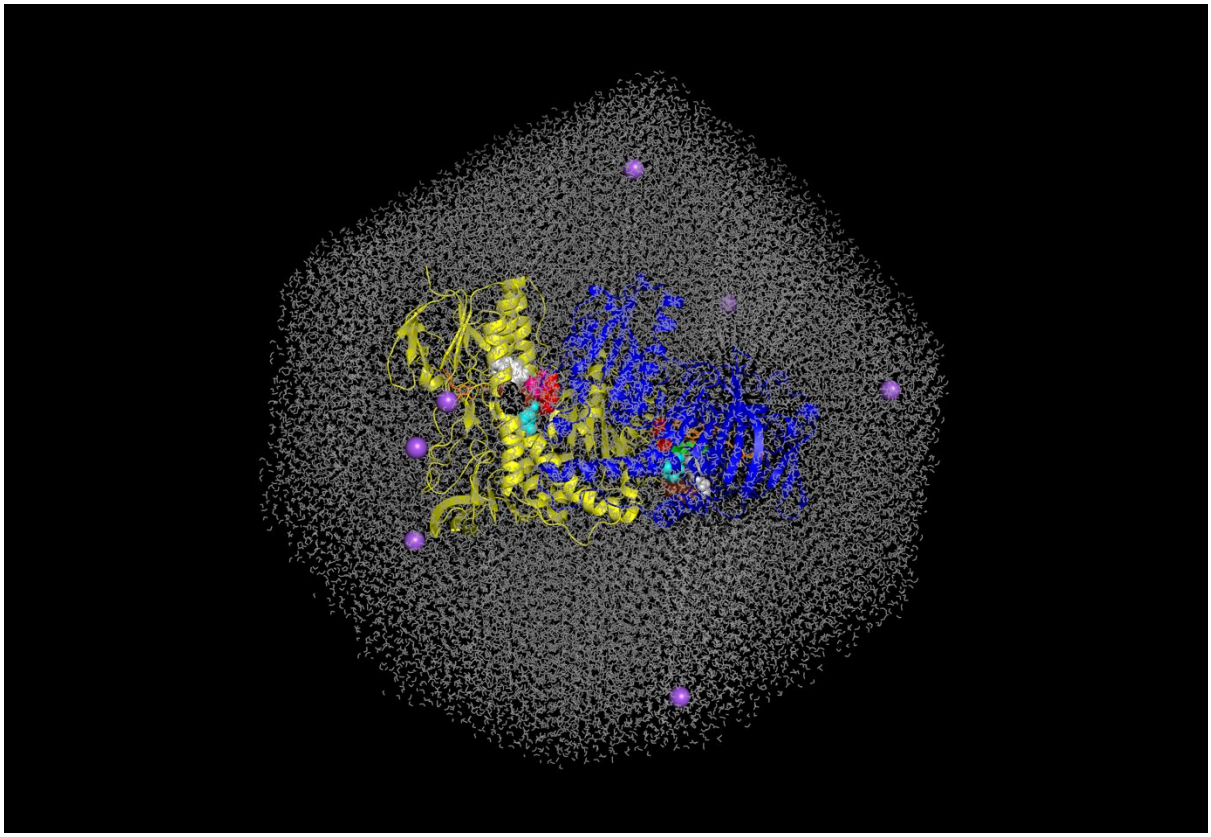

Figure S1.
Starting configuration for the MD simulation of the full TrxR dimer, embedded in explicit OPC water, with 7 Na+ counter ions.

MOVIE_A_SS_md10_16_1_210_DETAIL.mpg
Dynamics of the complete TrxR dimer in water.
The central dimer chains C (yellow) and D (blue) of 2J3N. pdb. FADs are orange, the Cys59/64 active site pairs are green. The Cys-488/489 shuttles are magenta. Tyr-116 is white. Leu-103 is brown. Ile-65 is Cyan, and His-472 is red.
Dynamics of the system with the shuttle in disulfide state, 37 ^{0}C. Each frame is 1 ns. Total simulation was 500 ns, here showing the first 200 ns. Water molecules have been removed for the movie. The movie starts with the shuttle disulfide docked against Tyr-116 and Leu-103 at around 11 Å from Cys-59/64 as in the crystal structure. At 88 ns shuttle is fully at the "left" of Tyr-116, Leu-103, Ile-65 and His-472, which form a barricade for shuttle access to the active site. At 201 ns the shuttle has broken through the barricade and is at 4.7 Å of Cys -59.

MOVIE_B_SS_md10_16_1_501_ALL.mpg
Dynamics of the complete TrxR dimer in water.
The central dimer chains C (yellow) and D (blue) of 2J3N. pdb. FADs are orange, the Cys59/64 active site pairs are green. The Cys-488/489 shuttles are magenta. Tyr-116 are white. Leu-103 is brown. Ile-65 is Cyan, and His-472 is red. Residues Ser-111 (black) indicate the (approximate) docking site of Thioredoxin.
Dynamics of the system with the shuttle in disulfide state, 37 ^{0}C. Each frame is 1 ns. Total simulation was 500 ns. Starting position is with the shuttle docked against Tyr116 and Leu-103.

MOVIE_C_ANION_md8_1_1250.mpg
Dynamics of the complete TrxR dimer in water.
The central dimer chains C (yellow) and D (blue) of 2J3N. pdb. FADs are orange, the Cys59/64 active site pairs are green. The Cys-488/489 shuttles are magenta. Tyr-116 are white. Leu-103 is brown. Ile-65 is Cyan, and His-472 is red. Residues Ser-111 (black) indicate the (approximate) docking site of Thioredoxin.
Dynamics of the system with reduced shuttles, 37 ^{0}C. Each frame is 0.4 ns. Total simulation 500 ns. Water molecules have been removed for the movie. The simulation starts with the reduced shuttle of Chain D close to the Cys 59/64 disulfide of chain C (lower right). Both shuttles escape into solultion, but the latter one lingers longer in the vicinity of Ser-111. Details are shown in **MOVIE_D_ANION_md8_1_1250_ DETAIL.mpg**

MOVIE_D_ANION_md8_1_1250_ DETAIL.mpg
At first the shuttle is very close to the Cys 59/64 disulfide, but soon it moves to and interacts with Tyr116 (white) and-Leu103 (brown). This is the "resting position" as seen in the crystal structure. Each frame is 0.4 ns. At about 2/3 of the total time, the shuttle has passed Leu103, and moves to within 4 Å of Ser111 OH. Ultimately it escapes in solution.