SUPPORTING INFORMATION

The relaxation procedure before production MD is explained in detail as follows:

(1) 1000 steps of minimization using steepest descent method using a cutoff of 8.0 Å for truncation of nonbonded pairs while applying a harmonic restraint to all the backbone atoms of the enzyme with a force constant of 5.0 kcal/mol $Å^2$.

(2) 15 picoseconds of molecular dynamics with a timestep of 1 femtosecond at 300 K and constant pressure using periodic boundary conditions and Berendsen weak-coupling algorithm(*1*) with a temperature coupling time constant of 0.5 picoseconds and a pressure relaxation time of 0.5 picoseconds. The Particle Mesh Ewald Sum technique is used to calculate long range electrostatic interactions. Shake algorithm(*2*) is also used to constrain bonds involving hydrogen atoms. The constraints for the backbone atoms and the nonbonded cutoff value used in the 1^{st} step are kept.

(3) Three subsequent minimizations with the same procedure as in step 1 except decreasing the force constant for the backbone atoms to 2.0 kcal/mol $Å^2$, 0.1 kcal/mol $Å^2$ and finally to 0, respectively.

(4) 5 picoseconds of molecular dynamics with the same procedure as in step 2 except decreasing the restraint force constant to 1.0 kcal/ mol $Å^2$.

(5) 15 picoseconds of molecular dynamics with the same procedure as in step 2 except decreasing the restraint force constant to 0.5 kcal/ mol $Å^2$.

(6) 1 nanosecond of molecular dynamics with the same procedure as in step 2 except releasing the restraints and increasing the timestep to 2 femtoseconds.

1. Berendsen, H. J. C., Postma, J. P. M., Vangunsteren, W. F., Dinola, A., and Haak, J. R. (1984) Molecular-Dynamics with Coupling to an External Bath, *Journal of Chemical Physics 81*, 3684-3690.
2. Ryckaert, J.-P., Ciccotti, G., and Berendsen, H. J. C. (1977) Numerical integration of the cartesian equations of motion of a system with constraints: molecular dynamics of n-alkanes, *Journal of Computational Physics 23*, 327-341.

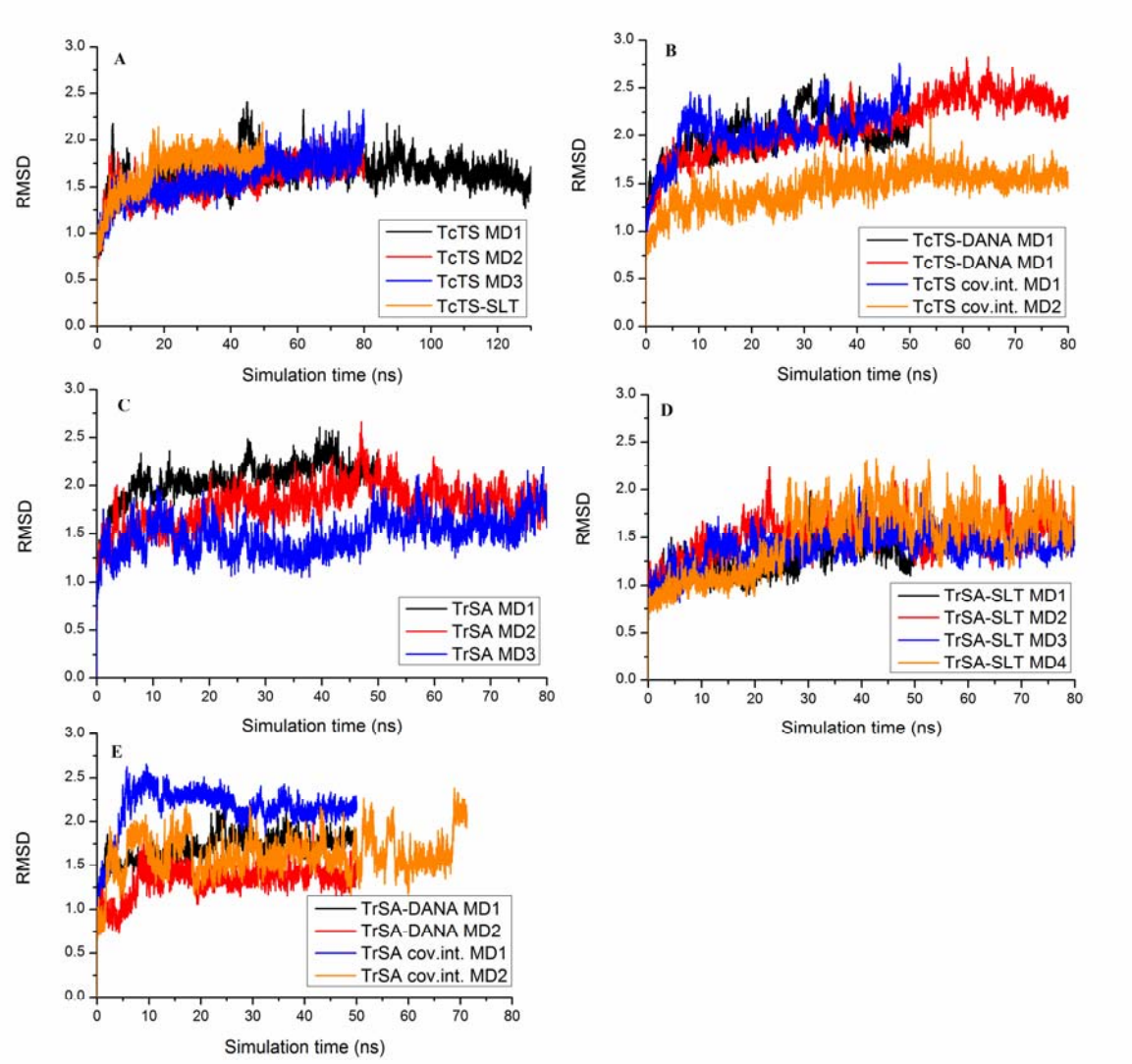

Figure S1. Root mean square deviations (RMSD) of C_α atoms of the systems during MD simulations (in Å). A) apo form of TcTS and sialyl-lactose-bound TcTS B) DANA-bound TcTS and TcTS covalent intermediate C) apo form of TrSA D) Sialyl-lactose-bound TrSA E) DANA-bound TrSA and TrSA covalent intermediate.

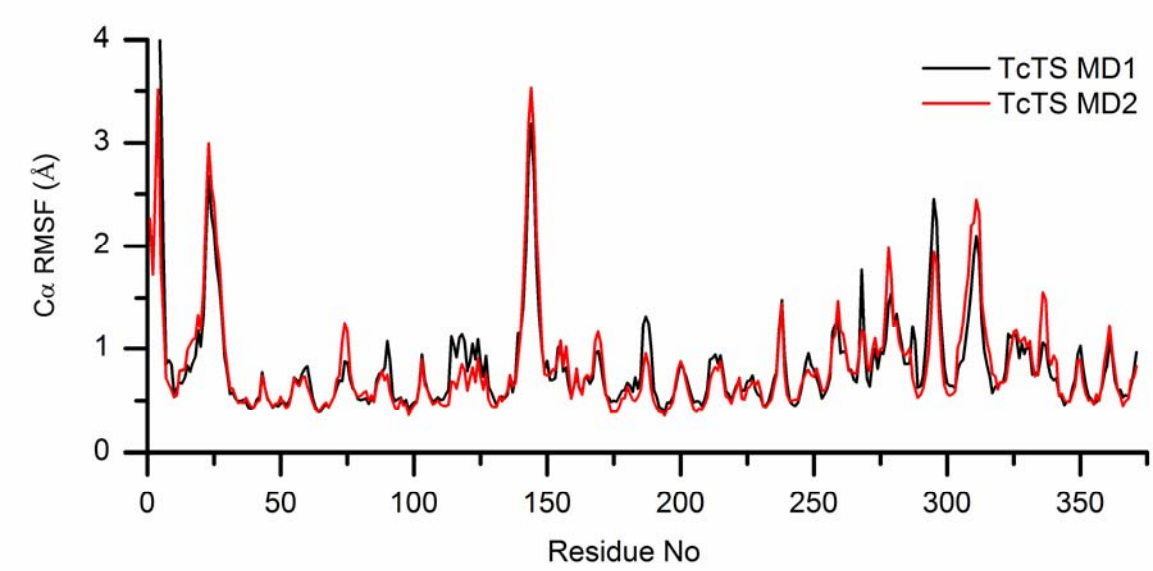

Figure S2. Mobilites of C_α for each residue in apo TcTS MD simulations. RMSF is a measurement of deviation of a particle from a reference structure—average structure of production run in our case—over time. RMSF is defined with $RMSF = \sqrt{\frac{1}{t}\sum_{t_j=0}^{t_j=t}(x(t_j)-\bar{x})^2}$ where t is time and $\bar{x}$ is the time-averaged position of the same particle. RMSF can be used as a measure of the mobility of a particle in a simulation and is related to experimental B-factors by the relationship given as: B-factor=$8\pi^2$ $(RMSF)^2$.