

Supplementary Figures

SFigure 1. Backbone RMSD of the SecY pore complex in the model implicit lipids during a 2 ns equilibration run.

SFigure 2. A series of snapshots from ball growth trajectory. at position Z_2 . Coloring scheme is the same as in Fig. 1a a) $R = 6 \text{ \AA}$; b) $R = 7 \text{ \AA}$; c) $R = 9 \text{ \AA}$; d) $R = 10 \text{ \AA}$; e) $R = 11 \text{ \AA}$; f) $R = 12 \text{ \AA}$.

SFigure 3. Comparison of residue based B-factors from the crystal structure and simulations.

SFigure 4. A ball with radius of 6 \AA being pushed into the cytoplasmic side by the resilience of the SecY complex. Gray ball indicate the initial location and green ball indicate the final location. Coloring scheme is the same as in Fig. 1a.

SFigure 5. Side view of the SecY complex, coloring scheme is the same as in Fig. 1a, a) When a soft ball of 20 \AA diameter is placed at position Z_2 . b) After 4 ns of relaxation with the soft ball removed.

SFigure 6. The front side of the SecY complex after a ball exited in between TM3 (green) and TM7 (orange). coloring scheme is the same as in Fig. 1a, a) $R = 7 \text{ \AA}$, helical structure of TM2 and TM7 are well preserved; a) $R = 8 \text{ \AA}$, helical structure of TM2 and TM7 are partially disrupted; a) $R = 10 \text{ \AA}$, helical structure of TM2 and TM7 are severely distorted.

SFigure 7. Top (a) and front side (b) view of a SecY complex after a ball laterally exit the pore in between TM2/3 and TM7. (Ball size: $R = 7 \text{ \AA}$; Pushing force: 2000 pN.)

SFigure 8. Top (a) and front side (b) view of a ball stuck above the plug in SecY complex (Ball size: $R = 6 \text{ \AA}$; Pushing force: 1500 pN.)

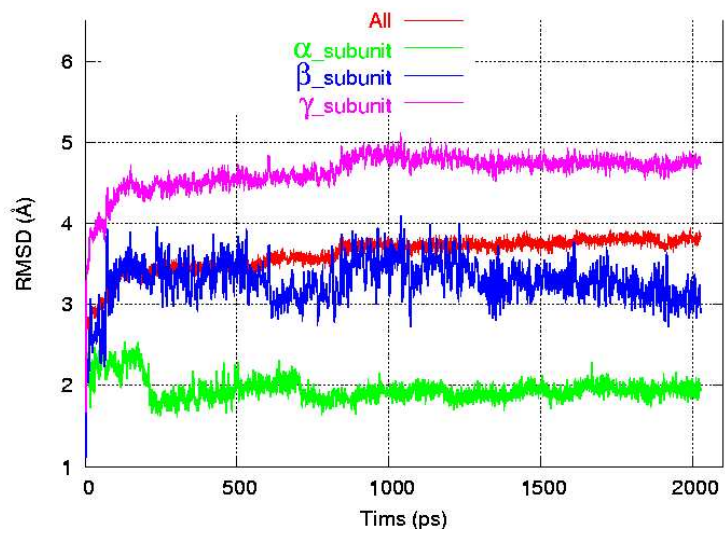


Figure 1:

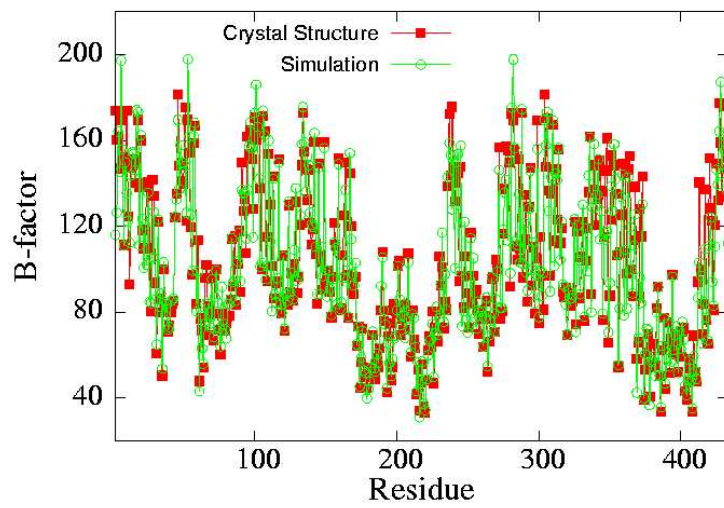


Figure 2:

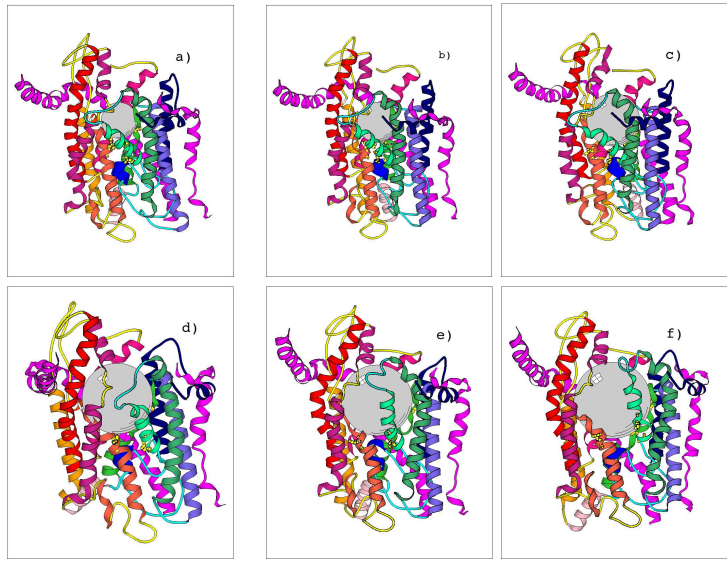


Figure 3:

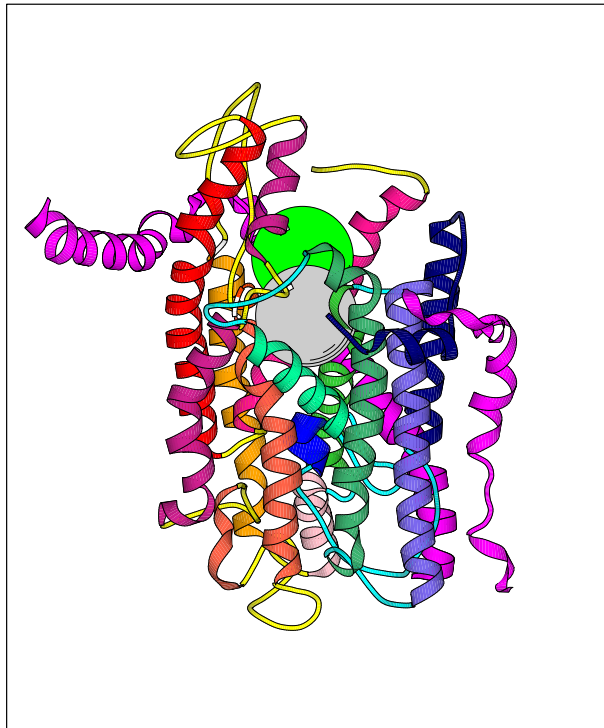


Figure 4:

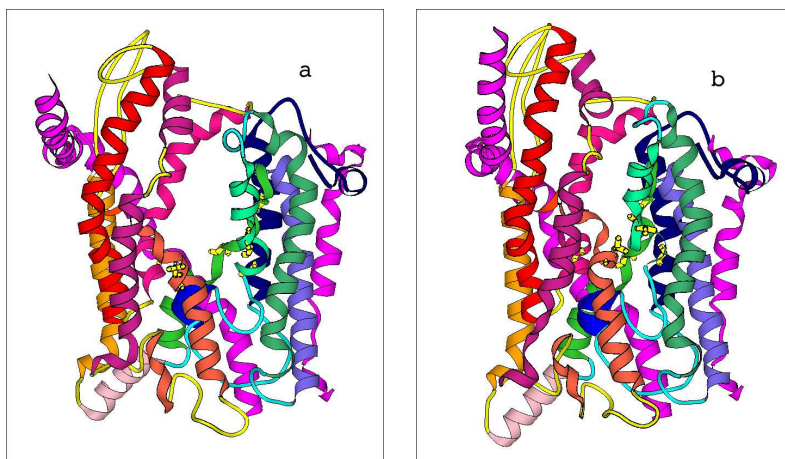


Figure 5:

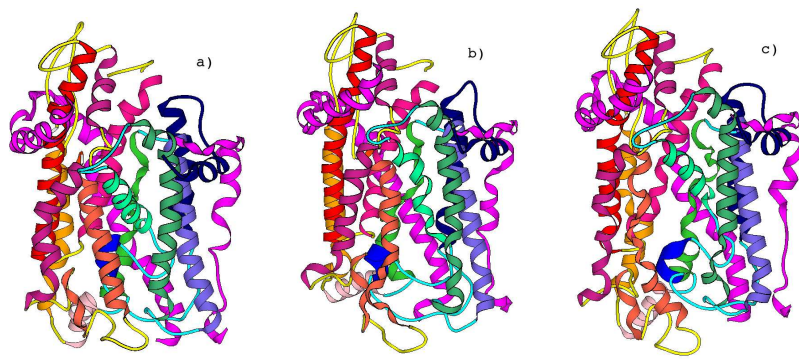


Figure 6:

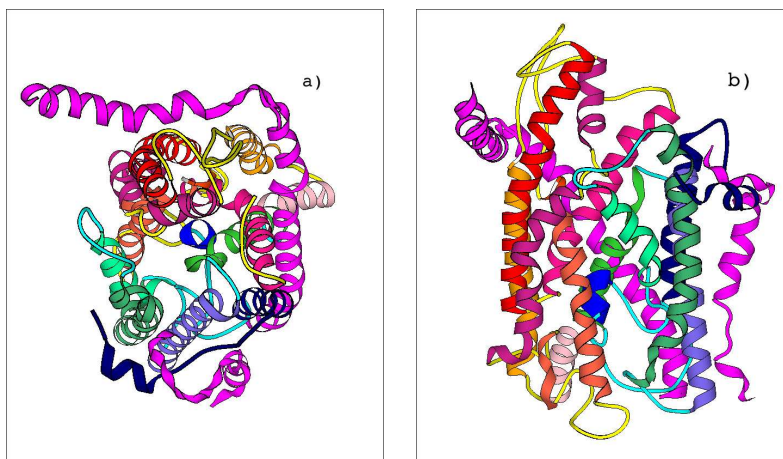


Figure 7:

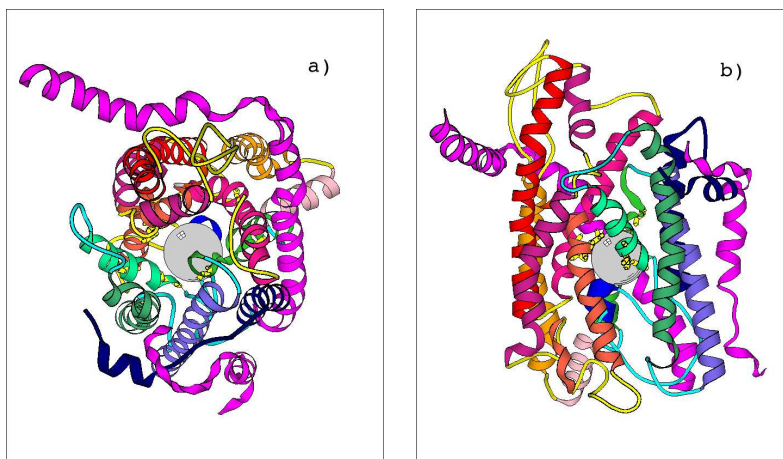


Figure 8: