Supporting Information for:

SIMULATIONS OF A PROTEIN TRANSLOCATION PORE: SECY

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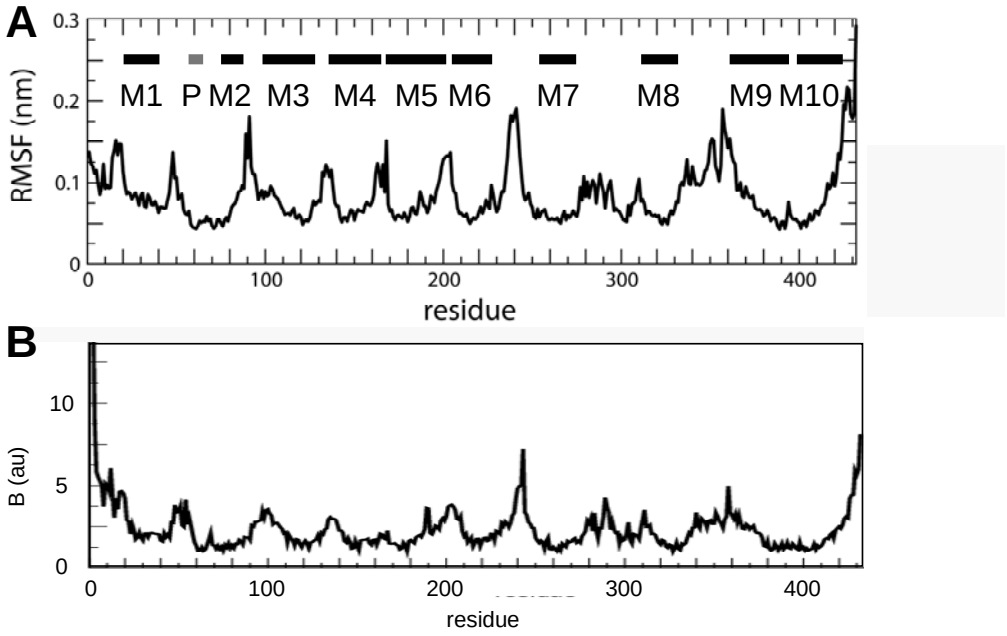
Figure S1
Comparison of **A** RMSF profile (from MD simulation of SecY in a bilayer) and **B** calculated B-value profile from a Gaussian network model analysis (*1*) of SecY. It can be seen that the two methods predict very similar profiles of residue-by-residue flexibility.



(1) Keskin, O., Jernigan, R. L., and Bahar, I. (2000) Proteins with similar architecture exhibit similar large-scale dynamic behavior. *Biophys. J. 78*, 2093-2106.