Supplemental Information

for

Cryo-Electron Microscopic Structure of SecA Bound to the 70S Ribosome

by

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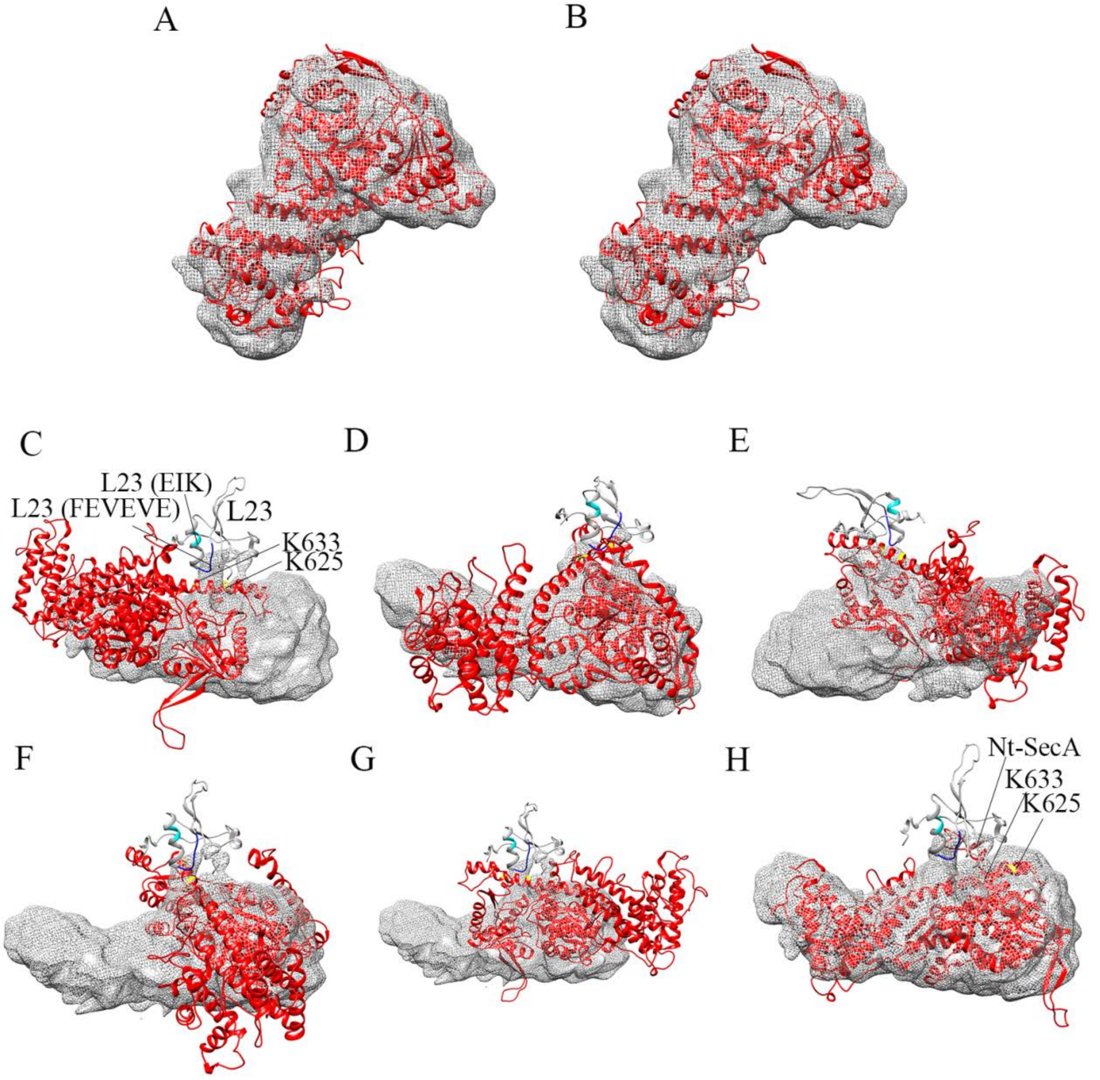
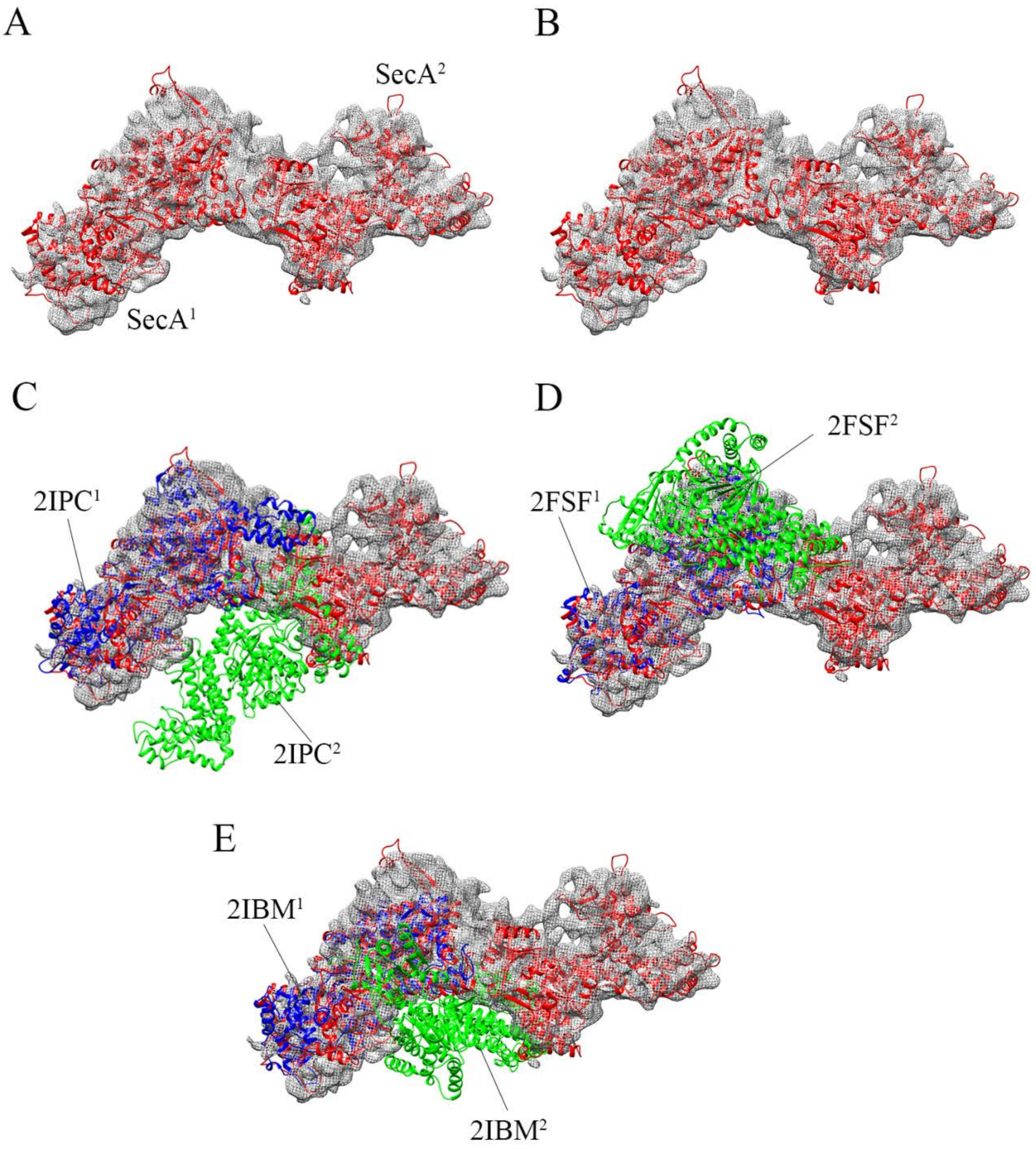
Supplemental Figures S1 - S2



Supplemental Figure S1. Modeling of a single copy of SecA in the ^{1}SecA-70S structure. A stereo-view representation of the fitting of SecA homology model (generated from the PDB id 1M74 in an open conformation) in the ^{1}SecA density with a cross-correlation value of 0.45 calculated with Chimera (A-B). Alternative fitting of SecA model by placing Lysine 625 and 633 in the close proximity to L23 protein (C-G), or with a rigid body followed by manual fitting (A,B and H). The cross-correlation values for C-H are 0.07, 0.15, 0.19, 0.23, 0.27, and 0.45, respectively. The highest cross-correlation is only obtained when the N-terminus of SecA is in the close proximity to L23 protein (A-B and H). The EM density for SecA is shown in grey color mesh, the SecA model is in red, protein L23 is in grey, Lysine 625 and 633 are in yellow, and two regions important for SecA binding in L23 protein are in cyan (EIK) and blue (FEVEVE).



Supplemental Figure S2. Modeling of the two SecA molecules in the ^{2}SecA-70S structure. A stereo-view representation of the fitting of the two SecA homology models (generated from the PDB id 1TF2 in a partially open conformation) in the ^{2}SecA density with a cross-correlation value of 0.61 calculated with Chimera (A-B). Docking of the dimeric structures of SecA (PDB id; 2IPC, 2FSF, and 2IBM) in the ^{2}SecA density resulted in only one of the two copies of SecA present in the dimer fitting into the density (C-E). The cross-correlation values for C-E are 0.36, 0.37, and 0.37, respectively. The EM density for SecA is shown in grey color mesh. SecA^1 and SecA^2 homology models in the partially open conformation are colored in red, two monomers of dimeric 2IPC, 2FSF, and 2IBM structure are in blue (2IPC^1, 2FSF^1, and 2IBM^1), and green (2IPC^2, 2FSF^2, and 2IBM^2), respectively.