FIGURE S1. Comparison of the SEC profiles of AtSOS1 purified following the initial (grey) and the final (black) purification protocols. The preliminary purification protocol yielded to a monomeric non functional protein.
The structure of the plant SOS1 antiporter

**FIGURE S2.** Representative electron microscopy field of (A) eluted Ni-NTA and (B) gel-filtered peak 2 SOS1 samples. Some particles are boxed. Representative averaged images are shown in the inset picture. Particles from eluted Ni-NTA sample (A) displayed a heterogeneous particle size distribution, although some 2-fold symmetry views were identified. Particles from Gel-filtered peak 2 SOS1 sample displayed a small, elongated shape and particles with 2-fold symmetry were scarcely observed.
FIGURE S3. Statistical information of the EM reconstruction. (A) Reference free class averages with their corresponding variance maps. (B) Angular distribution of Euler angles rot (Φ) and tilt (θ) for class 1 and class 2 reconstructions. (C) Fourier Shell Correlation plot for class 1 and class 2 reconstructions.
FIGURE S4: AtSOS1 and the CPA homologues EcNhaA and MjNhaP1. (A) Structural alignment of the N-terminal end of EcNhaA (14) and MjNhaP1 (17), compared with SOS1 predicted secondary structure elements. TM helices and β-strands are displayed in red and blue boxes, respectively. Helices are labeled as in (14) and (17). (B) Sequence alignment of AtSOS1 and MjNhaP1 TM regions. Sequence identity is 21%. Sequence conservation is shown. Helices from the MjNhaP1 7Å resolution 3D model are labeled and marked with red boxes. Conserved aspartates involved in ion binding or translocation are marked with green boxes (14).
**MOVIE S1:** Movie showing the differences between AtSOS1 class 1 and class 2.