Prediction of a New Ligand-Binding Site for Type 2 Motif Based on the Crystal Structure of ALG-2 by Dry and Wet Approaches

Supplementary Information

Figure S1. Blocking of predicted Pocket 3 in crystal. Surfaces of chain A and a crystallographic symmetry-related monomer (chain A'; not the partner of dimer, chain B) of PDB ID 2zn9 are drawn by PyMol. Views of front and side are shown similarly to Figure 2. Residues involved in forming Pocket 3 are colored in cyan in chain A and blue in chain A'.

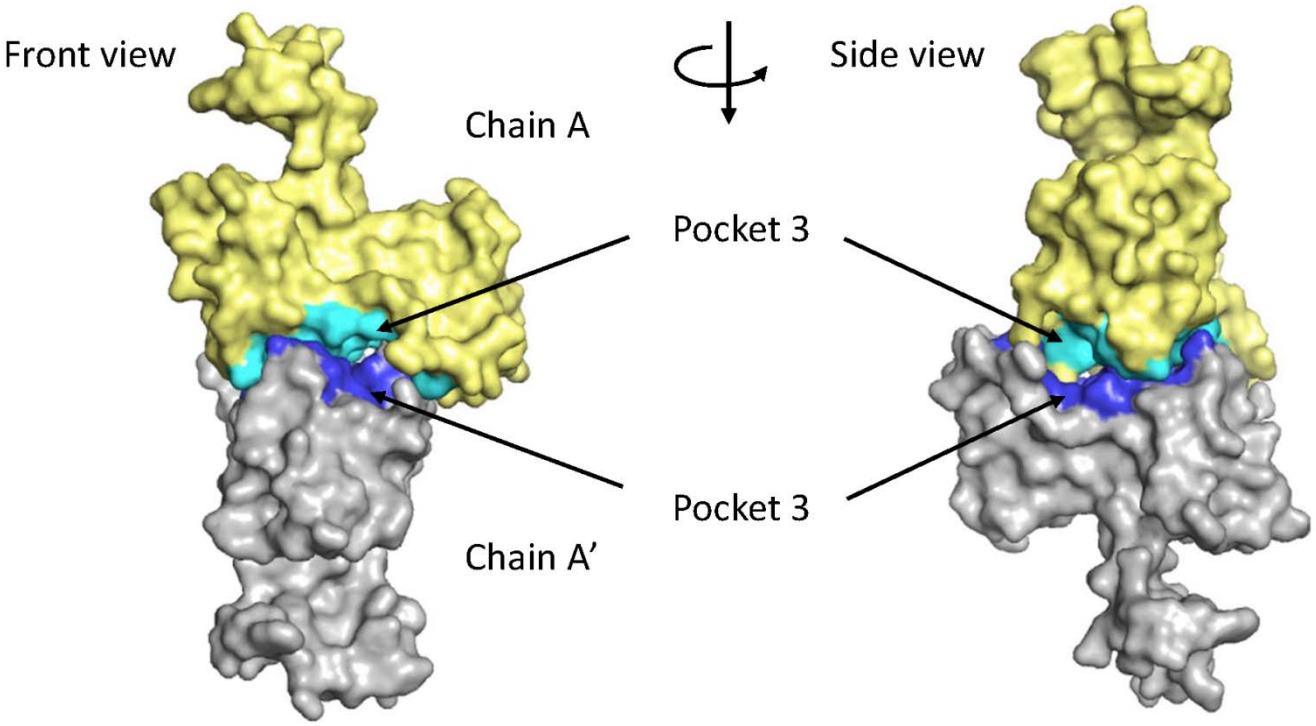

Figure S2. Ca^{2+}-dependent interaction of ALG-2 with PLSCR3. GST-pulldown assays were performed similarly to Figure 7 in the presence of 5 mM EGTA or 100 μM $CaCl_2$ using the lysates of HEK293T cells that expressed GFP-fused wild-type PLSCR3. Proteins bound to the glutathione Sepharose beads (pulldown fractions) were analyzed by Western blotting using an anti-GFP antibody.