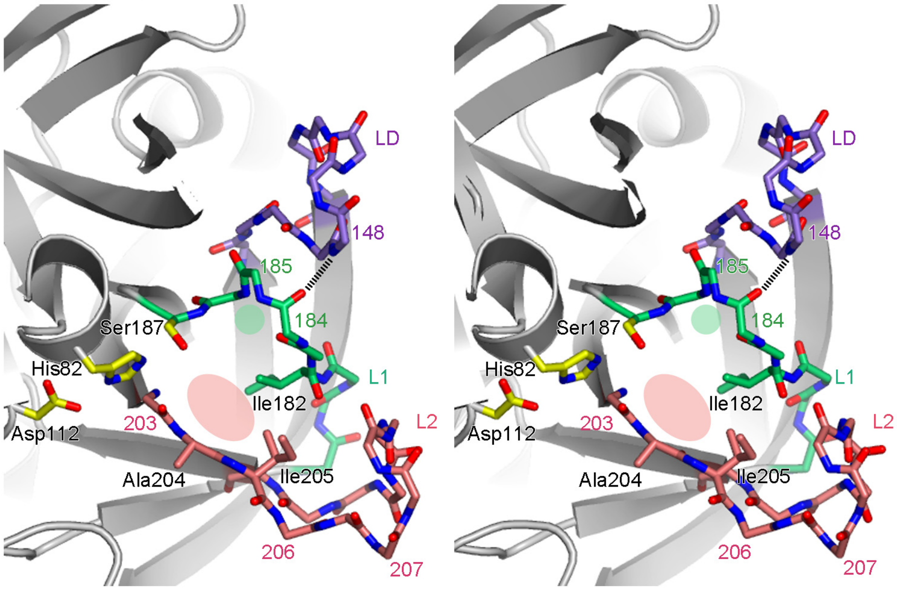
Figure S1 Sawa et al.

QProtPDZ1



QProt

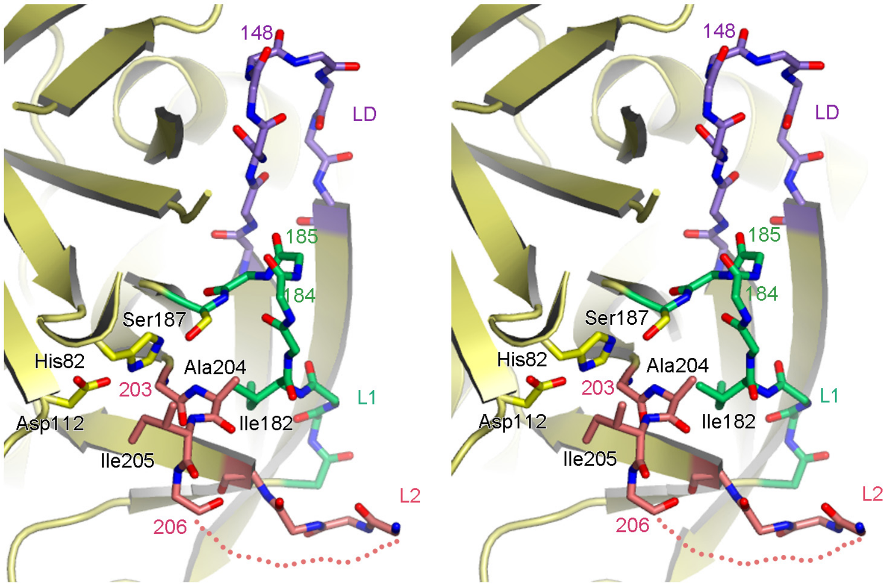


Fig. S1. **Structural details of the active site loops in proteolytically active QProtPDZ1 and inactive QProt.** Stereo view of QProtPDZ1 (top panel, grey) and QProt (bottom panel, light yellow). The backbone of the activation domain (loops L1, L2 and LD in green, light red and lilac, respectively) as well as the side chains of residues forming the S1 pocket formation (Ile182, Ala204 and Ile205, yellow) and the catalytic triad (His82, Asp112 and Ser187, yellow) are shown in stick mode. The position of the oxyanion hole is depicted as a green circle and residues engaged in its stabilization are labeled (Arg184, Gly185 and Phe148). For clarity, side chains of residues that are not discussed are omitted from the illustration.