**Figure S2 Sawa et al**.

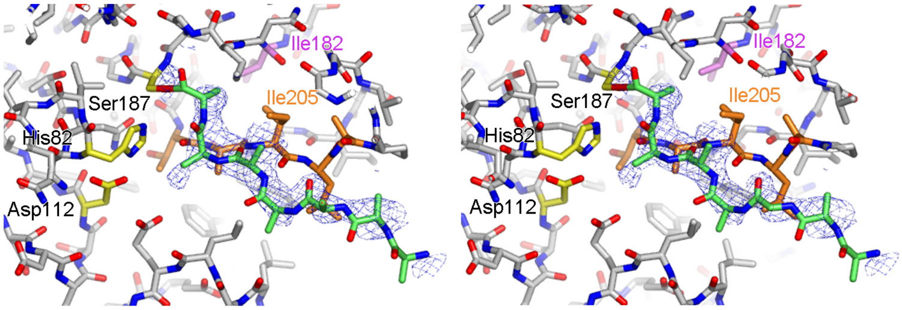

Fig. S2. **Peptide binding to the proteolytic site of QProtPDZ1.** Detailed stereo view of the proteolytic site with the bound peptide (green) that is attached via β-augmentation to the L2 loop (orange). The peptide P1 residue forms a covalent bond with the active site Ser187 (yellow, stick mode) and its side chain protrudes into the S1 specificity pocket defined by the side chains of Ile205 (orange) and Ile182 (magenta). The 2Fo–Fc electron density map, which is contoured at 1.3 σ, was calculated at 2.6 Å resolution without contribution of the bound peptide ligand.