

Figure S6 The acceptor ubiquitin can take various orientations.

(A-F) PDB structures of the E2~Ubi complexes (4AP4, 1FXT, 2KJH, 2GMI, 3A33 and 3JVZ) were each superimposed on the Ube2g2~Ub-Ube2g2 subcomplex model in cluster 2 by overlaying the E2 structures onto the acceptor Ube2g2. Six different acceptor ubiquitin orientations were generated (A-F). Note that Lys48 in acceptor ubiquitins are colored in red.

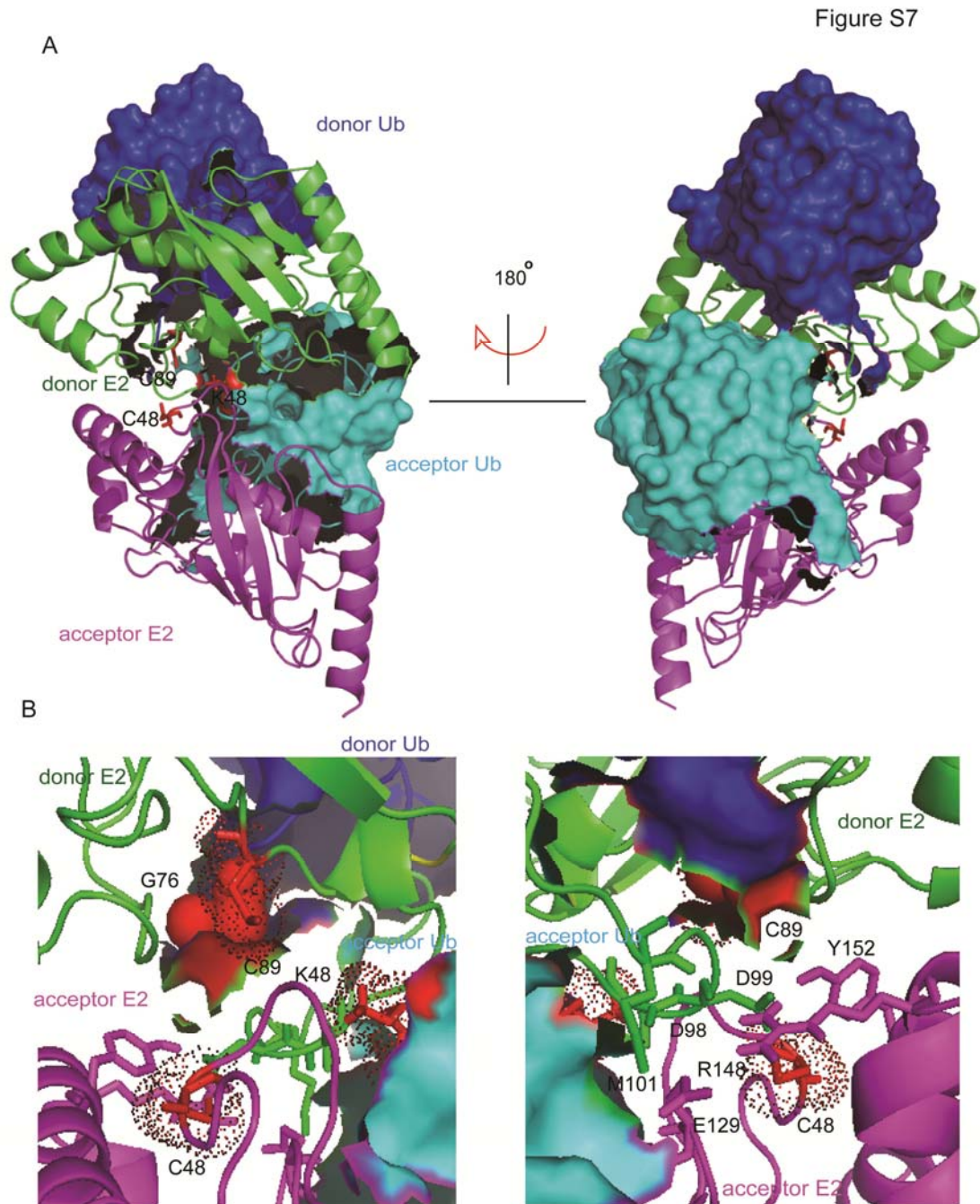


Figure S7 Characterization of the Ube2g2 dimer interface

(A) A structural model for the Ube2g2~Ub dimer. The two E2s form a front-to-back dimer that is jointed at the bottom. The top contains a 19 Å gap that harbors the donor and acceptor ubiquitins. Note that C48 in the acceptor E2 is in proximity to C89 in the donor E2.

(B) A close-up view of the E2 dimer interface. Dashed lines show ion pairings between the two E2s. Note that dimerization of Ube2g2 forms a deep pocket that houses the active site of the donor Ube2g2. The side chain of Lys48 of the acceptor ubiquitin is pointing directly at the donor active site.