

(Kleywegt and Jones, 1999) and AVE (Jones, 1992). This improved map allowed fitting of the amino acid sequence.

The ALIX<sub>Bro1</sub> and ALIX<sub>Bro1-v</sub> structures were solved by molecular replacement using PHASER (McCoy et al., 2005). The search model for ALIX<sub>Bro1</sub> was a mixed poly-Ser/homology model based on the yeast Bro1 structure (pdb code 1ZB1) (Kim et al., 2005). Search models for ALIX<sub>Bro1-v</sub> were the refined structures of ALIX<sub>Bro1</sub> and the two arms of ALIX<sub>v</sub>. Modelbuilding was with O (Jones et al., 1991) and COOT (Emsley and Cowtan, 2004). Structures were refined with CNS (Brunger et al., 1998) and in the final cycles using REFMAC5 with TLS refinement using TLSMD (Merritt and Painter, 2006; Painter and Merritt, 2006), and TLSANL (Howlin et al., 1993) in the CCP4 suite (Group, November 4. 1994). Figures of the structure were generated in PyMol (DeLano, 2002). Coordinates and data have been deposited in the Protein Data Bank, [www.pdb.org](http://www.pdb.org) (PDB code 2OEV, 2OEW, 2OEX).