et al., 2002). All measured reflections (except the test set) were used in refinement, regardless of I/σ(I) value, up to a Bragg spacing of 3.0 Å, at which point the $\sigma_A$ value falls precipitously (DeLaBarre and Brunger, 2006). No solvent molecules were included in the model. NCS restraints were set automatically in Phenix and only minor deviations from NCS are apparent. Stereochemistry was assessed using MolProbity (Davis et al., 2007), and the overall clashscore was 70% for the Blm10 portion of the structure in comparison with other structures reported at 3.4 Å resolution. The clashscore was 89% for the proteasome portion of the structure. Molprobity evaluated 87.8% of residues as possessing favored Ramachandran angles and 2.8% as being outliers. The following residues lacked defined density and have been omitted from the model. Blm10: N-terminus to Ser78, Asp155-Ala238, Arg1038-Asp1146. Proteasome: α1 before Ala10, α2 before Gln20, α3 before Ser14, α4 before Ile17, α7 before Gly4. All other proteasome residues that were present in the search model were also included in the Blm10 complex refinement. Crystallographic statistics are given in Table 1. The figures were made with PyMol (DeLano, 2002).