



Figure 2-figure supplement 2. Root-mean-square deviation(RMSD) of the nucleotide-interacting residues in the *cis* pockets among different proteasomal states. The RMSD of the nucleotide-interacting residues in the *cis* binding pockets among different proteasomal states was analyzed as described in methods 1. The first three comparisons were gated according to whether a pocket changed from ‘occupied’ to ‘empty’ or *vice versa*. The last two compare the pocket geometry in the EB, EC1,2 and ED1,2 states which have substrate peptide in the ATPase channel with the pocket geometry in the EA1 or ED1 state. In the last analysis, only pockets with identical nucleotide status (“occupied” or “empty”) are compared. The figure shows the box plot for the RMSD distributions.