



**Figure 1-figure supplement 1.** Schematics showing the key structural features and the nucleotide-binding status of the substrate-engaged proteasome identified in a cryo-EM study. Each ATPase subunit is arranged vertically according to the order, or the approximate distance, of its pore-1 loop to the 20S core particle. An open interface is represented by a large gap. The Rpt2-Rpt6 interface is marked separately. Subunits that are disengaged from substrate are blank-and-white. The engage/disengage status is predicted according to the proximity of pore-1 loop to the central axis in the  $E_{A1/2}$  and  $E_B$  states which do not exhibit substrate density in the translocation channel.