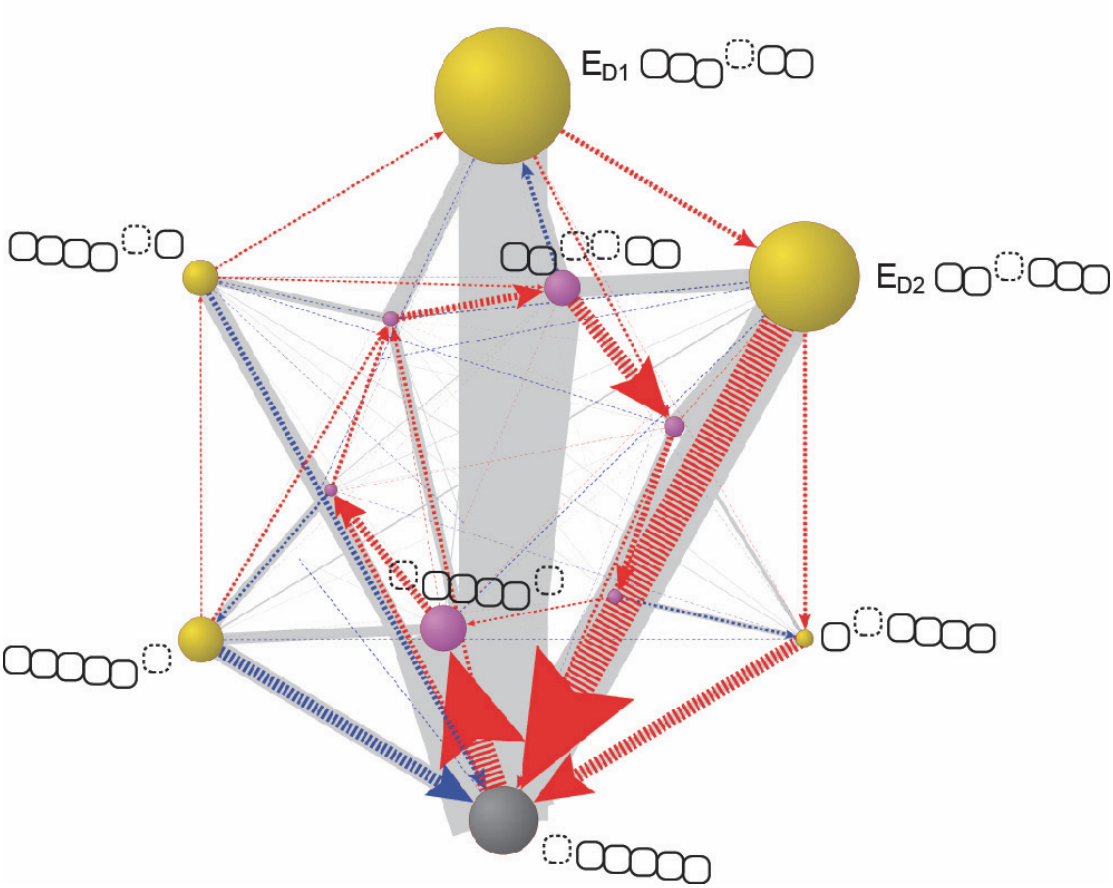

Figure 6-figure supplement 4. The Lid-ATPase interaction may account for the observed dissymmetry in conformational occupancies in previous cryo-EM studies. In a FEL model simulation, the standard free energy of the E_D-like conformation (gray) which mimics the ATPase architecture in the E_A-like states in the cryo-EM studies was lowered by an arbitrary 2.0 kcal/mol. The resulting transition network is presented using the same convention as in Fig. 5A. The size of the grey node was shrunk by 2.5fold for presentation. Varying the free energy difference from 1.6 to 4.0 kcal/mol gave qualitatively similar results. The ATPase architecture of each conformation is shown next to the node as in Fig. 5A.