



Movie 1. The transition between the conformations of dynein observed in the yeast (nucleotide free) and *Dictyostelium* (ADP bound) crystal structures. The yeast motor domain structure (PDB 3AKG) is coloured according to the scheme in Fig. 2C, with the exception that the C-terminal region after AAA6 is coloured hot pink. The structure is morphed into a model of the ADP-bound dynein that was built by aligning the individual domains of 3AKG on the 2.8Å *Dictyostelium* structure (PDB 3VKG). Discrepancies between the model and the 3VKG structure were corrected by manually with the program Coot using the electron density map of 3VKG as a guide. The AAA1L domain was used as a point of reference to align the nucleotide-free and ADP-bound conformations. The conformational changes include closure of the AAA1 site between AAA1L (blue) and AAA2L (cyan). The movement of a rigid block of domains from AAA2L (cyan) to AAA4L (yellow) allows the AAA5L domain (orange) to swing over and close the AAA4 site. This movement is accommodated by a large movement in the position of AAA6L (red) relative to AAA1L (blue). The linker (purple) moves slightly to contact AAA5L. Whether these changes are caused by ADP release or are due to structural differences between the two dyneins is discussed in the text.



Movie 2. The transition between chain A of the 2.8Å crystal structure the *Dictyostelium* motor domain and chain A of the 3.8Å crystal structure. Both structures have ADP in the AAA1 site, but in the 3.8Å structure chain A crystal packing contacts have driven a further closure of the AAA1 site. The structures are coloured as in supplementary material Movie 1. The extra C-terminal domain (that is not present in yeast dynein) is coloured grey. The structures are aligned on AAA1L. The conformational changes include the further closure of the AAA1 site compared with that observed in the presence of ADP. The AAA+ domains between AAA2L (cyan) and AAA5L (yellow) move as a rigid block, as observed in supplementary material movie 1. The N-terminal end of the linker (purple), which is close to the base of the stalk, moves around a hinge point close to the interface between linker subdomains 2 and 3 (the cleft).