

Fig. 1 Schematic illustration of the tubulin heterodimer assembly pathway [5]. CCT denotes cytosolic chaperonin, a ring-like protein complex involved in folding of tubulin subunits. Tubulin-folding cofactors B and E (TBCB and TBCE) are involved in the folding and dimerization pathway of a-tubulin monomers (light blue circle), while cofactors A and D (TBCA and TBCD) fulfil this function for b-tubulin monomers (dark blue circle). Note that TBCE (in addition to TBCD) can also dissociate tubulin dimers into a- and b-tubulin monomers (shown by backward directed arrows), leading to a reduction of the tubulin dimers pool available for microtubules polymerization. Modified from [27].

 

Fig. 2 Structural regions identified within the adenovirus L4-100 K protein: coiled-coil region (CCR, aa 439–458), RNA recognition motif (RRM, aa 383–458), Rev-like nuclear export signal (NES, aa 383–392), arginine-arginine-glycine (RGG) box (aa 727–743), containing

three RGG motifs and overlapping nuclear localization signal (NLS, aa 727–764) (from [98]).

 

Fig. 3 Visualisation of Ad L4-100 K protein alone and in the complex with hexon. a Gallery of eight EM images of the recombinant Ad2 L4-100 K protein, the averaged image, and the

structural model of the L4-100 K protein (from left to right, upper panel). The L4-100 K protein is a dumbbell-shaped molecule, consisting of two globular domains linked by a rod-like structure. The total length of the molecule is about 120 **Å**. b Gallery, the averaged image and the model of the recombinant Ad3 hexon-Ad2 L4-100 K protein complex, with the hexon in end-on view (from left to right, lower panel). One of the globular domains of the L4-100 K

protein is attached either to the distal domain or to the apical domain of the hexon trimer. c EM analysis of native proteins purified from Ad5-infected 293 cells. Scale bar 30 nm. Most of the visible structures are hexons. Some L4-100 K protein molecules and hexon–100 K protein complexes are marked with black and white arrows, respectively. The column on the right represents five images of hexon–100 K protein complexes and five images of 100 K protein

molecules (upper and lower columns, respectively) (from [94]).

 

Fig. 4 Schematic model of the predicted domains of HYPK chaperone, a Huntingtin-interacting protein. Domains are shown from left to right: acidic, putative SH3-binding and coiled coil (after [142]).