



Fig. S4 (Continued). Sequence alignments and secondary structures of Bro1 domains. Secondary structures of the Bro1 domain of ALIX (*Upper*) and Bro1p (*Lower*) (PDB entry 1zb1) are shown together with aligned primary sequences of ALIX_{Bro1} domains from 25 representative metazoan species (top sequence block), Bro1 domains from the human Brox and HD-PTP proteins (middle sequence block), and Bro1 domains from the yeast Rim20p and Bro1p proteins (bottom sequence block). ALIX_{Bro1} and Bro1p were aligned by least squares overlap of the two structures, and other sequence alignments were performed by using the ClustalW server http://npsa-pbil.ibcp.fr/NPSA/npsa_clustalw.html [Combet C, Blanchet C, Geourjon C, Deléage (2000) NPS@: Network protein sequence analysis. *Trends Biochem Sci* 25:147–150]. Residues highlighted in yellow make contacts with CHMP4A in the ALIXBro1-CHMP4A_{205–222} structure and residues italicized in bold and red block ALIX binding and HIV-1 budding when mutated to Asp.