

Supplemental Materials

Molecular Biology of the Cell

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Supplemental Figure. Sequence alignment of human ESCRT-III family proteins discussed in this study with the *Sulfolobus acidocaldarius* ESCRT-III ortholog Saci_1373. Note that residues 1-211 of Saci_1373 were used in the alignment, removing the archaeal-specific winged helix-like domain of this protein (Samson et al., 2011). Sequence alignment was achieved with ClustalW (<http://www.ebi.ac.uk/Tools/msa/clustalw2/>) and shading performed with Boxshade (http://www.ch.embnet.org/software/BOX_form.html). Residues identical in >50% of the sequences are outlined in black, and residues homologous in >50% of the sequences in gray. The table of pairwise comparisons gives percent sequence identity and homology for each pair. Values were generated using Needle (http://www.ebi.ac.uk/Tools/psa/emboss_needle/) with default parameters. ND- it was not possible to generate a meaningful pairwise alignment of IST1 and Saci_1373.

