

Supplemental Materials

Molecular Biology of the Cell

Dobro et al.

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.

CHMP1B 1 -----MSNMEKHLFNLKFAAKELSRSAKKCDKKEEKAEKAKIKKAIQ
 CHMP2a 1 ----MDLL-FGRRKT---PEELLRQNQRALNRAMRELDREERQKLETQEKKIADIKKMAK
 CHMP3 1 ----MGLFGKTQEKP---PKELVNEWSLKIIRKEMRVVDRQIRDIQREEEKVKRSVKDAAK
 Saci_1373 1 MFDKLSIIFNSDRKRKVHLSKATTEISLKLKEQODRLDEAIRRLRERDKDLFEKVIIRSQI
 IST1 1 -MHKLSVEAPPKILVERYLIEIAKNYNVPYEPDSVVMMAEAPPGVETDLIDVGFDDVKKG

CHMP1B 42 KGNMEVARTHAENAIROKNOAVNFLRMSARVDAVAARVOTAVTMGKVTKSMAGVVKSMDA
 CHMP2a 53 QGQMDAVRIMAKDLVRTRRYVRKFVILMRANIQAVSLKIQTLSNNSMAQAMKGVTKAMGT
 CHMP3 54 KGQKDVCIVLAKEMIRSRKAVSKLYASKAHMNSVLMGMKNQI AVLRLVAGSLQKSTEVKKA
 Saci_1373 61 EGDIA RATIYAQEI SDIRKMIKI IYTAYLAIEKVR LKLDTVQELQGVSLVLPV MRILGE
 IST1 60 GPGRGGSGGFTAPVGGPDGTVPMPPMPMPMPMP SANTPFSYPLP-KGPSDFNGLPMGTYQA

CHMP1B 102 TLKTMN--LEKISALMDKFEHQFETLDVQTTQOMEDTMSSTTTLTTPQNQVDMLLQEMADE
 CHMP2a 113 MNRQLK--LPQIQKIMMEFERQAEIMDMKEEMNDAIDDAMGDEEDEEESDAVVSQVLDE
 CHMP3 114 MQSLVK--IPEIQATMRELSKEMMKAGIIEEMLEDTFESMDDQEMEEEAEMEIDRILFE
 Saci_1373 121 LKEQVRGIAPEVALALDSITSSVNSTAIETGALSEKTFVPTVADEQAKQIMEEAOKMAEV
 IST1 119 FPNIHPPQIPATPPSYESVDDINADKNISSAQIVGPGPKPEASAKLPSRPADNYDNFVLP

CHMP1B 160 AGLDINMELP-----QGQTSVGTSVASAEQDELSQRLARLRDQV
 CHMP2a 171 LGLSLTDELSNLPSTGGSLSVAAGGKKAEEAASALADADADLEERLKNLRD-
 CHMP3 172 ITAGALGKAPS KVTDALPEPEPPGAMAASEDEEEEEEALEAMQSRLATLRS--
 Saci_1373 181 KVRELLPELP-----HPPSELPKRVAKQVQSSNKKS-----
 IST1 179 ELPSVPDTLP-----TASAGASTSASEDIDFDDLSRRFEE LKKKT

	CHMP1B	CHMP2A	CHMP3	Saci_1373	IST1
CHMP1B		26/45	21/49	15/39	15/26
CHMP2A			27/52	18/36	14/24
CHMP3				19/37	18/31
Saci_1373					ND
IST1					