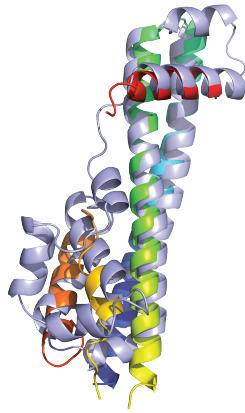
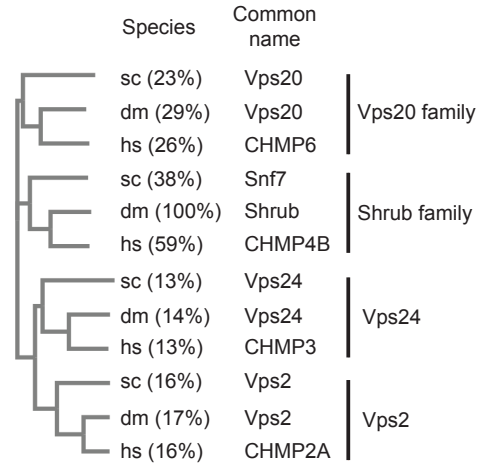


A

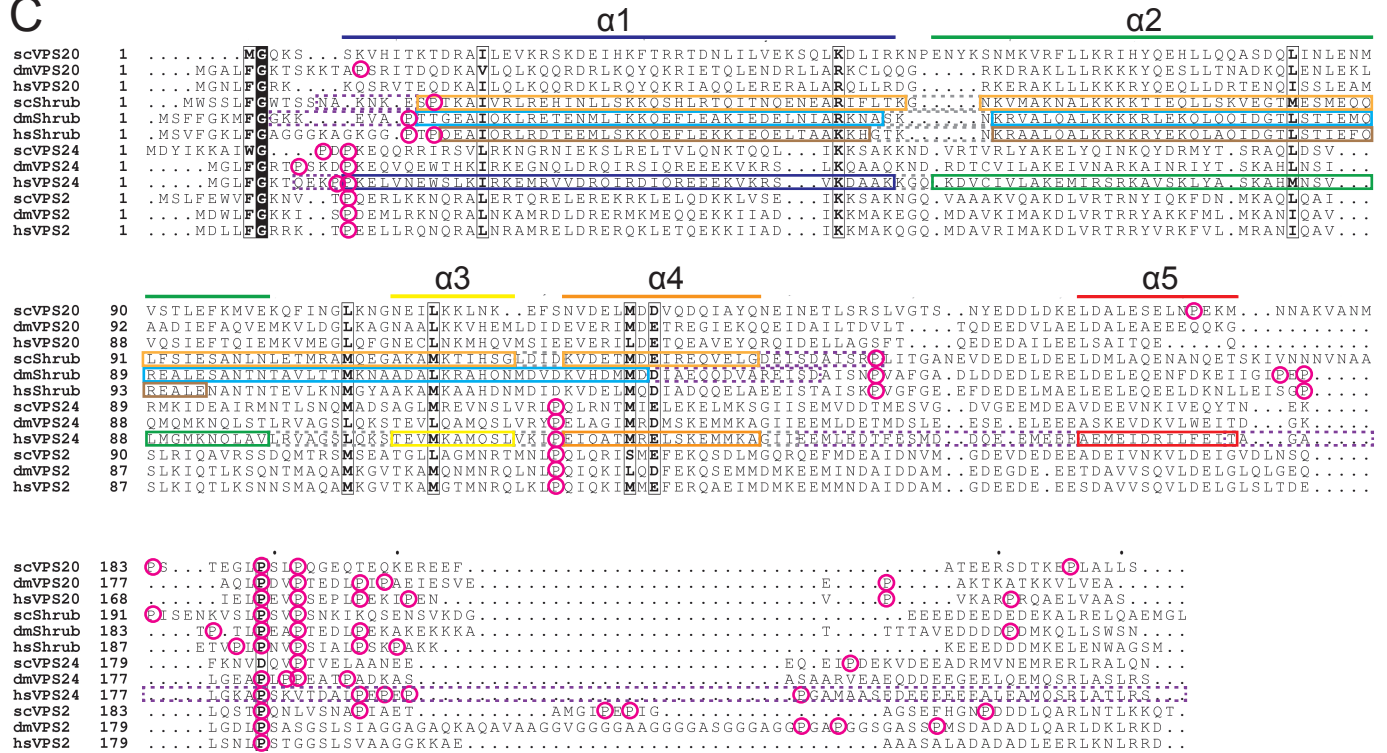


hsVps24/CHMP3 (PDB 3FRT)
scIST1 (PDB 3GGY)

B



C

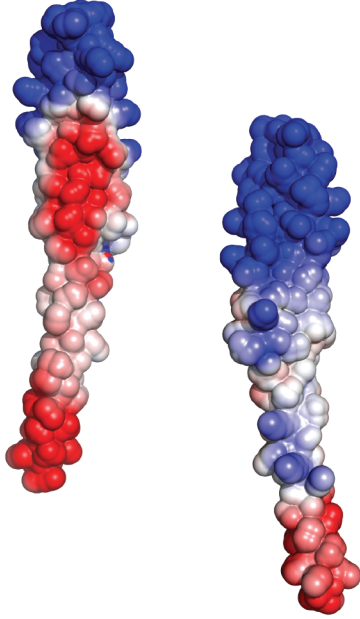


Unstructured in crystal: Structured Linker: Proline

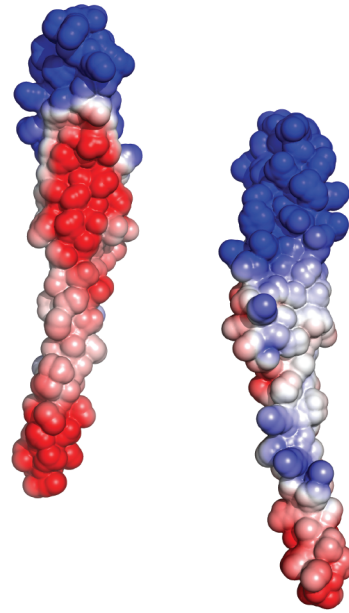
hsShrub (CHMP4B): PDB 4ABM
scShrub (SNF7): PDBs 5FD7, 5FD9
hsVps24 (CHMP3): PDBs 3FRT, 2GD5

Figure S1, related to Figure 1. *A*, Superposition of the closed helical bundles of human Vps24/CHMP3 (colored on a sliding scale from N- (blue) to C-terminus (red)) and yeast IST1 (light blue) *B*, Phylogenetic tree of four core ESCRT-III members across yeast, fly and human sequences. The percent identity relative to the Shrub protein from *Drosophila melanogaster* is listed in parentheses. *D*, Primary sequence alignment of proteins in the phylogenetic tree, annotated using crystal structures information when available. Helical numbering is based on the representative crystal structure. Sc: *Saccharomyces cerevesiae*; dm: *Drosophila melanogaster*; hs: *homo sapiens*.

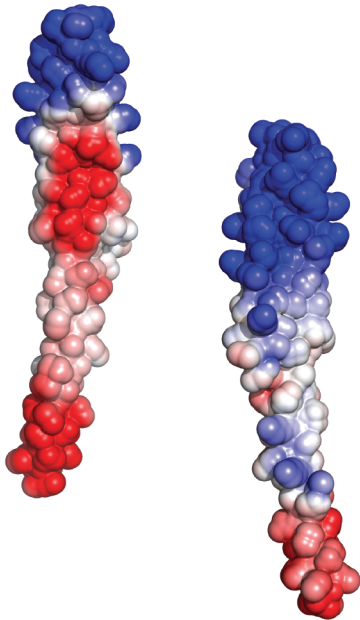
Porifera
(*Amphimedon queenslandica*)



Placozoa
(*Trichoplax adherens*)



Cnidaria
(*Nematostella vectensis*)



Bilateria
(*Drosophila melanogaster*)

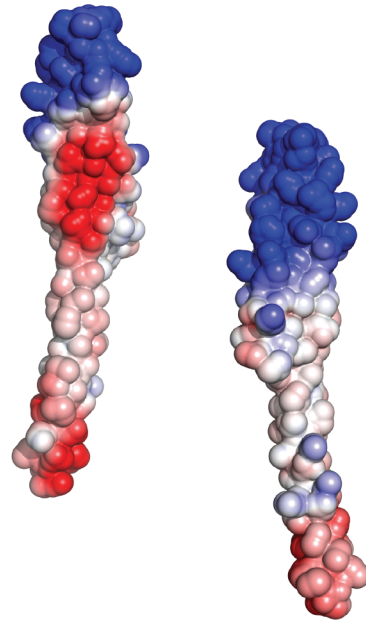


Figure S2, related to Figure 2. Homology models for diverse metazoan orthologs based on the structure of fly Shrub. The structures are shown as an open book representation of the putative monomer-monomer interface, and colored by charge (blue, positive to red, negative).

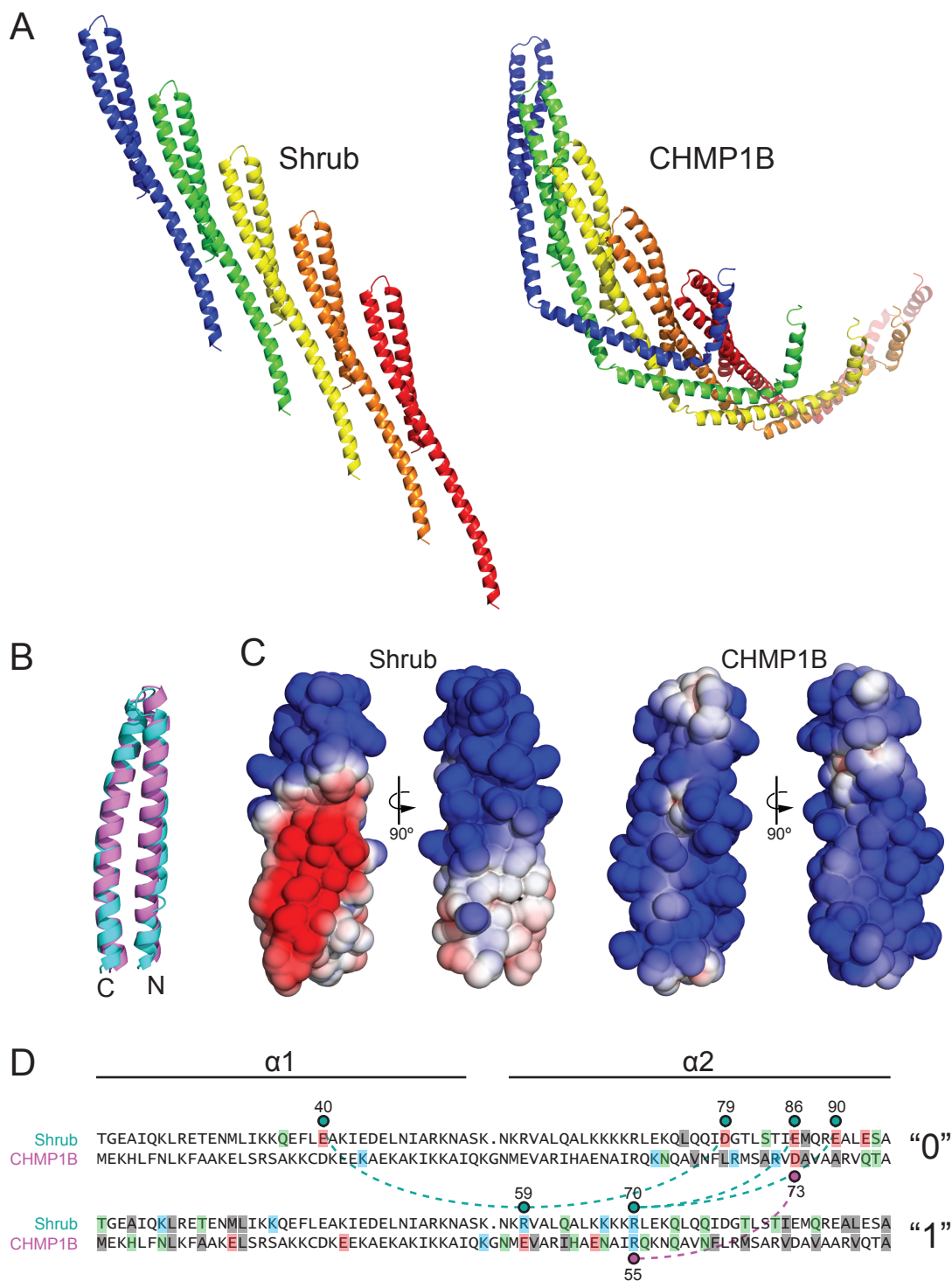


Figure S3, related to Figure 1. Comparison of the Shrub lattice with packing of CHMP1B subunits of a CHMP1B/IST1 copolymer. *A*, Cartoon representation of a five protomer unit from the Shrub lattice and the CHMP1B subunit in CHMP1B/IST1 copolymer filaments. Structures are aligned based on the helical hairpin of each “yellow” protomer. *B*, Superposition of the core helical hairpins from Shrub (18-95) and CHMP1B (4-82). *C*, Electrostatic surface representation of the Shrub and CHMP1B hairpins (blue, positive to red, negative). *D*, Primary sequence alignment of Shrub (18-95) and CHMP1B (4-82). Residues at the contact interfaces (within 5 Å of the neighboring protomer) are boxed and colored by class (acidic, red; basic, blue; polar, green; non-polar, gray). Residues involved in salt-bridge interactions (dotted lines) indicated by residue number and with a colored circle above (Shrub) or below (CHMP1B) the aligned sequences.