Supplemental information

Structure of the endosomal Commander

complex linked to Ritscher-Schinzel syndrome

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Table S1. Cryo-EM data collection, refinement, and validation statistics. Related to Figures 1 and 4.

	Retriever VPS35L-VPS26C-VPS29	CCC COMMD1 to COMMD10-CCDC22-CCDC93	
Data collection and processing			
Magnification	130,000	75,000	
Voltage (kV)	200	300	
Electron exposure (e⁻/Å²) Defocus range (μm)	$61.7\ e^-/\text{Å}^2$ -2, -1.6, -1.2, -0.8 μm	$43.55/42.73\ e^-/\text{Å}^2$ -2, -1.8, -1.6, -1.4, -1.2 μm	
Pixel size (Å)	0.525	1.084	
Symmetry imposed	C1	C1	
Programme used	RELION/cryoSPARC	cryoSPARC	RELION
Initial particle images (no.)	297,077	2,666,858	1,321,587
Final particle images (no.)	119,564	153,104	20,034
Map resolution (Å)	4.3[a]	3.12	3.53
FSC threshold	0.143	0.143	0.143
Refinement			
Initial model used		Colabfold	CryoSPARC/Colabfold
Model resolution range (Å)		3.49	3.98
FSC threshold		0.5	0.5
Map sharpening B factor (Å²)		83	- 24
Model composition			
Non-hydrogen atoms		29276	36574
Protein residues		1837	2298
R.m.s. deviations			
Bond lengths (Å)		0.005	0.002

Bond angles (°)		1.118	0.561
Validation			
MolProbity score		1.41	1.49
Clashscore		6.01	6.24 (90th percentile)
Poor rotamers (%)		0.12	0
Ramachandran plot			
Favored (%)		97.63	97.18
Outliers (%)		0.17	0
EMDB ID		EMD-28825	EMD-28827
PDB ID		8F2R	8F2U

a. This is significantly overestimated due to preferred particle orientations.