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Supplemental Information

An unconventional TOG domain

is required for CLASP localization

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| Α | HR AHR BHR CHR DHR EHR F HR AHR BHR CHF | R DHR EHR F | Model confidence Very low (pl | : LDDT < 50) | Very high (pLDDT > 90) |
|---|---|-------------|----------------------------------|-----------------|--|
| | | A | ItCLASP | | |
| | | | CeCLS-1 | | |
| | | | CeCLS-2 | | Contraction of the second s |
| | | > | CeCLS-3 | | Contraction of the second seco |
| | | · · | CiCLASP | | Contraction of the second seco |
| | | <i>•</i> | mMAST | | |
| | | Dr | CLASP1 | | |
| L | | Dri | CLASP2 | | |
| C | | Gg | CLASP1 | | |
| G | | Ggi | CLASP2 | ÷ | |
| ŀ | | Hs | CLASP1 | | |
| ŀ | | Hst Hst | CLASP2 | | |
| М | | Mm | CLASP1 | | Contraction of the second s |
| М | | Mm(| CLASP2 | | |
| x | | хіс | LASP1a | | |
| x | | хіс | LASP1b | | |
| | × | 5 | - | 7 | $\overline{\mathbf{v}}$ |

FIGURE S1 related to Figure 1. The CTD of CLASP proteins folds like a TOG domain.

(A-B) AlphaFold2 3D structure prediction of the CTDs of 16 CLASP proteins from various species. Left: side view. Right: end-on view. (A) Heat Repeats (HR) A-F are color-coded. (B) Model confidence is color-coded based on the AlphaFold2 pLDDT score (Local Distance Difference Test)³². (*At: Arabidopsis thaliana, Ce: Caenorhabditis elegans, Ci: Ciona intestinalis, Dm: Drosophila melanogaster, Dr: Danio rerio, Gg: Gallus gallus, Hs: Homo sapiens, Mm: Mus musculus, XI: Xenopus laevis*).



FIGURE S2 related to Figure 2. A conserved arginine in the CTD of CLASP proteins is essential for their proper sub-cellular localizations.

(A) Size exclusion chromatography of the CLS-2-CTD with or without tubulin, and of tubulin alone. Coomassie staining of the fractions of interest is shown on the right. (B-F) Left: Immunofluorescence images of (B,C) HeLa or (D-F) DLD-1 cells transiently expressing (B) WT or R1481A EGFP-*Hs*CLASP1, (C-F) WT or R1458A EGFP-*Hs*CLASP2, and stained for (B-D) the centromeric marker ACA (bottom right: zoom on one kinetochore pair. Scale bar on zoom, 1 μ m), (E) the trans-Golgi marker TGN46, (F) the focal adhesion marker Paxillin. Scale bars, 5 μ m. Right: Quantification of mean intensity of WT or mutant CLASPs at (B-D) kinetochores, (E) the Golgi and (F) the cell cortex. Error bars: SEM for B-D, SD for E,F. Sample sizes (N kinetochores, n areas) are indicated on each graph. Unpaired t-tests, p<0.0001. (G) Yeast-two-hybrid interaction tests between the CLS-2-binding domain (CBD) of CeHCP-1, and the TOG2, TOG3 and wild-type or R970A CTD of CeCLS-2. In the presence of 5 mM 3-AT (3-Amino-1,2,4-Triazole), only the wild-type *Ce*CLS-2 CTD interacts with the CBD of *Ce*HCP-1.



FIGURE S3 related to Figure 3. GOLGA4 is required for *Hs*CLASP1 Golgi localization.

(A) Western blot of wild-type and CRISPR/Cas9-engineered mNG-mAID-*Hs*CLASP1 DLD-1 cells using an anti-*Hs*CLASP1 antibody. (B) Immunofluorescent images of the trans-Golgi marker TGN46 (red), endogenously-tagged mNeonGreen-*Hs*CLASP1 (green), the Golgin protein GOLGA4 (magenta) and DNA (blue) in DLD-1 cells transfected with Luciferase- (top) or GOLGA4-targeting siRNAs (bottom). Scale bars, 5 μ m. (C) Quantification of GOLGA4 intensity at the Golgi relative to TGN46 in siLuciferase or siGOLGA4-transfected DLD-1 cells. Unpaired t-test, p<0.0001. (D) Quantification of mean mNeonGreen-*Hs*CLASP1 intensity at the Golgi relative to TGN46 in siLuciferase or siGOLGA4-transfected DLD-1 cells. Error bars, SD. Sample sizes (n areas) are indicated on each graph. Unpaired t-test, p<0.0001.