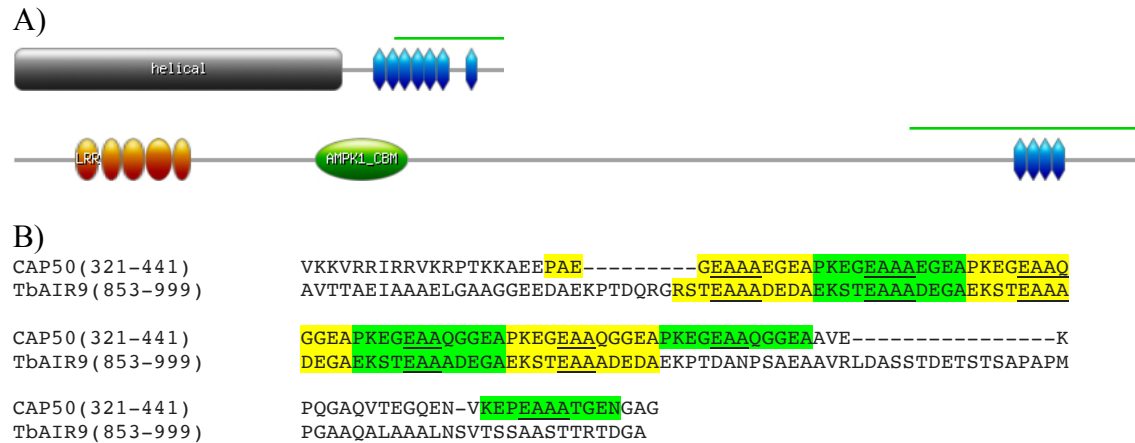


Supplementary table 1: DNA oligonucleotides used in this study

Name	Purpose, Restriction site	Sequence
pHD BirA for	BirA* amplification, <i>Ascl</i>	ATAGGGCGCGCCGAACAAAACTCATCTCAGAAG
pHD BirA rev	BirA* amplification, <i>PacI</i>	TATTTAATTAAGTCGAGCTTCTCTCGCTTCTC
CAP5.5ORFfor	CAP5.5 ORF amplification, <i>FseI</i>	ATAGGCCGGCCATGGGTTGTGGTGGATCAAAG
CAP5.5ORFrev	CAP5.5 ORF amplification, <i>Ascl</i>	TATGGCGCGCCCATCACTGTCACTTTCATCAC
Tb927.6.5070_RNAi_for	CAP52 RNAi, <i>BamHI</i> , <i>HindIII</i>	ATAGGATCCAAGCTTCTGTTCTTGCAATGAGC
Tb927.6.5070_RNAi_rev	CAP52 RNAi, <i>XhoI</i> , <i>XbaI</i>	ATACTCGAGTCTAGAGGAACCTTGAGCCTTC
Tb927.4.1300_RNAi_for	CAP42 RNAi, <i>BamHI</i> , <i>HindIII</i>	ATAGGATCCAAGCTTATGTGACTGCTCTGTTTCG
Tb927.4.1300_RNAi_rev	CAP42 RNAi, <i>XhoI</i> , <i>XbaI</i>	ATACTCGAGTCTAGATGACAACCATAATGTTG
Tb927.11.2610RNAi2_for	CAP50 RNAi, <i>BamHI</i> , <i>HindIII</i>	ATAGGATCCAAGCTTGTACGGAGAAAGAAATCACC
Tb927.11.2610RNAi2_rev	CAP50 RNAi, <i>XhoI</i> , <i>XbaI</i>	ATACTCGAGTCTAGACCTGCTGGCGAGGCGGTCAACAGC
Tb927.6.5070_ORF_for	CAP52 ORF amplification, <i>FseI</i>	ATAGGCCGGCCATGCGAGCAAACCAATTGAGCG
Tb927.6.5070_ORF_rev	CAP52 ORF amplification, <i>Ascl</i>	TATGGCGCGCCCATACGCCCTCCACAGTGGACC
Tb927.4.1300_ORF_for	CAP42 ORF amplification, <i>FseI</i>	ATAGGCCGGCCATGTCGACTGCTCTGTTCTGTTTC
Tb927.4.1300_ORF_rev	CAP42 ORF amplification, <i>Ascl</i>	TATGGCGCGCCCGCAACCGCCGCTTAAATGTC
Tb927.11.2610_ORF_for	CAP50 ORF and ΔC amplification, <i>FseI</i>	ATAGGCCGGCCATGGCAGCCGCTGTTACAATTG
Tb927.11.2610_ORF_rev	CAP50 ORF and ΔN amplification, <i>Ascl</i>	TATGGCGCGCCCCGACGTGCGTTTCGACTTGGGTG
Tb927.11.2610 ΔC _rev	CAP50 ΔN amplification, <i>Ascl</i>	TATGGCGCGCCCATCAATTTGGTCAAAAGCGATTTCAGC
Tb927.11.2610 ΔN _for	CAP50 ΔC amplification, <i>FseI</i>	ATAGGCCGGCCATGCGTAATGGACCCCGCATC
PFRAqPCRf	qPCR	CGTTGGAGATGTTTGGACCT
PFRAqPCRr	qPCR	GCACGGTACTCCACCATCTT
1300q_for	qPCR	CGGTTGGAGGAGGATGCTGG
1300q_rev	qPCR	GTATTGACATGGAGTCACCGACA
5070q_for	qPCR	GATTCCAGTGGAGAGCCTGGGAAG
5070q_rev	qPCR	GCTTCCACGCCAATGGTGCG
Tb927.11.2610qfor	qPCR	GGAGGTTGAGGAACAGCACG
Tb927.11.2610qrev	qPCR	CTCCATCTCGGCGGGCAGTT

Supplementary Figure 1



Sequence Analysis of CAP50 and AIR9. A) Domain organization. CAP50 contains a N-terminal α -helical region (grey box). Several repeats can be detected in the C-terminal, unstructured region (green bar). In AIR9, Leucin-Rich repeats (LRR, orange) and a AMP-activated protein kinase (green) can be identified in the N-terminal region, followed by longer, structured repeats (not shown here). Again, repeats can be identified in the intrinsically unstructured region at the C-terminus. B) Sequence alignment of the two repeat-containing regions of CAP50 and TbAIR9. The individual repeats are highlighted. The common EAAA-motif is underlined.

Method: Sequence Analysis

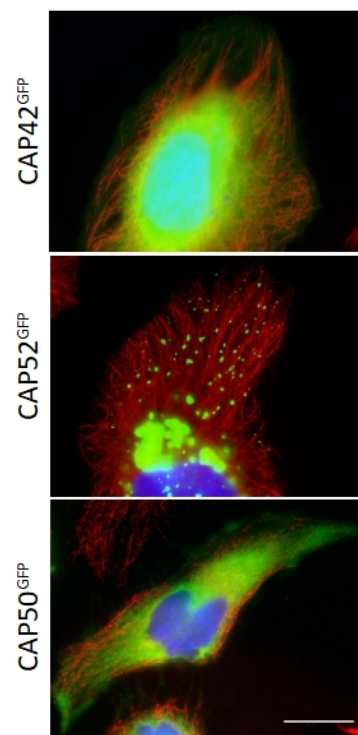
NCBI BLAST have been used to identify similarities to other sequences using the UniProt database. Domain analysis were performed, using SMART (Letunic et al. (2020) Nucleic Acids Res doi: 10.1093/nar/gkaa937), prediction of intrinsically unstructured regions using IUPRED2 (Mészáros et al. 2008, doi.org/10.1093/nar/gky384). Repeats have been identified using EMBOSS dotplot (Rice et al 2010, [10.1016/s0168-9525\(00\)02024-2](https://doi.org/10.1016/s0168-9525(00)02024-2)) & HHRepID (Zimmermann, et al. 2018, doi.org/10.1016/j.jmb.2017.12.007).

>CAP52_Tb927.6.5070
MRANPI¹RRKERETALS²VRQRELEELR³QKAQLGEELGMELSALEGDNLAAAF⁴PVIQYCGSRPKDKAKKIPVESLGSVMN⁵
QFEIAIKAISQNNRDIEQQITDLNRTIGVEAQRFTKLKRHSKELADATGVSLDPNAVQHLAGKSRDGEDCSGGLKELEET⁶
TVVLEERKALVEKEIRAARQLVKKKEEAVLAMSSALESRQEEIDQLNRLYNDIRVVDRDIKCEKETLREIISEHDIVDTK⁷
LNEA⁸IERNVSRTRL⁹LIEQG¹⁰INEIKTEIADSVSVSRRGQ¹¹ERV¹²MKAQEF¹³RIDQLEKRLDCINKALKNNHLTRDVEAIVSHKW¹⁴
AAAGDALVAAT¹⁵PEDESMYDIEAI¹⁶IP¹⁷QERCHPAIYNLLTEKERLAR¹⁸RIISLGI¹⁹IAKEKVEIDALACKAEALARECQQA²⁰I
QELDHVASAAAYEEMORVEAMEY²¹IO²²KORLHYS²³DLFLKEMWKLKTKNOGPI²⁴LWRAY²⁵

>Tb927.9.11540
MADVSAADSAQVELERLNDVIDKYTCQVEHIDNLLQEEENNDSVSRQIAEYQSALESHPENIPAEDALEVITRLNT
LKIVQRRNHLLKENGQTQNRLLERSNVLLNATKTFDHIVDVTGWHDKFLFDAEDLRKSVADIREMSNIEAVVQKELRVA
QGI IKKKEAALRQLLEELVEQGKEQEAVLNNVYNDIRVKERDCSEVEMQLVRLRKSVAKTDEALAVFDLHNQNASLAYMES
DRDYLRDSVAEMKSTTRRQDNV IKAQLTRQQQLQTRLDVIMKSLREMKLDDKKYERNIPKSALVPSASREEPEDVSKILPE
SECIPVPTYRLLHKNNAELRVIMRKNMPLVLEKNAVIEAMLEAGLAKYGSALITTYKEQQDLRQNKMDLIELMDDLQQQH
SNYLEKLEFELRLQNAALKKKMYRSTROHAPLKGTRPMR

Pairwise alignment of CAP52 with Tb927.9.11540 using EMBOSS Needle (www.ebi.ac.uk/Tools). Sequences are 24% identical and 42.2% similar.

Supplementary Figure 3



Expression of GFP-tagged CAP42, CAP52 and CAP50 in HeLa cells showed no co-localization of the proteins with mammalian microtubules. Cells were stained with anti-tubulin (red), anti-GFP (green) and the DNA was stained with DAPI. Scale bar = 20 μm