

**Ska3 Ensures Timely Mitotic Progression by Interacting Directly With Microtubules
and Ska1 Microtubule Binding Domain**

Maria Alba Abad¹, Juan Zou¹, Bethan Medina-Pritchard¹, Erich, A. Nigg², Juri Rappsilber¹,
Anna Santamaria³ and A. Arockia Jeyaprkash^{1*}.

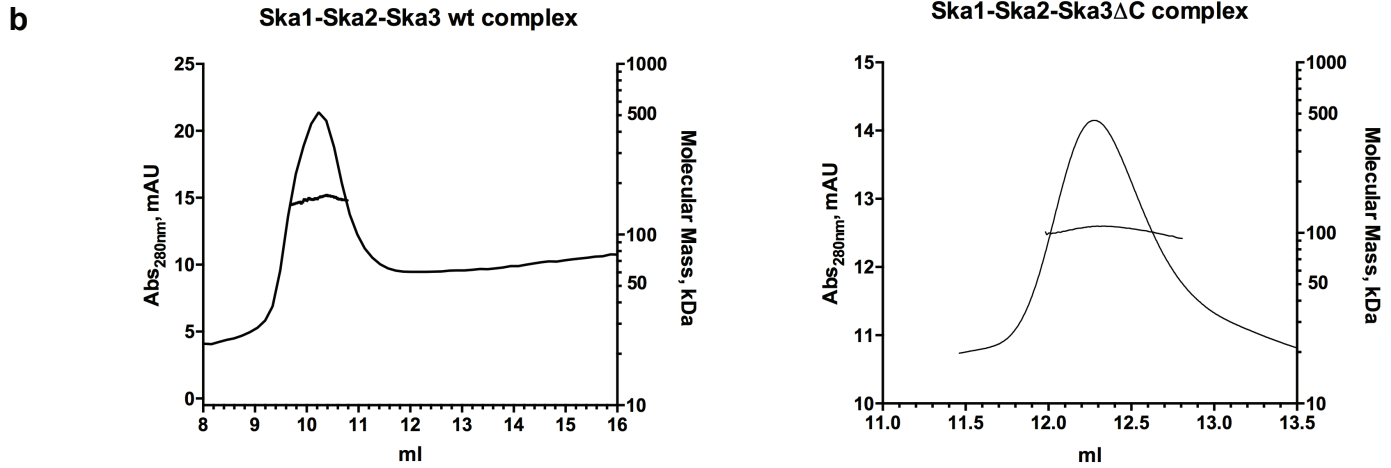
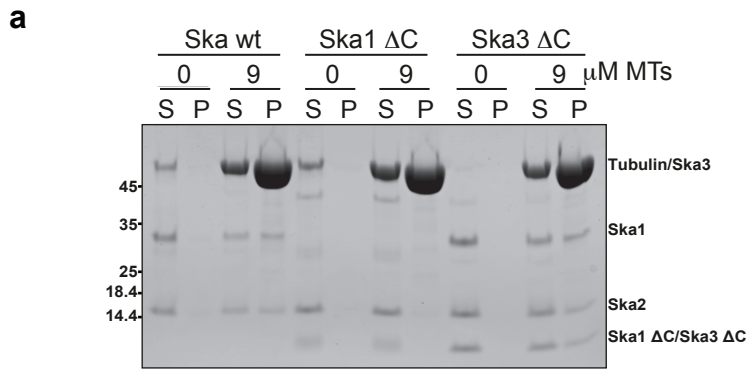
¹*Wellcome Trust Centre for Cell Biology, University of Edinburgh, Michael Swann Building, Max
Born Crescent, Edinburgh, EH9 3BF*

²*Biozentrum, University of Basel, Klingelbergstrasse 50/70, CH-4056 Basel, Switzerland*

³*Cell Cycle and Cancer, Group of Biomedical Research in Gynecology, Vall d'Hebron Research
Institute, Barcelona, Spain*

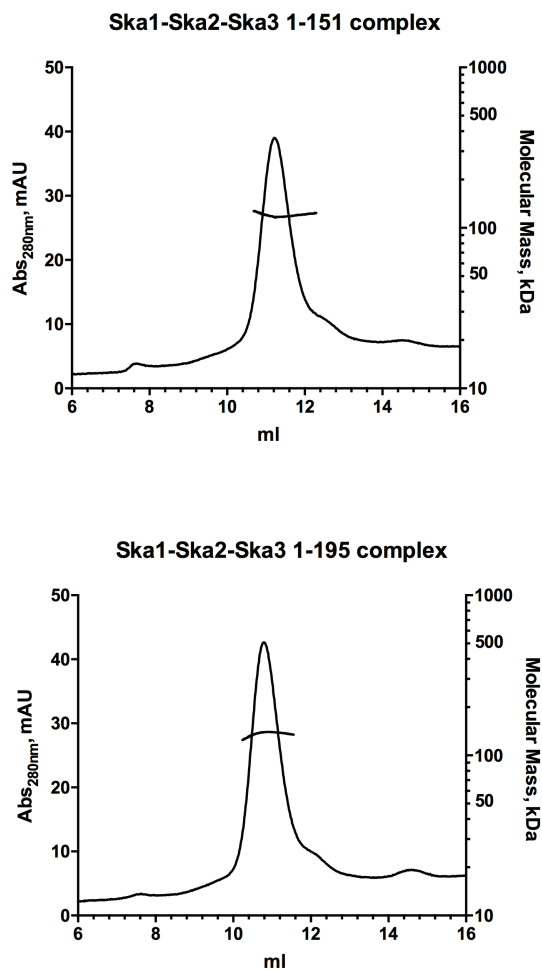
Correspondence: ajeyapra@staffmail.ed.ac.uk

Running title: Ska3-microtubule interactions



	Measured MW in kDa (Calculated MW)	Quaternary Structure
Ska1-Ska2-Ska3	169kDa (180kDa)	Homodimer
Ska1-Ska2-Ska3 Δ C	121kDa (112kDa)	Homodimer

Figure S1. a) Representative SDS-PAGE gels of cosedimentation assays comparing the microtubule binding ability of the wt Ska complex, Ska1 Δ C and Ska3 Δ C as shown in **Fig. 1d**. **b)** SEC-MALS profile of the wt Ska complex (left) and Ska3 Δ C (right). The analysis shows that the deletion of the C-terminal domain of Ska3 does not alter the overall oligomeric state of the complex.

a

	Measured MW in kDa (Calculated MW)	Quaternary Structure
Ska1-Ska2-Ska3 1-151	121.8kDa (122kDa)	Homodimer
Ska1-Ska2-Ska3 1-195	132.9kDa (132kDa)	Homodimer

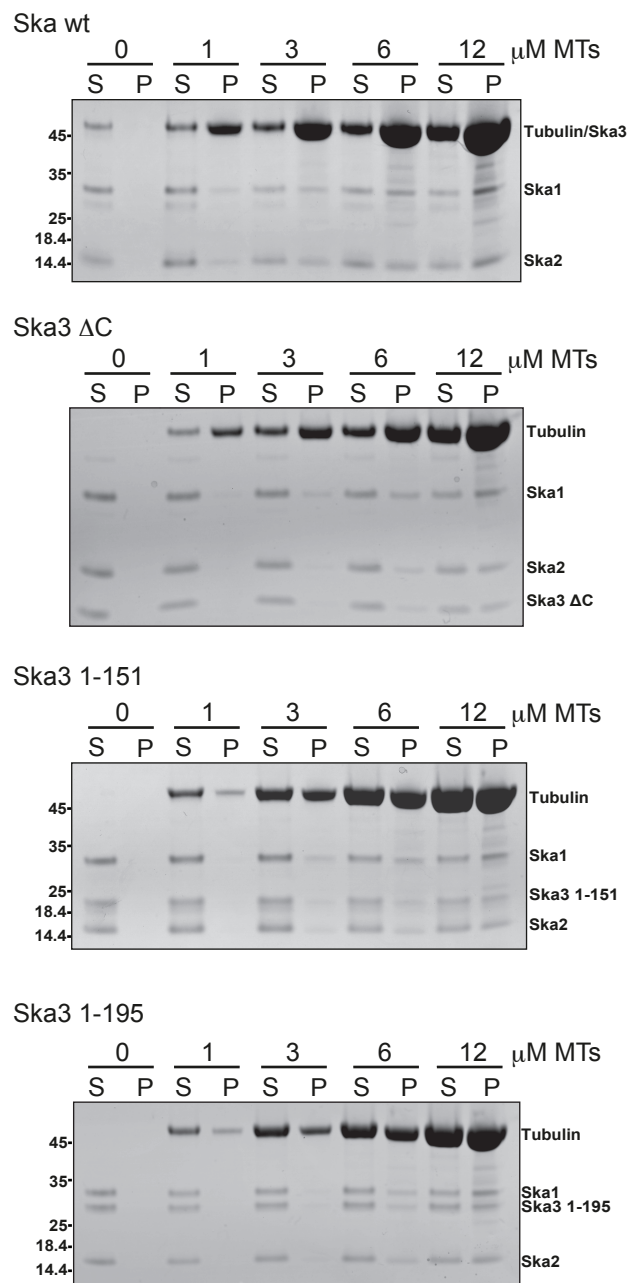
b**c**

Figure S2. a) SEC-MALS profiles of the Ska1-Ska2-Ska3 1-151 (top) and Ska1-Ska2-Ska3 1-195 (bottom) complexes. The analysis shows that the truncations do not affect the oligomeric structure of the complex. **b)** Representative SDS-PAGE gels of cosedimentation assays comparing wt Ska complex and Ska3 Δ C with Ska1-Ska2-Ska3 1-151 and Ska1-Ska2-Ska3 1-195 as shown in **Fig. 2a**. **c)** Representative western blot showing the level of depletion obtained in HEK293T with Ska1 and Ska3 double siRNA after 72 hours of treatment.

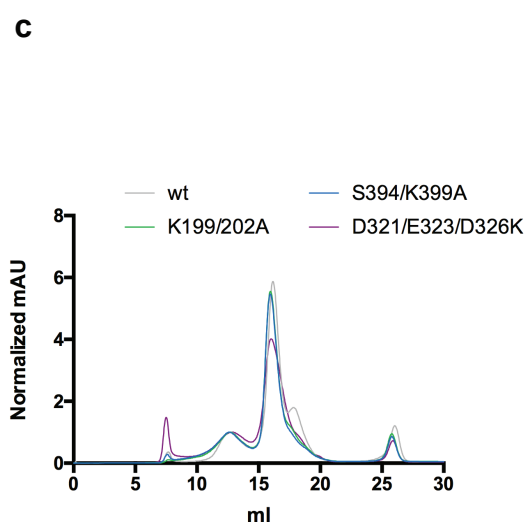
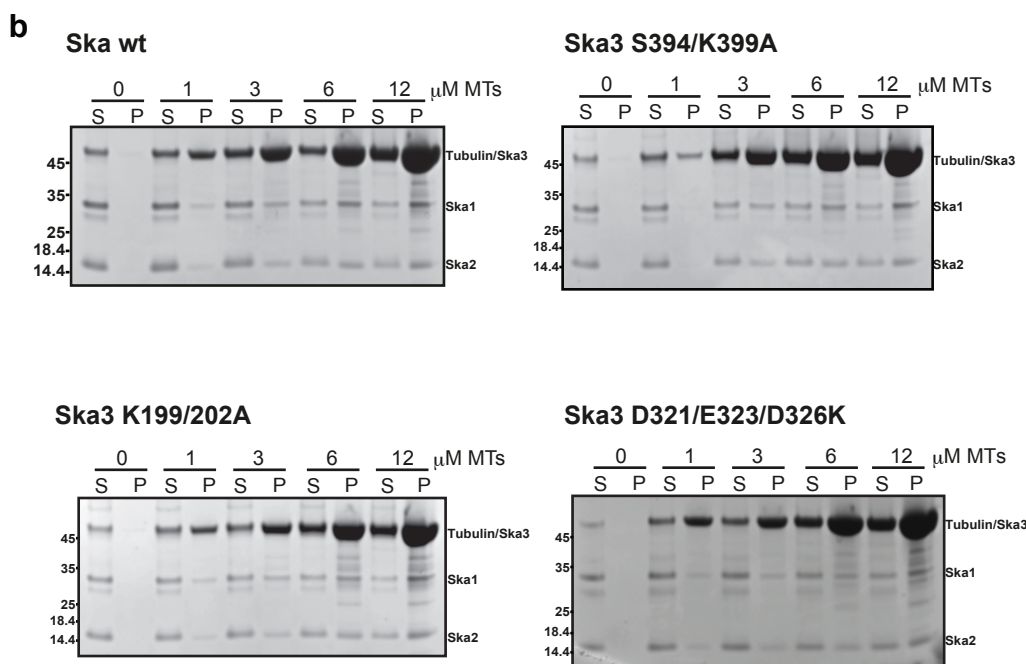
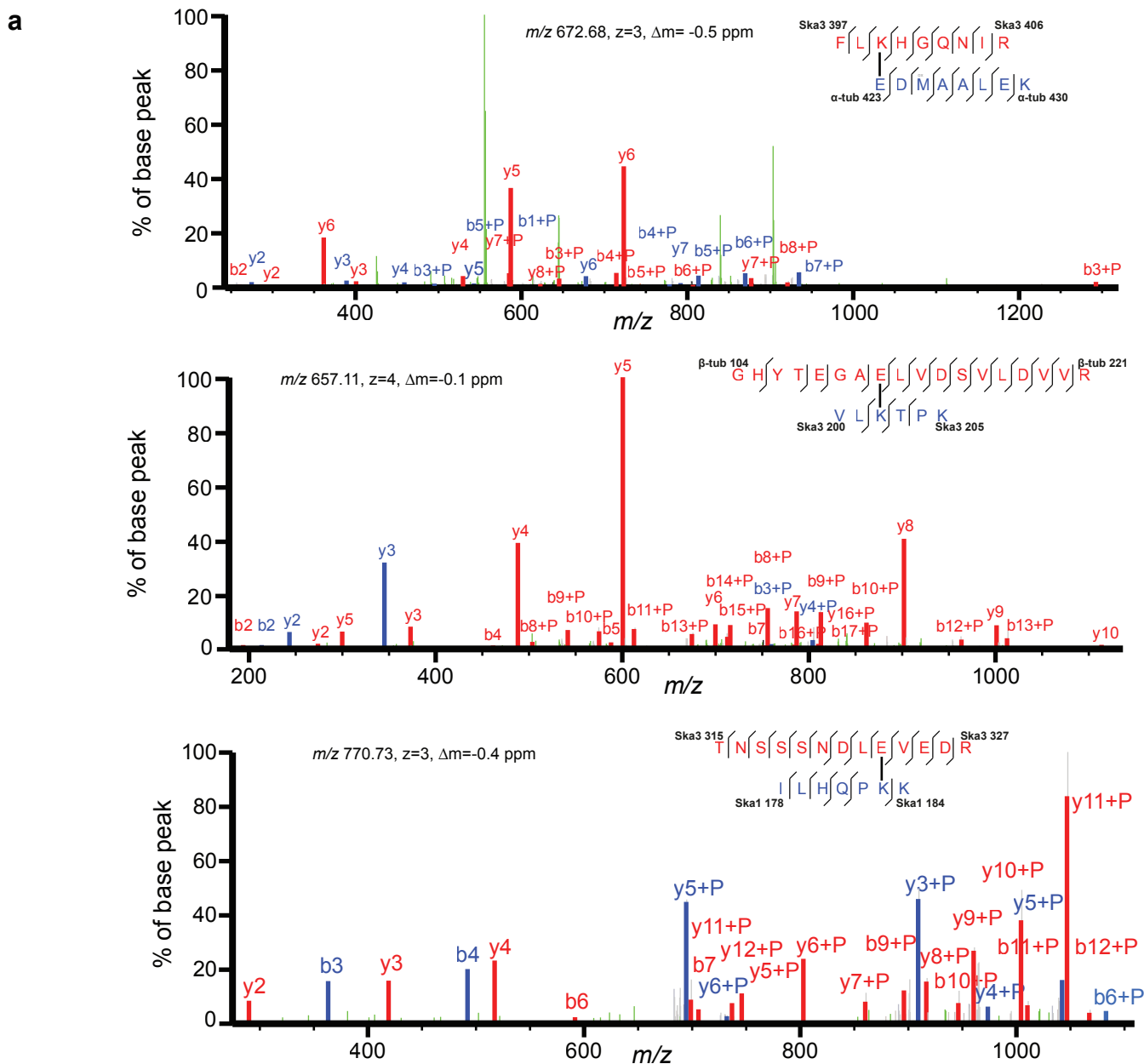


Figure S3. a) High resolution fragmentation spectra of a few representative cross-linked peptides. **b)** Representative SDS-PAGE gels of MT-cosedimentation assays comparing wt Ska complex and Ska3 point mutants (Ska3 K199/202A, S394/K399A and D321/E323/D326K) as shown in Fig. 3c and d. **c)** Comparison of the size exclusion chromatograms of all the mutants tested in MT-cosedimentation assays shown in Fig. 3c and d. Analysis shows that all mutants behave identically to the wt Ska complex.

Myc-V	+	-	-	-	-	+	-	-	-	-
Myc-Ska1	-	+	+	+	+	-	+	+	+	+
mCherry-V	+	-	-	-	-	+	-	-	-	-
mCherry-Ska3	-	+	-	-	-	-	+	-	-	-
mCherry-Ska3 K199/202A	-	-	+	-	-	-	-	+	-	-
mCherry-Ska3 K394/399A	-	-	-	+	-	-	-	-	+	-
mCherry-Ska3 D321/323/326K	-	-	-	-	+	-	-	-	-	+

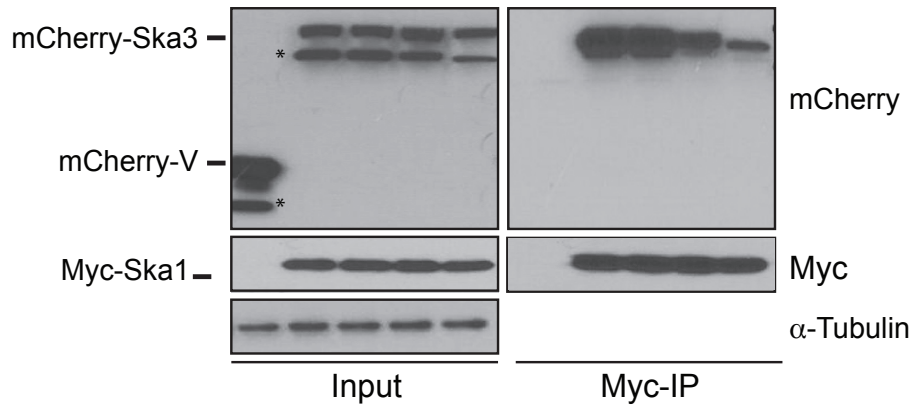


Figure S4. Combinations of Myc-Ska1 and mCherry-Ska3 versions as depicted in the figure were expressed in HEK-293T cells and cells were harvested after 36 hours. Myc-empty vector or Myc-Ska1 was then immunoprecipitated using anti-Myc antibodies, resolved by SDS-PAGE and co-immunoprecipitation of mCherry-Ska3 versions was resolved by Western blotting.