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## **Supplemental Information**

## Structural Characterization of the Chaetomium

### thermophilum TREX-2 Complex and its Interaction

## with the mRNA Nuclear Export Factor Mex67:Mtr2

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#### SUPPLEMENTARY MATERIAL

# Structural Characterization of the *Chaetomium thermophilum* TREX-2 Complex and its Interaction with the mRNA Nuclear Export Factor Mex67:Mtr2

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#### **Supplementary Experimental Procedures**

**Strains and plasmids:** *ctTHP1* was cloned into the BamHI and EcoRI sites of pET-Duet-1 (Novagen) in frame with the His<sub>6</sub> tag, with *ctSEM1* cloned in the second multiple cloning site (MCS) via NdeI/XhoI. *ctSAC3-*<sup>M415-755</sup> together with an additional ribosomal binding site was cloned into EcoRI/Pst1 sites of pET-Duet-1-HIS<sub>6</sub>-*ctTHP1-ctSEM1*. *ctSUS1* was cloned into BamHI/SacI in frame with a HIS<sub>6</sub> tag, whereas *ctCDC31* was cloned between the NdeI and XhoI sites in the second MCS. *ctSAC3-CID*<sup>1085-1170</sup> was inserted between NdeI and BamHI sites of pET24d-GST-TEV. For TREX-2, reconstitution *ctSAC3*<sup>1-1191</sup>-FLAG was inserted at the NdeI/BamHI sites of YEplac112(TRP1)-pGal1-10-pA-TEV(Leu2d). His<sub>6</sub>-*ctSUS1* was cloned in the P1 site of YEplac195(URA1)-P2-pGal1-10-P1 and *ctCDC31* was cloned in the P2 site. For pull-down assays, *ctMLP1-C* and truncations, *ctSAC3*<sup>1-755</sup> and truncations, Nup145<sup>213-567</sup>, *ctCRM1*, *ctKAP104* were cloned into the NdeI/BamHI sites of pET24d-GST-TEV. *ctMEX67* truncations and *ctMTR2* were cloned into the BamHI/EcoRI sites and NdeI/XhoI sites of pET-Duet-1, respectively. For the growth and mRNA export assays *sac3A(*G1) strain was transformed with pRS314(TRP), pRS314-Sac3 and pRS314-Sac3<sup>140-1301</sup>. To check the localization of wt and mutant Sac3, GFP was inserted at a BamHI site at the Sac3 N-terminus.

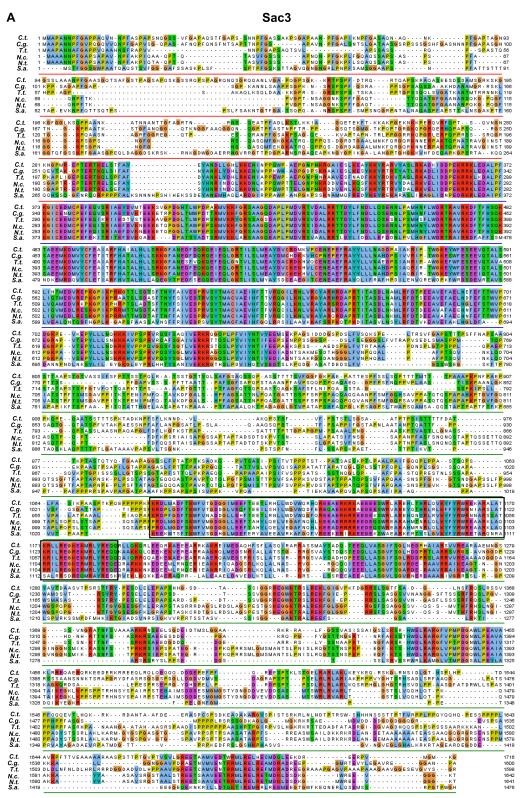
*Growth Assays* Cells were freshly plated overnight on SDC-TRP plates. On the following day, they were diluted to  $OD_{600} = 1$  after which they were spotted in 10 fold dilutions on SDC-TRP and grown for 3 days at 23°C, 30°C and 37°C.

Analysis of mRNA nuclear export by in situ hybridization and fluorescent microscopy GFP labelled SAC3 and mutant were grown in selective media at 30°C to logarithmic growth. For the *in situ* hybridization cells were grown at 30°C at selective media before being fixed. Analysis of poly(A)<sup>+</sup> RNA export by *in situ* hybridization was carried out using Cy3-labeled oligo(dT) probes essentially as described in Amberg et al. (1992). For fluorescence microscopy, an Imager Z1 (Carl Zeiss) with a 63× NA 1.4 plan apochromat oil immersion lens (Carl Zeiss) and DICIII, 4',6-diamidino-2-phenylindole, HECy3 or HEeGFP filter sets were used. Images were acquired with an AxioCamMRm camera (Carl Zeiss) and AxioVision 4.3 (Carl Zeiss) at resolution 1,388 × 1,040 (Binning 1×1, gain factor 1).

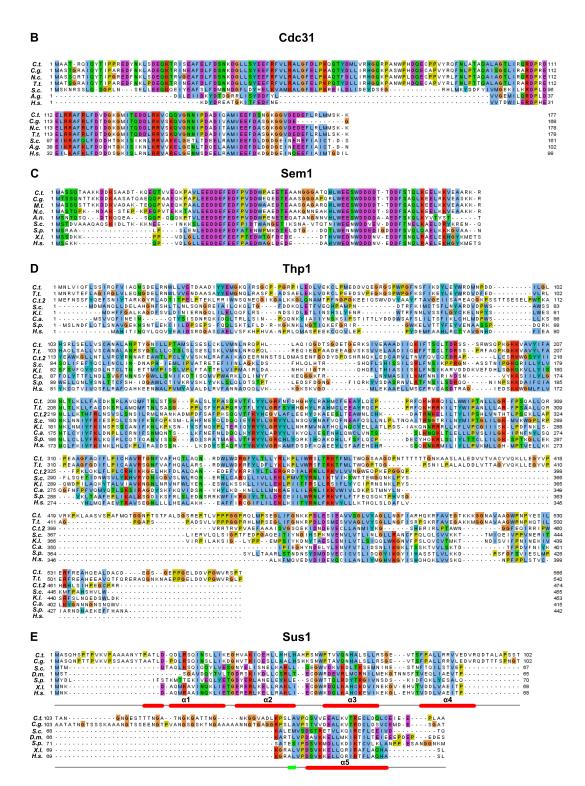
Plasmids	Origin
pET-Duet-1-HIS6-ctTHP1-ctSEM1	This study
pET-Duet-1-HIS6-ctTHP1-ctSAC3M(415-	
755)-ctSEM1	This study
pET-Duet-1- <i>HIS6-ctSUS1-ctCDC31</i>	This study
pET24d- <i>GST-TEV- ctSAC3-CID</i> (1085- 1170)	This study
YEplac112 (TRP1)-pGAL1-10-pA-TEV- ctSac3(1-1191)-FLAG	This study
YEplac195(URA1)-ctCDC31-pGAL1-10- HIS6-ctSUS1	This study
pET24d-GST-TEV- ctSAC3(1-784)	This study
pET24d-GST-TEV- ctSAC3(1-112)	This study
pET24d-GST-TEV- ctSAC3(1-112)	This study
pET24d-GST-TEV- ctSAC3(21-784)	This study
pET24d-GST-TEV- ctSAC3(44-784)	This study
pET24d-GST-TEV- ctSAC3(105-784)	This study
pET24d-GST-TEV- ctNUP145(213-567)	This study
pET24d-GST-TEV- ctKAP104	Kressler et al. (2012)
pET24d-GST-TEV- ctCRM1	Monecke et al. (2013)
pETDuet-1- HIS6-ctMEX67()-ctMTR2	This study
pETDuet-1-HIS6-TEV-ctMEX67(NTF2L)- ctMTR2	This study
pETDuet-1-HIS6-MEX67(UBA)	This study
pET24d-HIS6-TEV- ctSac3(44-94)	This study
pET24d-GST-TEV- ctMLP1(1797-2085)	This study
pET24d-GST-TEV- ctMLP1(1797-1960)	This study
pET24d-GST-TEV- ctMLP1(1797-1916)	This study
pET24d-GST-TEV- <i>ctMLP1</i> (1797-1887)	This study
pET24d-GST-TEV- <i>ctMLP1</i> (1959-2085)	This study
pRS314(TRP)	Sikorski and Hieter (1989)
pRS314- <i>SAC3</i>	Ellisdon et al. (2012)
pRS314-SAC3 (140-1301)	This study
pRS314-GFP-SAC3	This study

Table S1. Plasmids and yeast strains, related to Experimental Procedures

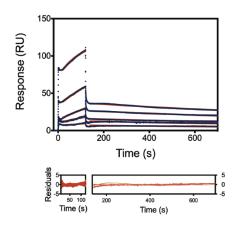
Strains	Origin
DS1-2b	Nissan et al. (2002)
<i>sac3Δ</i> (G1)	Fischer et al. (2002)



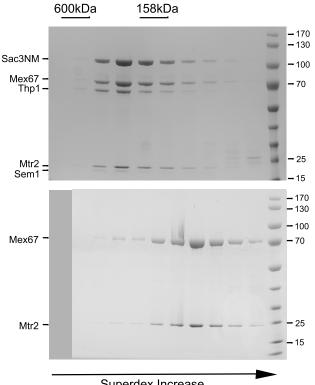
**Supplementary Figure S1A, related to Figure 1:** (A) Multiple sequence alignment of Sac3 (*Chaetomium thermophilum* (*C.t.*), *Chaetomium globosum* (*C.g.*), *Thielavia terrestris* (*T.t.*), *Neurospora crassa* (*N.c.*), *Nurospora tetrasperma* (*N.t.*) and *Scedosporium apiospermum* (*S.a.*).



**Supplementary Figure S1 B-E, related to Figure 1:** Multiple sequence alignments for Cdc31 (B), Sem1 (C),Thp1 (D) and Sus1 (E) from *C. thermophilum* (*C.t.*), *T. terrestris* (*T.t.*), *C. thermophilum2* (CTHT\_0056910) (*C.t.2*), *Chaetomium globosum* (*C.g.*), *S. cerevisiae* (*S.c.*), *K. lactis* (*K.l.*), *C. albicans* (*C.a.*), *S. pombe* (*S.p.*), *Homo sapien* (*H.s.*), *Drosophila melanogaster* (*D.m.*), *Xenopus laevis* (*X.l.*), *Neurospora crassa* (*N.c.*) and *Aspergillus nidulans* (*A.n.*).



Supplementary Figure S2, related to Figure 2. Binding of the Sac3<sup>CID</sup>:Cdc31:Sus1 complex to the Sac3 N-terminus analyzed by Surface Plasmon Resonance. Both the on- and off-rate constants were very slow ( $k_a = 235 \text{ M}^{-1} \text{ s}^{-1}$  and  $k_d = 5.2 \text{ x} 10^{-4} \text{ s}^{-1}$  with the overall equilibrium constant  $K_d$  equating to 2.2  $\mu$ M).

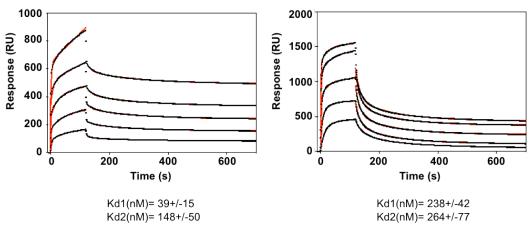


Superdex Increase

Supplementary Figure S3, related to Figure 4. Comparison of the size exclusion chromatography of the ctSac3NM:Thp1:Sem1:Mex67:Mtr2 pentameric complex and the ctMex67:Mtr2 complex. The in vitro reconstituted pentameric complex and ctMex67:Mtr2 were loaded onto a Superdex 200 increase size exclusion column. The fractions were analysed by SDS-PAGE and stained by Coommassie.

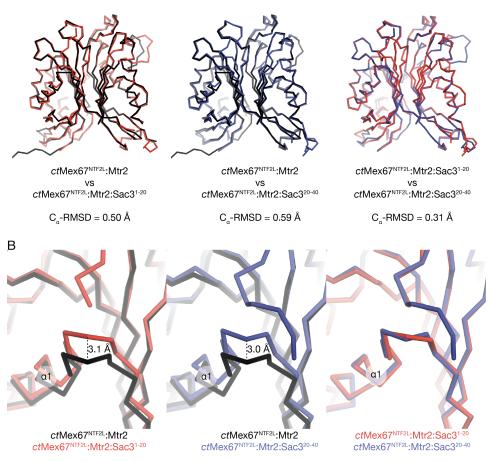
Mex67:Mtr2 vs GST-ct Sac3 (1-210)

Mex67:Mtr2 vs GST-ct Nup145 (213-567)

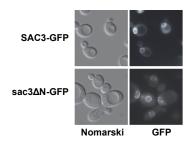


Supplementary Figure S4, related to Table 2 and Figure 5. SPR analysis of the binding of ctMex67:Mtr2 to ctSac3 (1-210) and ctNup145N. The data were fitted to a two-phase model with K<sub>d</sub>1 and K<sub>d</sub>2 depicted under the sensograms.

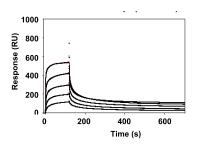
А



Supplementary Figure S5, related to Figure 5. Conformational changes in the pre- $\alpha$ 1 loop of Mex67<sup>NTF2L</sup> on binding different peptides. Whereas binding of either Sac3<sup>1-20</sup> or Sac3<sup>20-40</sup> produced a ~3 Å shift in the pre- $\alpha$ 1 loop, binding a FG peptide produced little change.



**Supplementary Figure S6, related to Figure 6. Deletion of Sac3N residues 1-136 does not inhibit Sac3-GFP binding to NPCs.** Both SAC3-GFP (pRS315-GFP-SAC3) and Sac3 (140-1301)-GFP shown nuclear rim staining in *S. cerevisiae* cells.



Supplementary Figure S7, related to Table 2 and Figure 7. SPR analysis of the binding of *ct*Mlp1 NPFG motifs to *ct*Mex67:Mtr2.

#### SUPPLEMENTARY REFERENCES

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