Structural insights into crista junction formation by the Mic60-Mic19 complex

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Mitochondrial cristae membranes are the oxidative phosphorylation sites in cells. Crista junctions (CJs) form the highly curved neck regions of cristae and are thought to function as selective entry gates into the cristae space. Little is known about how CJs are generated and maintained. We show that the central coiled-coil (CC) domain of the mitochondrial contact site and cristae organizing system subunit Mic60 forms an elongated, bow tie–shaped tetrameric assembly. Mic19 promotes Mic60 tetramerization via a conserved interface between the Mic60 mitofilin and Mic19 CHCH (CC-helix-CC-helix) domains. Dimerization of mitofilin domains exposes a crescent-shaped membrane-binding site with convex curvature tailored to interact with the curved CJ neck. Our study suggests that the Mic60-Mic19 subcomplex traverses CJs as a molecular strut, thereby controlling CJ architecture and function.

The conserved multisubunit mitochondrial contact site and cristae organizing system (MICOS) localizes to CJs (13–18). It is crucial for the formation and stabilization of CJs from yeast to humans and likely plays an important role for the regulation of CJ permeability. MICOS is composed of the Mic60 and Mic10 subcomplexes that both have membrane-shaping activity (fig. S1) (19–25). Mic60 is anchored in the inner mitochondrial membrane (IMM) via an N-terminal transmembrane (TM) segment and exposes a large domain into the intermembrane space (Fig. 1A) that associates with Mic19 (and in metazoan additionally Mic25). The Mic60 module of MICOS links CJs to the mitochondrial outer membrane through the formation of membrane contact sites with different partner protein complexes, such as the sorting and assembly machinery for β barrel proteins (SAM complex) (5, 6, 14–16, 26, 27). Mic12 in yeast or MIC13/QIL1 in higher eukaryotes connects the Mic60 and Mic10 modules of MICOS (21, 28). Loss of MICOS components leads to a massively altered cristae morphology in all organisms examined so far. The strongest phenotype with a nearly complete loss of CJs and accumulation of detached sheets of lamellar cristae membranes are observed upon ablation of Mic60 (5, 12–16, 18). How exactly MICOS controls CJ architecture and function is, however, unclear since no structural information of any MICOS component is available.

Here, we found that the central coiled-coil (CC) domain of Mic60 forms a bow tie–shaped tetrameric assembly. Mic19 promotes Mic60 tetramerization. The C-terminal mitofilin domains of Mic60 dimerize to form two crescent-shaped membrane-binding modules on each side of the CC. Our structural study suggests that the Mic60-Mic19 complex traverses CJs, therefore controlling their diameter and function.

RESULTS

The CC domain of Mic60 forms an antiparallel tetramer

In tomograms of fixed Saccharomyces cerevisiae cells, we frequently observed filamentous densities in the mitochondrial CJs (fig. S1, C and E, and movie S1). Because of its specific localization, we reasoned that the density may constitute part of the MICOS complex and, for its elongated shape, the predicted CC region of Mic60. To obtain high-resolution structural information of the CC domain,
we determined its crystal structure from the thermostable yeast *Lachancea thermotolerans* (amino acids 207 to 382; ltMic60 CC) (Fig. 1, A and B, and tables S1 and S2). ltMic60 CC forms an elongated α helix (α1C) with two short α helices (α2C and α3C) tightly packed onto the C-terminal ends of α1C (Fig. 1B). In agreement with size exclusion chromatography (SEC) and Blue native polyacrylamide gel electrophoresis (BN-PAGE) analysis, four ltMic60CC molecules assembled into a tetramer via a hydrophobic, highly conserved interface (Fig. 1, B to D; and figs. S2A; S3, A and B; and S4). An antiparallel dimeric CC further dimerized to form a bow tie–shaped tetrameric assembly. In agreement with the structure, a double amino acid substitution in this interface (M291D/F297D) leads to disruption of the ltMic60CC tetramer into monomers (Fig. 1D and fig. S2A).

**Mic19 promotes Mic60 tetramerization to stabilize CJs**

Since longer constructs of *L. thermotolerans* Mic60 (ltMic60) could not be expressed in a soluble form, we resorted to Mic60 from *Chaetomium thermophilum* (ctMic60) for further biochemical analysis. In agreement with previous data (23), an almost full-length construct of ctMic60 excluding the TM region (residues 208 to 691, ctMic60 sol) migrated as a dimer in BN-PAGE, with some minor higher-order assemblies (Fig. 2, A and B, and table S2). Notably, addition of purified ctMic19 induced the formation of a heteromeric species, likely containing four molecules of Mic60 and Mic19 each (Fig. 2B).

To prove the involvement of the tetrameric interface in this assembly, we introduced a structure-based disulfide bridge in ctMic60 sol (R525C) that can only form in the tetrameric context (fig. S3C). Under oxidizing conditions, ctMic60 sol R525C formed a tetramer even in the absence of Mic19 (Fig. 2B and fig. S2B). In the presence of Mic19, the assembly was shifted to a hetero-oligomeric complex of comparable size to ctMic60 sol-Mic19 in BN-PAGE. This indicates that the cross-link stabilizes a native form of the Mic60-Mic19 assembly. Furthermore, a double amino acid substitution in the tetrameric interface, V455D/F461D, greatly reduced higher-order assembly of Mic60 in the absence and presence of Mic19 (Fig. 2B).

ctMic60 sol protein cosedimented with Folch liposomes derived from bovine brain lipids and dragged ctMic19 into the pellet fraction (fig. S2, C and D) (23). ctMic60 sol R525C and ctMic60 sol V455D/F461D proteins cosedimented with liposomes to a similar extent as ctMic60 sol. The ctMic60 sol V455D/F461D variant showed reduced recruitment of
Mic19 to Folch liposomes (fig. S2D) and a 30-fold reduced affinity to Mic19 in isothermal titration calorimetry (ITC) experiments compared to ctMic60sol (fig. S5, A, B, and L). This suggests that oligomerization of Mic60 via the tetrameric interface is required for a tight interaction with Mic19.

To analyze the physiological role of Mic60 tetramerization, we used *S. cerevisiae* as a model. Mic60-deficient *S. cerevisiae* cells showed massively reduced levels of Mic19 (Fig. 2C), as previously described (14, 16). Expression of a tetramer-disruptive *S. cerevisiae* Mic60 (scMic60) variant (I274D/F280D; fig. S4) restored mitochondrial accumulation of Mic19 in these cells (Fig. 2C) but interfered with the appearance of Mic60-containing tetrameric complexes, as revealed by BN-PAGE (Fig. 2D). In agreement with the BN-PAGE data obtained with ctMic60sol, the tetramerization-deficient Mic60 variant did not completely abolish self-assembly, as assessed in pull-down experiments, but the homotypic Mic60 interaction was weakened compared to the wild-type (WT) situation (fig. S6A). Mic60-deficient cells showed the expected loss of CJs and fragmentation of the mitochondrial network (16), which was rescued by reexpression of scMic60 (Fig. 2, E and F, and figs. S6B and S7A). Notably, reexpression of tetramerization-defective scMic60 variant in mic60Δ cells did neither restore CJ architecture (Fig. 2G) nor mitochondrial network morphology (fig. S7A). In EM tomograms of these mitochondria, the few remaining CJs did not show filamentous densities (fig. S1, D and E, and movie S2). Furthermore, their mean CJ diameter was reduced from 13.8 to 10.4 nm (fig. S1F). We conclude that tetramerization of Mic60 is required for the formation and/or maintenance of CJs.

**The Mic60 mitofilin domain binds to the Mic19 CHCH domain via a conserved interface**

We next aimed to characterize the molecular basis of the Mic60-Mic19 interaction, which requires the C-terminal mitofilin domain of Mic60 and the C-terminal CHCH domain of Mic19 (23). Because isolated mitofilin domain constructs tended to precipitate after purification, we determined the crystal structure of a fusion construct termed Mito1_CHCH, containing the C-terminal region of the ctMic60 mitofilin domain linked to the ctMic19 CHCH domain (table S1 and S2).

Each Mito1_CHCH monomer consists of one α helix from the mitofilin domain (α3M) and α1CH and α2CH of the Mic19 CHCH domain, which together form a three helical bundle (Fig. 3A). The mitofilin-CHCH domain interface has an area of 660 Å² and is...
dominated by conserved, hydrophobic interactions (Fig. 3B and figs. S3E, S4, and S8). Mutagenesis of the hydrophobic residues in the context of the longer ctMic60sol and ctMic19 constructs impaired formation of higher-order oligomers in BN-PAGE (fig. S2E) and strongly reduced binding affinity in ITC experiments (see color code in Fig. 3B and fig. S5, A and E to M) and Mic60-mediated recruitment of Mic19 to liposomes (Fig. 3C and fig. S2D). Thus, the interaction in the fusion construct faithfully reflects the interaction of Mic60 and Mic19. In contrast, disruption of the peripheral polar interactions in the interface showed only minor effects on oligomerization and a moderate reduction in binding affinity (Fig. 3B and figs. S2E and S5).

When reintroduced into Mic60-deficient S. cerevisiae cells, the scMic60 I532D variant with a defective Mic60-Mic19 interface displayed reduced levels of mitochondrial Mic19 in comparison to cells expressing WT scMic60 (figs. S4 and S6C). Isolated Mic60-containing oligomeric complexes were reduced for this variant (fig. S6F). Accordingly, scMic60 I532D–containing mitochondria were almost devoid of CJs and showed a strongly fragmented overall morphology (Fig. 3D and figs. S6B and S7A). By contrast, the scMic60 T539D substitution at the periphery of the interface did not reduce the number of CJs but still affected mitochondrial tubular network formation in cells (Fig. 3D and figs. S6B and S7A). When coexpressed with Protein A–tagged Mic19, both Mic60 variants showed reduced coisolation (fig. S6G) in pull-down experiments, but more pronounced for scMic60 I532D.

Similarly, scMic19 variants with amino acid substitutions in the Mic60-Mic19 interface (scMic19 L143D and L147D; fig. S8) could not be coisolated with Protein A–tagged Mic60 (fig. S6H). When the

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**Fig. 3. Structural characterization of the Mic60 and Mic19 interaction.** (A) Structure of Mito1_CHCH fusion construct. Domains are colored as in Fig. 2A. The unresolved linker region is indicated as dashed line. (B) Magnification of the ctMic60-ctMic19 interface. Label colors represent the effect of single amino acid substitutions, as analyzed by ITC experiments: Green, up to 15× reduced; orange, up to 100× reduced; red, no binding, compared to the ctMic60sol-ctMic19 interaction. See fig. S5 for ITC data. (C) Liposome cosedimentation assays of ctMic60sol and ctMic19. S, supernatant; P, pellet. See also fig. S2 (C and D). (D) Quantification of CJs per mitochondrial section in S. cerevisiae mitochondria. ***P ≤ 0.001. ns, not significant. See also fig. S6B. Numbering of the corresponding ctMic60 residues is shown in parentheses.
Mic19 variants were reexpressed in a MIC19 deletion strain, reduced accumulation of Mic19 in mitochondria, a decreased number of CJs, and increased mitochondrial fragmentation were observed (Fig. 3D and figs. S6, B and D, and S7B). These data reveal the critical importance of the hydrophobic Mic60-Mic19 interface for protein stability and MICOS integrity in living cells.

The mitofilin dimer forms a convex membrane-binding site

Besides the N-terminal TM anchor, Mic60 interacts with membranes via two distinct lipid-binding sites (LBS 1 and LBS 2) in the C-terminal region of the protein (Fig. 2A) (23). Constructs including LBS 1 and LBS 2 did not crystallize. Coevolution analysis (29) predicted that LBS 2 is flexible (fig. S3D) and might therefore interfere with crystallization. Sourcing this information, we determined the crystal structure of the mitofilin domain including LBS 1, but without LBS 2, again fused to the CHCH domain of ctMic19 (Mito2_CHCH; tables S1 and S2).

The Mito2_CHCH structure revealed that the mitofilin domain is built of a four-helix bundle: α1M, α2M, and the LBS 1 from one monomer interact with α3M from an opposing monomer to form an interdomain swapped dimer with an interface area of 2000 Å² (Fig. 4A). The interaction of α3M with the CHCH domain of Mic19 is identical to the previously described structure containing the truncated mitofilin domain construct (Fig. 3A). L676 in the dimer interface points into a hydrophobic pocket of the interacting monomer (Fig. 4A and fig. S3F).

In agreement with the structural data, the Mito2_CHCH construct was a dimer in analytical ultracentrifugation experiments, whereas the L676D amino acid substitution rendered the protein monomeric (Fig. 4B). In the longer ctMic60sol construct (amino acids 208 to 691),

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Fig. 4. The mitofilin dimer forms a convex membrane-binding site. (A) Cartoon representation of the mitofilin dimer in complex with the Mic19 CHCH domain (Mito2_CHCH). One monomer is colored as in Fig. 2A. Dimer interface residues (boxed in straight lines) and potential membrane binding residues (boxed in dashed lines) are shown in the close-up views. The deduced curved membrane binding surface is indicated. (B) Association states of Mito2_CHCH (black) and Mito2_CHCHL676D (red) were analyzed at a concentration of 1 mg/ml by sedimentation equilibrium analysis. Top: The original data (dots) and the fit of the data (line): Mito2_CHCH: molecular mass (Mr) = 34 ± 4 kDa. Mito2_CHCHL676D: Mr = 16 ± 2 kDa (molecular weight of the monomer: 17 kDa). Bottom: The deviation of the fit to the data. (C) BN-PAGE analysis of different ctMic60sol variants and their complexes with ctMic19. (D) Quantification of CJs per mitochondrial section in S. cerevisiae mitochondria. **P < 0.001. See also see fig. S6B. Numbering of the corresponding C. thermophilum residues is shown in parentheses. (E) Liposome cosedimentation assays of ctMic60sol and membrane binding variants (see also fig. S2C).
the L676D variant showed a similar behavior as the WT protein in BN-PAGE, forming mostly a dimer (Fig. 4C). Liposome binding of the variant was also comparable to that of unmodified ctMic60sol (fig. S2C). However, complex formation with ctMic19 in BN-PAGE (Fig. 4C) and ITC (fig. S5, C and L), as well as Mic60-mediated Mic19 recruitment to liposomes, was reduced (fig. S2D), indicating that dimerization of the Mic60 mitofilin domain supports Mic19 recruitment. Simultaneous disruption of the tetrameric and the dimeric interface in the V455D/F461D/L676D variant had an even more drastic effect, completely preventing higher-order oligomer formation of ctMic60sol alone and in complex with ctMic19 (Fig. 4C). In addition, Mic60-dependent Mic19 recruitment to liposomes was severely affected (fig. S2D). Having both interfaces disrupted, the number of CJs per mitochondrial section and the formation of a tubular mitochondrial network in the respective S. cerevisiae variant (scMic60I274D/F280D/V530D) were impaired to a similar extent as in the mic60 knockout strain (Fig. 4D and fig. S6, B and E, and S7A), showing the additive effect of both assembly sites for tetramerization.

The dimeric arrangement positions the two positively charged LBS 1 helices on the outside of the dimer on a convex membrane-binding surface (Fig. 4A). Replacement of the positively charged amino acids on this convex surface led to reduced membrane binding (Fig. 4, A and E, fig. S2C, and table S2), supporting the idea that the convex surface in the mitofilin dimer comprises the membrane-binding site of Mic60.

### DISCUSSION

Proper mitochondrial ultrastructure is a prerequisite for mitochondrial functions in cellular energy metabolism and signaling. CJs form a highly curved membrane microdomain at the transition between the inner boundary and cristae membrane. With this study, we provide the first structural insights into CJ architecture leading to an advanced mechanistic understanding of CJ formation, stabilization, and function. The CC domain of Mic60 forms an elongated bow tie–shaped antiparallel CC. Mic19 promotes tetramerization of Mic60 into an active MICOS subcomplex. We reveal the structural basis of the heteromeric interaction of Mic60 and Mic19 and show that the mitofilin domain of Mic60 forms a convex-shaped dimeric membrane-binding module that is tailored to bind to the highly curved CJ membrane. Complementary mutational analysis in yeast demonstrates the critical role of these structural elements for CJ formation and MICOS function in vivo. Together, our findings can be compiled into a structural model of the Mic60-Mic19 complex at CJs (Fig. 5).

Each of the widely separated endings of the antiparallel Mic60 CC tetramer contains two connections to the mitofilin domain. Since the linker between the two domains is short, the two dimeric membrane-binding mitofilin modules within a tetramer must be localized on opposite sides of the CC. In a cellular context, this implies that the tetrameric CC spans over the CJ, and the two mitofilin domain dimers bind to opposite membrane surfaces in the CJ (Fig. 5, A and B). In this scenario, the convex-shaped membrane-binding sites of the mitofilin dimer are complementary to the membrane curvature of the CJ. The N-terminal TM regions of Mic60 would anchor the complex in the CJ membrane.

The proposed model of the Mic60-Mic19 complex is in agreement with the filamentous density in CJs observed in tomograms of fixed yeast mitochondria (fig. S1). However, the exact molecular identity of the filamentous density and its detailed localization in CJs is not known, and we cannot exclude that it is only indirectly related to the presence of the Mic60 tetramer. Previously proposed ring-like assemblies of Mic60 in CJs are difficult to reconcile with the fourfold symmetry of the tetrameric CC and the twofold symmetry of the mitofilin domain. Super-resolution microscopy of

![Fig. 5. Model of Mic60-Mic19 function at CJs. (A) Top view and (B) side view showing the proposed architecture of the Mic60-Mic19 complex at CJs. Each monomer has a different color. Regions not determined by x-ray crystallography are modeled as unstructured elements.](image-url)
human Mic60 suggests that up to 10 Mic60 molecules are located at one CJ (30), corresponding to two to three tetramers.

Our model has functional implications for the Mic60-Mic19 complex that can be tested in future experiments. For example, the N-terminal region of Mic19, together with parts of Mic60, is available to extend to the outer mitochondrial membrane (OMM). By interacting with SAM and translocase of the outer membrane (TOM) complexes (14, 16, 31), membrane contact sites would be formed (fig. S1). These contact sites have been implicated, among others, in lipid transfer between the IMM and OMM (32). In this context, our structural data would support the idea of an arch dome-like assembly that vaults the entry into cristae.

Our model also explains the uniform diameters of circular or slit-like CJs, which would be governed by the length of the traversing tetrameric CC of the Mic60-Mic19 complex. In line with this idea, vertebrates have longer Mic60 CC sequences and larger CJ diameters. The soluble portion of Mic60 has membrane-remodeling activity that is stimulated by Mic19 binding (23). Thus, one function of the Mic60-Mic19 complex may relate to the generation of membrane curvature at CJs, for example, by membrane scaffolding via the convex-shaped membrane-binding site or by the membrane insertion of hydrophobic residues from LBS 1 and 2. In addition, destabilization of the Mic60 tetramer through site-directed mutagenesis leads to significantly reduced CJ diameters in yeast cells (fig. S1F). This suggests a second function of the Mic60-Mic19 tetramer in preventing the collapse of CJs, for example, by counteracting membrane curvature generation of other membrane-remodeling proteins at cristae. Consequently, the lack of CJs in the absence of Mic60 may be explained by increased CJ scission induced by other membrane-remodeling proteins at CJs. A candidate for membrane curvature generation is Mic10, which forms a small wedge-shaped TM hairpin. Its oligomerization into higher-order assemblies within the membrane was shown to induce membrane curvature (19, 20). Further contributions to cristae remodeling may originate from dynamin-like Mgm1/OPA1 filaments or ATP synthase dimers (9, 33). A recent study shed first light on how these complexes may work together and orchestrate their membrane-remodeling functions, which has paved the ground for further studies on this exciting topic (34).

Last, by spanning across CJs, the Mic60-Mic19 complex is tailored to serve as a physical barrier preventing the free diffusion of proteins and metabolites in and out of the cristae space. Notably, an intrinsically disordered region is predicted between the N-terminal TM and the central CC domain of Mic60 proteins (Fig. 5, A and B) (35). Similar to the FG (phenylalanine-glycine) repeats in nuclear pore gates and carboxypeptidase A.

To remove the C-terminal His6-tag, carboxypeptidase A (from bovine pancreas, Sigma-Aldrich) treatment was applied during overnight dialysis using 50 mM Hepes/NaOH (pH 8.0), 100 mM NaCl, and 10% glycerol. A second Ni²⁺ sepharose column was used to separate cleaved from uncleaved protein. Last, a SEC run using a S200 column and SEC buffer [50 mM Hepes/NaOH (pH 8.0), 500 mM NaCl, and 10% glycerol] was used to separate pure protein from aggregates and carboxypeptidase A. Pure protein was concentrated to 31 mg/ml, flash-frozen in liquid nitrogen, and stored at −80°C until further use.

All ctMic60 and ctMic19 constructs were purified in a similar manner as described for ltMic60. However, the lysis buffer contained 50 mM Hepes/NaOH (pH 7.5), 500 mM NaCl, and 20 mM imidazole. The N-terminal His₆-tag was cleaved using recombinant His₆-tagged HRV-3C protease during overnight dialysis using 50 mM Hepes/NaOH (pH 7.5), 150 mM NaCl, and 25 mM imidazole. The final SEC was performed using S200 and S75 SEC columns (GE Healthcare Life Science) at 500 mM NaCl, 1 mM TCEP (GE Healthcare Life Science) to separate pure protein from aggregates and carboxypeptidase A. Pure protein was concentrated to 31 mg/ml, flash-frozen in liquid nitrogen, and stored at −80°C until further use.

Expression and purification

Expression plasmids were freshly transformed into Escherichia coli BL21 (DE3) cells. Protein expression was carried out in terrific broth supplemented with kanamycin (50 µg/ml) or ampicillin (100 µg/ml). The cultures were grown until OD₆₀₀ (optical density at 600 nm) reached 0.8 at 37°C and 80 rpm and protein expression subsequently induced by the addition of 300 µM isopropyl-β-D-1-thiogalactopyranoside and incubated at 20°C for another 20 hours. The cells were centrifuged at 4000g, collected, and frozen at −20°C until needed.

ltMic60 expression plasmid containing cells were diluted in lysis buffer [50 mM Hepes/NaOH (pH 8.0), 500 mM NaCl, 20 mM imidazole, 10% glycerol, 1 mM 3,3′,3′′-phosphanetriyltripropanoic acid (TCEP), and deoxyribonuclease I (1 mg/ml) (Roche)] before disruption using a microfluidizer (Microfluidics). To remove insoluble parts, the solution was centrifuged at 100,000g for 45 min at 4°C. The cleared supernatant was applied onto a prepacked Ni²⁺ sepharose High Performance IMAC (immobilized metal affinity chromatography) resin (GE Healthcare Life Science) containing gravity flow column loaded with 100 mM nickel sulfate and equilibrated in lysis buffer. The column was washed using lysis buffer and bound proteins eluted with lysis buffer containing 50 and 500 mM imidazole, respectively. To remove the C-terminal His₆-tag, carboxypeptidase A (from bovine pancreas, Sigma-Aldrich) treatment was applied during overnight dialysis at 4°C against dialysis buffer [50 mM Hepes/NaOH (pH 8.0), 500 mM NaCl, and 10% glycerol]. A second Ni²⁺ sepharose column was used to separate cleaved from uncleaved protein. Last, a SEC run using a S200 column and SEC buffer [50 mM Hepes/NaOH (pH 8.0), 500 mM NaCl, 10% glycerol, and 1 mM TCEP] (GE Healthcare Life Science) was applied to separate pure protein from aggre gates and carboxypeptidase A. Pure protein was concentrated to 31 mg/ml, flash-frozen in liquid nitrogen, and stored at −80°C until further use.

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Mass spectrometry

Mass spectrometry (MS) analysis using liquid chromatography–electrospray ionization–time-of-flight MS (LC-ESI-TOF-MS) indicated that a disulfide bridge was formed in all ctMic19 CHCH domain-containing
from the CCP4 software packaging (41, 42). For ltMic60cc, four ideal α helices build by 20 alanine residues have been placed, and AutoBuild from the PHENIX suite was used for initial model building (43, 44). For Mito1_CHCH, three ideal α helices built by 30 alanine residues could be placed. Additional helices have been identified using Phaser-MR (44, 45) from the PHENIX suite. SHELXE (46) and AutoBuild were used to obtain the initial model. The structure of Mito2_CHCH was solved by molecular replacement with Phaser-MR using the final refined structure of Mito1_CHCH as search model. ltMic60cc crystallized in space group P4212 with one monomer, Mito1_CHCH in P1 with six monomers and Mito2_CHCH in P221 with four monomers arranged as two dimers in the asymmetric unit. For ltMic60cc only amino acids 235 to 382 are visible in the structure. Residues ctMic60661–691 and ctMic19118–158 are visible in all monomers of Mito1_CHCH. In case of Mito2_CHCH, ctMic60656–586, ctMic60622–689, and ctMic19118–160 are visible in all monomers.

Refinement was carried out using iterative steps of manual model building in Coot (47) and maximum likelihood refinement with individual B factors, Translation-Libration-Screw-rotation (TLS), and secondary structure restraints using phenix.refine (48). Final structure validation was carried out with MolProbity (49). All statistics for data collection and refinement as well as the corresponding Protein Data Bank (PDB) codes can be found in table S1.

Surface conservation plot were created using the ConSurf Server (50) with standard settings and multiple sequence alignments using MULTALIN64. Figures were prepared with PyMOL (The PyMOL Molecular Graphics System, Version 1.8.2.3 Schrödinger LLC). PDBePISA web server (51) was used to calculate the interface area between the mitofilin domain and the CHCH domain.

Evolutionary coupling analysis
Structure prediction of the C-terminal region of Mic60 was done using the EVCoupling server (29). Structure predictions of ctMic60557–685 were obtained using the input sequence ctMic60550–693 (monomer pipeline, version 1, bitscore 0.1). The highest scoring folding candidate is shown.

Oxidation of cysteines
To artificially induce disulfide bridge formation, 30 μM of the respective protein has been diazylated against 20 mM tris-HCl (pH 7.5) and 150 mM NaCl overnight. The next day, oxidation of free cysteines was performed using 500 μM CuSO4 for 15 min at 4°C, followed by the addition of 50 mM EDTA. The residual CuSO4 and EDTA were removed using a PD-10 column (GE Healthcare Life Science). The concentration of the final oxidized protein was set to 1 mg/ml for further analysis.

Blue native polyacrylamide gel electrophoresis
BN-PAGE analysis of recombinant purified proteins was performed using the NativePAGE bis-tris system (Thermo Fisher Scientific). Five micrograms (μg) of single proteins or 5 μg of Mic60 variants incubated for 15 min with 2 μg of Mic19 variants were applied on 4 to 16% acrylamide BN-PAGE gradient gels and run for 2 hours at 150 V on ice. Proteins were visualized by Coomassie Brilliant Blue (CBB) staining. Immunoprecipitated mitochondrial protein complexes eluted in digitonin buffer (see below) were mixed with 10x BN-PAGE loading buffer [5% (w/v) CBB G250, 500 mM 6-aminocaproic acid, and 100 mM bis-tris/HCl (pH 7.0)] and loaded on home-made 4 to 13% BN-PAGE gradient gels that were run for 2 to 3 hours at 150 V
in a water-cooled Hoefer gel chamber at 6°C. Proteins were blotted on polyvinylidene difluoride (PVDF) membranes and visualized using specific antibodies together with an enhanced chemiluminescence (ECL) detection system.

**Isothermal titration calorimetry**
ITC experiments were performed using the PEAQ-ITC system (Malvern) in 20 mM Hepes/NaOH (pH 7.5) and 150 mM NaCl at 10°C. Mic60 concentration in the sample cell varied between the variants in the range of 44 to 81 μM, and Mic19 concentration in the syringe varied between 391 and 809 μM. The Malvern analysis software was used to integrate the binding isotherms and calculate the binding parameters. At least two biological replicates per run were conducted, while one of them is shown.

**Liposome cosedimentation assay**
Folch lipids (total bovine brain lipids fraction I, Sigma-Aldrich) were dried under an argon stream, dissolved in 20 mM Hepes/NaOH (pH 7.5) and 150 mM NaCl, incubated overnight at 4°C, and sonified for 15 min in a sonification bath. Forty microliters of a reaction mixture containing liposomes (0.6 mg/ml) and 5 μM protein (or complex) was incubated for 30 min at room temperature (RT) and centrifuged at 200,000g for 16 min at 20°C. The respective supernatant and pellet fractions were analyzed by SDS-PAGE, and the protein bands were quantified using ImageJ (version 1.50i) (52).

**Analytical ultracentrifugation**
The fusion constructs Mito2_CHCH and Mito2_CHCH<sup>676D</sup> were analyzed at protein concentrations of 0.05 to 1 mg/ml in 20 mM Hepes/NaOH (pH 7.5) and 150 mM NaCl using a Beckman Optima XL-1 centrifuge equipped with an An50Ti rotor and double sector cells. Sedimentation equilibrium measurements were carried out at 20°C and 16,000 rpm. The data were recorded at a wavelength of 230 or 280 nm and analyzed using the software Sedfit (53). No concentration-dependent assembly was observed for either construct in the applied concentration range.

**S. cerevisiae strains and plasmids**
*S. cerevisiae* strains are derivatives of YPH499 (54). Deletion strains mic60Δ and mic19Δ were described previously (16). For generation of different Mic60 and Mic19 variants containing individual amino acid substitutions, PCR fragments containing either the MIC60 or the MIC19 open reading frames together with their natural promoter and terminator regions were cloned into plasmid pRS416, and the respective mutations were generated via site-directed mutagenesis (see table S3 for a list of plasmids and table S4 for a list of *S. cerevisiae* strains used in this study). *S. cerevisiae* strains expressing Mic19 fused to a C-terminal Protein A tag for immunoprecipitation were generated by homologous recombination using a transformation cassette that consists of a tobacco etch virus protease cleavage site, a ZZ domain of *S. aureus* Protein A for immunoglobulin G (IgG) binding, and a HIS3 marker gene for selection (55). For isolation of mitochondria, *S. cerevisiae* cells were grown in liquid minimal glycerol medium [0.67% (w/v) yeast nitrogen base, 0.07% (w/v) complete supplement mixture (CSM) amino acid mix minus uracil, and 3% (v/v) glycerol] at 30°C.

**Isolation of *S. cerevisiae* mitochondria**
Cells were grown in minimal glycerol medium to midlog phase and harvested by centrifugation at 1200g for 5 min at RT. Pellets were resuspended in wet weight DTT softening buffer (2 ml/g) [0.1 M tris/H<sub>2</sub>SO<sub>4</sub> (pH 9.4) and 10 mM DTT] and incubated for 20 min at 30°C. After centrifugation (2000g for 5 min at RT), cell pellets were washed with Zymolyase buffer [1.2 M sorbitol and 20 mM KP, (pH 7.4)]. Cells were resuspended in 6.5 ml of Zymolyase buffer containing 4 mg of Zymolyase per gram of cells (wet weight) and incubated for 30 min at 30°C for enzymatic digestion of the cell wall. The resulting spheroplasts were harvested by centrifugation (2000g for 5 min at RT), washed again with Zymolyase buffer, and resuspended in 6.5 ml of homogenization buffer [0.6 M sorbitol, 10 mM tris/H<sub>Cl</sub> (pH 7.4), 1 mM EDTA, 0.2% (w/v) bovine serum albumin, and 1 mM phenylmethylsulfonyl fluoride (PMSF)] per gram of cells. Spheroplasts were then homogenized using a glass-teflon Dounce homogenizer (15 strokes). The suspension was centrifuged (1500g for 5 min at 4°C) to remove cell debris. The supernatant was transferred into a new tube and again centrifuged (15,000g for 10 min at 4°C). The mitochondria-containing pellet was resuspended in SEM buffer [250 mM sucrose, 10 mM MOPS (pH 7.2), and 1 mM EDTA]. Protein concentration was measured via a Bradford assay and adjusted to 10 mg of total protein/ml of suspension. Isolated mitochondria were flash-frozen in liquid nitrogen and stored at −80°C.

**Steady-state levels of mitochondrial proteins**
For comparing the steady-state levels of individual proteins in WT and mutant mitochondria, frozen samples were thawed slowly on ice and centrifuged (15,000g for 10 min at 4°C). The mitochondrial pellet was resuspended in Laemmli buffer [60 mM tris/H<sub>Cl</sub> (pH 6.8), 2% (w/v) SDS, 10% (v/v) glycerol, 0.01% bromophenol blue, and 1% β-mercaptoethanol]. The samples were incubated for 10 min at 65°C and loaded on SDS-PAGE gels for protein separation. Subsequently, proteins were blotted on PVDF membranes and visualized using specific antibodies together with an ECL detection system (see table S5 for a list of the used antibodies).

**Immunoprecipitation**
For IgG affinity chromatography, 0.9 mg of isolated *S. cerevisiae* mitochondria (total protein content) containing Protein A–tagged Mic19 or Mic60 was resuspended in solubilization buffer [20 mM tris/H<sub>Cl</sub> (pH 7.4), 50 mM NaCl, 0.1 mM EDTA, 10% (v/v) glycerol, 2 mM PMSF, 1× Roche protein inhibitor cocktail, and 1% (w/v) digitonin] and incubated for 30 min at 4°C. Mitochondrial detergent extracts were centrifuged (20,000g for 10 min at 4°C), and the supernatant was incubated with 50 μl of human IgG–coupled Sepharose beads [pre-equilibrated with 0.5 M acetate (pH 3.4)] for 90 min at 4°C. Beads were washed 10× with digitonin buffer [20 mM tris/H<sub>Cl</sub> (pH 7.4), 0.5 mM EDTA, 60 mM NaCl, 10% (v/v) glycerol, 2 mM PMSF, and 0.3% digitonin], followed by centrifugation (700g for 30 s at 4°C). Bound proteins were eluted either by tobacco etch virus protease cleavage over night at 4°C and centrifugation (1200g for 30 s at 4°C) or by incubation with 50 mM glycine (pH 2.5) and subsequent neutralization with 1 M tris (pH 8.0), followed by centrifugation (1200g for 1 min at 4°C).

**Quantification of Western blots**
Western blots analyses of immunoprecipitation experiments were quantified using ImageJ2 Version 2.3.0/1.53q. Background-corrected signals obtained with the relevant antibodies were quantified in total and eluate samples. The signal intensities of the total samples were set to 100% to determine the relative amount of signal in eluate samples.
Relative coisolation efficiencies were calculated by determining the ratio of WT/WT and WT/variant setting the WT/WT ratio to 100% for each protein analyzed.

EM of S. cerevisiae mitochondria
S. cerevisiae cells grown in minimal medium supplemented with 2% glucose for 24 hours at 30°C were diluted in minimal glycerol medium and grown until early log phase. Cells were handled as previously described (56). Cells were fixed for 3 hours with freshly prepared 4% (w/v) paraformaldehyde and 0.5% (v/v) glutaraldehyde (GA) in 0.1 M citrate buffer adjusted to pH 7.5. After washing with citrate buffer, cells were permeabilized for 1 hour with 1% (w/v) sodium metaperiodate at 4°C. Cells were washed with 0.1 M phosphate buffer and then embedded in 12% gelatine by cooling the 37°C warm gelatine in ice after 10 min of incubation. Cubes (1 mm³) were cut, infiltrated overnight with 2.3 M sucrose, mounted onto specimen chucks, and frozen in liquid nitrogen. Ultrathin sections were cut using an UC7 ultramicrotome (Leica) at −110°C and collected on formvar/carbon-coated copper grids (Plano). The gelatine was removed by washing with PBS at 37°C and water before staining with 3% (w/v) silicotungstic acid hydrate (Fluka) in 2.8% (w/v) polyvinyl alcohol (Sigma-Aldrich) in water for 5 min. Grids were imaged after drying with the transmission electron microscope EM910 (Zeiss) operating at 80 kV and equipped with a Quemesa charge-coupled device (CCD) camera and the imaging software iTEM (Emsis) at ×10,000 magnification. All data are presented as means ± SD, and value differences were compared statistically. Data analysis and plotting were done with the statistic program R. The normal distribution was tested using the Kolmogorov-Smirnov test and the Q-Q plot. Since data were not normally distributed, the two-sided Wilcoxon distribution was tested using the Kolmogorov-Smirnov test and the Q-Q plot. Since data were not normally distributed, the two-sided Wilcoxon distribution was tested using the Kolmogorov-Smirnov test and the Q-Q plot. Since data were not normally distributed, the two-sided Wilcoxon distribution was tested using the Kolmogorov-Smirnov test and the Q-Q plot. Since data were not normally distributed, the two-sided Wilcoxon distribution was tested using the Kolmogorov-Smirnov test and the Q-Q plot. Since data were not normally distributed, the two-sided Wilcoxon distribution was tested using the Kolmogorov-Smirnov test and the Q-Q plot. Since data were not normally distributed, the two-sided Wilcoxon distribution was tested using the Kolmogorov-Smirnov test and the Q-Q plot. Since data were not normally distributed, the two-sided Wilcoxon distribution was tested using the Kolmogorov-Smirnov test and the Q-Q plot. Since data were not normally distributed, the two-sided Wilcoxon distribution was tested using the Kolmogorov-Smirnov test and the Q-Q plot. Since data were not normally distributed, the two-sided Wilcoxon distribution was tested using the Kolmogorov-Smirnov test and the Q-Q plot. Since data were not normally distributed, the two-sided Wilcoxon distribution was tested using the Kolmogorov-Smirnov test and the Q-Q plot. Since data were not normally distributed, the two-sided Wilcoxon distribution was tested using the Kolmogorov-Smirnov test and the Q-Q plot. Since data were not normally distributed, the two-sided Wilcoxon distribution was tested using the Kolmogorov-Smirnov test and the Q-Q plot. Since data were not normally distributed, the two-sided Wilcoxon distribution was tested using the Kolmogorov-Smirnov test and the Q-Q plot. Since data were not normally distributed, the two-sided Wilcoxon distribution was tested using the Kolmogorov-Smirnov test and the Q-Q plot. Since data were not normally distributed, the two-sided Wilcoxon distribution was tested using the Kolmogorov-Smirnov test and the Q-Q plot. Since data were not normally distributed, the two-sided Wilcoxon distribution was tested using the Kolmogorov-Smirnov test and the Q-Q plot. Since data were not normally distributed, the two-sided Wilcoxon distribution was tested using the Kolmogorov-Smirnov test and the Q-Q plot.

Analysis of mitochondrial networks
S. cerevisiae cells were grown in liquid minimal medium [0.67% (w/v) yeast nitrogen base, 0.07% (w/v) CSN amino acid mix minus uracil, and 3% (w/v) glucose] at 24°C until an OD600 of 1.0. Cells were pelleted by centrifugation for 3 min at 400g. Mitochondrial networks of the S. cerevisiae cells were stained using 175 nM 3,3′-dihexyloxacarbocyanine iodide in buffer A [10 mM Hepes (pH 7.2) and 5% glucose] for 10 min at RT. Cells were washed once with buffer A. For imaging, cells were transferred on a microscopy slide, and the sample was covered with a cover slip. Images were taken immediately at a Leica DMi8 fluorescence microscope with a 63×/1.40 objective and a Leica DFC3000 G CCD camera. Z-stacks, covering the whole cell, were recorded for each image. For each cell, sections of 8 μm by 8 μm were cropped and deconvoluted with Huygens Essential (Scientific Volume Imaging, Netherlands, http://svi.nl). Maximum intensity projections were created in Fiji. For quantification of mitochondrial morphology, tubular versus nontubular mitochondrial networks were assessed by the experimenter in cells from three independent and blinded experiments (for each individual culture, approximately 300 cells were counted). Percentages were calculated and the P values were derived by an unpaired t test using GraphPad Prism.

Preparation of the Mic60-Mic19 model within CJs
The model of Mic60 and Mic19 in CJs was created and prepared by E. Werner, RNS Berlin (www.rns.berlin), who granted copyrights. The model comprises the crystal structures of the CC region of Mic60 from L. thermotolerans (ltMic60CC, residues 235 to 382), the LBS 1 and mitofilin domain of ctMic60, and the CHC domain of ctMic19 (Mito2 CHCH). In this, the sequence of ltMic60 was used to create the Mic60-Mic19 model within CJs. The model was generated using the Maya software from Autodesk Inc. (www.autodesk.com/products/maya/) and Modeling kit and Rigging kit of the plugin Molecular Maya (mMaya) from Digizyme Inc. (https://clarafi.com/tools/mmaya/).

SUPPLEMENTARY MATERIALS
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REFERENCES AND NOTES


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Structural insights into crista junction formation by the Mic60-Mic19 complex

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