Tim23, a Protein Import Component of the Mitochondrial Inner Membrane, Is Required for Normal Activity of the Multiple Conductance Channel, MCC

Timothy A. Lohret,* Robert E. Jensen,[‡] and Kathleen W. Kinnally*[§]

*Department of Biological Sciences, University at Albany, SUNY, Albany, New York 12222; [‡]Department of Cell Biology, Johns Hopkins University School of Medicine, Baltimore, Maryland 21205; and [§]Department of Molecular Medicine, Wadsworth Center, NYS Department of Health, Empire State Plaza, Albany, New York 12201-0509

Abstract. We previously showed that the conductance of a mitochondrial inner membrane channel, called MCC, was specifically blocked by peptides corresponding to mitochondrial import signals. To determine if MCC plays a role in protein import, we examined the relationship between MCC and Tim23p, a component of the protein import complex of the mitochondrial inner membrane. We find that antibodies against Tim23p, previously shown to inhibit mitochondrial protein import, inhibit MCC activity. We also find that MCC activity is altered in mitochondria isolated from yeast carrying the *tim23-1* mutation. In contrast to wild-type MCC, we find that the conductance of MCC from the *tim23-1* mutant is not significantly blocked by mitochondrial presequence peptides. Tim23 antibodies and the *tim23-1* mutation do not, however, alter the activity of PSC, a presequence-peptide sensitive channel in the mitochondrial outer membrane. Our results show that Tim23p is required for normal MCC activity and raise the possibility that precursors are translocated across the inner membrane through the pore of MCC.

"N eukaryotic cells, a key step in the sorting of proteins to intracellular compartments is the translocation of polypeptides across organelle membranes. Although the mechanisms of these processes are not well understood, it has been suggested that proteins may cross membranes through pores or channels (Blobel and Dobberstein, 1975). Recently, Simon and Blobel (Simon and Blobel, 1991, Simon and Blobel, 1992) used electrophysiological techniques to identify potential protein-translocating channels in the endoplasmic reticulum and in the bacterial plasma membrane. In mitochondria, proteins imported from the cytosol utilize import complexes in both the inner and outer membranes (Pfanner et al., 1994; Ryan and Jensen, 1995; Pfanner and Meijer, 1995; Lithgow et al., 1995). However, the mechanism by which imported proteins cross either mitochondrial membrane is unclear.

Most mitochondrial proteins are synthesized in the cytosol as precursor proteins, carrying amino-terminal extensions called presequences. Presequences carry the information that targets proteins to the mitochondrion and are removed during or after import into the organelle. Precursor proteins are imported via a multi-step process that includes binding to outer membrane receptors, and translocation across one or both mitochondrial membranes. Translocation of the precursor across the mitochondrial inner membrane requires an electrochemical potential which is set up by the electron transport chain (Gasser et al., 1982; Schleyer et al., 1982). In addition, a matrix-localized member of the hsp70 family (mt-hsp70) plays an important role in the translocation of precursors across the inner membrane (Kang et al., 1990; Ungermann et al., 1994, 1996). The Tim44 protein is associated with the matrix face of the inner membrane (Blom et al., 1993; Horst et al., 1993; Maarse et al., 1992; Scherer et al., 1992) and interacts with mt-hsp70 during the translocation reaction (Kronidou et al., 1994; Rassow et al., 1994; Schneider et al., 1994).

Tim23 is an integral protein of the inner membrane essential for import (Emtage and Jensen, 1993; Dekker et al., 1993). Mitochondria isolated from yeast strains carrying the *tim23-1* mutation are defective in the import of at least five different precursor proteins (Emtage and Jensen, 1993). Furthermore, antibodies to Tim23p inhibit import across the inner membrane (Emtage and Jensen, 1993). Tim23p can be chemically cross-linked to a precursor arrested in transit across the inner membrane (Ryan and Jensen, 1993; Kübrich et al., 1994), and depletion of Tim23p from cells results in a defect in import (Emtage and Jensen, 1993). Tim17p is another essential inner membrane import component (Maarse et al., 1994; Ryan et al., 1994) that associates with Tim23p (Blom et al., 1995; Berthold et al., 1996; Ryan, K.R., R. Leung, and R.E. Jensen, manu-

Please address all correspondence to Kathleen Kinnally, Wadsworth Center, Empire State Plaza, P.O. Box 509, Albany, NY 12201-0509. Tel.: (518) 474-4229. Fax: (518) 474-7992. E-mail: kinnally@wadsworth.org

Timothy A. Lohret's present address is Department of Anatomy and Cell Biology, Emory University School of Medicine, Atlanta, GA 30322-3030.

script submitted for publication). While the exact function of Tim23p and Tim17p in import is not known, it has been suggested that both proteins form part of a channel in the inner membrane through which precursors are translocated into the matrix.

Both mitochondrial membranes contain a number of channel activities which have been identified using electrophysiological techniques (Kinnally et al., 1992; Sorgato and Moran, 1993). The multiple conductance channel (MCC^{1} or mitochondrial megachannel; Kinnally et al., 1996; Zoratti and Szabó, 1994) is a channel activity found in the mitochondrial inner membrane of mammals and yeast. MCC has a large conductance and allows the passage of a variety of different ions across the membrane in patch-clamp studies (Lohret and Kinnally, 1995a). This channel is normally closed under metabolizing conditions unless activated (Kinnally et al., 1991, 1992, 1996). However, MCC activity is usually detected after its reconstitution into proteoliposomes, suggesting that regulatory components may be lost during the fractionation procedure (Lohret et al., 1996).

We have recently shown that the conductance of MCC is transiently blocked by synthetic peptides corresponding to mitochondrial presequences (Lohret and Kinnally, 1995b). Presequence peptides caused a momentary closure of MCC (a flicker blockade) that is reversible, voltage-, and dose-dependent. To determine whether MCC plays a role in mitochondrial protein import, we have examined the relationship between MCC and Tim23p, an inner membrane import component. Below we find that antibodies to Tim23p inhibit MCC activity. We also find the peptide sensitivity of MCC is altered in mitochondria isolated from the *tim23-1* mutant. Our results indicate that Tim23p is required for normal MCC activity, and suggest that precursors are translocated across the inner membrane through the pore of the MCC.

Materials and Methods

Isolation of Mitochondria and Preparation of Proteoliposomes

Mitochondria were isolated from wild-type strain AH216 and the tim23-1 mutant as described (Emtage and Jensen, 1993; Daum et al., 1982). Mitochondrial membranes were prepared by the French press method (Decker and Greenawalt, 1977), and the outer membrane was separated from the inner membrane as described by Mannella (1982). The purity of the membrane fractions was assayed in two ways. First, immunoblotting showed, for the most part, that the outer membrane protein, voltage-dependent anion-selective channel (VDAC), was found only in the outer membrane preparations, and that the inner membrane protein Tim23 was found solely in the inner membrane preparation (see Fig. 1). Second, we found that VDAC activity detected by patch-clamp analysis was found only in outer membrane, but not in inner membrane preparations (Lohret and Kinnally, 1995a; Lohret et al., 1996). Inner and outer membranes were separately reconstituted into giant proteoliposomes (Sigma Type IV-S soybean L-a-phosphatidylcholine) by dehydration-rehydration (Criado and Keller, 1987) as previously described (Lohret and Kinnally, 1995a,b; Lohret et al., 1996). To eliminate the contribution of VDAC to the channel activity of outer membrane preparations, strain M22-2 (Blachly-Dyson et al., 1990), which is disrupted for VDAC, was used as the source of outer

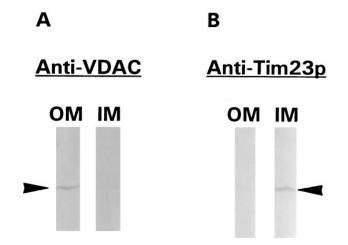


Figure 1. Analysis of mitochondrial inner and outer membrane preparations. Immune blots indicate the presence of Tim23 in the inner and VDAC in the outer membrane preparations. Aliquots from inner (IM) and outer (OM) membrane preparations from wild-type mitochondria were subjected to SDS-PAGE and immune blots were decorated with antibodies to VDAC (A) and Tim23 (B) proteins. Immune complexes were visualized using AuroProbe BLplus secondary antibody reaction.

membranes in studies of the Tim23 antibody on PSC (Lohret and Kinnally, 1995a).

Patch Clamp Analysis

The patch-clamp procedures and analysis used were as previously described (Lohret and Kinnally, 1995a,b; Lohret et al., 1996). Briefly, membrane patches were excised from proteoliposomes after formation of a giga-seal using micropipettes with $\sim 0.4 \ \mu m$ diameter tips and resistances of 10-20 MΩ (program courtesy of A.K. Dean, Sutter Instruments, Novato, CA). Unless otherwise stated, the solution in the micropipettes and bath was 150 mM KCl, 5 mM Hepes, 1 mM EGTA, 1.05 mM CaCl₂ (10⁻⁵M free calcium), pH 7.4, and the experiments were carried out at room temperature (~23°C). Peptides were either introduced and removed by perfusion of the bath (0.5 mL vol) with 3-5 mL of media or included in the micropipette filling solution. Voltage clamp was performed with the inside-out excised configuration of the patch-clamp technique (Hamill et al., 1981) using a Dagan 3900 patch clamp amplifier in the inside-out mode. Voltages across patches excised from proteoliposomes are reported as bath (i.e., matrix) potentials. Channel open probability was calculated as the fraction of the total time the channel spent in the fully open state from total amplitude histograms generated with PAT program (Strathclyde Electrophysiological Software, courtesy of J. Dempster, U. of Strathclyde, UK). Mean open times were determined from current traces usually 20-40 s in duration, band-width limited to 2 kHz by a low pass filter, and sampled at 5 kHz using the PAT program. Flicker rate was the number of transition events/sec from the open state to lower conductance states with a 50% threshold of the predominant event (typically \sim 500 pS). In comparisons of tim23-1 and wild-type MCC, the percent reduction in flicker rate was [1-(N from tim23-1/N from wild-type)]100, where N was the increase in flicker rate induced by the addition of the presequence peptide [N = (rate with peptide) - (rate without peptide)]. Only single channel patches were used for the analysis of flicker blockade. Permeability ratios were calculated from the reversal potential in the presence of a 150:30 mM KCl gradient as previously described (Lohret and Kinnally, 1995a).

Antibody Inhibition

Preimmune IgG and IgG against Tim23p were prepared from serum as described (Emtage and Jensen, 1993). To examine the effect of antibodies on the intermembrane space face of the inner membrane, preimmune IgG and IgG against Tim23p, VDAC (Stanley et al., 1995), and the Rieske iron-sulfur protein (Beckmann et al., 1987) were added to proteoliposomes (25

^{1.} *Abbreviations used in this paper*: MCC, multiple conductance channel; PSC, peptide-sensitive channel; VDAC, voltage-dependent anion-selective channel.

 μ g antibody/ μ g inner membrane protein) and incubated on ice for 60 min before the patch-clamp experiments.

Peptides

Peptides were prepared by the Wadsworth Center's peptide synthesis core facility using a 431A automated peptide synthesizer as previously described (Applied Biosystems, Foster City, CA) (Lohret and Kinnally, 1995b). As shown in Table I, the presequence peptides used were based on amino acids 1-13 and 1-22 from the amino terminus of cytochrome oxidase subunit IV of *S. cerevisiae* (yCOX-IV₁₋₁₃ and yCOX-IV₁₋₂₂), amino acids 3-22 of *N. crassa* subunit IV (fCOX-IV), and amino acids 1-20 from subunit VI of *S. cerevisiae* (yCOX-VI). Control peptides were the amino and carboxy termini and an internal segment of *N. crassa* VDAC (nVDAC, cVDAC, and iVDAC, respectively; Guo et al., 1995), the binding domain of antithrombin III (pAT-III; Smith and Knauer, 1987), and a synthetic mitochondrial presequence, synB2 (Allison and Schatz, 1986). Peptides were subjected to mass spectroscopy to determine impurities and proper composition.

Immune Blotting

Mitochondrial proteins were separated by SDS-PAGE (Laemmli, 1970) and transferred to nitrocellulose or Immobilon filters (Towbin et al., 1979). Filters were decorated with antibodies and visualized with an Auro-Probe BLplus secondary antibody reaction (Amersham, Amersham, UK) or by chemiluminescence (ECL; Amersham).

Results

Conductance of MCC Is Transiently Blocked by Presequence Peptides

We previously showed that peptides based on two mitochondrial presequences transiently block the conductance of MCC (Lohret and Kinnally, 1995b). We have extended this investigation by examining the effect of additional peptides on MCC activity. Mitochondrial inner membranes were isolated from wild-type yeast strains and fused with small phosphatidylcholine liposomes to form large proteoliposomes. Membrane patches were excised from the proteoliposomes with a micropipette and the conductance was examined in the presence or absence of peptides. Peptides were either added to the bath solution, which represents the mitochondrial matrix, or added to the micropipette buffer, representing the intermembrane space.

As shown previously, MCC in the absence of peptide had a predominant transition size of \sim 500 pS, a peak conductance of ~ 1 nS, a mean open time of ~ 25 ms at 20 mV, and a cation selectivity (Lohret and Kinnally, 1995a; see also Figs. 2 and 3). When a peptide based on the first 13 residues of the Saccharomyces cerevisiae cytochrome oxidase subunit IV presequence (yCOX-IV₁₋₁₃) was added to the bath solution, a transient blockade of MCC conductance was induced during perfusion of the chamber as indicated by the decrease in mean current (Fig. 2 A). While transitions to lower conductance levels were relatively infrequent in the absence of presequence peptide (seen as downward deflections in the current trace of Fig. 2 B), large amplitude, rapid flickering between the open and lower conductance states developed in the current trace during the introduction of yCOX-IV₁₋₁₃ (Fig. 2 C) and persisted after the perfusion was complete (Fig. 2 D).

The reduced occupancy of the open state of MCC and rapid flickering between open, sub-, and closed states brought on by presequence peptides is further illustrated by comparing the current amplitude diagrams and single

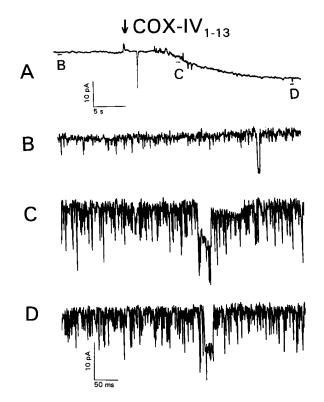


Figure 2. Presequence peptides rapidly induce a transient blockade of MCC conductance. The patch containing two MCC was excised with a micropipette from a proteoliposome prepared with mitochondrial inner membranes from the wild-type strain and the patch conductance was measured at 20 mV as described in Materials and Methods. The current trace shows the time course of the effect on the two channels of perfusing 3 ml of media containing 50 μ M yCOX-IV₁₋₁₃ into the 0.5-ml bath solution. (A) The current trace shown was obtained using an Omniscribe recorder whose effective filtration rate is 0.05 kHz. This current trace was also analyzed using the PAT computer program at 2 kHz as detailed in the Materials and Methods section and 0.5-s regions show the current trace before (B), during (C), and after (D) the introduction of yCOX-IV₁₋₁₃ to the bath by perfusion on a faster time scale. Media were 0.15 M KCl, 5 mM Hepes, 1 mM EGTA, 1.05 mM CaCl₂, pH 7.4.

channel current traces in the absence (control) and presence of yCOX-IV₁₋₁₃ in Fig. 3. The peptide-induced reduction in open probability from 0.9 (control) to 0.4 (yCOX- IV_{1-13}) was seen as a decrease in the fraction of the total time spent in the open state peak of the amplitude diagrams. The transient blockade of MCC conductance by presequence peptide was seen from either side of the membrane, but the effect was voltage-dependent. When the presequence peptide was added to the bath, the rapid flickering was seen at bath positive potentials (negative in the micropipette), but not at bath negative potentials (Lohret and Kinnally, 1995b). When the peptide was included in the micropipette, the blockade of MCC conductance was seen only at bath negative potentials. Several additional presequence peptides induced rapid flickering and reduced open probability of MCC, including peptides based on the amino terminus of yeast cytochrome oxidase subunit IV (yCOX-IV₁₋₂₂) and subunit VI (yCOX-VI), as

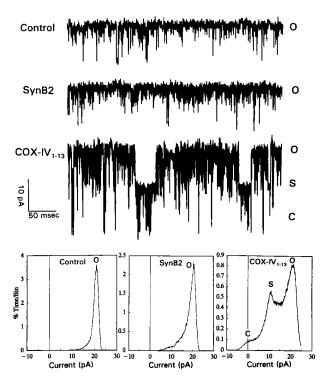


Figure 3. Presequence peptides specifically induce a transient blockade of MCC conductance. The conductance of a patch excised from a proteoliposome-containing mitochondrial inner membranes from the wild-type strain was measured at 20 mV. The single channel current traces in the absence of peptide (control) and in the presence of 50 μ M synB2 or yCOX-IV₁₋₁₃ peptide in the bath solution were band-width limited to 2 kHz. Total current amplitude diagrams and current traces show the occupancy of open (O), substate (S) and closed (C) conductance levels. The probability of occupying the open state was 0.9, 0.8, and 0.4 in the absence of peptide (control), in the presence of synB2, and in the presence of yCOX-IV₁₋₁₃, respectively.

well as subunit IV of cytochrome oxidase from *N. crassa* (fCOX-IV), and are scored positive in Table I.

Functional mitochondrial presequences contain several basic amino acids and are thought to fold into amphipathic α helices (Roise and Schatz, 1988). To test the specificity of the peptide inhibition of MCC conductance, we examined several peptides either previously shown or not pre-

dicted to act as mitochondrial presequences. For example, synB2 is a synthetic peptide that does not function as a mitochondrial targeting signal (Allison and Schatz, 1986). synB2 is cationic and predicted to be α -helical, but has low amphipathicity. We find that synB2 has little or no effect on MCC activity compared to mitochondrial presequences, e.g., yCOX-IV₁₋₁₃, as shown in Fig. 3. yCOX-IV₁₋₁₃ induced large-amplitude flickering and reduced the open probability of MCC while the current traces and amplitude diagrams in the presence of synB2 closely resembled the control (Fig. 3). Furthermore, we found that nVDAC, an α -helical peptide with one negative charge (Gou et al., 1995), cVDAC, an uncharged peptide that is not α -helical (Gou et al., 1995) as well as iVDAC, a cationic peptide predicted to form a β-sheet (Mannella et al., 1996), did not cause the flicker blockade in our MCC assays (scored as negative in Table I). Interestingly, pAT-III (another cationic α -helical peptide with low targeting activity; Glaser and Cumsky, 1990) had little effect on MCC activity if included in the micropipette but induced a flicker blockade of MCC if applied to the bath face.

Increasing the net positive charge and/or length of presequence peptides increased their ability to competitively inhibit protein import (Cumsky and Glaser, 1990) while similar changes in presequences increased the efficiency of protein import (Isaya et al., 1988; Martin et al., 1991). The ability of presequence peptides to induce rapid flickering of MCC was similarly sensitive, i.e., more positively charged or longer peptides had lower effective concentrations. In particular, 2 μ M yCOX-IV₁₋₂₂ or yCOX-VI (+5 net charge) had about the same effect on MCC as 20 μ M fCOX-IV or yCOX-IV₁₋₁₃ (+3 net charge, data not shown).

Antibodies to Tim23p Block MCC Activity

The specific blockade of MCC conductance by presequence peptides suggests that MCC plays a role in mitochondrial protein import. To further test this idea, we asked if antibodies to the Tim23 protein affect the activity of MCC. Tim23p is a component of the protein import machinery and has been proposed to be part of a protein-translocating channel in the inner membrane (Ryan and Jensen, 1993; Ryan et al., 1994; Dekker et al., 1993). For example, translocation of precursors across the inner membrane can be inhibited by antibodies to Tim23p (Emtage and Jensen,

Table I. The Effects of Synthetic Peptides on MCC Activity

Peptide	Sequence	Source	Net charge	Presequence	MCC block
yCOX-IV ₁₋₁₃	¹ MLSLRQSIRFFKY ₁₃	yeast	+3	+*	+
yCOX-IV ₁₋₂₂	¹ MLSLRQSIRFFKPATRTLCSSR ₂₂	yeast	+5	+*	+
yCOX-VI	¹ MLSRAIFRNPVINRTLLRAR ₂₀	yeast	+5	$+^{\ddagger}$	+
fCOX-IV	³ RAPALRRSIATTVVRCNAET ₂₂	N. crassa	+3	$+^{\ddagger}$	+
SynB2	MLSRQQSQRQSRQQSQRQSR	synthetic	+5	§	_
pAT-III	RNASVLKSSKNAKRYLRCNLKA	antithrombin III binding domain	+7	_*	\pm
iVDAC	¹⁰⁹ RGAKFNLHFKQ ₁₁₉	N. crassa	+3	_‡	_
nVDAC	¹ MAVPAFSDIAKSANDLLNKD ₂₀	N. crassa	-1	_‡	_
cVDAC	²⁷² THKVGTSFTFES ₂₈₃	N. crassa	0	_*	-

*Glaser, S.M., and M.G. Cumsky. 1990. J. Biol. Chem. 265:8817-8822.

*Predicted but not determined.

[§]Allison, D.S., and G. Schatz. 1986. Proc. Natl. Acad. Sci. USA. 83:9011–9015.

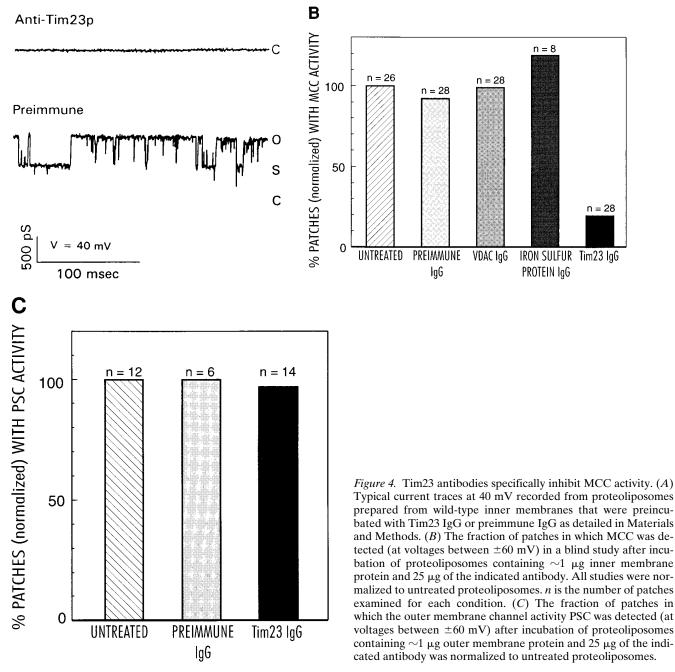
pAT-III blocked from the bath side but not micropipette side.

1993). We preincubated proteoliposomes prepared with mitochondrial inner membranes with antibodies to Tim23p and then examined the conductance of patches excised from the treated vesicles. As shown in the current traces of Fig. 4 *A*, antibodies to Tim23p blocked MCC activity. When the conductance of patches from proteoliposomes preincubated with Tim23 IgG was measured, MCC was virtually absent. Tim23 IgG blocked essentially all conductance through MCC (Fig. 4 *A*) and blocked the effect of yCOX-IV₁₋₁₃ peptide. In contrast, equivalent amounts of preimmune IgG did not affect MCC activity (Fig. 4 *A*). To quantify the effect of Tim23 antibodies, several patches were taken from proteoliposomes treated with Tim23 IgG

A

and their conductance was measured. As controls, proteoliposomes were also incubated with IgG from preimmune serum, antibodies to the outer membrane VDAC channel (Stanley et al., 1995), or IgG to the Rieske iron-sulfur protein of the inner membrane electron transport chain (Beckmann et al., 1987) (Fig. 4 *B*). In a total of 28 patches from proteoliposomes treated with Tim23 IgG, no MCC activity was observed in 23 of the patches, whereas five patches had detectable MCC (Fig. 4 *B*). In all of the controls (90 total patches), MCC activity was found in normal amounts (Fig. 4 *B*).

To test the specificity of the inhibition of MCC by Tim23 antibodies, we examined the activity of an outer mem-



brane channel activity, PSC (Fig. 4 *C*). Proteoliposomes prepared using outer membranes were incubated with equivalent amounts of Tim23 IgG or antibody from preimmune serum. Neither IgG had any effect on the detection level of PSC, and activity similar to untreated proteoliposomes was found in the preparations preincubated with either preimmune or Tim23 IgG (Fig. 4 *C*). Thus, antibodies to Tim23p appear to specifically inhibit the inner membrane channel MCC, and further support the possibility that MCC plays a role in mitochondrial protein import.

Conductance of MCC Isolated from the tim23-1 Mutant Is Not Transiently Blocked by Presequence Peptides

To further test the connection between MCC and protein import, we examined MCC activity in mitochondria isolated from the *tim23-1* mutant. The *tim23-1* mutation results in a substitution of aspartate for glycine at position 186 in Tim23p (Emtage, 1994). Mitochondria isolated from *tim23-1* mutants are defective in the import of several different precursor proteins, including subunit IV of yeast cytochrome oxidase (Emtage and Jensen, 1993). We prepared mitochondrial inner membranes from either wildtype or the *tim23-1* mutant, reconstituted the membranes into proteoliposomes, and then measured the conductance of patches excised from the vesicles.

We found that the electrical properties of MCC isolated from wild-type and *tim23-1* strains were virtually identical (compare control current traces of Fig. 5 *A* with 5 *B* and Fig. 6 *A* with 6 *B*). In particular, MCC from both strains had the same peak conductance, predominant transition size, mean open time, and cation selectivity. Furthermore, permeability ratios for K⁺/Cl⁻ were ~6 for MCC from wildtype and *tim23-1* patches with a 150:30 mM KCl gradient. Conductance through MCC from both strains was voltage dependent, i.e., MCC is predominantly open at low (e.g., 20 mV) but not high potentials of either polarity. The V₀ (voltage where the probability of opening and closing are the same) at positive potentials was less than V₀ at negative potentials for MCC from both wild-type and *tim23-1* strains.

In the presence of presequence peptides, however, MCC activity from wild-type and tim23-1 strains differed dramatically. The conductance of MCC isolated from wild-type strains is transiently blocked by presequence peptides (Fig. 5 A, see also Figs. 2 and 3, and Table I). The flicker rate of MCC from the wild-type strain increased \sim 10-fold upon addition of the yCOX-IV₁₋₁₃ peptide to the bath solution at positive potentials (Fig. 5 A). Similarly, the flicker rate of wild-type MCC was ~10-fold higher at negative potentials if yCOX-IV₁₋₁₃ was included in the micropipette buffer (Fig. 6 A). The flicker rate of MCC isolated from wild-type cells increased with yCOX-IV₁₋₁₃ concentration in the bath and saturated by $\sim 25 \ \mu M$ (Fig. 7). This dose-dependent inhibition of MCC is similar to that required for the inhibition of protein import by presequence peptides (Glaser and Cumsky, 1990). In marked contrast, the activity of MCC isolated from the tim23-1 mutant was only slightly affected by the addition of yCOX-IV₁₋₁₃ peptide (Figs. 5 B and 6 B). Quantification showed that the tim23-1 mutation caused at least an 85%

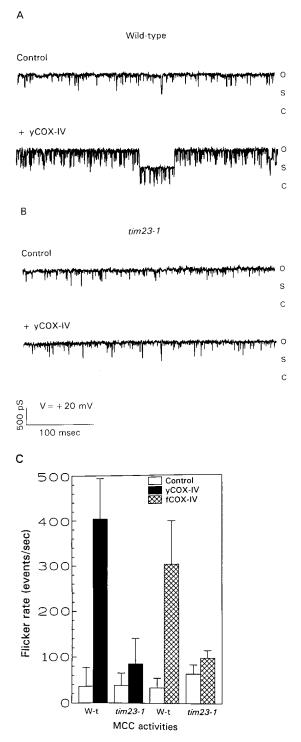


Figure 5. The conductance of MCC isolated from the *tim23-1* mutant is not blocked by presequence peptides in the bath. Proteoliposomes were prepared from inner membranes from wild-type cells (*A*) or the *tim23-1* mutant (*B*), and current traces of MCC activity were recorded from patches in the presence and absence of 50 μ M yCOX-IV₁₋₁₃ peptide in the bath solution. (*C*) The flicker rate (events/sec) from the open state to lower conductance states of MCC at 20 mV from wild-type and *tim23-1* strains was determined in the absence (control) and presence of 50 μ M of either yCOX-IV₁₋₁₃ or fCOX-IV₃₋₂₂. Error bars indicate standard deviations from a minimum of four determinations.

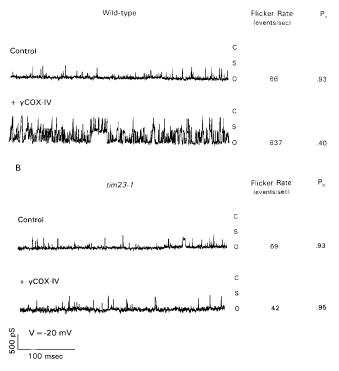


Figure 6. Rapid flickering induced by presequence peptides in the micropipette solution is reduced in MCC from the *tim23-1* mutant. Patches were excised from proteoliposomes containing wild-type (A) or *tim23-1* (B) mitochondrial inner membranes. Typical current traces of MCC activity at -20 mV recorded from different patches in the presence and absence of $100 \,\mu\text{M}$ yCOX-IV₁₋₁₃ peptide in the micropipette are shown. P_O corresponds to probability of occupying the open state.

reduction in the transient conductance blockade (or increased flicker rate) induced by yCOX-IV₁₋₁₃ and fCOX-IV in the bath (Fig. 5 *C*). Similar results were also found with yet another presequence peptide yCOX-VI at 2 μ M concentrations (data not shown). Furthermore, we found that peptides added to the micropipette, instead of the bath, failed to induce flickering of MCC isolated from the *tim23-1* mutant (Fig. 6). The flicker rate of wild-type MCC, but not *tim23-1* MCC, was ~10-fold higher at negative potentials when the yCOX-IV₁₋₁₃ peptide was present in the micropipette solution. At the same time, the lower open probability for wild-type MCC that is associated with the peptide-induced rapid flickering was not seen with MCC from the *tim23-1* strain (Fig. 6).

tim23-1 mutants are temperature-sensitive for growth and mitochondrial protein import, but mitochondria isolated from *tim23-1* cells are defective in protein import in vitro at all temperatures (Emtage and Jensen, 1993). We have recently found that the Tim23-1 protein is rapidly degraded during mitochondrial isolation from *tim23-1* strains (Ryan, K.R., R. Leung, and R.E. Jensen, manuscript submitted for publication). Similarly, we find that proteoliposomes prepared from *tim23-1* inner membranes contain greatly reduced levels of the Tim23-1 protein (Fig. 8). Equal amounts of proteoliposomes prepared from wildtype and *tim23-1* mitochondrial inner membranes were an-

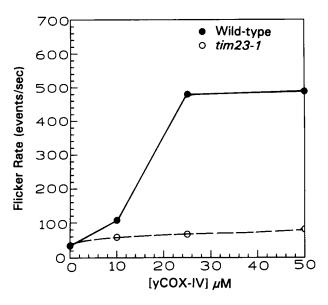
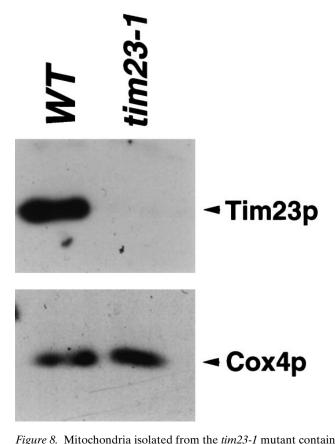


Figure 7. Dose dependence of blockade of MCC conductance by yCOX-IV₁₋₁₃ peptide. Flicker rates for typical MCC activity from wild-type (\bullet) or *tim23-1* (\bigcirc) strains at different concentrations of the yCOX-IV₁₋₁₃ peptide in the bath were determined from current traces (5–15 s) at 20 mV in single channel patches.

alyzed by immune blotting. While similar levels of cytochrome oxidase subunit IV (Cox4p; Fig. 8) and the β-subunit of the F1-ATPase (not shown) were seen in the two preparations, the level of the Tim23 protein was reduced at least 10-fold in the tim23-1 proteoliposomes. Importantly, the frequency of detecting MCC in proteoliposomes prepared from similar quantities of wild-type and *tim23-1* inner membrane protein was virtually the same. Twelve MCC were detected in thirteen patches from proteoliposomes prepared with 16 µg tim23-1 inner membrane protein/mg lipid, while 0, 7, and 32 MCC were recorded from fifteen patches each from proteoliposomes prepared with 3, 27, and 133 μ g wild-type inner membrane protein/ mg lipid, respectively. Hence, the reduced level of Tim23 protein in the inner membrane of *tim23-1* mitochondria may explain their defect in protein import, as well as the alteration (but not loss) of MCC activity.

tim23-1 Mutants Are Not Altered in the Activity of PSC, an Outer Membrane Peptide-sensitive Channel

To show that the *tim23-1* mutation specifically affected MCC activity, we examined the activity of the outer membrane peptide-sensitive channel, PSC. Like MCC in the inner membrane, the conductance of PSC is transiently blocked by presequence peptides (Henry et al., 1996; Fèvre et al., 1994; Theiffry et al., 1992; Juin et al., 1995). Outer membranes were isolated from mitochondria of wild-type cells and the *tim23-1* mutant, and then reconstituted into proteoliposomes. When membrane patches were examined, we found that the PSC activities from both preparations were comparable in terms of conductance, selectivity, and voltage dependence. Furthermore, addition of the yCOX-IV₁₋₁₃ peptide increased the flicker rate of PSC from both wild-type and *tim23-1* strains by \sim 10-



reduced amounts of the Tim23-1 protein. Mitochondria were isolated from wild-type cells and the *tim23-1* mutant, and proteoliposomes were prepared as described in Materials and Methods. Aliquots representing 30 μ g of proteoliposomes were immune blotted and decorated with antibodies to the Tim23 protein (Tim23p) and to cytochrome oxidase subunit IV (COX4p).

fold as shown by the current traces and histograms of Fig. 9. This inhibition was both dose- and voltage-dependent (data not shown). In addition, we previously found deletion of VDAC, or the adenine nucleotide translocator had no effect on MCC activity in proteoliposomes (Lohret and Kinnally, 1995*a*; Lohret et al., 1996). Our results indicate the *tim23-1* mutation specifically alters the activity of the inner membrane MCC, and has no effect on the outer membrane PSC activity. The Tim23 antibody and the *tim23-1* mutation allow discrimination between MCC and PSC activities.

Discussion

Our studies indicate a striking correlation between MCC activity and the translocation of precursors across the inner membrane. We find that Tim23p, an inner membrane import component, is required for peptide-sensitive activity of MCC. Antibodies to Tim23p block both protein import and the MCC channel. We find that MCC conductance is specifically blocked by presequence peptides. Furthermore, we find that the presequence peptide sensitivity of MCC isolated from the protein import deficient mutant *tim23-1* is dramatically reduced. MCC has several properties ex-

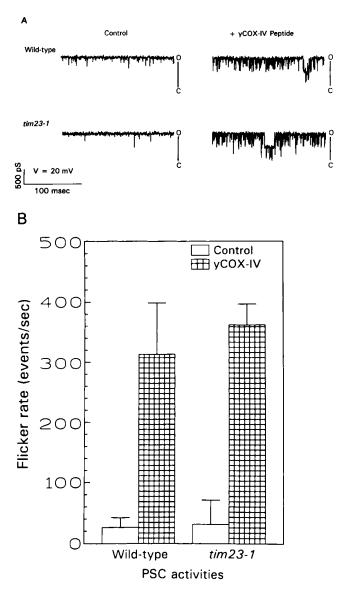


Figure 9. The *tim23-1* mutation does not affect the peptide-sensitive channel, PSC, of the mitochondrial outer membrane. (*A*) Sample current traces for PSC from proteoliposomes containing outer membranes from wild-type or *tim23-1* strains are shown in the presence and absence (control) of 50 μ M yCOX-IV₁₋₁₃ peptide in the bath. (*B*) The flicker rates of PSC of wild-type and *tim23-1* strains were determined from current traces represented by those in *A* above.

pected for a protein-translocating channel in the mitochondrial inner membrane. For example, the pore size of MCC is estimated at 2–3 nm (Zoratti and Szabó, 1994), which is sufficiently large to allow the passage of unfolded precursor proteins. In addition, the predominant transition size of MCC (500 pS) is similar to potential protein-conducting channels observed both in the endoplasmic reticulum and the bacterial plasma membrane (Simon and Blobel, 1991, 1992).

Biochemical studies indicate that the membrane potential drives the initial movement of the presequence through the inner membrane and that the presequence in transit is not tightly bound to the import apparatus (Martin et al.,

1991; Berthold et al., 1995; Ungermann et al., 1996). Thus, the inner membrane import channel is proposed to be a passive pore interacting only weakly with translocating polypeptide chains (Ungermann et al., 1994). Consistent with this idea, we found that the transient blockade of wild-type MCC by presequence peptides could occur from either side of the membrane in a potential-dependent manner, i.e., at positive potentials (pipette negative) when the presequence peptide was added to the bath and at negative potentials (pipette positive) when peptide was included in the pipette. In addition, flicker rate increased with the magnitude of the voltage. Moreover, the reduction in open probability and increase in flickering induced by addition of presequence peptide to the bath was reversed by perfusion with fresh media, suggesting the presequence peptides are not tightly bound. The peptideinduced flickering, however, was specific for presequence peptides. For example, peptides shown not to function as presequences, such as synB2 (Allison and Schatz, 1986; Roise et al., 1988), or peptides that were not cationic, did not affect MCC activity.

The presequence peptide-induced flickering between open and subconductance states seen in wild-type MCC may be due to the momentary occlusion of the channel during translocation of the peptide from one side of the membrane to the other. Although direct demonstration of peptide translocation through MCC will likely require reconstitution of MCC using purified components, a similar peptide-induced flickering seen in studies with the outer membrane channel, PSC, was shown to be associated with the movement of peptide across the membrane (Thieffry et al., 1992; Juin et al., 1995; Henry et al., 1996). Alternatively, the rapid flickering of MCC may result from a destabilization of the open state upon binding of the peptide to one or more sites on MCC. Since MCC isolated from the tim23-1 mutant is not blocked by presequence peptides added to either side of the membrane, we suggest that the tim23-1 mutation may either hinder translocation of presequence peptides through MCC or alter presequence peptide recognition by MCC.

Mitochondria must maintain an electrochemical gradient for ATP synthesis. Therefore, any protein-translocating channel in the inner membrane must be tightly regulated. While MCC is normally closed in mitochondria under metabolizing conditions, it is usually detected after inner membranes are reconstituted in liposomes. Presumably a regulatory component is lost during reconstitution that normally maintains MCC in a closed state in the absence of protein import. In preliminary studies, we find that an inner membrane pore, presumably MCC, can be opened in isolated mammalian mitochondria and mitoplasts under normal conditions by presequence peptides (Sokolove and Kinnally, 1996; Campo, M.L., and K.W. Kinnally, unpublished data).

The *tim23-1* mutation results in a substantial reduction in the import of several different precursors into isolated mitochondria (Emtage and Jensen, 1993). Although *tim23-1* strains are temperature-sensitive for viability, the protein import defect in vitro was seen at the permissive temperature. Consistent with previous results (Ryan, K.R., R. Leung, and R.E. Jensen, manuscript submitted for publication), we found the Tim23 protein was reduced 10–20-fold in mitochondria isolated from the tim23-1 mutant as compared to the wild-type strain. Associated with loss of Tim23 protein and a defect in protein import, we found that the activity of MCC from *tim23-1* mitochondria was markedly insensitive to presequence peptides. In the absence of peptide, however, MCC activity from wild-type strains and the tim23-1 mutant was similar. For example, no significant differences in pore size (as reflected by peak conductance), predominant transition size, voltage dependence, or ion selectivity were seen. Furthermore, the number of channels detected in the wild-type and *tim23-1* membrane preparations was virtually the same. Our findings that the Tim23 protein is reduced in *tim23-1* mitochondria suggests that Tim23p is not a structural component of the pore of MCC. Instead, we argue that Tim23p plays a regulatory function in MCC activity.

The Tim23 protein contains a 9-kD hydrophilic aminoterminal domain facing the intermembrane space, and four potential carboxyl-terminal membrane-spanning segments (Bauer et al., 1996; Emtage, J.L.T., and R.E. Jensen, manuscript submitted for publication). The amino terminus of Tim23p appears to function as a receptor for presequences as they are translocated through the outer membrane import machinery (Emtage et al., 1993; Bauer et al., 1996). In addition, Tim23p has been shown to form dimers in mitochondria in a potential-dependent manner (Bauer et al., 1996). Dimerization of Tim23p is disrupted upon the binding of precursors. The role of Tim23, therefore, may be to bind the presequence and pass the precursor to the inner membrane import channel. In this view, tim23-1 mutants would be defective in the recognition of the presequence, but MCC activity would not otherwise be affected. To further test the relationship between MCC and mitochondrial protein import, we are currently analyzing MCC defective in or lacking different import components.

We thank Carmen Mannella, Robert Murphy, and Richard Zitomer for their helpful discussions and for reading this manuscript. We thank Andre Moodie, Roxanne Leung, and Ana Rodriguez for technical assistance. Antibody raised against *N. crassa* VDAC was graciously provided by C.A. Mannella (Wadsworth Center, NYS Dept. of Health [NYSDOH], Albany, NY). Strain M22-2 was graciously provided by Michael Forte (Oregon Health Science University, Portland, OR). We also thank J. Dias (Wadsworth Center, NYSDOH, Albany, NY) for the synthesis of peptides and B. Trumpower (Dartmouth) for antibodies against the iron sulfur protein of complex I.

This research was supported by National Science Foundation grant MCB9513439 (K.W. Kinnally) and U.S. Public Health Service grant RO1-GM46803 (R.E. Jensen).

Received for publication 6 June 1996 and in revised form 22 January 1997.

References

- Allison, D.S., and G. Schatz. 1986. Artificial mitochondrial presequences. Proc. Natl. Acad. Sci. USA. 83:9011-9015.
- Bauer, M.F., C. Sirrenberg, W. Neupert, and M. Brunner. 1996. The role of Tim23 as voltage sensor and presequence receptor in protein import into mitochondria. *Cell*. 87:33–41.
- Beckmann, J.D., P.O. Ljungdahl, J.L. Lopez, and B.L. Trumpower. 1987. Isolation and characterization of the nuclear gene encoding the Rieske iron-sulfur protein (RIP1) from *Saccharomyces cerevisiae*. J. Biol. Chem. 262:8901– 8909.
- Berthold, J., M.F. Bauer, H.-C. Schneider, C. Klaus, K. Dietmeir, W. Neupert, and M. Brunner. 1995. The MIM complex mediates preprotein translocation across the mitochondrial inner membrane and couples it to the mt-Hsp70/ ATP driving system. *Cell*. 81:1085–1093.
- Blachly-Dyson, E., S. Peng, M. Colombini, and M. Forte. 1990. Selectivity

changes in site-directed mutants of the VDAC ion channel: structural implications. Science (Wash. DC). 247:1233–1236.

- Blobel, G., and B. Dobberstein. 1975. Transfer of proteins across membranes. I. Presence of proteolytically processed and unprocessed nascent immunoglobulin light chains on membrane-bound ribosomes of murine myeloma. J. Cell Biol. 67:835–851.
- Blom, J., M. Kübrich, J. Rassow, W. Voos, P.J.T. Dekker, A.C. Maarse, M. Meijer, and N. Pfanner. 1993. The essential yeast protein MIM44 (encoded by MPI1) is involved in an early step of preprotein translocation across the mitochondrial inner membrane. *Mol. Cell. Biol.* 13:7364–7371.
- Criado, M., and B.U. Keller. 1987. A membrane fusion strategy for single channel recordings of membranes usually non-accessible to patch-clamp pipette electrodes. *FEBS Lett.* 224:172–176.
- Daum, G., P. Böhni, and G. Schatz. 1982. Import of proteins into mitochondria. J. Biol. Chem. 257:13028-13033.
- Decker, G.L., and J.W. Greenawalt. 1977. Ultrastructural and biochemical studies of mitoplasts and outer membranes derived from french-pressed mitochondria. J. Ultrastr. Res. 59:44–56.
- Dekker, P.J., P. Keil, R. Rassow, A.C. Maarse, N. Pfanner, and M. Meijer. 1993. Identification of MIM23, a putative component of the protein import machinery of the mitochondrial inner membrane. *FEBS Lett.* 330:66–70.
- Emtage, J.L.T. 1994. The role of mas6p in mitochondrial protein import. Ph. D. thesis, Johns Hopkins University. 1–228.
- Emtage, J.L.T., and R.E. Jensen. 1993. mas6 encodes an essential inner membrane component of the yeast mitochondrial protein import pathway. J. Cell Biol. 122:1003–1012.
- Fèvre, F., J.-P. Henry, and M. Thieffry. 1994. Reversible and irreversible effects of basic peptides on the mitochondrial cationic channel. *Biophys. J.* 66:1887– 1894.
- Gasser, S.M., G. Daum, and G. Schatz. 1982. Import of proteins into mitochondria. Energy-dependent uptake of precursors by isolated mitochondria. J. Biol. Chem. 257:13034–13041.
- Glaser, S.M., and M.G. Cumsky. 1990. Localization of a synthetic presequence that blocks protein import into mitochondria. J. Biol. Chem. 265:8817–8822.
- Guo, X.W., P.R. Smith, B. Cognon, D. D'Arcangelis, E. Dolginova, and C.A. Mannella. 1995. Molecular design of the voltage-dependent, anion-selective channel in the mitochondrial outer membrane. J. Struct. Biol. 114:41–59.
- Hamill, O.P., A. Marty, E. Neher, B. Sakmann, and F.J. Sigworth. 1981. Improved patch-clamp techniques for high-resolution current recording from cells and cell-free membrane patches. *Pflügers Arch.* 381:85–100.
- Henry, J.-P., P. Juin, F. Vallette, and M. Thieffry. 1996. Characterization and function of the mitochondrial outer membrane peptide-sensitive channel. J. Bioenerg. Biomembr. 28:101–108.
- Horst, M., P. Jeno, N.G. Kronidou, L. Bolliger, W. Oppliger, P. Scherer, U. Manning-Kreig, T. Jascur, and G. Schatz. 1993. Protein import into yeast mitochondria: the inner membrane import site protein ISP45 is the MPI1 gene product. *EMBO (Eur. Mol. Biol. Organ.) J.* 12:3035–3041.
- Isaya, G., W.A. Fenton, J.P. Hendrick, K. Furtak, F. Kalousek, and L.E. Rosenberg. 1988. Mitochondrial import and processing of mutant human ornithine transcarbamylase precursors in cultured cells. *Mol. Cell. Biol.* 8:5150–5158.
- Juin, P., M. Pelleschi, C. Sagné, J.-P. Henry, M. Thieffry, and F.-M. Vallette. 1995. Involvement of the peptide sensitive channel in the translocation of basic peptides into mitochondria. *Biochim. Biophys. Res. Commun.* 211:92–99.
- Kang, P.-J., J. Ostermann, J. Shilling, W. Neupert, E.A. Craig, and N. Pfanner. 1990. Requirement for hsp70 in the mitochondrial matrix for translocation and folding of precursor proteins. *Nature (Lond.)*. 348:137–143.
- Kinnally, K.W., T.A. Lohret, M.L. Campo, and C.A. Mannella. 1996. Perspectives on the mitochondrial multiple conductance channel. J. Bioenerg. Biomembr. 28:115–121.
- Kinnally, K.W., D.B. Zorov, Yu. Antonenko, and S. Perini. 1991. Calcium modulation of inner mitochondrial channel activity. *Biochem. Biophys. Res. Commun.* 176:1183–1188.
- Kinnally, K.W., D.B. Zorov, and Yu. Antonenko. 1992. Modulation of inner mitochondrial membrane channels activities. J. Bioenerg. Biomembr. 24: 99–110.
- Kronidou, N.G., W. Oppliger, L. Bolliger, K. Hannavy, B.S. Glick, G. Schatz, and M. Horst. 1994. Dynamic interaction between ISP45 and mitochondrial hsp70 in the protein import system of the yeast mitochondrial inner membrane. *Proc. Natl. Acad. Sci. USA*. 91:12818–12822.
- Kübrich, M., P. Keil, J. Rassow, P.J.T. Dekker, J. Blom, M. Miejer, and N. Pfanner. 1994. The polytopic mitochondrial inner membrane proteins MIM17 and MIM23 operate at the same preprotein import site. *FEBS Lett.* 349:222–228.
- Laemmli, U.K. 1970. Cleavage of structural proteins during assembly of the head of bacteriophage T4. *Nature (Lond.)*. 227:680–685.
- Lithgow, T., B.S. Glick, and G. Schatz. 1995. The protein import receptor of mitochondria. *TIBS*. 20:98–101.
- Lohret, T.A., and K.W. Kinnally. 1995a. Multiple conductance channel activity of wild-type and VDAC-less yeast mitochondria. *Biophys. J.* 68:2299–2309. Lohret, T.A., and K.W. Kinnally. 1995b. Targeting peptides transiently block a

mitochondrial channel. J. Biol. Chem. 270:15950-15953.

- Lohret, T.A., R. Murphy, T. Drgoñ, and K.W. Kinnally. 1996. Evidence that the mitochondrial multiple conductance channel, MCC, is not related to the adenine nucleotide translocator. J. Biol. Chem. 271:4846–4849.
- Maarse, A.C, J. Blom, L.A. Grivell, and M. Miejer. 1992. MPI1, an essential gene encoding a mitochondrial membrane protein, is possibly involved in protein import in yeast mitochondria. *EMBO (Eur. Mol. Biol. Organ.) J.* 11: 3619–3628.
- Maarse, A.C., J. Blom, P. Keil, N. Pfanner, and M. Miejer. 1994. Identification of the essential yeast protein MIM17, an integral mitochondrial inner membrane protein involved in protein import. *FEBS Lett.* 349:215–221.
- Mannella, C.A. 1982. Structure of the outer mitochondrial membrane: ordered arrays of pore-like subunits in outer membrane fractions from *Neurospora* crassa mitochondria. J. Cell Biol. 94:680–687.
- Mannella, C.A., A.F. Neuwald, and C.E. Lawrence. 1996. Detection of likely transmembrane β -strand regions in sequences of mitochondrial pore proteins using the Gibbs sampler. *J. Bioenerg. Biomembr.* 28:163–169.
- Martin, J., K. Mahlke, and N. Pfanner. 1991. Role of an energized inner membrane in mitochondrial protein import. J. Biol. Chem. 266:18051–18057.
- Pfanner, N., and M. Meijer. 1995. Pulling in the proteins. *Curr. Biol.* 5:132–135.Pfanner, N., E. Craig, and M. Meijer. 1994. The protein import machinery of the mitochondrial inner membrane. *TIBS*. 19:368–372.
- Rassow, J., A.C. Maarse, E. Krainer, M. Kubrich, H. Muller, M. Miejer, E.A. Craig, and N. Pfanner. 1994. Mitochondrial protein import: biochemical and genetic evidence for interaction of matrix hsp70 and the inner membrane protein MIM44. J. Cell Biol. 127:1547–1556.
- Roise, D., and G. Schatz. 1988. Mitochondrial presequences. J. Biol. Chem. 263: 4509–4511.
- Ryan, K.R., and R.E. Jensen. 1993. mas6p can be cross-linked to an arrested precursor and interacts with other proteins during mitochondrial protein import. J. Biol. Chem. 268:23743–23746.
- Ryan, K.R., and R.E. Jensen. 1995. Protein translocation across mitochondrial membranes: What a long, strange trip it is. *Cell*. 83:517–519.
- Ryan, K.R., M.M. Menold, S. Garrett, and R.E. Jensen. 1994. SMS1, a highcopy suppressor of the yeast *mas6* mutant, encodes an essential inner membrane protein required for mitochondrial protein import. *Mol. Biol. Cell*. 5: 529–538.
- Schatz, G., and B. Dobberstein. 1996. Common principles of protein translocation across membranes. *Science (Wash. DC)*. 271:1519–1526.
- Scherer, P.E., U.C. Manning-Krieg, P. Jeno, G. Schatz, and M. Horst. 1992. Identification of a 45-kDa protein at the protein import site of the yeast mitochondrial inner membrane. *Proc. Natl. Acad. Sci. USA*. 89:11930–11934.
- Schleyer, M., B. Schmidt, and W. Neupert. 1982. Requirement of a membrane potential for the posttranslational transfer of proteins into mitochondria. *Eur. J. Biochem.* 125:109–116.
- Schneider, H.C., J. Berthold, M.F. Bauer, K. Dietmeier, B. Guiard, M. Brunner, and W. Neupert. 1994. Mitochondrial hsp70/MIM44 complex facilitates protein import. *Nature (Lond.)*. 371:768–774.
- Simon, S.M., and G. Blobel. 1991. A protein-conducting channel in the endoplasmic reticulum. *Cell*. 65:371–380.
- Simon, S.M., and G. Blobel. 1992. Signal peptides open protein-conducting channels in *E. coli. Cell*. 69:677–684.
- Smith, J.W., and D.J. Knauer. 1987. A heparin binding site in antithrombin III. Identification, purification and amino acid sequence. J. Biol. Chem. 262: 11964–11972.
- Sokolove, P.M., and K.W. Kinnally. 1996. A mitochondrial signal peptide from *Neurospora crassa* increases the permeability of isolated rat liver mitochondria. *Archives Biochem. Biophys.* 336:69–76.
- Sorgato, C., and O. Moran. 1993. Channels in the mitochondrial membranes: knowns, unknowns and prospects for the future. *Crit. Rev. Biochem. Mol. Biol.* 28:127–171.
- Stanley, S., J.A. Dias, D. D'Arcangelis, and C.A. Mannella. 1995. Peptide-specific antibodies as probes of the topography of the voltage-gated channel in the mitochondrial outer membranes of *Neurospora crassa* mitochondria. J. Biol. Chem. 270:23743–23748.
- Thieffry, M., J. Neyton, M. Pelleschi, F. Fèvre, and J.-P. Henry. 1992. Properties of the mitochondrial peptide-sensitive cationic channel studied in planar bilayers and patches of giant liposomes. *Biophys. J.* 63:333–339.
- Towbin, H., T. Staehelin, and J. Gordon. 1979. Electrophoretic transfer of proteins for polyacrylamide gels to nitrocellulose sheets: procedure and some applications. *Proc. Natl. Acad. Sci. USA*. 76:4350–4354.
- Ungermann, C., W. Neupert, and D.M. Cyr. 1994. The role of Hsp70 in conferring unidirectionality on protein translocation into mitochondria. *Science* (*Wash. DC*). 266:1197–1198.
- Ungermann, C., B. Guiard, W. Neupert, and D.M. Cyr. 1996. The delta psi- and Hsp70/MIM44-dependent reaction cycle driving the early steps of protein import into mitochondria. *EMBO (Eur. Mol. Biol. Organ.) J.* 15:735–744.
- Zoratti, M., and I. Szabó. 1994. Electrophysiology of the inner mitochondrial membrane. J. Bioenerg. Biomembr. 26:543–553.