The cytochrome bc1 complexis a highly conserved enzyme of the mitochondrial respiratory chain. In S. cerevisiae it consists of three catalytic subunits, Cobp, Rip1p, and Cyt1p, plus seven additional subunits: Cor1p, Qcr2p, Qcr6p, Qcr7p, Qcr8p, Qcr9p, and Qcr10p. The crystal structure of the complex shows that two functional units, each containing these ten subunits, associate with each other in the mitochondrial inner membrane. Assembly of a functional complex requires two proteins, Cbp3p and Cbp4p, that are not components of the complex but may associate with it during assembly. It also requires Bcs1p, an AAA-family ATPase that interacts with a precursor of the complex to mediate incorporation of the Rip1p and Qcr10p subunits. The mechanism of energy transfer by the complex, known as the protonmotive Q cycle, has been studied in detail. The net result of the Q cycle is the stepwise transfer of an electron through the complex from ubiquinol to cytochrome c, coupled with the translocation of a proton across the mitochondrial inner membrane. The function of the cytochrome bc1 complex is essential to the energy-generating process of oxidative phosphorylation, which is carried out by the enzyme complexes of the mitochondrial respiratory chain. Cytochrome b, which contains two b-type heme groups, is one of the catalytic subunits of the cytochrome bc1 complex and comprises a major part of the site at which ubiquinol is oxidized, termed center P of the enzyme.Cytochrome b, encoded by the mitochondrial COB gene, is the only mitochondrially-encoded subunit of the cytochrome bc1 complex. The structure and expression of the COB gene are extremely complex: it contains multiple introns, whose number varies between strains, and its mRNA maturation and translation require multiple nuclear-encoded proteins. Generation of the correct 5' end of the COB mRNA, which is cotranscribed with an upstream tRNA gene, requires the action of Cbp1p and Cbt1p. The COB gene of the genome reference strain S288C has five introns, named bI1 through bI5. The first intron, bI1, is a group II, self-splicing intron; the other introns are group I. The second through fourth intronscontain open reading frames that are contiguous with the upstream COB exons, such that translation of alternately spliced mRNAs produces fusion proteins comprised of both cytochrome b sequences and intron-encoded sequences. These proteins have maturase activity and are involved in splicing of introns from both the COB and COX1 genes. Splicing of the fifth intron, bI5, requires the nuclear-encoded protein Cbp2p. Translation of mRNAs bearing the COB 5'-untranslated leader requires the specific translational activators Cbs1p and Cbs2p.Cytochrome b is highly conserved across bacteria and all eukaryotes. Mutations of the human ortholog MTCYBcause a variety of disease syndromes due to complex III deficiency. Mutations conveying resistance to the anti-malarial and antifungal drug atovaquone are known to arise in the cytochrome b orthologs of parasites and fungi such as Plasmodium falciparum, Toxoplasma gondii, and Pneumocystis jirovecii.