



Front cover image: A schematic structural representation of subunits I (brown) and II (blue) of the *Rhodobacter sphaeroides* aa₃ cytochrome c oxidase (PDB ID: 1M56). These two subunits contain all the redox-active co-factors, Cu, heme a and the catalytic site, which consists of heme a₃ and Cu. Amino-acid residues and water molecules (red spheres) defining the K and D proton pathways are shown. During turnover, electrons are transferred from cytochrome c to Cu, heme a and the catalytic site as indicated by the red arrow. Oxygen enters to the catalytic site through a channel located in the membrane-spanning part of the protein as indicated by the bold arrow. Protons are transferred along the black arrows. A proton-exit pathway has not been identified and the black arrow above the hemes is shown at an arbitrary location. Figure courtesy of C. von Ballmoos. For further details, see corresponding article on p. 650 of this issue.

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