Cytochrome *c* oxidase (CcO) catalyzes the oxygen reduction coupled to the electron and proton transfer. Previous biochemical studies indicated that Zinc (Zn) inhibited proton transfer by binding either inside or outside surface of CcO. Similar inhibition is also caused by (Cadmium) Cd. To identify the Zn/Cd inhibitory sites, we have carried out the X-ray structural analyses of bovine heart CcO–Zn/Cd complex. We found several Zn/Cd-binding sites by using the crystal of dimeric CcO. The highest affinity Zn/Cd-binding site (Zn2/Cd1 site) is located at the inside surface of the subunit III. The second highest affinity site (Zn3/Cd2 site) on the inside surface is located at the D-pathway entrance. The zinc binding affinity for the second site suggests that the zinc site is tightly coupled with the proton-pumping site. Recently, we analyzed Zn/Cd-binding to monomeric CcO which gives crystal packing different from that in the dimeric CcO crystal. The X-ray structural analysis showed Zn-binding to the Zn2, Zn3 and additional sites including the site near the K-pathway entrance. Several Zn-binding sites have been found on the outside surface. However none of them is located on the subunit I surface from which pumping protons exit.

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S11.28 The finding of the CBB_3-oxidase gene and the evidence for enzyme expression in extremely alkaliphilic bacteria

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The aim of this study was to determine whether the *cbb*$_3$-oxidase is expressed in new representatives of extremely alkaliphilic bacteria *Thioalkalivibrio* with the optimum of growth at pH = 10. For this purpose we used the synthetic oligopeptides identical to the C-terminal parts of the catalytic subunit and then worked out the specific antibodies against the catalytic subunit. A *cbb*$_3$-type oxidase was shown to be expressed in membranes of extremely alkaliphilic bacterium *Thioalkalivibrio versutus* using polyclonal rabbit anti-ccoN antibodies. The expressed oxidase is composed of 48, 34 and 29 kDa subunits, the two smaller of them being presented by cytochromes *c*. The 48 kDa subunit cross reacting with anti-ccoN antibodies was detected as a catalytic one. Sequence of the 5′-end terminal fragment of the catalytic subunit gene produced significant alignment with sequences of *Methylobacillus flagellatus* KT and *Thiobacillus denitrificans cbb*$_3$-type oxidase *ccoN*, displaying only distant phylogenetic relationship to them. Acknowledgments: authors thanks N. Pozdnyakova for assistance in work with animals.

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S11.29 Possible proton transfer mechanism through peptide groups in the H-pathway of the bovine cytochrome *c* oxidase

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A recently proposed proton transfer path (H-path) in bovine cytochrome *c* oxidase involves the peptide group connecting Tyr440 and Ser441 and interrupts the continuous hydrogen-bond network across which protons are expected to propagate. Our first-principles calculations show that the porpagation is not hindered, but occurs via a multi-step process. A proton is initially transferred to the carbonyl oxygen of a keto form of the Tyr440-Ser441 peptide group [–CO–NH–], producing an imidic acid [–C(OH)–NH–] as a metastable state. The amide proton of the imidic acid is then transferred in a barrierless way to the deprotonated carboxyl group of the Asp51 side chain, leading to the formation of an enol form [–C(OH)=N–]. Eventually, an enol-to-keto tautomerization is realized via a double proton transfer in the two adjacent Tyr440-Ser441 and Ser441-Asp442 peptide groups. An analysis of the pathway shows that each elementary process occurs through the shortest distance, thus preserving the X-ray structure, and the path is characterized by a reasonable activation barrier.

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S11.30 Oxygen reaction in the *cbb*$_3$-type cytochrome *c* oxidase from *Rhodobacter Sphaeroides*

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The *cbb*$_3$-type cytochrome *c* oxidase is a proton-pumping terminal oxidase present solely in bacteria. The enzyme is expressed mainly under very low oxygen tension and it has been shown to have a high apparent affinity for oxygen. Therefore it is of interest to investigate the properties of the enzyme that allow it to function under such conditions. In this work we have studied directly the reaction of cytochrome *cbb*$_3$ with molecular oxygen using fast kinetic approaches. The flow-flash method, where a reduced carbon monoxide inhibited enzyme is mixed with oxygenated buffer and the reaction is started by a laser flash, allowed us to follow the optical changes during the catalytic reaction at different oxygen concentrations as well as the potential generation across the membrane that takes place as a result of the charge transfer. The initial reaction with oxygen was found to be relatively slow ($k_{on} \sim 2 \times 10^7$ 10^7 M^{-1} s^{-1}) and the consequent steps of reduction were coupled to potential generation. Therefore the efficiency in reducing molecular oxygen at low oxygen concentration is not based on a particularly fast binding of O_2, but rather on the irreversibility of the oxygen binding to the enzyme.

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S11.31 Nitric oxide reductase from *Paracoccus Denitrificans* —what are the five conserved glutamates in NorB good for?

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The *c*-type nitric oxide reductase (NOR) from *Paracoccus denitrificans* is an odd member of the heme copper oxidase superfamily. It catalyses NO reduction; $2NO + 2e^- + 2H^+ \rightarrow N_2O$ $N_2O + H_2O$ and also oxygen reduction as a side reaction. All known *c*-type NORs have been shown to have five conserved glutamates (E) in the catalytic subunit (here NorB). These are, by *Paracoccus denitrificans* numbering, the E122, E125, E198, E202 and E267. The E122 and E125 are presumed to face the periplasm and the E198, E202 and E267 are thought to be located in the interior of the membrane, not far from the catalytic site.