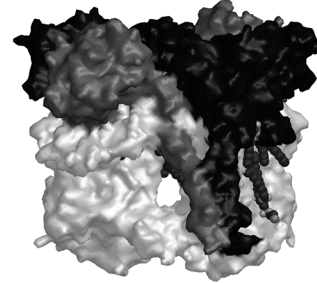


W0007

**The bc1 Complex from *Rhodobacter Sphaeroides* at 2.85 Å Resolution.** Lothar Esser<sup>1</sup>, Maria Elberry<sup>2</sup>, Chang-An Yu<sup>2</sup>, Linda Yu<sup>2</sup>, Di Xia<sup>1</sup>, <sup>1</sup>National Institutes of Health, National Cancer Inst., Bethesda, MD 20892, <sup>2</sup>Dept. of Biochemistry and Molecular Biology, Oklahoma State Univ., Stillwater, OK 74078.

Proton-translocating quinol/quinone oxido-reductases are membrane embedded protein complexes (bc1) that play a central role in the ATP production of the majority of organisms. The structures of mutant *Rhodobacter Sphaeroides* bc1 inhibited by stigmatellin (1) and stigmatellin and antimycin (2) have been determined. These crystals are monoclinic (C2) with cell dimensions of  $a=353.4\text{Å}$ ,  $b=147.1\text{Å}$ ,  $c=162.3\text{Å}$ ,  $\beta=104.5^\circ$  and diffract between 2.85 and 3.10 Å. The structures were solved by MR using a dimeric model of beef bc1. The asymmetric unit contains three dimers of cyt b, cyt c1 and ISP with clearly visible density for the respective inhibitors. However, there was no density for subunit IV.  $\Delta$ -Sub IV *R.S.* bc1



crystals are triclinic and contain two independent dimers. The appearance of interpretable electron density for *R.S.*-specific sequences as well as lipid and detergent molecules proved the solution to be correct. The difficulties in crystallizing this membrane protein, the function of the longer bacterial sequences and the role of the lipids will be discussed. The current best model (1) containing 42,192 atoms refined to  $R(\text{cryst}) = 0.24$  and  $R(\text{free}) = 0.28$ .