

**Experiment title:**

Low resolution phasing of datasets of human LDL particles by MAD and MASC.

Experiment number:

LS-1746

Beamline: ID14-4	Date of experiment: from: 30 November 2000 to: 02 December 2000	Date of report: 28.2.03
Shifts: 6	Local contact(s): Dr. Raimond RAVELLI	<i>Received at ESRF:</i>

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¹ This paper is dedicated to the memory of Prof. Joseph Keul (1932-2000)

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Synopsis

A preliminary crystallographic model for the Low-Density Lipoprotein (LDL) particle was obtained at a resolution of 27 Å using several *ab initio* phasing methods.

Abstract

The knowledge of the molecular structure of LDL, a large lipoprotein complex, is of great interest for medical investigations. Currently available LDL crystals do not diffract to high resolution and do not allow the application of standard crystallographic techniques. Additional difficulties arise due to a very dense crystal packing and due to the presence of several components with quite different mean densities. Several *ab initio* phasing methods previously reported by the authors have been successfully applied to find a crystallographic image of LDL at a resolution of 27 Å. The most promising results have been obtained using direct phasing with a connectivity analysis of the electron-density maps. The current image makes it possible to discern a single particle covered by a layer of relatively high density that is asymmetrically distributed on the particle surface. It shows a partition of high and low densities inside the particle and, in particular, strips of varying density in the lipid core.