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Experiment title:

S100A12 protein from Human neutrophils

Experiment number:

LS1383

Beamline: Date of experiment:

ID14-4 from:

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Shifts:

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Report:

S100A12 belongs to the calgranulin subfamily of the S100 family of proteins with the sequence identity between members of the subfamily varying between 70-78%. S100A12 possesses extracellular activities and triggers various types of cellular activation. It has been shown that ligation of the RAGE cellular receptor with S100A12 mediates activation of endothelial cells, macrophages and lymphocytes, cells which are central to inflammatory response. Involvement of S100A12 in exocytosis has also been proposed. Recently it was found that three anti-allergy drugs, amlexanox, cromolyn and tranilast, which inhibit IgE-mediated degranulation of mast cells, bind to S100A12. These studies indicate that S100A12 may play a significant role in the process of degranulation, which remains a poorly understood aspect of exocytosis, involving a large number of genes and their products.

Crystals of S100A12 usually grow in R3 space group with unit cell dimensions of a = b = 99.6 Å, c = 64.2 Å. These crystals contain two monomers, each with the molecular weight of 10.4 kDa, in the asymmetric part, resulting in the solvent content of 57.9%. Unfortunately, most of these crystals are twinned, and only a small number of crystals could be grown from limited amounts of non-recombinant protein isolated from human blood. An initial data set was collected in February 1999 at ID14-4 from the only crystal which grew in a different space group, P2, with a=53.8 A, b = 100.5 A, c = 113.0 A, β =94.5°. The structure solution by molecular replacement using the data set in P2, proved to be difficult, owing to the presence

of 8 to 12 molecules in the asymmetric unit (12 molecules correspond to a solvent content of 48%). The structure was solved using 2.7 Å data collected in-house from a tiny crystal in space group R3, which appeared to be non-twinned. The same crystal was used to extend the resolution to 1.95 Å at ID14-2 station in December 1999. The structure refinement using the recent high resolution data is in progress.