dreamed regions suggest that the folding of CHM and GDI may be similar. Site-directed mutagenesis of a region defined by two of the SCR5S which forms a compact structure at the apex of domain I reveals a critical role for this region in the binding of Rab proteins. The crystal structure of GDI has been determined using MIRAS method and refined to crystallographic R-value of 19.8% and R-free=27.5% for a total of 450 residues of the molecule in the asymmetric unit.

**MS04.07b.03 THE STRUCTURE OF EF-Tu-(EF-Ts)2 COMPLEX SUGGESTS A MECHANISM FOR NUCLEOTIDE RELEASE.** Takemasa Kawashima, Carmen Berthet-Colominas, Michael Wulff,6* Stephen Cusack, and Reuben Leberman, EMBL Grenoble Outstation, Grenoble, France, *European Synchrotron Radiation Facility, B.P. 220, 38043 Grenoble Cedex, France.

The crystal structure of the bacterial elongation factor complex EF-Tu-(EF-Ts)2 from Escherichia coli has been determined at 2.5 Å resolution. It reveals a typical guanine nucleotide binding protein in interaction with its guanine nucleotide release factor. The complex is a tetramer where two EF-Ts form a tight dimer and each EF-Tu binds essentially to one EF-Ts, with barely any contact between EF-Tu, such that the complex is best described by the formula EF-Tu-(EF-Ts)2·EF-Tu. Comparison of EF-Tu·GDP and EF-Tu·EF-Ts shows that the conformational change between the two structures mainly alters the magnesium binding site, by disrupting the coordination of the ion. This suggests a molecular mechanism by which EF-Ts releases the GDP bound to EF-Tu where the affinity of EF-Tu for GDP is lowered by the loss of the magnesium ion.


**MS04.07b.04 GAMMA-FIBRINOGEN: CRYSTAL STRUCTURE OF A 30 KDA C-TERMINUS FRAGMENT AT 2.1 Å RESOLUTION.** V.C. Yee, K.P. Pratt, H.C. Cote, E. Le Trong, D.W. Chung, R.E. Stenkamp, and D.C. Teller, Departments of Biochemistry and Biological Structure, University of Washington, Seattle, WA 98195.

The crystal structure of a 30 kDa carboxy terminus fragment of the fibrinogen gamma chain has been determined using MIR phases to 2.5 Å resolution, and refined against diffraction data to 2.1 Å resolution. Fibrinogen is the central structural protein in the blood coagulation process. Cleavage of fibrinogen by the serine protease thrombin yields fibrin, which spontaneously polymerizes to form a clot matrix. Subsequent covalent crosslinking by factor XIIIa, a transglutaminase, produces a mechanically and proteolytically stable blood clot.

Fibrinogen is a disulfide-crosslinked dimer of heterotrimers, and contains two copies each of the alpha, beta, and gamma chains. A recombinant 30 kDa C-terminus fragment of the gamma chain containing the principle factor XIIIa crosslinking site, the calcium-binding site, the platelet receptor recognition domain, part of the polymerization surface, and one of the sites which activate t-PA through plasminogen, has been the focus of our crystallographic studies. This fragment crystallizes in space group P21, and its structure has been determined using MIR phases to 2.5Å resolution. The model has been refined against 2.1 Å resolution diffraction data to give Rcryst=15.5% and Rfree=22.7%.

This first structure of a large fibrinogen fragment provides fresh insight into the polymerizing and crosslinking events important during blood clot formation. In other work, we have determined several crystal structures of factor XIII in various forms. Our structural characterization of both enzyme and substrate extends our understanding of the transglutaminase reaction, and provides information that will be helpful in continuing studies toward obtaining the structure of an enzyme-substrate complex.

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