ESRF	Experiment title: Spliceosmal U5 snRNP-specific 15 K protein	Experiment number: LS 915
Beamline: BM 14	Date of experiment:from:29-Nov-97to:0 1 -Dee-97	Date of report: 29-Jul-98
<b>Shifts:</b> 8	Local contact(s): Leonard Gordon	Received at ESRF:

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## **Report:**

The splicing of mRNA is catalyzed by the spliceosome which is formed by the ordered interaction of the Ul, U2, U5, and U4/U6 snRNPs and numerous additional proteins. We had obtained single crystals of the spliceosomal U5 snRNP-specific 15 K protein. Since this protein does not display any significant sequence homology to a protein of known three-dimensional structure, we considered to solve the crystal structure by means of MAD using selenomethionine containing protein.

The crystals belong to space group  $P2_12_12$  (cell constants a=61.3 Å, b=65.2 Å, c=36.4 Å) and contain one molecule in the asymmetric unit. They showed diffraction beyond 1.4 Å resolution using the synchrotron radiation at beam line BM14. First the MAD experiment was carried out collecting data of one frozen crystal at three wavelengths (Table 1). Also a complete data set of native crystal was collected at a maximum resolution of 1.4 A. These diffraction data enabled us to solve and refine the novel crystal structure of the U5 snRNPspecific 15 K protein (Figure 1). The globular fold of the U5 15 K protein resembles the thioredoxin fold. However the canonical Cys-X-X-Cys motif found in thioredoxin and thioredoxin like proteins is replaced by Asp-X-X-Cys. Surpringsly, a disuflide bond is present almost in the same location formed by Cys38 and Cys79. The Cys79 is part of the loop connecting P-strands 3 and 4.

Data set	Resolution	No. of	No of unique	Completeness	R <sub>merg</sub>
		observations	reflections		
λ1	30 1.9	113,639	11,601	95.0 %	4.3 %
λ2	30 1.9	113,617	11,533	95,9 %	4.3 %
λ3	30 1.9	114,335	11,464	95.5 %	4.1 %
Native	30 1.4	381,393	28,054	95,2 %	2.9%

Table 1: Summary of Data Sets collected at BL19

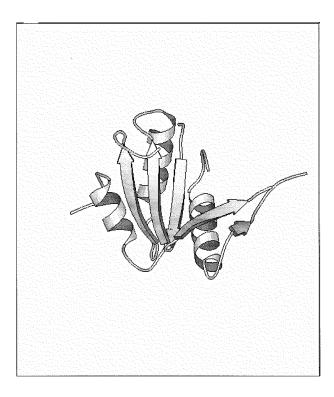


Figure 1: Structure of the U5 snRNP-specific 15 K protein