

	Experiment title: BAG-LEBS-2007-1	Experiment number: 30-01-796
Beamline: BM30A	Date of experiment: from: Saturday 20/07/2007 at 8:30 to: Monday 21/07/2007 at 8:00	Date of report: 28/2/07
Shifts: 3	Local contact(s): Dr. L. Serre	<i>Received at ESRF:</i>
Names and affiliations of applicants (* indicates experimentalists): Jenny Keller* (PhD Student): Herman Van Tilbeurgh's Group, Institut de Biochimie et de Biophysique Moléculaire et Cellulaire (IBBMC), Equipe Génomique Structurale, CNRS UMR8619, Université Paris-Sud, Orsay, France		

Report:

Jenny Keller* (3 shifts) : yeast multi-protein complexes involved in DNA replication, ribosome biogenesis, mRNA quality control pathway and cell signalling and archeophage structural genomics project

1) Virar79

Spacegroup: P₆₁22 with a=b=62 Å and c=111Å

Resolution: 2.33 Å.

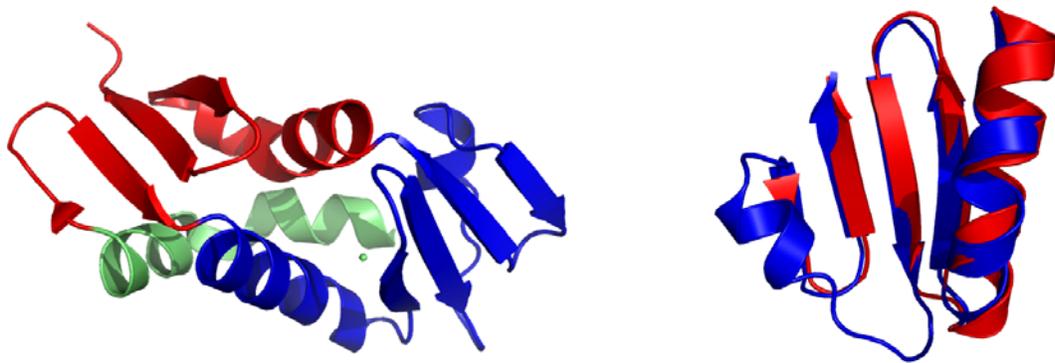
Rsym=0.098

Completion 100%)

We solved the structure of virar79, a 15kD protein from Acidianus Filamentus virus 1. X-ray diffraction data from a crystal of the SeMet substituted virar79 were collected on beamline BM30A (ESRF) at the Se K-edge. The crystal diffracted to 2.33 Å and belongs to P₆₁22 space group with one molecule per asymmetric unit. From these data, we could obtain high quality experimental phases that allowed us to build the protein. The structure was further refined against 1.9 Å resolution native data collected on the ESRF ID29 beamline. The protein consists in a beta-alpha-beta sandwich. Two anti parallel 4-stranded beta sheets surround 3 alpha helices with a $\beta_1\beta_2\alpha_1\beta_3\beta_4\alpha_2\beta_5\beta_6\alpha_3\beta_7\beta_8$ topology. One sheet is composed of $\beta_1\beta_2\beta_7\beta_8$ and the other of $\beta_3\beta_4\beta_5\beta_6$. The connection between the two sheets is performed by α_1 in one side and by α_3 in the opposite side (α_1 connects β_2 to β_3 and α_3 connects β_6 to β_7) while α_2 connects two strands from the same sheet (β_4 to β_5). The tree helices establish few hydrophobic contacts between them.

The protein is composed of two quasi identical domains related by a two fold symmetry axis. The first domain is comprises $\beta_1\beta_2\alpha_3\beta_7\beta_8$ and the second $\beta_3\beta_4\alpha_2\beta_5\beta_6\alpha_1$. An rmsd of 1.34 Å is observed for 29C α of the two domains. The main difference between the two domains comes from the insertion of 14 residues forming the helix α_2 and the linker between α_2 and β_4 .

No such fold has been reported in public databases according to DALI and the SSM server of EBI.



Structure of virar79:

Left: cartoon representation of the protein colored as left. Right: superposition of the two domains.