	Experiment title: Structural studies of protein-protein interactions in model oligomeric proteins.	Experiment number: LS-1685		
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Report:

This project aims at studying the structural determinants of proteinprotein association in different oligomeric proteins (model systems) using a combination of X-ray crystallography, molecular modeling, sitedirected mutagenesis and protein binding studies.

During the last six months, we have collected various diffraction data sets from wild-type or mutant forms of three proteins: dihydrofolate reductase (DHFR), glyceraldehyde-3-phosphate dehydrogenase (GPDH) from insect cells, and the constant domains (FC) of distinct immunoglobulin isotypes.

Data collection is summarized in table 1. All the crystal structures have been solved using molecular replacement techniques, and the crystallographic refinements are currently in progress (except for the DHFR crystal form collected at 0.9Å resolution, for which the data processing is preliminary and should be improved before starting the crystallographic refinement at atomic resolution).

Crystal form	Beam- line	λ (Å)	No. of images	Space group	a (Å)	b (Å)	c (Å)	Data resolution (Å)	Data complet. (%)	R merge (%)	Multipli- city
DHFR (single mutant form- dimer)	ID-14.3	0.931	190	P2 ₁ 2 ₁ 2 ₁	39.53	44.99	85.44	2.5	98.1	8.3	6.6
DHFR (two single mutant forms – heterotetramer)	ID-14.3	0.931	100	I422	67.55	67.55	52.02	1.4	99.3	2.9	7.2
DHFR (two single mutant forms - heterotetramer)	ID-14.3	0.931	190	I422	67.55	67.55	52.02	0.9 (*)	1	-	-
FC (wild-type)	ID-14.3	0.931	100	P2 ₁ 2 ₁ 2 ₁	49.38	79.10	137.7	2.1	98.3	7.3	3.8
GPDH (wild-type)	ID-14.3	0.931	180	F222	97.34	101.7	165.0	2.8	99.9	6.2	7.3

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