



Participant Profile

for the
Turkish-German Strategy Workshop 2006
TÜBİTAK Marmara Research Center,
Istanbul- Gebze Turkey
13 – 15 December 2006



International Bureau (IB)
of the Federal Ministry of
Education and Research
(BMBF)

1. Contact details and personal information

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Role/function¹:	Project Leader BioSAXS beamline	Fax:	++49 40 89902-149
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Postcode and City:	22603 Hamburg		

¹ **Role/function** e.g. working group leader, managing director, postdoc, PhD etc.

² **Organisation type** e.g. university, research institution, small and medium enterprise (SME), industry etc.

Working Group:

- | |
|---|
| <input type="checkbox"/> 1 Material Technologies |
| <input checked="" type="checkbox"/> 2 Biotechnology, Genomics and Food |
| <input type="checkbox"/> 3 Energy |
| <input type="checkbox"/> 4 Information and Communication Technologies |
| <input type="checkbox"/> 5 Environmental Protection, Climate Change and Sustainable Development |

Areas of activity:

- | | |
|---|--|
| <input checked="" type="checkbox"/> research | <input checked="" type="checkbox"/> training |
| <input type="checkbox"/> technology development | <input type="checkbox"/> dissemination |
| <input type="checkbox"/> demonstration | <input type="checkbox"/> other: |

Keywords characterising your area of research:

Please choose the appropriate key words (max. 5) from the following list:
<http://www.cordis.lu/fp6/keywords>

Structural biology

Expertise, technologies and infrastructures available in your institution:

Research activities / expertise:

Methods: Protein Crystallography, Small angle x-ray scattering on proteins in solutions (SAXS)

Key technologies: Structure determination of proteins

Infrastructures: Synchrotron based X-ray experiments for scattering and diffraction, high throughput protein crystallization facility, computational infrastructure structure determination/modelling

Key publications:

The SAXS solution structure of RF1 differs from its crystal structure and is similar to its ribosome bound cryo-EM structure.

Vestergaard, B., Sanyal, S., Roessle, M., Mora, L., Buckingham, R.H., Kastrop, J.S., Gajhede, M., Svergun, D.I. & Ehrenberg, M. Mol Cell. 2005 Dec 22;20(6):929-38.

Structure of the metal-independent restriction enzyme BfiI reveals fusion of a specific DNA-binding domain with a nonspecific nuclease.

Grazulis, S., Manakova, E., Roessle, M., Bochtler, M., Tamulaitiene, G., Huber, R. & Siksnys, V. Proc Natl Acad Sci U S A 2005 Nov 1;102(44):15797-802. Epub 2005 Oct 24.

Strong binding of myosin heads stretches and twists the actin helix.

Tsaturyan, A.K., Koubassova, N., Ferenczi, M.A., Narayanan, T., Roessle, M. & Bershitsky, S.Y. Biophys J. 2005 Mar;88(3):1902-10. Epub 2004 Dec 13.

The "roll and lock" mechanism of force generation in muscle.

Ferenczi, M.A., Bershitsky, S.Y., Koubassova, N., Siththanandan, V., Helsby, W.I., Panine, P., Roessle, M., Narayanan, T. & Tsaturyan, A.K. Structure. 2005 Jan;13(1):131



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2. Past and present research collaborations

Are you familiar
with the European
Framework
Programme?

<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No
<input type="checkbox"/> with Framework Programme 5	
<input checked="" type="checkbox"/> with Framework Programme 6	
<input type="checkbox"/> with Framework Programme 7	

EU-projects you are
involved in:

**Programme title / contract number / title / acronym / your function
(coordinator / partner / contractor)** Design Study / RIDS 011934 / SAXIER /
EMBL Hamburg is Coordinator

Past projects

Present projects

Other international
collaborations:

Collaboration with Sabanci University; Istanbul
Collaboration with University of Milano; Milano
Collaboration with european users groups supported by I3 / IA-SFS

Name(s) and
contact details of
potential partners:

**If you would like to suggest the participation of particular partners from the
partner country based on existing contacts or collaboration experience,
you are welcome to indicate their names and contact details below:**

3. Presentation at the Workshop

I will give a presentation at the workshop (approx. 10 min.) to present my institution, my expertise, and my collaboration interests. The contents of my presentations is summarised below (max. 1 page).

The European Molecular Biology Laboratory (EMBL) is one of the leading research institutes for Life Science in Europe. The EMBL Hamburg is a specialized unit for structural biology using synchrotron radiation provided by the Deutsches Elektronen-Synchrotron (DESY) and operates five X-ray beamlines for protein crystallography, one beamline for X-ray absorption spectroscopy and a small angle X-ray scattering (SAXS) beamline dedicated for proteins in solution. In addition a high throughput crystallisation facility was opened 2005. These facilities are open for the international user community and accessible over a proposal system. SAXS is versatile tool for structural investigations of biological macromolecules in solution and the structure of native particles can be investigated at low resolution. In contrast with other methods SAXS allows one to investigated structural changes of proteins upon response to variations in external conditions such as temperature, pH etc. Developments in data evaluation software and experiment hardware permits now fast and reliable model building out of the experimental data. The available software packages on the BioSAXS station cover all steps in data analysis ranging from semi-automatic data reduction, data analysis and indirect Fourier transformation up the ab initio low resolution model building. Ab initio model building technique as well as rigid body modeling allows one to analyze the overall shape of the macromolecule based only on the scattering data, and taking advantage of already available high or low resolution structures. Semi-automatic modeling up to completely automatic rigid body modeling using distance constrains are possible with our present software packages. This software is freely available for the academic user community (ATSAS program suite) and widely used. The new BioSAXS beamline planned for the german synchrotron project Petra III will operational 2009-2010. This beamline will adequately exploit the exceptionally high brilliance of the Petra-III source to further improve the efficiency of structural analysis using the small-angle scattering technique accompanying new and fast analysis methods developed at the EMBL. The BioSAXS station will share the infrastructure for biological sample preparation and handling with the other EMBL beamlines and will lead towards a unique environment for cutting edge research in life science.



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I agree with the publication of my data on the Workshop website!

PLEASE FILL IN THIS FORM **UNTIL 22 SEPT. 2006 AND RETURN IT TO:**

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