## EMBL Hamburg: Brief History

EMBL Hamburg is the oldest unit of EMBL. In 1969, Ken Holmes was developing new methods using synchrotron radiation beams as a source for X-ray diffraction from muscle fibres. At that time, the facility he used at the Deutsches Elektronensynchrotron (DESY) in Hamburg was the first of its kind in the world. Holmes suggested to Sir John Kendrew, who became the first Director General of EMBL, to coordinate the international use of DESY's beams for biological structure research. Initially, EMBO gave modest funds to pursue experiments at DESY, and an Outstation at Hamburg was added to the EMBL proposal, along with another Outstation in Grenoble, where EMBL would coordinate the biological uses of the neutron beams produced by the Institut Laue-Langevin (ILL) in Grenoble, France.

During the late seventies, under the leadership of Heinrich Stuhrmann, the Hamburg Outstation created a boom in synchrotron radiation experiments, both by EMBL and guest scientists. New equipment and beam lines were added, providing increasing access to the radiation for small-angle scattering, high-resolution X-ray spectroscopy and protein crystallography experiments. Eventually, EMBL Hamburg became a leading facility in the world for such research. The demand for access to this radiation by visiting scientists had intensified considerably and EMBL Hamburg, under Michel Koch, Juan Bordas and later Keith Wilson, directed considerable efforts to increasing the number of beam lines and improving the associated technology. This required the development of two-dimensional detectors, and EMBL Hamburg produced the first online imaging plate scanner for protein crystallography, which is now commercialised and very widely used. Wilson continued to strengthen Hamburg's in-house research, based on the knowledge that EMBL scientists with a vested interest in the technology were the most likely to fuel technical improvements and provide effective support to visitors. A major interest of the crystallography group has been the study of proteins at atomic resolution.

In part because of the success of so many experiments performed at the EMBL Hamburg beamlines, a need for state-of-the-art synchrotron radiation facilities across Europe and other parts of the world became evident. In 1992, DESY decided to convert the DORIS storage ring into a dedicated synchrotron radiation facility. A new bypass was built allowing to set-up a number of wiggler beamlines with substantially enhanced intensities. One such wiggler fan was split into two halves allowing to construct two additional beamlines in protein crystallography, one for applications requiring energy tuneability and the other one optimised for high photon flux. During the late nineties, EMBL Hamburg experienced the largest numbers of external users, exceeding 500 in some of the years, and close to 15% of the structures of biological macromolecules produced worldwide came from Hamburg.

During the last decade, the emerging availability of sequence data from entire genomes revolutionised life sciences and had its impact on structural biology as well. Key words such as 'structural genomics' and 'high throughput' became basic vocabulary, and it became evident that, by moving into more complex systems for high-resolution structure determination, the most serious bottlenecks are in the preparation of samples. Consequently, the EMBL Hamburg started to complement its synchrotron beamlines with advanced facilities for expression of the corresponding genes, and purification and characterisation of biological samples. In 2005, one of the largest automatic crystallisation facilities with a storage 'hotel' for 10 000 trays was established. Taking advantage of these new infrastructures, several research groups from EMBL Hamburg became involved in structural proteomics projects such as the European pilot consortium SPINE, and more specific projects focused on targets from mycobacteria and viruses. In parallel, EMBL Hamburg became an important contributor for software packages allowing the automatic interpretation of data collected using synchrotron radiation. The most well known suites are ARP/wARPfrom Victor Lamzin for applications in protein crystallography, and ATSAS from Dmitri Svergun for applications in Small Angle X-ray Scattering.

In 2002, DESY decided to convert the next bigger storage ring PETRA into a dedicated synchrotron facility. According to calculations by DESY, the new PETRA-III ring could generate synchrotron light with extremely low emittance, permitting state-of-the-art future applications. EMBL has proposed to build an integrated life science facility, with synchrotron experiment stations for applications in protein crystallography and Small Angle X-ray Scatttering, plus equipment for sample preparation and crystallisation.

*Written by Matthias Wilmanns, Head of EMBL Hamburg*
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