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European boost for structural genomics

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The aim of the BIOXHIT project, which is funded for four years, is to build a common platform for European researchers working in structural biology, and to facilitate the high-throughput solving of protein structures. Current technologies available at major European research centers will be developed further, integrated and standardized. "We already have all the single components necessary to solve molecular structures," says Victor Lamzin, who is the grant coordinator at EMBL-Hamburg. "We have synchrotrons, we can grow protein crystals, we have the software components and we can obtain structures. But the tools we use were not originally designed for high-throughput work. This is what is needed now because of the tens of thousands of new molecules we have discovered in the many genome sequencing projects," Lamzin adds.

BIOXHIT (pronounced BIO-X-HIT) will soon reduce the time it takes to obtain the structure of a given molecule. Robots can replace time-consuming manual steps, and BIOXHIT is specifically aimed at improving the process by which samples are handled, the equipment needed to detect X-rays, and the computers and software needed to model structures. This is intended to encourage more researchers to work on protein structures.

"Biocrystallography used to be a field for specialists," explains Lamzin, "but today, researchers from all walks of biology want to solve molecular structures at the synchrotrons. The new platform will make this process very user-friendly; it will even allow them to send us their samples and work remotely, from their own institutions."

References

1. The BIOXHIT Project, [http://www.embl-hamburg.de/BIOXHIT/]

2. The EMBL Hamburg Outstation, [http://www.embl-hamburg.de/]