

# Unique partnership produces life-critical 3D structures

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Most diseases are caused by malfunctions in the body's complex protein machinery. The next generation of drugs will be designed on the basis of 3D protein models that scientists are creating. The Structural Genomics Consortium laboratory at Swedish medical university Karolinska Institutet has now made available the structure of PARP3, the four hundredth structure in this unique project to chart the body's proteins.

The Structural Genomics Consortium (SGC) is a collaborative project involving scientists in Sweden, Britain and Canada. Since 2004, the SGC has devoted itself to determining the structure of human proteins of particular medical and therapeutic relevance. The four hundredth protein structure PARP3, which today is made freely available to other scientists, can be used in the development of cancer therapies.

"The structural data from the SGC will be a unique resource for accelerating the early phase of drug development projects," says Jan Lundberg, Executive Vice President Discovery Research at AstraZeneca. "We see great value in this kind of focused and effective work identifying human proteins, and congratulate the SGC on its advances."

Since the SGC's goal – to have 386 structures available by June 2007 – has been met by a wide margin, it is also a victory for the unusual partnership between the public and private sectors. The SGC is a charitable organization and publishes the 3D structural models it determines without delay or priority rights for its private or public

financers.

"This result wouldn't have been possible if it had been done by individual research groups focusing on their own special interests," says Professor Jan Carlstedt-Duke, Dean at Karolinska Institutet. "The dialogue with the scientific community has also ensured that the results come to the benefit of other scientists."

The structural models are not only powerful tools for drug development, they are also of fundamental importance to our understanding of disease mechanisms and of how proteins operate.

Source: Karolinska Institutet

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