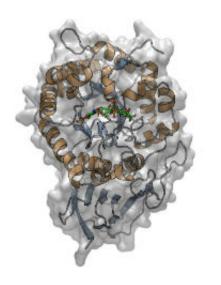


## Scientists reveal structure of key cancer target enzyme

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3D structure of heparanase bound to a sugar ligand

A team from the University of York has published research unveiling the 3-D structure of human heparanase, a sugar-degrading enzyme which has received significant attention as a key target in anti-cancer treatments.

Though naturally regulated in a healthy organism, heparanase is an enzyme which is produced in excessive quantities in a cancer situation. The sugar-degrading activity of this excess heparanase leads to exaggerated degradation of the sugars in the extracellular 'matrix' (the molecules surrounding cells), making it easier for cancer cells to proliferate.



This is one of many biological processes involved in tumour cell metastasis - the spread of cancer from one organ to another - but its importance as a therapeutic target has led to the development of a number of anti-heparanase compounds, which are now at advanced clinical trial stage.

The knowledge of the 3-D <u>structure</u> of this enzyme identified by the team from the Structural Biology Laboratory (YSBL) in the Department of Chemistry at York, will boost work on understanding and targeting heparanase worldwide. The study, which was supported by the European Research Council and the Medical Research Council, is published in *Nature Structural and Molecular Biology*.

Knowledge of the structure will enable a more rational approach to drug design. It will improve scientists' ability to predict and design chemicals that will bind to heparanase to obtain more specific and effective antiheparanase compounds.

Professor Gideon Davies, one of the authors of the study, said: "The 3-D structure of human heparanase will allow the design and application of novel therapeutic agents based upon the intimate details of its structure. All groups worldwide will now be able to benefit from understanding of its 3-D shape and interaction with sugars."

**More information:** Liang Wu et al. Structural characterization of human heparanase reveals insights into substrate recognition, *Nature Structural & Molecular Biology* (2015). DOI: 10.1038/nsmb.3136

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