## Structural Studies of Human *a*-thrombin

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Thrombin is a member of the serine proteinase family. The structure consists of two chains. Thrombin plays an important role in the coagulation of blood; contact with fibrinogen results in the formation of fibrin that polymerize into a blood clot.

X-ray data have been measured at ESRF ID 14.4, SRS MPW10 and at APS SBC. The four X-ray diffraction data sets achieved thus far are between 1.26 and 1.4 Å based on  $\langle F/\sigma(F) \rangle > 2$  and completeness > 50%, two bound with hirugen only, and two with an inhibitor as well. We wish to identify hydrogen atoms at the active site and other key water hydrogens that are involved in the cleavage of fibrinogen.

In addition we wish to use neutron crystallography because the scattering factor for neutrons of deuterium equals that of C, N and O. We have so far grown a large (0.7x0.7x-0.3mm) thrombin crystal. Tests of the diffraction on the ILL LAue DIffractometer are imminent.

Overall, we plan to understand better how inhibitors bind to thrombin, so as to design enhanced drugs.

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