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Screening with X-rays

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In the October Nature Biotechnology, Nienaber *et al*. demonstrate that drug or inhibitor leads can be identified by high throughput X-ray crystallography (*Nat. Biotech*. 2000, **18**:1105-1108). Pre-formed protein crystals are soaked in solvents containing mixtures of 100 compounds before the crystals are examined by X-ray crystallography. Nienaber *et al*. look for changes in the electron-density map caused by ligand binding. The compounds in each mixture are chosen to be diverse in shape so that they can be differentiated readily, and the technique allows the site and orientation of binding to be identified. Nienaber *et al*. use this method to screen thousands of compounds per day in a successful search for a high affinity inhibitor of the anti-cancer target urokinase.

References

1. *Nature Biotechnology*, [http://www.nature.com/nbt/]