

Finding the lock for a key - Identification of the targets of screening hit molecules

Nadine Homeyer[⊗], Bernardo Ochoa-Montaño[▽], Ruud van Deursen[⊗], Kathrin Heikamp[⊗],
Fabio Zuccotto[⊗], Tom Blundell[▽], Ian Gilbert[⊗]

[⊗] Drug Discovery Unit, Division of Biological Chemistry and Drug Discovery, School of Life Sciences, University of Dundee, Sir James Black Centre, DD1 5EH, UK

[▽] Department of Biochemistry, University of Cambridge, Old Addenbrooke's Site, 80 Tennis Court Road, Cambridge CB2 1GA, UK

When molecules from phenotypic screens have been identified as hits the main question is: What are the targets of these hit molecules? Targets could be primary target molecules that are affected directly by the hit molecule or secondary targets associated with side effects or polypharmacology. Knowing the targets and potential binding sites of a hit molecule can provide the basis for further optimization of the initial hit, e. g. by structure-based design. But, how can targets and binding sites be identified?

We developed a target identification procedure that is based on hit molecule fragmentation and binding site analogy search using structures from the Protein Data Bank [1], the Credo Database [2], and models of *Mycobacterium tuberculosis* (Mtb) proteins from the Chopin Database [3]. The initial system was developed for Mtb, because tuberculosis is still a wide-spread disease today [4] and a number of drug design efforts have been initiated in recent years in order to fight this disease [5]. The target identification procedure was implemented into a database-based web platform that can be easily handled by medicinal chemists. Furthermore, the database of protein structures can be extended to proteins of other organisms, so that in the future target identification beyond *M. tuberculosis* proteins will be possible. We therefore believe that the developed platform will largely facilitate target identification for phenotypic screening hit molecules.

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