In silico-guided target identification for a new molecular scaffold

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A collection of 2,150 active sites[1] from the Protein Data Bank was screened by high-throughput docking to identify putative targets for five representative molecules of a combinatorial library sharing a triazepanedione scaffold. Five targets were prioritized for experimental evaluation by computing enrichment in individual protein entries among the top 2% scoring targets. Out of the five proposed proteins, phospholipase A2 was shown to be a true target for a panel of triazepanediones which exihibited micromolar affinities toward several isoforms of the latter enzyme.

[1] Paul N. *et al.*, Proteins 2004 – **54**:671-80