Use of computational Grid based methodology for bioactive compounds design in plant virology

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Drug discovery is an extended process that can take as many as 15 years from the first compound synthesis in the laboratory until the therapeutic agent, or drug, is brought to market.

Gridock is a molecular modeling software developed to identify potentially bioactive compounds (hit-compounds) in order to speed-up the drug discovery process. It's based on the virtual-screening approach in which the activity of a large set of molecules is predicted by multiple molecular docking calculations distributed on a Grid system. More in details, GriDock joints the VEGA flexibility and the AutoDock 4 power to take full advantage of the Grid technology.

The applications were ported on the Sicilian Grid infrastructure, solving parallelization problem and adjusting compilation time directives. This effort leaded to a ready and run process able to produce results on the Grid. The platform has been used to analyze different aspects of advanced biology as protein involved in inflammatory response, inhibitors of HIV integrase, inhibitor of human receptors. Recently a study was undertaken in order to test the features implemented in GriDock on plant pathology, the *Citrus tristeza virus* (CTV) case was considered. The RNA-dependent-RNA polymerase (RdRp) was identified as possible therapeutic target because this enzyme plays a pivotal role in the CTV replication. The viral RdRp was modelled and the potential inhibitors of this enzyme were identified through virtual screenings calculations. Three hit compounds have been selected after a screening of about 1.000.000 molecules and are in testing for *in vivo* and *in vitro* experiments.

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