

FragMAX research

Clues to block replication of SARS-CoV-2 found with FragMAX platform

An international collaboration of scientists used FragMAX to identify four fragments that interact with the nsp10 protein of the SARS-CoV-2 virus. The fragments could be used to develop inhibitors that supplant key enzymes activated by the protein – an application with the potential to block the viral replication process.

Full article:



Contact us



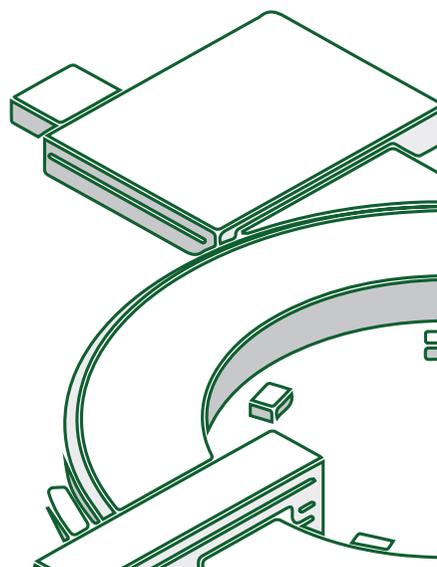
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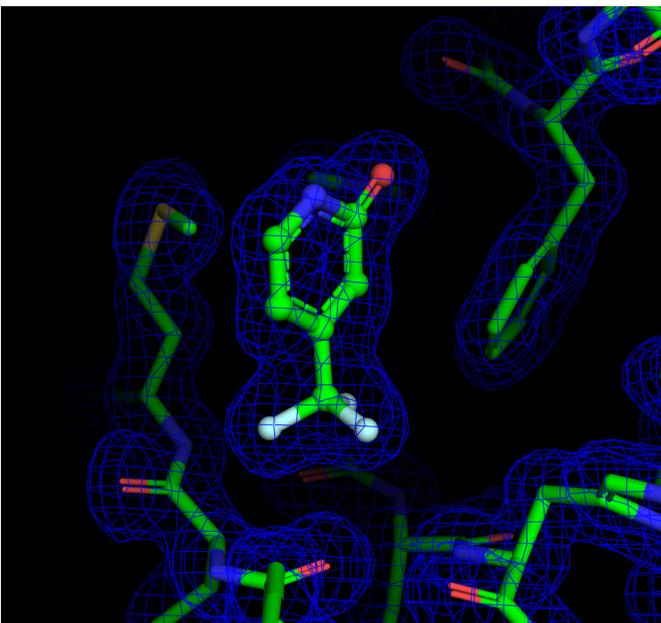


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Fragment screening at MAX IV

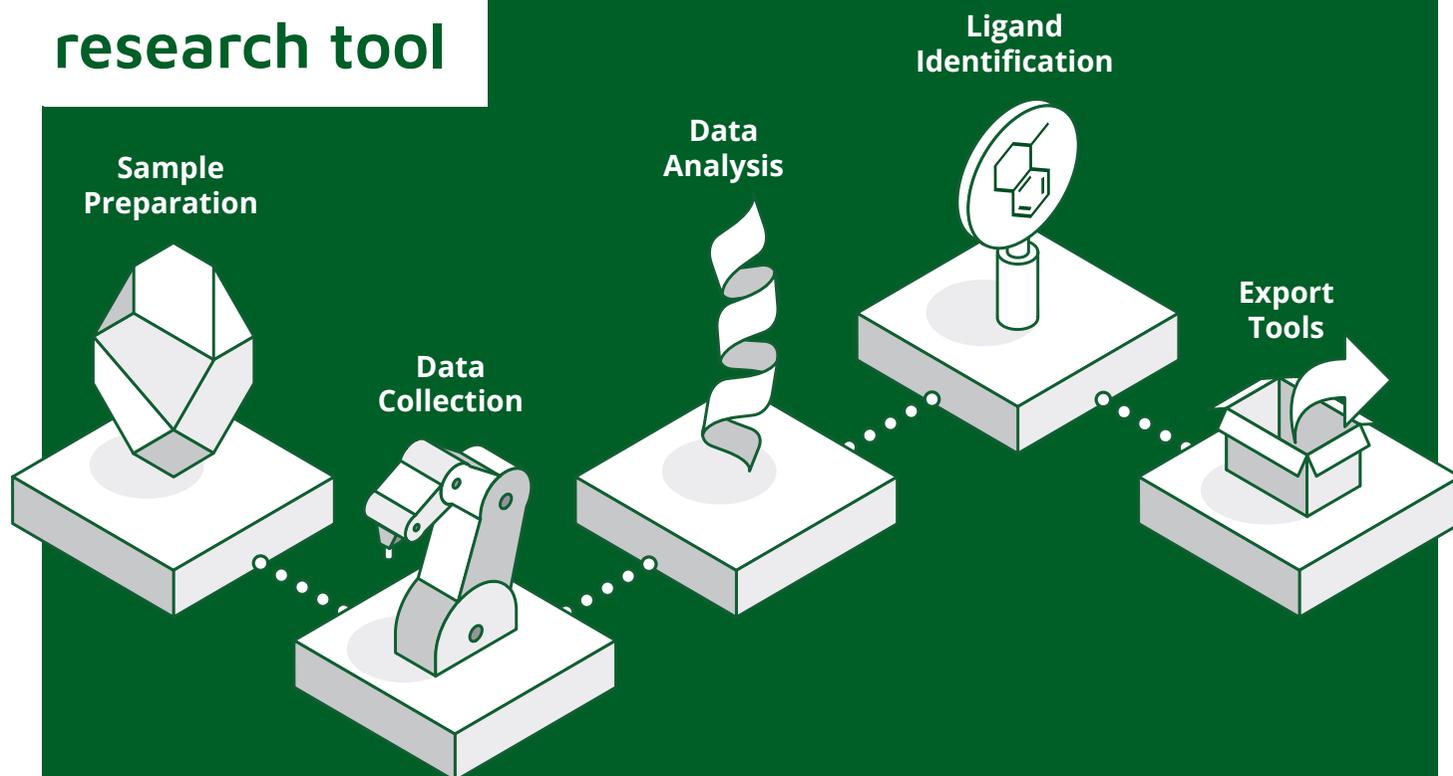
MAX IV



Explore new possibilities

For the discovery of new and better pharmaceutical drugs, crystallographic fragment screening is a powerful method to map the binding sites of target proteins and find new functionalities to exploit. It reveals the three-dimensional structures of protein-ligand complexes and enables the identification of chemical groups that interact with the target.

An all-in-one research tool



MAX IV's modular screening facility FragMAX is equipped for all types of protein-ligand studies. It offers crystal preparation, data collection, fast data analysis tools, and diverse fragment libraries including FragMAXlib (172 compounds) and DSI (860 compounds). Researchers may also work with their own samples. Our dedicated staff will assist you every step of the way, from experimental design and sample preparation to data processing – FragMAX offers end-to-end user support.

All projects are supported by a database system which tracks every step of the experiment and provides comprehensive data capture. Additionally, we offer software tools for rapid online and offline data processing and refinement.

Read more:



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