



Contribution ID: 199

Type: Poster

Hundreds of starting points to develop protein-protein interaction modulators

Tuesday, 15 March 2022 18:14 (1 minute)

Crystallographic fragment screening facilitates the identification of weak but efficient small molecules (fragments) while elucidating their binding mode and position. This enables structure-guided optimization of bound fragments into potent modulators. Here, the ~1000-fragment large F2X-Universal Library was screened against a spliceosomal protein-protein complex and resulted in hundreds of hits.

Primary authors: BARTHEL, Tatjana (Helmholtz-Zentrum Berlin); WOLLENHAUPT, Jan (Helmholtz-Zentrum Berlin); Dr LIMA, Gustavo M. A.; Prof. WAHL, Markus C. (Freie Universität Berlin); WEISS, Manfred (Macromolecular Crystallography, Helmholtz-Zentrum Berlin für Materialien und Energie (HZB-MX))

Presenter: BARTHEL, Tatjana (Helmholtz-Zentrum Berlin)

Session Classification: Postersession

Track Classification: Main conference: Biologic Structure, Function, Reactivity, and Regulation