Poster Presentation

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Fragment-screening at the BESSY II MX-beamlines of the Helmholtz-Zentrum Berlin

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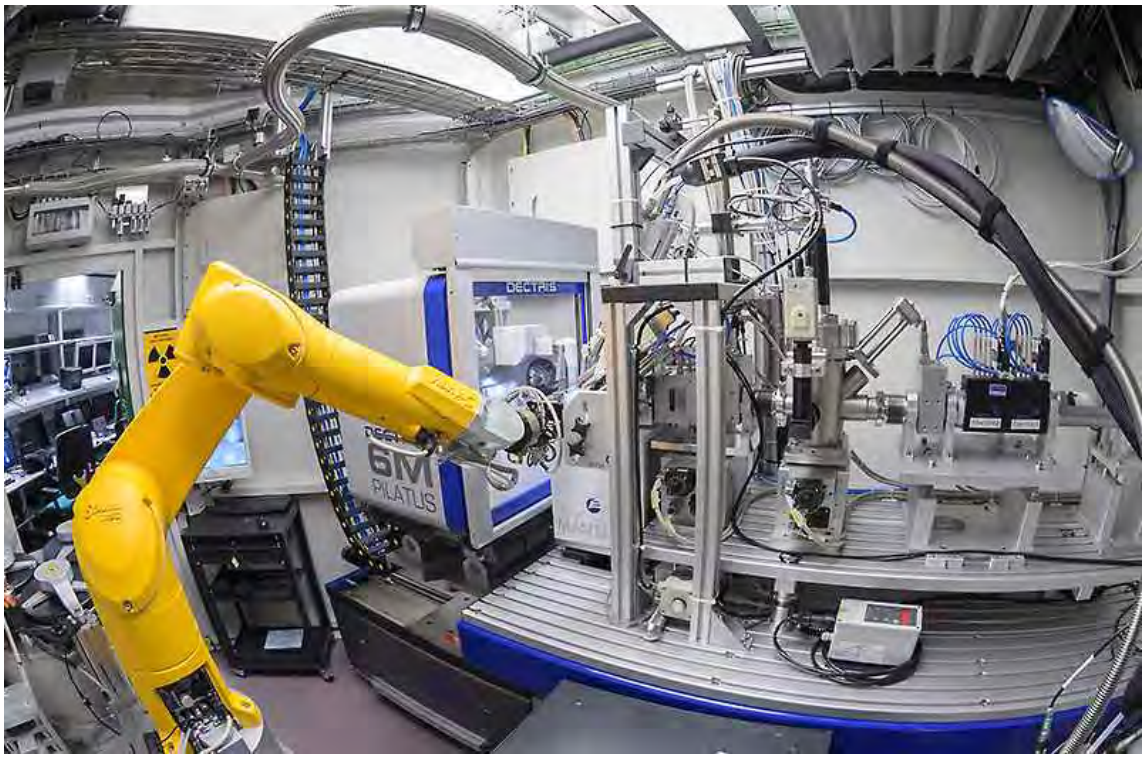
Within the last decade, the fragment-based screening approach has been matured to a reliable and powerful instrument of pharmaceutical drug discovery. The success of fragment screening strongly depends on the quality of the chosen fragment library (100-200 Da), the quality of the target protein diffraction as well as the possibility to use high throughput methods for the screen application. A thorough crystallographic analysis of many protein-fragment complex structures and their binding modes has the perspective to result in the development of new potential lead structures and to map the interaction landscape of protein surfaces. Recently we started the development of a dedicated experimental facility for high throughput fragment screening at the BESSY II storage ring. The in house data processing pipeline "XDSAPP" [1] has been developed to speed up the data evaluation of large amounts of diffraction data. We have assembled a fragment library of 96 compounds and have validated this library against two target proteins. These first results suggest that our library is capable of identifying binding partners at a hit rate of close to 10%. This library together with a fully automated beam line [2] will be made accessible to users, thus enabling fragment-screening experiments on a much broader basis.

[1] *M. Krug, M.S. Weiss, U. Heinemann, U. Mueller, 2012, J. Appl. Cryst. 45, 568-572,* ***[2]*** *U. Mueller, N. Darowski, M.R. Fuchs, et al., 2012. , J. Syn. Rad., 19, 442*



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