The aim of this project is to advance novel strategies for efficient and fast development of compounds for fighting emerging (zoonotic) viral diseases. A key problem in drug development via fragment screening is that the organic chemistry necessary for fragment linking is relatively slow, labor-intensive and not easily accessible. In contrast, synthesis of peptides and many peptidomimetics can be conducted in a highly automated and parallel fashion. In this project, the researchers will establish technologies for fast and efficient development of potent inhibitors of two proteases as targets for antiviral therapy: SARS-Cov-2 main protease and the NS2B-NS3 protease of the Zika virus. This strategy relies on crystallographic fragment screening using fragments that enable inhibitor synthesis via automated parallel solid phase synthesis. Computational tools will be developed for the generation of biased fragment libraries increasing the hit rate, and for fragment linking as well as extension. In addition to the results obtained for the highly relevant viral targets studied, the technology developed in this work will be highly accessible and practicable also for other laboratories, including an academic environment as well as small and medium enterprises.

Projektbeteiligte

Prof. Dr. Norbert Sträter
Universität Leipzig
Fakultät für Chemie und Mineralogie
Institut für Bioanalytische Chemie
Leipzig

Prof. Dr. Ralf Hoffmann
Universität Leipzig
Fakultät für Chemie und Mineralogie
Institut für Bioanalytische Chemie / Bioanalytik
BBZ
Leipzig

Prof. Dr. Jens Meiler
Universität Leipzig
Medizinische Fakultät
Institut für Wirkstoffentwicklung
Leipzig
Es werden die Institutionen genannt, an denen das Vorhaben durchgeführt wurde, und nicht die aktuelle Adresse.

19.01.2024