15 international PhD positions in structure-based drug discovery in the European Innovative Training Network AEGIS

AEGIS (Accelerated Early staGe drug dIScovery) is a Marie Skłodowska -Curie Innovative Training Network (ITN) for early stage researchers (ESR) funded by the European Commission under the H2020 Programme, the EU framework programme for research and innovation.

A key research aim of AEGIS is improving the efficiency and success of early stage drug development by combining innovative methods and techniques to tackle difficult but promising targets (i.e. protein-protein interactions), as potentially valuable drug targets are often neglected due to the high risk associated with their validation. AEGIS is a collaborative action of 11 groups in 7 countries from academia and pharmaceutical industry, combining a balanced portfolio of excellent expertise knowledge of structural and computational based drug design.

Further information: www.aegis-itn.eu

AEGIS will provide a comprehensive and cross-disciplinary structured curriculum for doctoral students in early drug discovery. **15 doctoral thesis fellowships** are available in the areas structural biology using NMR and crystallography, computational structural biology and medicinal chemistry.

Contact and information: e-mail to info"at"aegis-itn.eu

Applications must be submitted online at www.aegis-itn.eu.

Eligible applicants must fulfill the Marie-Curie mobility criteria, and must not have stayed in the country of the host lab for more than 1 year during the last 3 years.

Deadline for applications: 20 Dec 2015

- ESR1: *Structural biology (NMR, crystallography) detection of conformational dynamics and transient pockets in protein targets.* (Helmholtz Zentrum München, Germany)
- ESR2: *Computational approaches for combining fragment-based screening and multicomponent reactions* (Helmholtz Zentrum München, Germany)
- ESR3: *Fragment-based approach to perturb PPI formation* (Phillips-University Marburg, Germany)
- ESR4: *Characterization and comparative analysis of fragment binding by X-rays and complementary biophysical methods* (Phillips-University Marburg, Germany)
- ESR5: *Design, synthesis and in vitro screening of novel molecules to control the oligomeric state of malate dehydrogenase* (University Groningen, Netherlands)
- ESR6: *Using binding kinetics for drug discovery,* (University Uppsala, Sweden)
- ESR7: *Design, synthesis and use of compounds to identify and characterize allosteric sites of UMPK* (Institut Pasteur, France)
- ESR8: *Innovative inhibition strategy against functional structural transitions of essential pathogenic virulence factors*(Institut Pasteur, France)
- ESR9*: Structural analysis of fragment-protein and ligand-protein complexes.* (Jagellonian University in Kraków, Poland)
- ESR10: *Computational analysis of compound libraries and screening* (ETH Zurich, Switzerland)
- ESR11: *Characterization of intracellular molecular interactions in living cells* (Ridgeview Instruments AB, Sweden)
- ESR12: *Discovery of novel chemotypes for the treatment of trypanosomatid and apicomplexan protozoal infections* (Novartis Pharma AG, Switzerland)
- ESR13: *Fragment based-MCR platform and web-based implementation* (University Groningen, Netherlands)
- ESR14: *Characterization of 14-3-3 PPI and identification of isoform-specific small molecule modulators* (AstraZeneca AB, Sweden)
- ESR15: *Design, synthesis and optimization of paramagnetic tags. Hit optimization.* (Giotto Biotech Srl, Italy)