

sh-miR designer v2.0

an upgraded tool for construction of RNA
interference reagents: sh-miRs

AMU-Poznan Team

Instructors:

Marcin Borkowski

Michał Ren

Student Members:

Martyna Urbanek

Mateusz Flieger

Sylwester Brzęczkowski

Michał Rostecki

Piotr Rogulski

--== iGEM 2013 ==--

Faculty of Mathematics and Computer Science
Adam Mickiewicz University in Poznan

An upgraded version of the sh-miR Designer software will have extended functionality. In contrast to v1.0, where the user had to provide the sequence of tested siRNA to insert to the miRNA scaffold, in the v2.0 providing only the transcript name (or the number from NCBI database) will be enough to construct the desired sh-miR. It will be possible thanks to the included blast-like algorithm which will search through the transcript sequence to find the appropriate siRNA sequence.

Furthermore the pri-miRNA database will be expanded and more flanking sequences will be added. sh-miR designer v1.0 had only 5 flanking sequences in its database.

We also plan to add a feature to prepare DNA constructs ready to clone into a couple of widely used plasmid vectors (e.g. pCDH-MCS-EF1-GFP) with added sequences containing restriction fragments to digest by widely used restriction enzymes.

Also we want to add a function to check if known immunostimulatory motifs are present in the prepared sh-miR molecule. In some cases, immunostimulatory effect caused by RNAi reagents is desired (in therapy against viral infections or oncology), but in most cases designed reagents should be safe for cells.

To improve the specificity of designed reagents, we will be testing off-target effects using a blast tool to search through the reference transcript sequences from the NCBI database.