Target sequences in FASTA format

Off-target database Feature tables (e.g. SNPs)

Identification of CAN repeats and other regions with sequences of low complexity

In silico ‘dicing’ of target sequences into all siRNAs of 19 nt (default) length

Prediction of specificity (perfect homology, ‘seed’ homology) and efficiency for each ‘diced’ siRNA

Discard siRNAs predicted to be unspecific, inefficient, of low complexity or containing unwanted features from target regions

Design of long dsRNAs: primer design for optimized target regions (only allow primer pairs with penalty below selected cut-off)

Ranking of designs by sorting for (i) predicted specificity, (ii) predicted efficiency and (iii) number of seed-matches (siRNAs only)

Evaluation of reagents for homology and content of selected features (e.g. SNPs, UTR), mapping reagents to the genome

Write long dsRNA / siRNA design(s) to flat files and generate HTML report
Visualization of reagents (GBrowse)