

MysiRNA-Designer: A workflow for Efficient siRNA Design Considering splice-variants, Multi-score filtration, Target Accessibility and both perfect and seed-matching off-targets

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Abstract: Designing of small interfering RNA (siRNA) is a multi factorial problem that gathered the attention of researchers in the area of therapeutic and functional genomics. Here, a new program MysiRNA-Designer which integrates several factors in an automated work-flow considering mRNA transcripts variations, siRNA and mRNA target accessibility and both near-perfect and mRNAs 3-UTR seed off- target matches is presented. Furthermore, a unique siRNA scores filtration technique using a combination of the top scoring algorithms that predict siRNA activity. This multi-score filtration layer isolate siRNA that pass the 90% threshold assigned. MysiRNA-Designer takes an accession, finds conserved regions among its transcript space (clustalw/cons), finds accessible regions within the mRNA (RNAs), designs all possible siRNAs for these regions, and filters them based on multi-scoring and then performs SNP and off-target filtration (Blastall against refseq/3UTR). These strict selection criteria were tested against human genes where at least one active siRNA was designed from 95.65% of total genes. In addition, when tested against experimental dataset it was capable of rejecting 95% of the false positive siRNA. MysiRNA is a freely accessible desktop application that used for siRNA designing with high accuracy and specificity and it is expected to play an important role in this area.

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