**sh-miR designer** is a software aimed for fast and efficient design of effective RNA interference (RNAi) reagents - sh-miRs, also known as artificial miRNAs. sh-miRs are RNA particles whose structure is based on miRNA precursor pri-miRNA, but sequence interacting with transcript is changed depending on research purpose. Maintenance of structure of pri-miRNA is very important to enable cellular processing (performed mainly by endonucleases Drosha and Dicer) and therefore ensure functionality of artificial particles. sh-miRs delivered to cells on genetic vectors - plasmids or viral vectors - enter natural RNAi pathway and silence target mRNA. They can be used in genetic therapies and basic biomedical research.

**Input:**
One strand or two strands in 5'-3' orientation of siRNA of known efficiency:
```
aggaagauugggcaauacucggacagucaguca
```

**Concatenation of both given siRNA strands (or one given strand and one added) with flanking sequences and loop sequence of pri-miRNA (caps) taken from created pri-miRNA database.**
```
CAUACACGAAAGGGAUUGUUGUCUUACUCGGACAGGGGAGAGGCAACGGCAUGCGCAUG
GGUUGACUGGGAACCCCAUGUCCACUGCUUGUCCUCGCUUGUCU
```

**Analysis of sh-miRNA structure with mfold program. Comparison with structure of endogenous pri-miRNAs**

**Scoring:**
1. Structure
2. Same first nucleotides of siRNA and miRNA sequence
3. Endogenous pri-miRNA product homogeneity (isomirs)

**Output:**
2-3 sh-miRs with best scoring results ordered from the best one with 2D structure web link to miRBase site of pri-miRNA, which flanking sequences were used.

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sh-miRNA with siRNA targeted on luciferase transcript in 155 pri-miRNA flanking sequence