**Requirements:**

* FASTA36
* ViennaRNA package
* SeqIO, SeqUtils, Seq module of Bio package
* Biopython
* Python packages: Pandas, Numpy, sci-kit learn, joblib

**Usage:**

* **Windows:**

**For Potential off-target site prediction:**

py Fasta36\_SeqSearch.py input\_filename.fasta

**For target efficiency prediction:**

py main.py input\_filename.fasta

* **Linux based systems:**

**For Potential off-target site prediction:**

Python3 Fasta36\_SeqSearch.py input\_filename.fasta

**For target efficiency prediction:**

Python3 main.py input\_filename.fasta