We have developed our own software which provides a database of stem loops. When users upload their own sequence, the software can find out corresponding stem loops and store them into the database. Moreover, when users need proteins expressed in specific quantity, such as inputting the ratio of two different proteins, the software can provide suitable stem loops according to the ratio. The relationship between the quantitative expression of protein and the folding energy is based on our modeling.

With the help of this database, we can regulate the protein expression level more rationally, more precisely and more quickly. We believe that our toolbox will play a part in prokaryotic regulation field.

The C++ code is origin from 2ndscore program

This database is based on Apache/PHP/MySQL environment. If you want to see our source code and operation guide. Please download this zip.

We also provided a temporary online server for you to know the UI (But the performance of server is limited). Please visit:

http://115.28.14.24

This URL will offer the code when updated.

References:

[1]Kingsford, Carleton L., Kunmi Ayanbule, and Steven L. Salzberg. "Rapid, accurate, computational discovery of Rho-independent transcription terminators illuminates their relationship to DNA uptake." Genome biology 8.2 (2007): 1.

[2]Ermolaeva, Maria D., et al. "Prediction of transcription terminators in bacterial genomes." Journal of molecular biology 301.1 (2000): 27-33.

[3]Zuker, Michael, David H. Mathews, and Douglas H. Turner. "Algorithms and thermodynamics for RNA secondary structure prediction: a practical guide." RNA biochemistry and biotechnology. Springer Netherlands, 1999. 11-43.
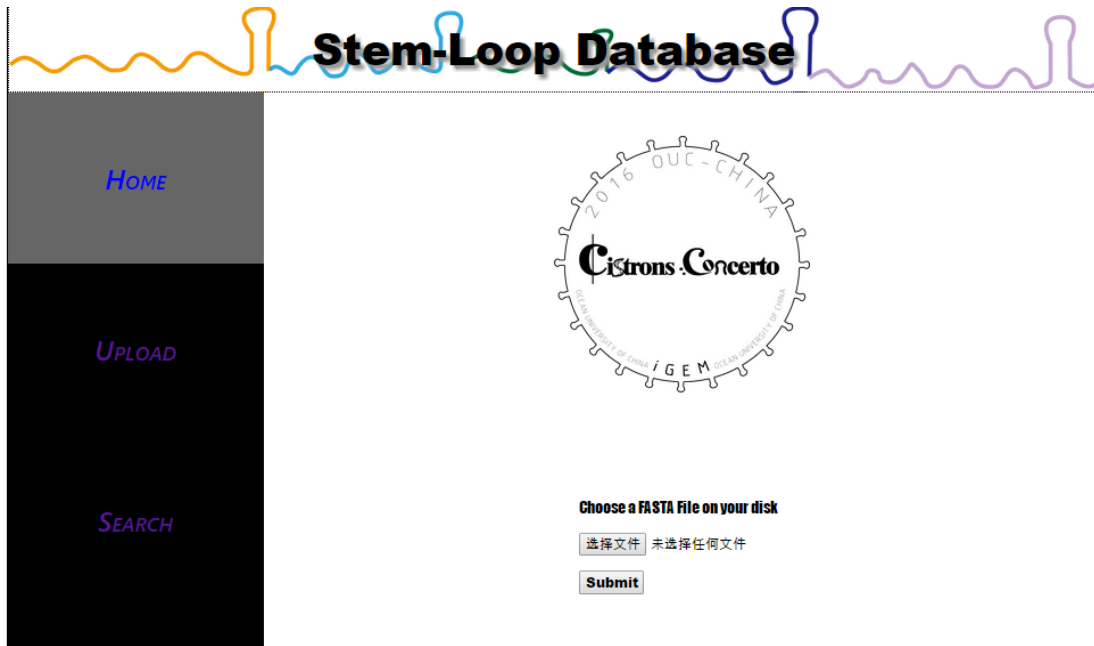
[4]Rouillard, Jean-Marie, Michael Zuker, and Erdogan Gulari. "OligoArray 2.0: design of oligonucleotide probes for DNA microarrays using a thermodynamic approach." Nucleic acids research31.12 (2003): 3057-3062.
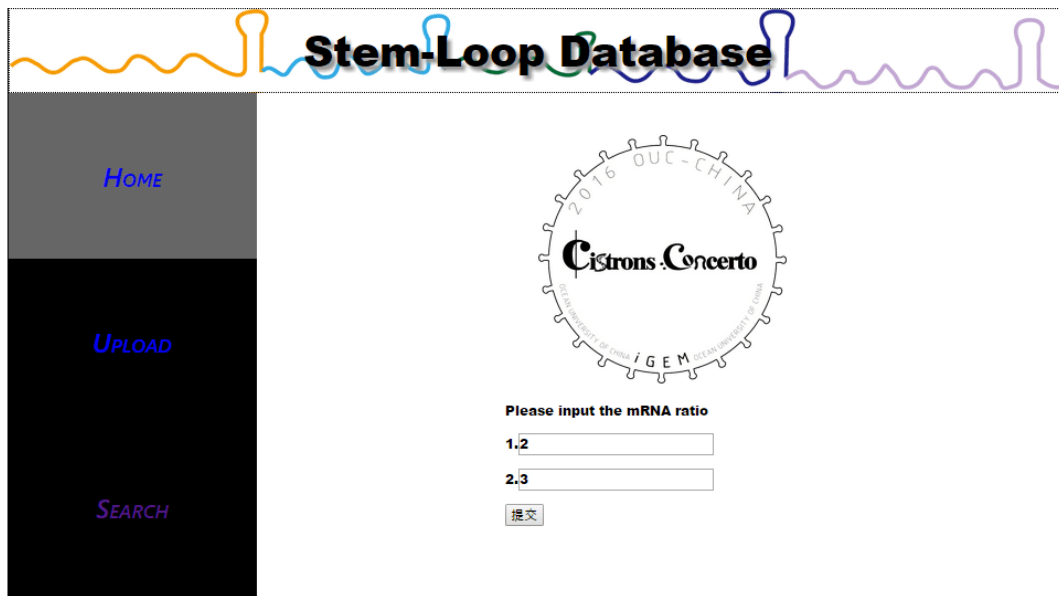
[5]http://unafold.rna.albany.edu/

[6]http://transterm.cbcb.umd.edu/

User's Guide:
1. First go to the upload page to upload your own sequence to the server.

2.Wait a minute.

3.Enter the ratio of Max[mRNA]

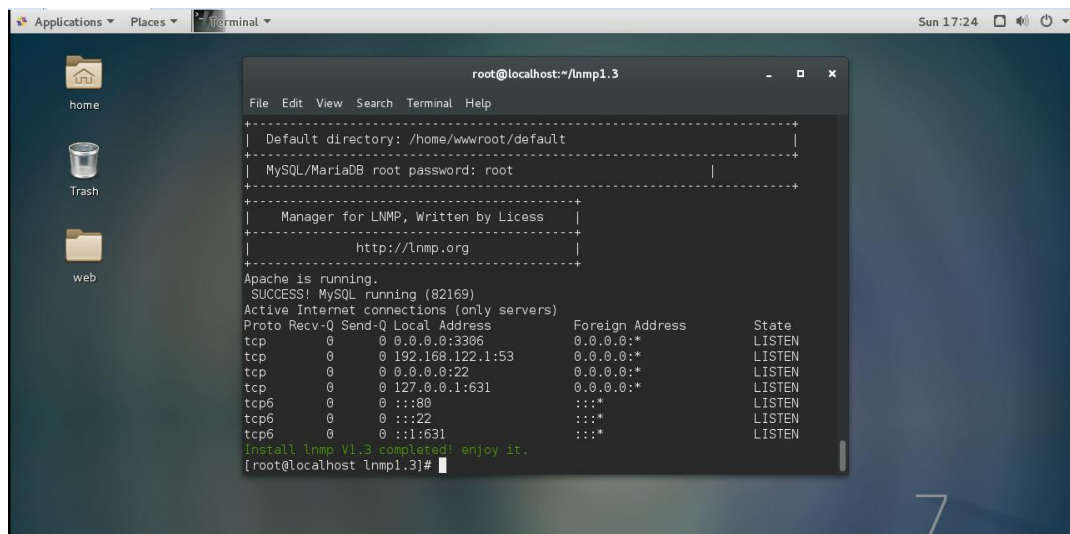4.Receive a Stem loop that can control the expression of proteins.

Connect Success
Folding Energy ratio=-5.4217068422261
Seq1:GATCGCCTGATCCCGGTGCACCCGGGATCAGGCCGCG
Energy:-25.6
Seq2:GATCGCCTGATCCCGGTGCACCCGGGCAGCTGCAGAGTCTGGGTGCACCGGGATCAGGCCGCG
Energy:-51.4

5.Add stem loops to your gene sequence.

6.We also provide a stem-loop database file to enrich your own database.

Install Guide:

1. First you need a Linux system with Apache/PHP/MySQL environment and gcc compiler.

2. Copy the HTML&PHP code to Apache Web Document Root.

3. Edit PHP.ini to allow PHP to execute system function.

4.Using SQL query to create a database.

←T→				id	seq		energy
☐	🖊 Edit	🔢 Copy	🚫 Delete	1	GATCGCCTGATCCCGGT		-25.6
☐	🖊 Edit	🔢 Copy	🚫 Delete	2	GATCGCCTGATCCCGGTGCACCCGGGCAGCTGCAGAGTCTGGGTGCACCG...		-51.4
☐	🖊 Edit	🔢 Copy	🚫 Delete	3	GATCGCGTCCAAGTTACATGATTCTTGGACGCCGCG		-14.9
☐	🖊 Edit	🔢 Copy	🚫 Delete	4	GAUCGUUGCG GGCGGGGCGA GAGUCUCGCC CCGCCCGCGA CCGCG		-38.7
☐	🖊 Edit	🔢 Copy	🚫 Delete	5	GAUCCUGUUG UCUUACAUGA UUGACAACAG CGCG		-10
☐	🖊 Edit	🔢 Copy	🚫 Delete	6	GAUCCGAUCG CUUGUCUUAC AUGAUUGACA AGCGAUCGCG CG		-20
☐	🖊 Edit	🔢 Copy	🚫 Delete	7	GAUCGUCUCA CACGUGCUCA UUACAUGAUU UGAGCACGUG UGAGAC...		-30.1
☐	🖊 Edit	🔢 Copy	🚫 Delete	8	GAUCCUAGUC UCUACUCAGA GUCGUCUGUU ACAUGAUUCA GACGAC...		-44.9
☐	🖊 Edit	🔢 Copy	🚫 Delete	9	GAUCGUCGUC ACACAGUGCU CAUUACAUGA UUUGAGCACU GUGUGA...		-34.4
☐	🖊 Edit	🔢 Copy	🚫 Delete	10	GAUCCUGCUC UACUCAAGUC GUCUGUUACA UGAUUCAGAC GACUUG...		-38.8
☐	🖊 Edit	🔢 Copy	🚫 Delete	11	GAUCCUGCUC UACUCAGACU GCUGUUACAU GAUUCAGCAG UCUGAG...		-38.5
☐	🖊 Edit	🔢 Copy	🚫 Delete	12	GAUCCUGUCU ACAUCAGACA UGCUUGAUCU ACAAGCAUGU CUGAUG...		-38.8

CREATE TABLE `hp`.`loops` (`id` INT NOT NULL AUTO_INCREMENT , `seq` VARCHAR(255) NOT NULL , `energy` FLOAT NULL , PRIMARY KEY (`id`)) ENGINE =InnoDB;

5.You need to change the login information in insert.php so that you can connect with your database.