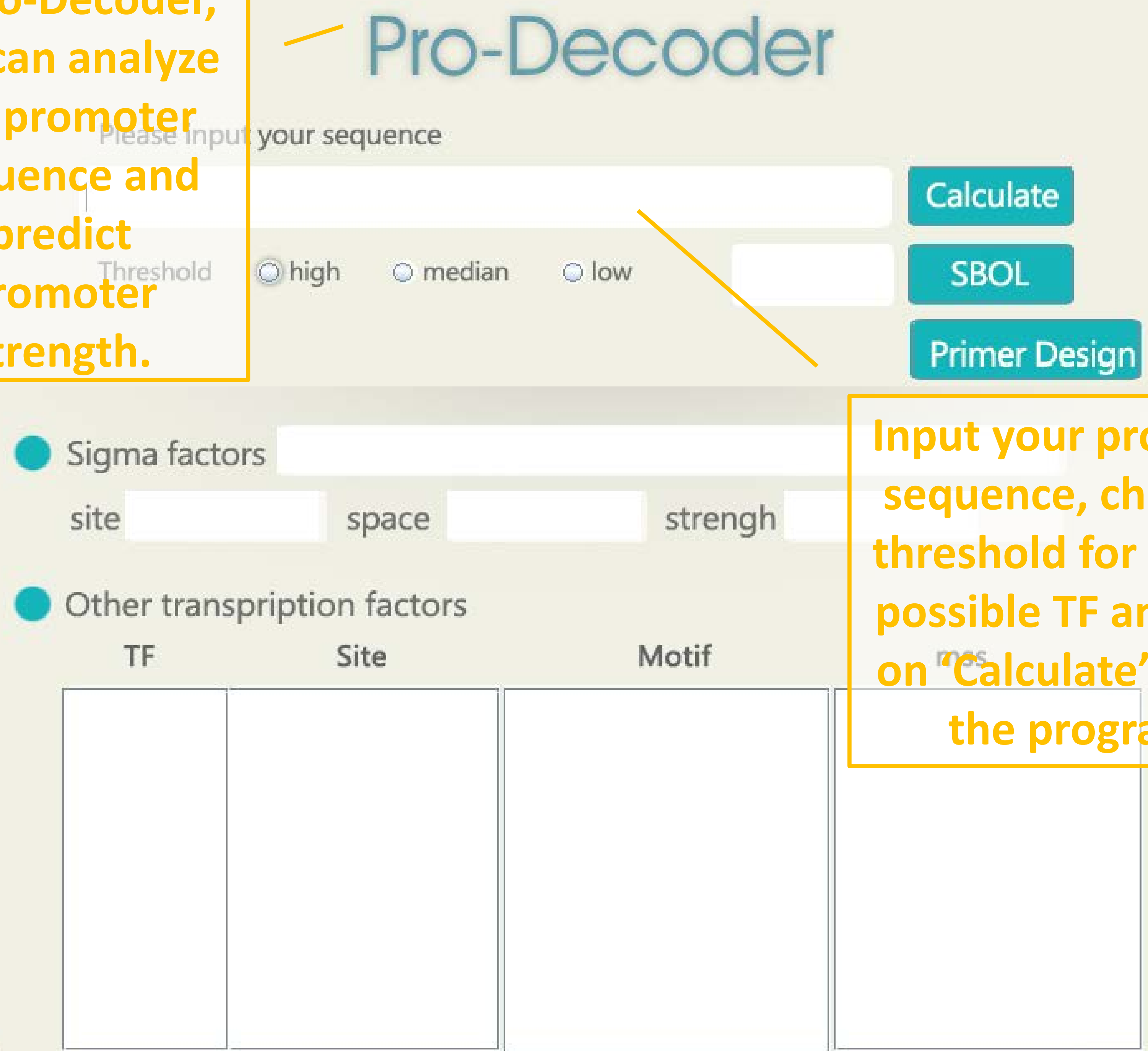
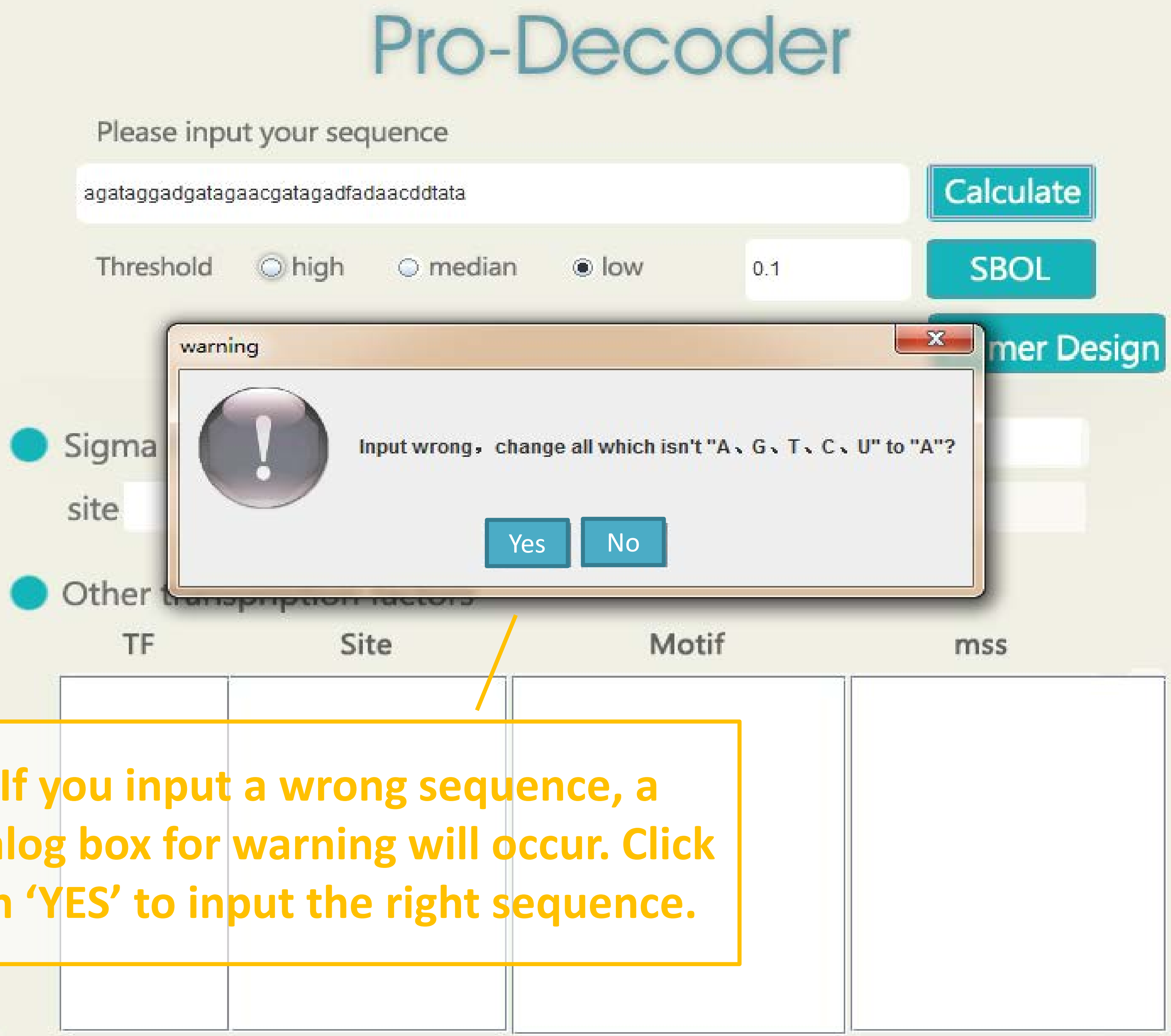
Welcome to use our software-Brick Worker. This brilliant tool can help you with analyzing and optimizing biobrick sequences.

Want a try? Click on one of the function keys and start to analyze biobricks!

In Pro-Decoder, you can analyze the promoter sequence and predict promoter strength.



Input your promoter sequence, choose a threshold for finding possible TF and click on 'Calculate' to run the program.

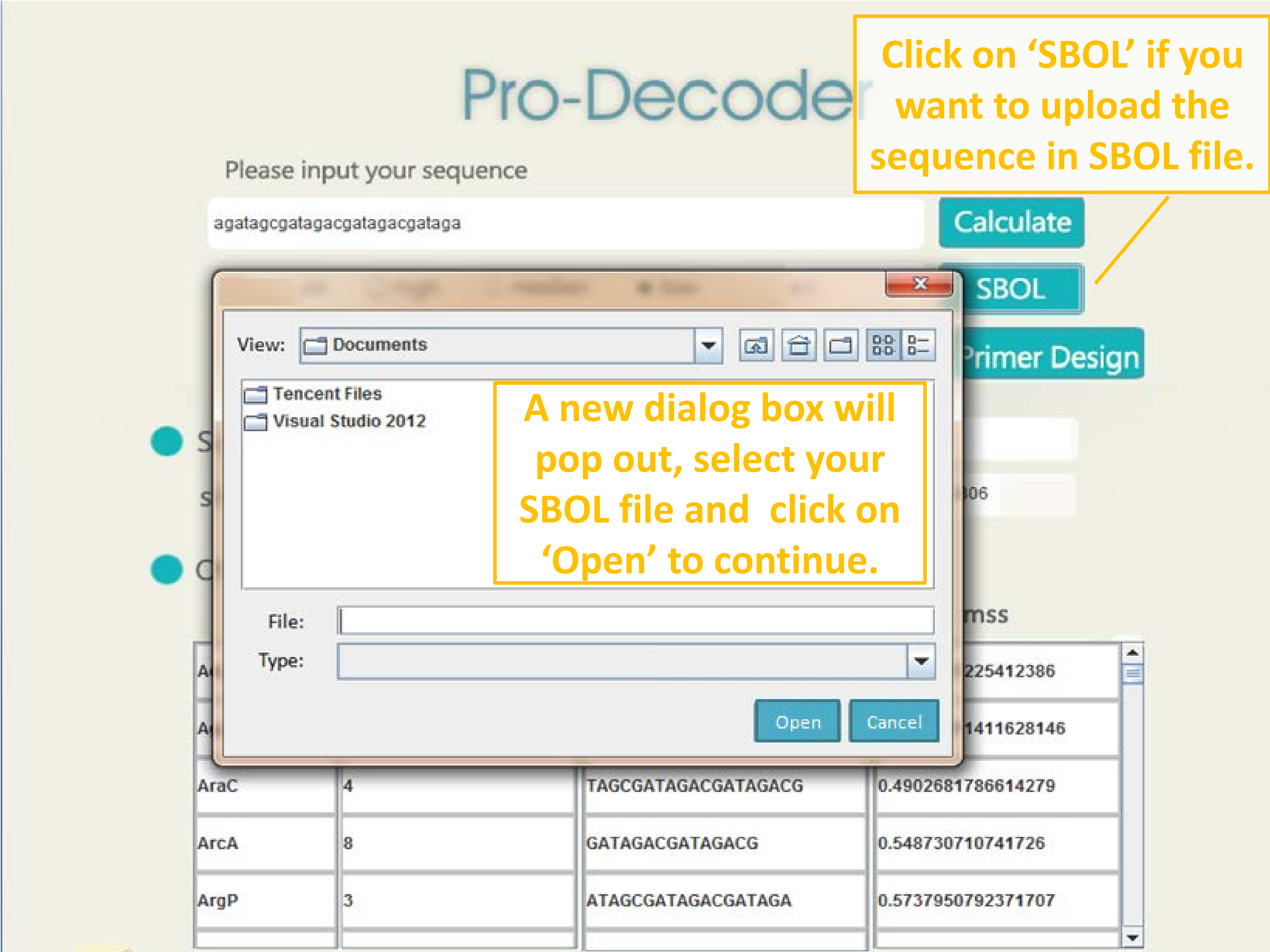


Please input your sequence: agataggadgatagaacgatagadfadaacddtata

Threshold ○ high ○ median ● low 0.1

Input wrong，change all which isn't "A、G、T、C、U" to "A"?

If you input a wrong sequence, a dialog box for warning will occur. Click on ‘YES’ to input the right sequence.



agatagcgatagacgatagacgataga

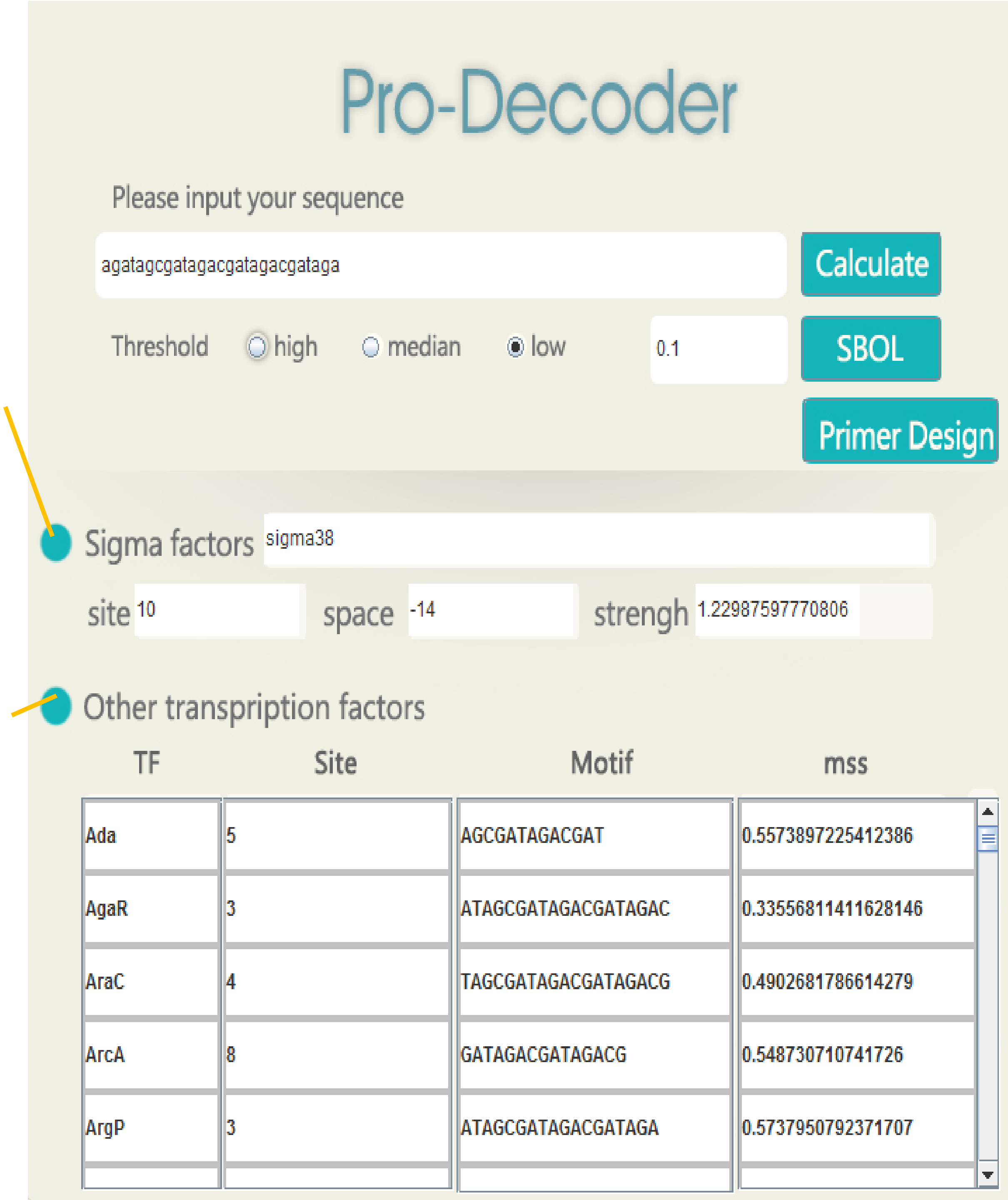
			mss
A			225412386
A			1411628146
AraC	4	TAGCGATAGACGATAGACG	0.4902681786614279
ArcA	8	GATAGACGATAGACG	0.548730710741726
ArgP	3	ATAGCGATAGACGATAGA	0.5737950792371707

Click on ‘SBOL’ if you want to upload the sequence in SBOL file.

A new dialog box will pop out, select your SBOL file and click on ‘Open’ to continue.

This part of output give you information about sigma factor type, the location of sigma factor binding site, the spacer length and the predicted relative strength.

This part of output is about the possible TFBS in the promoter, the TF type, the location, sequence and similarity score of TFBS.



Please input your sequence: agatagcgatagacgatagacgataga

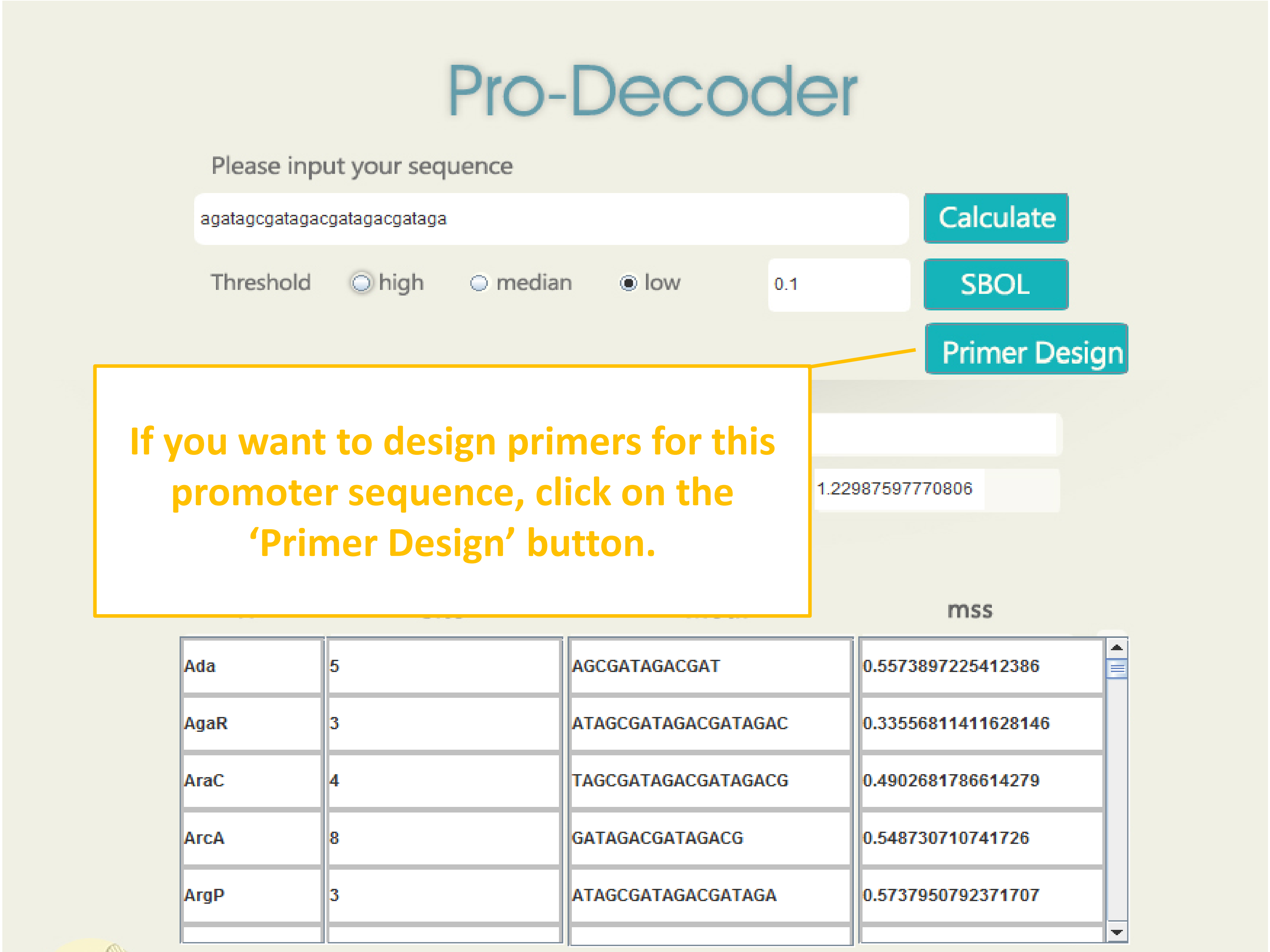
Threshold ○ high ○ median ● low 0.1

Sigma factors: sigma38

site: 10 space: -14 strengh: 1.22987597770806

Other transpription factors

TF	Site	Motif	mss
Ada	5	AGCGATAGACGAT	0.5573897225412386
AgaR	3	ATAGCGATAGACGATAGAC	0.33556811411628146
AraC	4	TAGCGATAGACGATAGACG	0.4902681786614279
ArcA	8	GATAGACGATAGACG	0.548730710741726
ArgP	3	ATAGCGATAGACGATAGA	0.5737950792371707



Please input your sequence

agatagcgatagacgatagacgataga

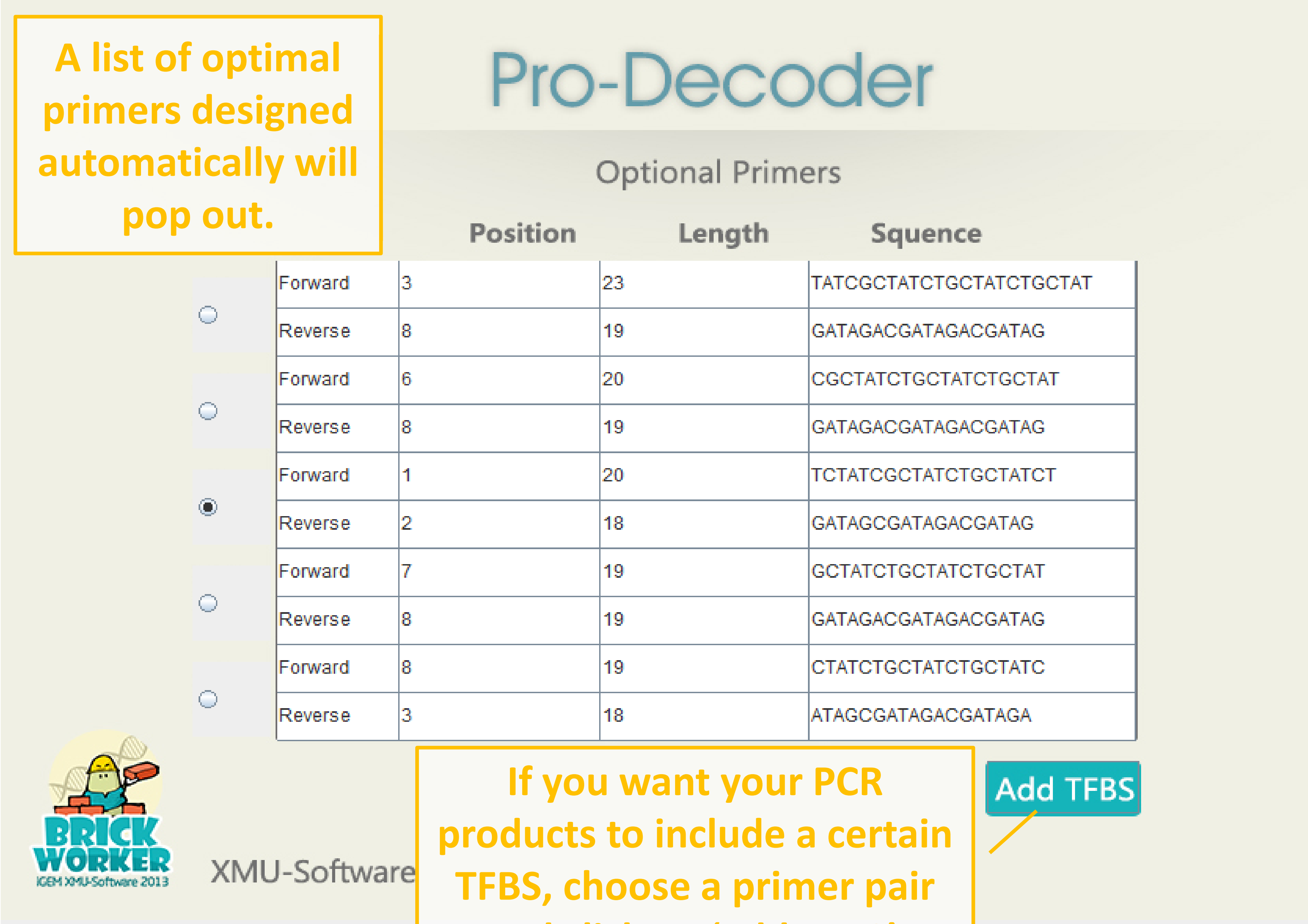
Threshold ○ high ○ median ● low 0.1

1.22987597770806

If you want to design primers for this promoter sequence, click on the ‘Primer Design’ button.

			mss
Ada	5	AGCGATAGACGAT	0.5573897225412386
AgaR	3	ATAGCGATAGACGATAGAC	0.33556811411628146
AraC	4	TAGCGATAGACGATAGACG	0.4902681786614279
ArcA	8	GATAGACGATAGACG	0.548730710741726
ArgP	3	ATAGCGATAGACGATAGA	0.5737950792371707

A list of optimal primers designed automatically will pop out.



Pro-Decoder

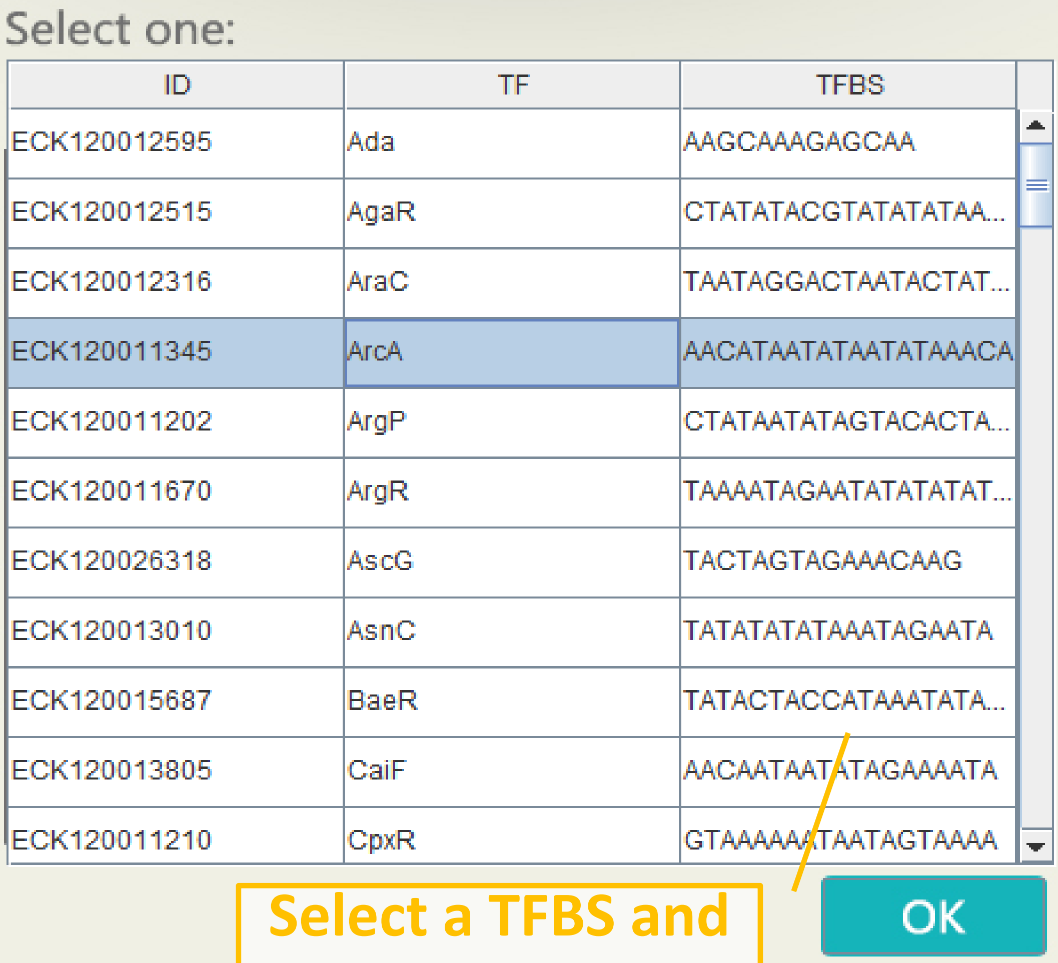
Optional Primers

		Position	Length	Squence
○	Forward	3	23	TATCGCTATCTGCTATCTGCTAT
	Reverse	8	19	GATAGACGATAGACGATAG
○	Forward	6	20	CGCTATCTGCTATCTGCTAT
	Reverse	8	19	GATAGACGATAGACGATAG
●	Forward	1	20	TCTATCGCTATCTGCTATCT
	Reverse	2	18	GATAGCGATAGACGATAG
○	Forward	7	19	GCTATCTGCTATCTGCTAT
	Reverse	8	19	GATAGACGATAGACGATAG
○	Forward	8	19	CTATCTGCTATCTGCTATC
	Reverse	3	18	ATAGCGATAGACGATAGA

If you want your PCR products to include a certain TFBS, choose a primer pair and click on ‘Add TFBS’.

Pro-Decoder

A list of all the TFBS will occur.



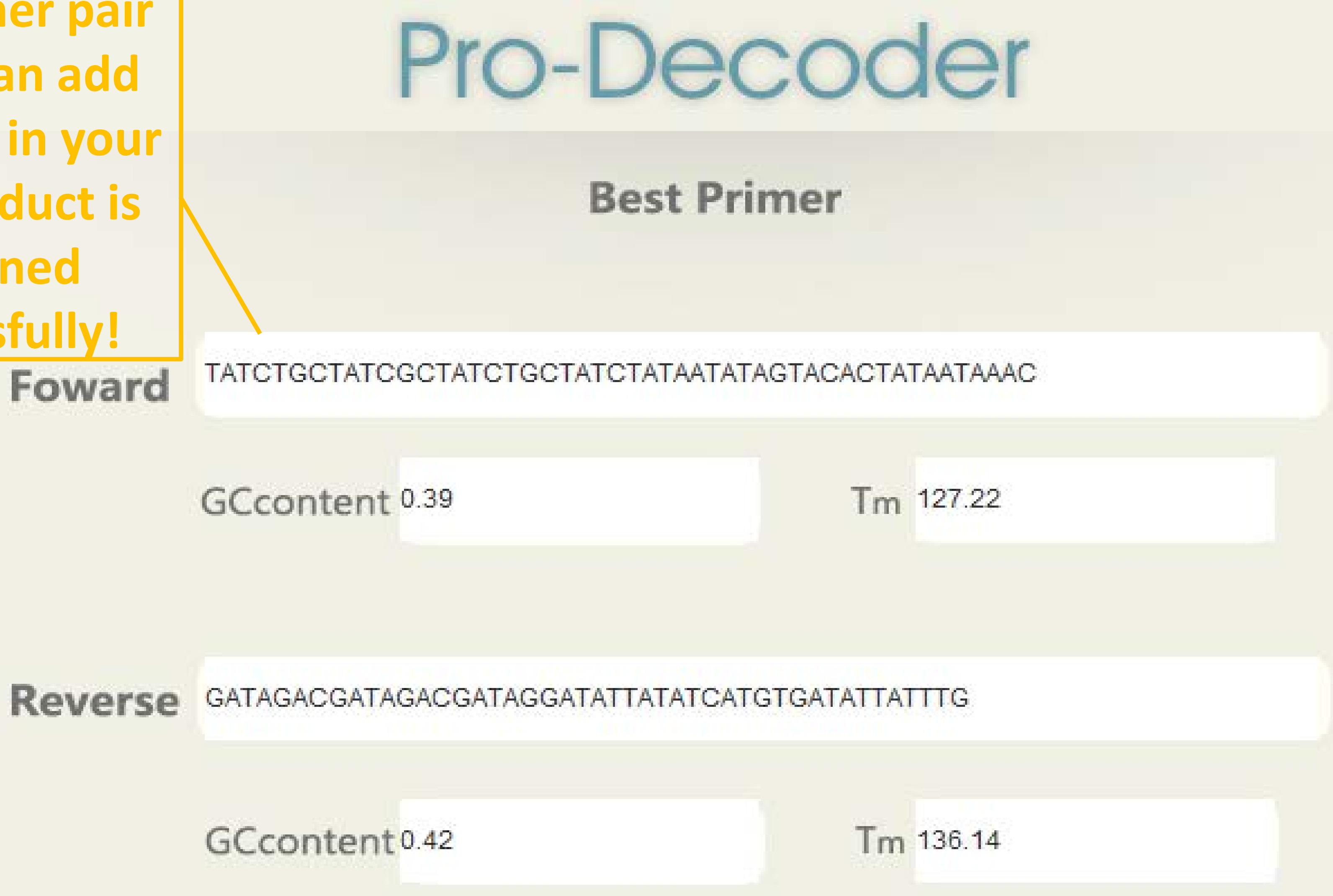
Select one:

ID	TF	TFBS
ECK120012595	Ada	AAGCAAAGAGCAA
ECK120012515	AgaR	CTATATACGTATATATAA...
ECK120012316	AraC	TAATAGGACTAATACTAT...
ECK120011345	ArcA	AACATAATATAATATAAACA
ECK120011202	ArgP	CTATAATATAGTACACTA...
ECK120011670	ArgR	TAAAATAGAATATATATAT...
ECK120026318	AscG	TACTAGTAGAAACAAG
ECK120013010	AsnC	TATATATATAAATAGAATA
ECK120015687	BaeR	TATACTACCATAAATATA...
ECK120013805	CaiF	AACAATAATATAGAAAATA
ECK120011210	CpxR	GTAAAAAATAATAGTAAAA

Select a TFBS and click on ‘OK’ to add the TFBS to the PCR product.

XMU-Software

The primer pair which can add the TFBS in your PCR product is designed successfully!



Pro-Decoder

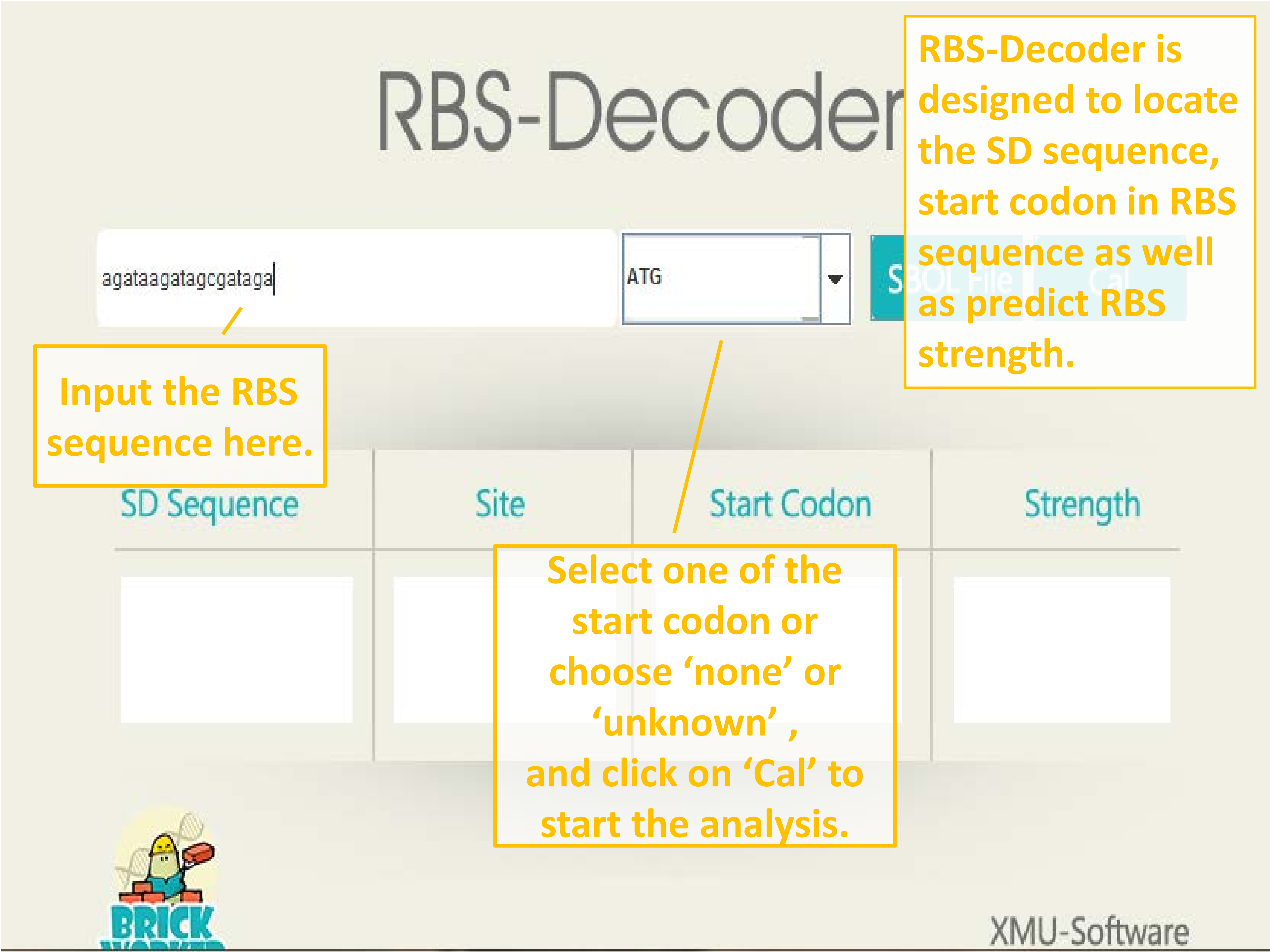
Best Primer

Foward TATCTGCTATCGCTATCTGCTATCTATAATATAGTACACTATAATAAAC

GCcontent 0.39 Tm 127.22

Reverse GATAGACGATAGACGATAGGATATTATATCATGTGATATTATTTG

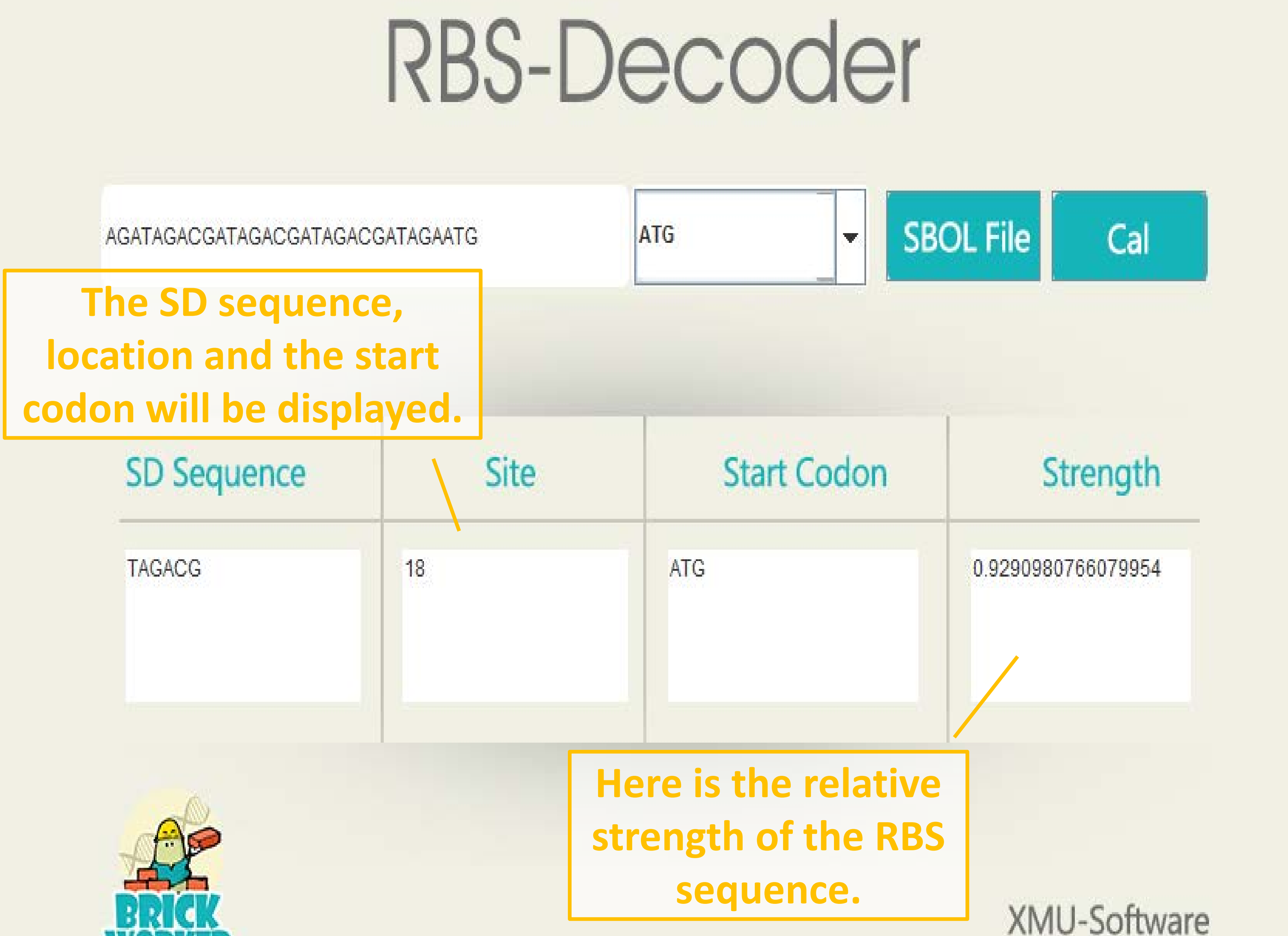
GCcontent 0.42 Tm 136.14



RBS-Decoder is designed to locate the SD sequence, start codon in RBS sequence as well as predict RBS strength.

Input the RBS sequence here.

Select one of the start codon or choose ‘none’ or ‘unknown’ , and click on ‘Cal’ to start the analysis.



RBS-Decoder

AGATAGACGATAGACGATAGACGATAGAATG

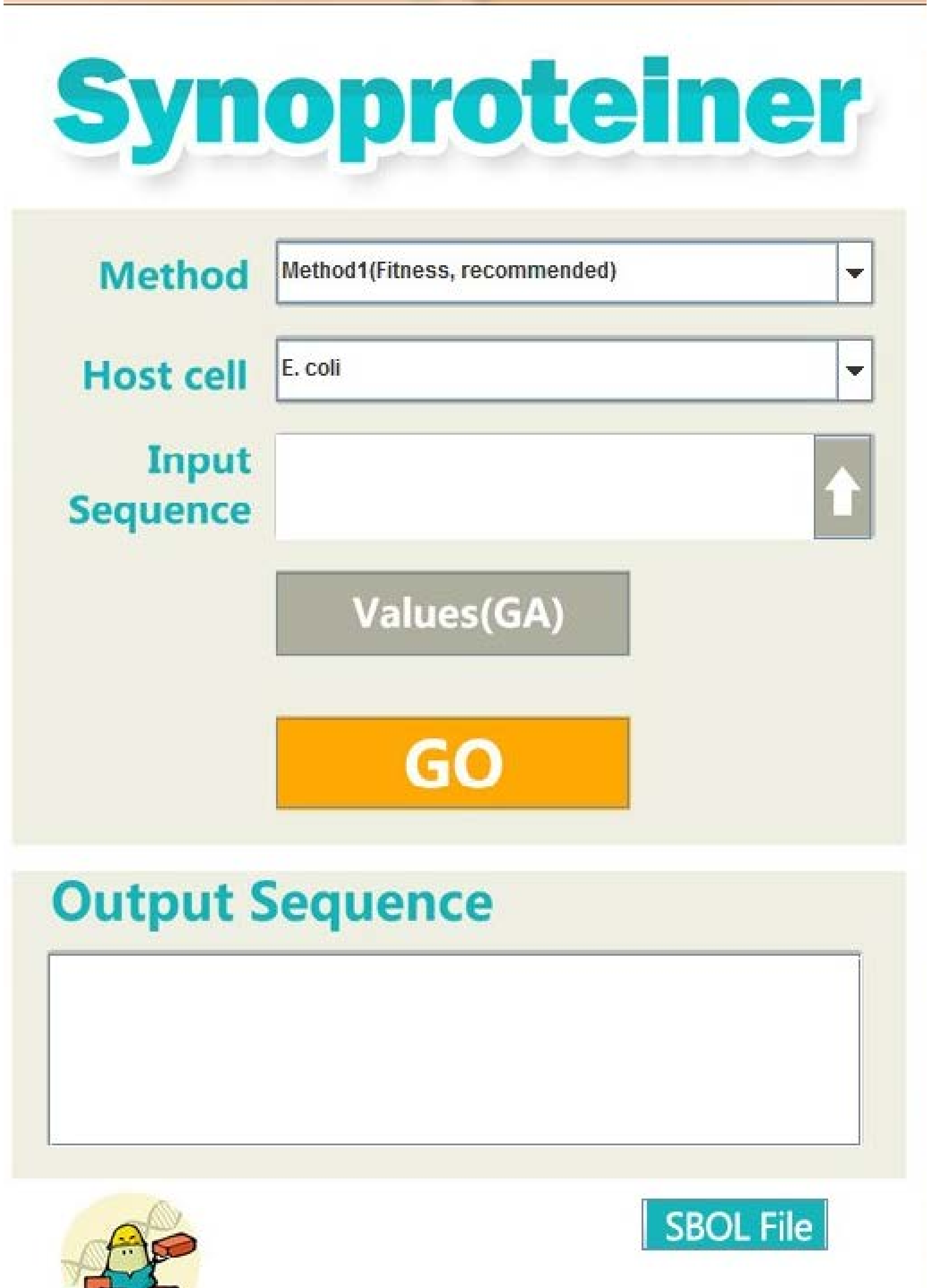
ATG

The SD sequence, location and the start codon will be displayed.

SD Sequence	Site	Start Codon	Strength
TAGACG	18	ATG	0.9290980766079954

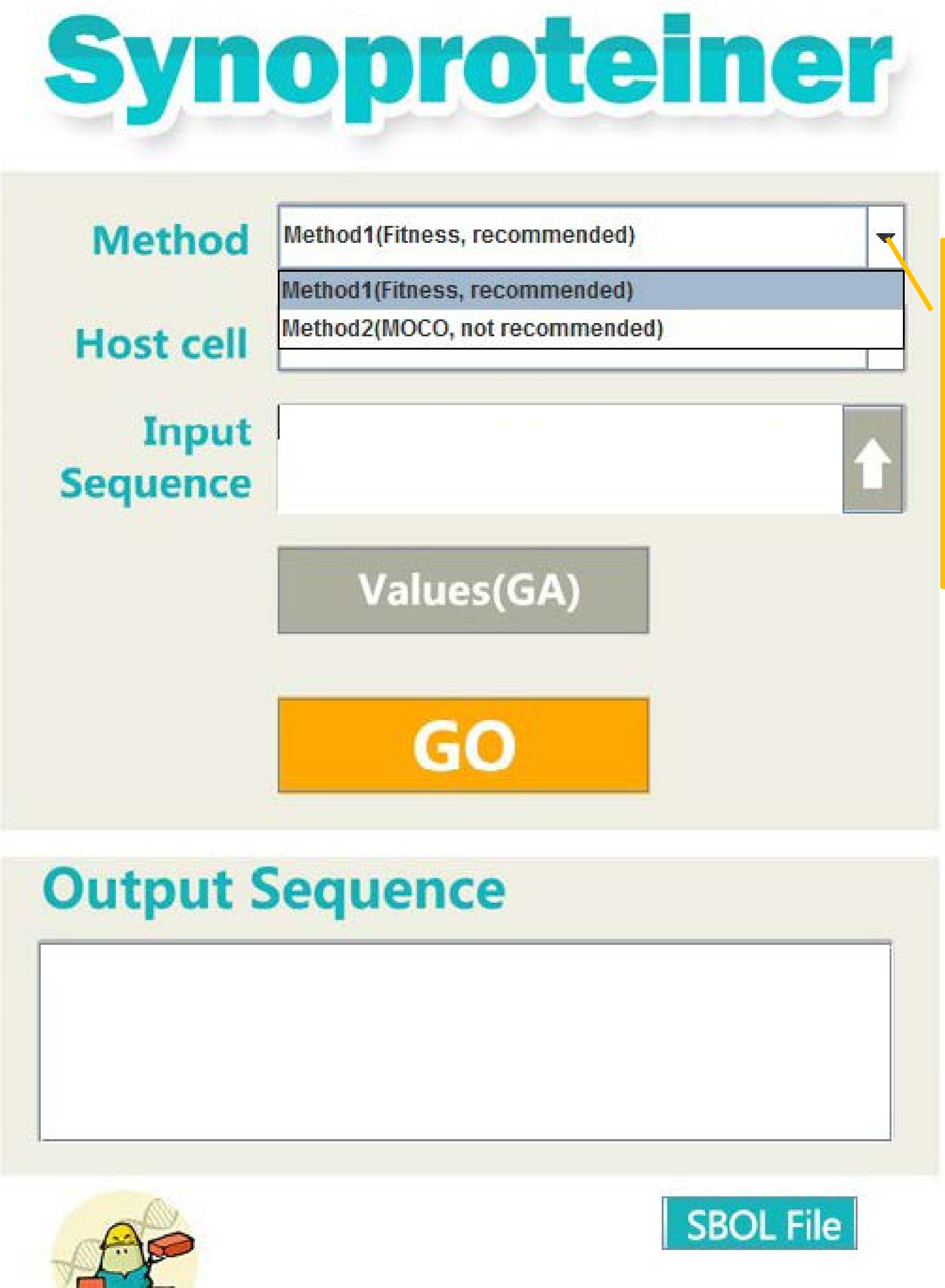
Here is the relative strength of the RBS sequence.

In this part
we provide
two methods
to optimize
the sequence.



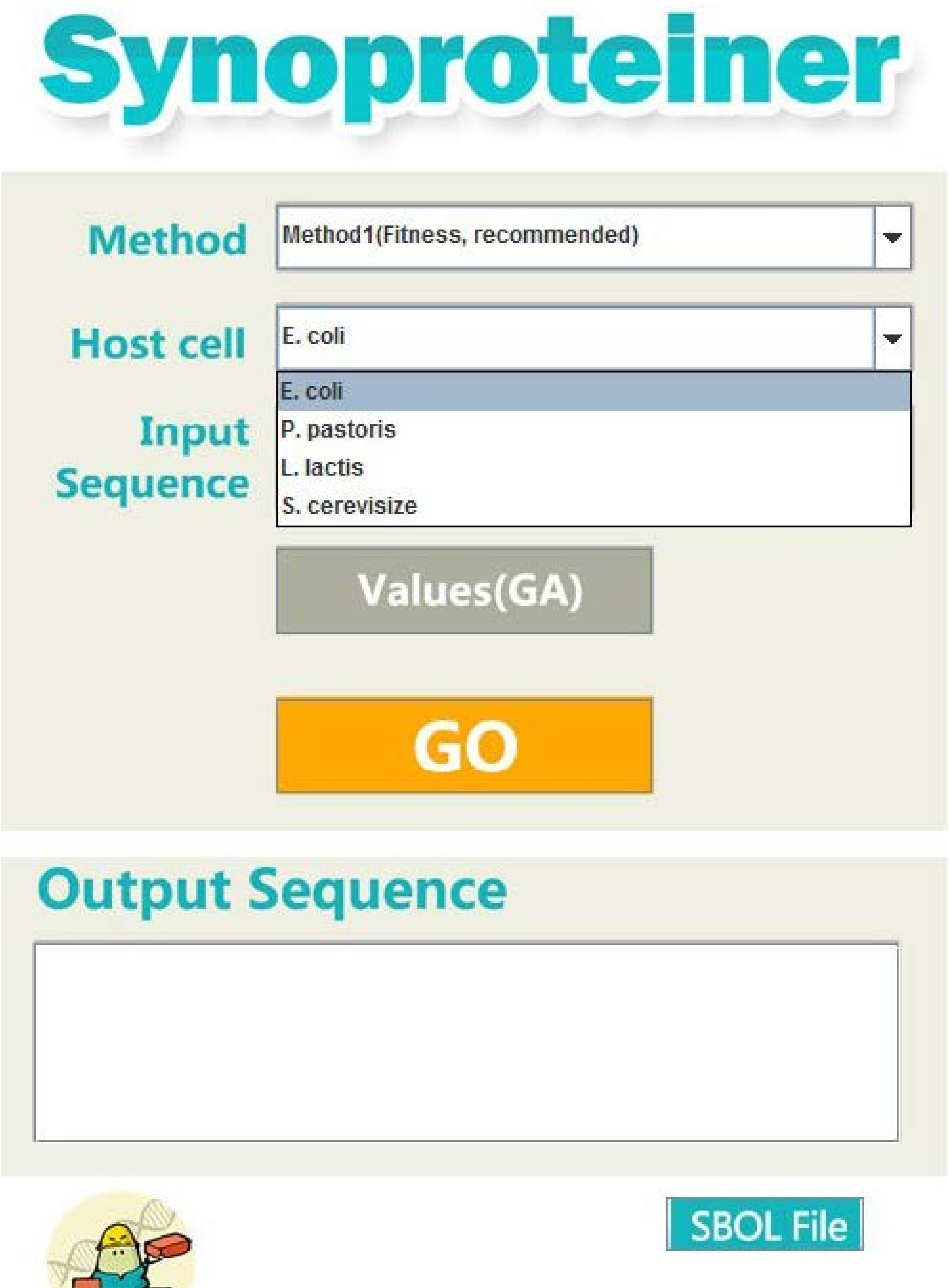
Method: Method1(Fitness, recommended)

Host cell: E. coli



Method: Method1(Fitness, recommended)

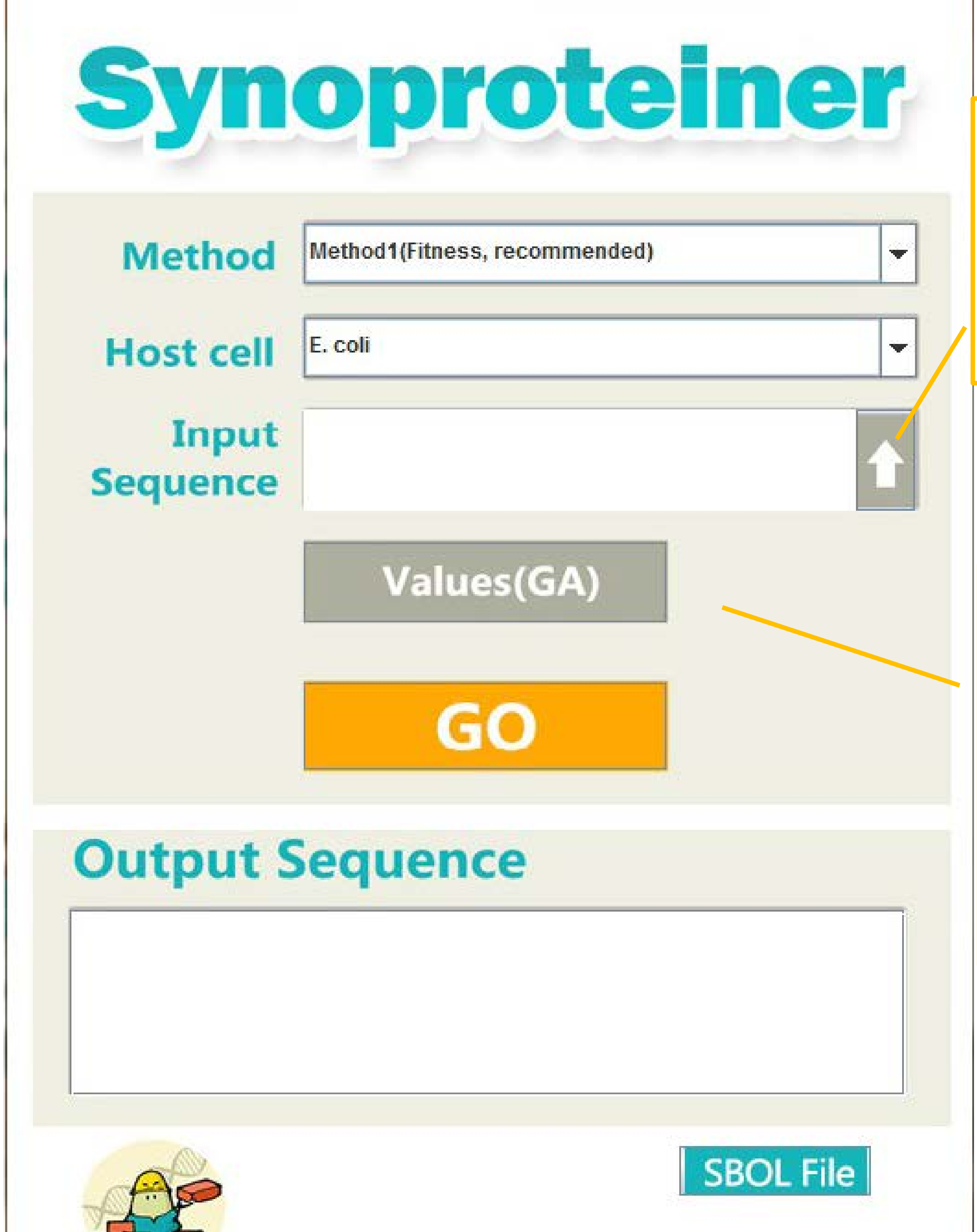
Choose one algorithm for the optimization.


Synoproteiner

Method: Method1(Fitness, recommended)

Host cell: E. coli

Choose the host cell.



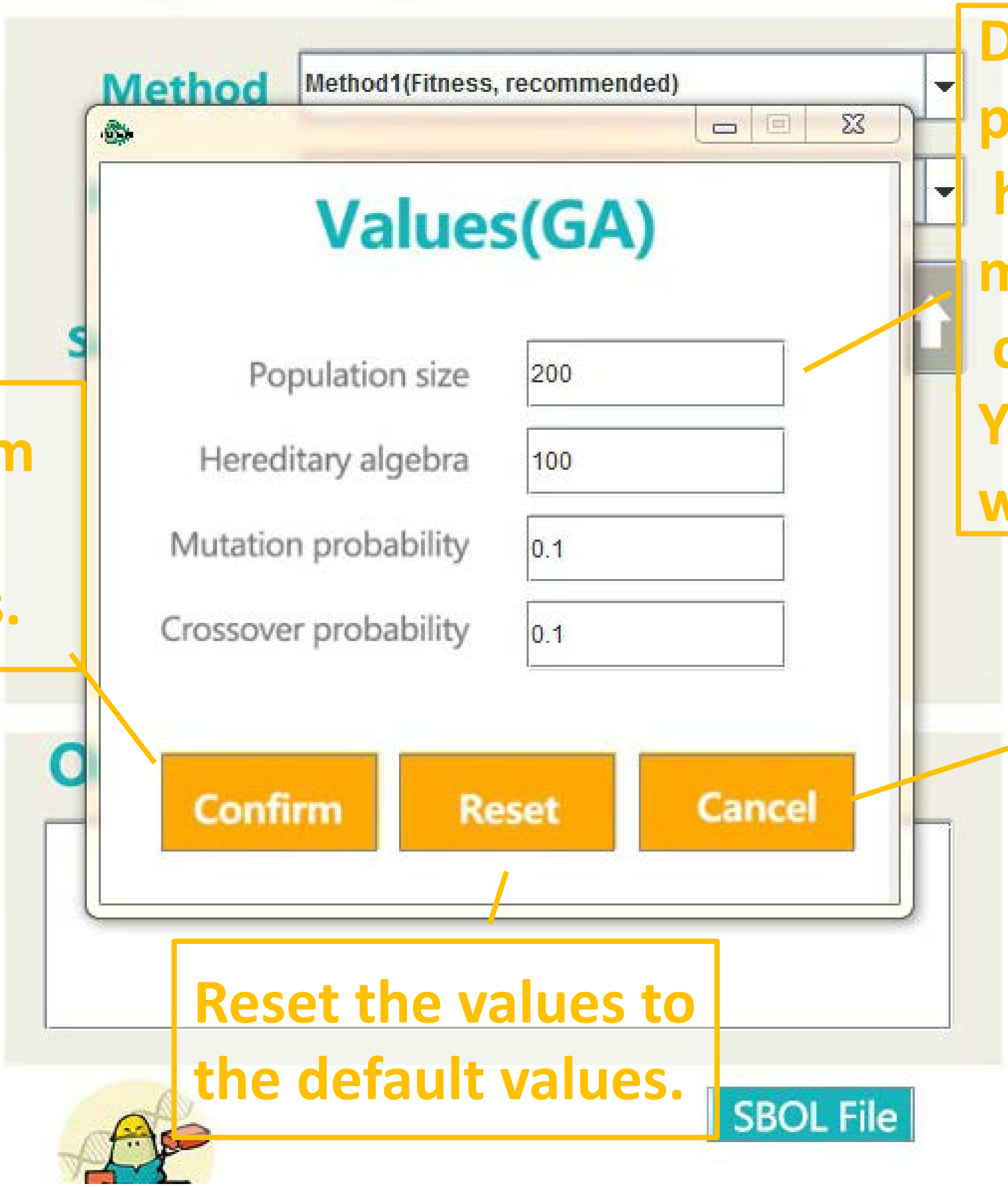
Method: Method1(Fitness, recommended)

Host cell: E. coli

Input an original sequence. Or upload an SBOL file.

Users can click the ‘Values(GA)’ button to input values of the parameter needed in genetic algorithm.

Synoproteiner



Method: Method1(Fitness, recommended)

Values(GA)

Population size: 200

Hereditary algebra: 100

Mutation probability: 0.1

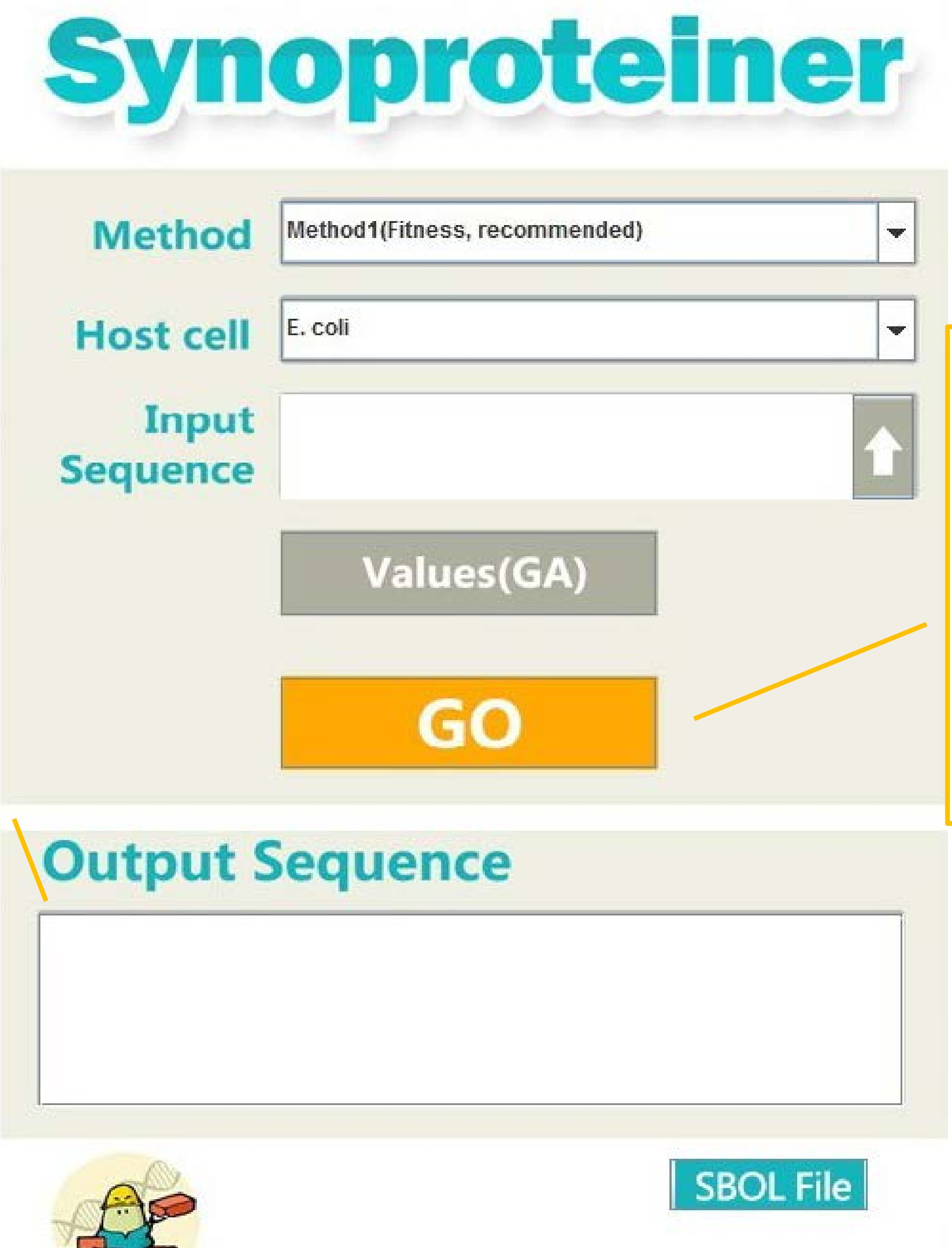
Crossover probability: 0.1

Default value:
population size—200,
hereditary algebra—100,
mutation probability--0.1,
crossover probability--0.1
You can input what you want.

Confirm the values.

Cancel the dialog box. And the default values will be applied.

Reset the values to the default values.

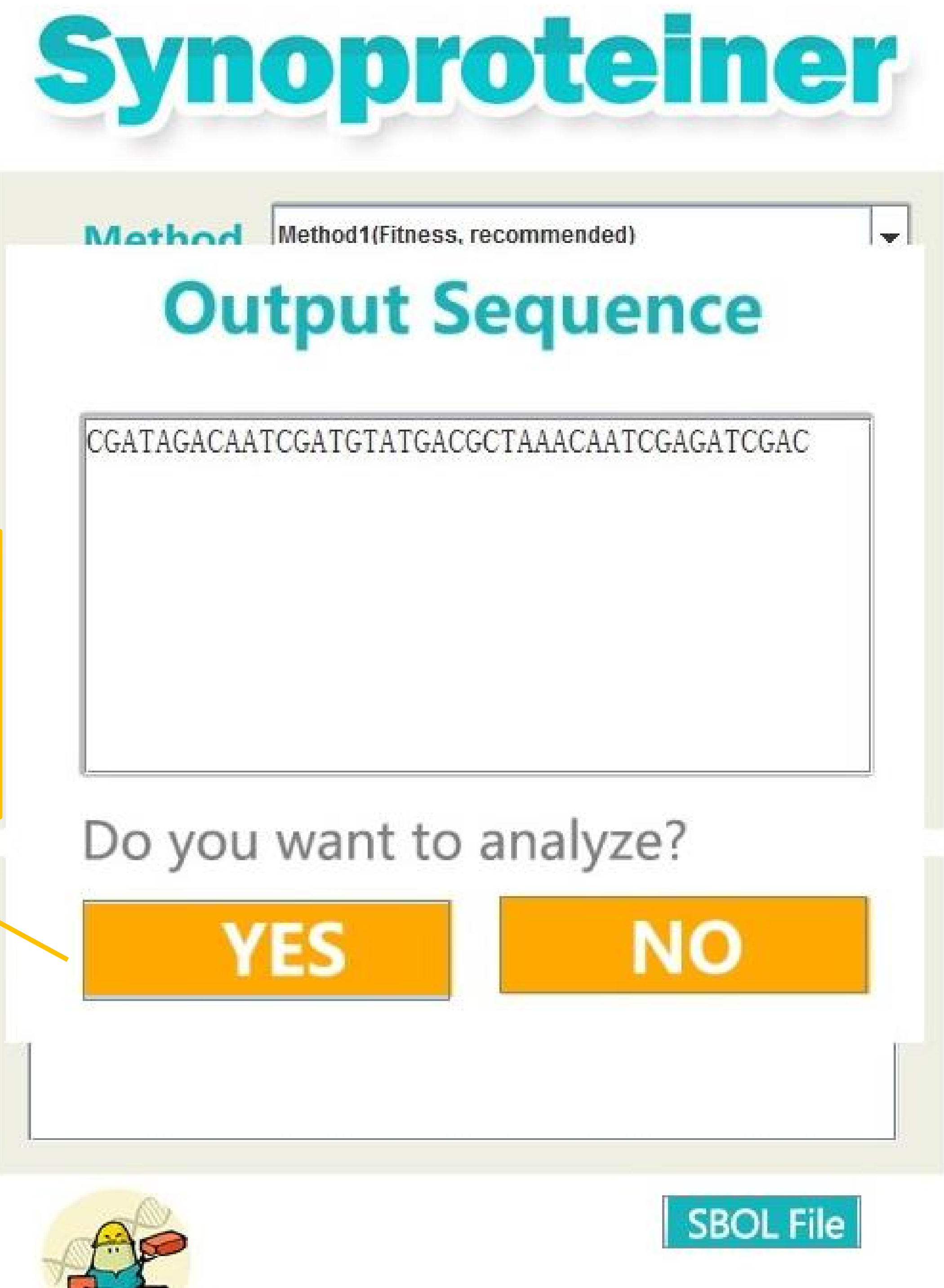


Method: Method1(Fitness, recommended)

Host cell: E. coli

When all above has been done, click ‘GO’ button to run the calculation.

This is a place for output of the sequence optimized.



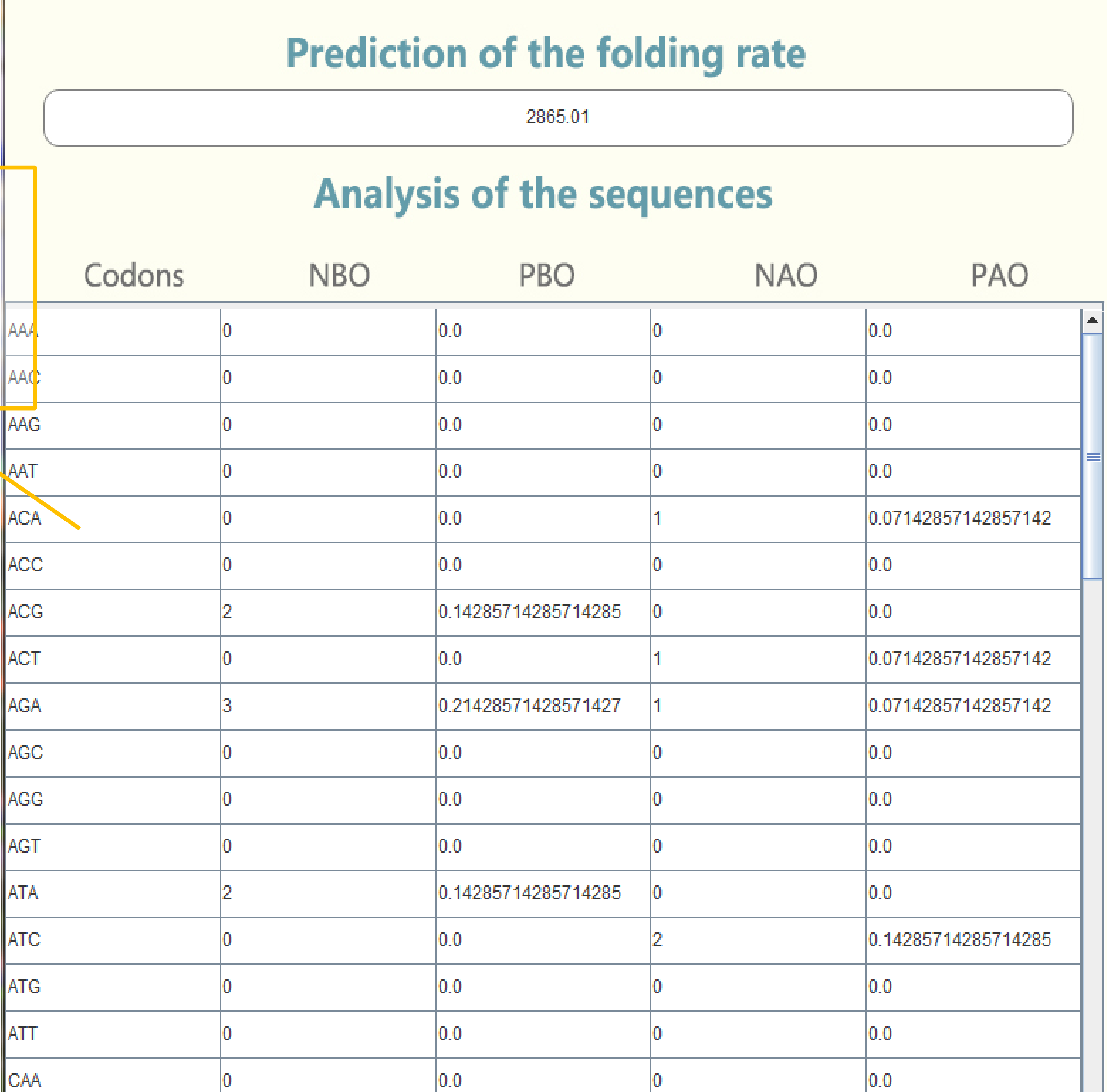
Method: Method1(Fitness, recommended)

Output Sequence

CGATAGACAATCGATGTATGACGCTAAACAATCGAGATCGAC

Do you want to analyze?

Click on 'YES' to analyze the sequence and predict the folding rate.



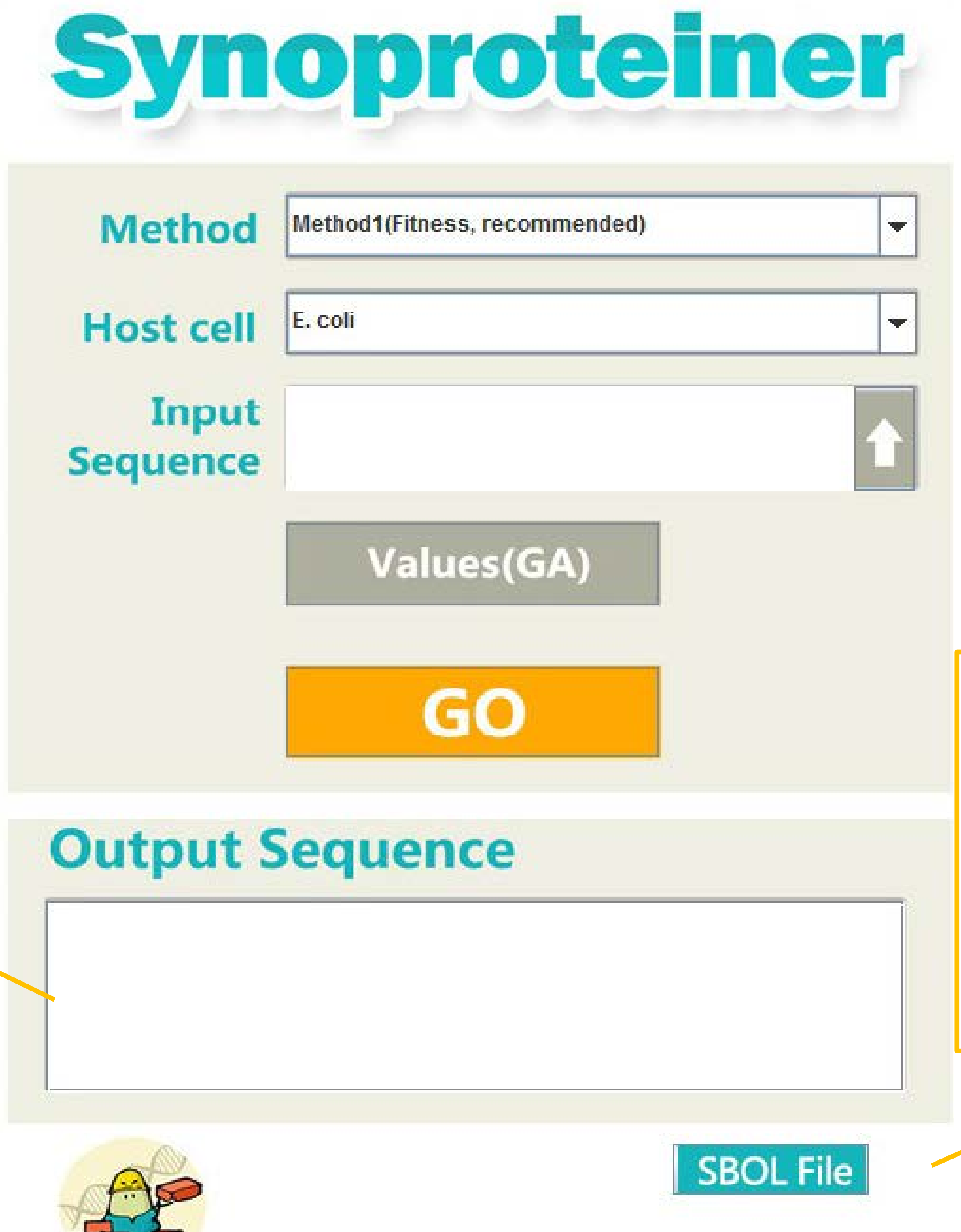
Prediction of the folding rate

2865.01

Analysis of the sequences

Codons	NBO	PBO	NAO	PAO
AAA	0	0.0	0	0.0
AAC	0	0.0	0	0.0
AAG	0	0.0	0	0.0
AAT	0	0.0	0	0.0
ACA	0	0.0	1	0.07142857142857142
ACC	0	0.0	0	0.0
ACG	2	0.14285714285714285	0	0.0
ACT	0	0.0	1	0.07142857142857142
AGA	3	0.21428571428571427	1	0.07142857142857142
AGC	0	0.0	0	0.0
AGG	0	0.0	0	0.0
AGT	0	0.0	0	0.0
ATA	2	0.14285714285714285	0	0.0
ATC	0	0.0	2	0.14285714285714285
ATG	0	0.0	0	0.0
ATT	0	0.0	0	0.0
CAA	0	0.0	0	0.0

This is the result of the prediction and the analysis.

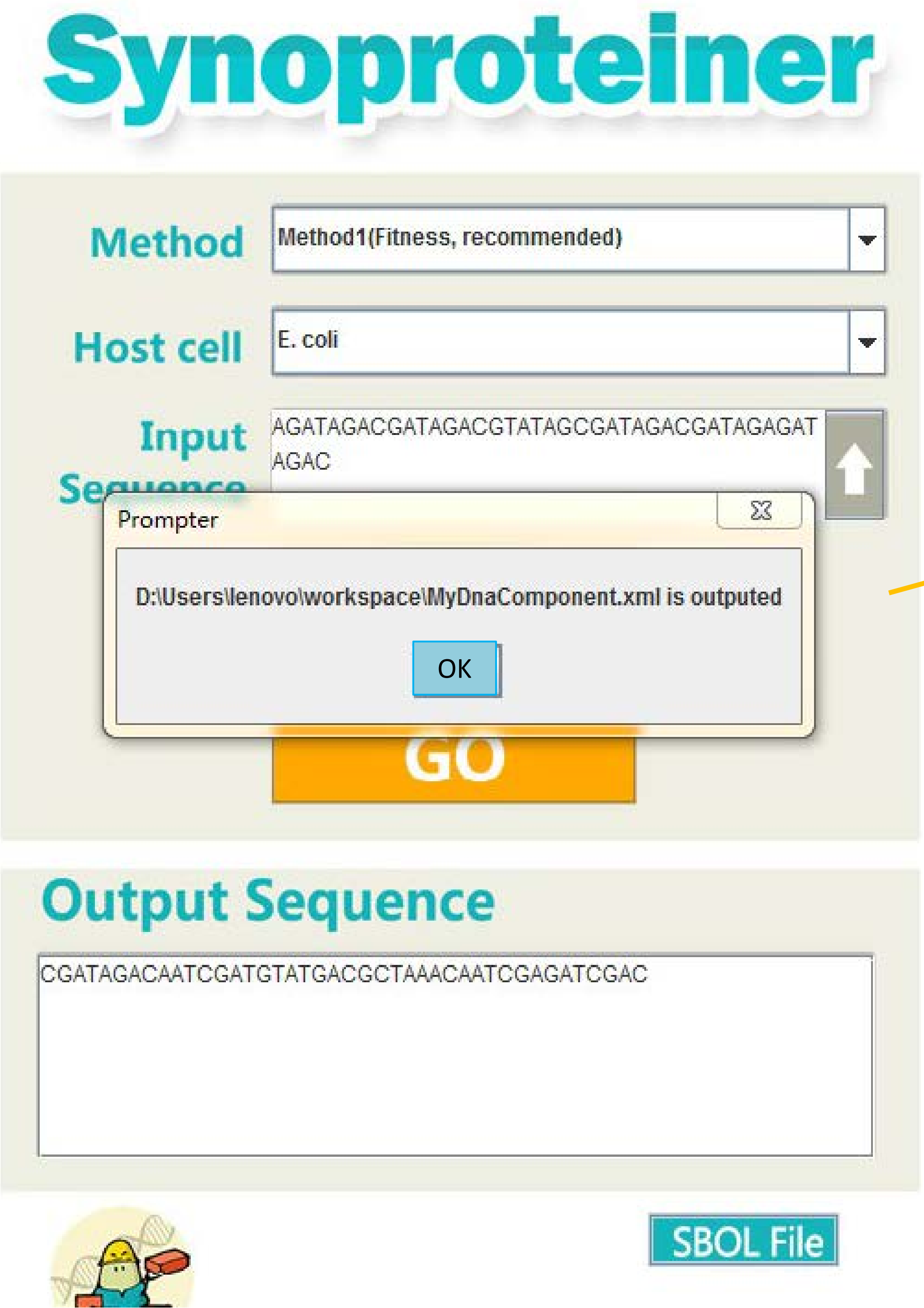


Method: Method1(Fitness, recommended)

Host cell: E. coli

This is a place for output of the sequence optimized.

Click on ‘SBOL File’ if you want to save the results.



Method: Method1(Fitness, recommended)

Host cell: E. coli

Input Sequence: AGATAGACGATAGACGTATAGCGATAGACGATAGAGATAGAC

Prompter

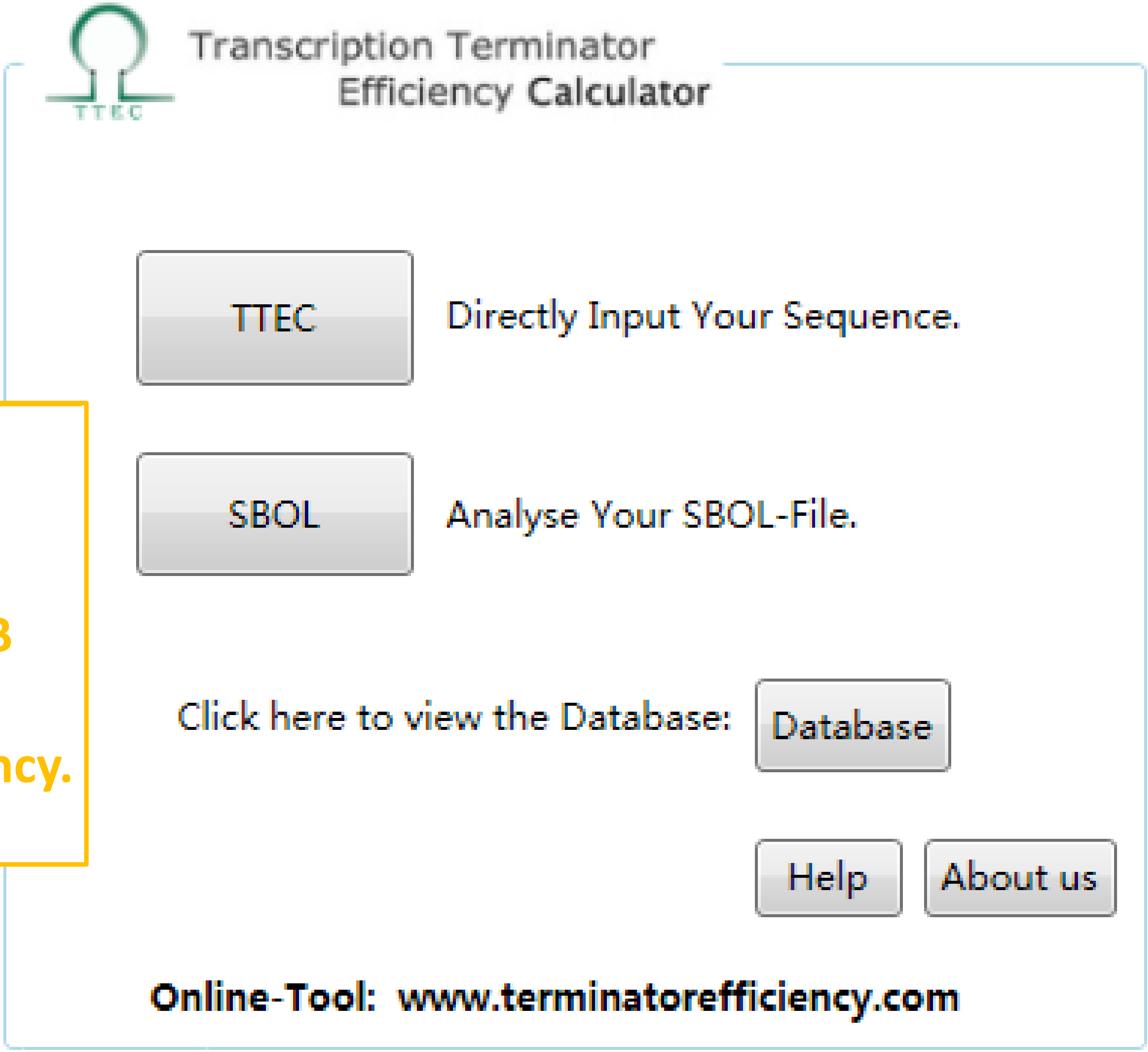
D:\Users\lenovo\workspace\MyDnaComponent.xml is outputted

Output Sequence

CGATAGACAATCGATGTATGACGCTAAACAATCGAGATCGAC

The SBOL file has been saved.

TTEC is a software designed by SUSTC-Shenzhen-B to calculate the terminator efficiency.



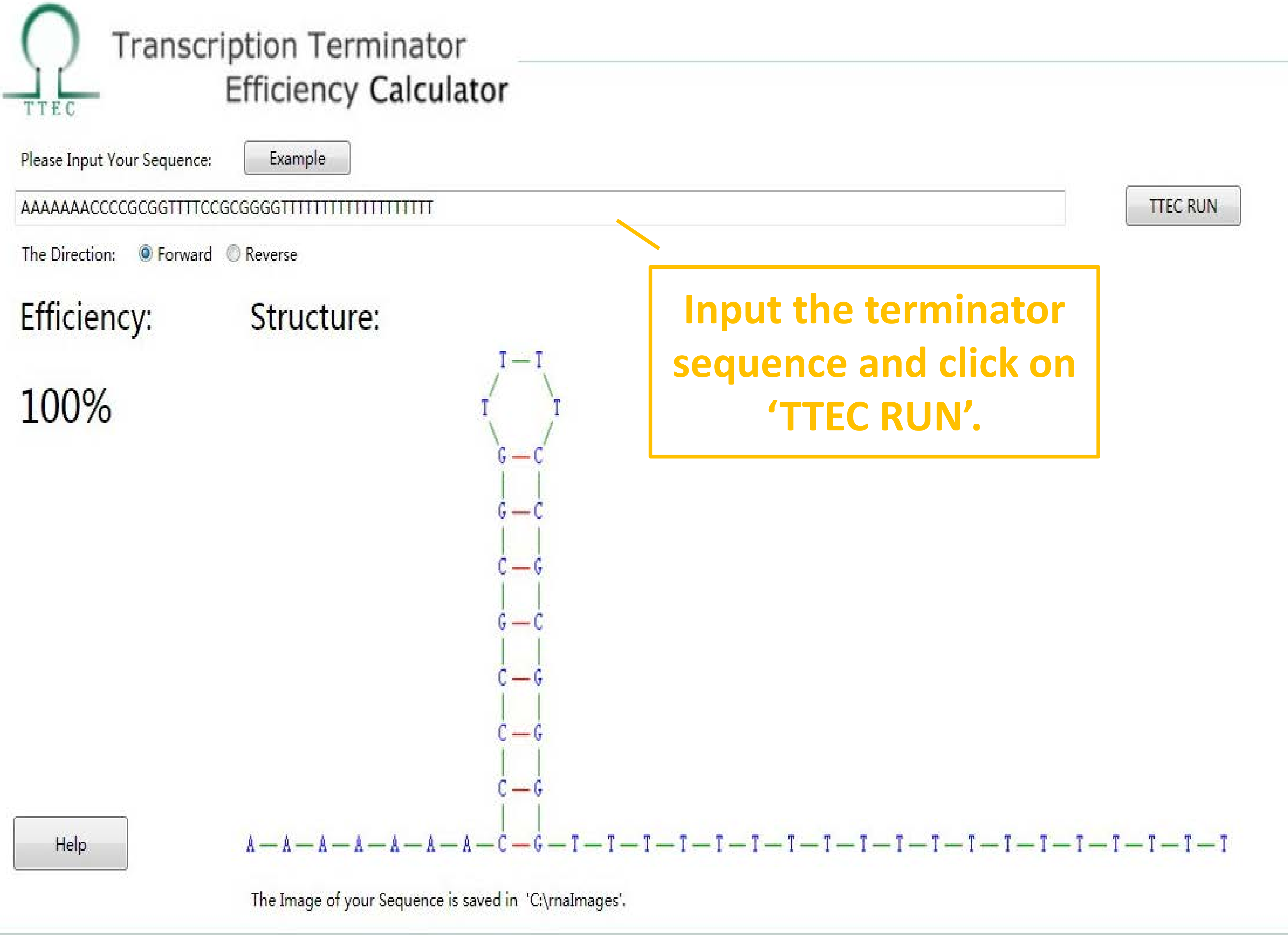
Transcription Terminator Efficiency Calculator

Directly Input Your Sequence.

Analyse Your SBOL-File.

Click here to view the Database:

Online-Tool: www.terminatorefficiency.com



Transcription Terminator Efficiency Calculator

Please Input Your Sequence: Example

AAAAAAACCCCGCGGTTTTCCGCGGGGTTTTTTTTTTTTTTTTTTT

TTEC RUN

The Direction: ● Forward ○ Reverse

Efficiency:

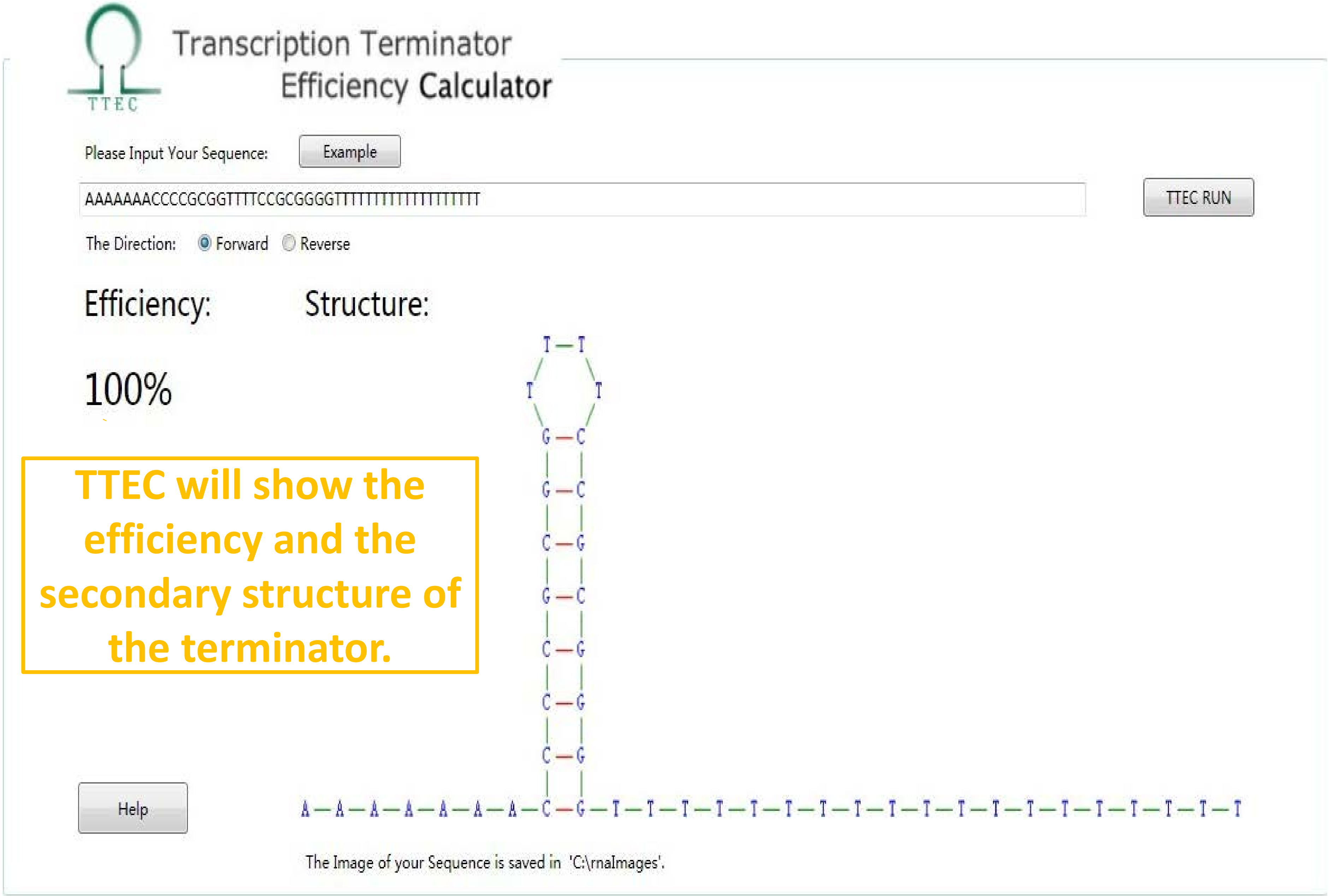
100%

Structure:

Help

The Image of your Sequence is saved in 'C:\rnaImages'.

Input the terminator sequence and click on ‘TTEC RUN’.



Please Input Your Sequence: AAAAAAACCCCGCGGTTTTCCGCGGGGTTTTTTTTTTTTTTTTTTT

The Direction: ● Forward ○ Reverse

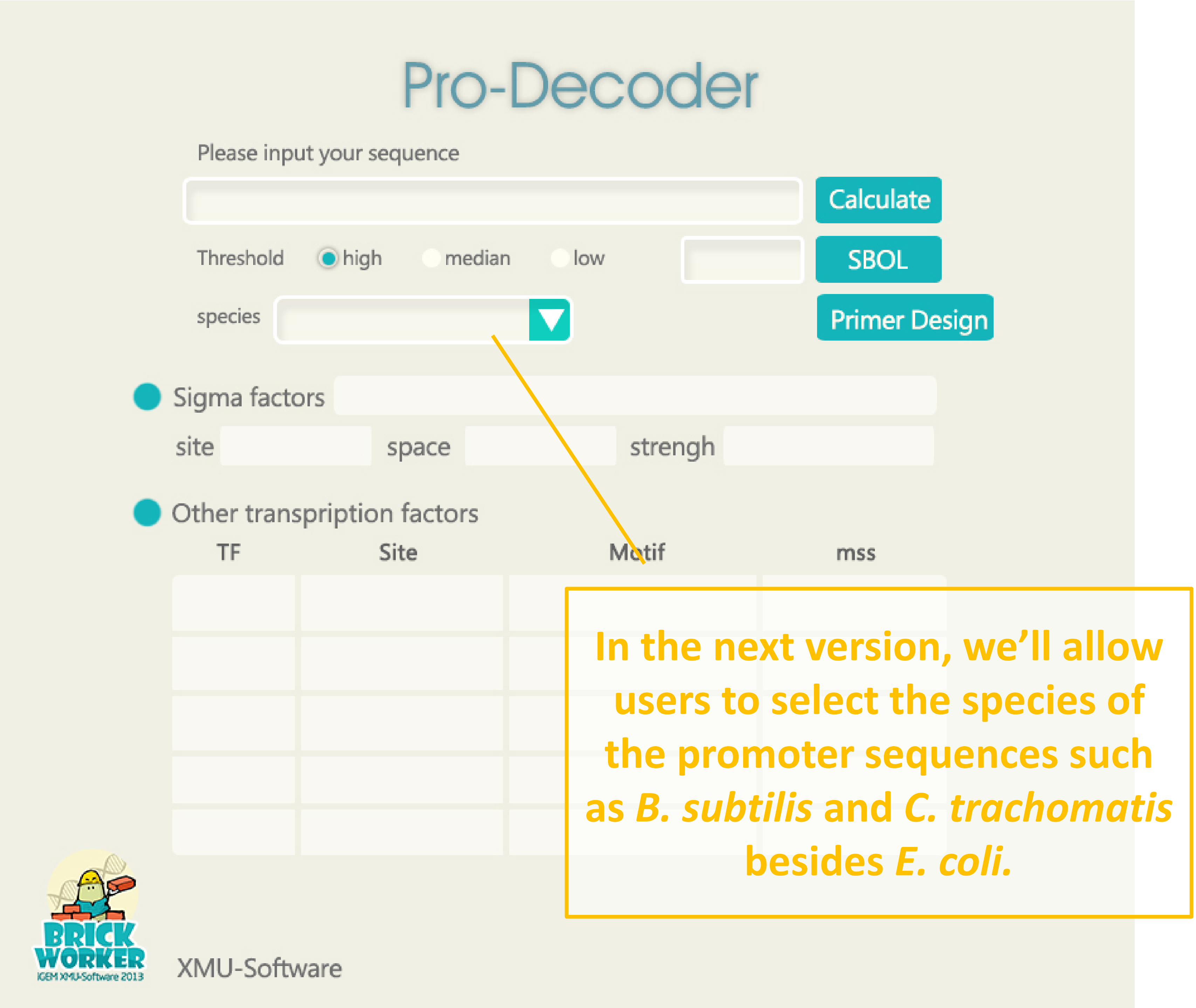
Efficiency: 100%

Structure:

The Image of your Sequence is saved in 'C:\rnaImages'.

TTEC will show the efficiency and the secondary structure of the terminator.

In next version,
YOU CAN……



In the next version, we'll allow users to select the species of the promoter sequences such as *B. subtilis* and *C. trachomatis* besides *E. coli.*

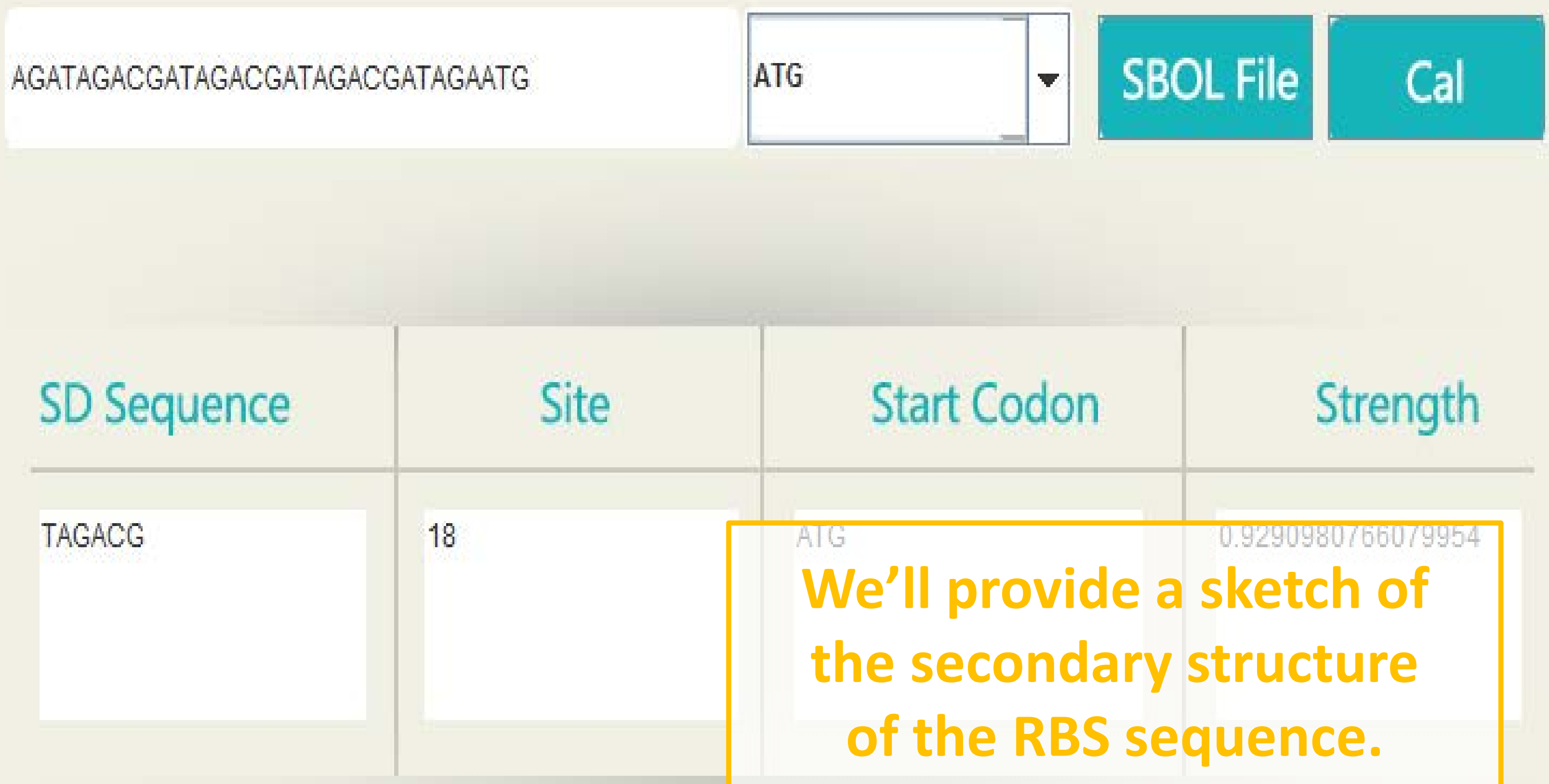
agataagatagcgataga

ATG

SD Sequence	Site	Start Codon	Strength

RBS-Decoder will also integrate the RBS model of more species such as *H. influenzae* and *M. genitalium*

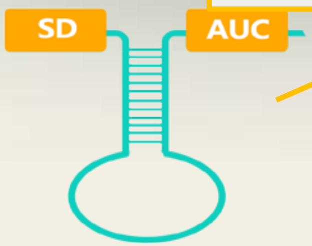
RBS-Decoder

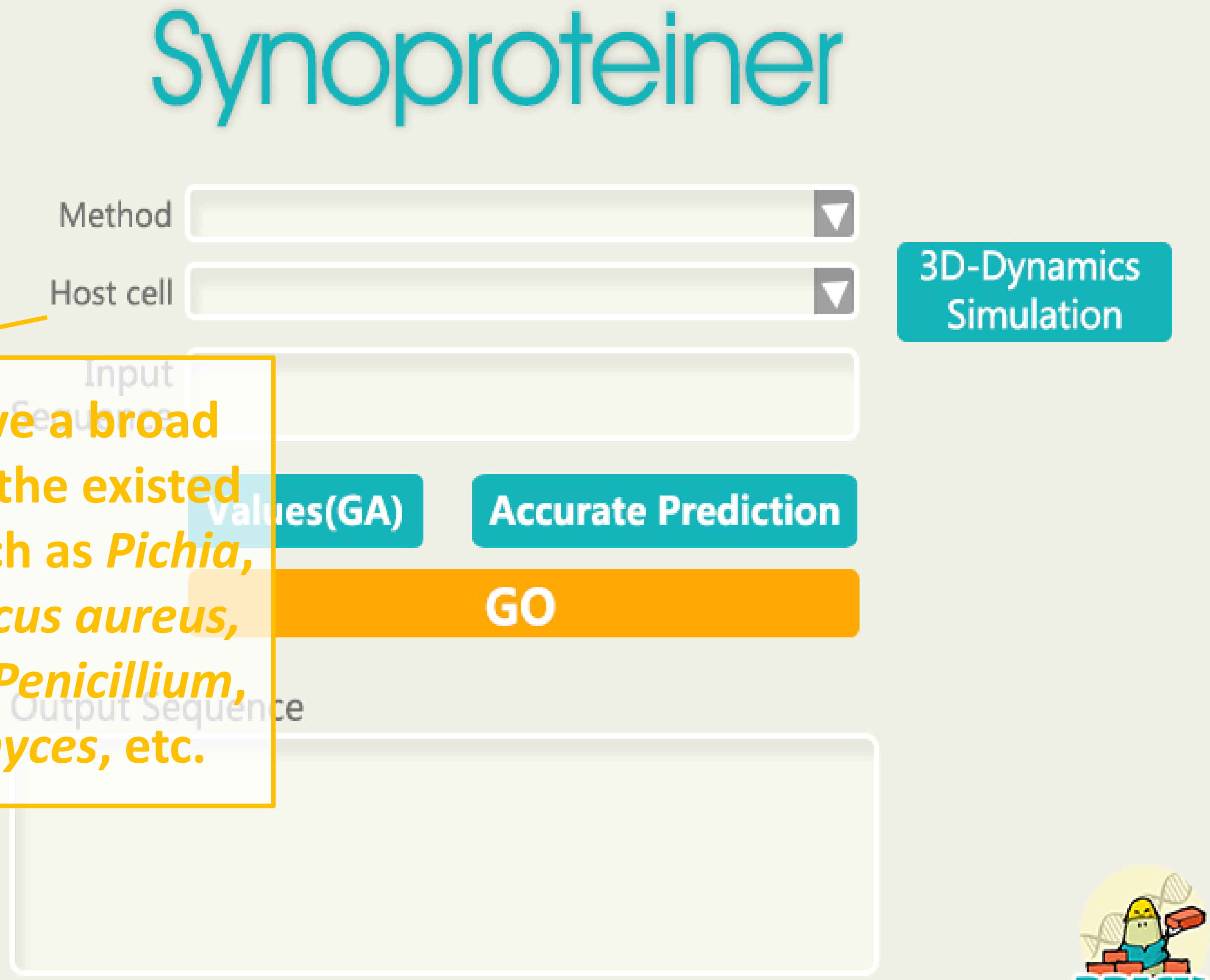


SD Sequence	Site	Start Codon	Strength
TAGACG	18	ATG	0.9290980766079954

We’ll provide a sketch of the secondary structure of the RBS sequence.

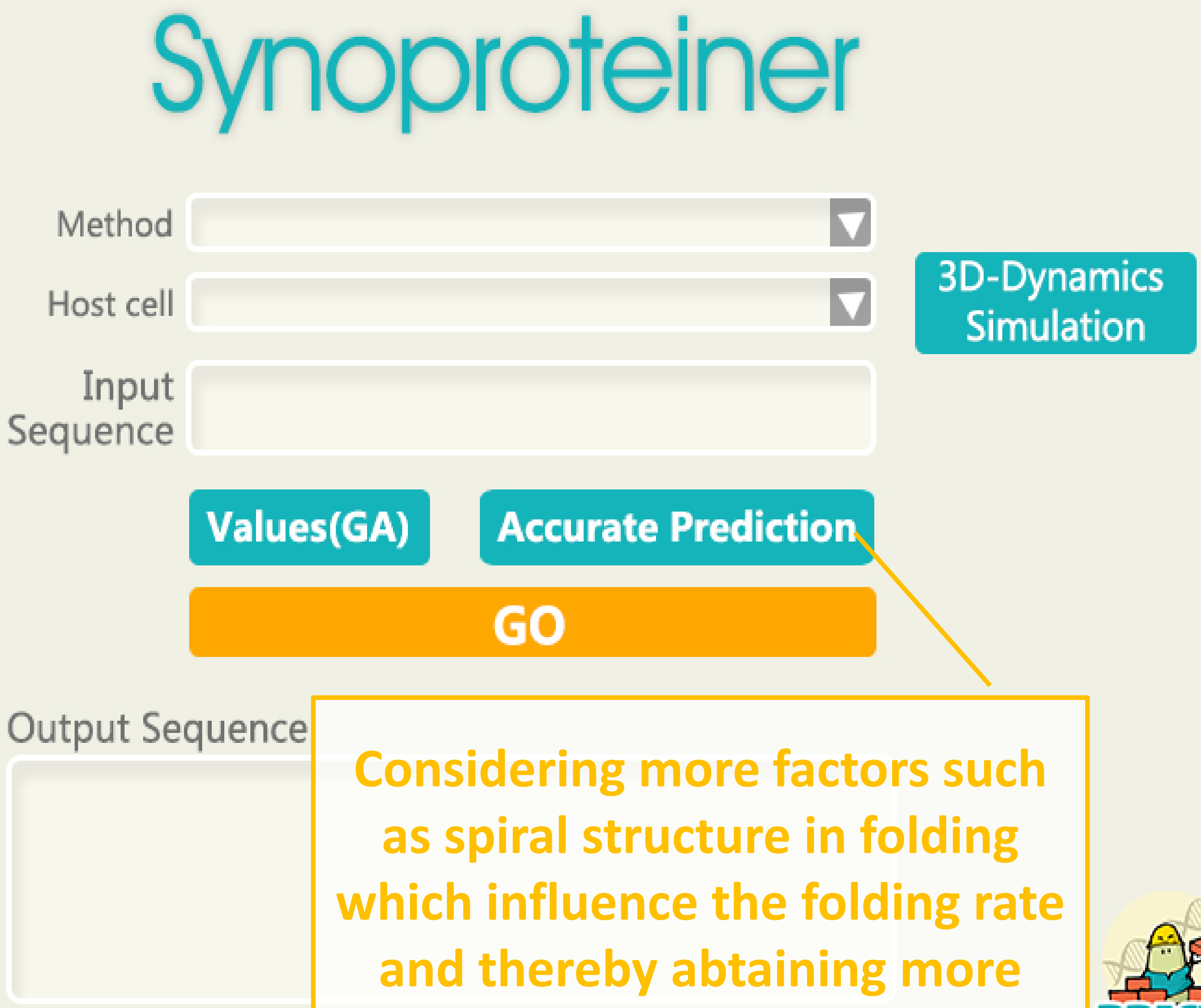
Structure:





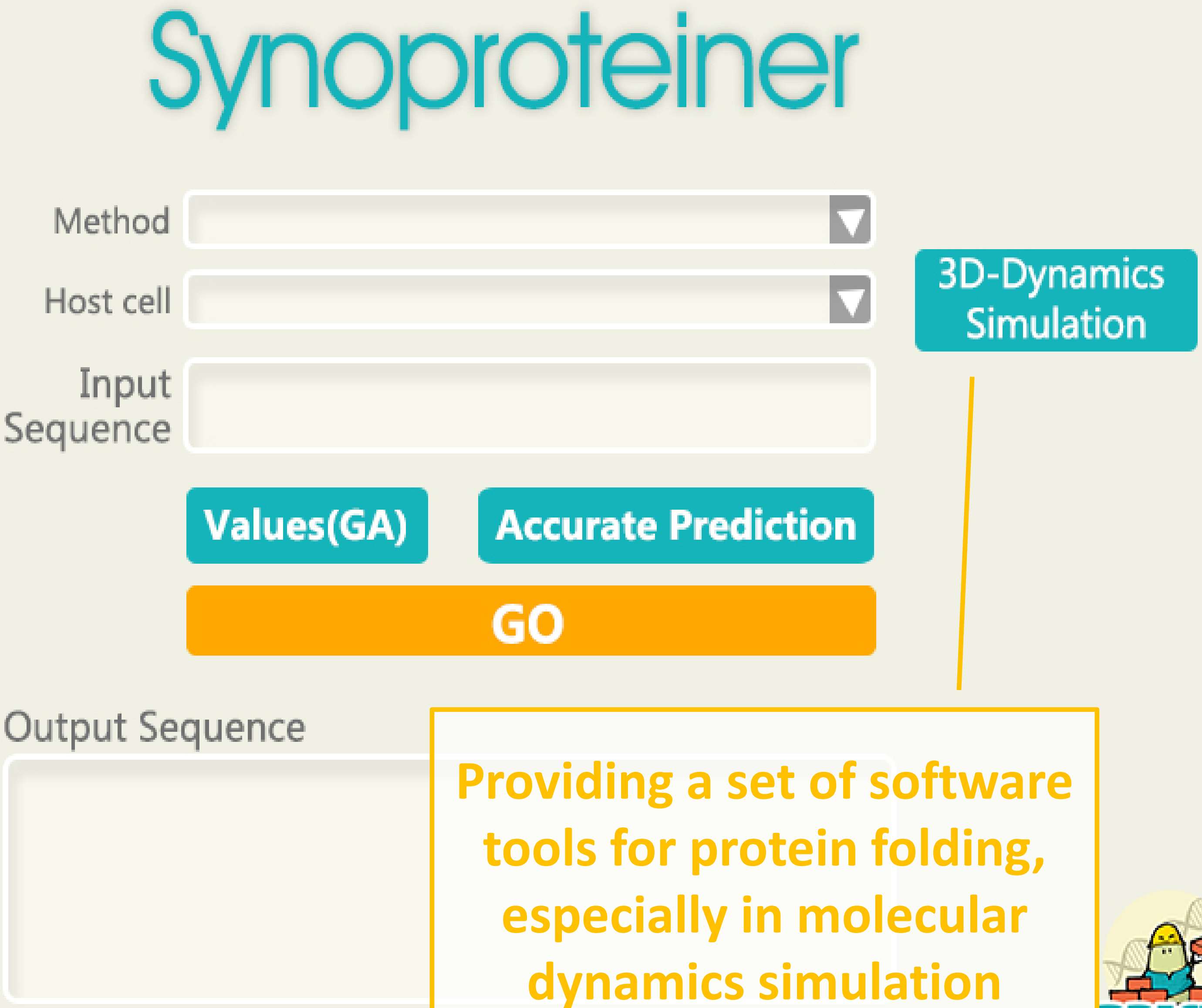
You can have a broad coverage of the existed host cells such as *Pichia*, *Staphylococcus aureus*, *Aspergillus*, *Penicillium*, *Saccharomyces*, etc.

BRICK WORKER
iGEM XMU-Software 2013



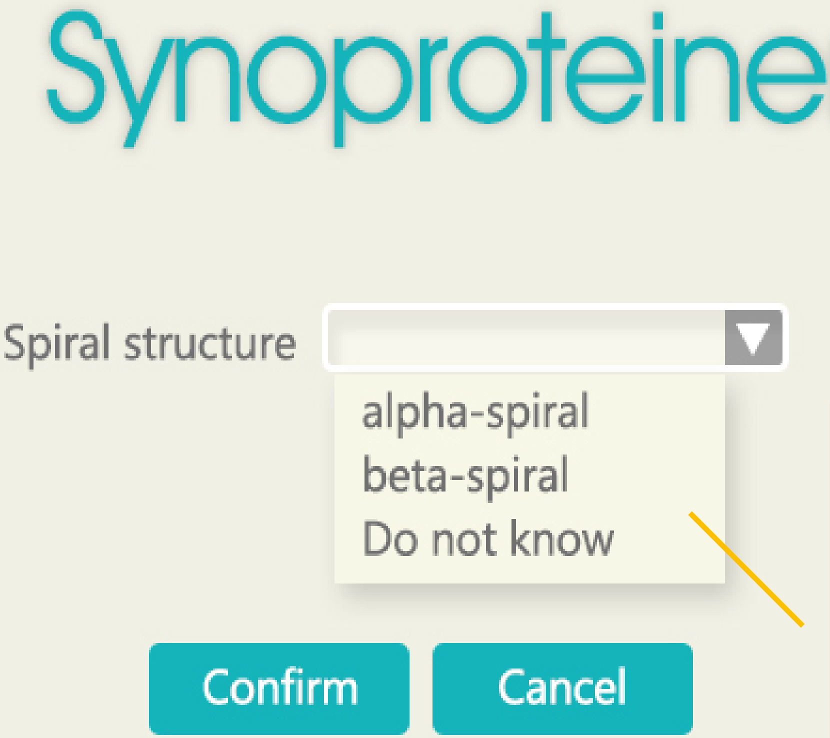
Considering more factors such as spiral structure in folding which influence the folding rate and thereby abtaining more accurate prediction rate.

BRICK WORKER
iGEM XMU-Software 2013



Providing a set of software tools for protein folding, especially in molecular dynamics simulation of protein folding.

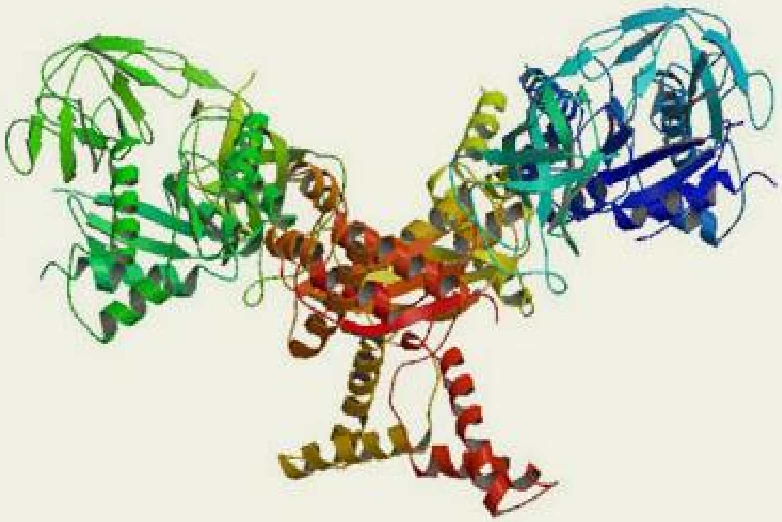
BRICK WORKER
iGEM XMU-Software 2013



These spiral structure will help you predict the rate more accurately.

Synoproteiner

3D-Dynamics Simulation



The 3D-structure of proteins can help users find the active center and simulate the reaction between the protein and the substrate to find an optimal configuration. And the users can obtain more optimized protein by figuring out the new gene sequence reversely (with structure information, not the amino acid sequence).

BRICK WORKER

IGEM XMU-Software 2013