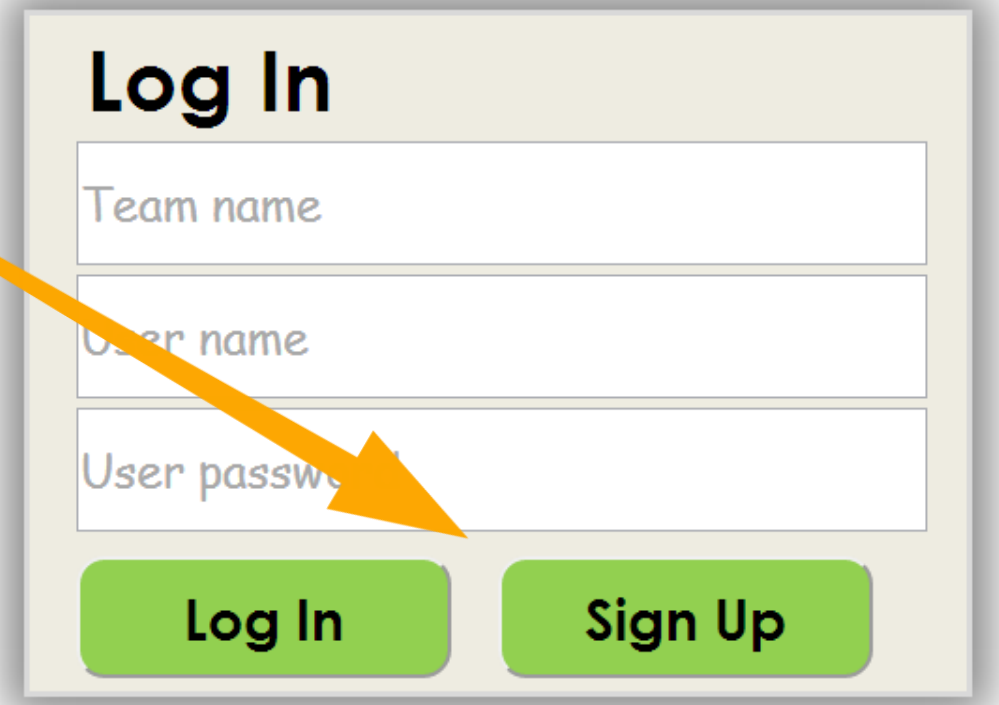
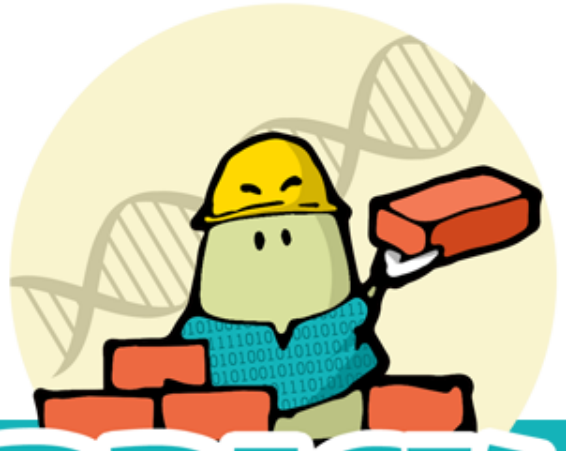
You will need to sign up the first time you use it.
We offer two kinds of accounts for you.





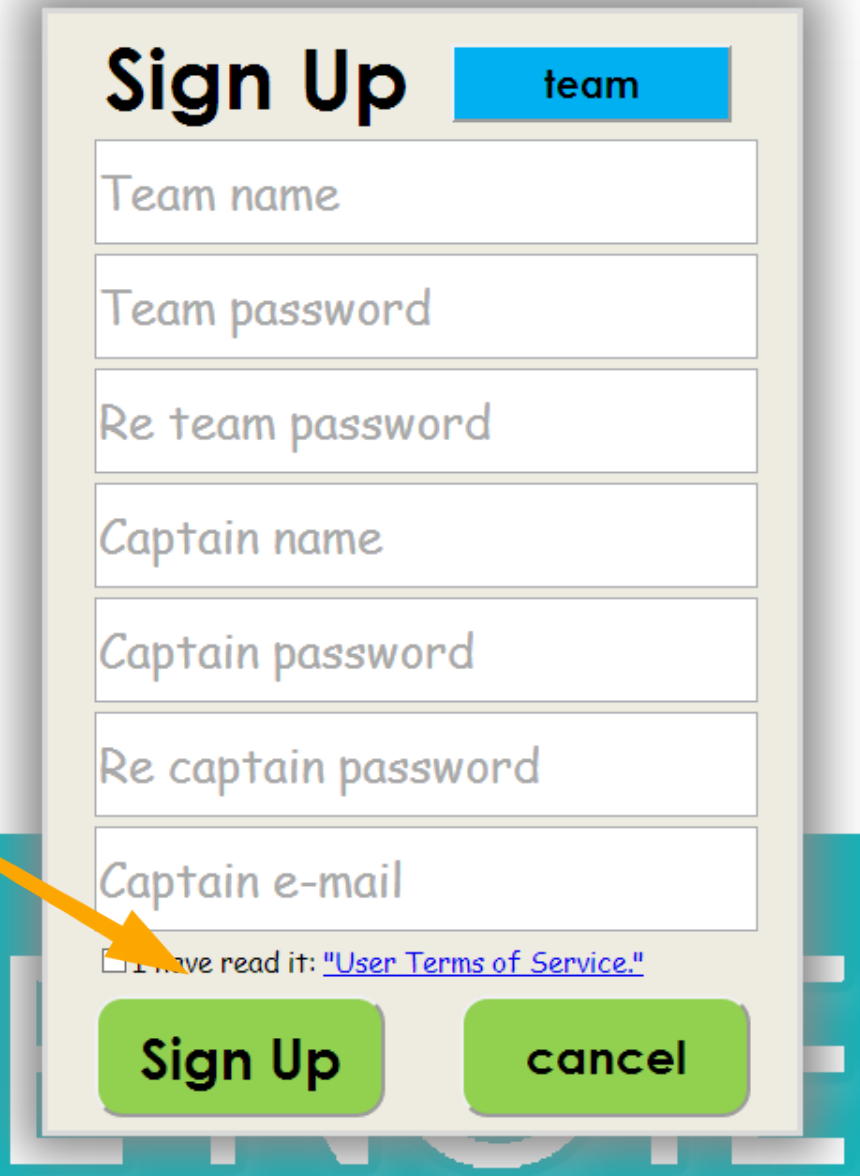
BRICK WORKER

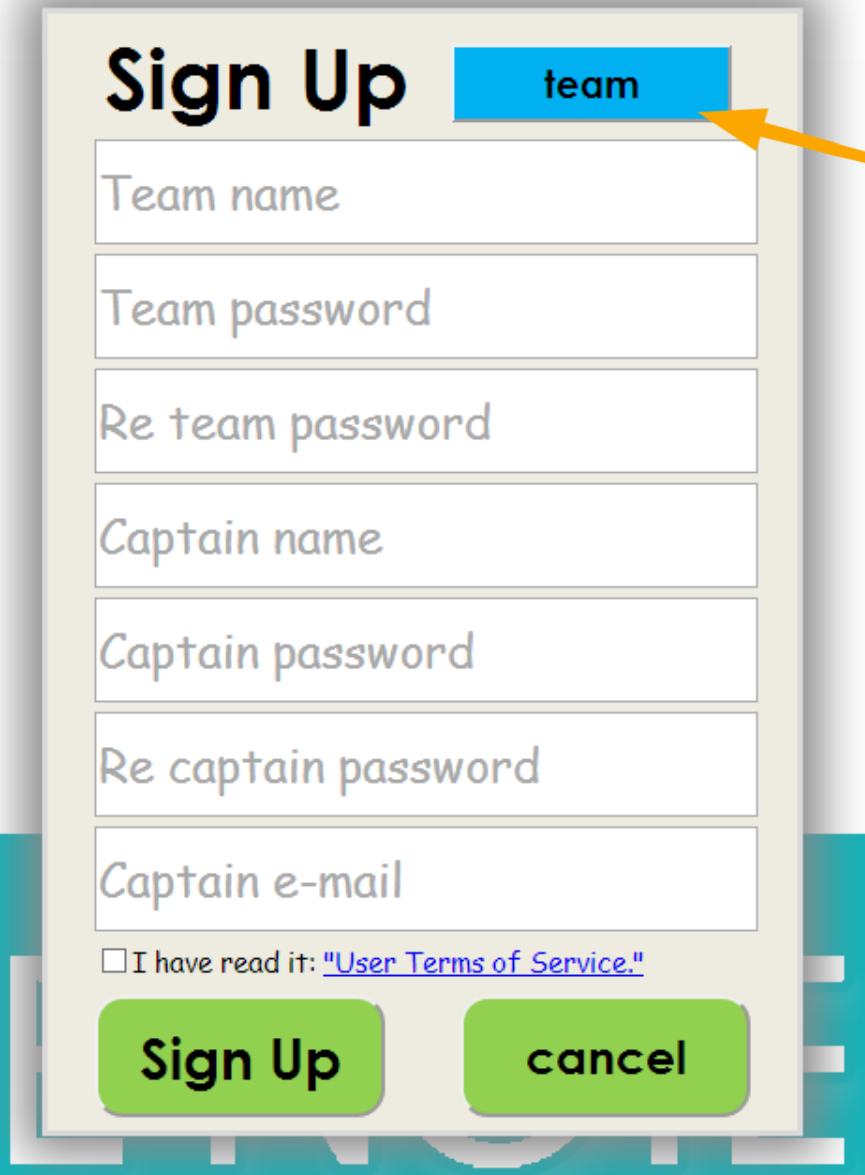
iGEM XMU-Software 2013

E'NOTE

A team account allows you to share your note. Anybody can join in the group after the leader accept.

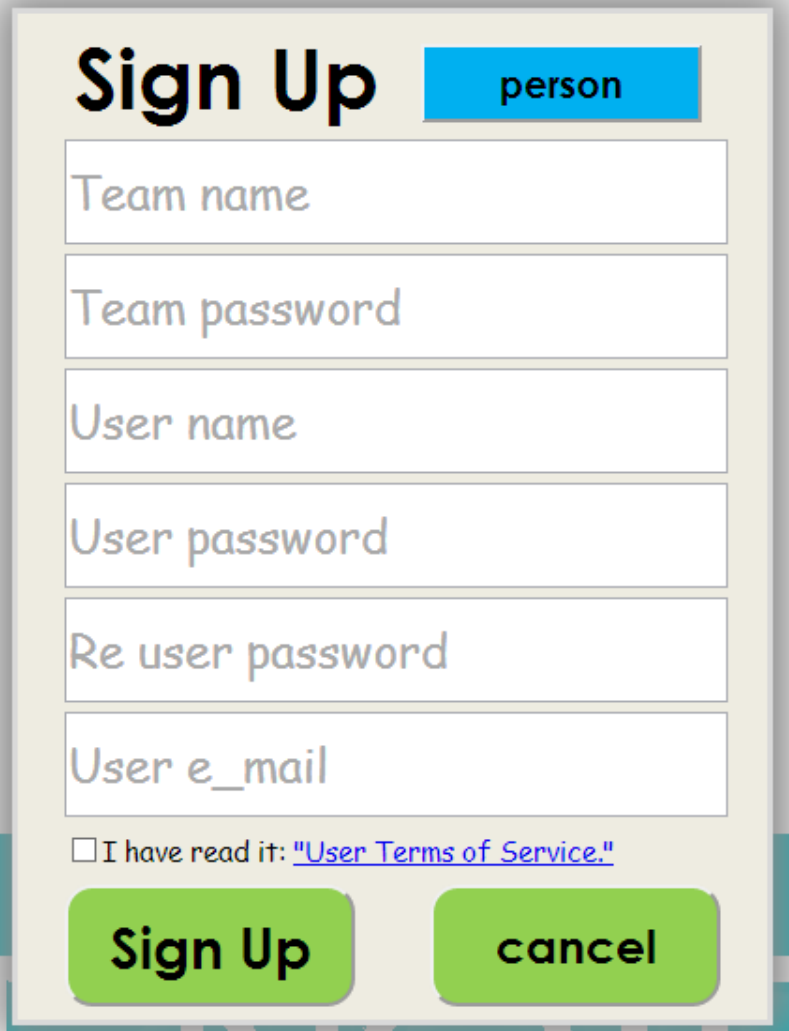
Remember to read this.





Click here to change the user's type.

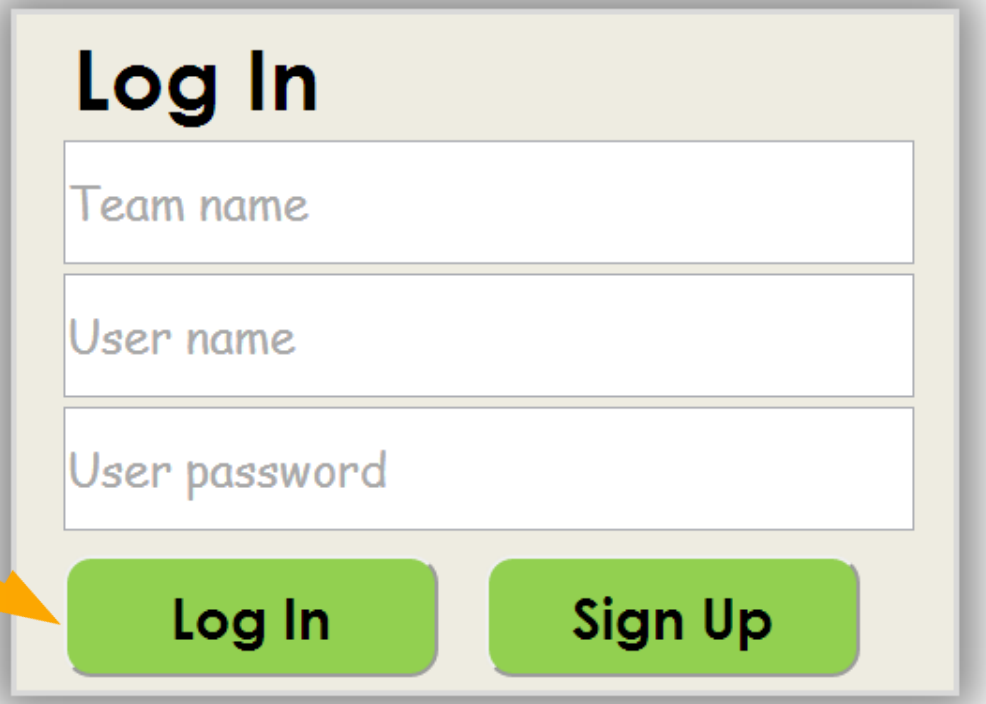
By the team name and password, you can have access to registration and share team journals.



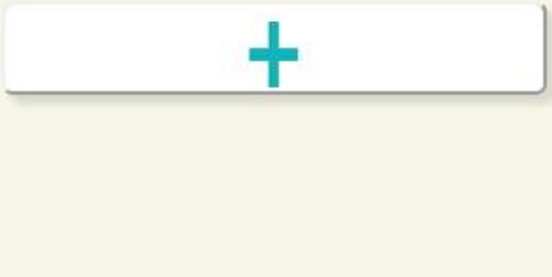
BRICK WORKER

iGEM XMU-Software 2013

Log in with your account after signing up.



E'NOTE

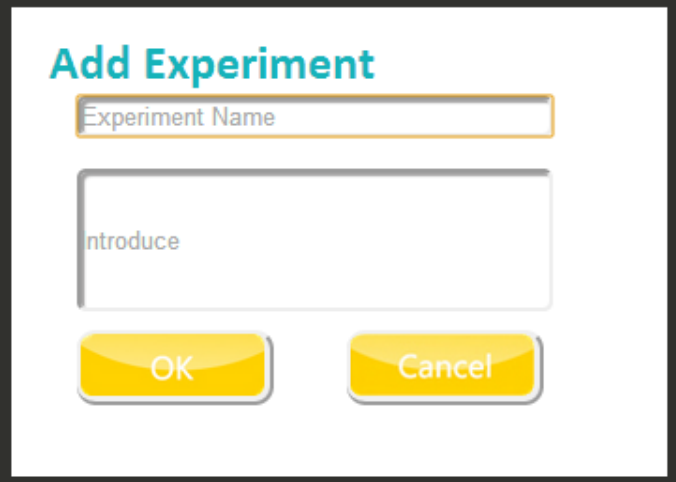


Click here to create a new file.

ENOTE
EasyExperiment

XS
HJ

+



Take a name and write a short introduction for your note .

ENOTE
Easy Experiment

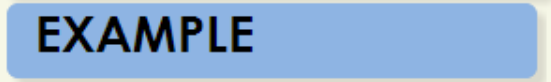
XMU Software
HJ

Create a new experiment.

Click here to show the note.

XMU Software
HJ

EXAMPLE



no name

EXAMPLE

no name 2013/10/23 01:58:55--HJ

You can edit the note's name by double clicking here.

XMU Software
HJ

EXAMPLE

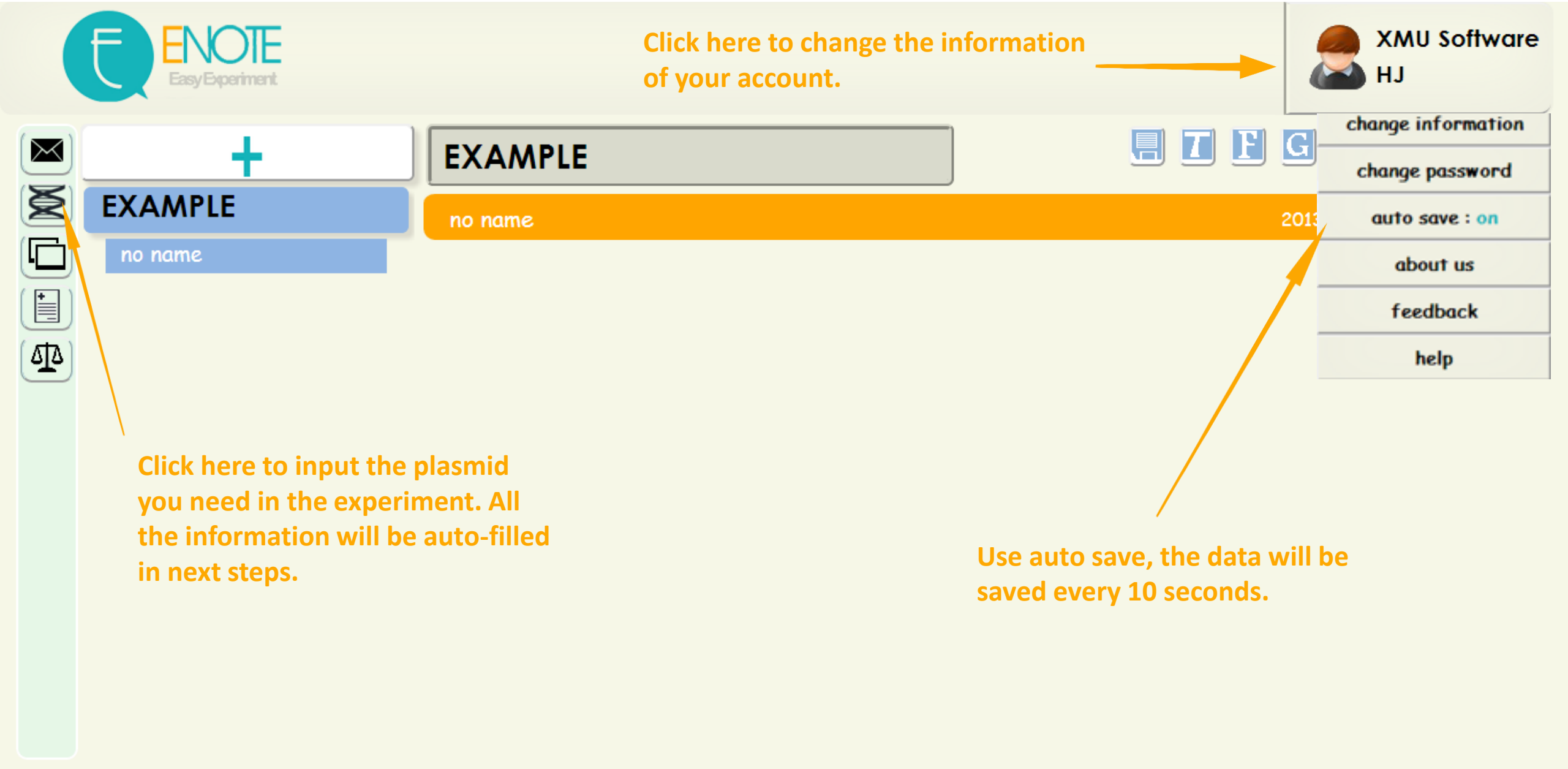
no name

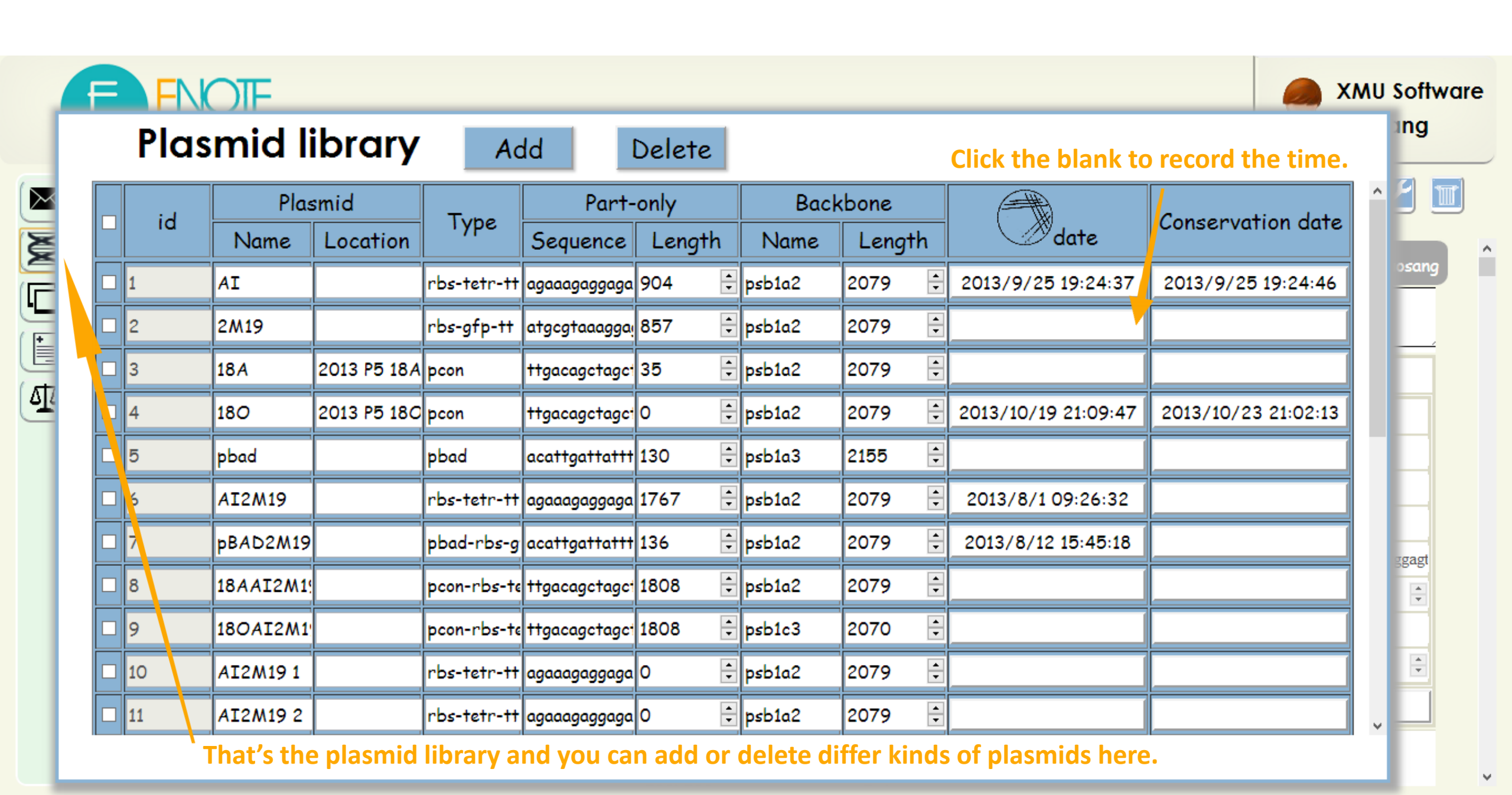
EXAMPLE

no name 2013/1 /23 01:58:55--HJ

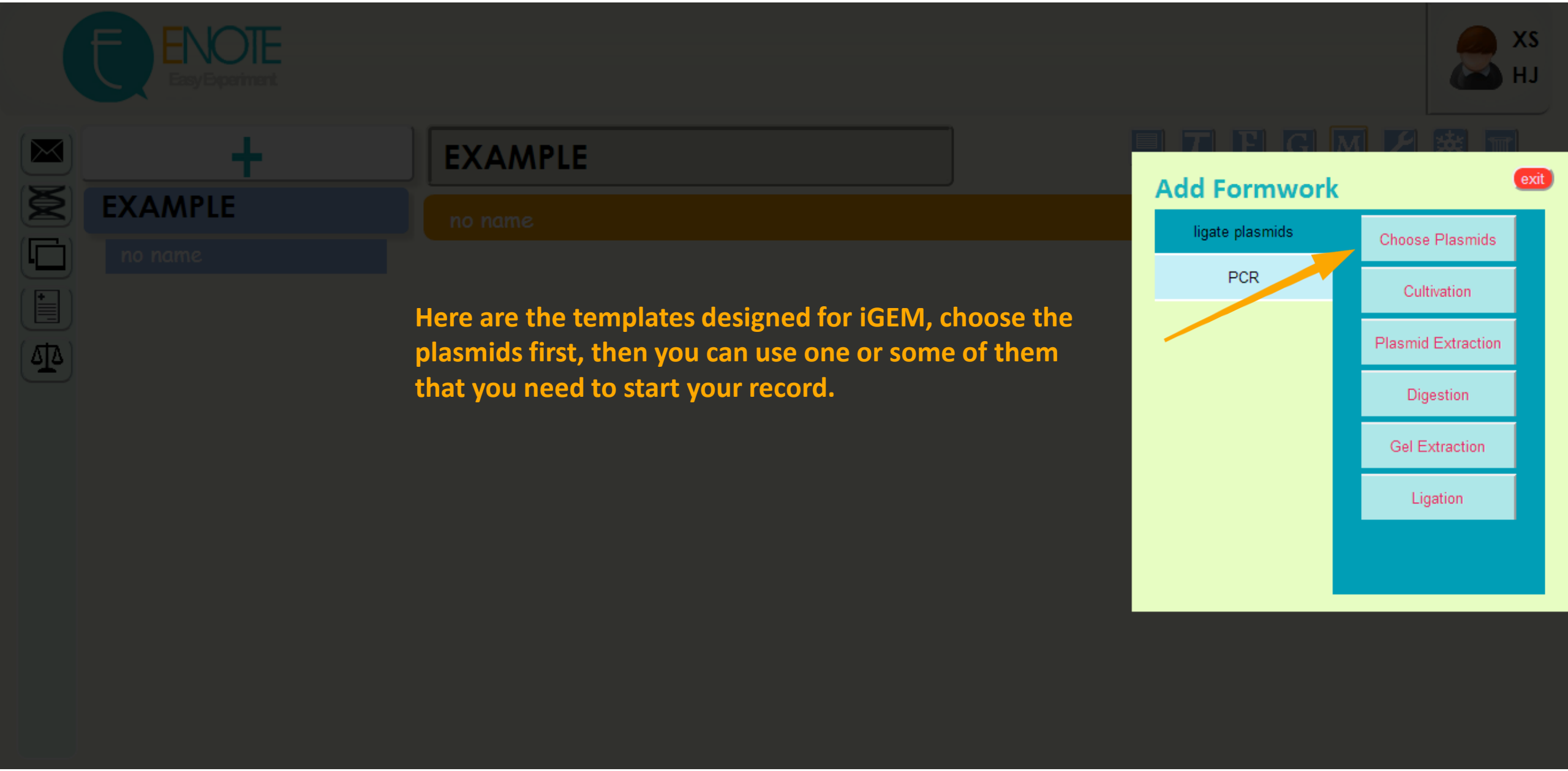
Click here to get tools.

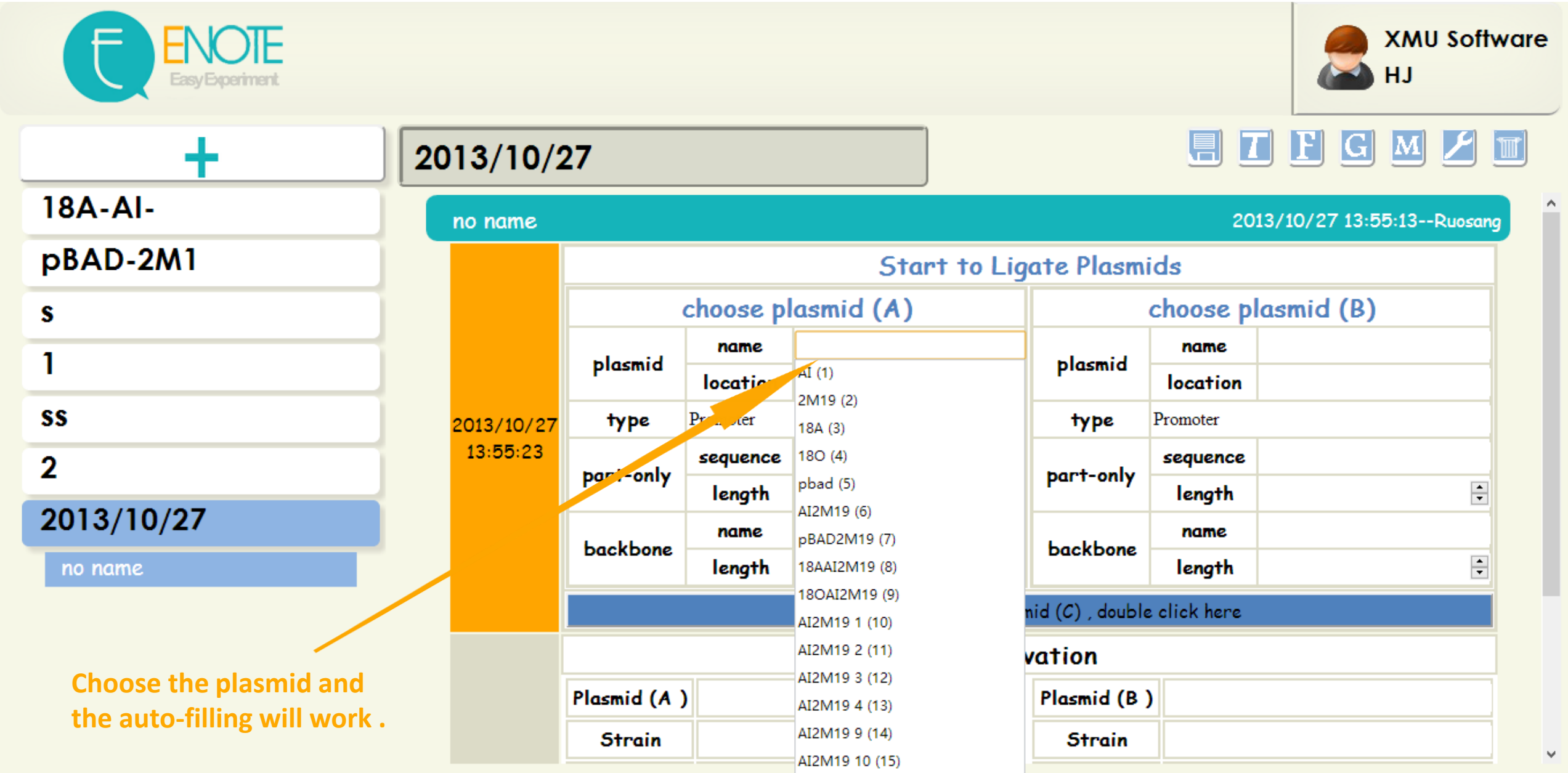
Click here or press ‘Alt’ + ‘t’ to show the tools bar on the left.


ENOTE
Easy Experiment
Click here to change the information of your account.
XMU Software
HJ
change information
change password
auto save : on
about us
feedback
help
EXAMPLE
EXAMPLE
no name
no name
Click here to input the plasmid you need in the experiment. All the information will be auto-filled in next steps.
Use auto save, the data will be saved every 10 seconds.



id	Plasmid		Type	Part-only		Backbone		date	Conservation date
	Name	Location		Sequence	Length	Name	Length		
1	AI		rbs-tetr-tt	agaaagaggaga	904	psb1a2	2079	2013/9/25 19:24:37	2013/9/25 19:24:46
2	2M19		rbs-gfp-tt	atgcgtaaagga	857	psb1a2	2079		
3	18A	2013 P5 18A	pcon	ttgacagctagc	35	psb1a2	2079		
4	18O	2013 P5 18O	pcon	ttgacagctagc	0	psb1a2	2079	2013/10/19 21:09:47	2013/10/23 21:02:13
5	pbad		pbad	acattgattattt	130	psb1a3	2155		
6	AI2M19		rbs-tetr-tt	agaaagaggaga	1767	psb1a2	2079	2013/8/1 09:26:32	
7	pBAD2M19		pbad-rbs-g	acattgattattt	136	psb1a2	2079	2013/8/12 15:45:18	
8	18AAI2M1		pcon-rbs-te	ttgacagctagc	1808	psb1a2	2079		
9	18OAI2M1		pcon-rbs-te	ttgacagctagc	1808	psb1c3	2070		
10	AI2M19 1		rbs-tetr-tt	agaaagaggaga	0	psb1a2	2079		
11	AI2M19 2		rbs-tetr-tt	agaaagaggaga	0	psb1a2	2079		


ENOTE
EasyExperiment
XS
HJ
EXAMPLE
EXAMPLE
no name
EXAMPLE
no name
Here are the templates designed for iGEM, choose the plasmids first, then you can use one or some of them that you need to start your record.
Add Formwork
exit
ligate plasmids
PCR
Choose Plasmids
Cultivation
Plasmid Extraction
Digestion
Gel Extraction
Ligation


ENOTE
Easy Experiment
XMU Software
HJ
2013/10/27
18A-AI-
pBAD-2M1
s
1
ss
2
2013/10/27
no name
no name
2013/10/27 13:55:13--Ruosang
2013/10/27 13:55:23
Start to Ligate Plasmids
choose plasmid (A)
choose plasmid (B)
plasmid
name
location
type
Promoter
part-only
sequence
length
backbone
name
length
AI (1)
2M19 (2)
18A (3)
18O (4)
pbad (5)
AI2M19 (6)
pBAD2M19 (7)
18AAI2M19 (8)
18OAI2M19 (9)
AI2M19 1 (10)
AI2M19 2 (11)
AI2M19 3 (12)
AI2M19 4 (13)
AI2M19 9 (14)
AI2M19 10 (15)
id (C) , double click here
vation
Plasmid (A)
Plasmid (B)
Strain
Choose the plasmid and
the auto-filling will work .

When you choose or input the name of plasmid, the other information will be filled automatically.

XMU Software
HJ

+

18A-AI-

pBAD-2M1

s

1

no name

no name

ss

2

1

2013/10/22 19:51:38

choose plasmid (A)			choose plasmid (B)		
plasmid	name	AI2M19 14 (16)	plasmid	name	
	location			location	
type		rbs-tetr-tt-ptetr-rbs-gfp-tt	type		
part-only	sequence	agaaagaggagaaatactagatgtccagatt	part-only	sequence	
	length	1775		length	
backbone	name	psb1a2	backbone	name	
	length	2079		length	

if you need another plasmid (C) , double click here

2013/10/22 19:51:43

electrophoretogram and gel extraction

Analyse Electrophoretogram

	$A_{260/280}$	ng/μL	bp	
AI2M19 14 (A)				Correct
(B)				

ENOTE
Easy Experiment

XMU Software
HJ

+

EXAMPLE

no name

EXAMPLE

no name 2013/10/23 01:58:55--HJ

2013/10/23 17:35:24

Start to Ligate Plasmids

choose plasmid (A)			choose plasmid (B)		
plasmid	name		plasmid	name	
	location			location	
type	Promoter		type	Promoter	
part-only	sequence		part-only	sequence	
	length			length	
backbone	name		backbone	name	
	length			length	

if you need another plasmid (C) , double click here

Double click here to get another plasmid.

Cultivation

Plasmid (A)		Plasmid (B)	
Strain		Strain	

ENOTE
Easy Experiment

XMU Software
HJ

EXAMPLE

EXAMPLE

no name

no name

2013/10/23 01:58:55--HJ

2013/10/23 17:35:24

Start to Ligate Plasmids

choose plasmid (A)			choose plasmid (B)			choose plasmid (C)		
plasmid	name		plasmid	name		plasmid	name	
	location			location			location	
type	Promoter		type	Promoter		type	Promoter	
part-only	sequence		part-only	sequence		part-only	sequence	
	length			length			length	
backbone	name		backbone	name		backbone	name	
	length			length			length	

if you don't need the plasmid (C) , double click here

Cultivation

Plasmid (A)		Plasmid (B)		Plasmid (C)	
Strain		Strain		Strain	

That is the plasmid C.
The templates below
will change for it as well.

ENOTE
Easy Experiment

XMU Software
HJ

EXAMPLE

EXAMPLE

no name

Cultivation settings.

if you don't need the plasmid (C) , double click here

2013/10/23
17:35:26

Cultivation								
Plasmid (A)			Plasmid (B)			Plasmid (C)		
Strain			Strain			Strain		
antibiotics	none	none none	antibiotics	none	none none	antibiotics	none	none none
Medium			Medium			Medium		
Volume	20	μ	Volume	20	μ	Volume	20	μ
Temperature	37	℃	Temperature	37	℃	Temperature	37	℃
Speed	200	rpm	Speed	200	rpm	Speed	200	rpm

2013/10/23
17:35:29

Plasmid Extraction		
	$A_{260/280}$	ng/μL
(A)		
(B)		
(C)		

ENOTE
Easy Experiment

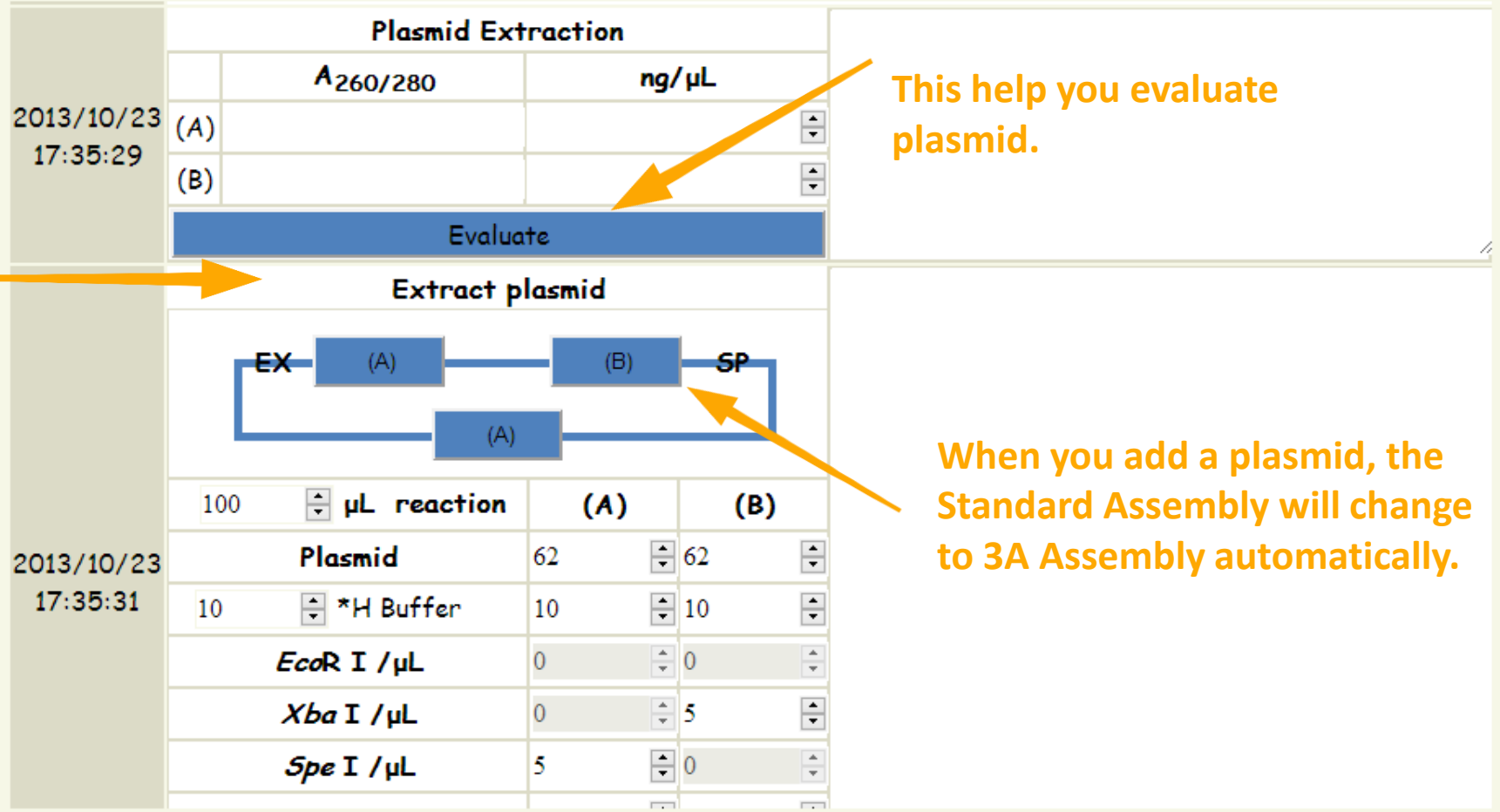
XMU Software
HJ

+

EXAMPLE

no name

EXAMPLE



This help you evaluate plasmid.

'Extract plasmid' can Change according to the number of plasmids.

When you add a plasmid, the Standard Assembly will change to 3A Assembly automatically.

ENOTE
Easy Experiment

XMU Software
HJ

+

EXAMPLE

no name

EXAMPLE

2013/10/23 17:35:29

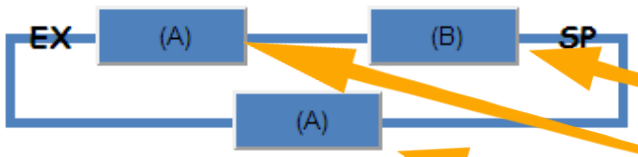
Plasmid Extraction

	$A_{260/280}$	ng/μL
(A)		
(B)		

Evaluate

2013/10/23 17:35:31

Extract plasmid



100 μL reaction	(A)	(B)
Plasmid	62	62
10 *H Buffer	10	10
EcoR I /μL	0	0
Xba I /μL	0	5
Spe I /μL	5	0

Choose the system.

Click on them to change the sequence.

ENOTE
Easy Experiment

XMU Software
HJ

+

EXAMPLE

no name

EXAMPLE

	Spe I /μL	5	5	
	Pst I /μL	5	5	
	H_2O /μL	18	18	

2013/10/23 17:35:33	electrophoretogram and gel extraction				
	Analyse Electrophoretogram				
		$A_{260/280}$	ng/μL	bp	Correct
	(A)			0	
	(B)			0	

2013/10/23 17:35:35	Ligation			
	10 μL reaction	Insert/Vector=	3	mol/mol
		Recommend	Actual use	
	A (vector) /μL			
	B (insert) /μL			
	10 *Buffer /μL	1		
	ligase /μL	1		

Here you can record the data and use it to analyze for the next step.

Input the concentration, the blanks will be filled automatically.

ENOTE
Easy Experiment

XMU Software
HJ

+

EXAMPLE

no name

EXAMPLE

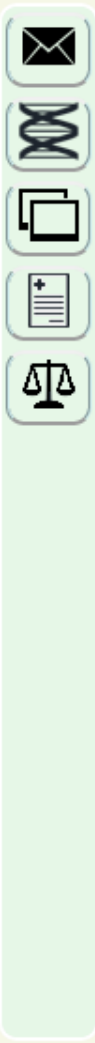
no name

2013/10/23 18:12:28--HJ

Click this three button to create your own templates.


ENOTE
EasyExperiment
XS
HJ
EXAMPLE
EXAMPLE
no name
EXAMPLE
no name
2013/10/23
18:12:33
no content
Add Table
Please set the row and col
Row
5
Col
5
OK
Cancel
Input the table you want.

XMU Software
HJ



EXAMPLE

no name

Add text board, table or picture wherever you want.

EXAMPLE

no name 2013/10/23 18:12:28--HJ

2013/10/23 18:12:33	no content
2013/10/23 18:13:17	
2013/10/23 18:14:15	

ENOTE
Easy Experiment

XMU Software
HJ

EXAMPLE

EXAMPLE

no name

EXAMPLE

2013/10/23
18:13:17

2013/10/23
18:14:15

Select File Not Select File

submit

Upload the graph you want to show to others and note it.

ENOTE
Easy Experiment

XMU Software
HJ

Don’t forget to save when you finish your record.

+

18A-AI-

pBAD-2M1

- pBAD
- PBAD-2M19
- PBAD-2M19 PBAD IS ...
- PBAD-2M19 2M19 IS ...
- PBAD2M19 4
- PBAD2M19 1 AND 2
- PBAD2M19 4
- PBAD2M10 5
- LINE 0,1,2 IN C3
- no name
- no name
- no name

pBAD-2M1

pBAD

2013/8/3 18:01:27--Ruosang

2013/8/3 18:01:51

Start to Ligate Plasmids

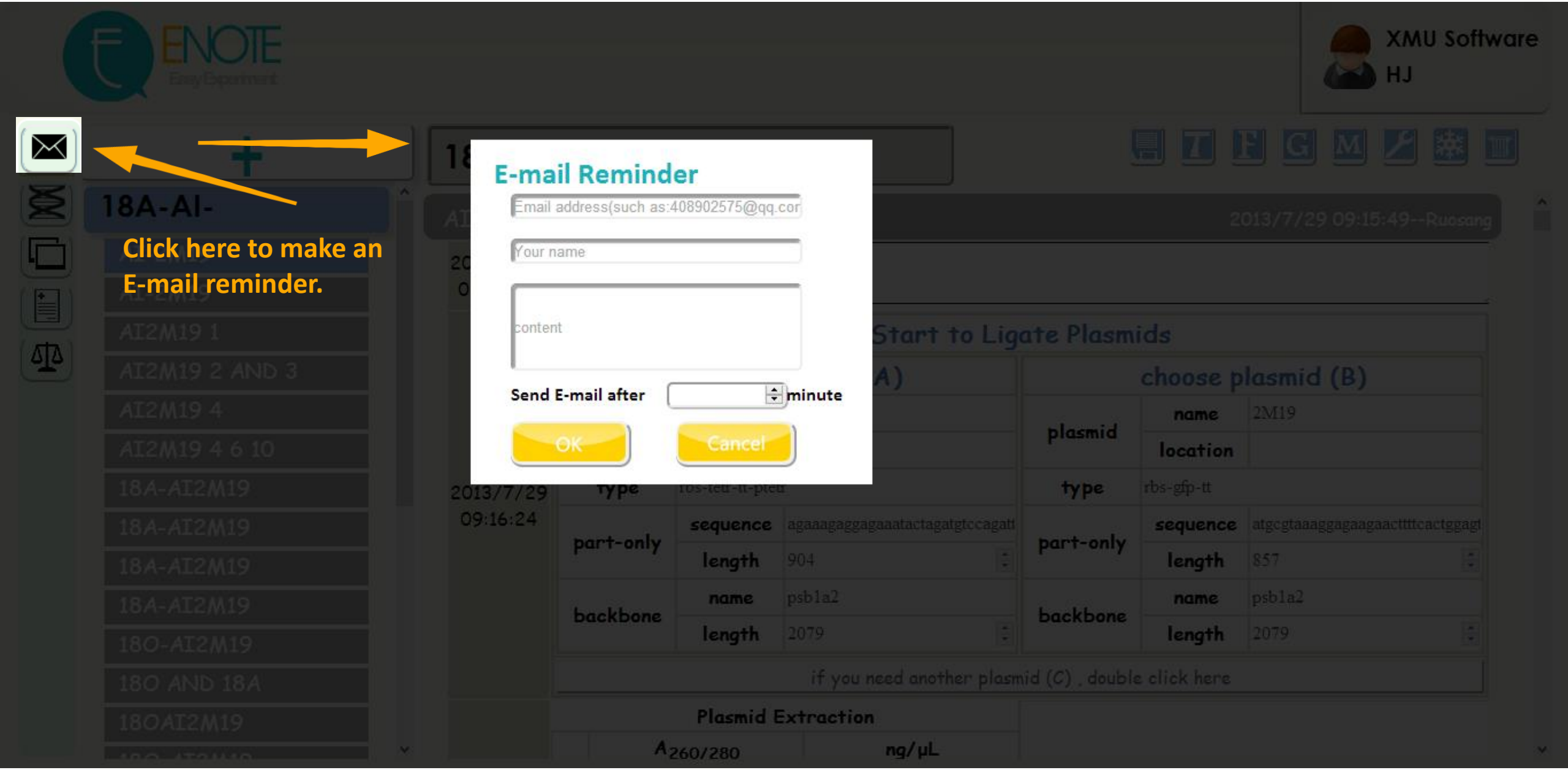
choose plasmid (A)			choose plasmid (B)		
plasmid	name	pbad	plasmid	name	
	location			location	
type	pbad		type		
part-only	sequence	acattgattatttgcacggcgtcacactttgcta	part-only	sequence	
	length	130		length	
backbone	name	psb1a3	backbone	name	
	length	2155		length	

if you need another plasmid (C) , double click here

2013/8/3 18:02:03

Plasmid Extraction

	$A_{260/280}$	ng/μL
(A)	1.88	19
(B)		


ENOTE
XMU Software
HJ
Click here to make an E-mail reminder.
E-mail Reminder
Email address(such as:408902575@qq.cor
Your name
content
Send E-mail after
minute
OK
Cancel
18A-AI-
AI2M19 1
AI2M19 2 AND 3
AI2M19 4
AI2M19 4 6 10
18A-AI2M19
18A-AI2M19
18A-AI2M19
18A-AI2M19
18O-AI2M19
18O AND 18A
18OAI2M19
Start to Ligate Plasmids
choose plasmid (B)
plasmid
name
2M19
location
type
rbs-gfp-tt
part-only
sequence
atgcgtaaaggagaagaacttttcactggagt
length
857
backbone
name
psb1a2
length
2079
2013/7/29 09:16:24
if you need another plasmid (C) , double click here
Plasmid Extraction
A260/280
ng/μL

ENOTE

XMU Software

The Tool from iGEM Software

Tools designed by other teams.

SYNBIO SEARCH

SynBio Search is an online tool that generates data sheets for over 2700 biological parts by aggregating data from various publicly available resources. It integrates and links information from various data sources, including the Registry of Standard Biological Parts, the iGEM Archive, Google Scholar, andPubMed. SynBio Search builds on the collected sources by providing a structured view that relates heterogeneous information, links back to original data sources, and allows users to customize and organize the display. It enables researchers to discover the most comprehensive view of freely available data about biological parts from a single online search. SynBio Search allows users to search by keyword (e.g. qiagen) or by part name.

From:2012 Wellesley HCI

The Tool from Internet

Tools from internet and you can use them for free.

Double Digest Finder

Use this tool to guide your reaction buffer selection when setting up double-digests, a common timesaving procedure. Choosing the right buffers will help you to avoid star activity and loss of product.

From:BioLabs:Double Digest Finder

Enzyme Finder

Use this tool to select restriction enzymes by name, sequence, overhang or type. Enter your sequence using single letter code nomenclature, and Enzyme Finder will identify the right enzyme for the job.

From:BioLabs:Enzyme Finder

NEBcutter

Use this tool to identify the restriction sites within your DNA sequence. Choose between Type II and commercially available Type III restriction enzymes to digest your DNA. NEBcutter® V2.0 will indicate cut frequency and methylation state sensitivity.

From:BioLabs:NEBcutter

www.synbiosearch.org

File output		
Experiment name	File path	source code
18A-AI-	http://trysomething-block.stor.sinaapp.com/t1e1.xml	<button
pBAD-2M1	http://trysomething-block.stor.sinaapp.com/t1e2.xml	<button
s	http://trysomething-block.stor.sinaapp.com/t1e17.xml	
1	http://trysomething-block.stor.sinaapp.com/t1e18.xml	
ss	http://trysomething-block.stor.sinaapp.com/t1e19.xml	
2	http://trysomething-block.stor.sinaapp.com/t1e20.xml	

1. Click here to output file.

2. That's the file path for you notes, and you can download it.

3. Or you can copy the source code to your wiki.

Please right click the path to download the data file

ENOTE

XMU Software

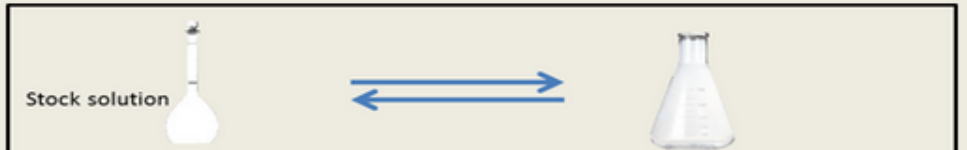
Calculate

In this board we support two kinds of calculated tools

An tool for dilution.

To dilute the solution of aX	
Please enter the prerequisite	
a =	
The final volume (mL) =	
Calculate	
Result:	
Desire the solution of ax	
Desire the solvent	

To dilute the stock solution			
Please enter the prerequisite			
solute =			
molar mass (g/mol) =			



The volume before dilution: V1 The concentration after dilution: C2
The concentration before dilution: C1 The volume after dilution: V2
The mass of solute: m The required volume adding to the reaction: V3

What do you want to cipher out			
V3	C1	V2	C2
Please enter the prerequisite			
C2 (mol/L)			
V2 (L)			
V3 (L)			
calculate			
C1		mol/L	

ENOTE
Easy Experiment

Click here to freeze the note,
and it won't be changed by anyone.

XMU Software
HJ

+

EXAMPLE

no name

EXAMPLE

no name 2013/10/23 20:40:53--HJ

2013/10/23 20:41:02

Start to Ligate Plasmids

choose plasmid (A)			choose plasmid (B)		
plasmid	name		plasmid	name	
	location			location	
type	Promoter		type	Promoter	
part-only	sequence		part-only	sequence	
	length			length	
backbone	name		backbone	name	
	length			length	

if you need another plasmid (C) , double click here

2013/10/23 20:41:04

Plasmid Extraction

	$A_{260/280}$	ng/μL
(A)		
(B)		

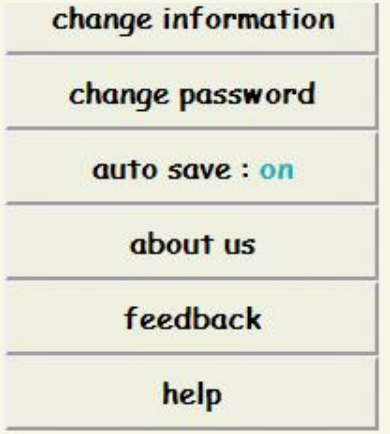
XMU Software
HJ

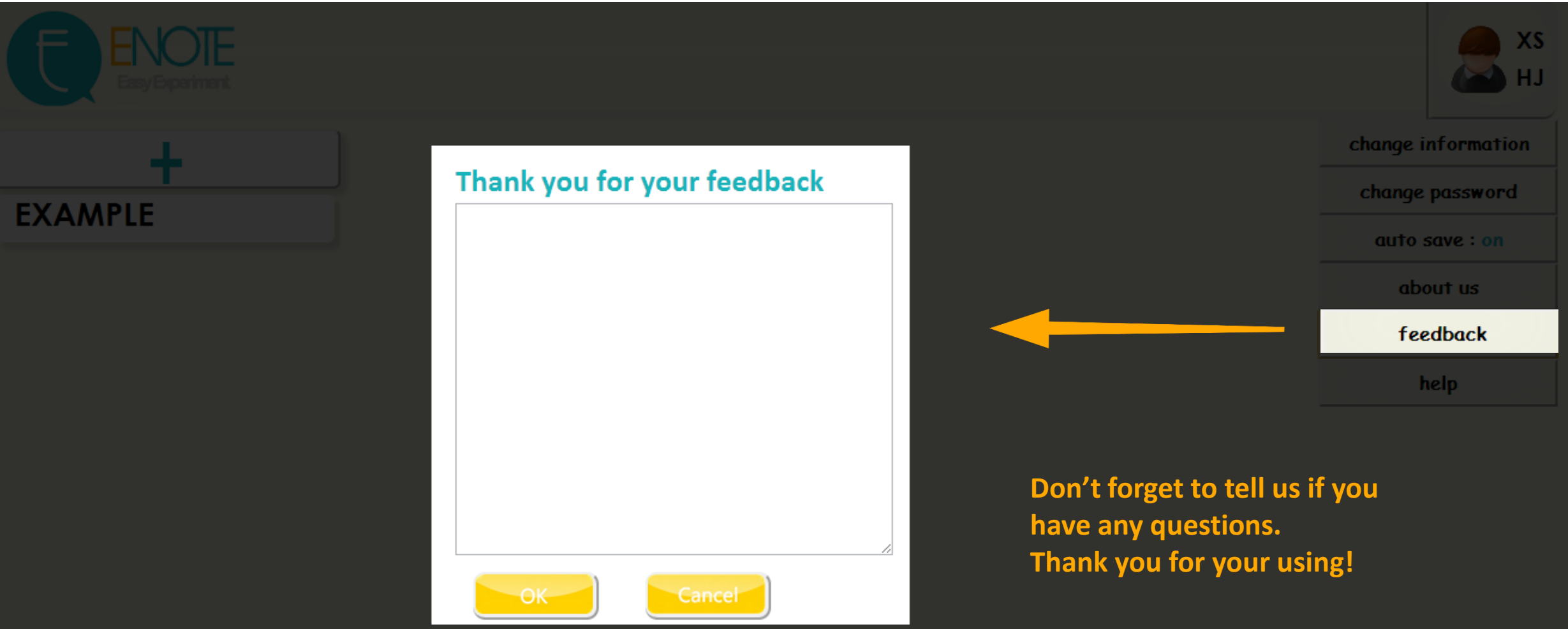
+

EXAMPLE

Click here to know more about us.

Change your settings and
you can e-mail us for help!




ENOTE
EasyExperiment
XS
HJ
change information
change password
auto save : on
about us
feedback
help
+
EXAMPLE
Thank you for your feedback
OK
Cancel
Don’t forget to tell us if you have any questions.
Thank you for your using!

In the next version YOU CAN.....

SHARING
platform

POST
You can post a message to share your experience

E' NOTE Share
Sharing your lab record or read lab record of others

TOOLS Share
Sharing your favourite Web tools or use others sharing

POST

Linda
[XMU-Software]
log out

Harry [XMU-Software]

What is SBOL?

2013.9.4 13:58

1

Thiago [XMU] 2013.9.4 17:44

Synthetic Biology Open Language (SBOL) is a language for the description and the exchange of standard biological part designs. You can start using SBOL in your software by reading about the file format, checking out the library libSBOLj, and for more details see the specification.

2

Harry [XMU-Software] 2013.9.4.18:09

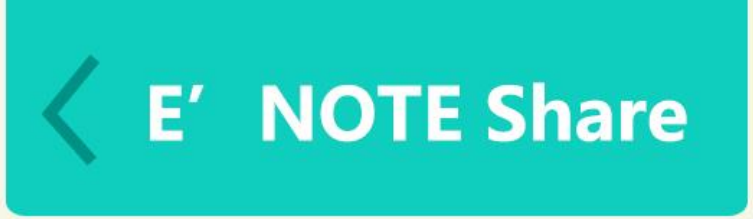
So...?

3

Thiago [XMU] 2013.9.4 19:48

It' s written in http://2013.igem.org/Software

Reply



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pBAD-RBS-GFP-TT
XMU-Software
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Experiment 4
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TOOLS Share

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Search software

- Protein
- Promoter
- Terminator
- Search
- Other

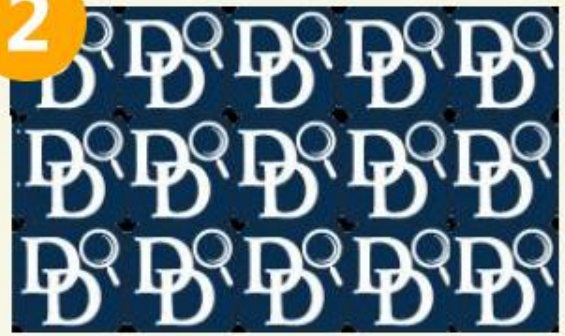
1

SYNBIO SEARCH

SynBio Search is an online tool that generates data sheets for over 2700 biological parts by aggregating data from various publicly available re-sources. It integrates and links information from various data sources, including the Registry of Standard Biological Parts, the iGEM Archive.....

From : 2012 Wellesley HCI

2



Double Digest Finder

Use this tool to guide your reaction buffer selection when setting up double-digests, a common timesaving procedure. Choosing the right buffers will help you to avoid star activity and loss of product.

From : BioLabs:Double Digest Finder

Classify your software and…

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Category of software

Protein

Links

http://trysomething.sinaapp.com/M.php

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