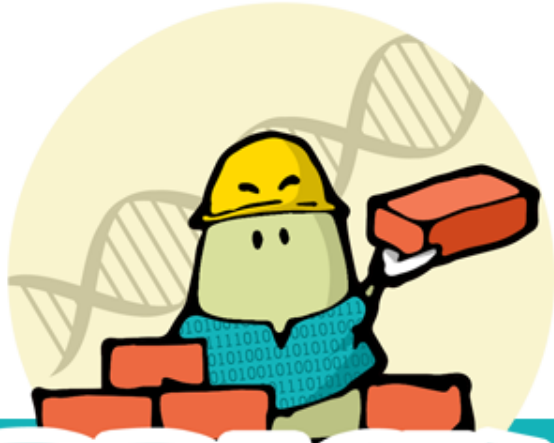




You will need to sign up the first time you use it. We offer two kinds of accounts for you.



**BRICK  
WORKER**  
iGEM XMU-Software 2013

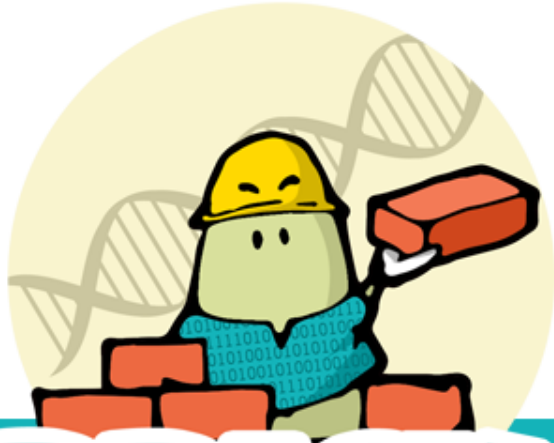
### Log In

E'NOTE



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



**BRICK  
WORKER**

iGEM XMU-Software 2013

Remember to read this.

## Sign Up

team

Team name

Team password

Re team password

Captain name

Captain password

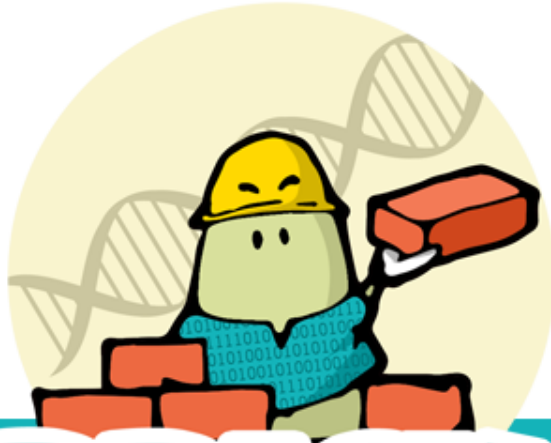
Re captain password

Captain e-mail

I have read it: ["User Terms of Service."](#)

Sign Up

cancel



**BRICK  
WORKER**

iGEM XMU-Software 2013

Sign Up

team

Team name

Team password

Re team password

Captain name

Captain password

Re captain password

Captain e-mail

I have read it: ["User Terms of Service."](#)

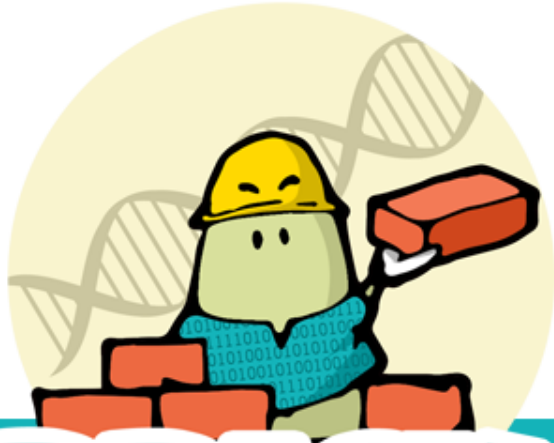
Sign Up

cancel

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

## Sign Up

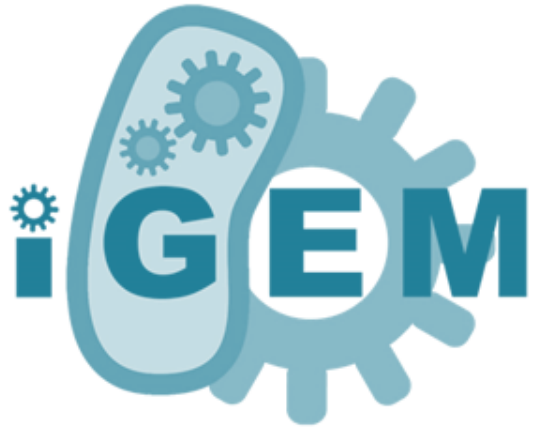
person

I have read it: ["User Terms of Service."](#)

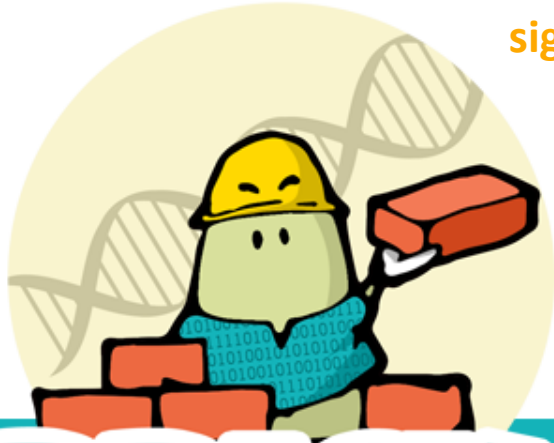
Sign Up

cancel

EINOTE



Log in with your account after signing up.



### Log In

Team name

User name

User password

[Log In](#) [Sign Up](#)

**BRICK  
WORKER**  
iGEM XMU-Software 2013

E'NOTE



Click here to create a new file.



### Add Experiment

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



EXAMPLE

EXAMPLE



Click here to show the note.



show the tool board

Create a new experiment.







**EXAMPLE**

no name


**EXAMPLE**

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



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





**EXAMPLE**

no name

**EXAMPLE**



no name 2013/11/23 01:58:55--HJ

Click here to get tools.

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

Click here to change the information of your account.



EXAMPLE



EXAMPLE

no name

2013



no name



change information

change password

auto save : on

about us

feedback

help

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.

# Plasmid library

Add

Delete

Click the blank to record the time.

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	atgcgtaaaggag	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		

That's the plasmid library and you can add or delete differ kinds of plasmids here.



EXAMPLE



EXAMPLE

no name



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

Choose Plasmids

PCR

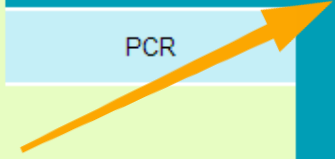
Cultivation

Plasmid Extraction

Digestion

Gel Extraction

Ligation





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

### Start to Ligate Plasmids

#### choose plasmid (A)

plasmid	name	location
	AI (1)	
	2M19 (2)	
type	Promoter	
	18A (3)	
part-only	sequence	18O (4)
	length	pbad (5)
backbone	name	AI2M19 (6)
	length	pBAD2M19 (7)
		18AAI2M19 (8)
		18OAI2M19 (9)
		AI2M19 1 (10)
		AI2M19 2 (11)
Plasmid (A )		AI2M19 3 (12)
		AI2M19 4 (13)
Strain		AI2M19 9 (14)
		AI2M19 10 (15)

#### choose plasmid (B)

plasmid	name	location
type	Promoter	
part-only	sequence	
	length	
backbone	name	
	length	
Plasmid (C) , double click here		
variation		
Plasmid (B )		
Strain		

2013/10/27  
13:55:23

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.

+

18A-AI-

pBAD-2M1

S

1








no name

no name

SS

2

1

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

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

electrophoretogram and gel extraction				
Analyse Electrophoretogram				
	A <sub>260/280</sub>	ng/μL	bp	Connect
AI2M19 14 (A)				
(B)				

+

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	<input type="text"/>		length	<input type="text"/>
backbone	name		backbone	name	
	length	<input type="text"/>		length	<input type="text"/>

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

Cultivation			
Plasmid ( A )	<input type="text"/>	Plasmid ( B )	<input type="text"/>
Strain	<input type="text"/>	Strain	<input type="text"/>

Double click here to get another plasmid.







+

EXAMPLE

no name

EXAMPLE

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



### 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	<input type="text"/>		length	<input type="text"/>		length	<input type="text"/>
backbone	name		backbone	name		backbone	name	
	length	<input type="text"/>		length	<input type="text"/>		length	<input type="text"/>

2013/10/23  
17:35:24

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

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

### Cultivation

Plasmid ( A )	<input type="text"/>	Plasmid ( B )	<input type="text"/>	Plasmid ( C )	<input type="text"/>
Strain	<input type="text"/>	Strain	<input type="text"/>	Strain	<input type="text"/>



+

EXAMPLE

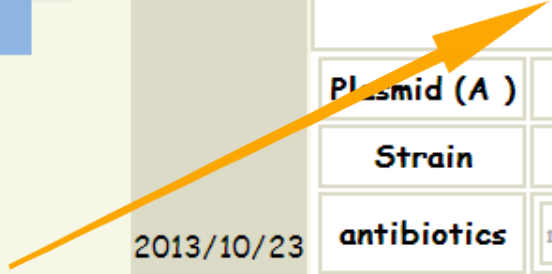
no name

EXAMPLE



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

Cultivation settings.



Cultivation												
2013/10/23 17:35:26	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	$\mu$	Volume	20	$\mu$	Volume	20	$\mu$			
	Temperature	37	$^{\circ}\text{C}$	Temperature	37	$^{\circ}\text{C}$	Temperature	37	$^{\circ}\text{C}$			
	Speed	200	r	Speed	200	r	Speed	200	r			

Plasmid Extraction		
	$A_{260/280}$	ng/ $\mu\text{L}$
2013/10/23 17:35:29	(A)	
	(B)	
	(C)	



EXAMPLE

no name

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

### EXAMPLE



		Plasmid Extraction			
		$A_{260/280}$	ng/ $\mu$ L		
2013/10/23 17:35:29	(A)				
	(B)				
		Evaluate			
		Extract plasmid			
	100 $\mu$ L reaction	(A)	(B)		
2013/10/23 17:35:31	Plasmid	62	62		
	10 *H Buffer	10	10		
	<i>EcoR</i> I / $\mu$ L	0	0		
	<i>Xba</i> I / $\mu$ L	0	5		
	<i>Spe</i> I / $\mu$ L	5	0		

This help you evaluate plasmid.

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



EXAMPLE

no name

### EXAMPLE

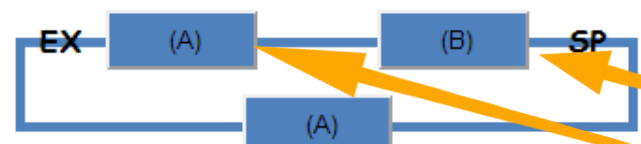


**Plasmid Extraction**

	$A_{260/280}$	ng/ $\mu$ L
2013/10/23 17:35:29 (A)		
(B)		

Evaluate

**Extract plasmid**



	100 $\mu$ L reaction	(A)	(B)
2013/10/23 17:35:31	<b>Plasmid</b>	62	62
	<b>*H Buffer</b>	10	10
	<b>EcoR I /<math>\mu</math>L</b>	0	0
	<b>Xba I /<math>\mu</math>L</b>	0	5
	<b>Spe I /<math>\mu</math>L</b>	5	0

Choose the system.



Click on them to change the sequence.





EXAMPLE

no name

### EXAMPLE



	<i>Spe I</i> / $\mu\text{L}$	5	5	
	<i>Pst I</i> / $\mu\text{L}$	5	5	
	H <sub>2</sub> O / $\mu\text{L}$	18	18	
<b>electrophoretogram and gel extraction</b>				
<b>Analyse Electrophoretogram</b>				
2013/10/23 17:35:33	A <sub>260/280</sub>	ng/ $\mu\text{L}$	bp	<b>Correct</b>
	(A)	0		
	(B)	0		
<b>Ligation</b>				
	10 $\mu\text{L}$ reaction	Insert/Vector=	3 mol/mol	
		Recommend	Actual use	
2013/10/23 17:35:35	A (vector) / $\mu\text{L}$			
	B (insert) / $\mu\text{L}$			
	10 *Buffer / $\mu\text{L}$	1		
	ligase / $\mu\text{L}$	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.



+ (Add button)

EXAMPLE

no name

EXAMPLE

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



Click this three button to create your own templates.



**+**

EXAMPLE

no name

EXAMPLE

no name	
2013/10/23 18:12:33	no content



### Add Table

Please set the row and col

Row

Col

Input the table you want.



+

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		
---------------------	--	--





+ [New]

**EXAMPLE**

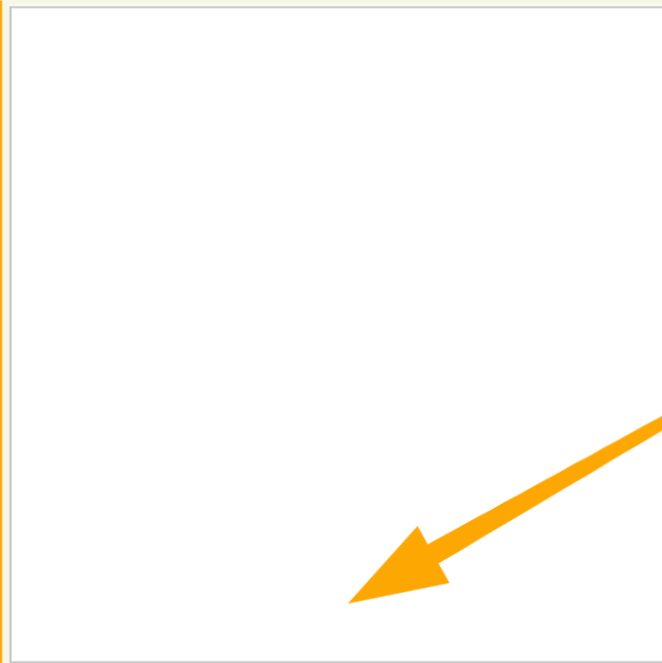
no name

**EXAMPLE**

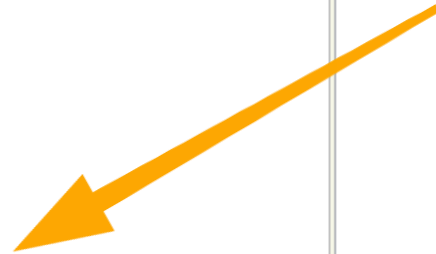


2013/10/23  
18:13:17


2013/10/23  
18:14:15



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



Select File Not Select File

submit

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

Start to Ligate Plasmids

choose plasmid (A)

choose plasmid (B)

plasmid	name	pbad
	location	
type	pbad	
part-only	sequence	acattgattattgcacggcgctcacactttgcta
	length	130
backbone	name	psb1a3
	length	2155

plasmid	name	
	location	
type		
part-only	sequence	
	length	
backbone	name	
	length	

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

Plasmid Extraction

	$A_{260/280}$	ng/ $\mu$ L
(A)	1.88	19
(B)		

2013/8/3 18:02:03



Click here to make an E-mail reminder.

### E-mail Reminder

Email address(such as:408902575@qq.com)

Your name

content

Send E-mail after  minute

OK

Cancel

### Start to Ligate Plasmids

choose plasmid (A)		choose plasmid (B)	
plasmid	name 2M19	plasmid	name 2M19
	location		location
type	rbs-gfp-tt	type	rbs-gfp-tt
part-only	sequence atgcgtaaaggagaagaacttttcactggagt	part-only	sequence atgcgtaaaggagaagaacttttcactggagt
	length 857		length 857
backbone	name psbla2	backbone	name psbla2
	length 2079		length 2079

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

### Plasmid Extraction

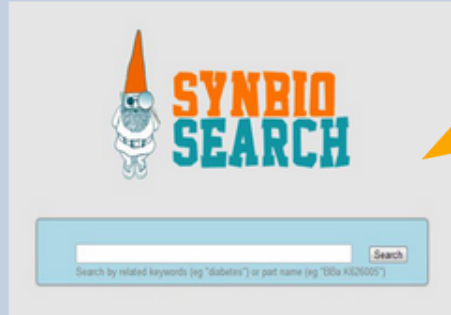
A<sub>260/280</sub>

ng/μL

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, and PubMed. 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](#)

File output		
Experiment name	File path	source code
18A-AI-	<a href="http://trysomething-block.stor.sinaapp.com/t1e1.xml">http://trysomething-block.stor.sinaapp.com/t1e1.xml</a>	<pre>&lt;div class="M1_exp_stepInfo" title="AI-2M19" id="sb0s0" style="background-color: rgb(166. 166. 166):"&gt; &lt;button</pre>
pBAD-2M1	<a href="http://trysomething-block.stor.sinaapp.com/t1e2.xml">http://trysomething-block.stor.sinaapp.com/t1e2.xml</a>	<pre>&lt;div class="M1_exp_stepInfo" title="pBAD" id="sb1s0" style="background-color: rgb(166. 166. 166):"&gt; &lt;button</pre>
s	<a href="http://trysomething-block.stor.sinaapp.com/t1e17.xml">http://trysomething-block.stor.sinaapp.com/t1e17.xml</a>	<pre>&lt;div class="M1_exp_stepInfo" title=" no name" id="sb2s0" style="background-color: rgb(166. 166. 166):"&gt;</pre>
1	<a href="http://trysomething-block.stor.sinaapp.com/t1e18.xml">http://trysomething-block.stor.sinaapp.com/t1e18.xml</a>	<pre>&lt;div class="M1_exp_stepInfo" title=" no name" id="sb3s0" style="background-color: rgb(166. 166. 166):"&gt;</pre>
ss	<a href="http://trysomething-block.stor.sinaapp.com/t1e19.xml">http://trysomething-block.stor.sinaapp.com/t1e19.xml</a>	<pre>&lt;div class="M1_exp_stepInfo" title=" no name" id="sb4s0" style="background-color: rgb(166. 166. 166):"&gt;</pre>
2	<a href="http://trysomething-block.stor.sinaapp.com/t1e20.xml">http://trysomething-block.stor.sinaapp.com/t1e20.xml</a>	<pre>&lt;div class="M1_exp_stepInfo" title="这是一个步骤" id="sb5s0" style="background-color: rgb(166. 166. 166):"&gt;</pre>

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

# 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

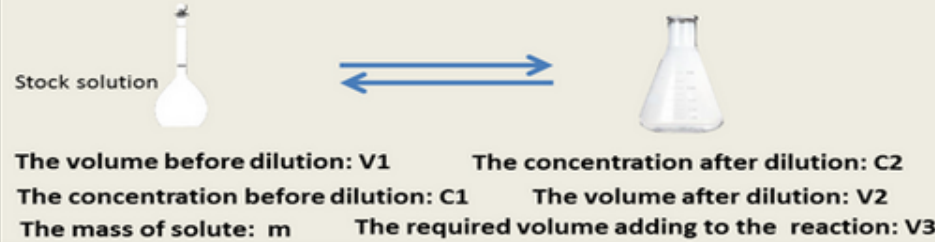
Desire the solvent

To dilute the stock solution

Please enter the prerequisite

solute =

molar mass (g/mol) =



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

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

Start to Ligate Plasmids						
choose plasmid (A)			choose plasmid (B)			
2013/10/23 20:41:02	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						
Plasmid Extraction						
		$A_{260/280}$		$ng/\mu L$		
2013/10/23 20:41:04	(A)					
	(B)					



EXAMPLE

[Click here to know more about us.](#)





EXAMPLE



XMU Software  
HJ

change information

change password

auto save : on

about us

feedback

help

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



EXAMPLE

**Thank you for your feedback**

**OK** **Cancel**

change information

change password

auto save : on

about us

**feedback**

help



**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



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

# < E' NOTE Share

Recent  
● Hot

# Share your recipes with iGEMers.

## pBAD-RBS-GFP-TT

XMU-Software  
2013.9.4 18:02 ★★★★★

## Experiment 2

XMU-Software  
2013.9.6 14:02 ★★★★★

## Experiment 3

XMU-Software  
2013.9.1 16:02 ★★★★★

## Experiment 4

XMU-Software  
2013.9.1 11:35 ★★★

## Experiment 5

XMU-Software  
2013.8.4 12:32 ★★

## Experiment 6

XMU-Software  
2013.9.2 12:27 ★

1 2 3.....23 24 Next

[Share your lab record](#)

# TOOLS Share

SHARE

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 resources. 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...

# TOOLS Share

## SHARE

Picture of software

Upload

Describe the software

Category of software

Links

OK

Cancel





# ENOTE

Design for iGEM

Easy Experiment