

Lab Journal

June 16, 2009

- meeting between Bogdan, Bryant, James and I
- finished the sequence for the surface expression construct
- figured out the to-do list
- mini-prepare the following:
 - linker K157013 *Plate 3, well 3G, plasmid Bba_K157000 (A)*
 - TEV protease
 - I712078 (C-terminus) *Plate 2, well 14M, plasmid J70003 (A)*
 - I712077 (N-terminus) *Plate 2, well 14K, plasmid J70003 (A)*
 - pLux
 - R0062 (not leaky) *plate 1, well 6O, pSB1A2 (A)*
 - R1062 (median strength in the absence of luxR/HSL) *plate 1, 8G, pSB1A2 (A)*
 - HO-*pcyA*
 - K098010 *plate 3, well 11N, plasmid pSB3K3 (K)*
 - terminator
 - B0015 *plate 1, well 23L, plasmid pSB1AK3 (AK)*
 - RFP
 - E1010 *plate 1, well 18F, plasmid pSB2K3 (K)*

2009-06-17

- transformed the following parts into Top10

1.	K157013	<i>Plate 3</i>	<i>well 3G</i>	<i>K157000</i>	<i>Resis:A</i>
2.	I712078	<i>Plate 2</i>	<i>well 14M</i>	<i>J70003</i>	<i>Resis:A</i>
3.	I712077	<i>Plate 2</i>	<i>well 14K</i>	<i>J70003</i>	<i>Resis:A</i>
4.	R0062	<i>Plate 1</i>	<i>well 6O</i>	<i>pSB1A2</i>	<i>Resis:A</i>
5.	R1062	<i>Plate 1</i>	<i>well 8G</i>	<i>pSB1A2</i>	<i>Resis:A</i>
6.	K098910	<i>Plate 3</i>	<i>well 11N</i>	<i>pSB3K3</i>	<i>Resis:K</i>
7.	B0015	<i>Plate 1</i>	<i>well 23L</i>	<i>pSB1AK3</i>	<i>Resis:AK</i>
8.	E1010	<i>Plate 2</i>	<i>well 18F</i>	<i>pSB2K3</i>	<i>Resis:K</i>
- left in 37C for four hours and left on the lab bench in room temperature overnight

2009-06-18

- no colonies were observed on the plates
- left the plates in 37C for four hours
- Picked one colony from each plate and made overnight broth culture for glycerol stock.
- K098010 plate did not grow, so it was left in the 37C overnight.

2009-06-19

- made the glycerol stocks from the overnight broth cultures
- started broth culture for K098010
- re-transformed the E1010 in Top10

2009-06-22

- re-started the broth culture for K098010 because it was overgrown (already in stationary phase)
- Observed no colonies on the E1010 plate. We found out that E101 should be on Kanamycin resistance plate.

Things to do

- get out the standard plasmid backbones
- High copy number assembly plasmid backbone
 - pSB1A3 *Plate 1, well 1K,*

2009-6-23

- submitted the VLA construct to Mr. GENE for synthesis
- placed orders for PCR primers

2009-6-24

- transformed the following parts into Top10
- | | | | | | | |
|-----|--------------|----------------|----------------|------------|----------------|------------------|
| 9. | RBS-luxR | <i>J37033</i> | <i>Plate 3</i> | <i>4O</i> | <i>pSB1A2</i> | <i>Resis: A</i> |
| 10. | RBS-LuxI-ter | <i>F1610</i> | <i>Plate 2</i> | <i>24G</i> | <i>pSB1AK3</i> | <i>Resis: AK</i> |
| 11. | RBS-LuxI | <i>K081008</i> | <i>Plate 2</i> | <i>10L</i> | <i>pSB1A2</i> | <i>Resis: A</i> |
| 12. | RBS-LuxR-ter | <i>I0462</i> | <i>Plate 1</i> | <i>8O</i> | <i>pSB1A2</i> | <i>Resis: A</i> |
| 13. | Pconst | <i>J23119</i> | <i>Plate1</i> | <i>18A</i> | <i>pSB1A2</i> | <i>Resis: A</i> |
| 14. | LuxR | <i>C0062</i> | <i>Plate1</i> | <i>4O</i> | <i>pSB1A2</i> | <i>Resis: A</i> |

2009-6-25

- purchased a QIAminiprep kit from BioBar
- picked colonies from plates and re-cultured in broth; left overnight
- ordered ITGA4 cDNA plasmid from OpenBioSystem.

2009-6-26

- made glycerol stocks for the parts transformed on 6-23
 - designed primer for PCR out VLA cDNA plasmid and primer for pLux-RBS-HindIII
 - Transformed the following parts into Top10 and left the plates in 37C overnight.
- | | | | | | | |
|-----|-------|----------------|---------------|------------|---------------|-----------------|
| 15. | RBS | <i>B0034</i> | <i>Plate1</i> | <i>2M</i> | <i>pSB1A2</i> | <i>Resis: A</i> |
| 16. | HemeC | <i>I716154</i> | <i>Plate1</i> | <i>17B</i> | <i>pSB1A2</i> | <i>Resis: A</i> |
| 17. | HemeD | <i>I716155</i> | <i>Plate1</i> | <i>17D</i> | <i>pSB1A2</i> | <i>Resis; A</i> |

2009-6-27

- picked colonies from plates and made glycerol stocks

2009-6-28

- transformed glycerol stocks into broth culture

2009-6-29

- purified plasmids containing parts 1-17 from Top10 using Qiagen Spin Miniprep Kit
- performed Agarose Gel Electrophoresis to check the size of the parts. Bands did not migrate very far, possibly due to the fact that circular plasmids migrate very slowly. We decided to digest the plasmids with a BioBrick restriction enzyme and then run gel again.

2009-7-2

- We rerun the Agarose Gel Electrophoresis to check the size of the parts. It worked.

2009-07-06

- We transformed the following parts into Top10

18. GFP	<i>E0040</i>	<i>Plate1</i>	<i>14K</i>	<i>pSB1A2</i>	<i>A</i>
19. GFP constr.	<i>E0840</i>	<i>Plate1</i>	<i>12O</i>	<i>pSB1A2</i>	<i>A</i>
20. pTet+GFP	<i>I13522</i>	<i>Plate2</i>	<i>8A</i>	<i>pSB1A2</i>	<i>A</i>
21. LuxR construct	<i>K091204</i>	<i>Plate2</i>	<i>8J</i>	<i>pSB1A2</i>	<i>A</i>
22. luxI + GFP	<i>J37034</i>	<i>Plate2</i>	<i>7I</i>	<i>pSB1A2</i>	<i>AK</i>
23. pSB1AC3		<i>Plate1</i>	<i>11A</i>	<i>pSB1AC3</i>	<i>AC</i>
24. pSB1AK3		<i>Plate1</i>	<i>13A</i>		<i>AK</i>
25. pSB1AT3		<i>Plate1</i>	<i>15A</i>		<i>AT</i>

2009-07-07

- We picked colonies from the plates and made broth culture, which was left to grow overnight.

2009-07-08

- We purified the plasmids of part 18 to 25 using QIA spin miniprep kit.

2009-07-09

- We ran a 1% Agarose gel electrophoresis to confirm the plasmid lengths of part 18 to 25.
- Gel loading and concentrations:

I.	<i>E0040</i>	120ug/uL	loaded 12ul
II.	<i>pSB1AC3</i>	120ug/uL	loaded 12ul
III.	<i>R0062</i>	120ug/uL	loaded 12ul
IV.	<i>pSB1AT3</i>	120ug/uL	loaded 12ul
V.	<i>J23119</i>	120ug/uL	loaded 12ul

VI.	J37034	120ug/uL	loaded 12ul
VII.	K091204	120ug/uL	loaded 12ul
VIII.	E0840	120ug/uL	loaded 10ul
IX.	B0034	50ug/uL	loaded 10ul
X.	F1610	50ug/uL	loaded 10ul
XI.	I13522	120ug/uL	loaded 10ul

- We figured out the relative concentrations of the parts by comparing the bands with the ladder (The 5,000bp ladder is about 120ng/ul)

- Parts digested

I.	R0062	P_{lux}	prefix	EcoR1+Spe1
II.	pSB1AT3		backbone	EcoR1+Pst1
III.	J23119	P_{const}	prefix	EcoR1+Spe1
IV.	B0034	RBS	suffix	Xba1+Pst1
V.	F1610	RBS-LuxI-STOP	suffix	Xba1+Pst1
VI.	B0015	Terminator	prefix	EcoR1+Spe1

- restriction digestion mix recipe:

- 600ng of DNA
- 4ul restriction buffer
- 0.5ul EcoR1 and 0.5ul Spe1, or
- 0.5ul Xba1 and 0.5ul Pst1
- Up to 35ul of ddH₂O

- We digested the parts using corresponding BioBrick restriction enzymes, and then purified the parts using QIAquick PCR Purification Kit.
- Stored the purified DNA in -20C overnight.

2009-07-10

- We ran a 1% Agarose gel electrophoresis to confirm the products of restriction digestions.
- The expected bands of the parts did not show up. This is probably due to the fact that most of the parts have lengths within 100bp and the QIA quick PCR Purification Kit removes DNA below 100bp length.
- The miniprep plasmids of the parts are digested again with corresponding restriction enzymes for 2 hours.
- Enzymes are deactivated (denatured) by heating at 65C

2009-07-13

- ligated the parts into the following constructs using the *T4 ligase protocol*.
 - P_{const} – RBS – LuxI – 2xSTOP
 - P_{lux} – RBS
 - P_{const} – RBS (Heme Oxygenase)
 - Terminator – RBS
- Transformed the ligated constructs into Top10

- made broth culture from the ITGA4 cDNA glycerol stock
- Transformed ANP construct and kill switch (I716462) into Top10.
I716462 *plate 2* *well 3C* *Amp*

-

2009-07-14

- purified the plasmid for ITGA4 using QIAminiprep spin kit.
- Recultured ITGA4 containing cells in broth.
- Picked colonies and made broth culture for the ligated constructs in triplicates.
- Picked colonies and made broth culture for ANP construct and the kill switch (I716462)
 - ANP construct plate was overgrown

2009-07-15

- PCR the colonies to check ligations
 - Broth culture for ANP construct did not contain cells. Therefore transformed Top10 cells were cultured in broth overnight again. Broth culture was also made for I716462.
 - Run gel to confirm ligations and ITGA4
 - working constructs from ligation
 - C1 (P_{const} – RBS)
 - PL3 (P_{lux} – RBS)
 - T3 (Ter- RBS)
- Note:* BioBrick primers worked for pSB1AT3 backbone.

Wed Sept 2

Summary:

- ① All Pur-MS-100 - 100% both culture were red upon harvest per
- ② All Pur-MS-100 - 100% 100% red
- ③ Pur-MS-100 - 100% plates yielded some white colonies

Action Items:

- ① Repeat both cultures from Pur-100 and Pur-100 - 100% plates; hope to improve biomass
- ② Get a gel (in fridge)
- ③ Send Pur-100 streaked ~~plates~~, using 10^8 and 10^7 , and the products from Pur-100 and Pur-100 from last time
 → tubes labeled 10^8 and 10^7
- ④ Pur-100 purify 10^8 + 10^7
- ⑤ Streak Pur-100 to 10^8 and 10^7 (1:10 - 1:10)
- ⑥ Streak gel on 10^8 samples (1:10 - 1:10)

Loading order:

1	2	3	4	5
10 ⁸	10 ⁷	10 ⁸	10 ⁷	10 ⁸

expected yield: ~250g by ~~10⁸~~

- 3:30 PM

James

- Actions
- PCR Purified run 2 → labelled loc¹, 1, -ve and
~~run 2~~ and run 3¹ ↑ actually run 3!
 - Set up new PCR w/ VF2 and R3
 - Image gel from run 2 → weak bands
 ~ 600 and < 200 bp. Will see how
 next run turns out.

- Phone call w/ Bryant:

- ↳ he has already done round 3.
- ↳ throw out current PCR and start
 again w/ VF2 and R4.
- ↳ he actually left in PCR machine and just
 installed program w/ new samples.

- (cont'd)
- New samples called loc¹, loc², -ve
 - Imaging round 3 on gel
- | | | | |
|--------|---|---|-----|
| folder | 1 | 2 | -ve |
| | ↓ | ↓ | ↓ |

Observations

- 1st set bands from previous gel ~ 600
 wanted 2nd set ~ 1000-2000 region.
- will see if repeat samples labore mistake
 with different.

To do

- PCR purifying round 4 samples
- Run gel for round 3 and round 4 samples.
- Recheck round 2 (overnight) if round 3 and 4 do not work.

Goal of run 3 and 4

ladder $\overbrace{\text{lot 1 lot 2}}$ -ve $\overbrace{\text{lot 1 lot 2}}$ -ve $\overbrace{\text{lot 1 lot 2}}$

* lot 1 and lot 2 loaded parity. Reported 4 and

Evening Update

- Gel 4 stored bands ~ 2000 bp, repeat PCR from step 2.
- Tubes labelled lot 1 rep 2, lot 2 rep 2 each -ve rep 2
- PCR running w/ QPC H₂O (now in rack w/ primers).
- will use commercial PCR machine in Kottersall

Time Sep 3

- PRR packet 401-02, rep 2 (and 3rd)
- Mapping: $\left\{ \begin{array}{l} P_{in} = 401-121-401 \\ P_{in} = 401-121-401 \end{array} \right\} \rightarrow$ (and 3rd handled out)

Digest

$\left. \begin{array}{l} s2 \text{ E/S} \\ s8 \text{ E/S} \\ 80015 \text{ X/P} \end{array} \right\} \begin{array}{l} (\text{print-RBS-SAA}) \\ \text{in PSBIAT3} \end{array}$

$\left. \begin{array}{l} \# 9 \text{ print-RBS-SAA E/S} \\ \# 10 \text{ print-RBS-SAA} \\ 80015 \text{ X/P} \end{array} \right\} \text{in PSBIAT3}$

Below digests are to put terminator onto SAA construct.

s2D are labels for digests
 s8D
 80015D
 #9D

~~CLS Master Mix $n=3+1=4$~~

~~Cell = $0.5 \times 4 = 2.0 \mu\text{l}$~~

~~Sp3 = $0.5 \times 4 = 2.0 \mu\text{l}$~~

~~Buffer Cell 4 $\times 4 = 16 \mu\text{l}$~~

~~BSA $1 \times 4 = 4 \mu\text{l}$~~

~~ddH₂O = $5 \mu\text{l}$~~

~~V_t = $40 \mu\text{l}$~~

~~final volume $\times 2$~~

~~2 μl backbone~~

~~$$\begin{array}{r} 2.0 \\ 2.0 \\ 16 \\ 4 \\ 5 \\ \hline 29 \\ + 11 \\ \hline 40 \mu\text{l} \end{array}$$~~

Setup of 2009 (Hany)

- Run PCR # 4 on $\frac{LDD1}{\text{rep}}$ + $\frac{LDD2}{\text{rep}}$, and on BSA
- Run gel for $\frac{LDD1}{\text{rep}}$ + $\frac{LDD2}{\text{rep}}$ + - C₁₂
- Ligated S₂ = B0015
- S₈ = B0015
- S₉ = B0015 $\times 2$ (duplexes)
- four digests with EcoRI + PstI
- run gel to check lengths (loading next page)
- transformed the ligation and placed on pSIRT5 plasmid

Gel loading

ladder, 2001 (mp), 2002, (mp), G-Bands, 50-Bands,
 5-Bands (1), 9-Bands (1), -CR (PCR)

Concentration of Ice

- Lower running temp to 3°C below top of R3.
- Use 8:10 on gel 1500 of purified R2 for R3.
- Try to re-amplify R2 and if OK use as R3 template.
- Remove aliquots @ 25 cycles.

Protocol 1600 - °C

50°C 5min

95°C 5min

95°C 30s

52°C 30s } x39

72°C 30s

72°C 10min

10°C 15min

4°C 6h

PCR R2 and R3

- | | | |
|-----|-------------------------|---------------------|
| A | * Dilute R2 → for R3 | } Pure final band |
| B | Regular R2 → for R3 | |
| ✓ C | * Dilute R2 → reamplify | |
| D | Regular R2 → reamplify | |
| E | * Dilute R2 → for R3 | } PCR Analysis Test |
| F | Regular R2 → for R3 | |
| G | * Dilute R2 → reamplify | |
| H | Regular R2 → reamplify | |

$$n = 8 + 1 = 9$$

$$n = 1$$

$$n = 9$$

$$10x \text{ PCR buffer } 6.0 \times 9 = 54$$

$$\text{dNTPs } 0.4 \times 9 = 3.6$$

$$\text{DEPC H}_2\text{O } 57.1 \times 9 = 513.9$$

SPLIT

$$n = 43$$

$$R2 = 36 \mu\text{l}$$

$$VF2 = 36 \mu\text{l}$$

$$R3 = 36 \mu\text{l}$$

$$VF2 = 36 \mu\text{l}$$

For R2
 $n = 5 (4+1)$

$n = 1$

$n = 5$

10X PCR Buffer $6 \times 5 = 30 \mu\text{l}$
 dNTPs $0.4 \times 5 = 2.0 \mu\text{l}$
 DEPC H_2O $32.1 \times 5 = 160.5 \mu\text{l}$
 R2 $6.0 \times 5 = 30 \mu\text{l}$
 VF2 $6.0 \times 5 = 30 \mu\text{l}$
 Total $0.5 \times 5 = 2.5 \mu\text{l}$
 + template

For R3

$n = 5 (4+1)$

(some no down fair R3 instead of R2)

Update

- first digest may not have worked - will retry w/ regular digest reagents.
 - Re-running R2's w/ updates as per above.
 - check plates: will have ladders to grow bigger.
- * Remove 7 μl of p20 PCR sample @ end of cycle 28 and decontaminate @ 72°C 10 min.

Gels Run

Cycle 28 aliquot loaded loader A → H, space, loader.

Full Run PCR loaded loader A → H, pair loading of wells B, D, G.

Gel 28 Cycle Observations

- All bands per 3 showing.
- Excess of all PB bands.
- * - 1m suggests hot start and separate MM for Hot cti (ie: reamplification)*

To Do

- Run PCR R4 with purified (gd) and Kit (sample) PCR 3 products.
 - Use protocol "10.0m - °C".
 - Pick colonies for later miniprep.
- Note: PCR products in the strip of tape, 10.0m Rock - 20°C.

Sept. 5 (Hany?)

- Run PCR on A, B, E, F (see page 52)
- picked colonies from P16-R11-S11-Ter 1+2
and plasm - P11-S11-Ter (S1-B105)
- plates for S1-B105 and S2-B105 were put back
into 37°C due to the lack of colonies.
- R - mislabeled pSR1A3 & pSR1A3 both ~~containing~~ ~~same~~
~~white~~ ~~in~~ ~~water~~ ~~residue~~ ~~both~~ ~~from~~ ~~glycerol~~ ~~stocks~~
(probe for pSR1A3 was pink)

PCR purification samples: (on green rack)

COB	COB	COB	COB
A	B	E	F

Sept 6 (Hany?)

- pick colonies from S1-B105 plate
(take 2+3)
- pick colonies from S2-B105
(tube 1)
- make glycerol stocks for ↑
- R - mislabeled P16-R11-S11-Ter
- placed in the green rack.

Gill from Harry Ritt

lanes A B E F B
 ↓
 1st

No bands > 500 bp. Ritt did not amplify. Check AT not reaction. Intensity.

↳ Wrong protocol was used!!! Repeat with protocol "1600" 1600°C.

6/

Tomorrow (Tues 6th Sept)

- PCR → if OK digest, ligate, transform
- Pick colonies
- Buy new sequencing lect
- Get order (10/15) Sent.

Jan

- digest PCR-DNA-SAA-Tor with EcoRI + PstI
- run gel to confirm.
- Return Myc to Peter.

Get of PCR products:
order = ladder, A, B, B, B, E, F

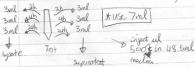
- Example: staining of SMT culture
Pct-RBS-SMT for called "SMT Full"
in freezer.

- ✓ PCR via digest for 2 + PstI to test in ladder
 - ✓ SMT + the cell growing for set up tomorrow.
 - ✓ Digest SMT to confirm.
 - Re-run B4 w/ PCR
- (Note: PCR amplified ADEF → test "E".)
- Re-run B4 on P. 57 gel w/ PCR purified samples

SAA experiment planning.

Collect 2 hrs, 4 hrs, overnight

- 3 ml for each timepoint
- 2x 50 ml Falcon tube. (1x100 overnight seal)



→ report w/ PSD IAT3 negative

+ media control

-ve

- Run procedure for normalizing
- re-run exp if req'd w/ normalizations
- Probe for SAA
- Lyse w/ 300 µl sample buffer (water) w/ 100 µl 1M DTT in 1:1 ratio. Boil 7 mins.
- Freeze @ -20°C remaining sample
- Measure OD upon collection.

Gel RH confirmation
 lanes A B ~~PF~~-ve SAA

- * Have digested and ligated previous RH for test purposes although gel did not show bands
- * ~~to~~ ~~be~~ ~~no~~ RH on above gel after new RH PCR run

SUCCESS! ALL WORKED!
 Excised band

To do

Recopying + digest + ligate PCR RH
 Gel purified samples labelled RH A, RH B, RH F
 overnight in Rotobell. (GA = gel purified A

FB
 F
 PA = PCR RH purified
 PB
 F

Gel of PCR samples:

lanes 1-6 GA GB GF PA PB PF

SAA Experiment Started @ 11:30

T₂ = 130

T₄ = 330

overnight = 11:30

OD Instructions / OD 600

- cassette w/ 1 ml media (blank)
- A or cassette sideways
- Press ref to blank
- OD > 1 means dilute sample or "..."

11:30
3ml
3ml
3ml
3ml

130
3ml
3ml
3ml
3ml

11:30	T ₂	OD 600
1.5ml	PSB143 sup	0.058
1.5ml	PSB143 ucl	0.063
1.5ml	SAA sup	0.040
1.5ml	SAA ucl	0.036

11:30	T ₂	OD 600	
3ml	PSB143 sup fl	0.560	→ lost -log
3ml	PSB143 ucl	0.600	11.2ml
3ml	SAA sup	0.190 0.330	pink
3ml	SAA ucl	0.324	20 _{ul}

30	T4	OD600	
3ml	psb1A13 sup	1.601	4.05 μ l
3ml	psb1A13 wcl	1.582	4.10 μ l
3ml	SAA sup	1.306	4.96 μ l
3ml	SAA wcl	1.321	4.91 μ l

30	T24	OD600	
3ml	psb1A13 sup	2.716	2.79 μ l
3ml	psb1A13 wcl	2.427	2.80 μ l
3ml	SAA sup	1.358	4.77 μ l
3ml	SAA wcl	2.841	2.49 μ l

1:10

Note: You must control for the volume of sample removed when resuspending whole cell lysates to lysate. You need to keep the same [2] of cells!
 For: 35 3ml removed, resuspend relative to sample if 1.5ml removed.

Also all lateral columns are λ -1 ml or 1ml range for OD600.

14 September 2009

- Western normalized against CD 0.324
 - Boiled ~~in~~ at 100°C for 5 mins.
- loaded as follows

	T0 + T2 on gel 1	
	T4 + T24 on gel 2	
left.	media ctrl	
	psb1AT3 sup	repeat for
T0	SAA sup	T4 / T24.
	psb1AT3 wcl	
	SAA wcl	
	ladder	
	psb1AT3 sup (missing for T2)	
	SAA sup	
T2	psb1AT3 wcl	
right	SAA wcl	

- transferred to nitrocellulose blot
- blocked at 4°C overnight

15 Sept. 2009

- made both cultures for ~~HB~~RBS - Cap-Spots - TBS + 1% BSA + 0.05% Triton
- [Washed the blots 3x 15 min in TBS]
- Incubated with 1st Ab (1:5000 in skim milk)
- Washed 3x 15 min in TBS-T
- Incubated with 2nd Ab (1:5000 in skim milk overnight at 4°C)

16 Sept. 2009

- both cultures did not grow \rightarrow need to remake both cultures
- To ligate RBS and Myc
 1. Digest RBS + Myc with $T3a$ I
 2. PCR purify electroporation
 3. Ligate

17 Sept. 2009

- Incubation do not work

- Digestion

1. ~~Schizosaccharomyces~~

PA, PB, PF, pSBUT3

EcoRI + PstI

2. RBS + Myc

DnaI

Looking volume (suggested by Peter)

Cell #1

+CTE 100	+CTE 100	-CTE 100	+CTE 100	Letter	To SAM cup 10	To SAM cup 10
To SAM cup 10	To SAM cup 10	Letter				

Cell #2

prim & water are the same +

To SAM cup 10	To SAM cup 10	To SAM cup 10
---------------------	---------------------	---------------------

Letter

Sept 28, 2007

- received SAM +CTE sample (100/10)

- SAM antibody (1:1000 dilution) → found in final solution

Sept 29 2009

Run SDS-PAGE on SAA samples

Sample preparation:

SAA + CTG (100 μ g/ml): ~~added~~

- conc. 10 : added 50 μ l and 11 μ l of 6x SDS buffer
- conc. 1 : added 5 μ l sample into 45 μ l of 6x SDS buffer, and mixed with 11 μ l of 6x SDS buffer

This method was used to prepare all samples:

- made 120 μ l of SAA To wcl and 120 μ l of 6x SDS buffer added: boiled)

Landing



Running 40 mA constant Amp for 70 min

- Maked in milk for 1 hr
- incubated with 1 μ Ab overnight at 4 $^{\circ}$ C

Sapota

Oct. 1, 2009

Run SDS-PAGE

Cell #1	+CTL 10	+CTL 1	-CTL 10	-CTL 1	Ladder	SAA T24 10 sup	SAA T24 1 sup
		SAA T24 10 10	SAA T24 10 1		Ladder		
Cell #2	+CTL 10	+CTL 1	-CTL 10	-CTL 1	Ladder	SAA T24 10 10	SAA T24 1 10

- transferred to nitrocellulose blue
- blocked for 1 hr
- 1° Ab overnight

Planning

Oct 2, 2009

1 PCR reactions

- ① PCR Psec-RBS using BioBack primers
- ② PCR consensus for cloning Psec-RBS
(using primer: Psec-seq FWD + PCR Whole REV)
- ③ PCR VEA9 using primer: VEA9 Partial FWD + REV
- ④ PCR Whole consensus to put into backbone
- ~~⑤ PCR~~

1 PCR purify; run gel to confirm band

2 PCR seq Psec-RBS to construct using overhang primers
(7.95 - 6.00)

3 PCR purify

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- PCR seq II to VEA

- Flusory ligase with T4R enzyme (K081018)

PCR round 1

tubes

- * 1. Psec-RBS amplified with BB primers
 - * 2. Mr. Cas PCR consensus amplified with Psec-seq FWD + VEA9 REV
 - * 3. VEA9 amplified with VEA9 partial FWD + VEA9 Full REV
 - * 4. Whole consensus amplified with PCR whole FWD + REV
- use it's evaporated, need to redo PCR

GAWA6ADE

PCR round 2

#5 Stitch Piece-RBS to consensus using primers:

BB FWD V2F + VLA stitch REV

- Note: this rxn contains 2-templates

#3 VLA4 amplified with VLA pair (FWD + REV)

Ran	gel of	1st	PCR	purified	products
order =	marker/ ladder	Ptet-RBS stitch (#1)	^{copy} Construct stitch (#2)	Amplified Construct (#4)	

Slanes

- when the gel was loaded some of the samples floated to the top

- gel file called: PCR Gel #1 - Oct 2 Bogdan

Checking gel

Construct stitch \rightarrow 492 bp \rightarrow farne band

amplified consensus \sim 750 bp \rightarrow worked

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Things to do:

- PER check VCA to constant
 template: "VCA check freq Oct. 2"
~~"Per-constant Oct. 2"~~
 "Per-constant Oct. 2"
 Primes - VAF B.B FWD
 - VCA Panel REV.

- Run Cal to confirm.
 template: "VCA check freq Oct. 2"
 "Per-constant Oct. 2"
 + produce from the new PER

- PER AMP out of constant
 template: Amplified Constant Oct. 2
 prims: AMP FWD + PER Whole REV.

Materials: 6.0 PER buffer x 5
 2.0 VAF x 5
 2.0 B.B x 5
 1.5 OGF x 5

Appendix 1 testing

Ladder, Rndg Constant, AMP, Blank, Rndg Constant, AMP - CS
 Per-SEC - Constant, VCA q very faint noted
faded

Plan

- simplify customer sketch with Price-customer FWD + VCA^{customer} REV.
- simplify binding customer with V&E and VCA^{customer} REV.
- simplify Price-customer with V&E and VCA^{customer} REV.
- simplify ANP with ANP FWD + PER^{customer} REV.
- simplify VCA using (partial V&E + VCA^{customer})
 primer VCA^{customer} FWD + VCA^{customer} REV.

important: x 8

Costs

Cost: PER cost. 6

Value: VCA^{customer}, $\frac{VCA_{customer}}{2}$, Price-customer, VCA^{customer}
 (customer)

FWD customer sketch, Binding customer

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- Parts that can be ligand into backbone:

- "VLA stick frag 2 Oct 6"
- "AMP 2 Oct 6"
- "Amplified GUS gene Oct 2"

Recom PCR 9L

11 samples "Proc-RBS stick Oct 2"

"GUS gene stick Oct 2"

primers: VLF + VLA check REV

- Sample labelled "Proc-GUS gene Oct 7"

Coel

ladder - 576 unpurified purified

200bp

200bp

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Recom 43

11 samples "Proc-RBS GUS gene Oct 7" add 9ul

"VLA stick frag 2 Oct 6" add 2ul

primers: VLF + VLA check REV

Samples: - 576

Binding GUS gene Oct 7 - unpurified sample

Binding 2 - unpurified sample