M2D2: Design gRNA for CRISPRi

10/11/19

- Pre-lab discussion
- Part 1: Load digests from M2D1 in agarose gels
- Mid-lab discussion: gRNA design considerations
- Part 2: Select target gene in fermentation pathway
- Part 3: Design gRNA for CRISPRi system

Announcements

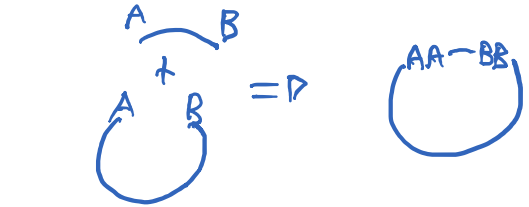
- Journal club starts next week! (See evaluation rubric on wiki. Also, if coming to office hours related to it, email us ahead of time so we can be sure to read your paper)
- Bring presentation slide homework for Comm Lab workshop at 1:30pm on Friday

From Last Time: Ligation Calculation

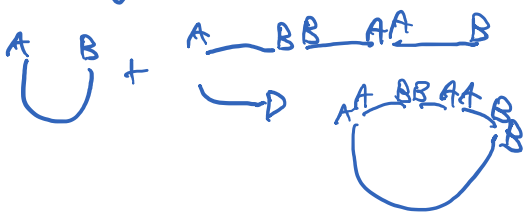
Optimal backbone-to-insert ratio

- Ideally, want 3:1 insert:backbone
  - molar ratio, ***not*** mass or volume

- What if too much insert?



- What if too much backbone?



↳ lead reannealing of digested vector (backbone)

Today Part 1:

Separate DNA by gel electrophoresis

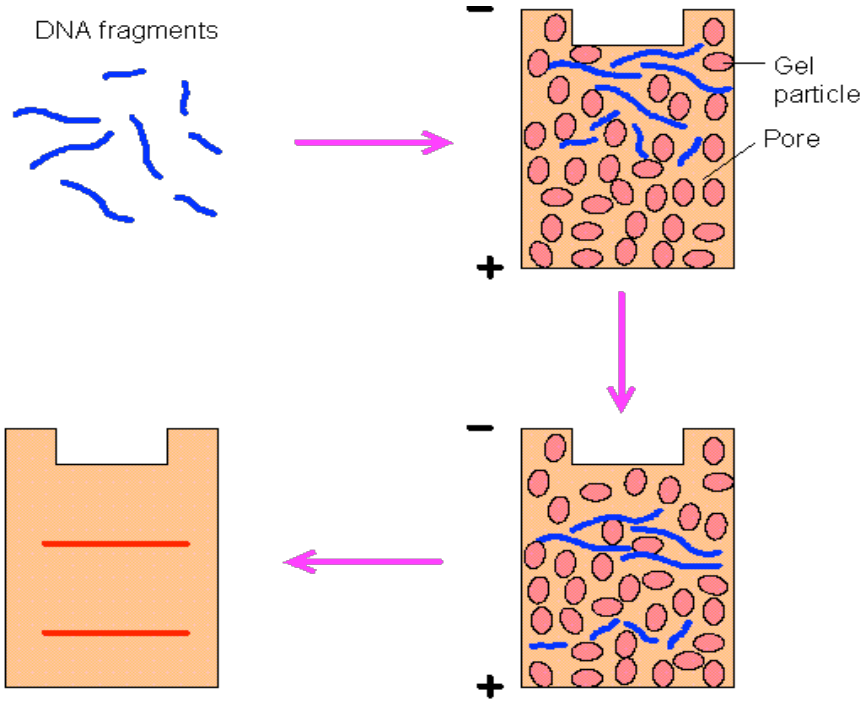
Agarose gel electrophoresis

– Driving force:

electric force (V)

– Separates DNA by:

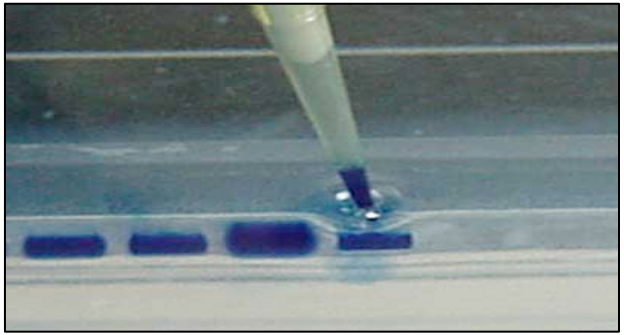
size

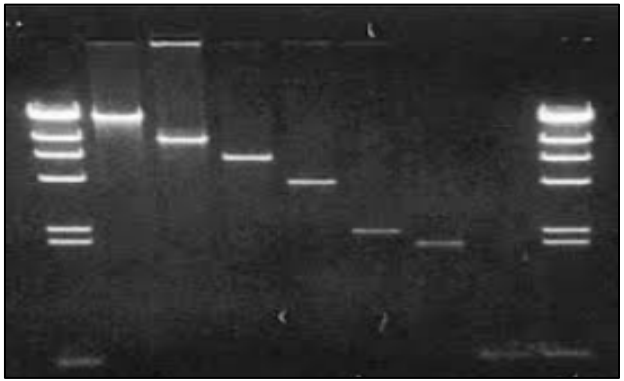


Today Part 1:

Visualize DNA + save a picture!

- DNA Loading dye (6X):
  Bromophenol blue
  L> dye for tracking your sample
- Sybr-Safe DNA stain:
  - intercalating agent for DNA (label)
  - fluorescence under UV



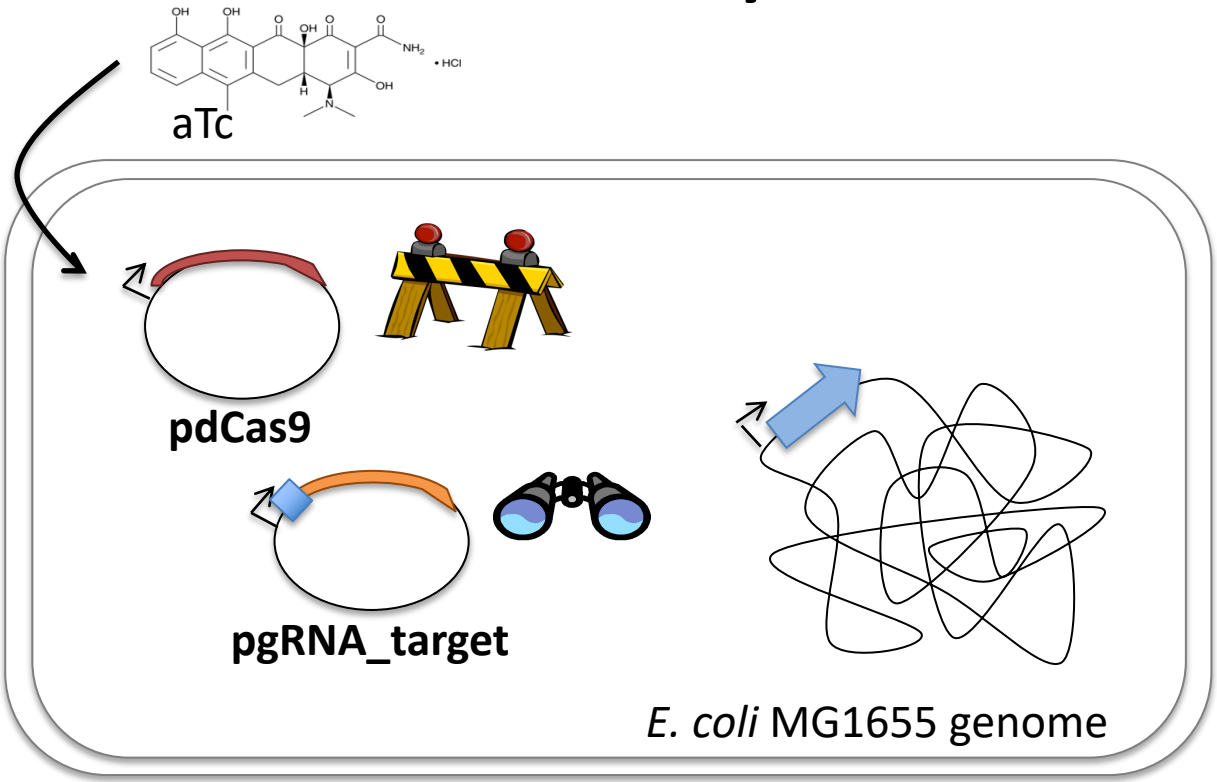


➢ Safety : wear nitrile gloves

Today’s goal:

Design gRNA sequence to repress a gene, such that the **production of ethanol or acetate will increase.**

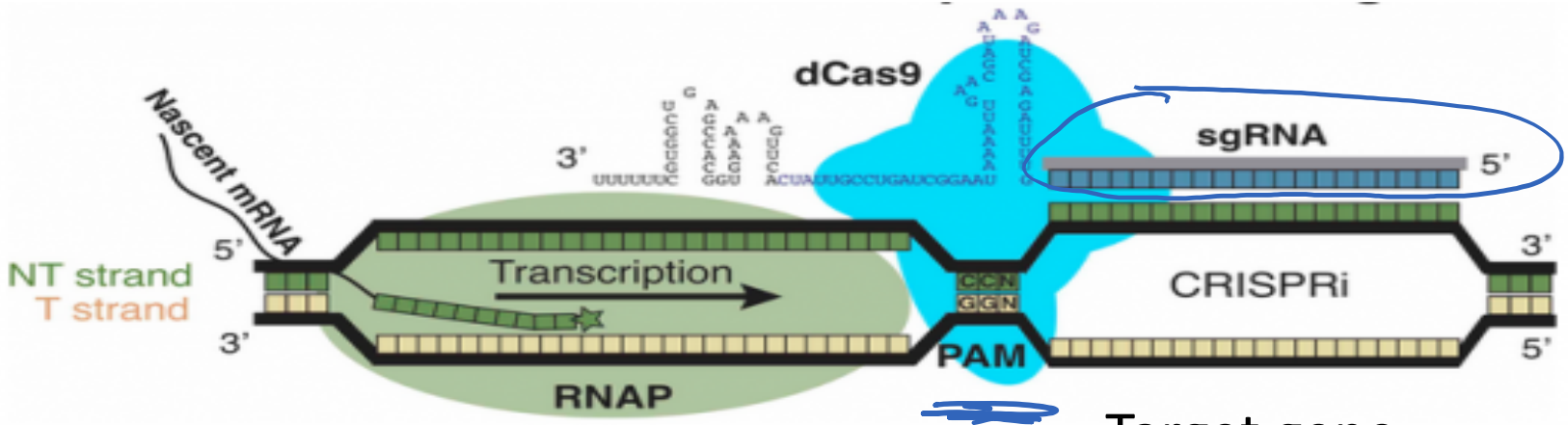
CRISPRi system overview



- Target gene
  silence / ↓ expression of GOI
- pgRNA_target
  ↳ tell where dCas9 will bind
- pdCas9
  ↳ bind to our target

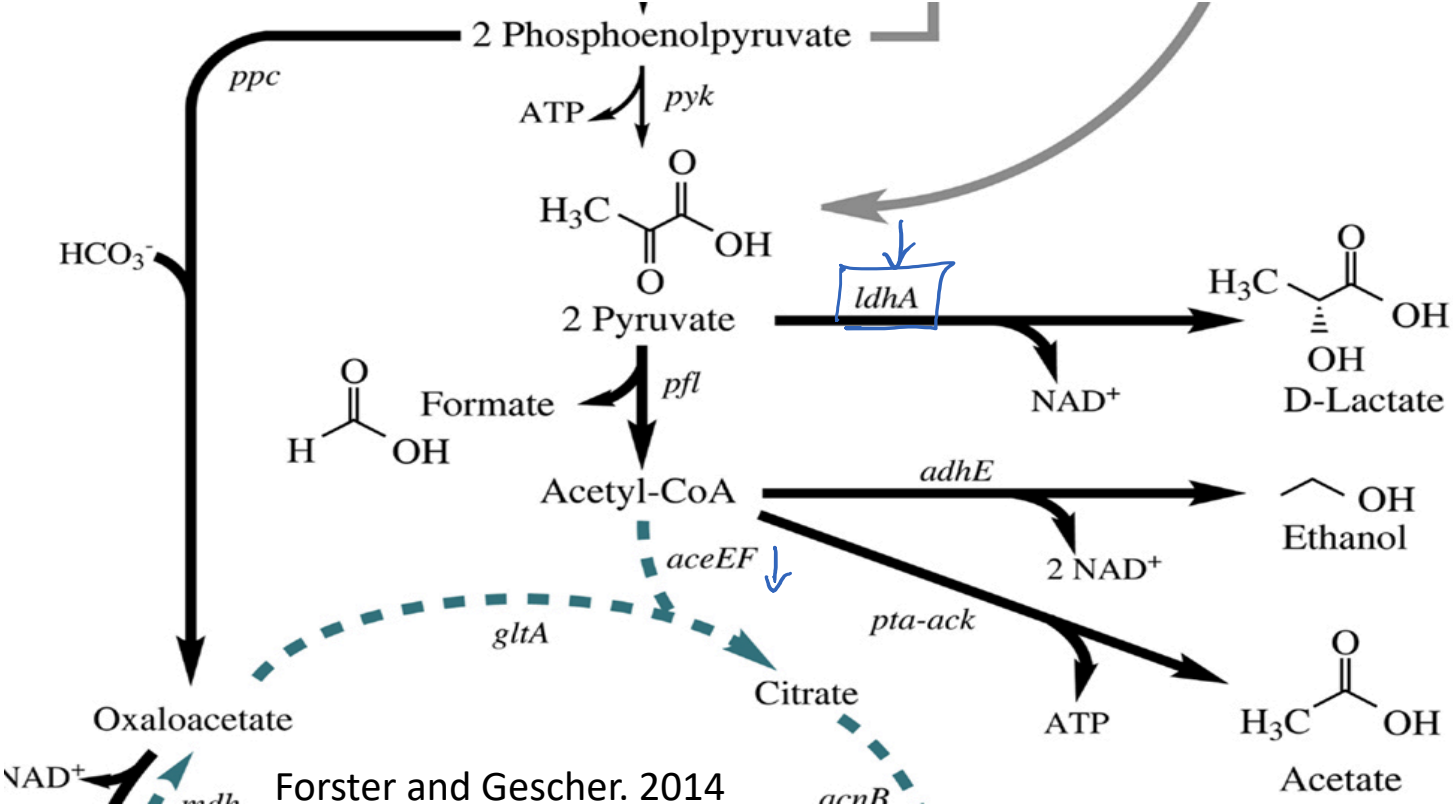
Dr. Noreen Lyell's lecture M2D1

CRISPRi system can block the RNA polymerase



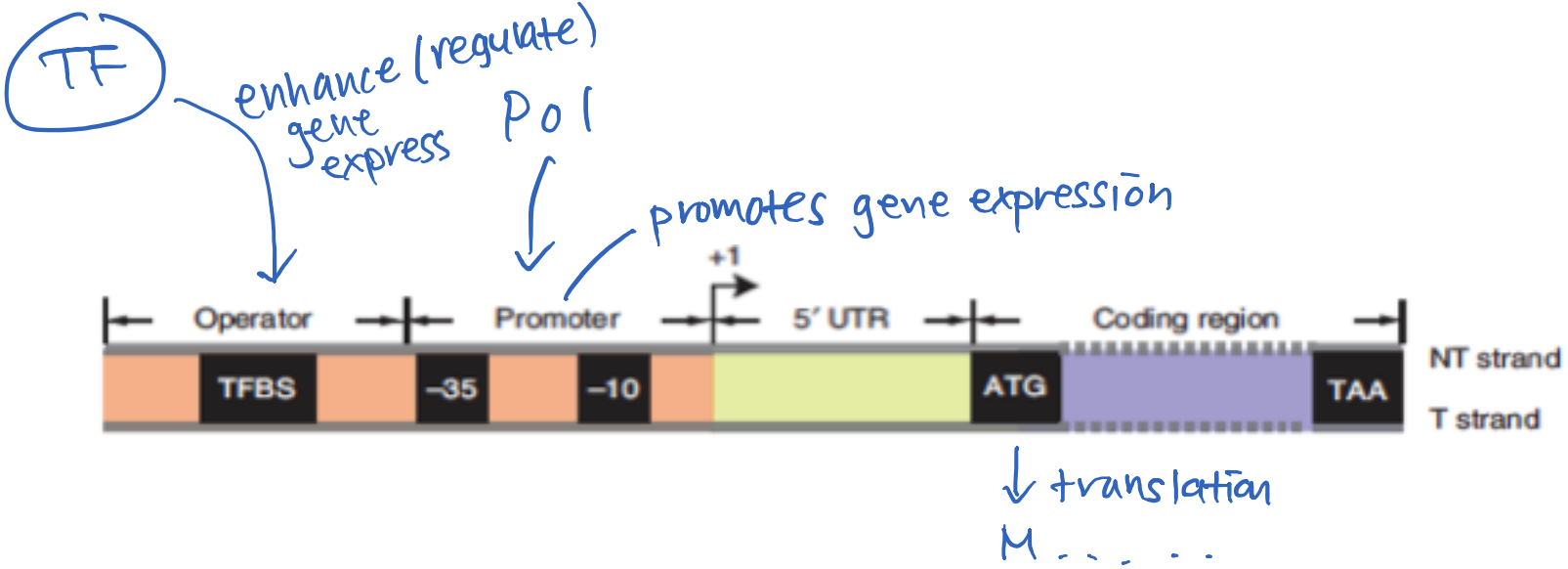
http://qi.ucsf.edu/CRISPR_transcription

How would you use CRISPRi to increase yield of the desired product?



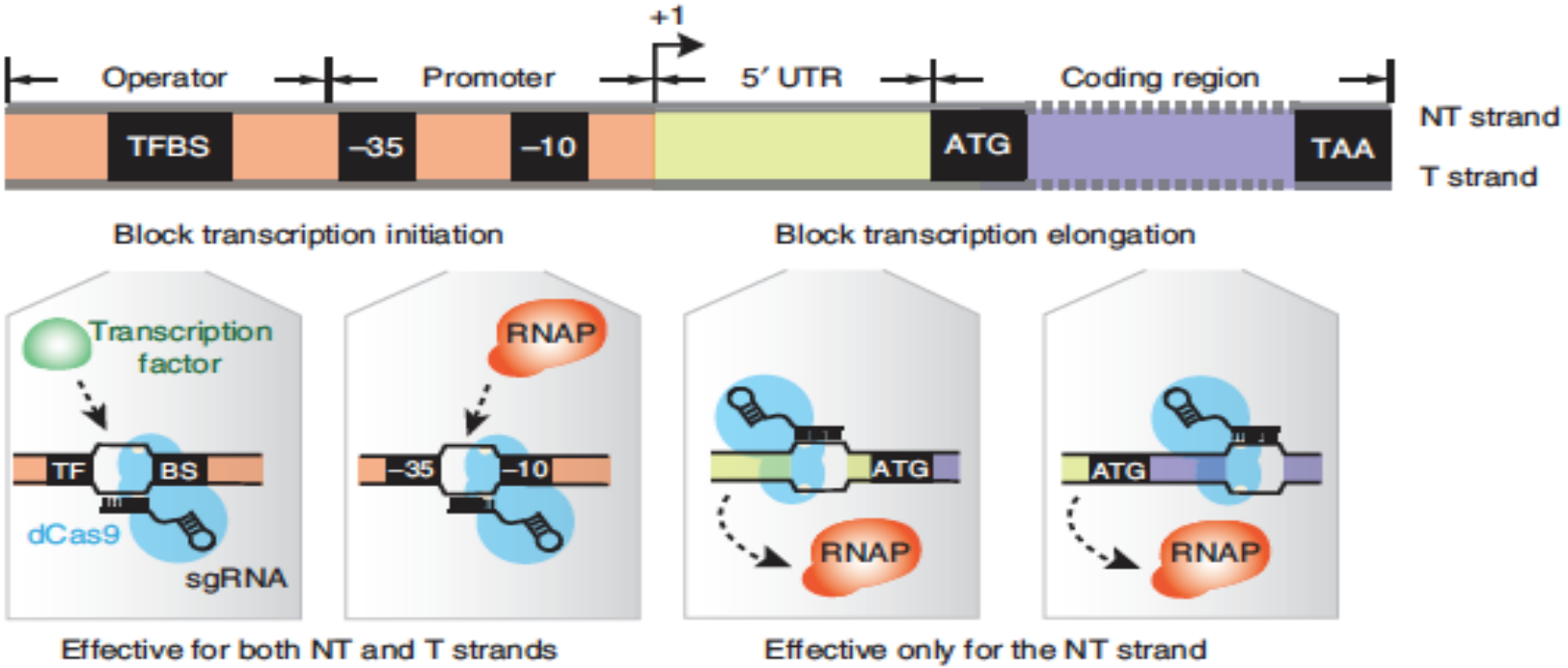
Forster and Gescher. 2014

Let's review binding partners:



Larson, et al. CRISPR interference for sequence-specific control of gene expression. *Nature Protocols.* 2013.

Which region of the gene will you target?

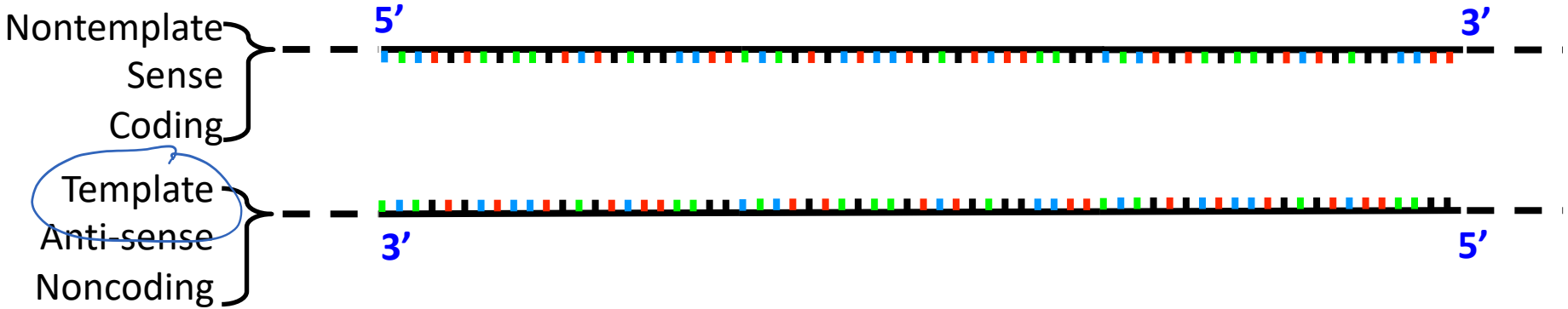


Larson, et al. CRISPR interference for sequence-specific control of gene expression. *Nature Protocols.* 2013.

Design of gRNA for CRISPRi system

(1) If you target the template DNA strand, the gRNA sequence will be the same as the transcribed (nontemplate) sequence.

(1) If you target the nontemplate strand, the gRNA sequence will be the reverse-complement of the transcribed sequence.



Design of gRNA for CRISPRi system

How do you use these principles to
Design the gRNA DNA sequence

Create a plasmid (pgRNA)

Generate the desired gRNA
when transcribed

Target gene of interest

See Handout

Handout:

gRNA (DNA sequence) Design for CRISPRi (fill in the blanks)

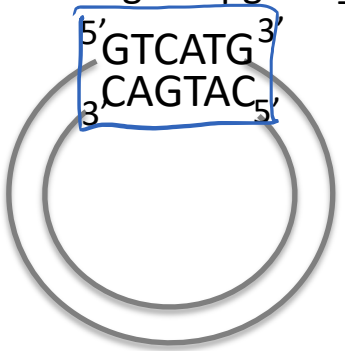
Target gene sequence: 5′ GTCATG 3′ ← Non-template (coding) strand

Complementary strand: 3′ CAGTAC 5′ ← Template (noncoding) strand

Scenario 1

gRNA (DNA sequence) is the same as the nontemplate (NT) strand: 5′ GTCATG 3′

The plasmid you generate after inserting the sequence would look something like pgRNA_target_1:



pgRNA_target_1

transcription

gRNA produced:

5′ GUCAUG 3′

This gRNA binds to the nontemplate/template (circle one) strand of the target gene.

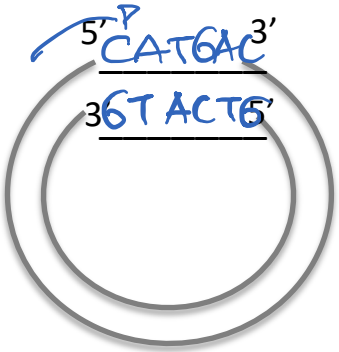
Handout:

gRNA (DNA sequence) Design for CRISPRi (fill in the blanks)

Scenario 2

gRNA (DNA sequence) is the same as the template (T) strand: 5’ CATGAC 3’

The plasmid you generate after inserting the sequence would look something like pgRNA_target_2:



pgRNA_target_2

transcription

gRNA produced:

5’ CAUGAC 3’

This gRNA binds to the nontemplate/template (circle one) strand of the target gene.

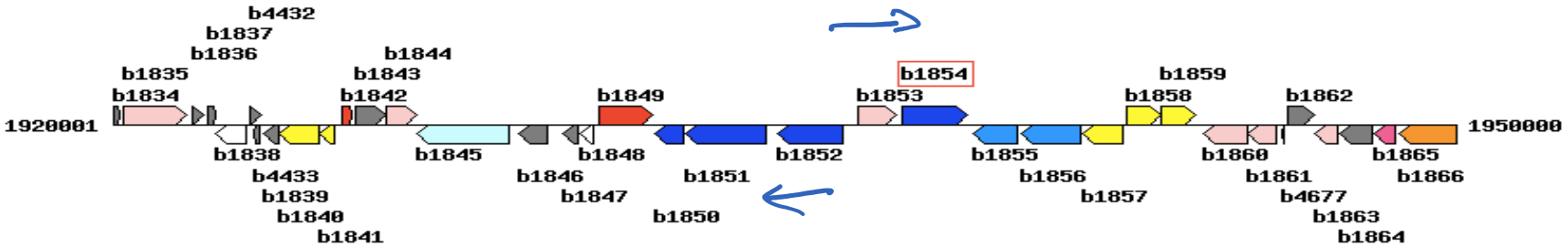
Practically: Using KEGG Database

Position	1937649..1939091 Genome map
AA seq	480 aa AA seq DB search MSRRLRRTKIVTTLGPATDRDNNLEKVIAAGANVVRMNFSHGSPEDHKMRADKVREIAAK LGRHVAILGDLQGPKIRVSTFKEGKVFLNIGDKFLLDANLGKGEGDKEKVGIDYKGLPAD VVPGDILLLDDGRVQLKVLEVQGMKVFTEVTVGGPLSNNKGINKLGGGLSAEALTEKDKA DIKTAALIGVDYLAVSFPRCGEDLNYARRLARDAGCDAKIVAKVERAEAVCSQDAMDDII LASDVVMVARGDLGVEIGDPELVGIQKALIRRARQLNRAVITATQMMESMITNPMPTRAE VMDVANAVLDGTDAVMLSAETAAGQYPSETVAAMARVCLGAEKIPSINVSKHRLDVQFDN VEEAIAMSAMYAANHLKGVTAIITMTESGRTALMTSRISSGLPIFAMSRHERTLNLTALY RGVTPVHFDSANDGVAAASEAVNLLRDKGYLMSGDLVIVTQGDVMSTVGSTNTTRILTVE
NT seq	1443 nt NT seq +upstream 0 nt +downstream 0 nt atgtccagaaggcttcgcagaacaaaaatcgttaccacgttaggcccagcaacagatcgc gataataatcttgaaaaagttatcgcggcgggtgccaacgttgtacgtatgaacttttct cacggctcgcctgaagatcacaaaatgcgcgcggataaagttcgtgagattgccgcaaaa ctggggcgtcatgtggctattctgggtgacctccaggggcccaaaatccgtgtatccacc tttaaagaaggcaaagttttcctcaatattggggataaattcctgctcgacgccaacctg ggtaaaggtgaaggcgacaaagaaaaagtcggtatcgactacaaaggcctgcctgctgac gtcgtgcctggtgacatcctgctgctggacgatggtcgcgtccagttaaaagtactggaa gttcagggcatgaaagtgttcaccgaagtcaccgtcggtggtcccctctccaacaataaa ggtatcaacaaacttggcggcggtttgtcggctgaagcgctgaccgaaaaagacaaagca gacattaagactgcggcgttgattggcgtagattacctggctgtctccttcccacgctgt ggcgaagatctgaactatgcccgtcgcctggcacgcgatgcaggatgtgatgcgaaaatt gttgccaaggttgaacgtgcggaagccgtttgcagccaggatgcaatggatgacatcatc ctcgcctctgacgtggtaatggttgcacgtggcgacctcggtgtggaaattggcgacccg gaactggtcggcattcagaaagcgttgatccgtcgtgcgcgtcagctaaaccgagcggta atcacggcgacccagatgatggagtcaatgattactaacccgatgccgacgcgtgcagaa gtcatggacgtagcaaacgccgttctggatggtactgacgctgtgatgctgtctgcagaa actgccgctgggcagtatccgtcagaaaccgttgcagccatggcgcgcgtttgcctgggt gcggaaaaaatcccgagcatcaacgtttctaaacaccgtctggacgttcagttcgacaat gtggaagaagctattgccatgtcagcaatgtacgcagctaaccacctgaaaggcgttacg gcgatcatcaccatgaccgaatcgggtcgtaccgcgctgatgacctcccgtatcagctct ggtctgccaattttcgccatgtcgcgccatgaacgtacgctgaacctgactgctctctat cgtggcgttacgccggtgcactttgatagcgctaatgacggcgtagcagctgccagcgaa gcggttaatctgctgcgcgataaaggttacttgatgtctggtgacctggtgattgtcacc cagggcgacgtgatgagtaccgtgggttctactaataccacgcgtattttaacggtagag taa

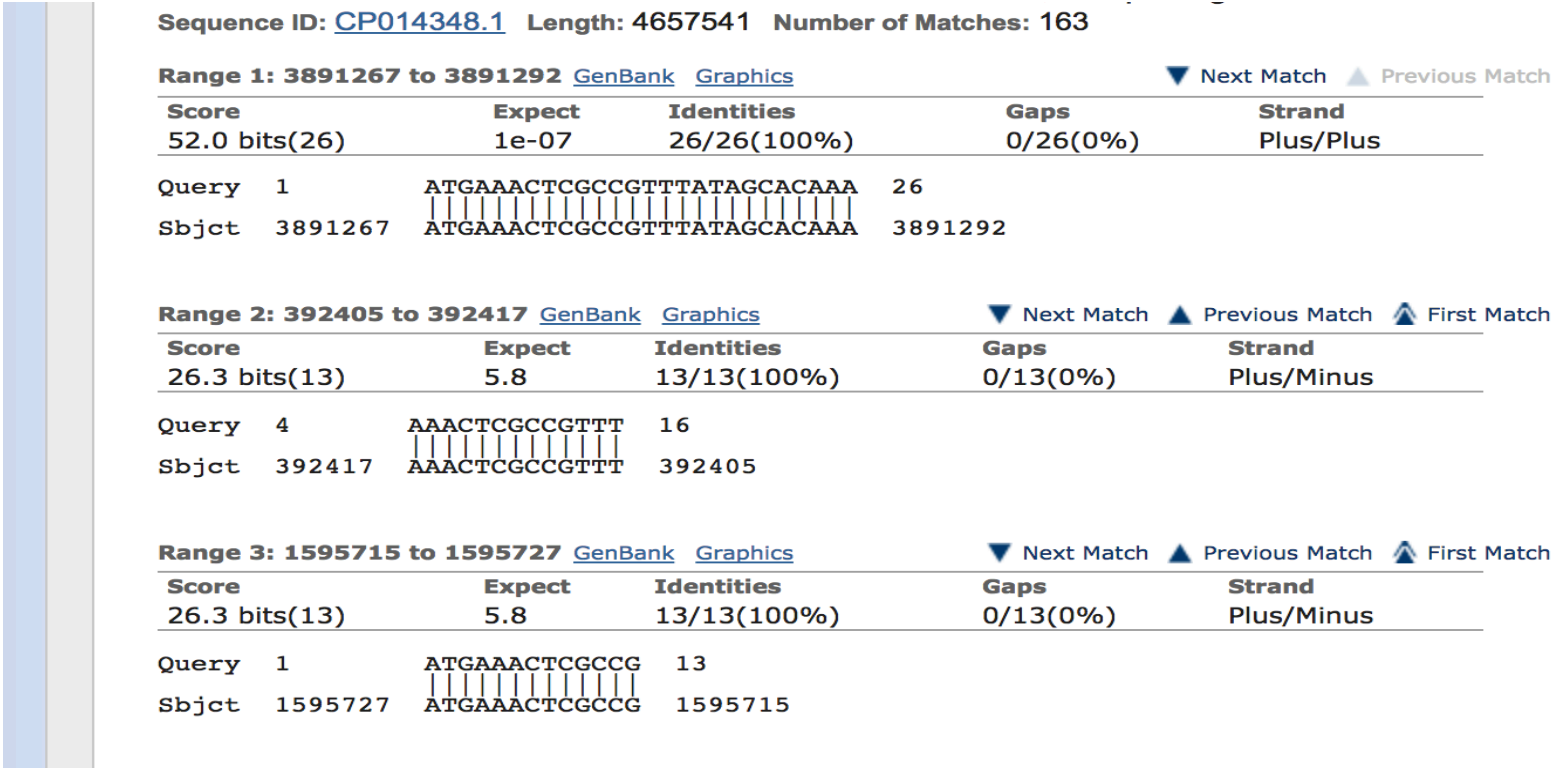
NT here means nucleotide sequence

Practically: Using KEGG Database

Genome Map



Practically: Using BLAST (Basic local alignment search tool) to assess off-target binding



Sequence ID: CP014348.1 **Length:** 4657541 **Number of Matches:** 163

Range 1: 3891267 to 3891292 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
52.0 bits(26)	1e-07	26/26(100%)	0/26(0%)	Plus/Plus

```
Query  1        ATGAAACTCGCCGTTTATAGCACAAA  26
               ||||||||||||||||||||||||||
Sbjct  3891267  ATGAAACTCGCCGTTTATAGCACAAA  3891292
```

Range 2: 392405 to 392417 GenBank Graphics ▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Identities	Gaps	Strand
26.3 bits(13)	5.8	13/13(100%)	0/13(0%)	Plus/Minus

```
Query  4       AAACTCGCCGTTT  16
               |||||||||||||
Sbjct  392417  AAACTCGCCGTTT  392405
```

Range 3: 1595715 to 1595727 GenBank Graphics ▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Identities	Gaps	Strand
26.3 bits(13)	5.8	13/13(100%)	0/13(0%)	Plus/Minus

```
Query  1        ATGAAACTCGCCG  13
               |||||||||||||
Sbjct  1595727  ATGAAACTCGCCG  1595715
```

M2D3 HW: Figure/Caption/Results

- Figure = agarose gel image with title and caption
  - don't add drawings/modification on top of image, next to image is sufficient
- Results **paragraph** should follow below figure and results subsection title (take-home message)
- Minimize interpretation in the results section in Mod2 report (separate discussion section; *M2D5HW*)
  - State the result of the experiment without discussing conclusions drawn from experiment
- Figure/text expectations same as Mod1 report, formatting major difference

In lecture discussion Thursday

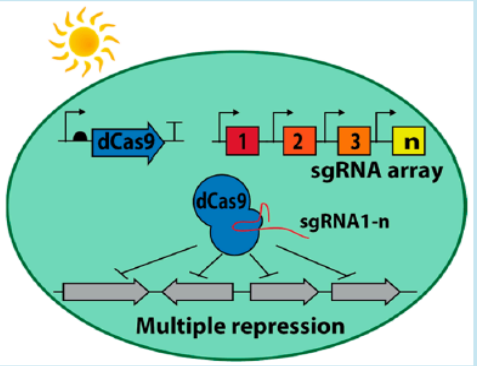
Multiple Gene Repression in Cyanobacteria Using CRISPRi

Lun Yao, Ivana Cengic, Josefine Anfelt, and Elton P. Hudson*

KTH—Royal Institute of Technology, Division of Proteomics and Nanobiotechnology, Science for Life Laboratory, Stockholm SE-171 21 Sweden

Supporting Information

ABSTRACT: We describe the application of clustered regularly interspaced short palindromic repeats interference (CRISPRi) for gene repression in the model cyanobacterium *Synechocystis* sp. PCC 6803. The nuclease-deficient Cas9 from the type-II CRISPR/Cas of *Streptrococcus pyogenes* was used to repress green fluorescent protein (GFP) to negligible levels. CRISPRi was also used to repress formation of carbon storage compounds polyhydroxybutryate (PHB) and glycogen during nitrogen starvation. As an example of the potential of CRISPRi for basic and applied cyanobacteria research, we simultaneously knocked down 4 putative aldehyde reductases and dehydrogenases at 50−95% repression. This work also demonstrates that tightly repressed promoters allow for inducible and reversible CRISPRi in cyanobacteria.



Fa19 20.109 Blog post

- Email to join class blog
- Suggested topics listed on blog
- For full credit you only need to complete 3 out of 4 blog posts– no late assignments accepted
- Details about use:
  - Do not publish MIT logo
  - Do not post photographs with names tagged
  - Do not write malicious content
  - Do not plagarize

Today

- Sign up for ethanol or acetate at front bench
- Write your gRNA (DNA) sequence on wiki and let me know so I can order them today

  Note: (your sequence + 35 bp tag) ≤ 60 bp