

Team 17

Improving CRISPR Off-Target Detection Using Transposases



DREXEL UNIVERSITY
School of
Biomedical Engineering,
Science and Health Systems

Members: Ann Abraham, Connor Gazda, Alexis Malamas, Olivia Wood

Advisor: William Dampier

NEED:

FUTURE:

Simplify DNA processing by combining separate **Cut** and **Label** steps into **1 Step**

Summary:

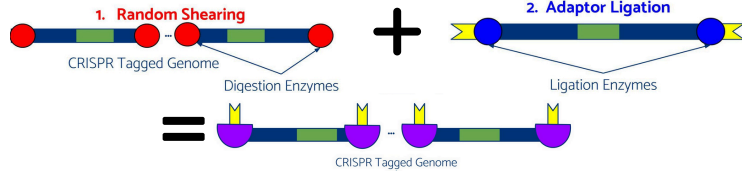
Combine 2 steps into 1, enhancing efficiency

Impact:

Simpler and quicker GUIDE-seq protocol.

Future Revisions:

Use an enzyme that can cut more TN5 reaction and directly test the sequencing (using comparable samples)



DESIGN INPUTS:

TESTING RESULTS

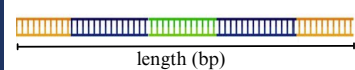
Constraints:

Compatible adapters: i5 and i7 ends needed for sequencing
Unique Molecular Index: needed to identify PCR duplicates

Requirements:

Fragment length: 100-2000 bp

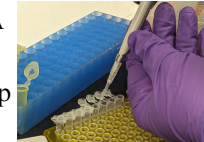
PCR Enrichment: higher DNA C. increase



DNA Fragmentation Test (R1) Run several TN5 Reaction

PCR Enrichment Test (R2) Run PCR, measure DNA concentration before and after

Results: **Pass** DNA fragments averaging ~1000 bp obtained

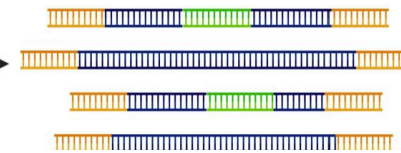
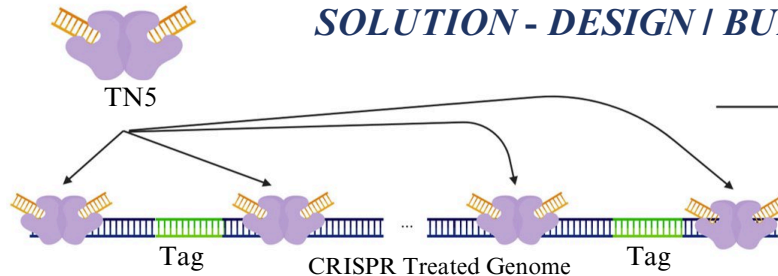


dna conc (ng/ul)	A1	A2	B1	B2
Before PCR	6.55	6.39	4.29	5.96
After PCR	10.75	12.35	21.25	19.3

Results: **Pass** adapter B samples showed 3x adapter A's DNA C. Increase.

SOLUTION - DESIGN / BUILD

Utilizes TN5 enzymes to **shear** and ligate **adapters** to an intact genome, produces same product as the GUIDE-seq **shearing** and **ligation** steps.



Random Fragments with Adapters

PCR
Enrichment
+
DNA
Sequencing