

Designing Artificial xrRNA

Leonhard Sidl

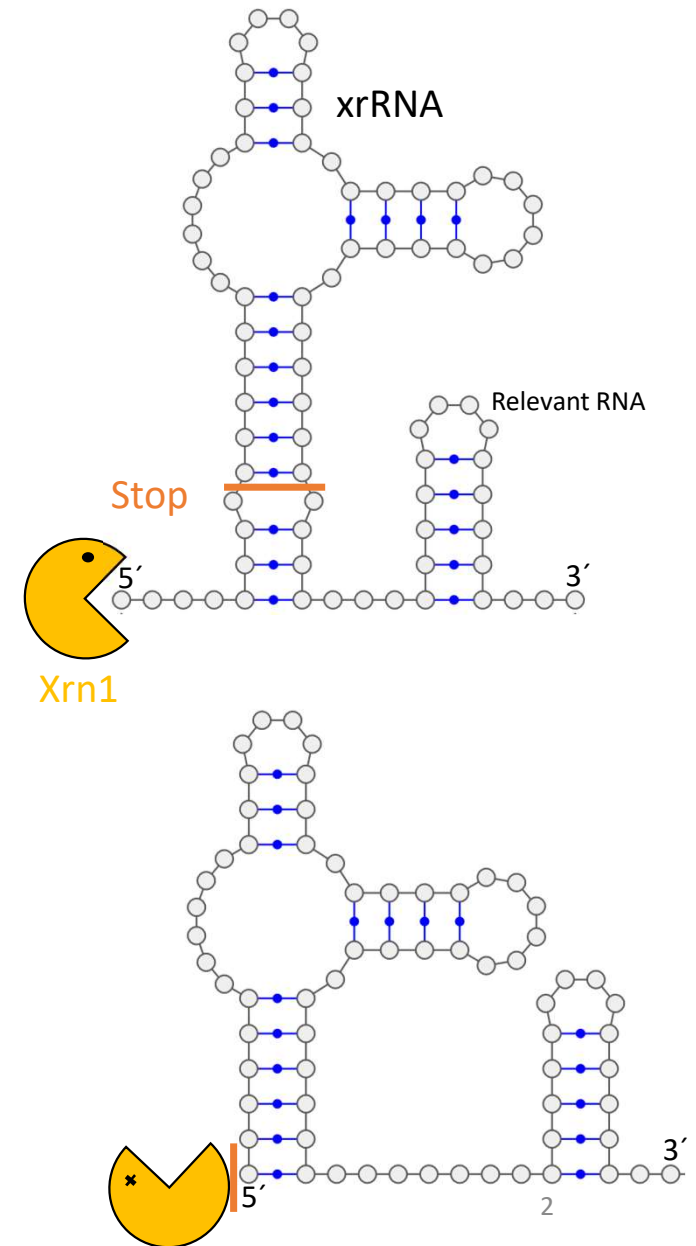


universität
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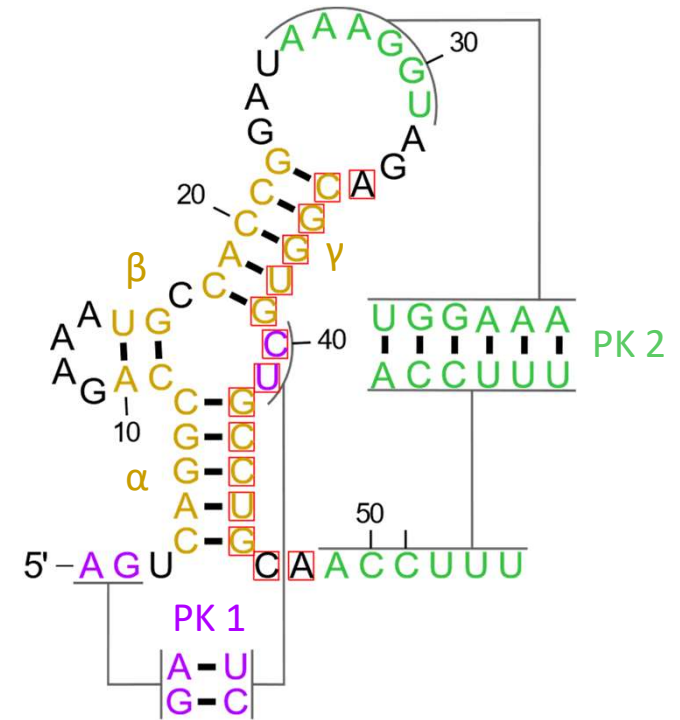
Introduction to xrRNA

- xrRNA stops exoribonuclease Xrn1



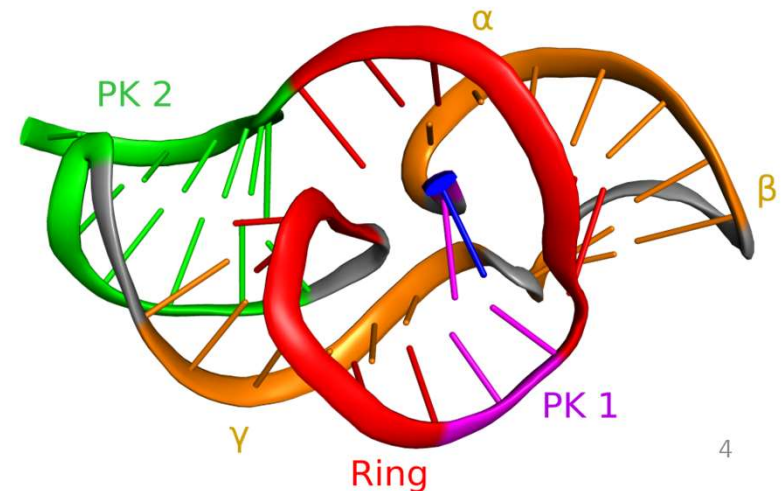
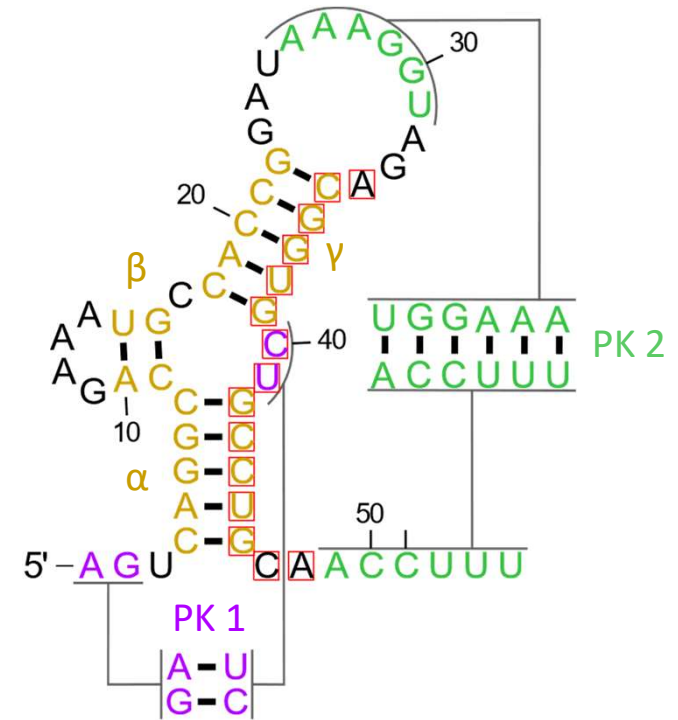
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- xrRNA stops exoribonuclease Xrn1
- Conserved secondary structure features:
 - Central 3-way junction with helices α - γ
 - Two pseudoknots PK1 and PK2



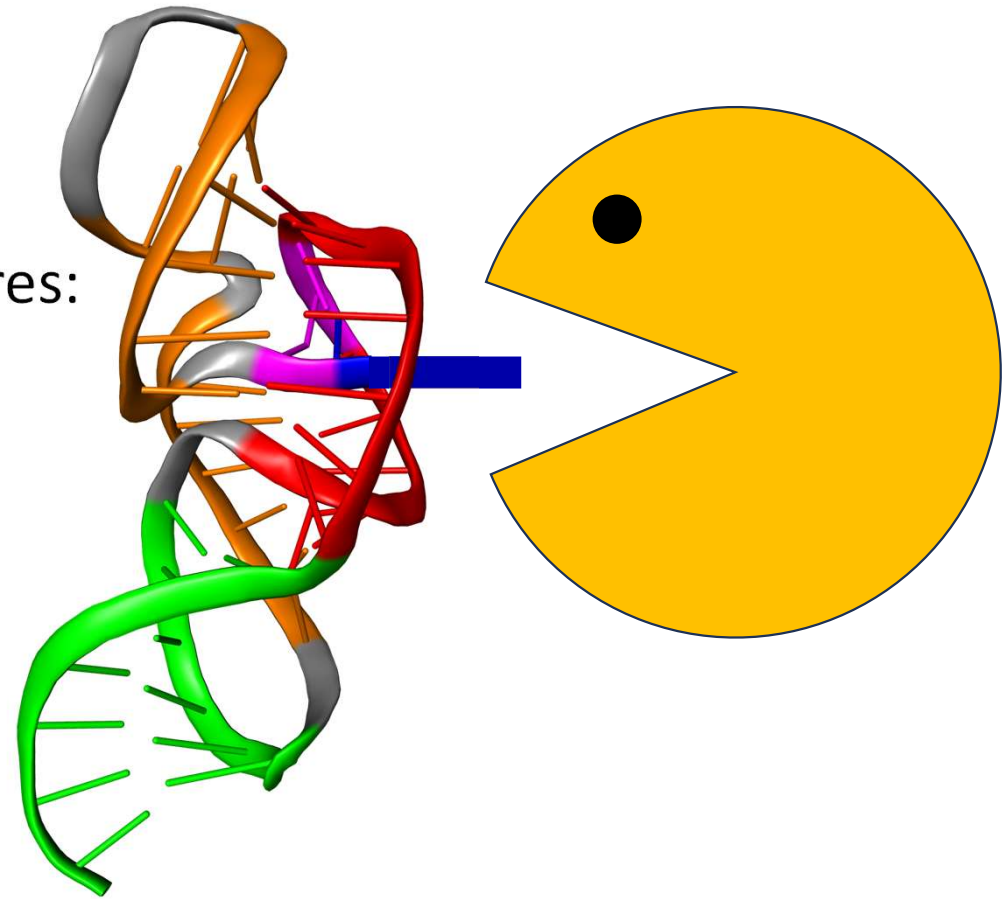
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 - Central 3-way junction with helices α - γ
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- Conserved tertiary structure feature:
 - Ringlike structure around the 5' end



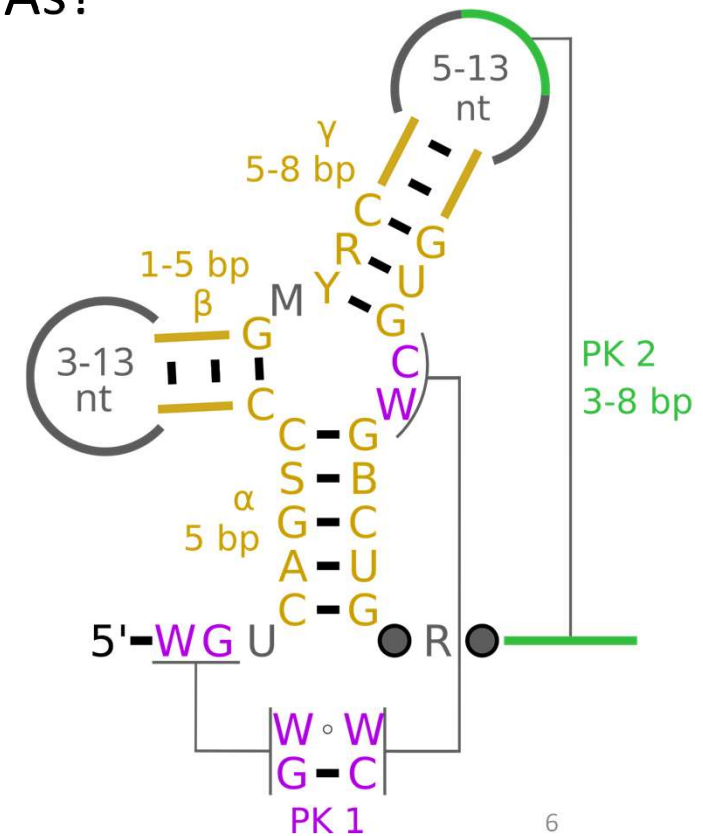
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- Conserved secondary structure features:
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- Mechanical block against Xrn1



Designing xrRNAs

1. Which features are essential for biological xrRNAs?

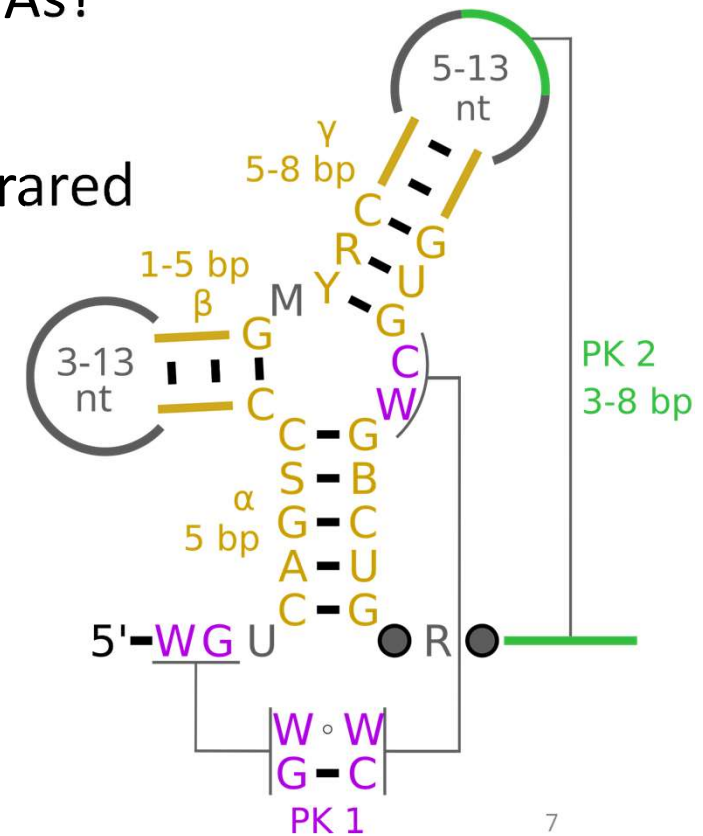


Designing xrRNAs



Yao, Hua-Ting, et al (2024)

1. Which features are essential for biological xrRNAs?
2. Design sequences with those features using Infrared

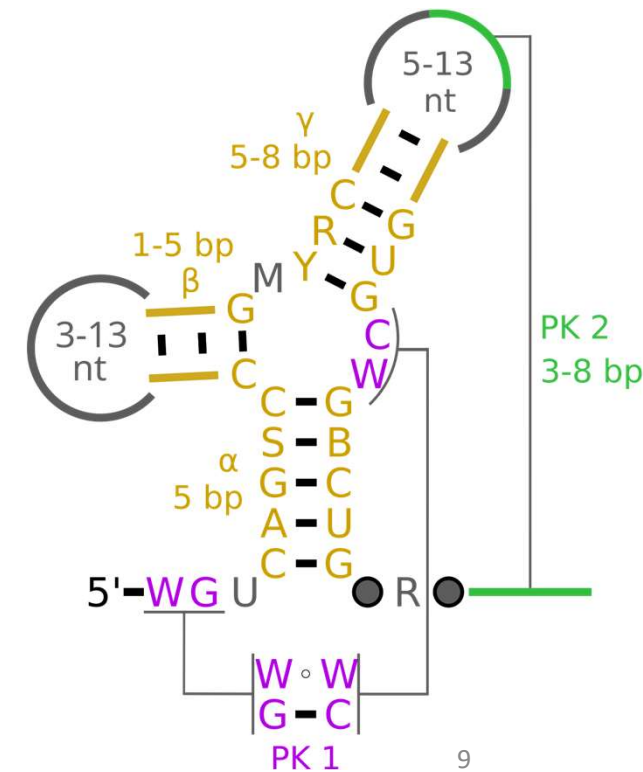


2. Infrared Model

- Sample sequences under a set of constraints and functions

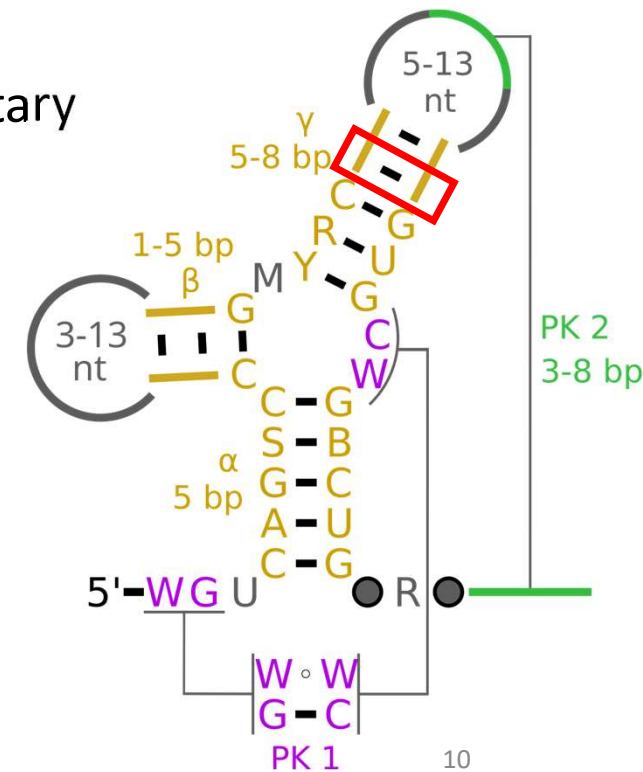
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- Sample sequences under a set of constraints and functions
- Constraints that lead to xrRNA designs:



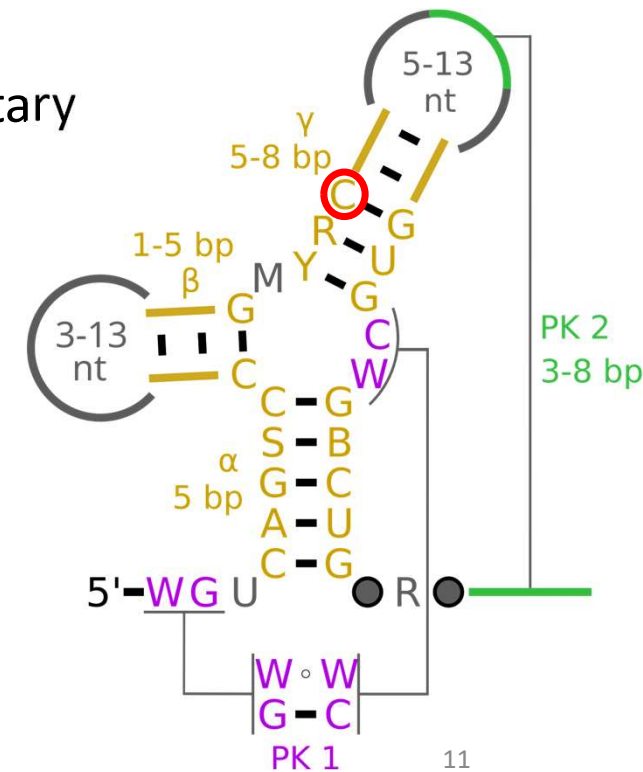
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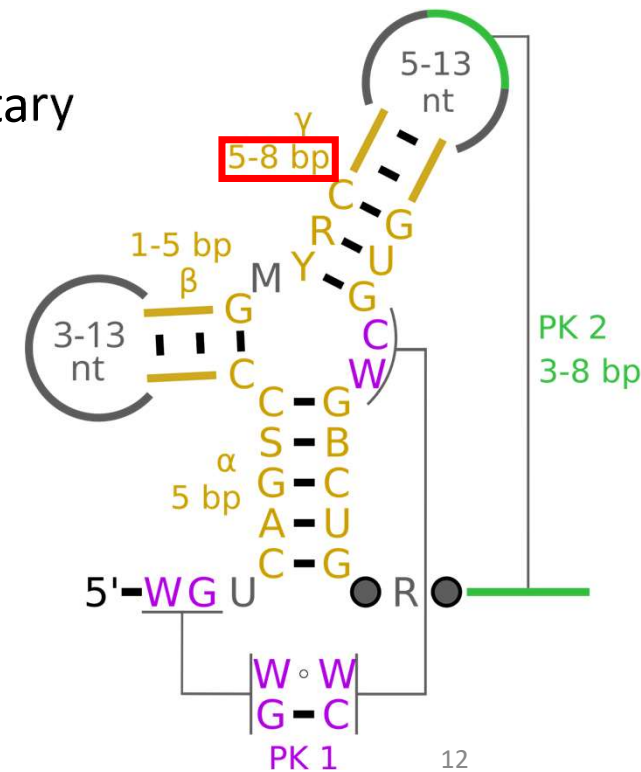
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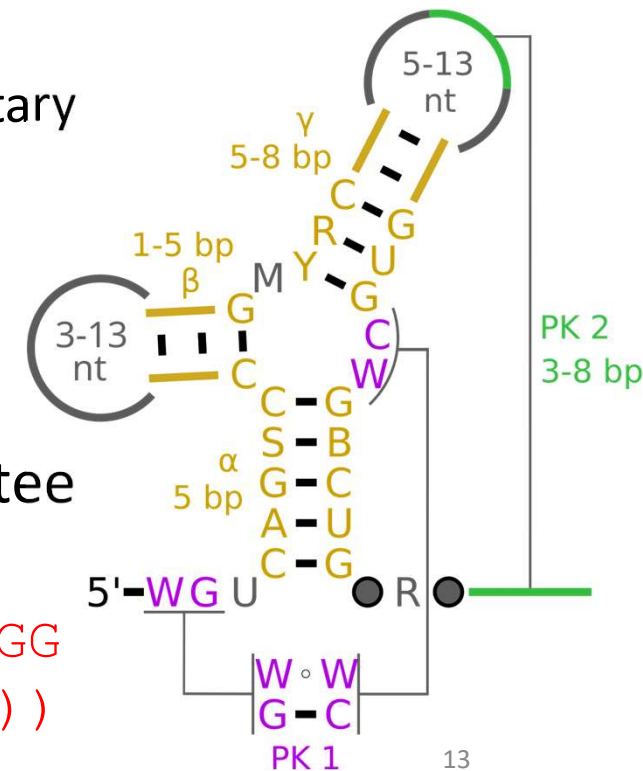
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2. Infrared Model

- Sample sequences under a set of constraints and functions
- Constraints that lead to xrRNA designs:
 - Bases that should form basepairs need to be complementary
 - Positions with conserved bases are fixed
 - Length of the individual features and total length
- Gaps only on one side of the helix/hairpin to guarantee uniform sampling

CC--AAAGG CC-A-AAGG CCA--AAGG
 ((.....)) ((.....)) ((.....))



2. Design Optimization

- Sample a starting sequence from global sequence space

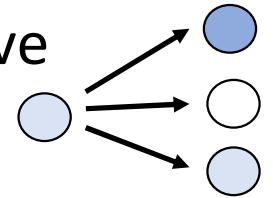
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- Sample a starting sequence from global sequence space
- This sequence will probably not fold into the correct structure



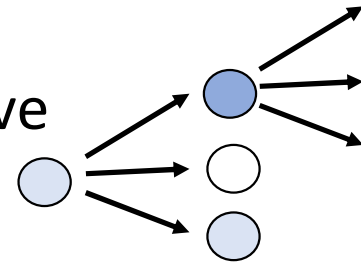
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- Sample a starting sequence from global sequence space
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- Move around the local neighborhood and improve the objective function



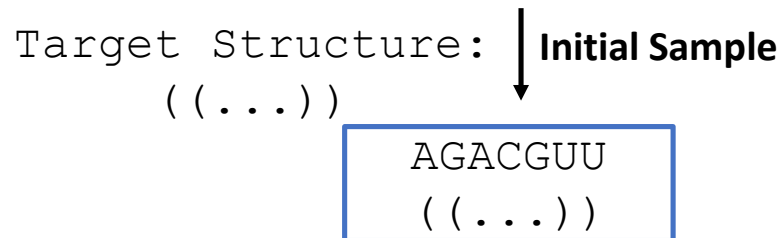
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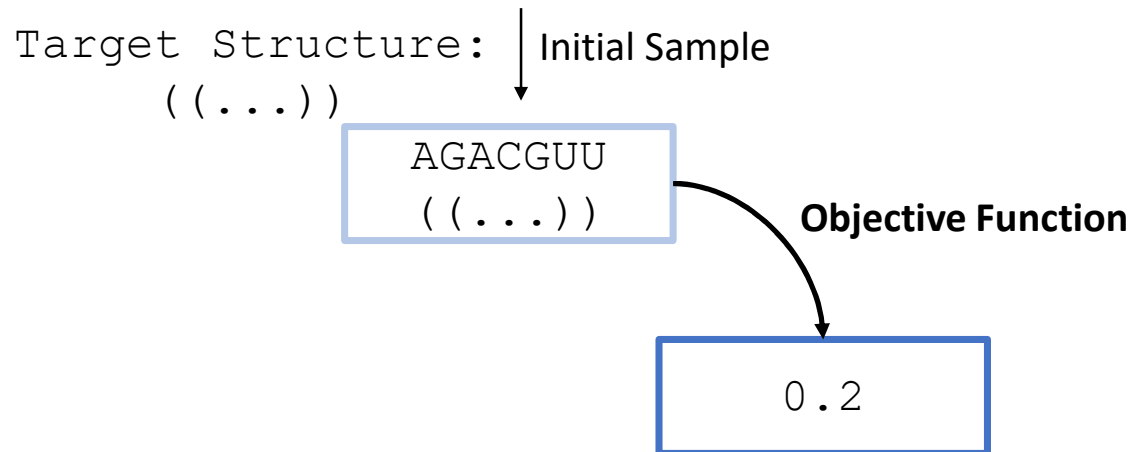
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Target Structure: ((...))

Initial Sample

AGACGUU
((...))

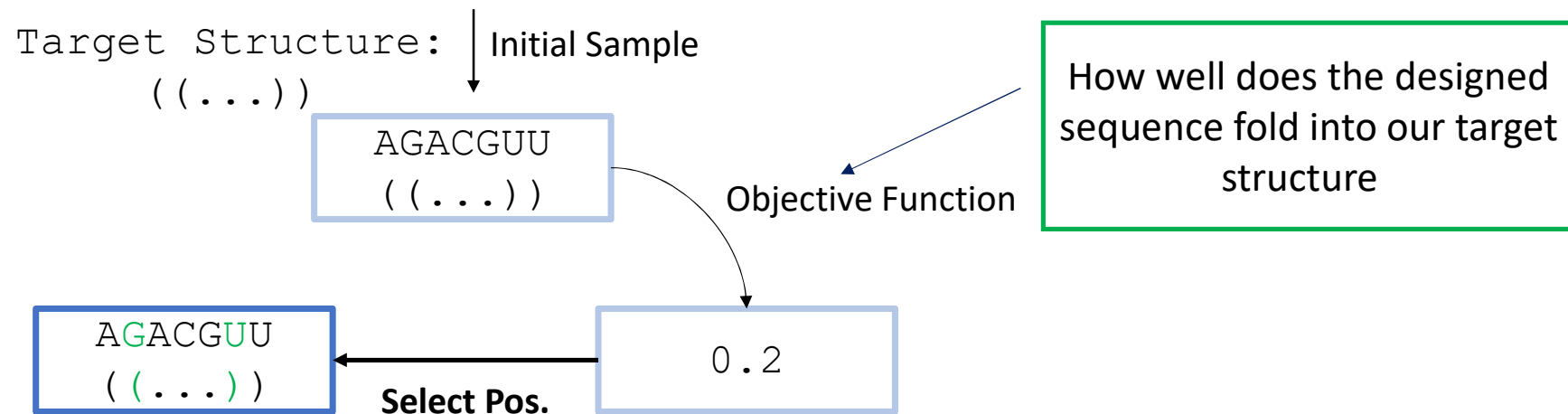
Objective Function

0.2

How well does the designed sequence fold into our target structure

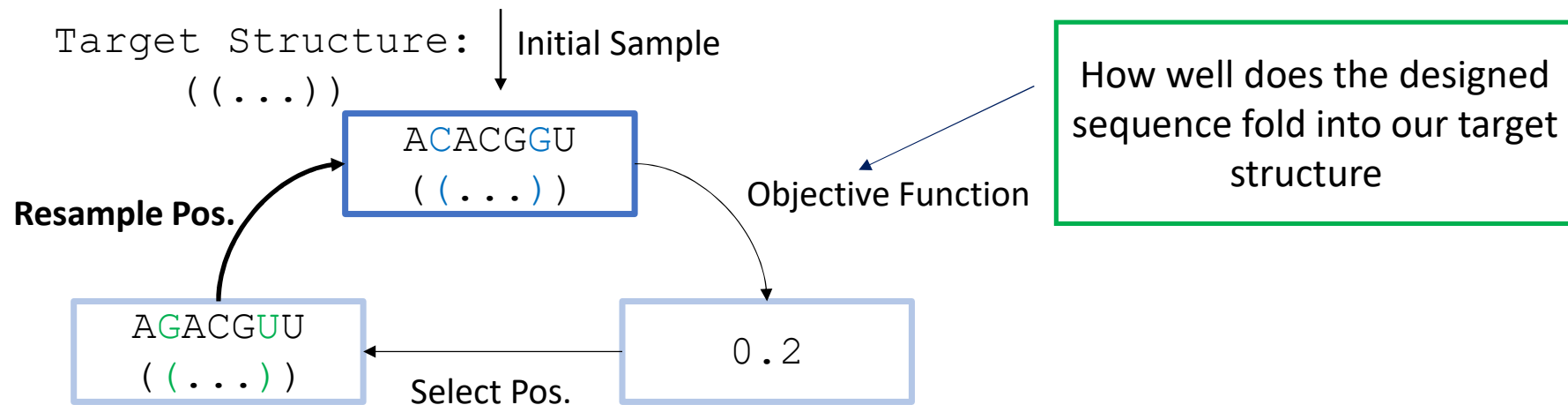
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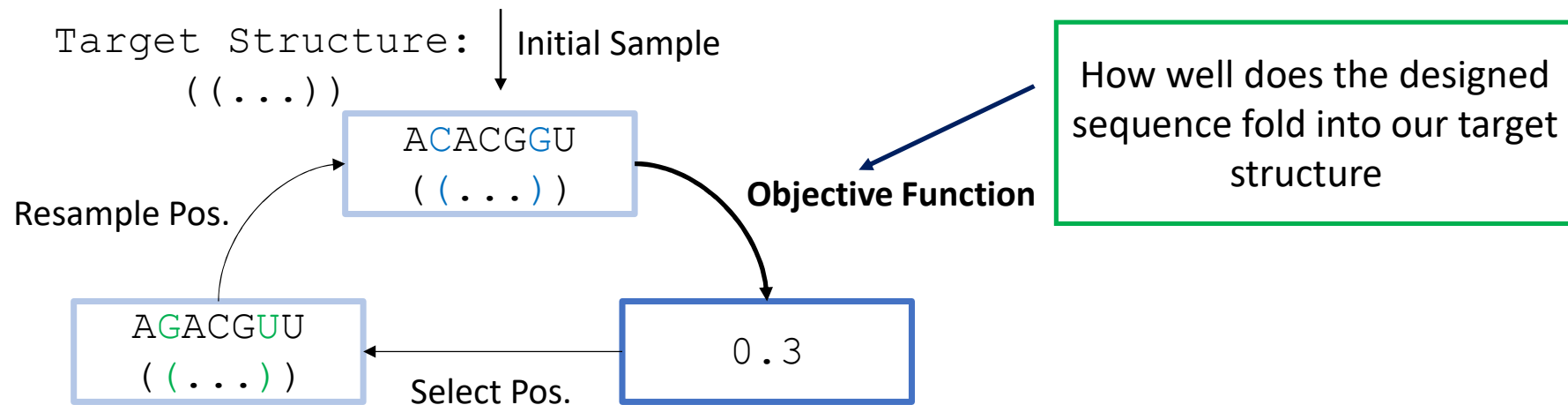
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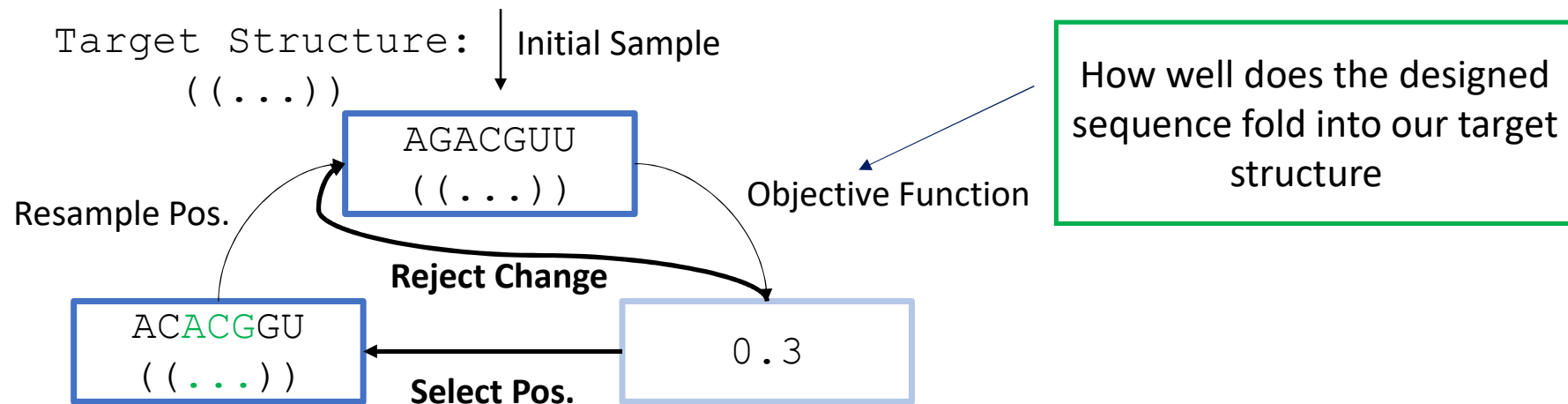
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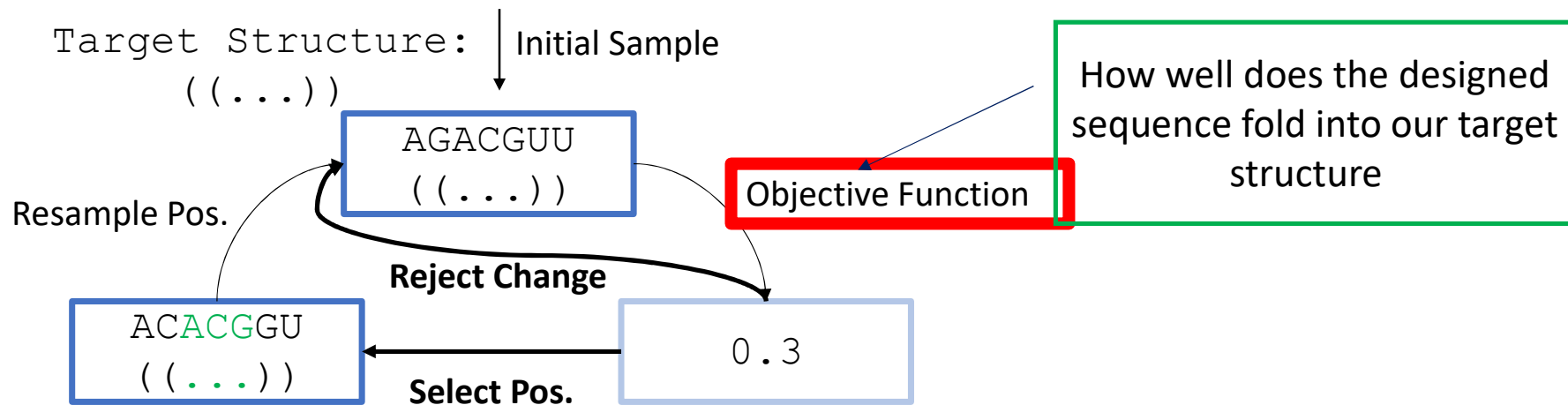
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2. Objective Functions - Target Probability

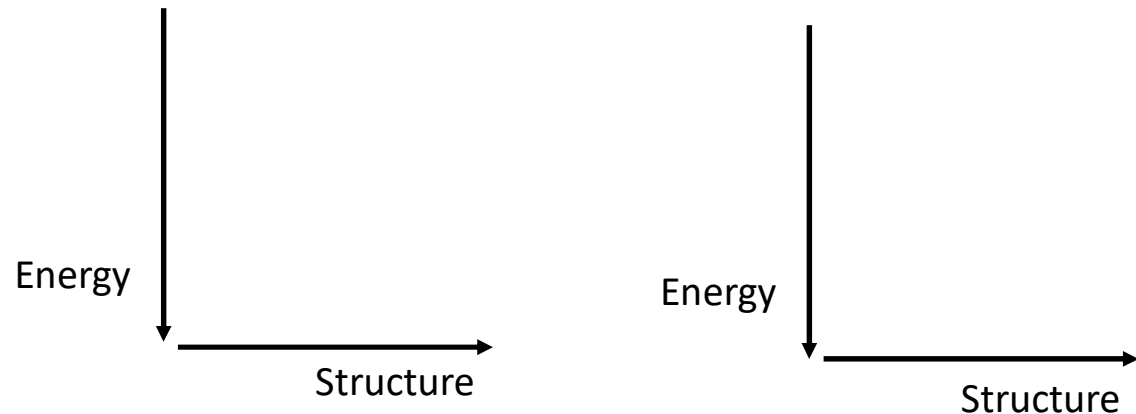
- Probability that sequence s folds into structure p

2. Objective Functions - Target Probability

- Probability that sequence s folds into structure p
- Sounds good, but RNAs don't fold into a single structure

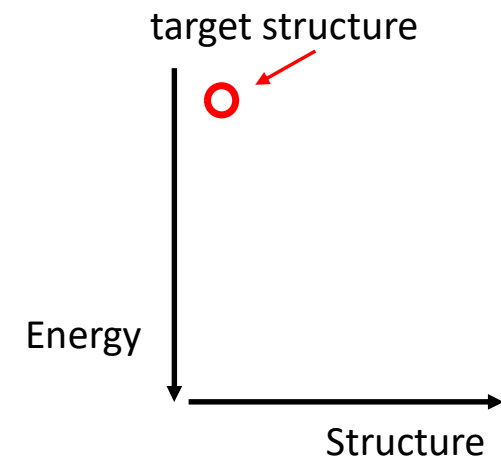
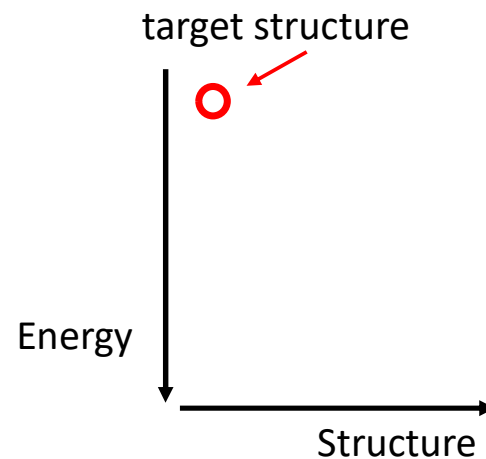
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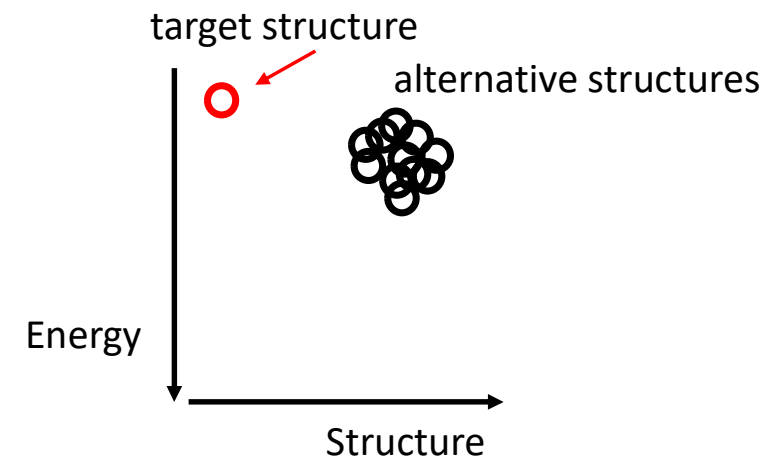
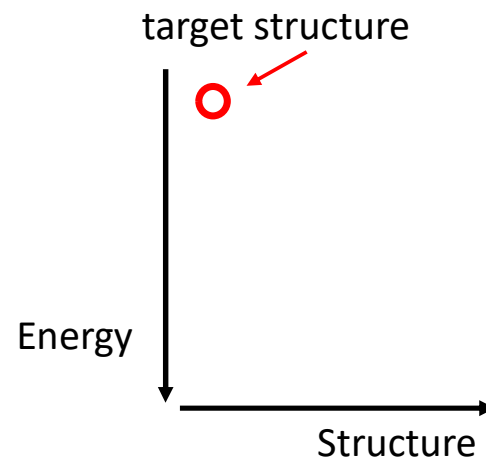
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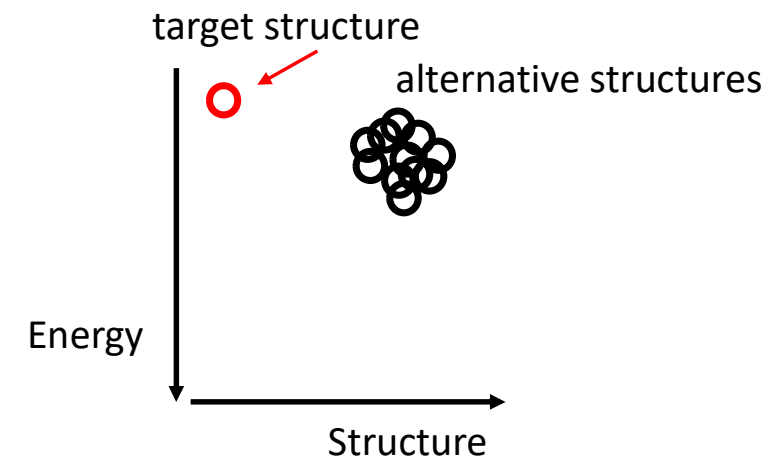
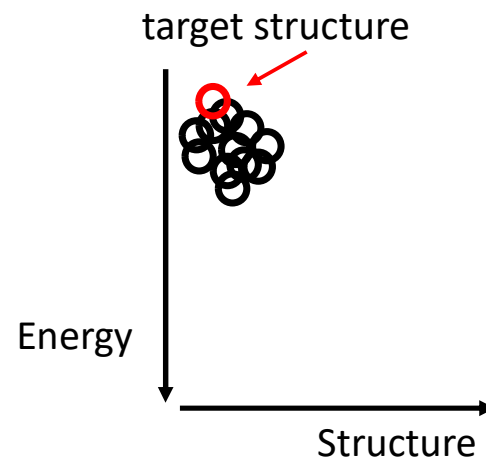
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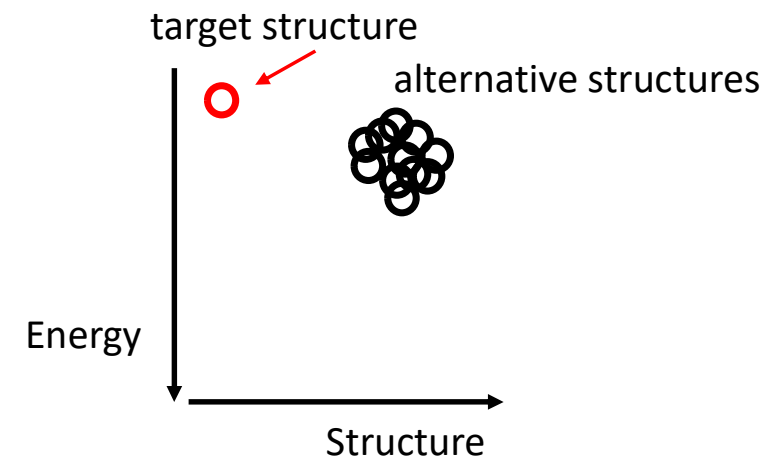
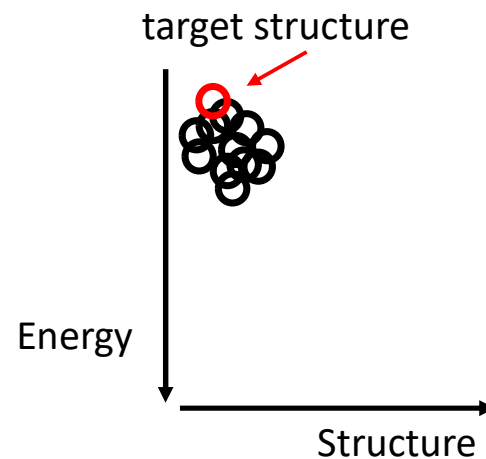
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- Same target probability

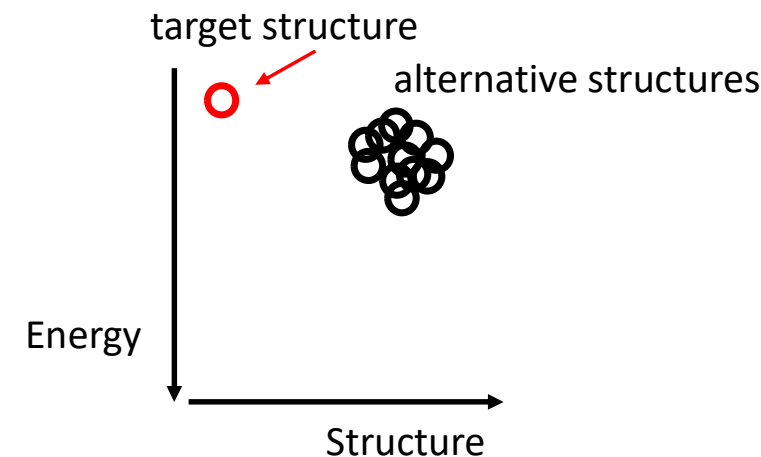
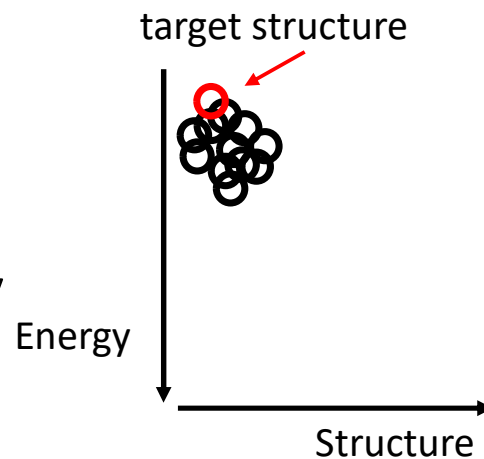


2. Objective Functions - Target Probability

- Probability that sequence s folds into structure p
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- Same target probability

- But one is a significantly better design



2. Objective Functions - Target Probability

- Probability that sequence s folds into structure p
- Sounds good, but RNAs don't fold into a single structure
- Same target probability
- But one is a significantly better design
- Also not a good optimization function if far away from the optimum

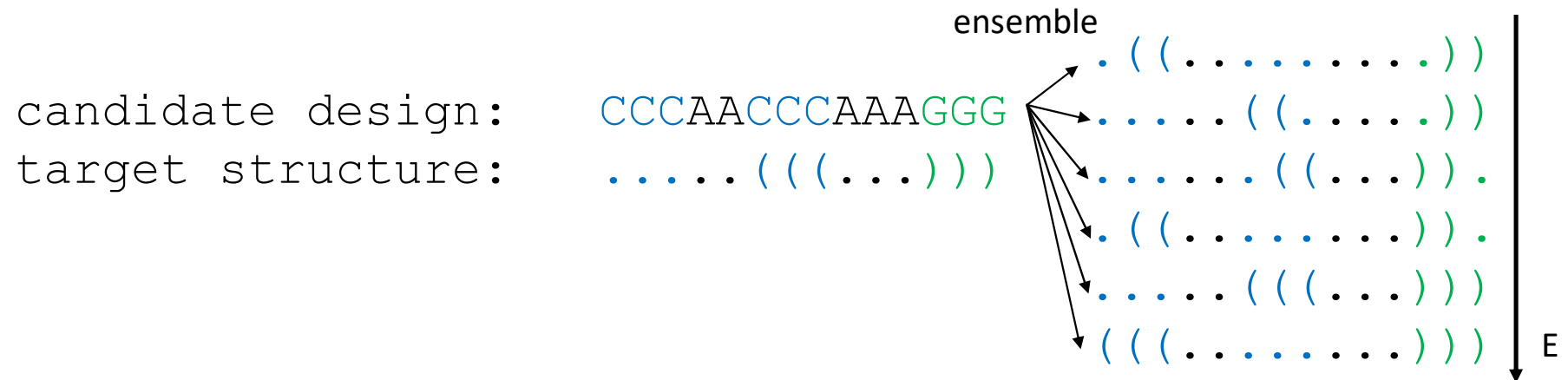
2. Objective Functions - Ensemble Defect

- Average number of incorrect nucleotides

candidate design: CCCAACCCAAAGGG
target structure: (((...)))

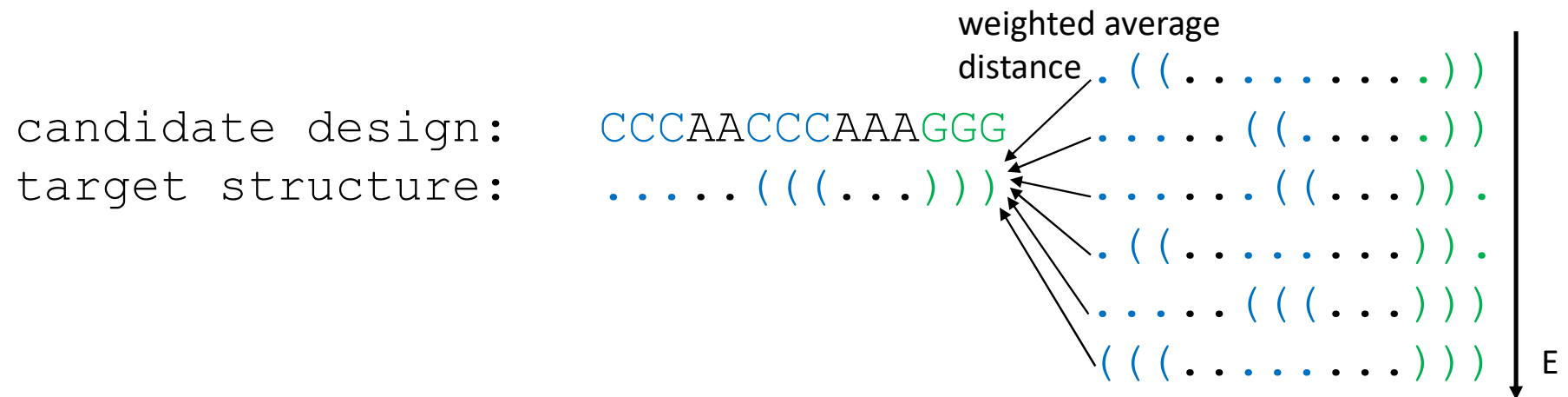
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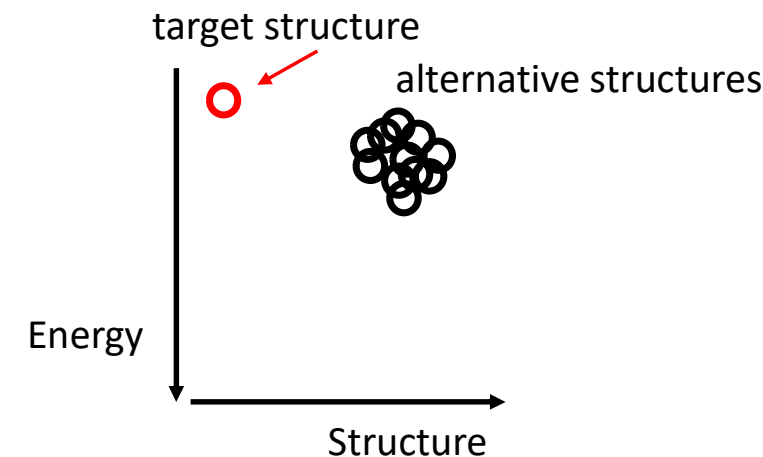
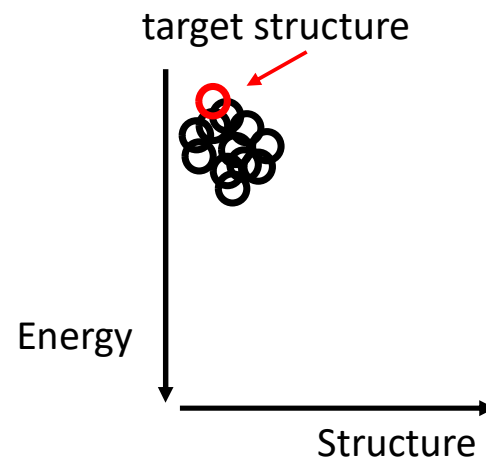
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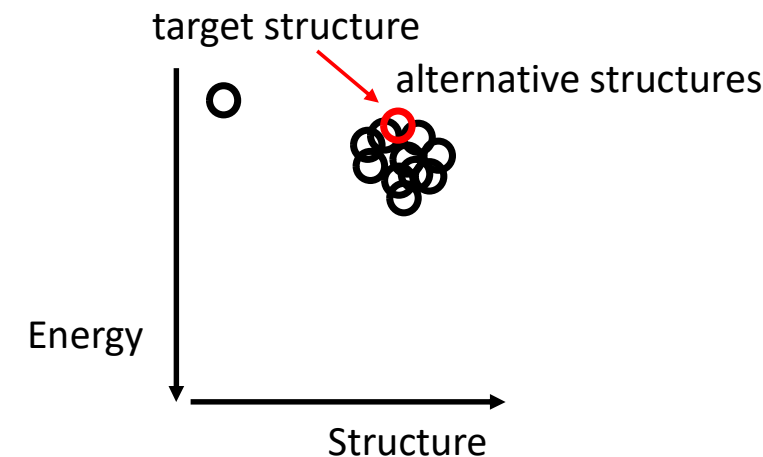
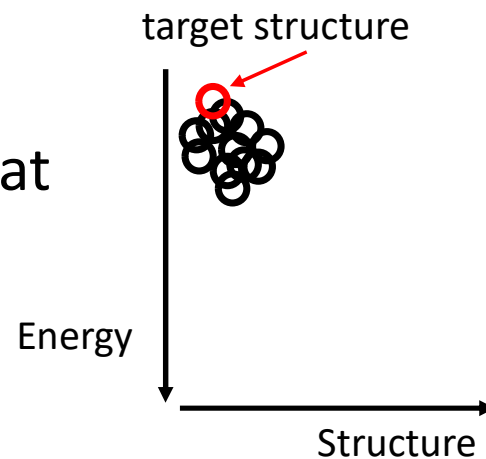
- Average number of incorrect nucleotides
- A sequence that can fold into many structures similar to the target structure has a good ED



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- Harder to find design that has the target as MFE



2. Objective Functions - Ensemble Defect

- Average number of incorrect nucleotides
- A sequence that can fold into many structures similar to the target structure has a good ED
- Harder to find design that has the target as MFE
- Works if far away from the optimum

2. Objective Functions - Ensemble Defect

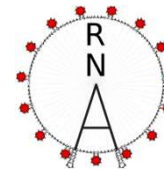
- Average number of incorrect nucleotides
- A sequence that can fold into many structures similar to the target structure has a good ED
- Harder to find design that has the target as MFE
- Works if far away from the optimum
- Start with ED; Use probability to make fine-grained optimizations

Designing xrRNAs

1. Characterize essential features conserved in biological xrRNAs
2. Sample sequences with those features using Infrared
3. Validate candidate designs in-silico

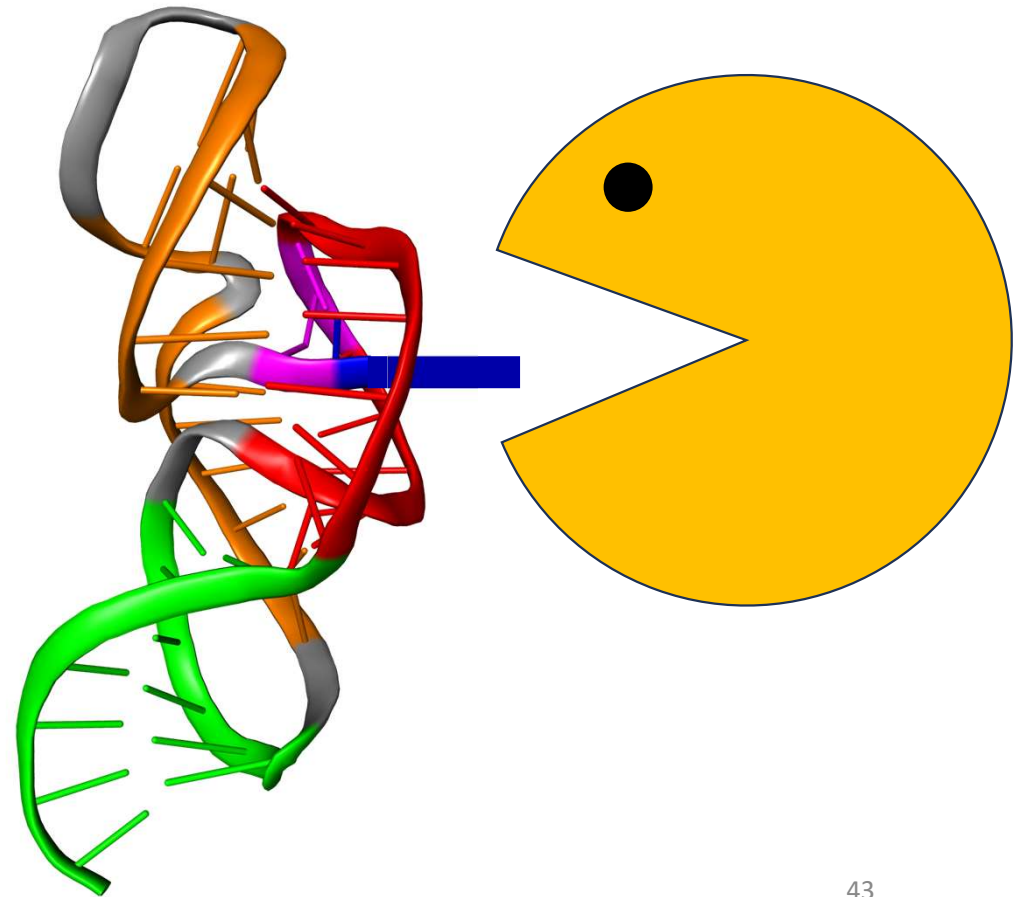


SimRNA



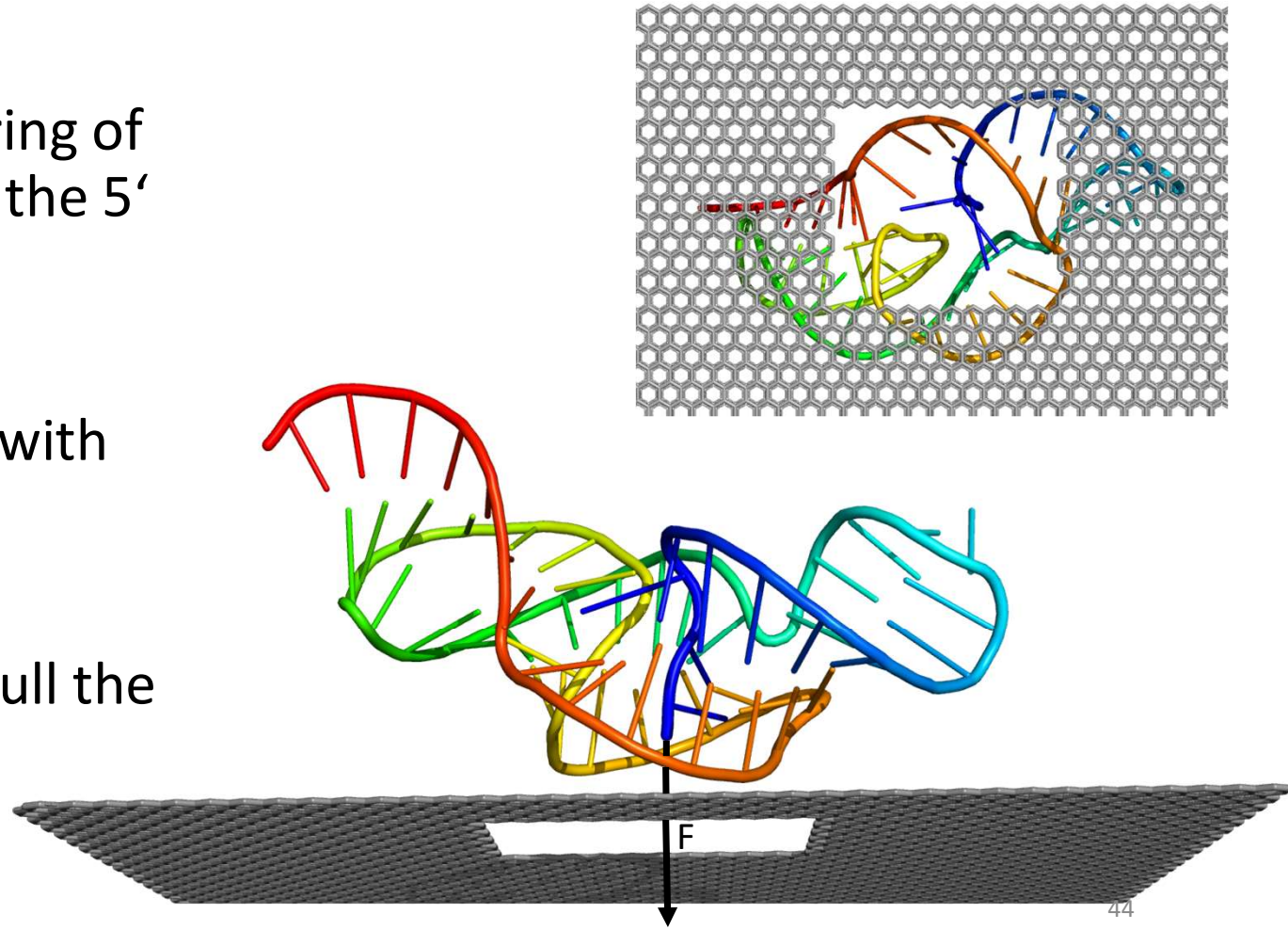
3. In-Silico Validation Using Steered MD

- Xrn1 braces against the ring of the xrRNA and can't pull the 5' end out

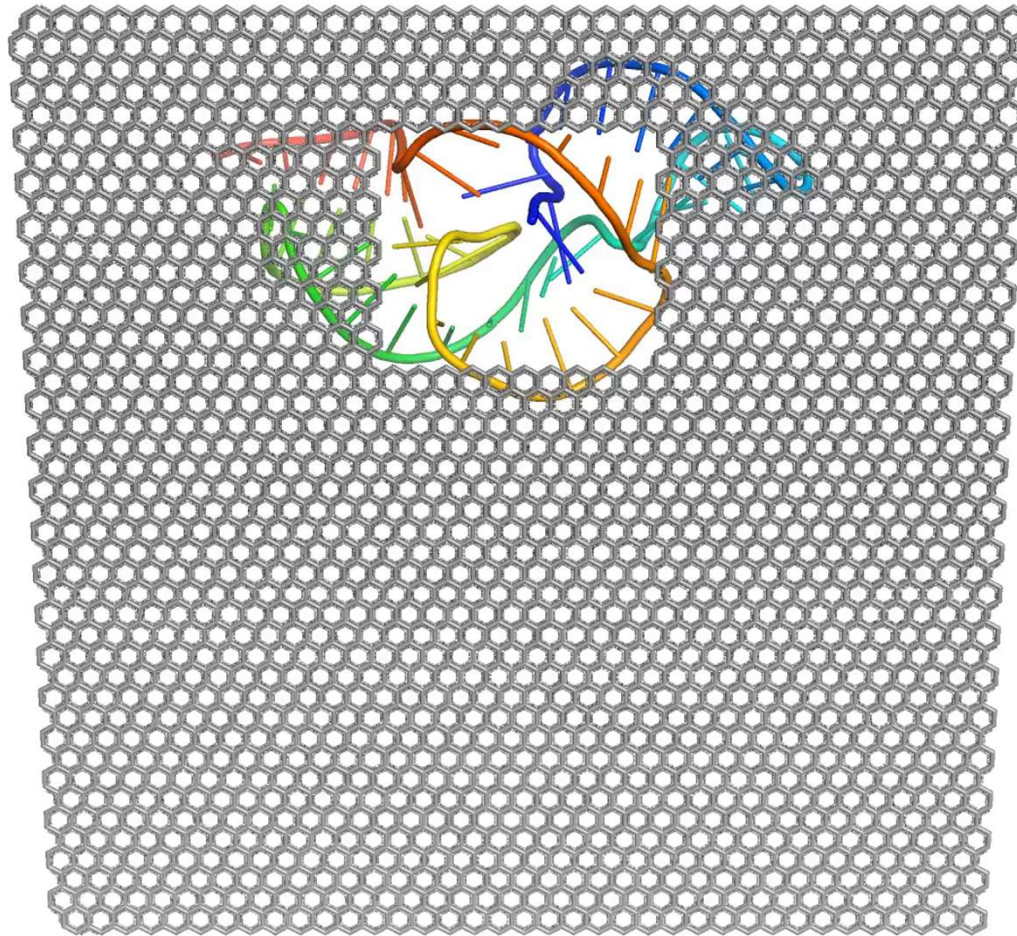


3. In-Silico Validation Using Steered MD

- Xrn1 braces against the ring of the xrRNA and can't pull the 5' end out
- Possible to approximate with steered MD
- Use a force gradient to pull the 5' end through a pore



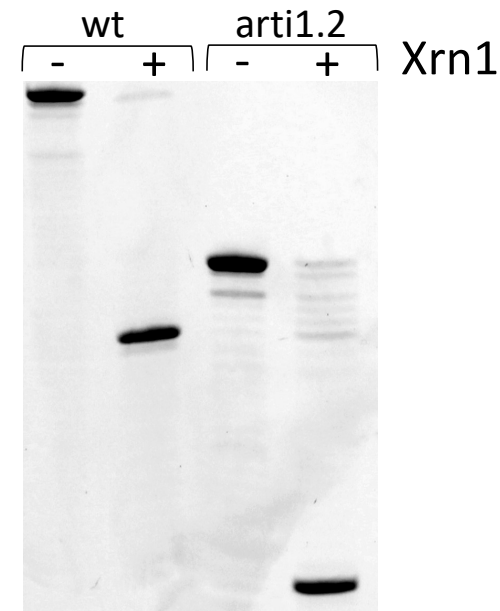
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MD Simulation, 400 pN external force, 2fs timestep, Amber OL3 RNA FF, 500 ns, implicit solvent GBn2, 0.15 mol/L Salt Conc.

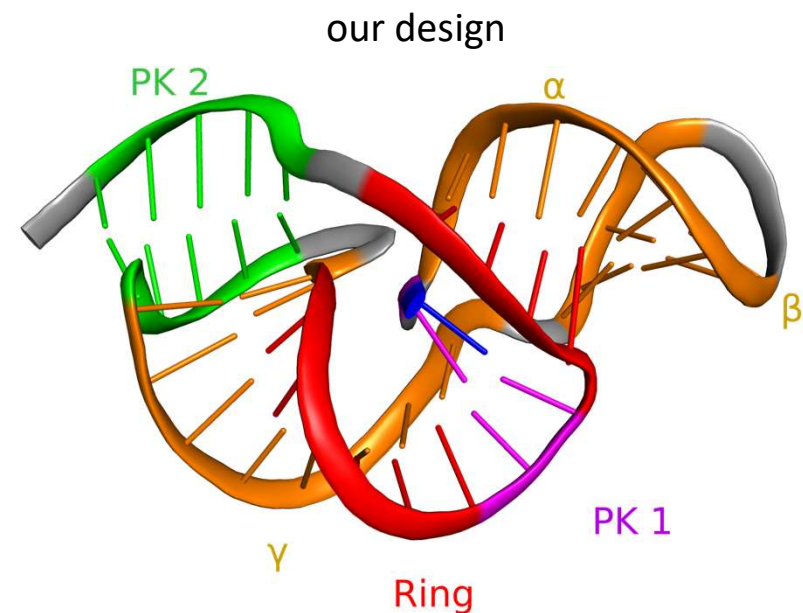
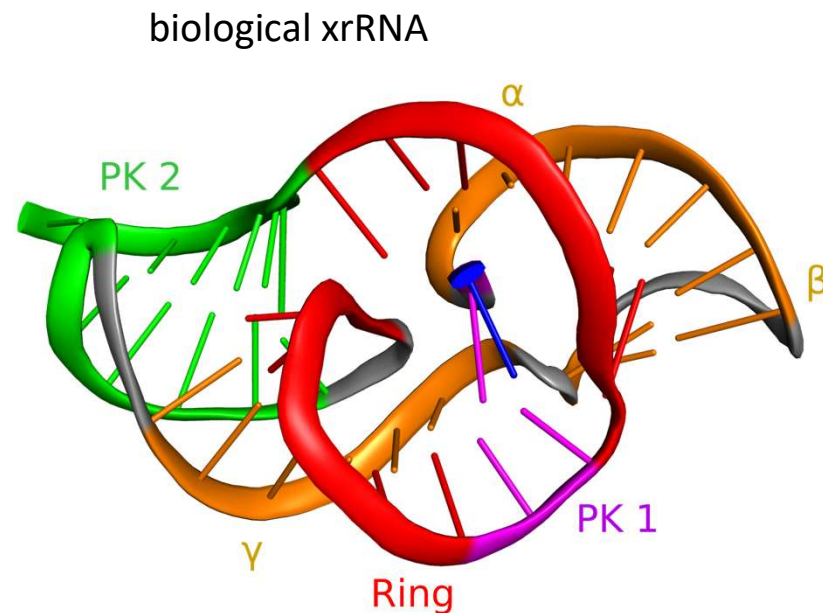
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4. Test designs in-vitro



4. In-Vitro Experiments Validate Designs

- In-vitro experiments show our artificial xrRNA exhibits resistance to Xrn1 like biological examples



Acknowledgments

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Jule Walter

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Thank you for your Attention