Our research aims to elucidate the structure of the HU-Junction complex to clarify the structural elements that lead to HU recognition of the Holliday Junction.

Elucidating the Structure of the HU-Junction Complex

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Methods & Results

- Purifying the HU Protein
- *E. coli* cells grown in Terrific Broth Media
- Pre-Induction, Post-Induction, and Fractions were run on 14% SDS-PAGE Gels (1)
- Purification done with SP Sepharose and Heparin HP Columns (2)

(1) SDS-PAGE – Mini Growths

(2) SDS-PAGE – SP Sepharose Column

(2) SDS-PAGE – Heparin HP Column

Pre Post F1 F3 F5 F7 F9 F11 F13 F15 F17 F19 F21 F23



HU

- a histone-like protein
- one of the most abundant proteins in *E. coli*
- significant roles in DNA packaging, recombination, replication, and repair
- binds with high affinity, in a non-sequence specific manner, to Holliday or 4-Way Junction



Holliday (HJ) or 4-Way Junction (4WJ)

- important intermediate in recombination and repair
- J20: an immobile Holliday Junction with 20 base pairs per strand



HU Standard Curve





X-Ray Crystallography

- used to visualize structural features of biomolecules
- will provide atomic details of the HU-HJ interaction



Future Directions

Crystal Trays



Determine stoichiometry of HU binding to J20

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Increasing [HU]

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Objectives

- Currently we are generating protein for crystal screens
- Assay protein to determine concentration for DNA binding activity
- Screen a wide range of conditions for trays Optimize screening conditions to generate diffraction-quality

- Is HU binding to J20 2:1, 4:1, 1:1?

Try crystal screens with Anabaena HU

- Cyanobacteria
- Homodimer
- Crystal structure of AHU and DNA
- Try crystal screens with different metal ions such as lanthanides
- Crystallophores, a part of the lanthanide family, have shown to promote crystal nucleation and solve the phase problem¹

⁵⁷La ⁵⁸Ce ⁵⁹Pr ⁶⁰Nd ⁶¹Pm ⁶²Sm ⁶³Eu ⁶⁴Gd ⁶⁵Tb ⁶⁵Dy ⁶⁶Dy ⁶⁷Ho ⁶⁸Er ⁶⁹Tm ⁷⁰Yb ⁷¹Lu ^{174,966}



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