

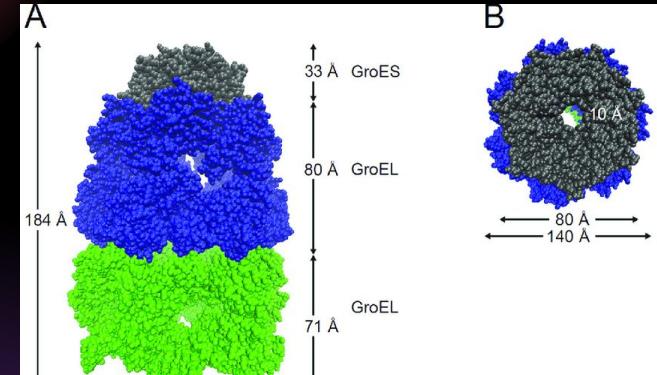
Haytham Zaami

ENM Analysis of GroEL Transitions in *E. coli*

What is GroEL?

GroEL is bacteria chaperone protein (typically found in E. Coli)

- Required for assisting in protein folding
- One part of two-part chaperone
- Put protein in chamber, come out folded correctly



Carlsen, Thomas & Bennike, Tue & Christiansen, Gunna & Birkelund, Svend. (2013). A role for anti-HSP60 antibodies in arthritis: a critical review. OA Arthritis. 1. 10.13172/2052-9554-1-2-879.

Additional animation:
<https://www.youtube.com/watch?v=-NcNeLc1mo>

GroEL–GroES chaperonin complex

T

T->R

- Unfolded protein binds inside one of GroEL's rings
- Taut to Relaxed
- GroES 'cap' not on yet
- Salt Bridges broken to conform

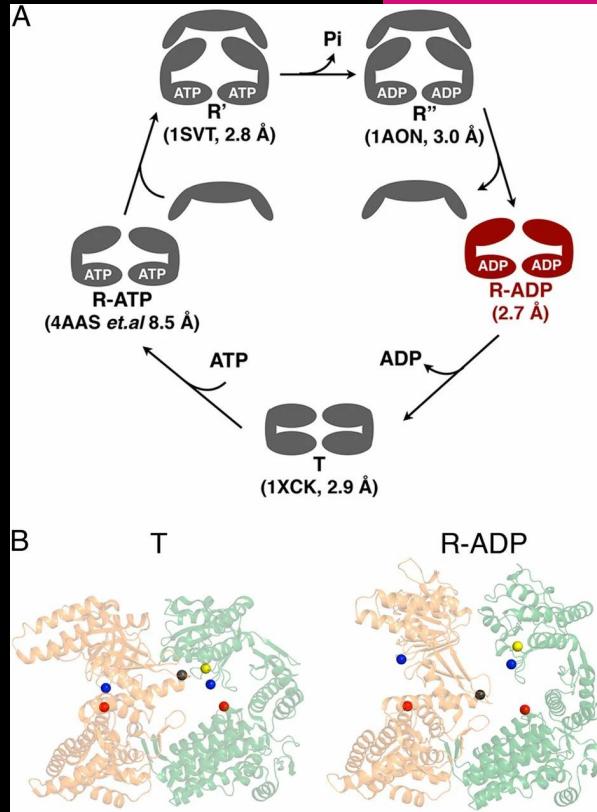
Bind with GroES -
After ATP Hydrolysis

R->R'

- GroES put on

R'->R''

- Convert ATP to ADP after GroES on
- Won't cover during research

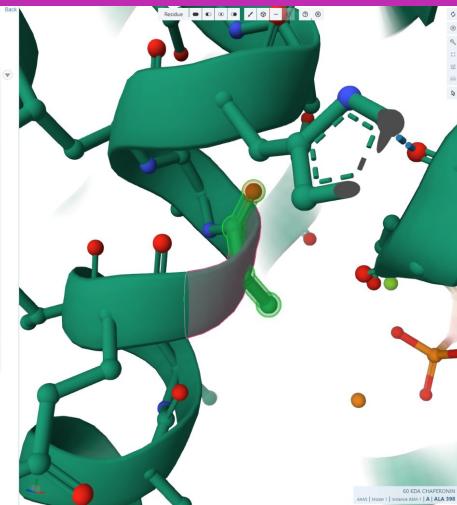
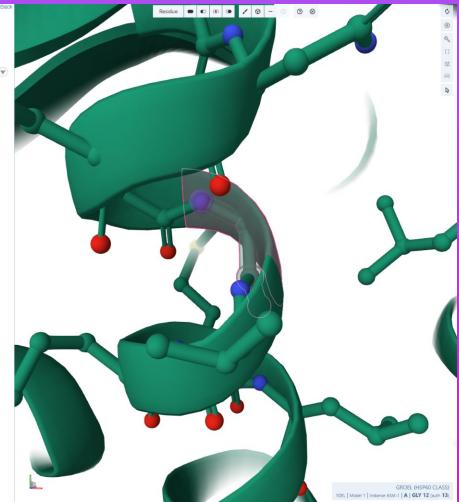


X. Fei, D. Yang, N. LaRonde-LeBlanc, & G.H. Lorimer, Crystal structure of a GroEL-ADP complex in the relaxed allosteric state at 2.7 Å resolution, Proc. Natl. Acad. Sci. U.S.A. 110 (32) E2958-E2966, <https://doi.org/10.1073/pnas.1311996110> (2013).

Proteins Used/ Caveates

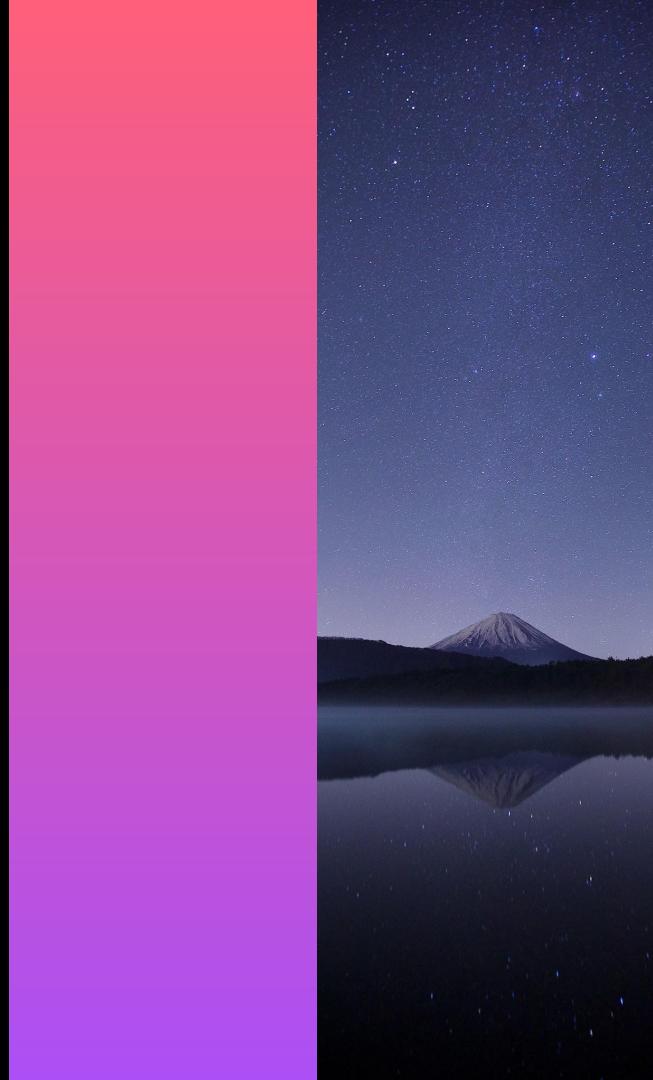
- T State: PDB ID 1OEL
 - Mutated; potentially for protein stabilization/disease study
 - Will neglect mutation
- R State: 4AAS
 - Mutated
 - Will neglect mutation
- R' State: 1SVT
 - Non Mutated

*Mutations could potentially impact research, but minimally



Central Topic:

How well do different types of Normal Mode Analysis predict the transitions that the chaperone protein goes through?



Type of analysis used

“

Analysis to see if theoretical motion
matches biological reality

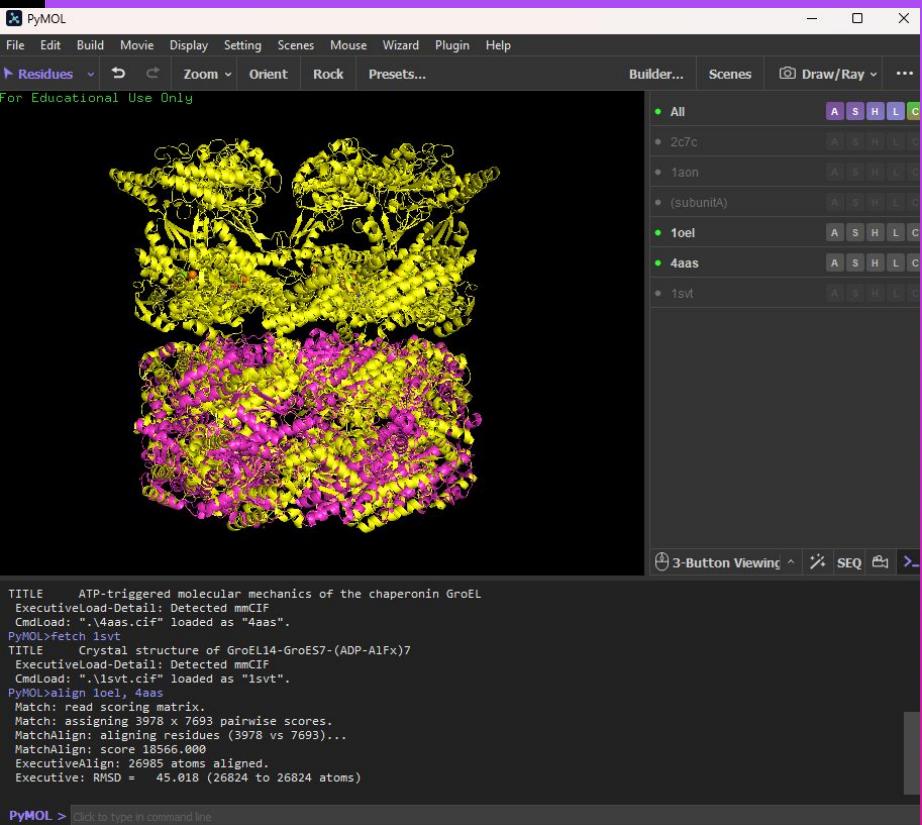
- ANM
- GNM
- *parameter-free ANM
- *RTB

<http://www.bahargroup.org/prody/>



Predictions

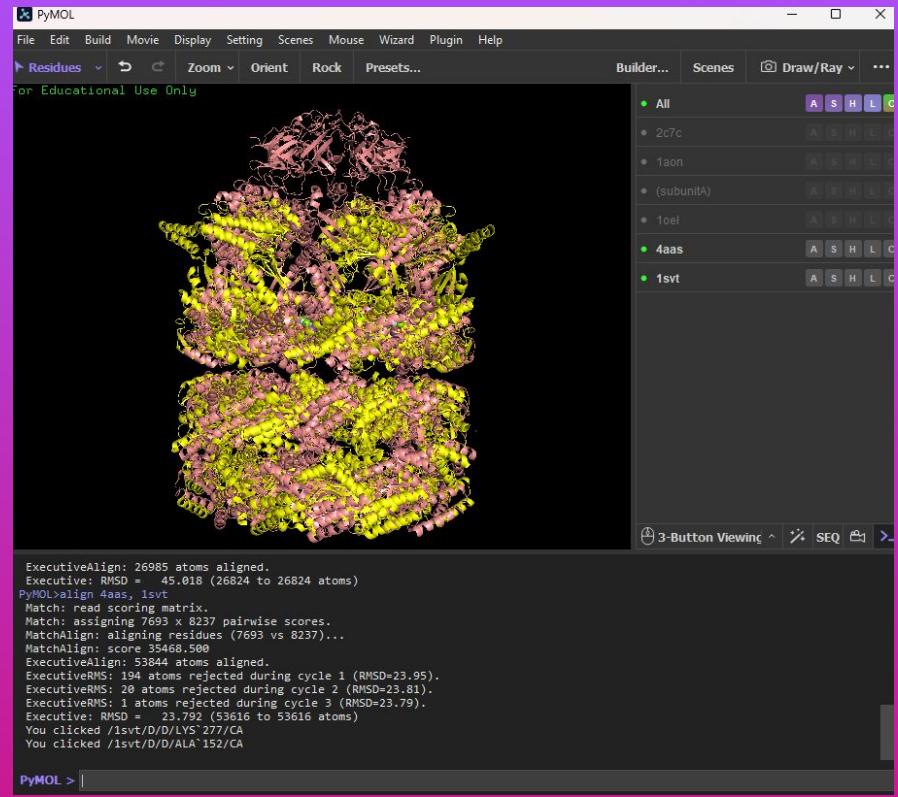
- 1OEL will conform similar, stretching
- May need to combine low frequency modes



1OEL - magenta
4AAS - Yellow

Predictions

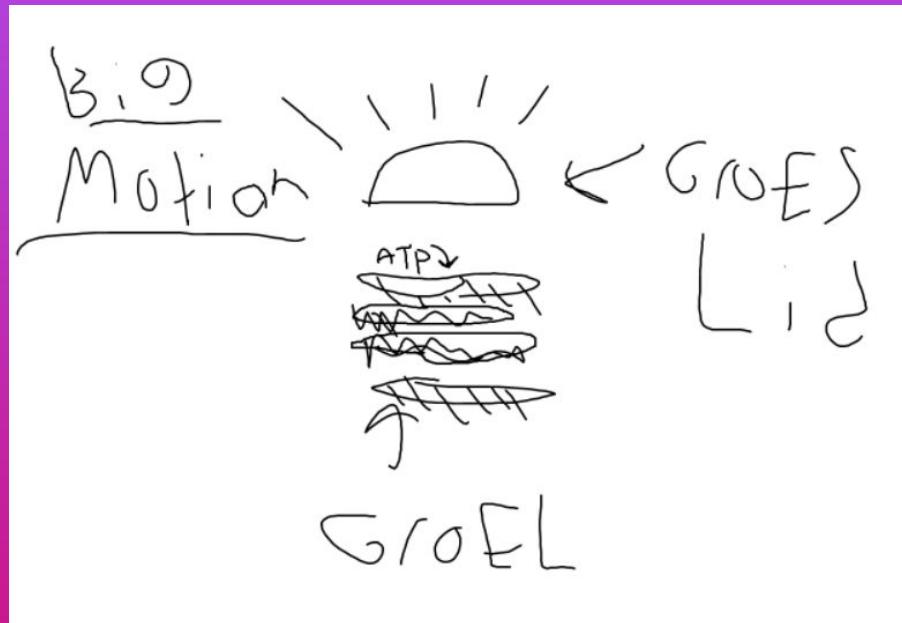
- 4AAS does not have the GroEL cap, will not get it from doing NMA
 - Has opening at top for ATP and protein to enter
- More overlap as structures similar in size/width



4AAS - Yellow
1SVT - Pink/Peach

Anticipated Issues

- Computation time
 - Based on method
- ATP Energy
 - NMA Constraint
 - Single energy minimum
- Large Scale motion prediction accuracy



Timeline of research*

NMA on 1OEL

- Try different methods
- Compute different modes
- Test for accuracy

NMA on 4AAS

- Try different methods
- Obtain different modes
- Test for accuracy

Visualize

- Visualize data to obtain insights
- Interpret accordingly
- Make changes if needed

Put Together

- Make inferences from findings

Current sources

Inspiration for proteins to use

[Crystal structure of a GroEL-ADP complex in the relaxed allosteric state at 2.7 Å resolution | PNAS](#)

Python library for analysis

[ProDy Project - Protein Dynamics and Sequence Analysis](#)

Chaperone protein transitions

[Dynamics of allosteric transitions in GroEL - PubMed](#)

More soon!