

Investigation of beta-Amyloid-(1-42)-DMPC lipid-protein system in Alzheimer diseased cells by Raman Spectroscopy and Molecular Dynamics

Supervised By:

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Presented by:

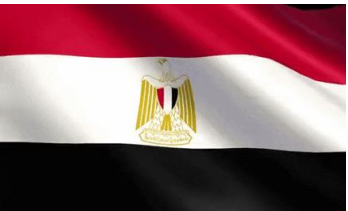
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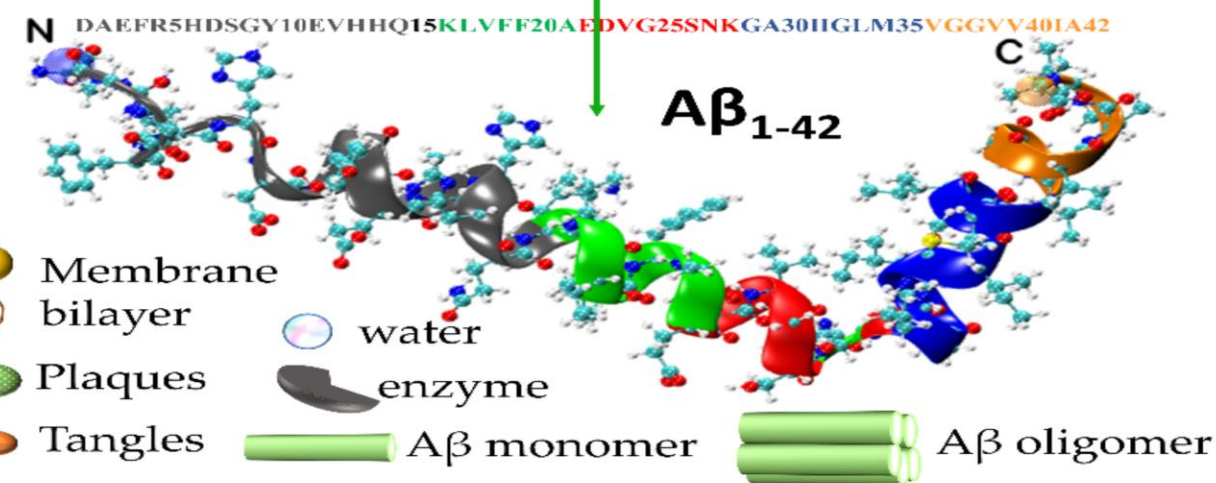
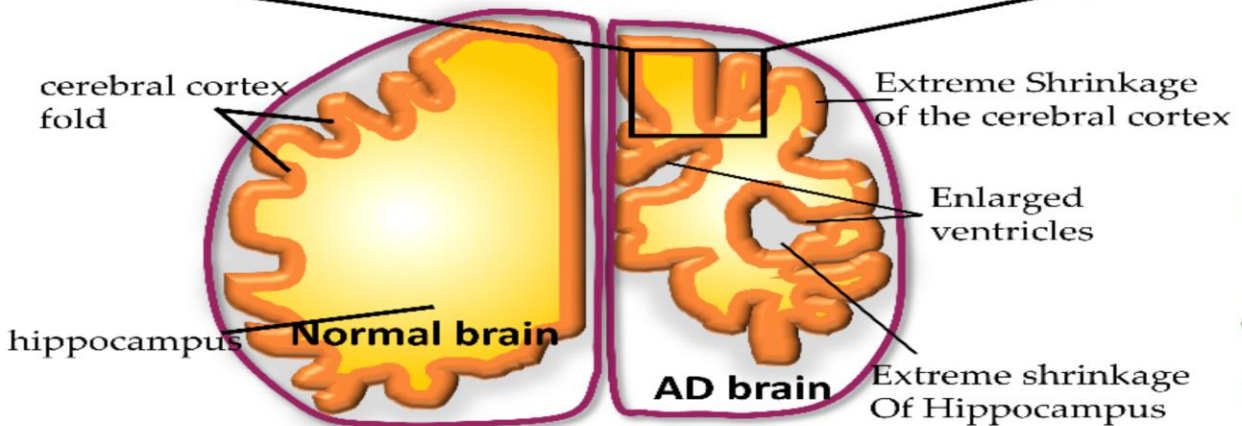
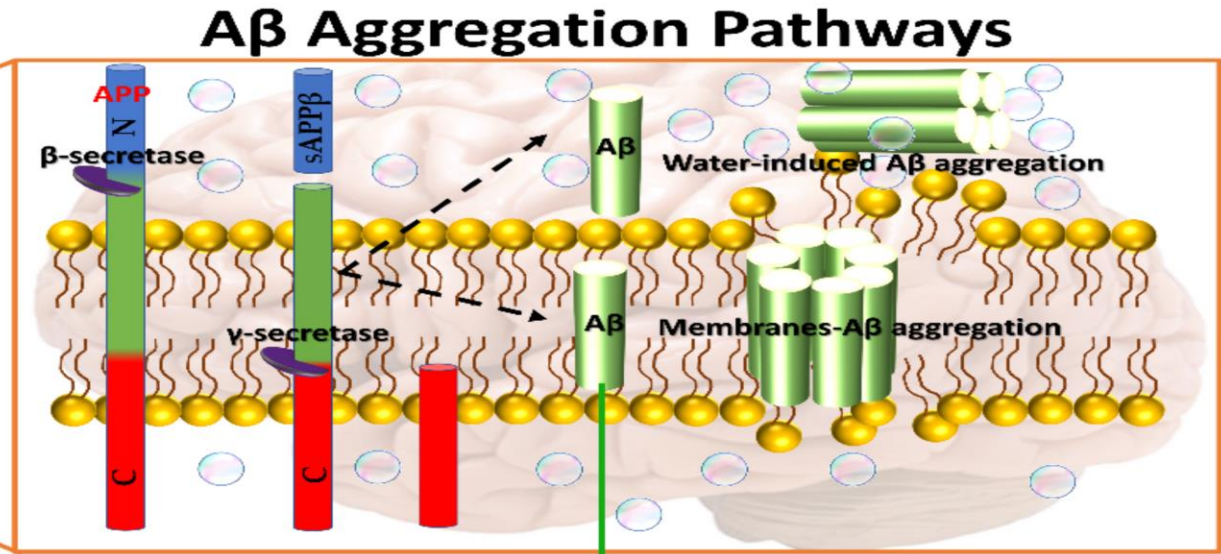
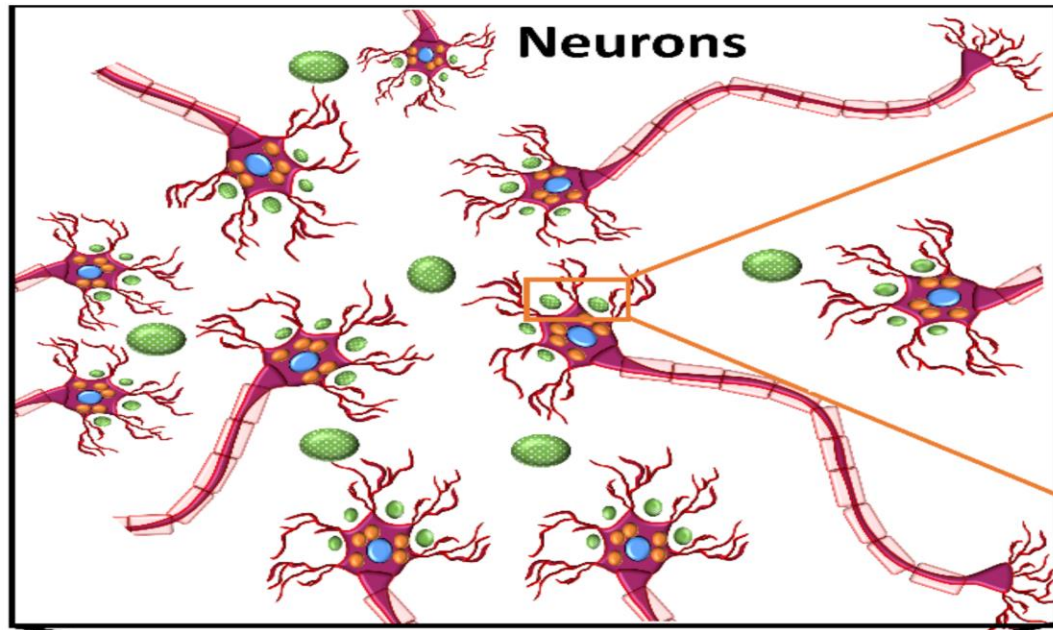
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The Grand Scheme of Our Project

Beta-amyloid 1-42 → Neurons accumulations → peptide aggregation in the bilayer membrane → Alzheimer

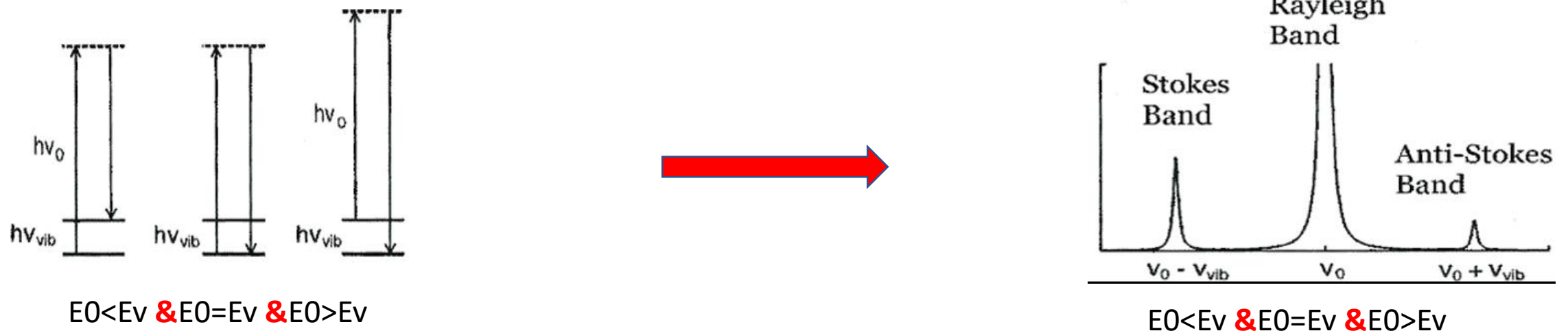


The Raman effect

Phenomenon in physics and spectroscopy where light interacts with matter, causing a shift in its energy level and resulting in the scattering of light with different wavelengths.



Diagram of the Rayleigh and Raman Scattering Processes



Raman spectra

Into Raman spectra:

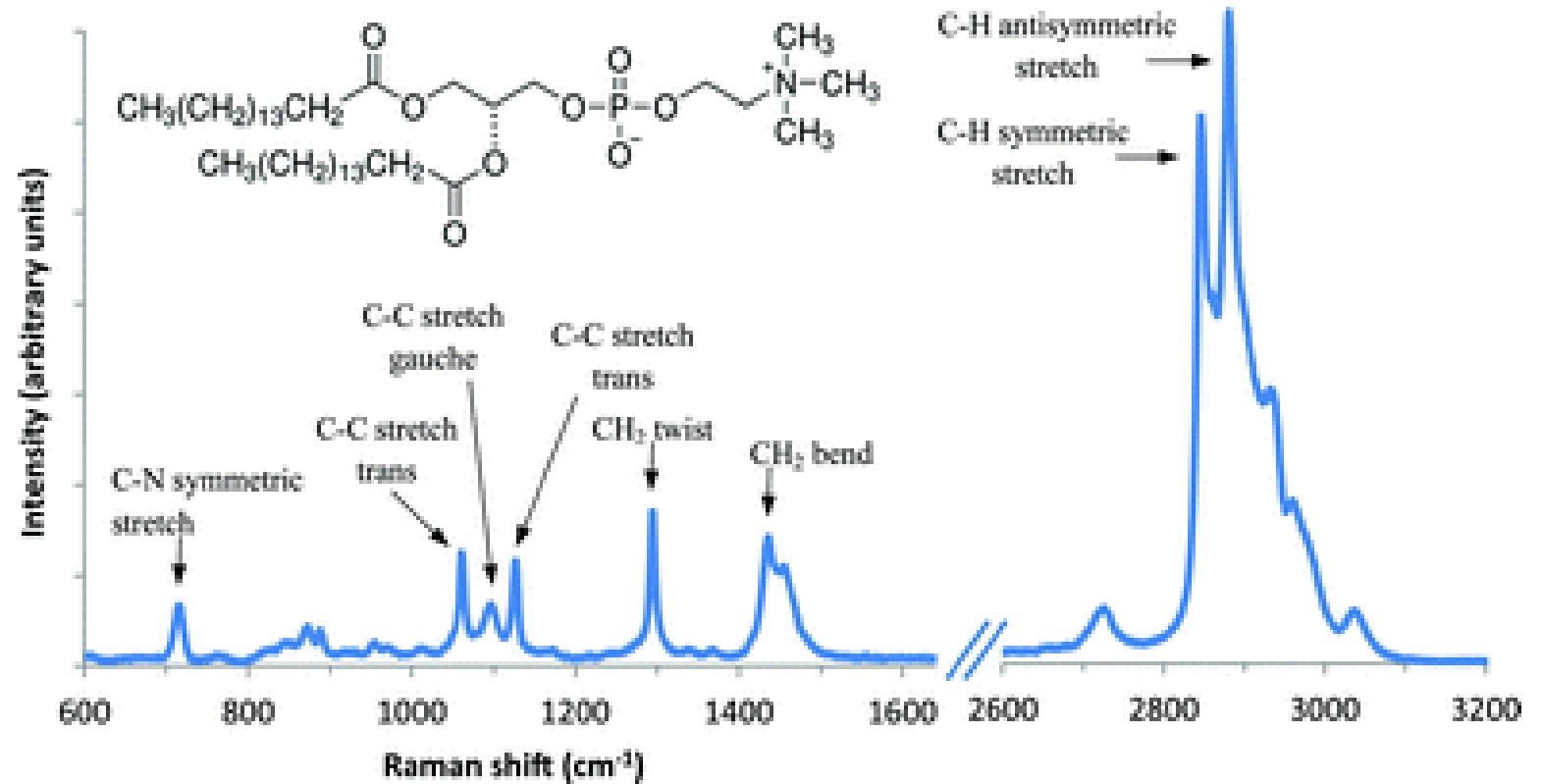
- ✓ Raman Shift:
- ✓ Vibrational Frequencies:
- ✓ Peak Intensity
- ✓ Bonds Between Atoms and Material Fingerprint

Raman spectra gives:

- ✓ Information about the molecular composition structure, and dynamics of materials
- ✓ Study solid, liquid and gaseous samples
- ✓ Fingerprint spectroscopy

Applications:

- ✓ Chemical analysis
- ✓ Material characterization
- ✓ Biomedical diagnostic
- ✓ Imaging: pharmaceuticals, forensics, art, etc



Life sciences



Materials science



Chemical sciences



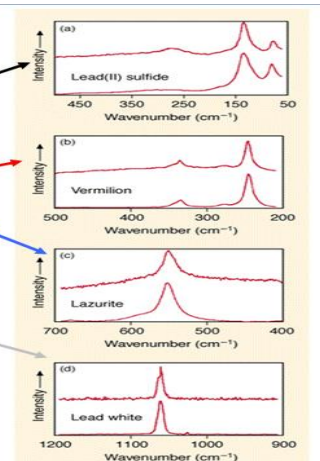
Earth sciences



Analytical sciences

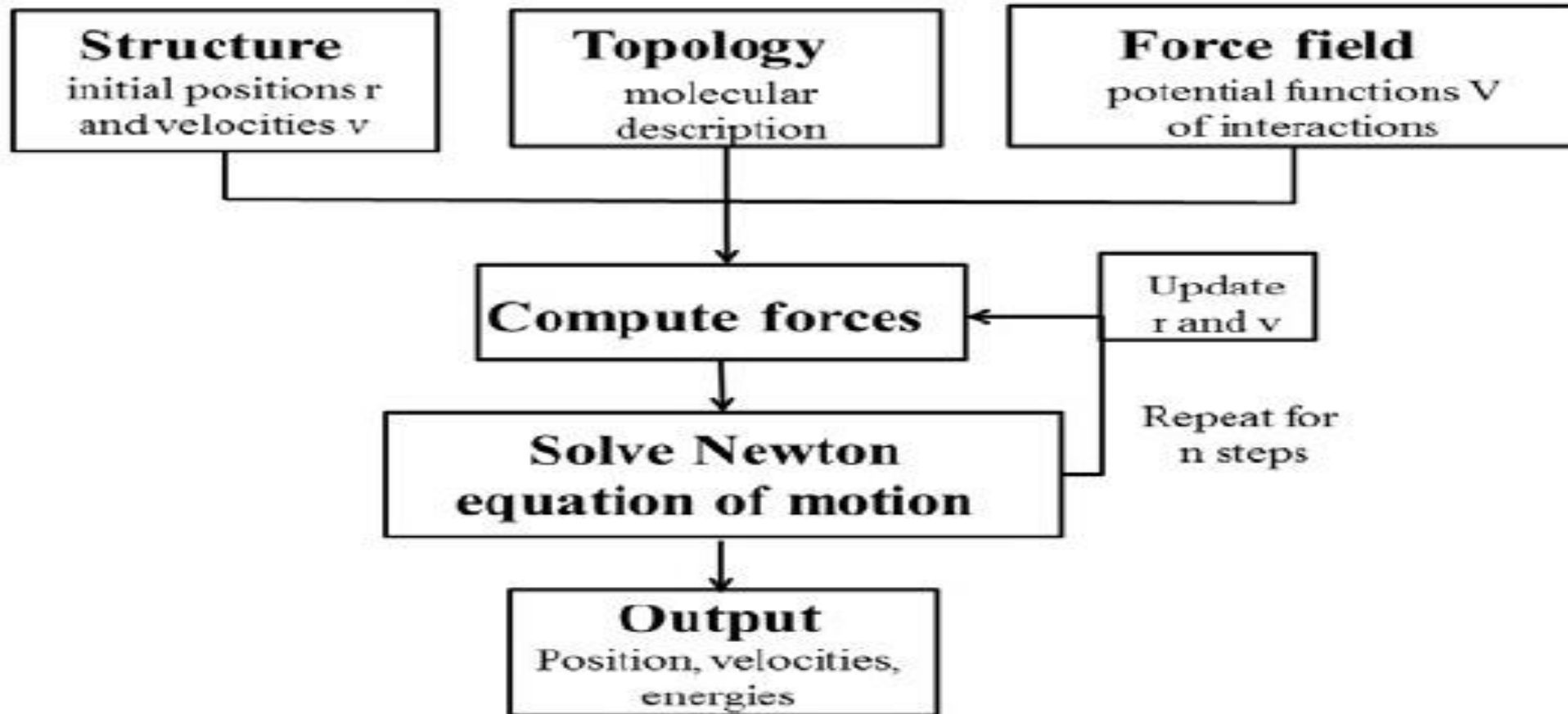


Paintings originality test



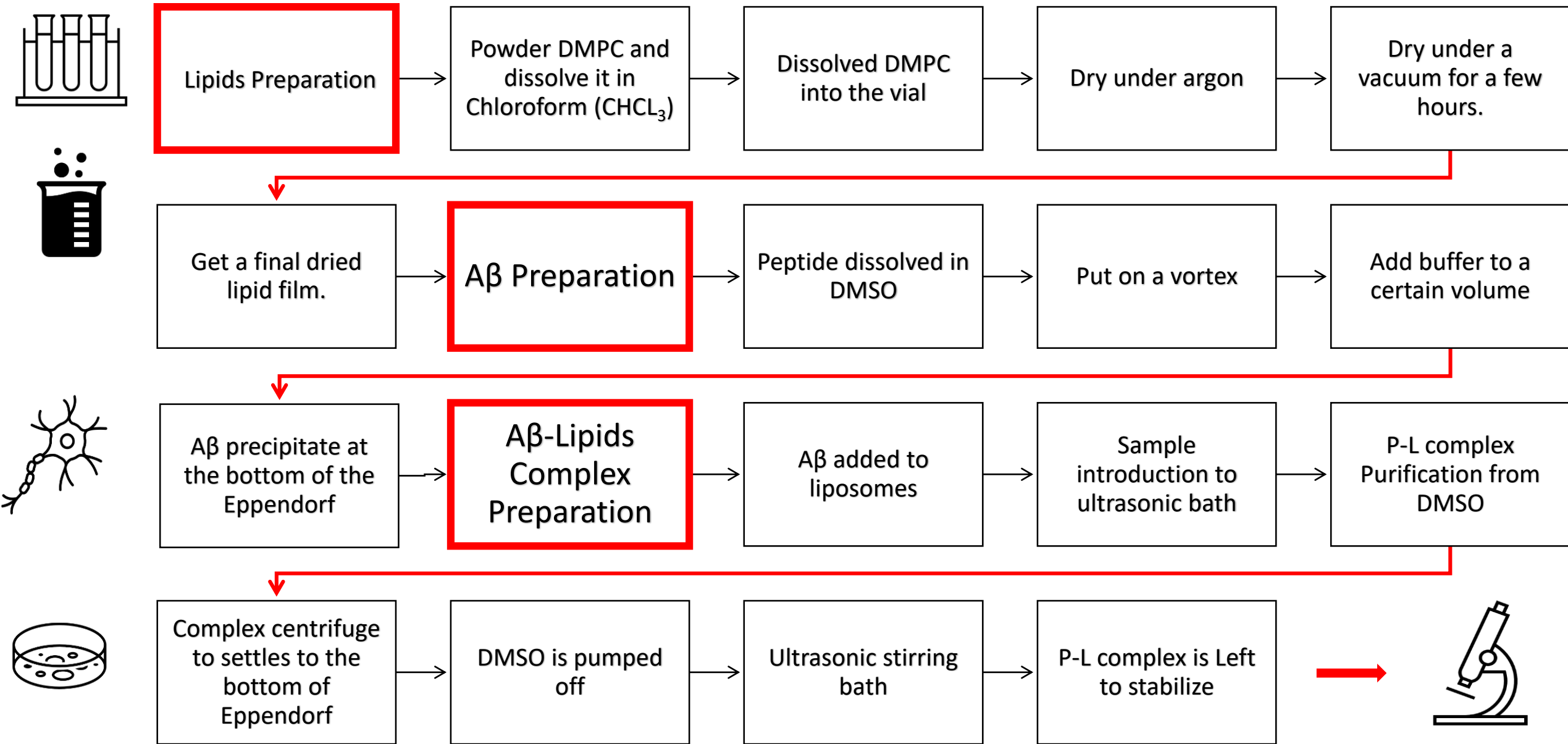
Molecular dynamics (MD)

Molecular dynamics is a computational simulation technique used to study the motion and behavior of atoms and molecules over time. It involves solving the equations of motion for each particle in a system to investigate their positions, velocities, and interactions, providing insights into the dynamic properties and processes of molecular systems at the atomic level

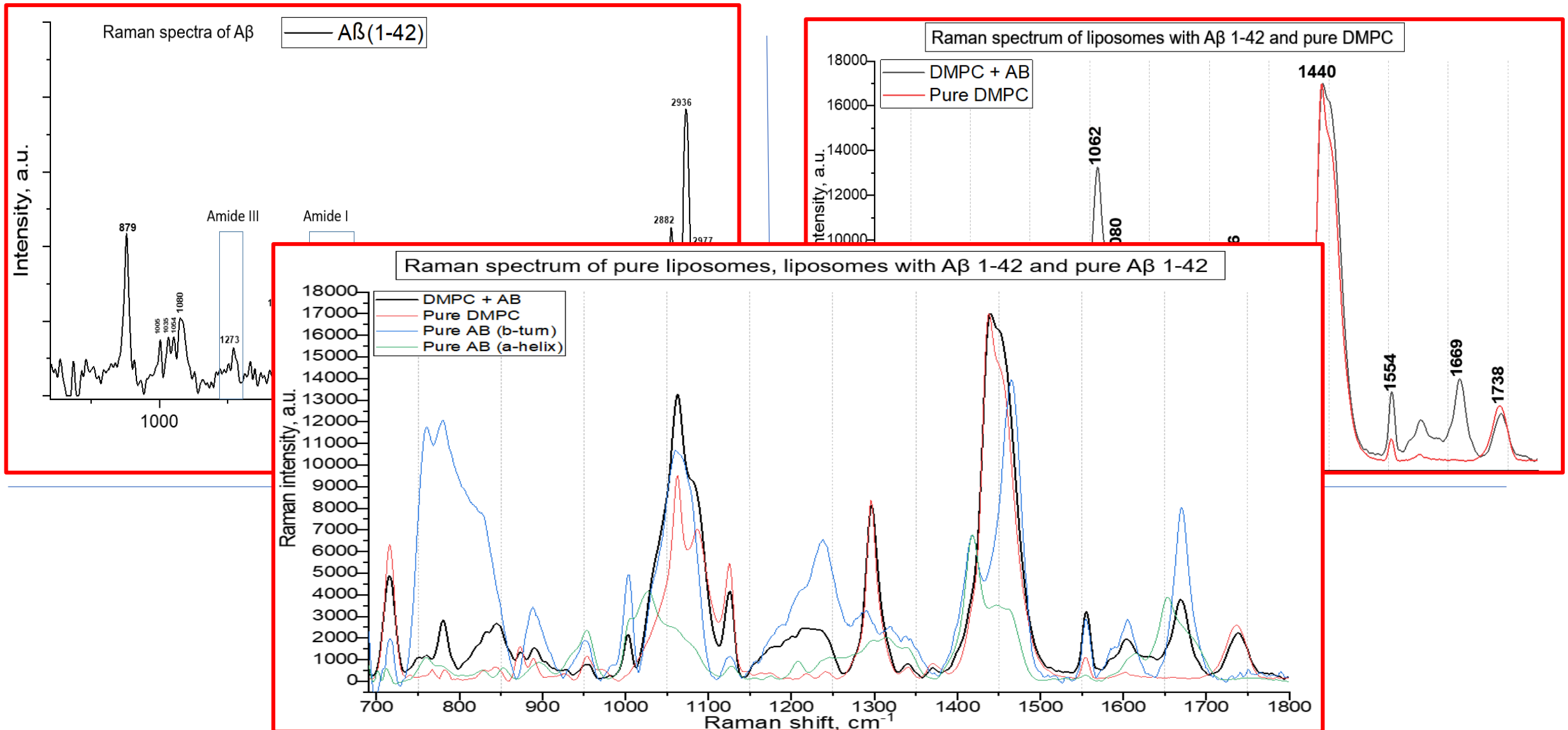


For our Protein-Lipid complex: MD will predict how every atom in a protein or p-L molecular system will move over time.

P-L System prep-protocol .

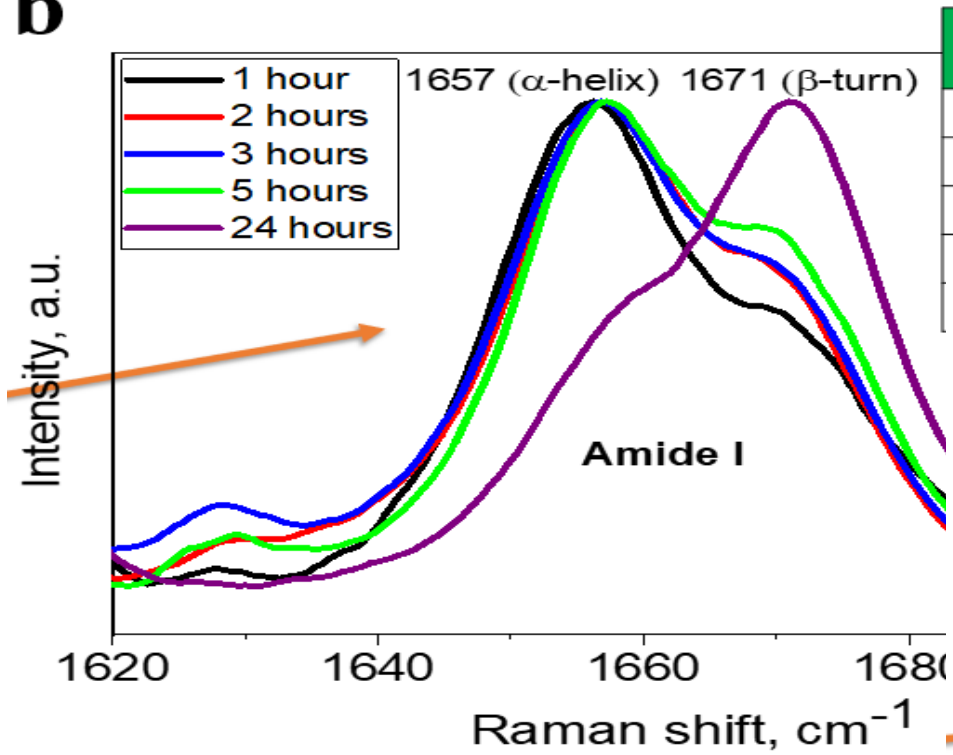


Spectroscopic analysis Results



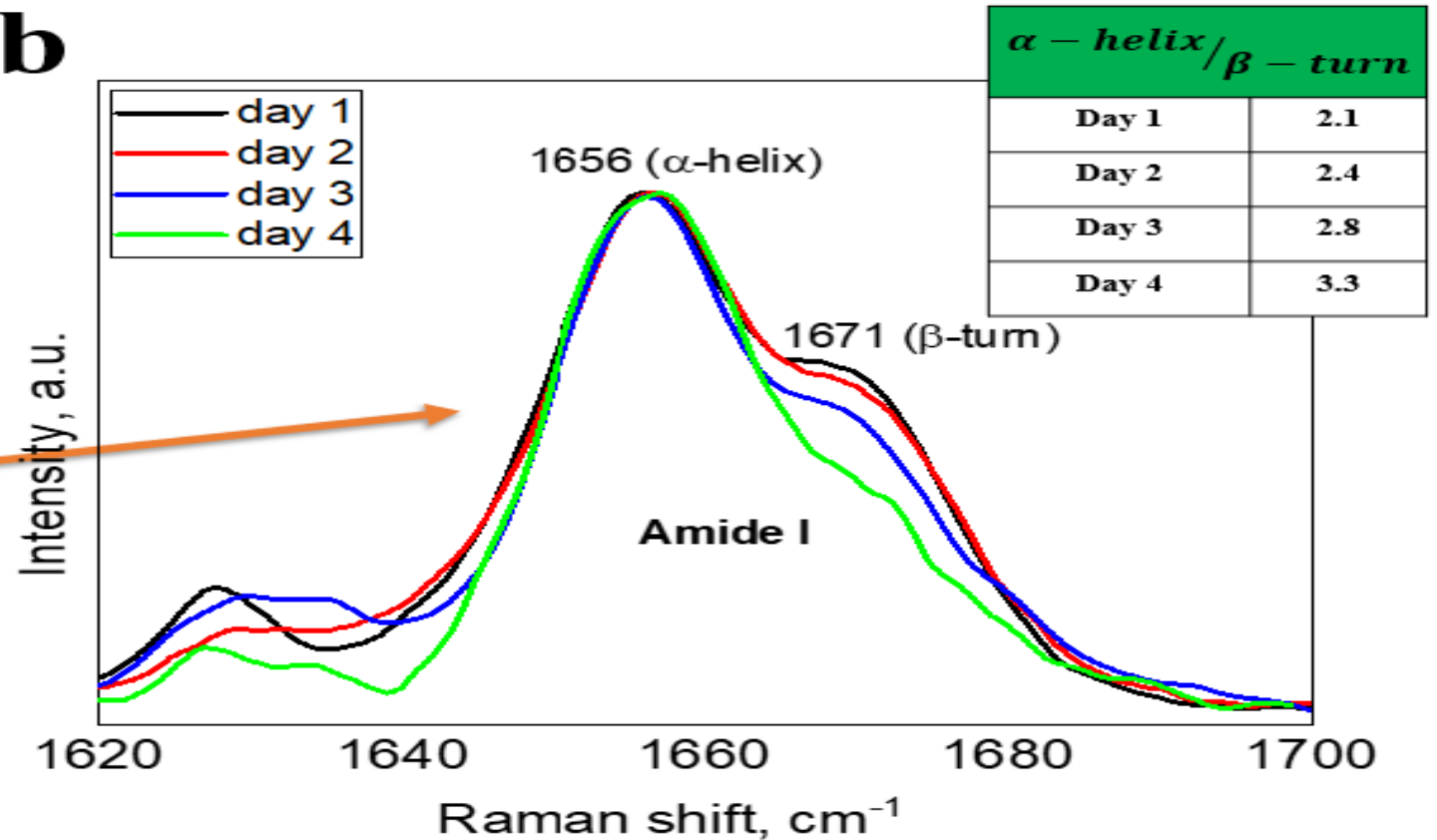
Spectroscopic analysis Results

b



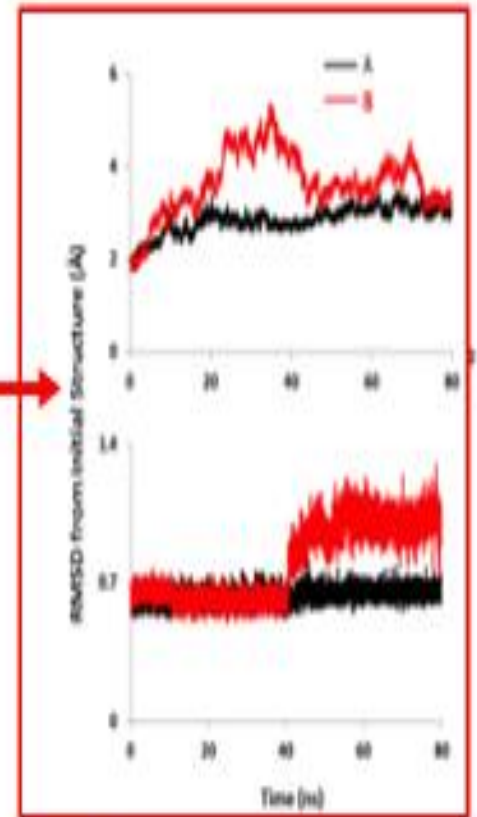
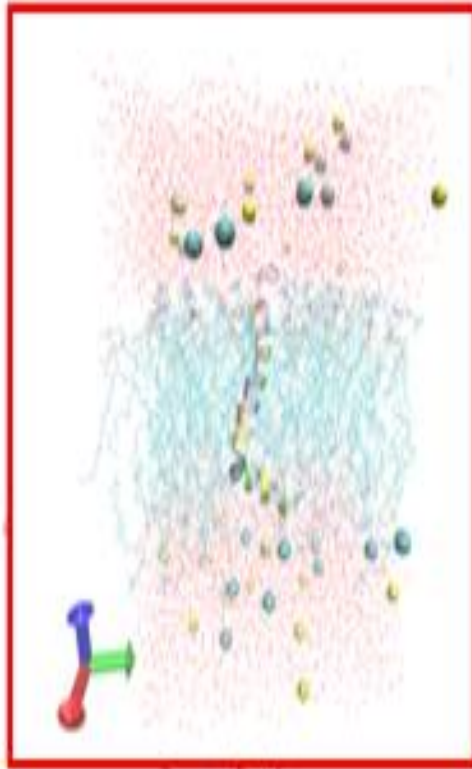
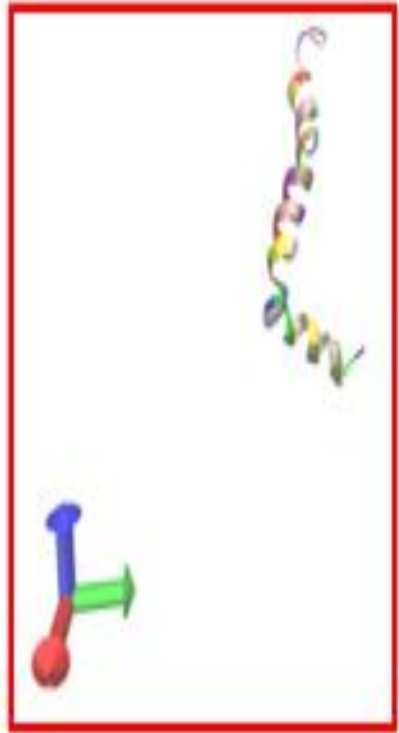
α -helix/ β -turn	
1 hours	2.6
2 hours	2.3
3 hours	2.2
5 hours	1.6

b



α -helix/ β -turn	
Day 1	2.1
Day 2	2.4
Day 3	2.8
Day 4	3.3

MD Workflow



1. Starting Structure

Structure Check
Protonation State
Solvation
Adding Salts

2. Preparation of the Simulation System

Select Simulation Protocol

3. Simulation Run

Post-processing

4. Trajectory Analysis

MD analysis Results

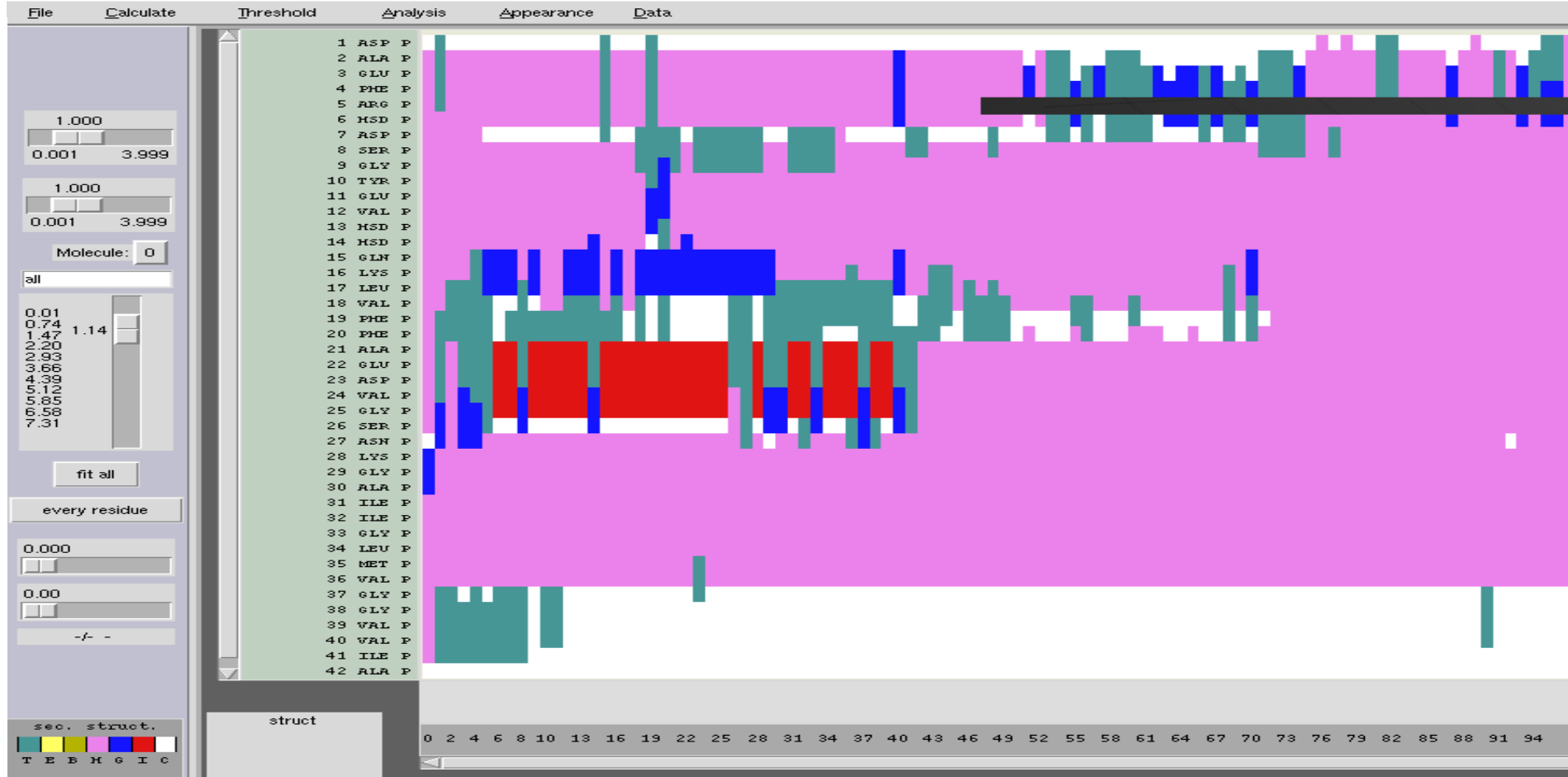
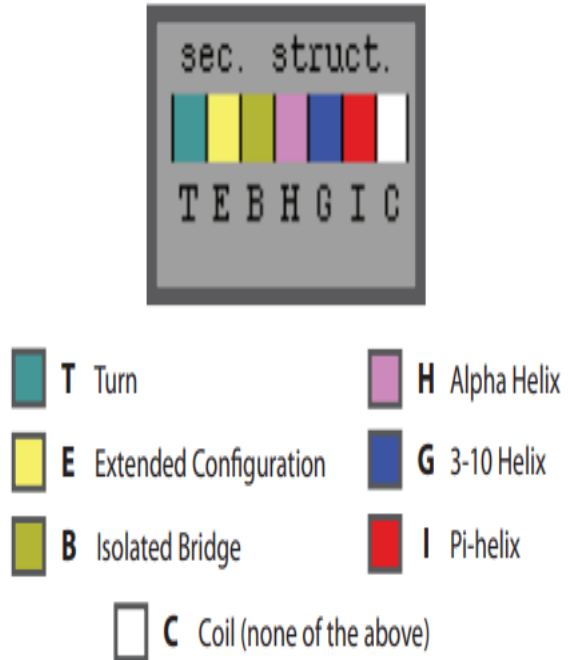
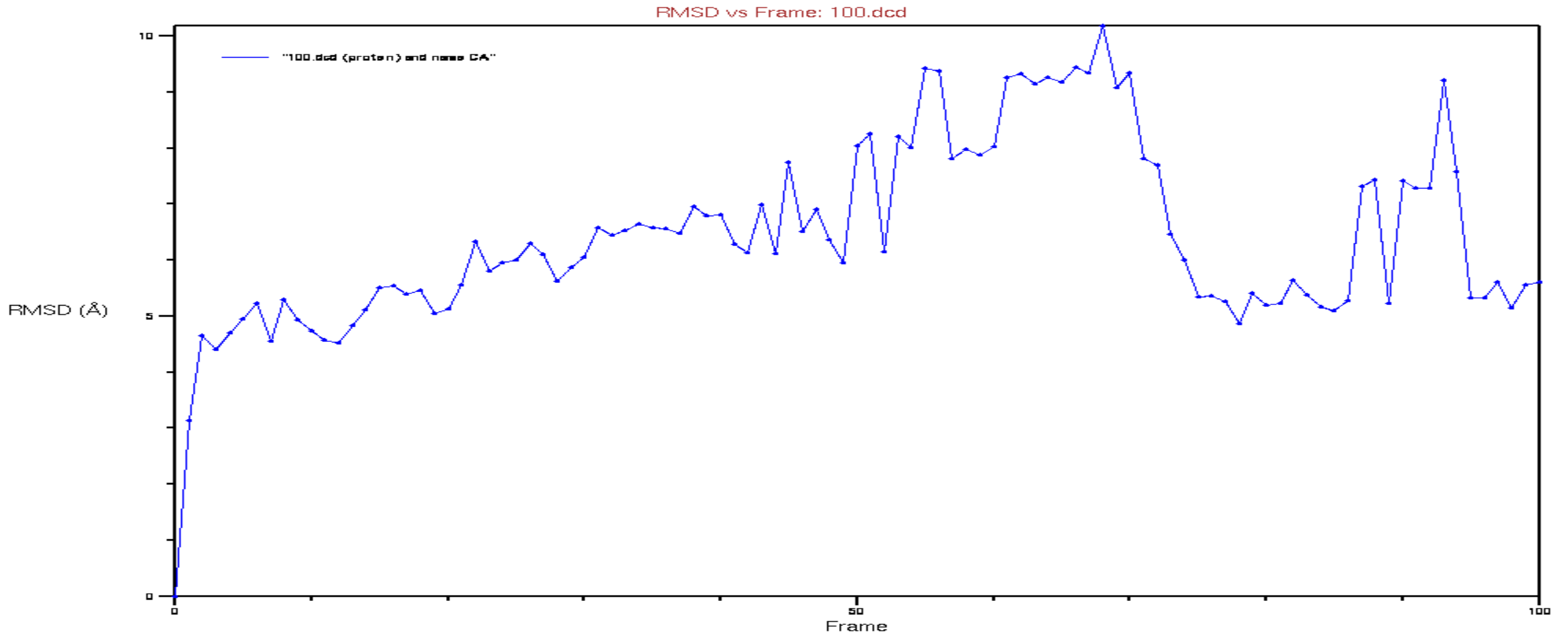


Figure 9: Color key for secondary structure plots.

Secondary structure analysis of peptide(1iyt) in liposome(lipid bilayer) during the 100ns.

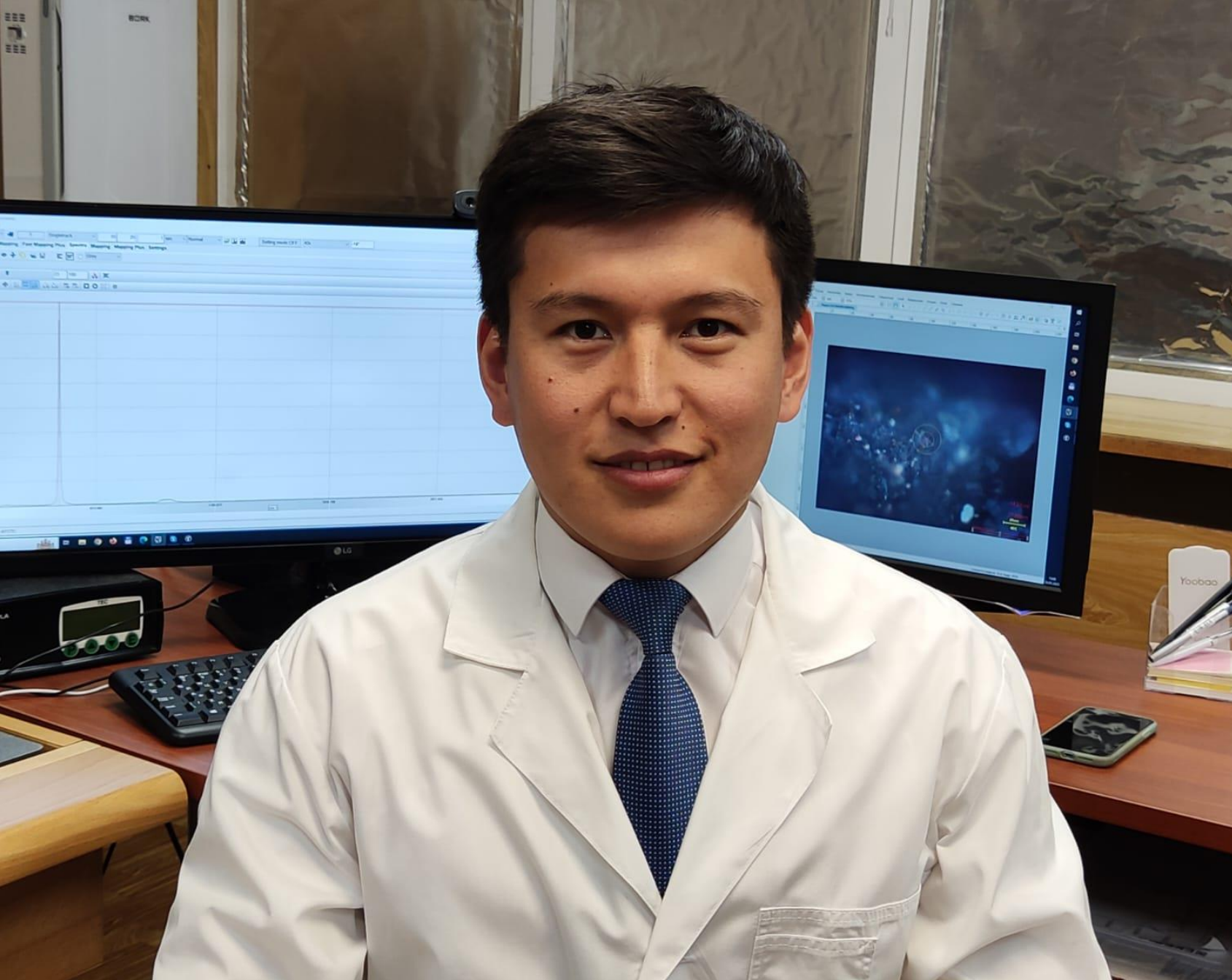
RMSD calculated by VMD



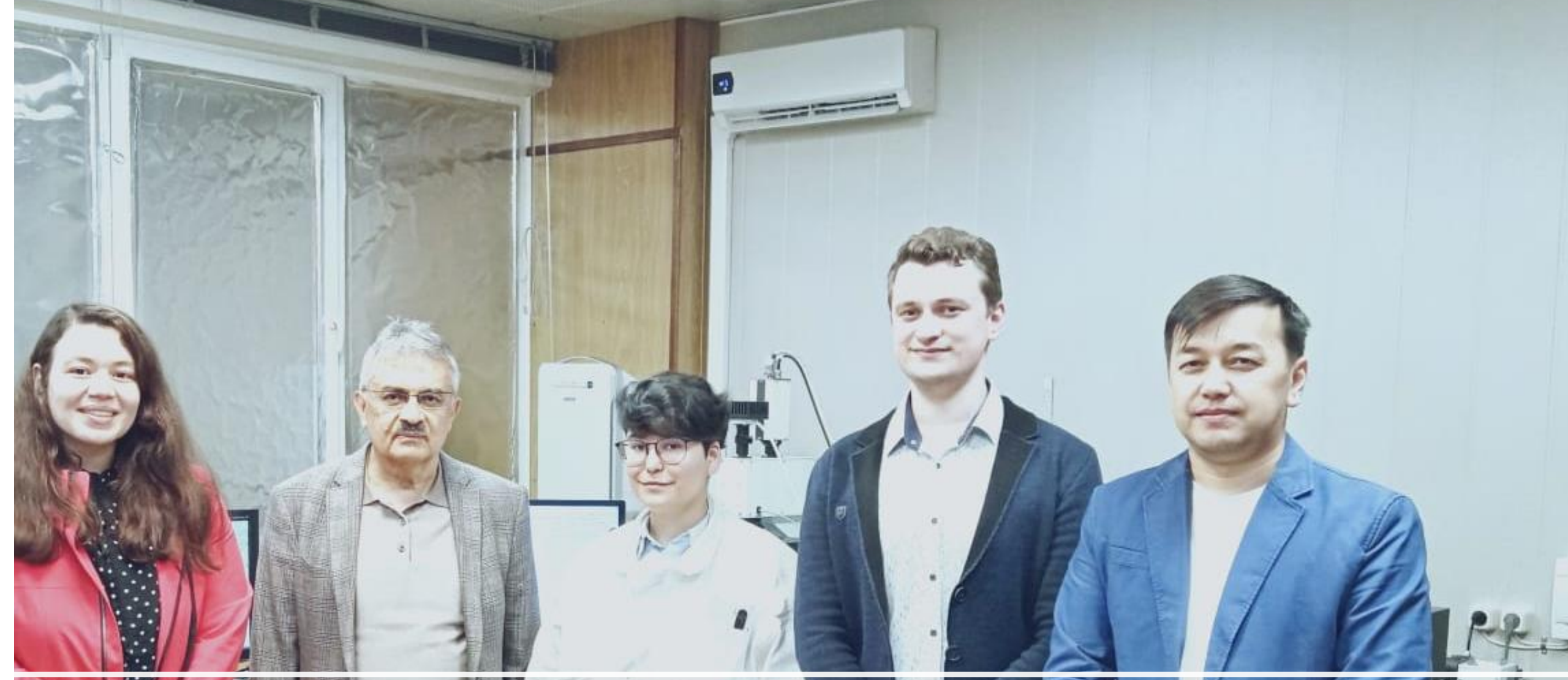
RMSD calculated by VMD

Super-Supervision

- ✓ Showed Professionalism
- ✓ Helped through molecular dynamics
- ✓ Showed patience
- ✓ Metaphorically illustrated and represented every single concept with academic and scientific integrity.
- ✓ Committed to be present every single day.
- ✓ Taught me so many in Molecular dynamics
- ✓ Sacrificed his lunchbreaks to keep working and searching for solutions when any error first appeared .



Yersultan Arynbeke



Thank you! Raman Spectroscopy Department

Prof. ArZumanyan & Darya & Artyom & Kahramon



Thank you! Erina!

Thank you!