

How small changes in molecular structure influence structure and mechanism of spontaneous self-assembly?: Insights from fully atomistic molecular dynamics simulations



Sangeeta Das, Rumela Adhikary, Argha Chakraborty and Avisek Das

School of Chemical Sciences, Indian Association for the Cultivation of Science, Jadavpur, Kolkata-700032

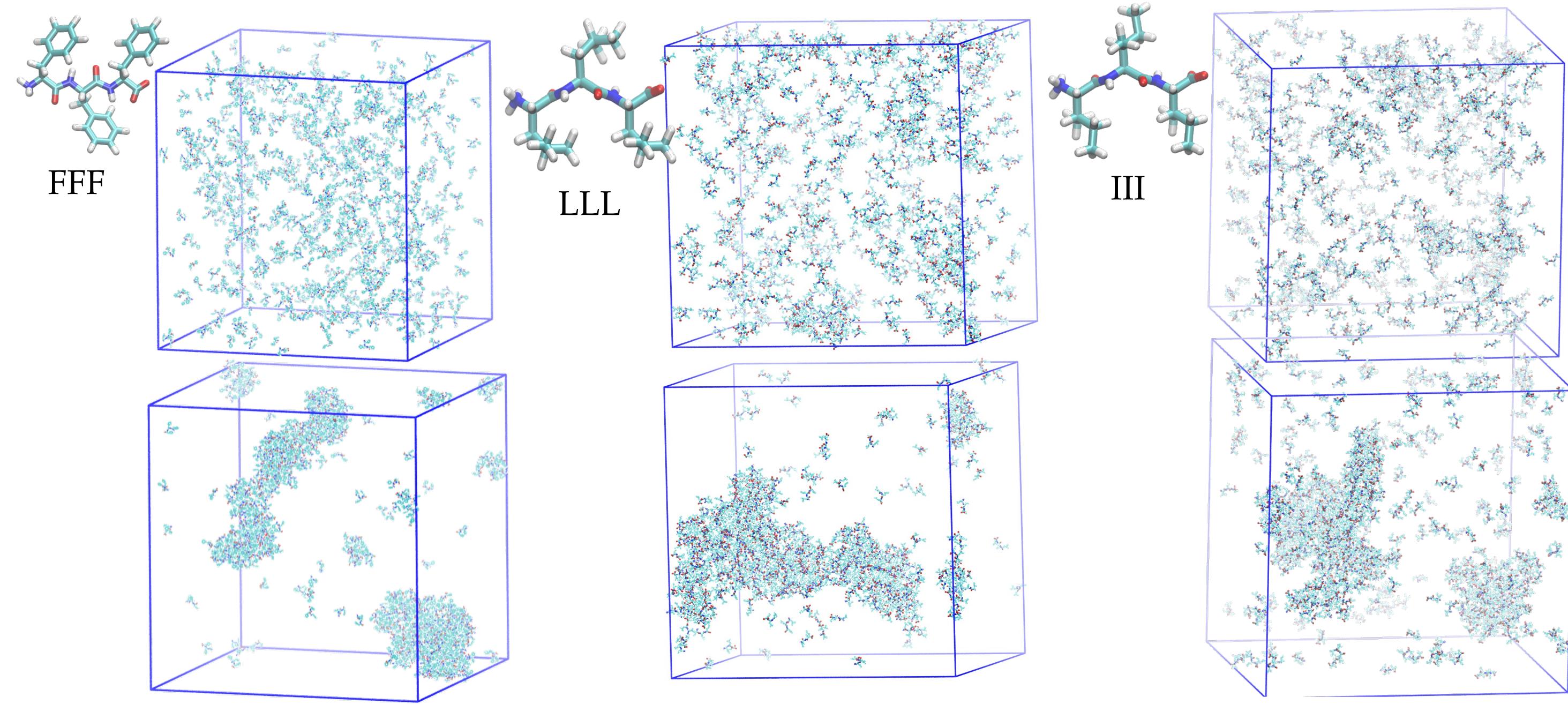
E-mail – intsd@iacs.res.in



Introduction

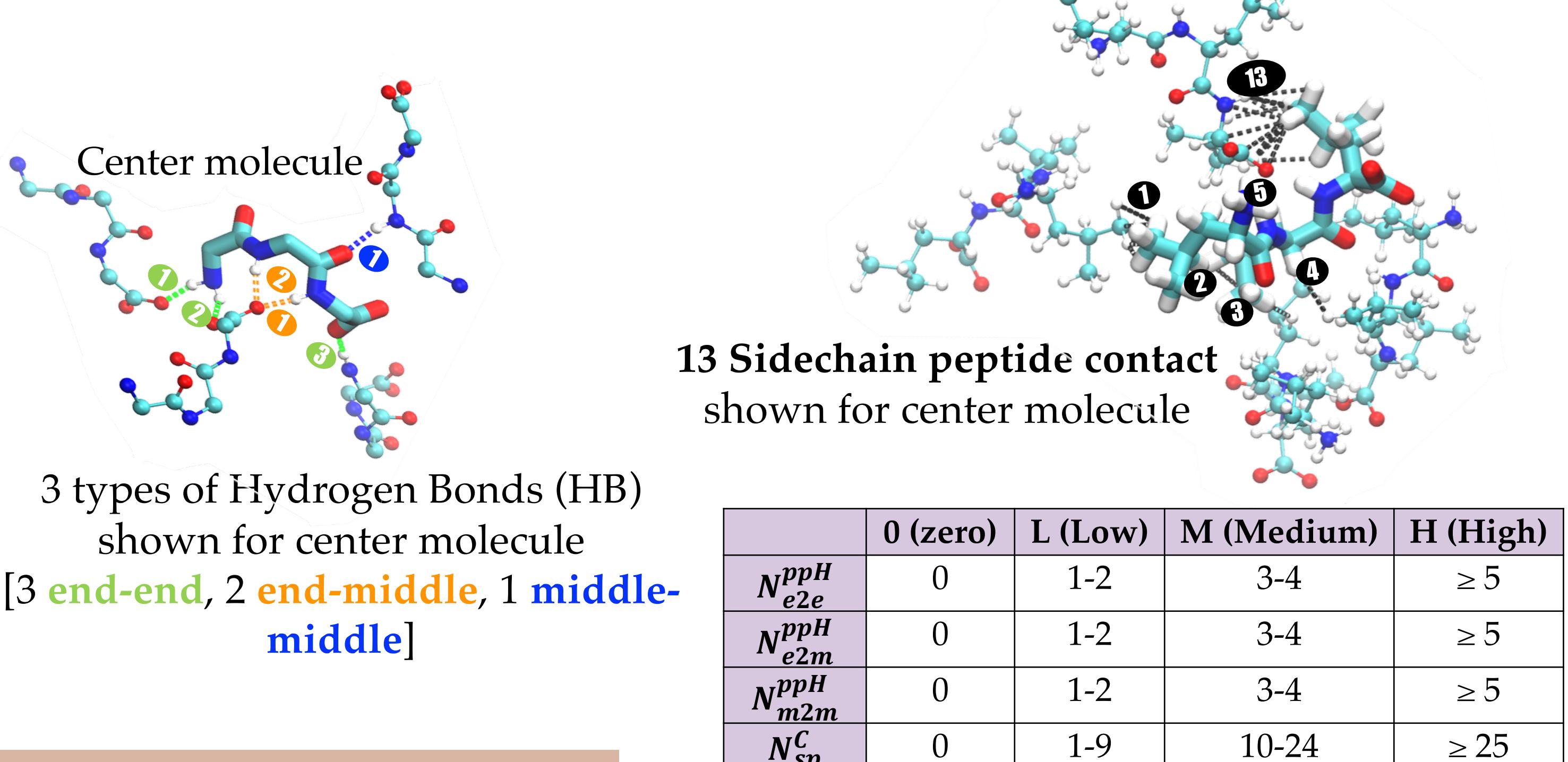
- Molecular self-assembly is a promising field in chemistry and materials science.
- The self-assembly process involves complex combinations of chemical interactions (Γ -space).
- To understand the time evolution in the Γ -space, we proposed Trajectory Analysis of Multidimensional Chemical Interaction Space (TAMCIS) method.
- TAMCIS is applied on to analysis of assembly mechanisms of three hydrophobic tripeptides (Phenylalanine tri-peptide (FFF), Isoleucine tripeptide (III) and Leucine tripeptide(LLL)) in water.
- In the FFF system (29.3mg/mL), a ~10nm bent fiber forms, while the LLL system (44.52mg/mL) produces longer ~16nm fiber. the III system (44.52mg/mL) yields a self-assembled state with one side ~11ns and the other side ~10ns in length.

Tri-peptide systems

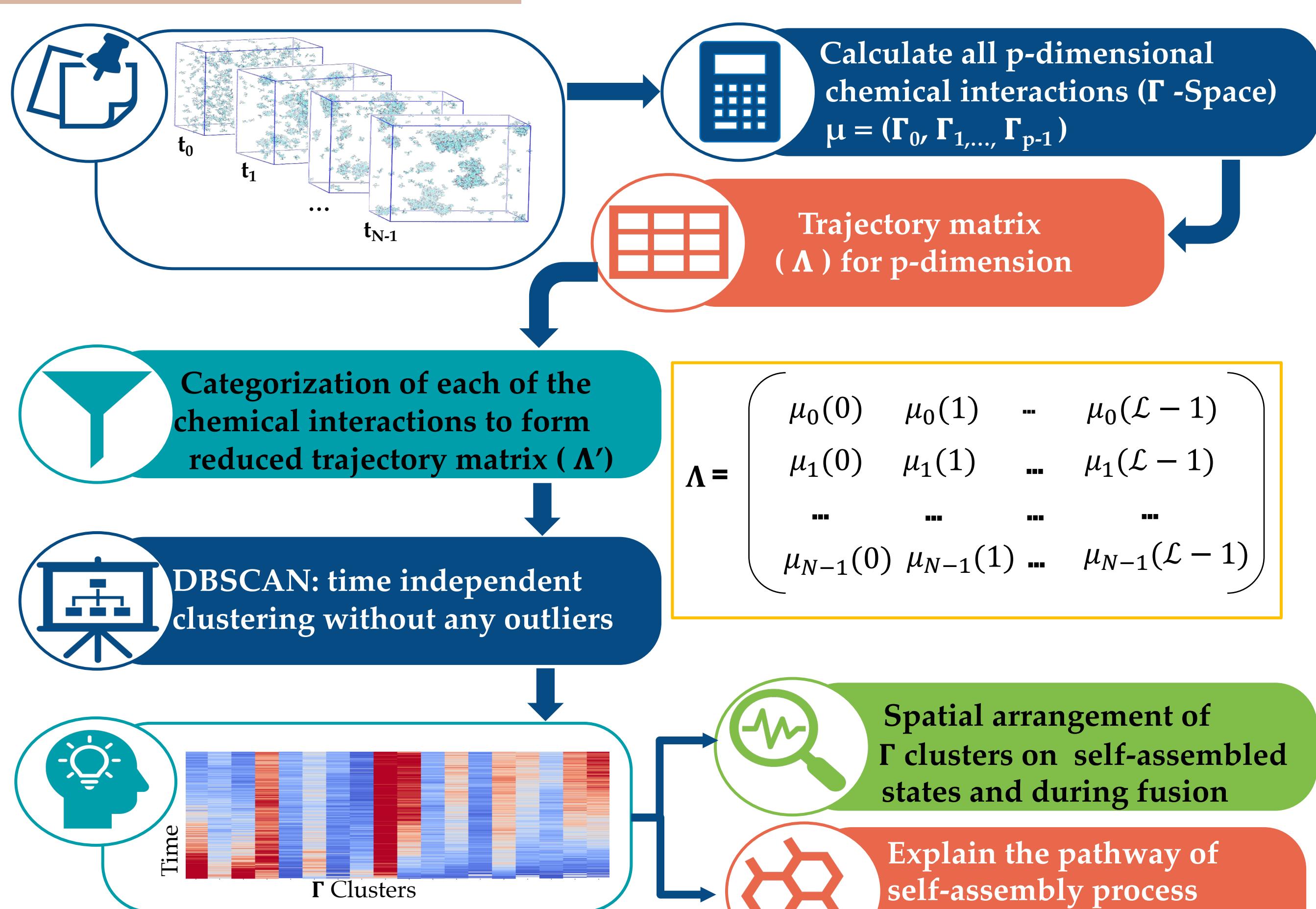


Multidimensional Chemical Interactions (Γ) Space

- Γ -space considered is of 4 dimension ($p=4$)
- $\mu_{it} = (N_{e2e}^{ppH} \text{ (end-end HB)}, N_{e2m}^{ppH} \text{ (end-middle HB)}, N_{m2m}^{ppH} \text{ (middle-middle HB)}, N_{sp}^C \text{ (sidechain peptide)})$ for i^{th} molecule at t^{th} time



TAMCIS Method



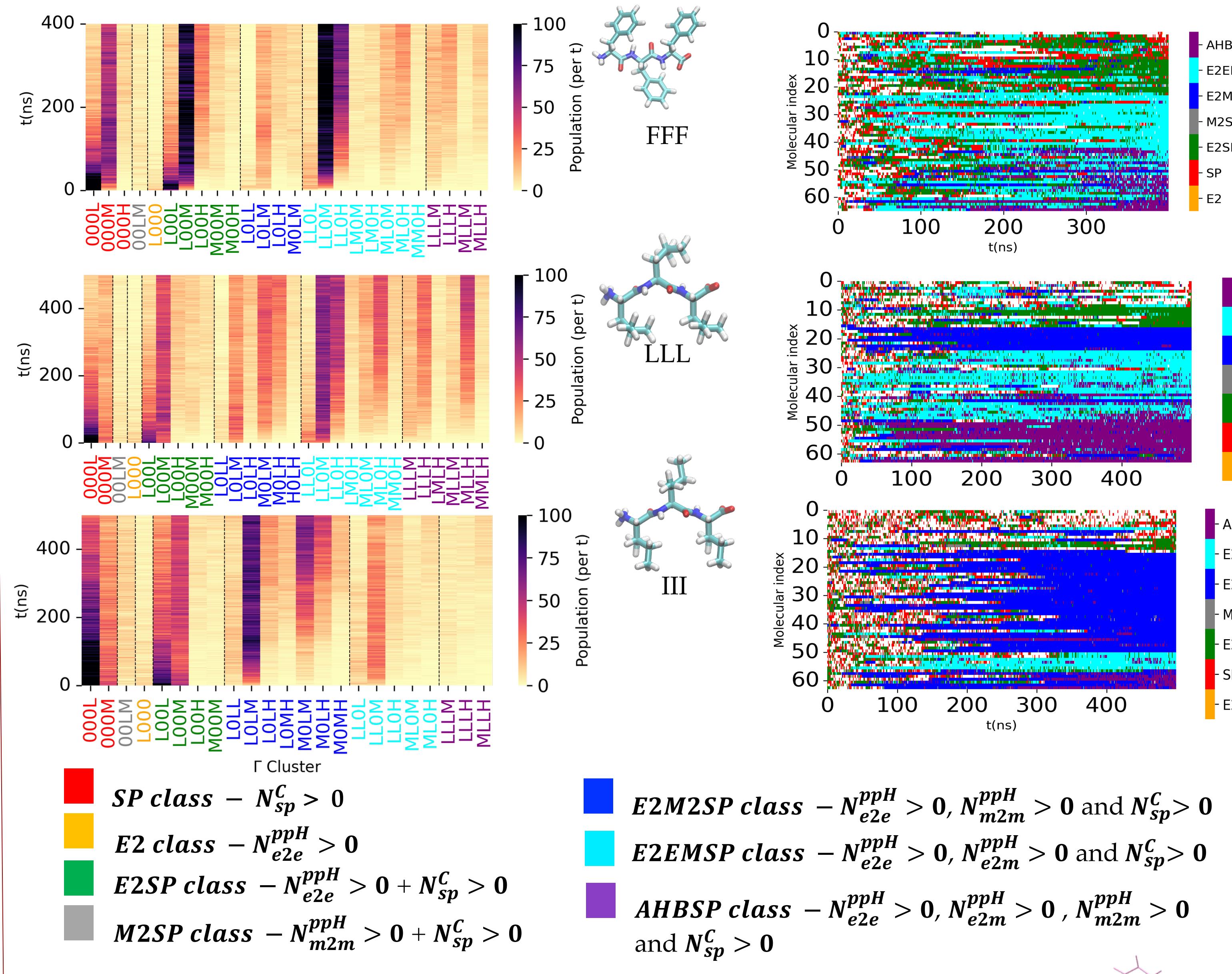
References

- Adhikary, R., & Das, A. (2022). *J. Phys. Chem. B*, 126(46), 9476-9492.
Zhou, P., Deng, L., Wang, Y., Lu, J. R., & Xu, H. (2016). *Langmuir*, 32(18), 4662-4672.

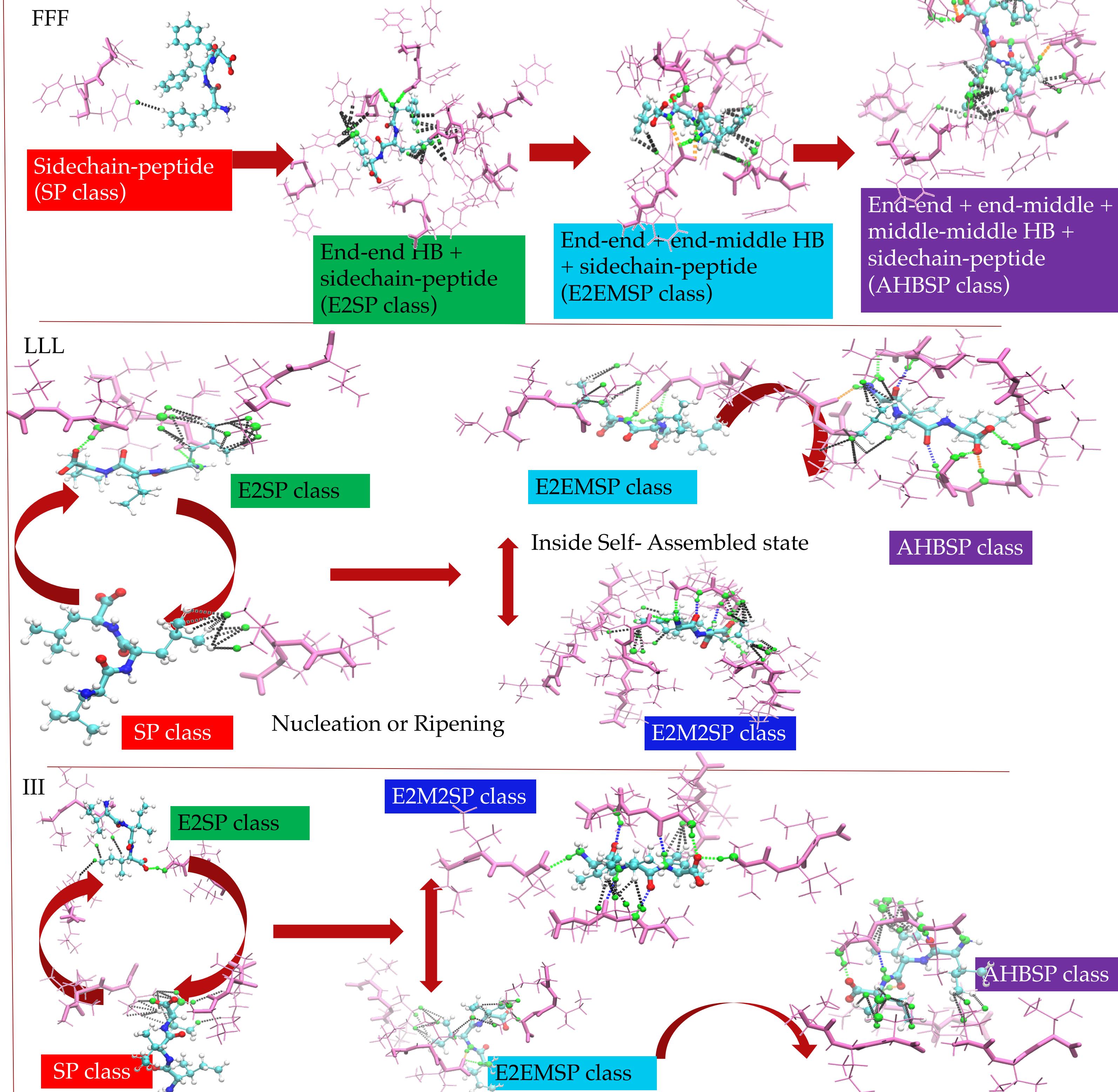
Acknowledgement



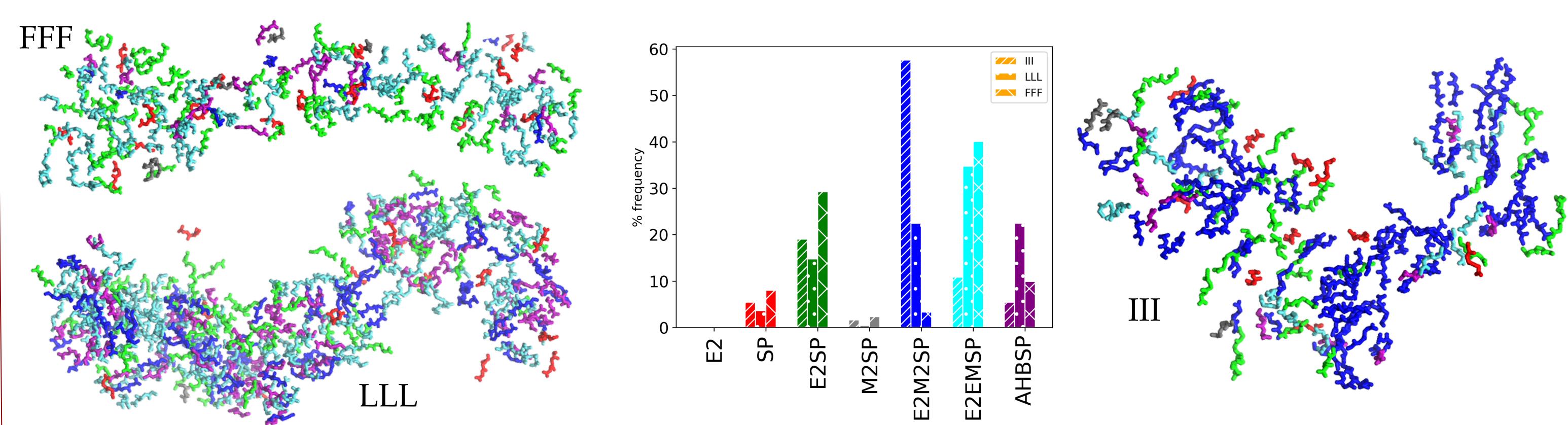
Comparison between Phenylalanine tri-peptide (FFF), Leucine tri-peptide (LLL) and Isoleucine tri-peptide(III) using TAMCIS



Pathway for Temporal Molecular Hopping in Γ -space



Spatial arrangement of Γ clusters in the final assembled states



Conclusions

- Dominant Γ clusters driving the self-assembly processes in FFF - end-end H-Bonds with sidechain peptide contacts (E2SP)+end-end, end-middle H-bonds with sidechain-peptide contacts (E2EMSP)
- LLL – combination of E2EMSP + end-end, end-middle H-Bonds with sidechain-peptide contacts (E2M2SP)
- III - end-end, middle-middle H-Bonds with sidechain contacts (E2M2SP)
- TAMCIS method has a generalized approach to analyze time-dependent hyperparameters to find similarities and differences in the pathway of any USPs self-assembly.

How small changes in molecular structure influence structure and mechanism of spontaneous self-assembly?: Insights from fully atomistic molecular dynamics simulations

Sangeeta Das, Rumela Adhikary, Argha Chakraborty and Avisek Das

School of Chemical Sciences, Indian Association for the Cultivation of Science, Jadavpur, Kolkata-700032

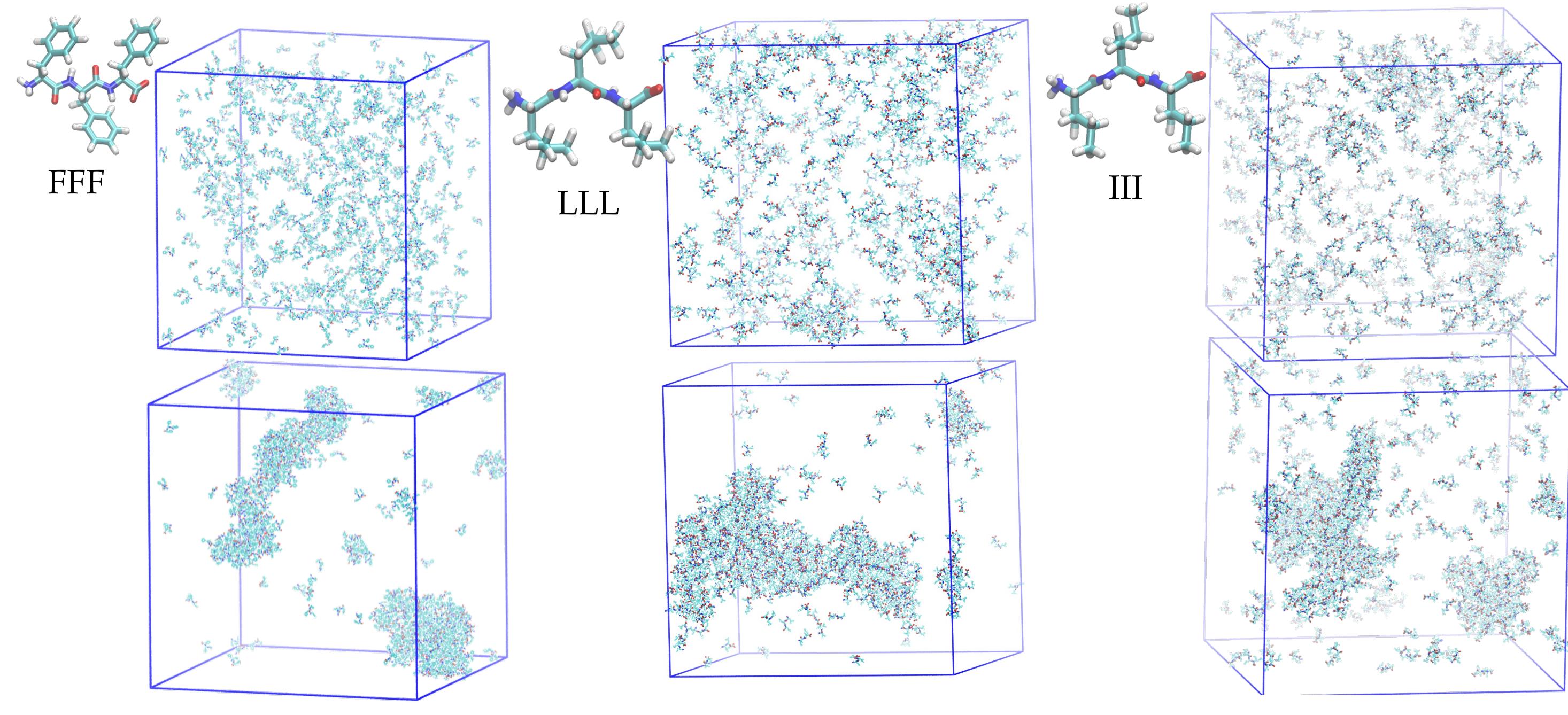


E-mail – intsd@iacs.res.in

Introduction

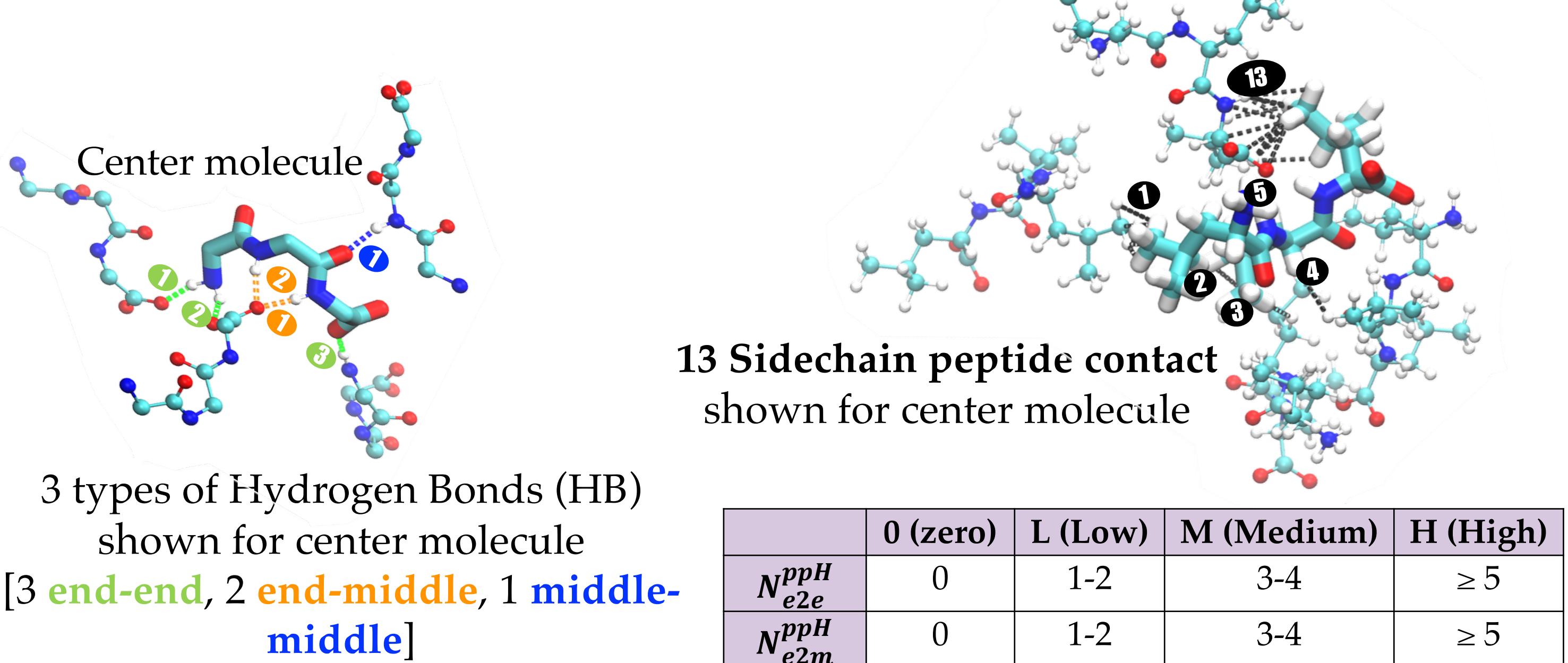
- Molecular self-assembly is a promising field in chemistry and materials science.
- The self-assembly process involves complex combinations of chemical interactions (Γ -space).
- To understand the time evolution in the Γ -space, we proposed Trajectory Analysis of Multidimensional Chemical Interaction Space (TAMCIS) method.
- TAMCIS is applied on to analysis of assembly mechanisms of three hydrophobic tripeptides (Phenylalanine tri-peptide (FFF), Isoleucine tri-peptide (III) and Leucine tri-peptide(LLL)) in water.
- In the FFF system (29.3mg/mL), a ~10nm bent fiber forms, while the LLL system (44.52mg/mL) produces longer ~16nm fiber. the III system (44.52mg/mL) yields a self-assembled state with one side ~11ns and the other side ~10ns in length.

Tripeptide systems

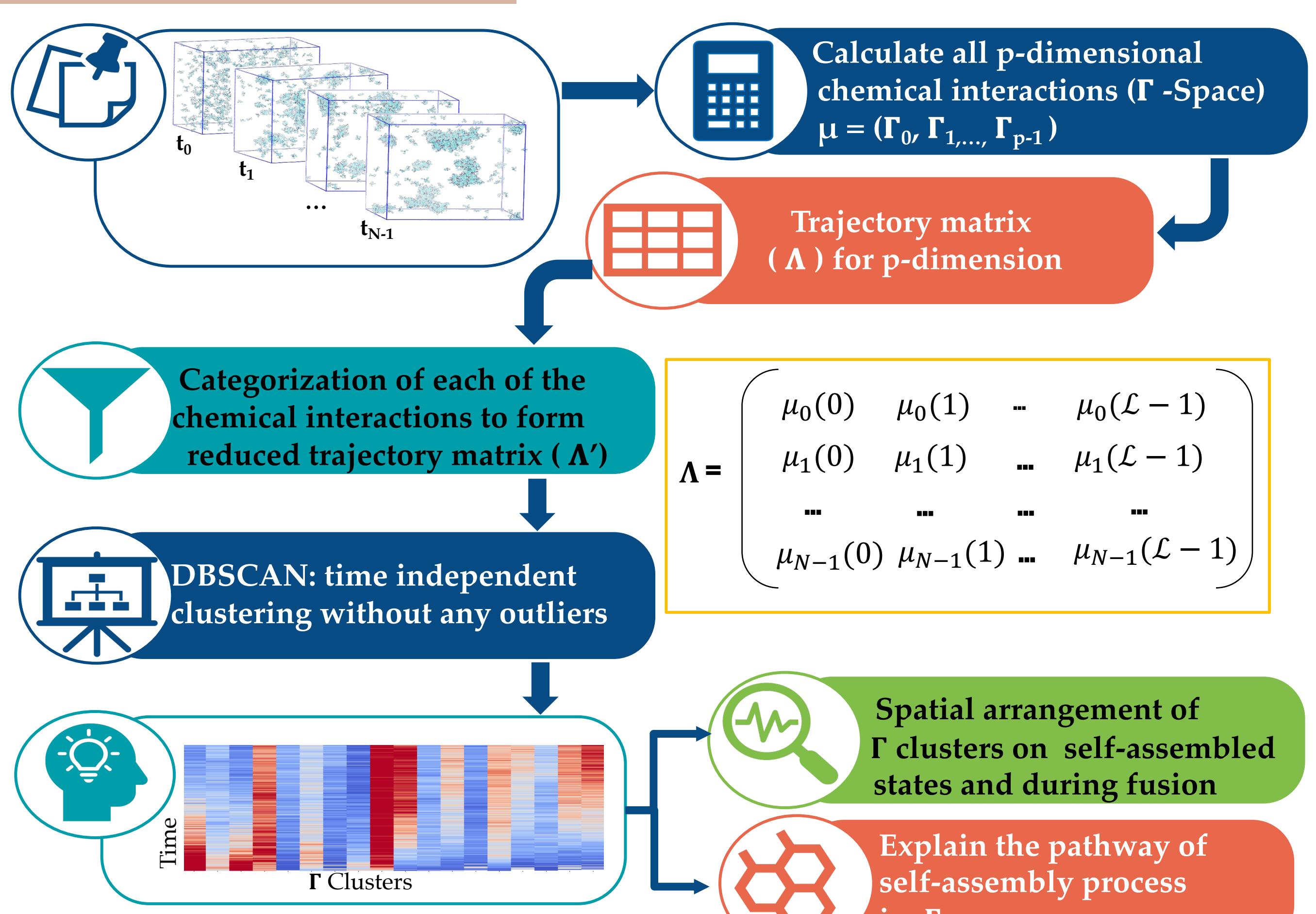


Multidimensional Chemical Interactions (Γ) Space

- Γ -space considered is of 4 dimension ($p=4$)
- $\mu_{it} = (N_{e2e}^{ppH} \text{ (end-end HB)}, N_{e2m}^{ppH} \text{ (end-middle HB)}, N_{m2m}^{ppH} \text{ (middle-middle HB)}, N_{sp}^C \text{ (sidechain peptide)})$ for i^{th} molecule at t^{th} time



TAMCIS Method



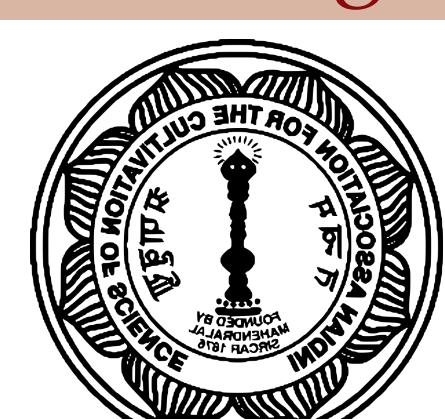
Features of TAMCIS Method:

- Multidimensional Clustering: Identifies significant interactions.
- Density-Based: No dimensionality constraints.
- Handle entire trajectory data

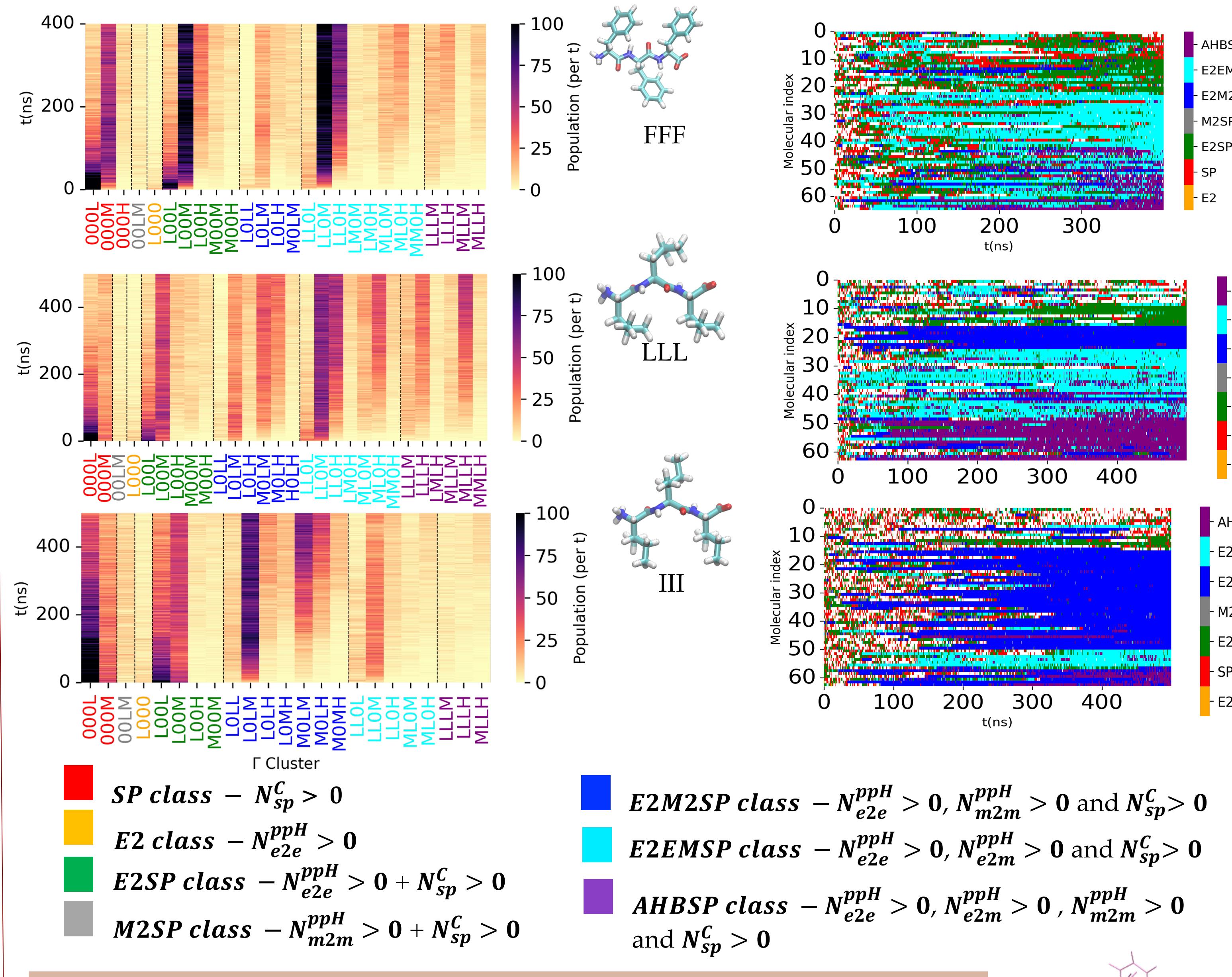
References

- Adhikary, R., & Das, A. (2022). *J. Phys. Chem. B*, 126(46), 9476-9492.
 Zhou, P., Deng, L., Wang, Y., Lu, J. R., & Xu, H. (2016). *Langmuir*, 32(18), 4662-4672.

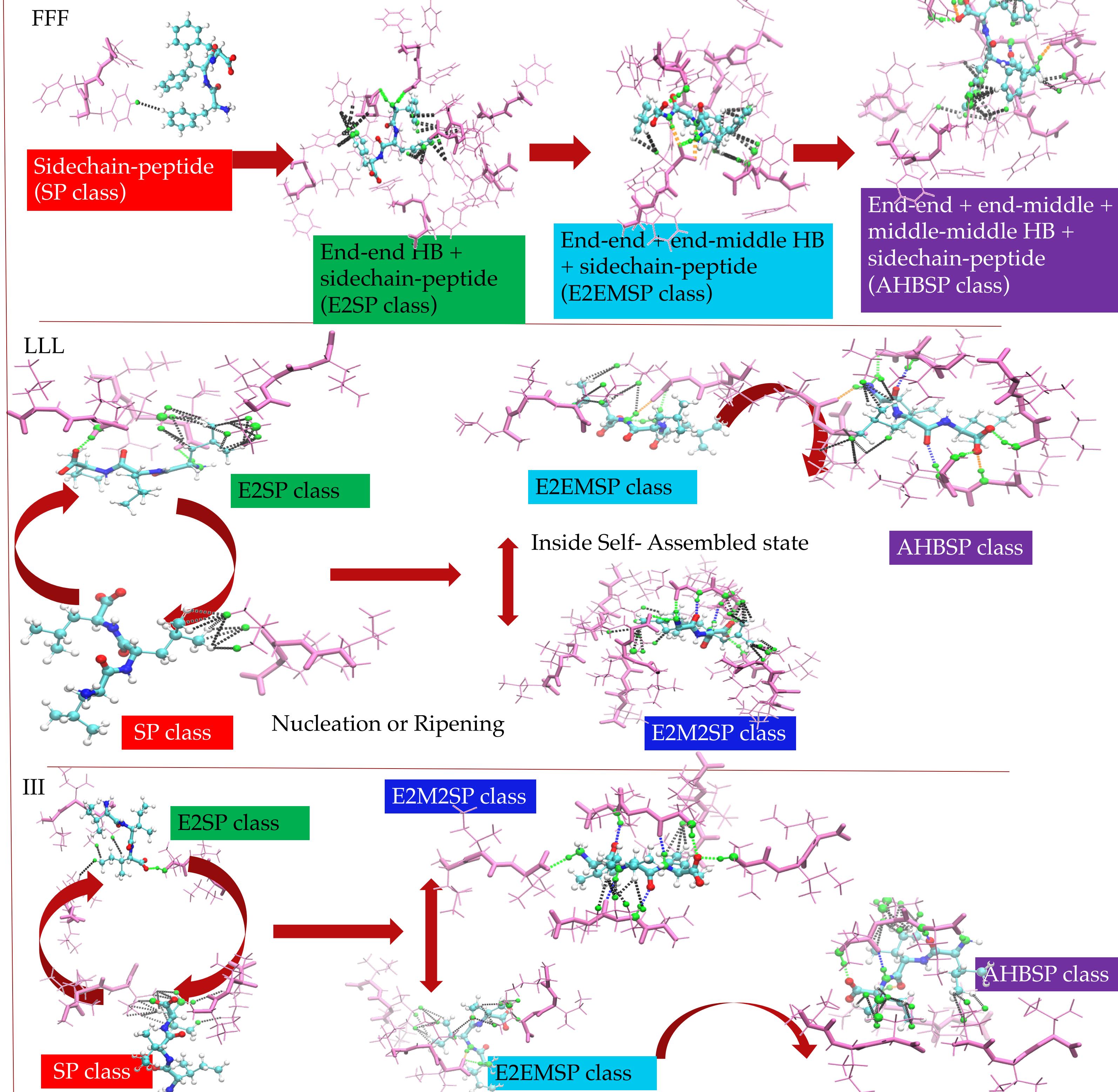
Acknowledgement



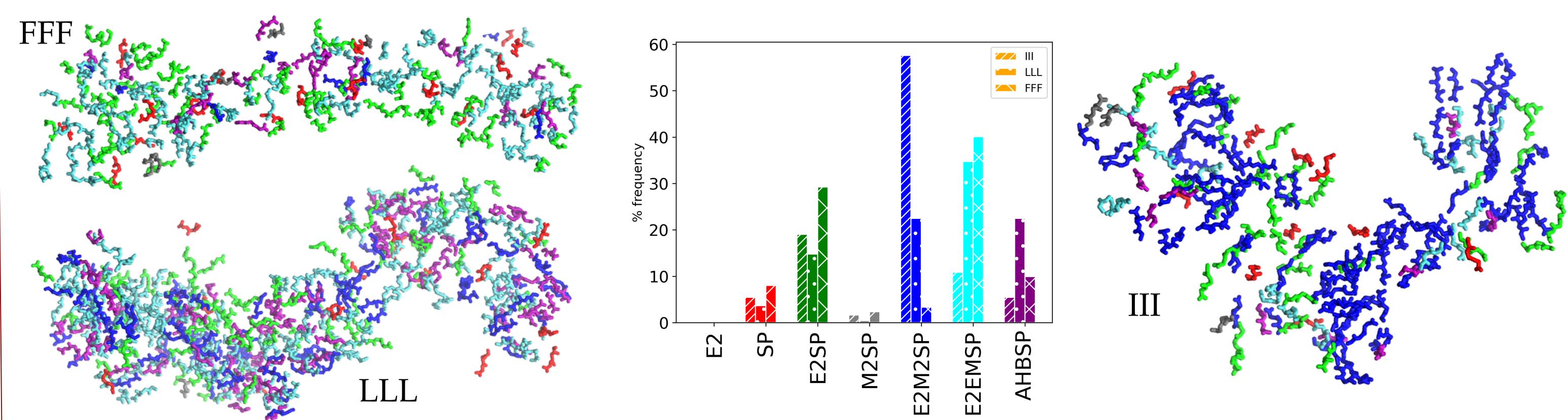
Comparison between Phenylalanine tri-peptide (FFF), Leucine tri-peptide (LLL) and Isoleucine tri-peptide(III) using TAMCIS



Pathway for Temporal Hopping in Γ -space



Spatial arrangement of Γ clusters in the final assembled states



Conclusions

Dominant Γ clusters driving the self-assembly processes

- In FFF, end-end H-Bonds with sidechain peptide contacts (E2SP)+end-end, end-middle H-bonds with sidechain-peptide contacts (E2EMSP)
- In LLL, combination of E2EMSP + end-end, end-middle H-Bonds with sidechain-peptide contacts (E2M2SP)
- In III, end-end, middle-middle H-Bonds with sidechain peptide contacts (E2M2SP)

TAMCIS method has a generalized approach to analyze time-dependent hyperparameters to find similarities and differences in the pathway of any USPs self-assembly.