#### Analyzing switch regions of human Rab7a and Rab10 by molecular dynamics simulations

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## **PROFESSIONAL TRAJECTORY**



#### **Levy Bueno Alves**

- 2015-2019: Degree in Biotechnology from the Federal University of Alfenas;
- 2020-2022: Master's Degree in Genetics from the University of São Paulo;
- 2022: PhD student in Genetics from the University of São Paulo.

#### Rab7a and Rab10 targets

- Belongs to the family of <u>Rab GTPases;</u>
- It is responsible for regulating intracellular traffic in various pathways of different cellular sublocations;
- Functional deregulation in the pathways of theses enzymes are implicated in ciliopathies, cancer and neurodegenerative diseases.

Figure 1. Rab7a and Rab10 cellular sub-locations





#### Rab7a and Rab10 in Alzheimer's disease

- Studies have shown that these enzymes play a relevant role in Alzheimer's disease.
  - Rab10 helps in the amyloidogenic processing of the amyloid precursor protein (APP);
  - > Rab7a is involved in the hyperphosphorylation of the Tau protein.

References: P. G. RIDGE et al., 2017; L. Rodriguez et al., 2017.

#### Rab7a and Rab10 in cancer

 Studies that correlate the inhibition of these enzymes with the induction of apoptosis in cancer cells;

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These enzymes can activate signaling pathways for cancer cells growth and survival, leading to cancer progression.

#### **Therapeutic** application

- Such evidences pave the way for the application of new drug targeting strategies for the treatment of various human diseases:
  - > The modulation of the activity of these enzymes using small molecules may represent a promising alternative to delay the progression of these diseases.

## **Cycle** of small GTPases

- Rab GTPases regulate cellular processes by alternating the nucleotides GTP and GDP;
  - When bound to GTP, these enzymes are in active state.
  - When bound to GDP, these enzymes are in inactive state.
- The switch 1 and switch 2 regions:
  - ➤ When activated, it has ↓ flexibility;
  - When inactivated, it has **1** flexibility;





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## **Cycle** of small GTPases

- Interactions with the phosphate-binding motifs (PMs):
  - **GTP** interacts with PM1, PM2 and PM3;
  - **GDP** interacts only with PM1.



#### **Figure 2.** The GTP $\rightarrow$ GDP cycle of small GTPases

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## OBJECTIVE

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- The present study aimed to detail the structural flexibility of the switch regions of Rab7a and Rab10 by molecular dynamics (MD) simulations.

Figure 3. Rab10 switch 1, interswitch and switch 2 regions



## OBJECTIVE

The present study aimed to detail the structural flexibility of the switch regions of Rab7a and Rab10 by molecular dynamics (MD) simulations.

- 2020: our research group performed MD simulations to investigate the internal movements of Rab10.
  - These results showed noticeable differences in local flexibility of switch1 when Rab10 was bound with GDP.

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In order to verify if the conformational change in the on-to-off process of Rab10 was not by chance, we extended our study considering Rab7a.

## **METHODS**

#### **Molecular docking**

We used molecular docking to form complexes with GDP and GTP.



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Figure 5. GDP docking at Rab's active site



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## **METHODS**

#### **Molecular dynamics (MD)**

The root mean square deviation (RMSD), root mean square fluctuation (RMSF), radius of gyration (Rg) and solvent accessible surface area (SASA) were used for the trajectory analysis.

Figure 6. Inactived and actived systems





Actived enzyme witch GTP

Reference: Author

#### **Molecular dynamics study**

 RMSD analysis: the trajectories reached stability after 40 ns of simulation. The complexes associated with the GTP have more restricted movements.

Figure 7. G-domain RMSD of Rab7a and Rab10.



RMSD of G-domain

#### **Molecular dynamics study**

RMSD analysis: switch 1 region showed significant differences when the Rab's was associated with the tested nucleotides.

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**Figure 7.** RMSD of switch regions of Rab7a and Rab10: (a) RMSD of Switch 1 and (b) RMSD of Switch 2.



#### **Molecular dynamics study**

 RMSF analysis: The residues composes the switch 1 region showed greater fluctuations when the Rab's is linked to GDP.

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Figure 8. RMSD of switch regions of Rab7a and Rab10: (a) RMSD of Switch 1 and (b) RMSD of Switch 2.



#### RMSF of proteins



#### **Molecular dynamics study**

**Rg analysis:** the Rg trajectories of the inactivated systems showed higher values than the activated state.

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**Figure 9.** Rg of G-domain of Rab7a and Rab10.

#### **Molecular dynamics study**

 SASA analysis: We can infer that the disordered movements of switch 1 and the absence of γ-phosphate in GDP contribute to the increase in SASA.

Figure 9. SASA of G-domain of Rab7a and Rab10.



## **CONCLUSIONS AND FUTURE WORK**

#### **Molecular dynamics study**

- MD simulations used in this study were able to obtain notable differences in the switch 1 region of Rab's, enabling the identification of its active and inactive states.
- We hypothesized <u>that the flexibility of the switch 1 sensitive region can be used as</u> an indicator of in silico studies that search potential competitive inhibitors based on nucleotides against these targets;
- The next steps of this research is to extend the analyzes to evaluate the on-to-off process of 44 representatives of human Rab GTPases.

# Thank you for your attention!

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