



# Innovative method to identify antidiabetic plant ingredients as protein tyrosine phosphatase 1B inhibitors



Carlos Shiraishi  
Estudante de Doutoramento  
shiraishi@ipb-pt

Carlos Seiti Hurtado Shiraishi<sup>1,2,3,4</sup>, Fábio G. Martins<sup>3</sup>, Sérgio F. Sousa<sup>3</sup>, Miguel A. Prieto<sup>4</sup>, Sandrina A. Heleno<sup>1,2</sup> e Rui M. V. Abreu<sup>1,2</sup>

<sup>1</sup> CIMO, School of Sciences and Technology, Polytechnic Institute of Bragança, Bragança, Portugal

<sup>2</sup> Associated Laboratory for Sustainability and Technology in Mountain Regions (SusTEC), Polytechnic Institute of Bragança, 5300-253 Bragança, Portugal

<sup>3</sup> LAQV/REQUIMTE, BioSIM-Departamento de Biomedicina, Faculdade de Medicina, Universidade do Porto, 4200-319 Porto, Portugal

<sup>4</sup> Nutrition and Bromatology Group, Universidad de Vigo, Department of Analytical Chemistry and Food Science, Faculty of Sciences, E-32004 Ourense, Spain;

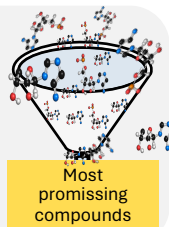


## Abstract

There is no disputing the huge costs involved in screening plants as a source of functional ingredients, from extracting compounds to evaluating their biological activity (SDGs 7 and 13). In this context, *in silico* tools are valuable for identifying natural compounds with greater potential for use in the food and pharmaceutical industry. This work aims to use the DiaNat-DB, a database of known antidiabetic compounds from medicinal plants [1], and perform a virtual screening analysis using human Protein Tyrosine Phosphatase (PTP1B) as the protein target. PTP1B inhibition is a promising mechanism in treating type 2 diabetes because its inhibition is related to insulin sensitivity improvement and, consequently, glycemic control. The *in silico* virtual screening methodology was performed using GOLD software for molecular docking and PLP scoring function. Currently, the DiaNat-DB database consists of 360 antidiabetic compounds from 211 plants [1].

## Methods

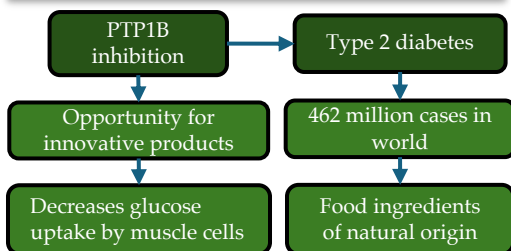
- 1 Human PTP1b protein selection
- 2 Protein preparation for molecular modeling
- 3 Database preparation in DataWarrior and Openbabel
- 4 Virtual Screening and Results Analysis



## Conclusion

From the virtual screening analysis performed, three compounds from the DiaNat-DB presented the best predicted inhibition activity: 6,6',3"-trihydroxy-7,3',7"-O-trimethylfloniflavone, Damnacanthal-3-O-beta-D-primeveroside and Demethoxycurcumin with significant PLP scores of -69,00, -63,56 and -63,30, respectively. The PLP scores compared well with the PLP score obtained for Sulfamic Acid (-34,30), the control compound used in this study. These compounds were found in the plant species: (A) *Salvia circinata*, (B) *Morinda citrifolia* and (C) *Curcuma longa*, respectively. This study presents an innovative method for identifying molecules and plants with potential antidiabetic activity as functional ingredients for the food and pharmaceutical industry.

## Contextualization of the theme



## Framework of the project in sustainability

Reuse	Identify Plants with Bioactivities
Reduce	Costs in identifying new ingredients
Innovate	Antidiabetic Ingredients

Figure 1. Protein Tyrosine Phosphatase 1B coupled with selective inhibitor

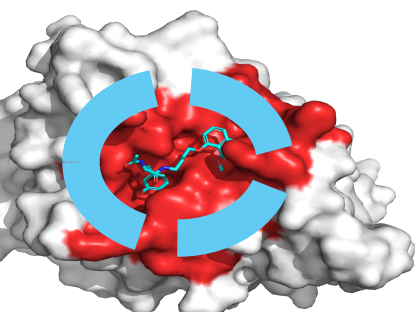
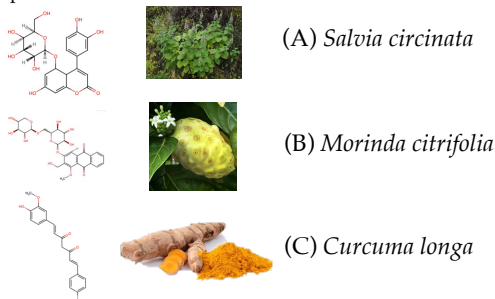


Figure 2. Natural compounds with antidiabetic potential



## References

[1] Madariaga-Mazón A, Naveja JJ, Medina-Franco JL, Noriega-Colima KO, Martínez-Mayorga K. DiaNat-DB: a molecular database of antidiabetic compounds from medicinal plants. RSC Adv. 2021 Jan 28;11(9):5172-5178

## Acknowledgements

National funds through FCT/MCTES (PIDDAC): CIMO, UIDB/00690/2020 (DOI: 10.54499/UIDB/00690/2020) and UIDP/00690/2020 (DOI:10.54499/UIDP/00690/2020); and SusTEC, LA/P/0007/2020 (DOI: 10.54499/LA/P/0007/2020); S.A. Heleno acknowledges FCT for her support through the institutional scientific employment program-contract; national funding by FCT, P.I. C.S.H.S thanks FCT, Portugal for the Ph.D. Grant 2023.04950.BD.