

***Araucaria heterophylla* oleogum resin essential oil is a novel aldose reductase and butyryl choline esterase enzymes inhibitor: *in vitro* and *in silico* evidence**

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Abstract

The essential oil isolated by hydrodistillation of the oleogum resin of *Araucaria heterophylla* has been analyzed by GC-MS. Twenty-four components accounting to 99.89 % of the total detected constituents of this essential oil were identified. The major ones were: caryophyllene oxide (14.8%), (+)-sabinene (12.07%), D-limonene (11.22%), caryophyllene (10.36%), α -copaene (8.00%), β -pinene (6.44%), trans-verbenol (5.88%) and α -pinene oxide (5.18%). The *in vitro* inhibitory activities of this oil against aldose reductase, BuCHE, COX-2 and SARS-CoV-2 M^{pro} enzymes were evaluated. This revealed promising inhibitory activity of the essential oil against both aldose reductase and BuCHE enzymes. The molecular docking study of the major components of the *Araucaria heterophylla* essential oil was carried out to correlate their binding modes and affinities for aldose reductase and BuCHE enzymes with the *in vitro* results. In conclusion, the *in vitro* inhibitory activity of the essential oil attributed to the synergistic effect between its components and the *in silico* study suggested that compounds containing epoxide and hydroxyl groups may be responsible for this activity. This study is preliminary screening for the oil to be used as antidiabetic cataract and Alzheimer's disease therapeutics and further investigations may be required.

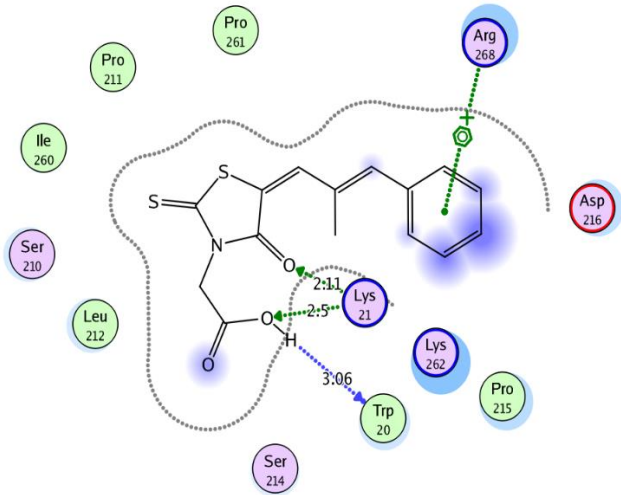
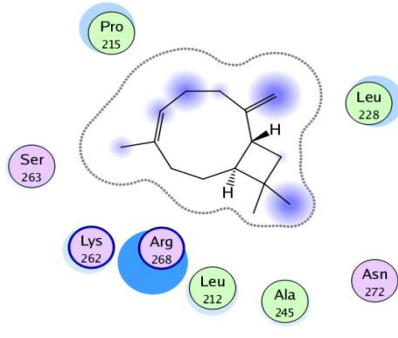
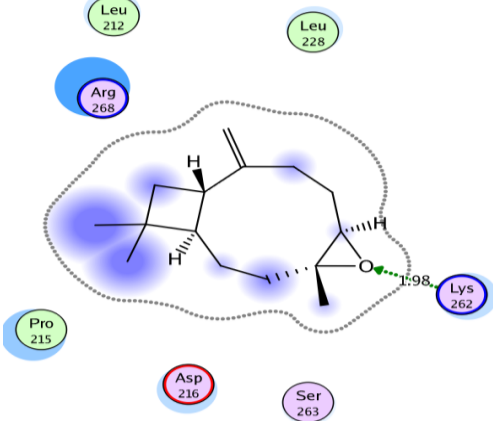
Keywords: *Araucaria heterophylla*, essential oil, enzymes inhibitor, molecular docking study.

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Table S1. The aldose reductase inhibition (IC_{50} $\mu g/ml$), docking scores^a and 2D pose of the major components of the essential oil and the reference compound (**Epalrestat**).

Comp.	Aldose reductase inhibition (IC_{50} $\mu g/ml$)	Binding energy (Kcal/mol) ^a (docking score)	2D pose
Ah (Isolated volatile oil)	0.133 ± 0.006		
Epalrestat	0.165 ± 0.008	-11.0	
Caryophyllene	NT	-8.0	
Caryophyllene oxide	NT	-9.0	

Ah major components

Comp.	Aldose reductase inhibition (IC ₅₀ ug/ml)	Binding energy (Kcal/mol) ^a (docking score)	2D pose
(+)- Sabinene	NT	-7.1	
D-limonene	NT	-6.7	
Alpha-Copaene	NT	-8.5	
Beta-pinene	NT	-6.8	
Trans-verbenol	NT	-7.9	

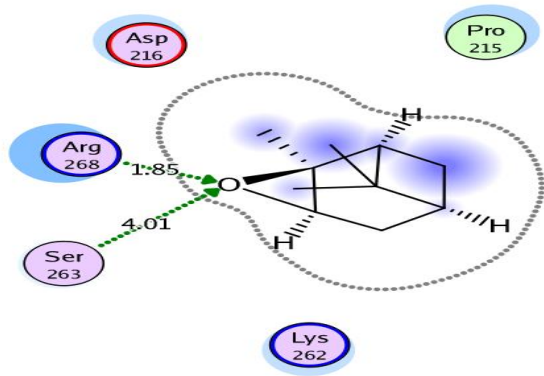
Comp.	Aldose reductase inhibition (IC ₅₀ ug/ml)	Binding energy (Kcal/mol) ^a (docking score)	2D pose
Alpha-pinene oxide	NT	-7.7	

Table S2. The aldose reductase inhibition (IC₅₀ ug/ml), docking scores^a and type of binding interactions of the major components of the essential oil and the reference compound (**Epalrestat**).

Interactions of the major components of the essential oil and the reference compound (Epalrestat).				
Comp.	aldose reductase inhibition (IC ₅₀ ug/ml)	Binding energy (Kcal/mol) ^a (docking score)	Type of binding interactions	
Ah (Isolated volatile oil)	0.133 ± 0.006			
Epalrestat	0.165 ± 0.008	-11.0	<ul style="list-style-type: none">Two H-bonds with Lys21H-bond with Trp20Arene-cation interaction with Arg268Strong hydrophobic interaction with Lys262, Pro215 and Asp216	
Ah major components	Caryophyllene	NT	-8.0	<ul style="list-style-type: none">Strong hydrophobic interaction with Arg268, Pro215 and Leu228
	Caryophyllene oxide	NT	-9.0	<ul style="list-style-type: none">H-bond with Lys262Strong hydrophobic interaction with Arg268 and Pro215
	(+)- Sabinene	NT	-7.1	<ul style="list-style-type: none">Strong hydrophobic interaction with Arg268 and Lys262
	D-limonene	NT	-6.7	<ul style="list-style-type: none">Strong hydrophobic interaction with Arg268 and Lys262
	Alpha-Copaene	NT	-8.5	<ul style="list-style-type: none">Strong hydrophobic interaction with Arg268 and Lys262
	Beta-pinene	NT	-6.8	<ul style="list-style-type: none">Strong hydrophobic interaction with Arg268 and Lys262
	Trans-verbenol	NT	-7.9	<ul style="list-style-type: none">Two H-bonds with Arg268 and Ser263Strong hydrophobic interaction with Pro215 and Lys262
	Alpha-pinene	NT	-7.7	<ul style="list-style-type: none">Two H-bonds with Arg268 and Ser263Strong hydrophobic interaction with Pro215, Asp216

Comp.	aldose reductase inhibition (IC ₅₀ ug/ml)	Binding energy (Kcal/mol) ^a (docking score)	Type of binding interactions
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oxide

and Lys262

- **Epalrestat** was used as reference aldose reductase inhibitor compound.
- All data are presented as mean value \pm SD for three independent experiments.
- Abbreviation: **NT**, not tested.
- Docking was carried out following the reported procedure [Zheng, et al., 2012] against the aldose reductase enzyme pocket (PDB code ID: 3RX2)
- ^a More negative score refers to better capability of a molecule to dock with the target and make more desirable interactions.

Fig. S1. 3D binding mode and residues involved in the recognition of (a) **epalrestat**, the compounds showing the best binding interactions (b) **caryophyllene oxide**, (c) **trans-verbenol** and (d) **alpha-pinene oxide** docked and minimized in the aldose reductase binding pocket

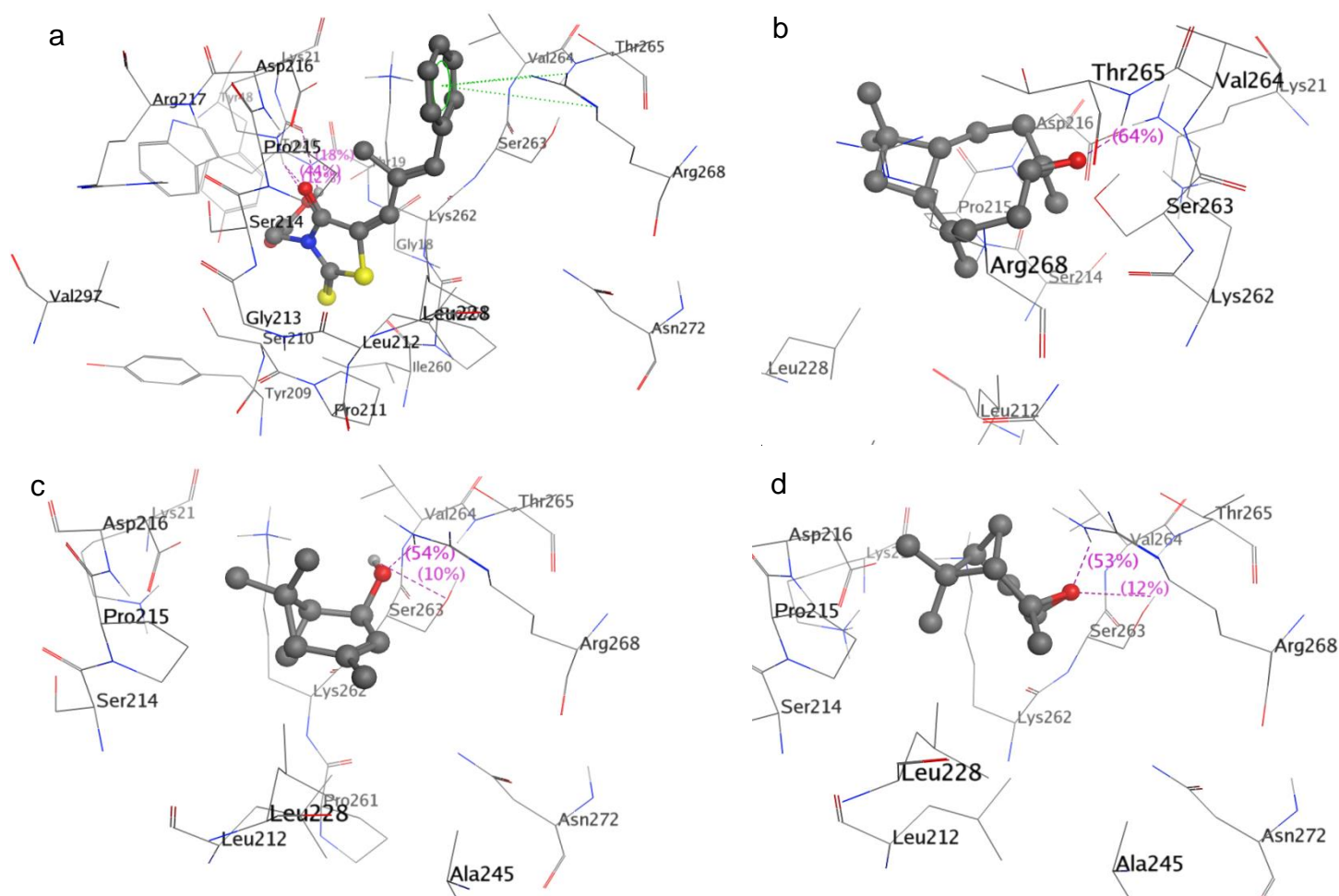
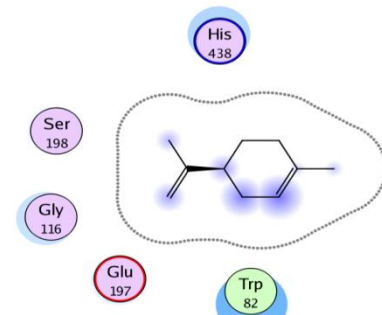
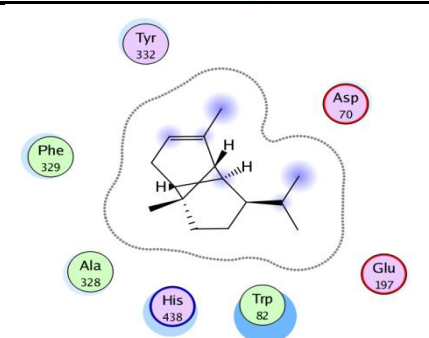
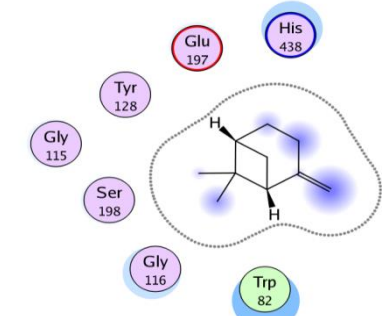
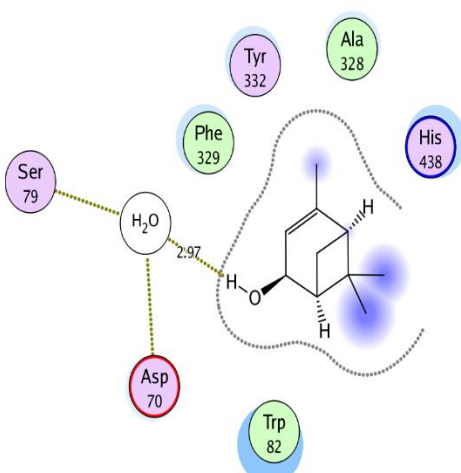


Fig. S1

Table S3. The BuChE inhibition (IC_{50} μ g/ml), docking scores^a and 2D pose of the major components of the essential oil and the reference compound (**Rivastigmine**).

Comp.	BuChE inhibition (IC_{50} μ g/ml)	Binding energy (Kcal/mol) ^a (docking score)	2D pose
Ah (Isolated volatile oil)	0.154 \pm 0.009		
Rivastigmine	0.078 \pm 0.005	-13.7	
Ah major components	Caryophyllene	NT	-8.9
	Caryophyllene oxide	NT	-12.0
	(+)- Sabinene	NT	-6.6

Comp.	BuChE inhibition (IC ₅₀ ug/ml)	Binding energy (Kcal/mol) ^a (docking score)	2D pose
D-limonene	NT	-6.7	
Alpha-Copaene	NT	-8.6	
Beta-pinene	NT	-7.0	
Trans-verbenol	NT	-7.8	

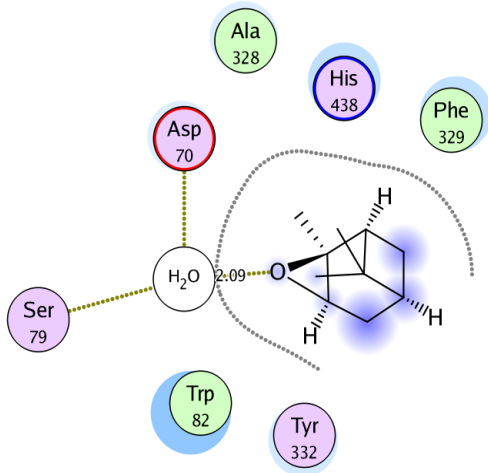
Comp.	BuChE inhibition (IC ₅₀ ug/ml)	Binding energy (Kcal/mol) ^a (docking score)	2D pose
Alpha-pinene oxide	NT	-9.5	

Table S4. The BuChE inhibition (IC₅₀ ug/ml), docking scores^a and type of binding interactions of the major components of the essential oil and the reference compound (**Rivastigmine**).

Major components of the essential oil and the reference compound (Rivastigmine).				
Comp.		BuChE inhibition (IC ₅₀ ug/ml)	Binding energy (Kcal/mol) ^a (docking score)	Type of binding interactions
Ah (Isolated volatile oil)		0.154 ± 0.009		
Rivastigmine		0.078 ± 0.005	-13.7	<ul style="list-style-type: none">Interaction with a water molecule of the binding site that form hydrogen bond with Asp70 and Ser79Strong hydrophobic interaction with Trp82, His438, Gly116 and Phe329
Ah major components	Caryophyllene	NT	-8.9	<ul style="list-style-type: none">Strong hydrophobic interaction with Trp82 and His438
	Caryophyllene oxide	NT	-12.0	<ul style="list-style-type: none">Interaction with a water molecule of the binding site that form hydrogen bond with Asp70 and Ser79Strong hydrophobic interaction with Trp82, His438 and Phe329
	(+)- Sabinene	NT	-6.6	<ul style="list-style-type: none">Strong hydrophobic interaction with Trp82 and His438
	D-limonene	NT	-6.7	<ul style="list-style-type: none">Strong hydrophobic interaction with Trp82 and His438
	Alpha-Copaene	NT	-8.6	<ul style="list-style-type: none">Strong hydrophobic interaction with Trp82 and His438
	Beta-pinene	NT	-7.0	<ul style="list-style-type: none">Strong hydrophobic interaction with Trp82 and His438
	Trans-verbenol	NT	-7.8	<ul style="list-style-type: none">Interaction with a water molecule of the binding site that form hydrogen bond with Asp70 and Ser79Strong hydrophobic interaction with Trp82 and His438

Comp.	BuChE inhibition (IC ₅₀ ug/ml)	Binding energy (Kcal/mol) ^a (docking score)	Type of binding interactions
Alpha-pinene oxide	NT	-9.5	<ul style="list-style-type: none"> Interaction with a water molecule of the binding site that form hydrogen bond with Asp70 and Ser79 Strong hydrophobic interaction with Trp82, His438 and Phe329

- **Rivastigmine** was used as reference BuChE inhibitor compound.
- Docking was carried out following the reported procedure [Nachon, et al., 2013] against the BuChE enzyme pocket (PDB code ID: 4BDS)
- All data are presented as mean value \pm SD for three independent experiments.
- Abbreviation: NT, not tested.
- ^a More negative score refers to better capability of a molecule to dock with the target and make more desirable interactions.

Fig. S2. 3D binding mode and residues involved in the recognition of (a) **rivastigmine**, the compounds showing the best binding interactions (b) **caryophyllene oxide**, (c) **trans-verbenol** and (d) **alpha-pinene oxide** docked and minimized in the BuChE binding pocket

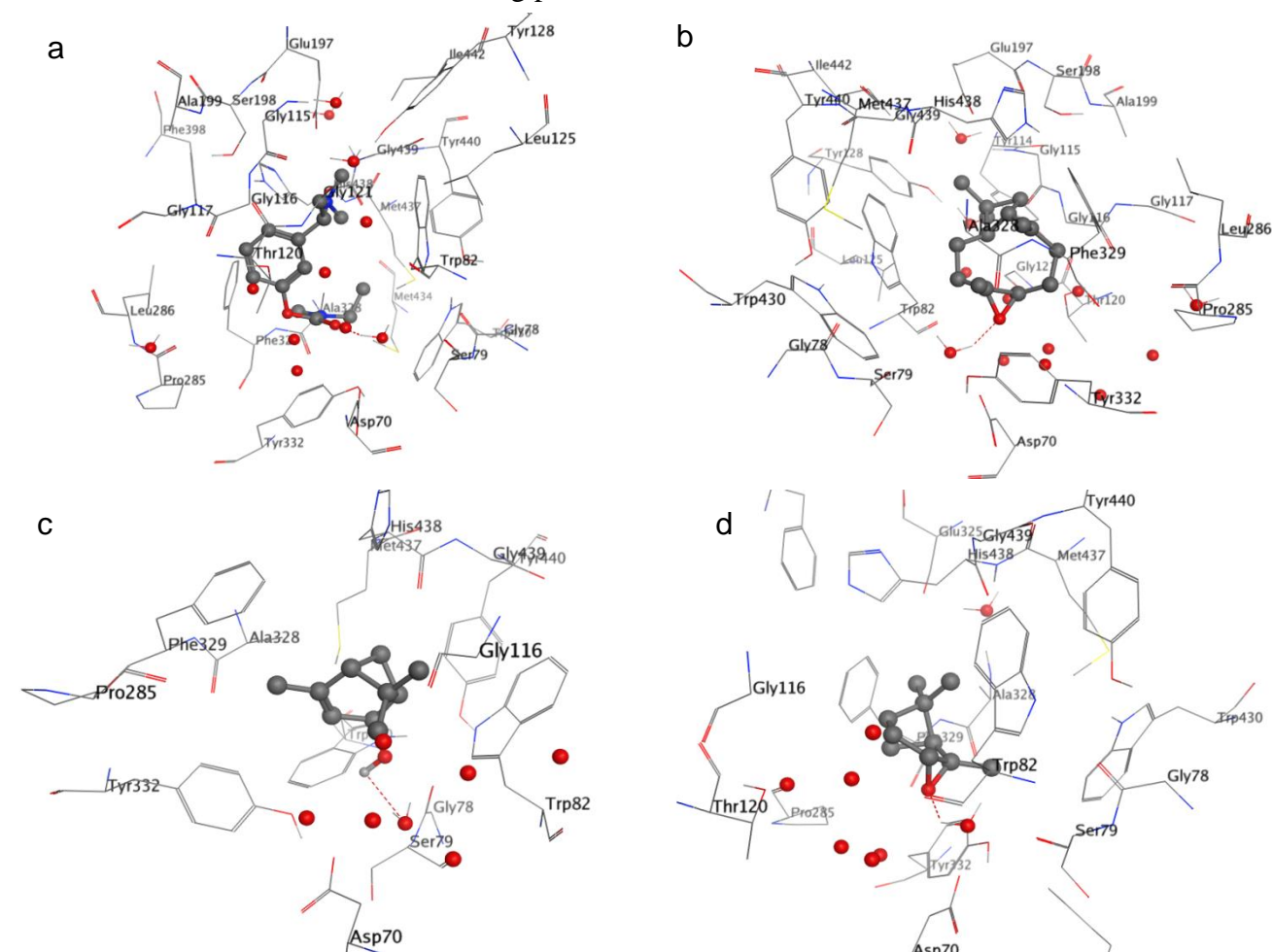


Fig. S2