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# **A combined** *in vitro–in silico* **approach for the discovery of novel endogenous enzymatic and ctDNA sequence of bioactive molecules from aerial and root parts of** *Centaurea sulphurea* **as antioxidant's agents**

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# <span id="page-1-0"></span>A combined in vitro–in silico approach for the discovery of novel endogenous enzymatic and ctDNA sequence of bioactive molecules from aerial and root parts of Centaurea sulphurea as antioxidant's agents

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#### ABSTRACT

The excess free radicals not neutralized by the antioxidant defenses damage the essential macromolecules of our cells, causing abnormalities in the expression of genes and membrane receptors, cell proliferation or death, immune disorders, mutagenesis, deposits of proteins or lipofuschin in tissues. The first objective of this study was to elucidate the composition of the essential oil of the aerial and root part of Centaurea sulphurea during beginning of the vegetative cycle (March), beginning of the flowering stage (April) and full bloom (May/June) using GC/FID and GC/MS. The second aim was to describe the antioxidant activity using three methods (2,2-diphenyl-1-picrylhydrazyl (DPPH), ferric-reducing antioxidant power (FRAP),  $\beta$ -carotene bleaching assay) and bioinformatical study of ctDNA sequence and three endogenous enzymes inhibition. The essential oils obtained from the root during the full bloom period consisted mainly of caryophyllene oxide, aplotaxene and (Z)-phytol. While, the aerial parts were dominated by caryophyllene oxide, verridiflorol and humulene epoxide II. The results showed that essential oil presented an excellent antioxidant activity with  $IC_{50}$  values of 2.06 g/L and 1.29 g/L, for aerial and root parts, compared to butylated hydroxyltoluene (BHT) and Ethylenediaminetetraacetic acid (EDTA) controls and the nicotinamide adenine dinucleotide phosphate (NADPH) co-crystallized inhibitor. The results of the molecular docking revealed that (Z)-phytol (Ligand 39) has an affinity to interact with ctDNA sequence, and three targets Endogenous enzymes. The molecular dynamics study was conducted for the best inhibitors (Z)-phytol. A few key residues were identified at the binding site of receptors. The in-silico assessment of the ADME properties and BOILED-Egg plot reveals that compound (Z)-phytol (L39) is permeable to the blood brain barrier and have high lipophilicity and high coefficient of skin permeability in the intestines with good bioavailability. The ADMET analysis also showed that this oxygenated diterpene is safer to replace the synthetic drugs with side effects. Further testing is needed to assess its effectiveness in reducing oxidative stress for use in the pharmaceutical industry.

#### ARTICLE HISTORY

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#### **KEYWORDS**

C. sulphurea; antioxidant; in silico; ctDNA binding; MOE (Molecular Operating Environment)

# 1. Introduction

Antioxidants have been widely used as additives to help maintain quality and increase the shelf life of the product. Also, antioxidants have an important role in the prevention of various diseases because they suppress active oxygen and lipid peroxidation (Noguchi & Niki, [1999\)](#page-21-0). The antioxidant capacity of essential oils can be evaluated either in vivo, on living organisms or in-vitro, by using methods that involve the mixture of oxidant species with a sample that contains antioxidants capable of inhibiting the generation of free radicals (Alam et al., [2013](#page-19-0)). The latter can act under different mechanisms such as free radical decomposition, free radical scavenging and to chelate ferrous ions (Cam et al., [2009](#page-20-0)). Synthetic antioxidants, such as butylated hydroxyanisole (BHA) and butylated hydroxyltoluene (BHT), have been widely used, but due to their undesirable effect, the naturally occurring antioxidants are highly desirable (Rodil et al., [2012](#page-21-0)). The Centaurea genus presents a great therapeutic interest. This genus belonging to the largest and important genera of Asteraceae family, it accounts for about more than five hundred species distributed all over the world (Trease et al., 1983). Forty-five species are cultivated in Algeria according to Quezel and Santa (Francisco et al., 1995). Among them, C. sulphurea which is an annual herbaceous species. Indeed, several phytochemical and pharmacological studies have shown its richness in natural bioactive substances. Many Centaurea species were used in traditional medicine to treat various diseases, such as diabetes, malaria, hemorrhoids, abscesses and colds (Kargı oğlu et al., [2010\)](#page-20-0). Similarly, it has been beneficial in the treatment of cancer and microbial infections (Kumarasamy et al., [2003;](#page-20-0) Panagouleas et al., [2003\)](#page-21-0). The flowering tops of C. sulphurea

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<span id="page-2-0"></span>are used in decoction against palpitations (Secilla et al., [2012](#page-21-0)). Previous phytochemical work of this species has shown that chloroform extracts of the aerial part were rich in sesquiterpene lactones such as sulfureidine (Lakhal et al., [2010](#page-20-0)) and flavonoid aglycones such cirsilineol, jaceosidin, 3- O-methyl-eupatorin, eptin and eupatilin (Kabouche et al., [2011](#page-20-0)). The endogenous enzymatic antioxidant defense system such as superoxide dismutase (SOD), catalase (CAT), glutathione peroxidase (GPxs), play an important role in homeostatic redox balance (Eddaikra et al., 2021). These defense systems are important and indispensable in the entire defense strategy of antioxidants, especially in reference to super oxide anion radical  $(^*O_2)$  (Ighodaro et al., [2018](#page-20-0)).

The computational technique known as "docking" can predict the binding of drug–target complex, as well as the conformation of the ligand upon binding to a protein target. It makes it possible to represent, interpret and predict biomolecular structures and functions (Mesli et al., [2013\)](#page-21-0).

To the best of our knowledge, no studies have investigated the chemical composition and the biological activities of C. sulphurea essential oil. The main interest of this study was to study first the chemical composition of essential oil of C. sulphurea during the three developmental stages and the investigation of their antioxidant properties. The second study was to try to elucidate how the molecules of this oil interact with three powerful endogenous enzyme (catalase (CAT), superoxide dismutase (SODs), glutathione peroxidase (GPx)) and ctDNA sequence. Knowing that these endogens are active in endothelial cells, cytoplasm and mitochondrial intermembrane matrix (Oury et al., [1996](#page-21-0)).

The previous studies have shown that the catalase activation with a natural antioxidant component, which doesn't have toxicity, can provide useful results in the health field (Najjar et al., [2017\)](#page-21-0). Also, other researchers have reported that catalase inhibition by wogonin led to  $H_2O_2$  accumulation and cytotoxicity in cancer cells through  $H_2O_2$ -mediated  $NF-\kappa B$  suppression and apoptosis activation (Pal et al., [2014;](#page-21-0) Yang et al., [2011](#page-22-0)). In this research, the plat form package MOE (Molecular Operating Environment) was used to study the modeling applications between all compounds of C. sulphurea essential oil and the catalase enzyme. After that, the compounds that achieved both good score in docking with catalase were docked with two endogenous enzymes: Superoxide Dismutase (Manjula et al., [2018](#page-20-0)), Glutathione Peroxidase (Tars et al., [2010\)](#page-21-0) enzymes and Ct-DNA sequence (CGCGAATTCGCG)2 dodecamer (Drew et al., [1980\)](#page-20-0), in order to validate the best interactions with the nucleotides and their affinities.

The main interest was to develop unique potential inhibitors of endogenous enzymatic (catalase (CAT), superoxide dismutase (SODs), glutathione peroxidase (GPx) and ctDNA sequence, to combat free radicals and protect the body from the damage caused by them. The docking studies predicted that the constituent molecules of the aerial and root parts of essential oil of C. sulphure possess more capability as inhibitors as compared to established drugs in the pharmaceutical industry. Further, five designed compounds were filtered

through Lipinski's rule of five, along with ADMET risk parameters assessments. Finally, the top hit compound Z-phytol was analyzed by system pharmacology approaches.

# 2. Material and methods

#### 2.1. Experimental procedures

#### 2.1.1. Chemicals used in the study

Solvents and reagents used were 2,2-diphenyl-1-picrylhydrazyl (DPPH) and 2,2'-azino-bis(3-ethylbenzothiazoline-6-sulfonic acid (ABTS), ethanol, methanol, potassium persulfate, iron chloride, ferrozine, BHT, EDTA, Quercetin and anhydrous sodium sulphate were purchased from Sigma (Sigma-Aldrich). In this study, we used analytical grade chemicals.

#### 2.1.2. Plant material and extraction of essential oil

The plant materials of C. sulphurea were collected in the Zarifet forestwit latitude: 1°19'08''O; longitude: 34°52'20''N; altitude: 990 m) about 10 km from Tlemcen (Algeria). The essential oils of the aerial and root parts used for the study were collected at the beginning of April (Vegetative stage), at mid-May (Floral budding stage) and at the end of June (Flowering stage). The plant was identified by the botanist BABA Ali from the Department of Agronomy of the University of Tlemcen (Algeria), where a voucher specimen of the plant has been deposited in the Herbarium. Plant materials were air-dried at room temperature and submitted to hydro-distillation for 4 hours using a Clevenger apparatus according to the procedure described in the European Pharmacopeia (Conseil de l'Europe, [1996](#page-19-0)). The essential oils were treated with anhydrous sodium sulphate ( $Na<sub>2</sub>SO<sub>4</sub>$ ) and stored in a sealed tube at  $-4^{\circ}$ C until further used for chemical analysis and antioxidant activity.

# 2.1.3. Identification of the oil components

2.1.3.1. Gas chromatography. The gas chromatography (GC) analysis was carried out using Clarus 500-Perkin-Elmer Auto system apparatus (Waltham, Massachusetts, USA) equipped by two flame ionization detectors (FID), with fused capillary columns (film thickness 0.25  $\mu$ m;50 m  $\times$  0.22 mm I. D), BP-1 (polymethyl-siloxane) and BP-20 (polyethylene glycol); carrier gas, helium; linear velocity, 0.8 mL/min (Bekhechi et al., [2010\)](#page-19-0). The oven temperature was fixed from  $60^{\circ}$ C to 220 °C at 2 °C/min and then held isotherm (20 min) (Bereksi et al., [2018](#page-19-0)), injector temperature was 250 $\degree$ C (injection mode: split  $1/60$ ; detector temperature 250 $^{\circ}$ C. The relative proportions of the essential oil constituents were expressed as percentages obtained by peak area normalization, without using correction factors, as described previously (Medbouhi et al., [2018](#page-20-0)).

2.1.3.2. Gas chromatography/mass spectrometry (GC/MS). Essential oils were analyzed with a Perkin ElmerTurbo-Mass quadrupole analyzer, coupled to a Perkin Elmer Auto system XL (France), equipped with two fused-silica capillary columns and operated with the same gas chromatography conditions <span id="page-3-0"></span>described above, except for a split of 1/80. Under the following conditions, EI mass spectra were acquired: Ion source temp. 150 $^{\circ}$ C, energy ionization 70 eV, mass range 35-350 Da (scan time: 1 s) (Zatla et al., [2017\)](#page-22-0).

#### 2.1.4. Component identification and quantification

Quantification and identification of the components were made (i) through the comparison of their GC retention indices (RI) on nonpolar and polar columns, determined relative to the retention time of a series of n-alkanes with linear interpolation, with those of authentic compounds or litera-ture data (Bouyanzer et al., [2006](#page-19-0); Jennings et al., 1980; König et al., [2004](#page-20-0)) and (ii) also through computer matching with commercial mass spectral libraries (National Institute of Standards and Technology, [1999](#page-21-0)) and comparison of spectra with those of in-library of laboratory of chemistry of natural products, University of Corsica (France). Component quantification was carried out using peak normalization % abundances calculated by integrating FID response factors relative to tridecane (0.7 g/100 g), used as an internal standard.

#### 2.1.5. Antioxidant assays

2.1.5.1. DPPH free radical scavenging assay. The essential oil from the **flowering stage (June)** was used for the evaluation of antioxidant activity. Radical scavenging activity of essential oil was measured by the standard method and determined by using spectrophotometer. A volume of 1000  $\mu$ l of various concentrations of oil ranging from (0.2–15 g/L) were prepared in ethanol and added 1 mL of 0.2 mM DPPH solution freshly prepared. After 30 min of incubation at  $37^{\circ}$ C in the dark, the anti DPPH activity was measured by recording the absorbance at 517 nm against blank and standard (BHT). The percentage inhibition activity was calculated by the following equation (Dhami et al., 2018).

$$
DPPH\ scavenging effect\% = \frac{(Acontrol - Asample)}{Acontrol}
$$
\n
$$
\times 100
$$
\n(1)

where  $A_{control}$  is absorbance of DPPH radical (without the test sample), and A<sub>sample</sub> is the absorbance of DPPH radical with the oil samples of various concentrations. The  $IC_{50}$  (Halfmaximal inhibitory concentration) was calculated graphically by the linear regression formula of the inhibition percentages as a function of different concentrations of the sample tested (Belabbes et al., [2017](#page-19-0)).

2.1.5.2. Metal chelating activity. The metal chelating assay by oils was examined by spectrophotometry method based on ability of essential oil to chelate transition metal ions  $Fe^{2+}$  by measuring the absorbance of iron-ferrozine complex formed at 562 nm (Kumar et al., [2012;](#page-20-0) Parki et al., [2017](#page-21-0)). In brief 100  $\mu$ l of (0.6 mM) FeCl<sub>2</sub>, 100  $\mu$ l of 5 mM ferrozine and 900  $\mu$ l mL of methanol were added to various concentrations of tested sample (0.2–15 mg/mL). The solutions were mixed thoroughly and incubated for 10 min (Dhami et al., 2018). The absorbance of test sample was measured in a UV spectrophotometer at 562 nm. All the readings were recorded in duplicate; EDTA

(0.01 mM) was used as the standard. The metal-chelating activity of tested samples, expressed as percentage was calculated by using the following formula (Dhami et al., 2018).

Chelating activity % = 
$$
\frac{(control - sample)}{control} \times 100
$$
 (2)

The  $IC_{50}$  was calculated graphically by the linear regression formula of the inhibition percentages as a function of different concentrations of the sample tested.

2.1.5.3.  $\beta$ -carotene bleaching assay. The ability of C. sulphurea essential oils to protect lipid peroxidation was assessed by using the  $\beta$ -carotene bleaching test (Sangwan et al., [2001\)](#page-21-0) this method is commonly used because  $\beta$ -carotene is an important physiological compound however it shows a strong biological activity (Kim et al., 2004). BHT was the positive control. Briefly, a mixture of  $\beta$ -carotene, Linoleic acid, and Tween 40 was prepared. The solvent was evaporated entirely by using a rotary evaporator. 100 mL of distilled water saturated with oxygen was added and shaken vigorously to form an emulsion. Then, 2.5 mL of the obtained emulsion was transferred into test tubes with 3.5 mL sample at different concentrations. The reaction mixture was maintained at  $50^{\circ}$ C for 120 min, and the absorbance was measured at 470 nm using spectrophotometer against a blank consisting of an emulsion without  $\beta$ -carotene (Stankovic et al., [2020](#page-21-0)). The  $\beta$ -carotene bleaching assay was calculated as follows (Stankovic et al., [2020\)](#page-21-0):

$$
\beta - \text{carotene activity } \% = \frac{(As(120) - AC(120))}{(AC(0) - AC(120))} \times 100
$$
\n(3)

where  $A_{s(120)}$  is the absorbance of the sample at  $t = 120$  min,  $A_{C(120)}$  is the absorbance of the control at t = 120 min, and  $A<sub>C(0)</sub>$  is the absorbance of the control at t = 0 min. The IC<sub>50</sub> was calculated graphically by the linear regression formula of the inhibition percentages as a function of different concentrations of the sample tested.

#### 2.2. Theoretical background and computational details

#### 2.2.1. Preparation and optimization of both enzyme and inhibitors

In this study, the structures of all compounds were downloaded from PubChem database ([https://pubchem.ncbi.nlm.](https://pubchem.ncbi.nlm.nih.gov) [nih.gov\)](https://pubchem.ncbi.nlm.nih.gov). The 3D structures of all compounds were pre-optimized by means of the Molecular Mechanics using Force Field  $MM+$ . After that, the resulted minimized structures were further refined using the semi-empirical method (AM1) (Stewart et al., [2007](#page-21-0)). All methods are implemented in Hyperchem 8.0.8 software (HyperChem v8, [2009\)](#page-20-0). At the end, the database was created in which all the compounds were converted into their 3D structures and this database was used as an input file in MOE-docking. Both crystallographic structures of the human catalase (PDB ID: 1dgb Resolution  $= 2.20 \text{ Å}$ ) as can be seen from [Figure 1](#page-6-0), R-Value Free 0.227 (Putnam et al., [2000\)](#page-21-0) and Ct-DNA sequenced (CGCGAATTCGCG)2 dodecamer (PDB ID: 1BNA; Resolution  $= 1.90 \text{ Å}$ ), R-Value Free 0.178 (Drew et al.,

<span id="page-4-0"></span>1980) (were retrieved from the Protein Data Bank (PDB) (PDB; <http://www.rcsb.org/pdb/home/home.do>). In general, the protein structure with a resolution between 1.5 and 2.5 Å have an excellent quality for further studies (Cl ement & Slenzka, [2006;](#page-19-0) Didierjean & Tête-Favier, [2016](#page-19-0)), whereas, the resolution value of catalase and B-DNA belongs to this interval. Receptor (DNA) and ligand (the complex) files were prepared using platform package MOE (Molecular Operating Environment). The complex was enclosed in a box with the number of grid points in  $x \times y \times z$  directions (122 × 72 × 6), and a grid spacing of 0.375 Å. All other parameters were default settings. For each of the docking cases, the lowest energy docked conformation, according to the package MOE (Molecular Operating Environment (MOE), 2013) scoring function, was selected as the binding mode.

#### 2.2.2. Molecular docking

In this research, the platform package MOE (Molecular Operating Environment) was used to study the modeling applications between all compounds and the catalase enzyme. After that, the compounds that achieved good score in docking with catalase were docked to two Endogenous enzymes: Superoxide Dismutase (PDB ID: 5ytu) (Manjula et al., [2018\)](#page-20-0), Glutathione Peroxidase (PDB ID: 2vcv) (Tars et al., [2010\)](#page-21-0) enzymes and Ct-DNA sequence (CGCGAATTCGCG)2 dodecamer (PDB ID: 1BNA) (Drew et al., 1980), in order to validate the best interactions with the nucleotides and their affinities. During the docking process the ligand was considered structurally rigid while the target was set as completely flexible. The wash setting was applied at pH6.0 and 300 K, hydrogen atoms were added, and protonation 3D were assigned. The minimum energy configuration was performed using the MMFF94x force field. OPLS-AA force field was used with conjugant gradient method (Jorgensen et al., [1996](#page-20-0)). To assign atom type and partial charges in receptor structure. The number of interactions varies between (0, n) where n is 10, the cut-off for coulomb interaction and Van der Waals interactions was 30 Å with the ability to study the hydrogen-electrostatic in the total active site of catalase was optimized and the results were discussed. Also, we followed the same protocol of Molecular docking simulation which is used in our previous studies (Chenafa et al., [2021](#page-19-0); Daoud et al., [2018\)](#page-19-0). The following default parameters were used: Placement: Triangle Matcher; Rescoring 1: London dG. The London dG scoring function was employed to estimate the lowest score energy of the complex for the best pose of the compounds tested. All simulations were run by using all explicit solvation models using TIP3P water. After that, the RMSD value was used to compare the differences between the atomic distances of the docked poses and the ligand molecule of reference pose (NADPH), where a threshold of 2.0 Å corresponding to the better solution (Cross et al., [2009](#page-19-0)). In the end, the binding energy between ligands and target catalase was calculated using molecular mechanics (MOE, 2013) and based on molecular mechanics (Halgren, [1996,](#page-20-0) [1999](#page-20-0)). The results of the top scoring complexes in the active site were selected for the further molecular dynamics simulation study.



# 2.2.3. Molecular dynamics simulation, ADMET, cytochromes P450 and pharmacophore mapping

The potent compound which has best binding affinity (Score) and one almost a stable interaction with the catalase target was subjected to Molecular dynamics simulations. Molecular dynamics simulations (MD) were run by Nanoscale Molecular Dynamics (NAMD) for 100 ns for the complex (1dgb-compound). The Langevin equation (Toda et al., [1991\)](#page-21-0) is used in NAMD to generate the Boltzmann distribution (canonical NVT, isobar-isotherm NPT) for units and simulations. The Brunger-Brooks-Karplus (BBK) method is used to integrate the Langevin equation (Brünger et al., [1984\)](#page-19-0). The equations of motion (position and velocity) are described by Fokker-Planck (Wang & Skeel, [2003](#page-22-0)). The detailed analysis of (MD) simulation results of complex-L39 with target catalase is summarized in [Figures 7](#page-16-0) and [8.](#page-17-0) Moreover, the stable conformation obtained in the MD simulation of the best complex was conducted by Internal coordinates normal mod analysis server (IMODS). Internal coordinate's normal mode analysis server (IMODS) is a web-based software system. It can be used to investigate the values of deformability, eigenvalues, variance, co-variance map and elastic network. The software package MOE (Molecular Operating Environment) has proven its performance in several recent studies and has been invoked, for example: Stitou et al. [\(2021\)](#page-21-0), Daoud et al. [\(2018\)](#page-19-0), Chenafa et al. ([2021](#page-19-0)), Mesli et al. [\(2019\)](#page-20-0), and Mesli et al. [\(2021\)](#page-21-0). Among the 60 (according to [Table 2\)](#page-5-0) selected compounds the molecular structures of the best compounds were analyzed using a SWISS ADME) server ([http://www.swis](http://www.swissadme.ch/)[sadme.ch/\)](http://www.swissadme.ch/). The results of absorption, distribution, metabolism and excretion (ADME) for selected compounds are listed in [Table 12](#page-12-0). These results prescribe that the ADMET-score would be a comprehensive index to estimate chemical druglikeness. The drug score associate drug likeness, cLogP, LogS, molecular weight and toxicity risks in one handy value than may be attuned to judge the compound's overall potential to quality for a drug (Geronikaki et al., [1999](#page-20-0); Lipinski et al., [1997](#page-20-0)). In this study, prediction and descriptors of druglikeness such as mutagenic, toxicological dosage level were predicted using a PreADMET server ([http://preadmet.bmdrc.org/\)](http://preadmet.bmdrc.org/) and admetSAR server [\(http://lmmd.ecust.edu.cn:8000/\)](http://lmmd.ecust.edu.cn:8000/). All results of toxicological pathways, including organ toxicity, toxicity and stress response pathways are given in [Table 13.](#page-12-0) To identify the toxicity of the selected best ligands Z-phytol, Eicosane, BHT, EDTA and analogues compounds of L39 and L42, we used Protox II (Banerjee et al., [2018\)](#page-19-0). Cytochromes P450 are key enzymes involved in the metabolism of various endogenous or exogenous molecules. The results of The P450 sites of metabolism (SOM) of the best compound L39 were determined by online tool, RS-WebPredictor 1.0 (Release, [2018](#page-21-0)) and listed in [supplementary Table S11.](https://doi.org/10.1080/07391102.2022.2090438) The

<span id="page-5-0"></span>Table 2. Chemical compositions of C. sulphurea essential oils during three developmental stages.

		Aerial part of C. sulphurea essential oils	



#### <span id="page-6-0"></span> $6 \Leftrightarrow$  B. LYNA ET AL.

#### Table 2. Continued.



RI: retention indices, MS: mass spectra in electronic impact mode. <sup>a</sup>Order of elution is given on apolar column (Rtx-1). <sup>b</sup>Retention indices of literature on the apolar column (IRIA).

<sup>c</sup>Retention indices on the apolar Rtx-1 column (RIA).

d Retention indices on the polar Rtx-Wax column.

Table 3. Antioxidant activity ( $IC_{50}$ s) of essential oils of C. sulphurea.



 $SD =$  standard deviation.



Figure 1. (a) The active site of isolated catalase. (b) Simplified model of catalase.



Figure 2. Distribution of variables of chemical composition of Centaurea sulphurea roots during the vegetative cycle.

pharmacophore mapping study of the best ligand was carried out by online server Pharm Mapper (Parr et al., 1989). It consists of identifying common binding elements that is responsible for the biological activity and determining the 3D relationship between pharmacophore elements in each conformation generated (Vyas et al., [2008](#page-21-0)). The pharmacophore modelling was done for the best ligand molecule among the 60 (according to [Table 2\)](#page-5-0) a selected molecule is summarized in [Figure 9](#page-18-0). However, in this study the P450 sites of metabolism (SOM), toxicological pathways, ligand-based pharmacophore modeling, drug likeness prediction and ADMET-calculations were carried out to determine and compare the biological

#### 3. Results and discussion

activities of the two best ligands.

#### 3.1. Experimental approach

#### 3.1.1. Essential oil yields

The essential oil yield of the aerial and root parts of C. sulphurea varied remarkably during the three stages of development of the plant. The essential oils yield of aerial and root parts was the lowest (0.05% and 0.15, respectively) during the first vegetative stage. Then it increased appreciably as the floral budding stage outset (0.16% and 0.29%) and reached 0.25% and 0.38% at the flowering stage, respectively [\(Table 1\)](#page-4-0). This increase in yield can be explained by the length of the vegetative cycle, summer heat and the effect of water stress (Kim et al., [2004;](#page-20-0) Sangwan et al., [2001](#page-21-0)).

## 3.1.2. Chemical composition of C. sulphurea essential oil

The analysis of essential oils of the aerial and root parts of C. sulphurea during three stages of development of the plant was analyzed by GC and GC/MS and identified by comparison of their retention indices and mass spectra with those of

<span id="page-7-0"></span>Table 4. Energy minimization of the best compounds for antioxidant drug.

Ligand compound		Toxic	LogP	Energies (kcal/mol)	LogS	$H$ don $+$ Hacc	Flexibility
L22	$\beta$ -Cadinene	No	4.58	$2.60161e + 001$	$-4.67$	don:0:acc:0	l out 1
L <sub>23</sub>	$\delta$ -Cadinene	No	4.58	$2.95608e + 001$	$-5.17$	don:0:acc:0	1 out 1
L24	3-(Z)-Hexenyl-benzoate	No	3.20	$3.01393e + 001$	$-3.30$	don:0:acc:1	$6$ out $6$
L30	Ƴ-Eudesmol	No	4.06	$3.84759e + 001$	$-3.67$	don:1:acc:1	1 out 1
L33	$\beta$ -Eudesmol	No	3.92	$4.47669e + 001$	$-4.36$	don:1:acc:1	1 out 1
L36	(Z.Z)-Farnesol	No	4.40	$1.60145e + 001$	$-4.25$	don:1:acc:1	7 out 7
L39	(Z)-Phytol	No	6.36	$1.72039e + 001$	$-8.27$	don:1:acc:1	13 out 13
L <sub>40</sub>	Heneicosane	No	8.44	$-8.49952e + 000$	$-10.66$	don:0:acc:0	18 out 18
L42	Eicosane	No	8.05	$-8.29676e + 000$	$-10.15$	don:0:acc:0	17 out 17
L50	Geranyl acetate	No	3.24	$9.02954e + 000$	$-3.02$	don:0:acc:1	6 out 6
L58	Aplotaxene	No	5.98	$1.22114e + 001$	$-7.27$	don:0:acc:0	11 out 11
L <sub>59</sub>	Hexadecanoic acid	No	5.55	$-1.46061e + 001$	$-6.49$	don:2:acc:1	14 out 14
L60	(E)-Phytol	No	8.27	$1.77210e + 001$	6.36	don:1; acc:1	13 out 13

Table 5. S-score (Energy) and interactions between best compounds and the active site residues of catalase target.



H = Conventional hydrogen bond, C = Carbon hydrogen bond, Aa = Alkyl-alkyl, Ap = Alkyl-Pi, Aps = Amide-Pi stacked, Ppt = Pi-pi T-shaped, X = Halogen.

the "Aromas" library specific to the laboratory of the University of Corsica. The chemical compositions are presented in [Tables 2](#page-5-0) and [3.](#page-6-0) Eight monoterpene hydrocarbons, nine sesquiterpene hydrocarbons, three oxygenated monoterpenes, sixteen oxygenated sesquiterpenes, four oxygenated diterpenes and two non-terpenic compounds were identified in the aerial parts. Throughout the vegetative cycle (May–June), the essential oil of aerial parts has been characterized by a high percentage of oxygenated sesquiterpenes characterized by caryophyllene oxide (10.5–29.6%), verridiflorol (4.9–12.8%) and humulene epoxide II (3.7–6.5%). At the vegetative stage and the floral budding stage, the hydrocarbon monoterpenes and the hydrocarbon sesquiterpenes were present in low amounts with percentages varying from 1.2–3.9% and 5.9–9.6%. Then at the flowering stage, they increased at 20.6% and 10.9%, respectively [\(Table 2\)](#page-5-0). At the vegetative stage (May), the aliphatic compounds were more predominant (14.9%) followed by heneicosane (7.3%) and eicosane (6.5%) [\(Table 2](#page-5-0)).

The chemical compositions of root parts are presented in [Table 3.](#page-6-0) Eighteen components were detected, accounting for 95.1% at the vegetative stage, 90.9% at the floral budding and 91.7% at the flowering stage. The essential oil of root parts of vegetative stage contains aliphatic compounds (35.8%), oxygenated sesquiterpenes (33.2%), hydrocarbon sesquiterpenes (10.6%) and oxygenated diterpenes (10.3%) ([Table 2](#page-5-0), [Figure 1](#page-6-0)). The oil contains caryophyllene oxide (32.1%), aplotaxene (27.9%) and (E)-phytol (10.3%) as main components. At the floral budding, the essential oil of C. sulphurea was dominated by oxygenated sesquiterpenes (29.8%) and aliphatic compounds (28.3%), followed by oxygenated diterpenes (15.4%) and hydrocarbon sesquiterpenes (12.3%) [\(Figure 1\)](#page-6-0). The main components were caryophyllene oxide (19.1%), aplotaxene (15.5%), (E)-phytol (15.4%) and hexadecanoic acid (12.3%). On the other hand, at the flowering stage, the oil of roots was dominated by oxygenated diterpenes (28.6%), oxygenated sesquiterpenes (18.4%), aliphatic compounds (17.9%), hydrocarbon sesquiterpenes (17.9%) and small amount of hydrocarbon monoterpenes (8.4%) ([Table 2](#page-5-0) and [Figure 2\)](#page-6-0). The main components were (E)-phytol (28.6%), (E)- $\beta$ -caryophyllene (16.6%), caryophyllene oxide (14.6%), aplotaxene (10.5%) and  $\beta$ -pinene (8.1%). It is noteworthy that the normalized percent abundances of major oil components varied greatly according to physiological stage.

A significant increase in hydrocarbons sesquiterpenes were observed with a percentage for 10% at the vegetative stage to 18% at the floral stage compared to oxygenate which decreased (33% to 18%). However, caryophyllene oxide and aplotaxene, showed a significant decrease of their percentage during vegetative monitoring (32 to 14%) and (27 to 10%), respectively. However, the content of oxygenated diterpenes increased significantly at the budding and flowering stages, with a percentage of 15.4% and 28.6% respectively. While the content of aliphatic compounds was at 35.8% decreased to 17.9% at the flowering stage [\(Table 2](#page-5-0)).

From our results cited in [Table 2](#page-5-0), we were able to trace the variation in the contents of the different chemical classes of essential oils from roots C. sulphurea see [Figure 2](#page-6-0). The distribution [\(Figure 2](#page-6-0)) showed that the essential oil was rich in oxygenated sesquiterpenes (18.4–33.2%) and aliphatic components (17.9–35.8%) during the month of April. However, the percentage of hydrocarbon sesquiterpenes was relatively

<span id="page-8-0"></span>Table 6. The docking energies of best DNA inhibitors.

Ligand	Compound	DE. (kcal/mol) ctDNA	$DE^*$ (kcal/mol) Catalase	ETOR (kT)	VDW (kT)	EIE (kT)
<b>BHT31404</b>		$-4.743$	$-5.052$	330.721	413.487	$-1942.09$
<b>EDTA6049</b>		$-4.965$	$-5.591$	330.722	413.486	$-1942.09$
Lref		$-5.900$	$-8.043$	330.722	413.486	$-1942.09$
L39	$(Z)$ -Phytol	$-6.978$	$-7.184$	330.723	413.317	$-1942.01$
L40	Heneicosane	$-6.819$	$-6.809$	330.724	413.316	$-1942.01$
L42	Eicosane	$-6.858$	$-7.158$	330.724	413.316	$-1942.01$
L59	Hexadecanoic acid	$-6.516$	$-6.266$	330.725	413.315	$-1942.01$
L60	(E)-Phytol	$-6.425$	$-6.908$	330.720	413.488	$-1942.09$

DE: Energy, ETOR: Energy Torsion, VDW: Van Der Walls, EIE: Electrostatic.

Table 7. Interaction profiles of the **potential** compounds for three *Endogenous Enzymatic* inhibitors.

No.	Compound	<b>Targets</b>	Energy (kcal/mol)	Energy torsion (kT)	Van Der Walls (kcal/mol)	Electrostatic (kcal/mol)
Lref	<b>NADPH</b>	CAT	$-8.043$	2603.149	8687.066	$-22,383.8$
		SOD	$-3.247$	637.836	3687.273	$-10,233.1$
		<b>GPX</b>	$-6.176$	1134.834	4767.672	$-12,474.1$
L39	(Z)-Phytol	<b>CAT</b>	$-7.184$	2537.734	8664.659	$-22,264.6$
		<b>SOD</b>	$-\overline{3.993}$	598.608	4192.510	$-10,291.6$
		<b>GPX</b>	$-4.413$	1091.834	4753.317	$-12,384.3$
L40	Heneicosane	<b>CAT</b>	$-6.809$	2522.562	8677.642	$-22,285.8$
		SOD	$-4.142$	581.009	3691.151	$-10,289.5$
		<b>GPX</b>	$-4.340$	1054.875	4788.068	$-12.421.7$
L42	Eicosane	CAT	$-7.158$	2515.807	8661.011	$-22,263.4$
		SOD	$-\overline{4.163}$	581.203	3704.941	$-10,281.9$
		<b>GPX</b>	$-\overline{4.686}$	1060.625	4773.694	$-12,419.8$
L <sub>59</sub>	Hexadecanoic acid	CAT	$-6.266$	2527.458	8649.425	$-22,338.3$
		SOD	$-3.617$	590.860	3763.376	$-10,415.7$
		<b>GPX</b>	$-4.748$	1077.965	4792.381	$-12,482.6$
L60	(E)-Phytol	CAT	$-6.882$	2533.186	8651.835	$-22,244.0$
		SOD	$-3.798$	598.256	3744.463	$-10,344.5$
		GPX	$-5.281$	1067.257	4775.731	$-12,435.8$

DE: docking energy; ETOR: Torsion energy; VDW: Van der Waals; EIE: Electrostatic Interaction Energy.

lower (4.2–8.4%) compared to oxygenated sesquiterpenes during the month of June. The, oxygenated monoterpenes (0.–-.09%) constitute the lowest percentage classes during the month of May. Previous work has shown that the main components of essential oils of C. dimorphaViv. and C. apiculata Lebed collected in Algeria and Bulgaria, respectively were rich in caryophyllene oxide with a percentage of (9.9% and 15.8%) (Belkassam et al., [2019](#page-19-0); Riccobono et al., [2017](#page-21-0)). However, hexadecanoic acid was detected as main constituent in essential oils of C. pterocaula Trautv (Sen et al., [2021](#page-21-0)), C. aggregata subsp. aggregata, C. balsamita and C. Behen (Erdogan et al., [2017\)](#page-20-0) from Turkey with a percentage ranging from 23.0% to 35.8%, similarly for essential oil from Lebanon (33.2%) (Senatore et al., [2005](#page-21-0)). On the other hand, the main component obtained from the essential oils of C. pumilio from Egypt was pentadecane (17.8%) (Naeim et al., [2020](#page-21-0)), C. damascena from Jordan was fokienol (11.4%) (Khleifat et al., [2019](#page-20-0)), C. polymorpha from Spain was Heptacosane (11.5%) (Formisano et al., [2006](#page-20-0)) and C. grinensis from Croatia was pvinyl guaiacol (21.5%) (Riccobono et al., [2017\)](#page-21-0). Benzyl benzoate (26.5%) and geranial (38.6%) were detected as the main constituents of essential oils of C. ispahanica Boiss and C. irritans from Iran, respectively (Formisano et al., [2006](#page-20-0); Khleifat et al., [2019](#page-20-0)). The essential oils of C. grisebachii subsp. Grisebachii and C. affinis Friv. from Greece were dominated by 6,10,14-trimethyl-pentadecan-2-one (12.9%) and tetracosane (7.8%) (Djeddi et al., [2011\)](#page-20-0). Essential oils of C. paniculata Subsp. Carueliana and C. rupestris from Italy were constituted by (Z)-3-hexenol (16.5%) and germacrene D (42.3%) (Tava et al., [2010](#page-21-0)).

# 3.1.3. Evaluation of the antioxidant activities of essential oils

The antioxidant activities were performed using the free radical scavenging activity (DPPH), metal chelating tests and  $\beta$ -carotene bleaching assay, using BHT and EDTA as a positive control ([Table 3\)](#page-5-0).

The free radical scavenging activity of C. sulphurea essential oil was analyzed using DPPH assay. Varying concentrations of the samples were used from 0.2 to 15 g/L. It has been observed that the free radical scavenging activity increases with the increase in concentration oils [\(Table 3\)](#page-5-0). It is also observed that the aerial and root parts of essential oils had good antioxidant activity, with  $IC_{50}$  values of 2.06 g/ L and 1.29 g/L, respectively, but this activity remains lower compared to the BHT control (IC<sub>50</sub> = 0.26 g/L).

Chelating activity on  $Fe^{+2}$  of essential oils of C. sulphurea was estimated using various amounts of oil from 0.2 to 15 mg/mL. From the  $IC_{50}$  values obtained, it was observed that the oil of the aerial part ( $IC_{50} = 2.02$  g/L) exhibited a greater inhibitory activity than the essential oil of the root part (IC<sub>50</sub> = 2.96 g/L), while that of the EDTA control, the  $IC_{50}$  was 1.03 g/L ([Table 3\)](#page-5-0). These oils either chelated metal ions or suppressed reactivity by occupying all coordination sites of metal ions (Mohaney et al., 1985).

 $\beta$ -carotene-linoleic acid activity of essential oils of C. sulphurea was estimated using various concentrations from 5.0 to 38 g/L for essential oils and 0.1 to 8.0 g/L for BHT. From the  $IC_{50}$  values obtained, it has been observed that the oil from the root part showed a greater inhibitory activity with an IC<sub>50</sub> of 36.6 g/L contrary to the aerial part (IC<sub>50</sub> = 38.4 g/

<span id="page-9-0"></span>L). The standard has the highest activity with an  $IC_{50}$  of 0.59 g/L. The rate of  $\beta$ -carotene bleaching can be slowed down in the presence of antioxidants (Oke et al., [2009](#page-21-0)). Indeed, this last one is a free radical mediated phenomenon resulting from the hydroperoxides formed from linoleic acid, which attack the highly unsaturated  $\beta$ -carotene molecules (Wang et al., [2008](#page-22-0)).

It can be concluded that the essential oils of C. sulphurea showed significant antioxidant potential, presumably due to qualitative and quantitative difference of their components. This antioxidant effectiveness of aerial and root parts essential oils may be attributed primarily to the presence of  $(E)$ - $\beta$ -caryophyllene and caryophyllene oxide in high concentrations. Indeed, it has been previously shown that species rich in these compounds possessed appreciable antioxidant activity (Figueiredo et al., [2019](#page-20-0); Sarikurkcu et al., [2018;](#page-21-0) Nafis et al., [2019](#page-21-0)). Also, the activity of the root part could be explained by the presence of the dominating compound aplotaxene, but to our knowledge there are no studies on evaluation of the antioxidant capacity of hydrocarbons compounds.

#### 3.2. Theoretical and computational methods

## 3.2.1. Evaluation of molecular docking

3.2.1.1. Properties of compounds. The information of best compounds after docking was obtained from MOE software (Molecular Operating Environment (MOE), [2019\)](#page-21-0) and Molegro Virtual Docker (MVD) software (Thomsen et al., [2006](#page-21-0)) given for ligands in [Table 4](#page-7-0) and properties of other compounds of aerial and root part of C. sulphurea are listed in [Tables S1](https://doi.org/10.1080/07391102.2022.2090438) and [S2](https://doi.org/10.1080/07391102.2022.2090438) ([Supplementary Materials\)](https://doi.org/10.1080/07391102.2022.2090438), respectively.

According to the table above, we note also that the five molecules (Z)-phytol, heneicosane, eicosane, hexadecanoic acid and (E)-phytol have a high value of flexibility compared to other molecules and also the results obtained show that these five ligands have a high value of torsion angle relative to other compounds. This shows that these compounds L39, L60, L59, L40 and L42 are more flexible. In addition, it is noted that the growth of the torsion angle depends on the binding number of the compound.

3.2.1.2. Identification of the best poses based on affinity of compounds with catalase target. The results obtained after the docking calculations and the five best poses received for the best compounds with the pocket of the catalase target have been listed in [Table 5](#page-7-0) and the results of energy (binding affinity) for other compounds are listed in [Tables S3](#page-6-0)–[S5](#page-7-0) [\(Supplementary Materials](https://doi.org/10.1080/07391102.2022.2090438)).

# 3.2.1.3. Interaction with catalase, CtDNA sequence and endogenous enzymatic antioxidant systems

3.2.1.3.1. Interaction with catalase. The results obtained show that the scores of binding free energies of all complexes (1dgb-compound) were between  $-3.819$  and 7.184 kcal/mol and the complexes formed by compounds: L39 and L42 have the lowest score of binding energy compared to the other complexes (see [Table 5](#page-7-0); Tables [S3](https://doi.org/10.1080/07391102.2022.2090438)–[S5,](https://doi.org/10.1080/07391102.2022.2090438) [Supplementary Materials](https://doi.org/10.1080/07391102.2022.2090438)). They give the best docking scores,

Table 8. Thermodynamic properties calculated in reels units.

Stage	Method	Н	U	EKT	P	v
SP <sub>1</sub>	<b>CATNVT</b>	$-548.001$	1239.506	7896.099	$-60.342$	70,733.242
	<b>CATNPT</b>	126.562	$-3738.745$	3258.956	$-166.790$	70.734.429
	<b>CATNVT</b>	$-3.077$	$-1794.187$	6340.632	$-6.647$	70,733.242
	<b>CATNPT</b>	0.607	$-4177.466$	3644.816	$-25.583$	70,129.531
	<b>CATNVT</b>	1.431	$-1872.646$	296.267	47.574	70,733.242
	<b>CATNPT</b>	0.856	$-4300.242$	3777.552	$-44.703$	68,616.622
SP <sub>2</sub>	<b>CATNVT</b>	1.794	$-1910.387$	6454.985	110.509	70,733.242
	<b>CATNPT</b>	1.732	$-4370.358$	3851.464	$-19.527$	68.023.101
	<b>CATNVT</b>	7.922	$-2034.435$	6380.051	$-48.245$	70,733,242
	<b>CATNPT</b>	15.996	$-4431.202$	3926.552	$-21.916$	66,554.343
	<b>CATNVT</b>	6.380	$-2223.329$	6466.652	$-91.712$	70,733.242
	<b>CATNPT</b>	24.248	$-4429.957$	3933.550	$-81.352$	65.744.632
SP <sub>3</sub>	<b>CATNVT</b>	$-1.253$	$-2267.157$	6466.531	50.258	70,733.242
	<b>CATNPT</b>	4.536	$-4482.546$	4055.145	108.319	58,992.375
	<b>CATNVT</b>	0.874	$-2352.489$	6388.428	$-44.417$	70,733.242
	<b>CATNPT</b>	44.459	$-4455.767$	4068.258	$-34.409$	55,208.097
	<b>CATNVT</b>	5.273	$-2387.140$	6402.313	61.308	70,733.242
	<b>CATNPT</b>	87.701	$-4490.880$	4146.594	153.381	51,238.800
	$\sim$	-3 - $\sim$	$\epsilon$ $\overline{\phantom{a}}$		.	

Pressure P =  $P^* \varepsilon / \sigma^{-3}$ . Energy of configuration  $U = U^* N \varepsilon$ . Translation Kinetic Energy EKT = EKT<sup>\*</sup> N $\varepsilon$  and Enthalpy H = H<sup>\*</sup> N $\varepsilon$ .

based on the binding free energy ([Table 5](#page-7-0)). This shows that these complexes are more stable. As can be seen from [Figure 3](#page-14-0) and [Figure 4.](#page-14-0)

We note that the complex formed by the compound L39 (1dgb-L39) has the lowest energy score compared to the other complexes formed by control test butyled hydroxyltoluene (BHT) and ethylenediaminetetraacetic acid (EDTA). Moreover, this compound forms one interaction with active site residue of the catalase target.

The complex formed by compound L42 gave a score value very close (slightly higher) to the value of the both best of control test butyled hydroxyltoluene (BHT) and ethylenediaminetetraacetic (EDTA) ([Table 5](#page-7-0)). Their binding free energies were  $-5.052$  and  $-5.591$  kcal/mol respectively. In addition, this compound establishes one interaction with active site residues of the catalase target.

In addition, other compounds that formed interactions with active site residues of the catalase target which are less stable than L39 and L42 are given in [Tables S3](https://doi.org/10.1080/07391102.2022.2090438)–[S5](https://doi.org/10.1080/07391102.2022.2090438) [\(Supplementary Materials\)](https://doi.org/10.1080/07391102.2022.2090438). These ligands are 3-(Z)-hexenylbenzoate,  $\beta$ -eudesmol and (E)-phytolligands L24, L33, L60, interacts with LYS 237 (pi-cation), PHE 198 and HOH 1558 at a distance of 3.83, 4.49 and 2.08 Å strong with energy of  $-1.3$ ,  $-0.7$  and  $-0.3$  kcal/mol respectively and p-cymene ligand L5 interacts with one amino acid PHE 198 pi-pi at a distance of 3.89 Å strong and energy binding of  $-0.04$ , similarly, the  $\alpha$ -copaene,  $\beta$ -cadinene, salvial-4(14)-en-1-one ligand (L14, L22 and L27) interacts with H-pi at a distance of 3.77, 4.00 and 3.80 Å (strong, low) respectively. Humuleneepoxyde II,  $\tau$ -muurolol and  $\beta$ -eudesmol ligands (L29, L32 and L33) interacts with HIS 305, H-pi, HOH 1444 and HOH 1533 at a distance of 3.75, 2060 and 2.72 Å (weak) respectively with energy binding of  $-1.0$ ;  $-1.1$  and  $-1.2$  kcal/mol respectively while (Z,Z)-farnesol ligand (L36) interacts with HOH 1465 Hdonor at a distance of 2.59 Å (strong) and energy binding of 0.6 kcal/mol. Hexadecanoic acid, linalool, methyl-salicylate and decanol interacts with one amino acid TYR 215, ARG203 and HOH 1414, HOH 1484 H-acceptor at a distance of 2.26, 2.63, 4.33 and 2.64, 2.34 Å average, strong interaction and energy binding of  $-6.6$ ,  $-1.5$ ,  $-0.7$  and  $-0.4$  kcal/mol, and

<span id="page-10-0"></span>



Green  $=$  good, yellow  $=$  tolerable, red  $=$  bad.

interaction with heneicosane,  $\alpha$ -thujene, methyl-salicylate, decanolanddec-3-en-2-one with HIS 305, PHE198, ASN 149 and HOH 1465, respectively, H-donor and H-pi at a distance of 3.62,4.21, 2.47 and 2.54 Å (strong, low, average interaction) and energy binding of  $-0.7$ ,  $-0.6.0.4$  and  $-0.8$  kcal/mol respectively. Dec-3-en-2-one, geranylacetate, dodecanal and caryophyllene oxide interact with HOH 1465–1533, HIS305, HOH1068 and HIS305 with energy binding of  $-1.7$ ,  $-3.6$ ,  $-2.7$  and  $-0.6$  kcal/mol.

In our research, all the compounds tested show stable hydrogen bonds. On the other hand, previous research (Sarwar et al., [2010,](#page-21-0) [2013\)](#page-21-0) proved that, halogen bonding similar to hydrogen bonding plays a crucial role for biological and chemical systems.

The binding affinity of L39, L42, L40, L60, and L59 ((Z)-phytol, eicosane, heneicosane, (E)-phytol and hexadecanoic acid) have considerably increased to  $-7.184$ , $-7.158$ ,  $-6.900$ ,  $-6.882$ , and  $-6.266$  kcal/mol respectively. Improved hydrogen bond was observed in L39 and L42. This bond not only contribute in increasing binding affinity, but also enhance the binding specificity (Bissantz et al., [2010](#page-19-0); Sarwar et al., [2013](#page-21-0)). This observation helped to confirm that compounds (L39 and L42) (oxygenated diterpene) are bound at the desired binding site of receptor protein after molecular docking.

3.2.1.3.2. Interaction mechanism of the complex with Ct-DNA sequence. According to the research of (Birben et al., [2012](#page-19-0)) reactive oxygen species (ROS) can lead to DNA modifications in several ways, which involves degradation of bases, single- or double-stranded DNA breaks, purine, pyrimidine, or sugar. Most of these DNA modifications are highly relevant to carcinogenesis, aging, and neurodegenerative, cardiovascular, and autoimmune diseases (Al-Dalaen et al., 2014). So, this study was to elucidate the interaction of the best ligands obtained by molecular docking with the CtDNA sequence, in order to validate the interactions with the nucleotides and their affinities. The results obtained after the docking calculations for the five best compounds with the pocket of the Ct-DNA sequence (CGCGAATTCGCG)2 dodecamer (PDBID:1BNA) have been listed in [Table 6.](#page-8-0) Energy (binding affinity) and interactions for other compounds are listed in [Table S6](http://dx.doi.org/10.1080/07391102.2022.2090438) [\(Supplementary Materials\)](https://doi.org/10.1080/07391102.2022.2090438).

The obtained results show that compounds with stronger electron—donating substituents have higher DNA-binding ability than the others; On the other hand, results show that some of the tested compounds are minor groove binders. Our results demonstrated that the five compounds: (Z)-phytol (Ligand 39), eicosane (Ligand 42), heneicosane (Ligand 40), hexadecanoic acid (Ligand 59), aplotaxene (Ligand 58), and (E)-phytol (Ligand 60), were the best interacting compounds (see [Table 6;](#page-8-0) [Supplementary Materials](https://doi.org/10.1080/07391102.2022.2090438) [Table S6\)](http://dx.doi.org/10.1080/07391102.2022.2090438).

The calculated docking energies for these compounds were respectively  $-6.978$ ,  $-6.858$ ,  $-6.819$ ,  $-6.516$ ,  $-6.425$ , and  $-6.4.6$  kcal mol<sup>-1</sup>. With the exception of  $\beta$ -cadinene,  $\Upsilon$ -eudesmoland  $\beta$ -eudesmol, other compounds are located in the small cDNA groove. The results of molecular docking showed that  $\beta$ -cadinene,  $\Upsilon$ -eudesmol and  $\beta$ -eudesmol, existed in the main groove region. The calculated docking energy of this compound was  $-4.741$ ,  $-4.824$  and  $-4.793$  kcal mol $^{-1}$ , respectively (See [Supplementary Materials](https://doi.org/10.1080/07391102.2022.2090438) [Table S6\)](http://dx.doi.org/10.1080/07391102.2022.2090438). Among, the test candidates in this study, (Z)-phytol (Ligand 39), eicosane (Ligand 42), displayed the lowest binding energy of  $-6.978$ ,  $-6.858$  kcal/mol for Ct-DNA sequence and  $-7.184$ ,  $-7.158$  kcal/mol for the enzyme. These energies are lower compared to those of the Lref (NADPH) and two control ligands butylated hydroxyltoluene (BHT) and ethylenediaminetetraacetic acid (EDTA). Their binding energies obtained are  $-4.743$ ,  $-4.965$  kcal/mol, respectively for DNA sequence and  $-5.052$ ,  $-5.591$  kcal/mol, respectively, for the enzyme were much higher than (Z)-phytol, as found in our study; thus (Z)-phytol (Ligand 39), eicosane (Ligand 42) displayed much better binding than the Lref (NADPH) and control molecule; butylated hydroxyltoluene (BHT) and ethylenediaminetetraacetic acid (EDTA). The two complexes are showing greater antioxidant activity than butyled hydroxytoluene (BHT) and ethylene diaminetetraacitic acid (EDTA).

The docking results reveal that the binding strength of complex-1 [(Z)-phytol-catalase] is higher than complex-2 [eicosane-catalase]. Molecular dynamics simulation studies suggest that compound (Z)-phytol has a strong DNA-binding affinity than compound eicosane. The more bonding strength of complex-1 is due to the presence of hydrophobic pi-pi interactions with nucleotide bases of DNA, along with hydrogen bonding interaction. On the other hand, complex-2 eicosane-catalase showed only a few pi-pi interactions with nucleotide bases of DNA. The bulkier aromatic group in complex-1 participated in pi-pi interactions with nucleotides. However, the group in eicosane-catalase showed no interactions with nucleotides. Thus, the absence of pi-pi interactions with DC15 and DT14 nucleotides lowers the binding affinity of complex-2.

From the docking results with the optimal energy, it was found that the complex [complex-1 (Z)-phytol-catalase] inserted into the groove of DNA fragments and hydrophobic forces play main roles in the binding of complex to ct-DNA.

The docking results reveal (Z)-phytol and eicosane displayed much better binding (See [Figure 5\)](#page-15-0). From our results, we can conclude that complex-1 showed greater DNA binding and antioxidant activity than complex-2.

3.2.1.3.3. Interaction with endogenous enzymes antioxidant systems. In order to complete this research, we deemed it

<span id="page-11-0"></span>Table 10. In silico Bioisosteric Replacement based on similarity comparison method using MolOpt.



useful to study the interaction of our best molecules with other defense systems antioxidant targets such as SOD and GPX.

The results of docking energies of three endogenous enzymes and five best inhibitors are shown in [\(Table 7](#page-8-0)). And results of other compounds are shown in [Table S7](http://dx.doi.org/10.1080/07391102.2022.2090438) ([Supplementary Materials\)](https://doi.org/10.1080/07391102.2022.2090438).

Molecular docking results revealed that (Z)-phytol (Ligand 39), eicosane (Ligand 42), (E)-phytol (Ligand 60), heneicosane (Ligand 40), hexadecanoic acid (Ligand 59), and aplotaxene (Ligand 58) were the best compounds interacting with the suspected binding residues at the active site catalase [\(Figure](#page-16-0) [6;](#page-16-0) [Supplementary Materials\)](https://doi.org/10.1080/07391102.2022.2090438). The calculated docking energies for these molecules were respectively  $-7.184$ ,  $-7.158$ ,  $-6.882$ ,  $-6.809$ ,  $-6.266$ , and  $-6.130$  kcal mol<sup>-1</sup>.  $\beta$ -eudesmol and *Y*-eudesmol were the weakest interacting compounds with this receptor [\(Table S7](http://dx.doi.org/10.1080/07391102.2022.2090438) [Supplementary Materials](https://doi.org/10.1080/07391102.2022.2090438)). The calculated docking energy, calculated for this compound was  $-5.070$  and  $-5.286$  kcal mol<sup>-1</sup>, respectively. The best compounds, interacting with the suspected binding residues at the active site superoxide dismutasesis (Z)-phytol (Ligand 39), eicosane (Ligand 42), (E)-geranyl acetate (Ligand 50), heneicosane (Ligand 40) ([Table 7;](#page-8-0) [Supplementary Materials](https://doi.org/10.1080/07391102.2022.2090438) [Table](http://dx.doi.org/10.1080/07391102.2022.2090438) [S7](http://dx.doi.org/10.1080/07391102.2022.2090438)). The calculated docking energies for these molecules were respectively  $-3.993$ ,  $-4.163$  and  $-4.173$ ,  $-4.142$  kcal mol<sup>-1</sup>.  $\beta$ -cadinene and Y-eudesmol ([Table S7,](http://dx.doi.org/10.1080/07391102.2022.2090438) [Supplementary Materials](https://doi.org/10.1080/07391102.2022.2090438)) was the weakest interacting compound with this receptor. The calculated docking energy calculated for this compound is  $-3.422$  and  $-3.182$  kcal mol<sup>-1</sup>, respectively. Additionally, the best compounds interacting with the suspected binding residues at the active site glutathione peroxidase were (E)-phytol (Ligand 60), hexadecanoic acid (Ligand 59), eicosane (Ligand 42), aplotaxene (Ligand 58) [\(Supplementary Materials](https://doi.org/10.1080/07391102.2022.2090438) [Table S7](http://dx.doi.org/10.1080/07391102.2022.2090438)). The calculated docking energies for these molecules were respectively  $-5.281$ ,  $-4.748$ ,  $-4.686$ , and  $-4.664$  kcal mol<sup>-1</sup>.  $\beta$ -eudesmol and  $\delta$ -cadinene were the weakest interacting compound with the receptor glutathione peroxidase. The calculated docking energy calculated for this compound are  $-4.000$  and  $-4.053$  kcal mol<sup>-1</sup>, respectively. We observed that (Z)-phytol (Ligand 39), eicosane (Ligand 42), heneicosane (Ligand 40), hexadecanoic acid (Ligand 59), aplotaxene (Ligand 58), and (E)-phytol (Ligand 60) showed a binding affinity for interacting with receptors for ctDNA and the same compounds showed a binding affinity for catalse and site of glutathione peroxidase but these compounds (Z)-phytol (Ligand 39), eicosane (Ligand 42), (E)-geranyl acetate (Ligand 50), heneicosane (Ligand 40) showed a binding affinity for interacting with receptors for superoxide dismutase. Representations of the best pose interactions (Z)-phytol (Ligand 39), eicosane (Ligand 42), with three targets (CAT, SOD and GPX) are shown in [Figure S1](http://dx.doi.org/10.1080/07391102.2022.2090438) [\(Supplementary Materials](https://doi.org/10.1080/07391102.2022.2090438)).

#### 3.2.2. Evaluation of molecular dynamics

Many previous studies (Chen et al., [2014,](#page-19-0) 2015; Hung et al., [2014\)](#page-20-0) confirmed that the highest dock score obtained by molecular docking does not mean that the compound is a potent lead. Therefore, to validate this result it is necessary to carry out molecular dynamics simulations. From the docking results, Z-phytol was found to possess the best binding affinity towards the Endogenous enzyme. Hence, the complex of Z-phytol with catalase was subjected to 100 ns of MD simulation.

3.2.2.1. Thermodynamic properties. We have studied the evolution thermodynamic properties of best ligand (Z)-phytol (Ligand39) in the NVT and NPT ensemble. We performed energy minimizations of the best complex after docking of 600 ps. Then carried out simulations up to (MD production cycles) 100 ns in three stages under constraints (see [Table 8\)](#page-9-0).

An important point is also obtained from [Table 8](#page-8-0). The translation and rotation energies of the complex formed by the ligand L39 in NPT are very important. Unlike the complex formed by the same ligand in NVT ensemble, these energies and its enthalpy are low. Pressure fluctuations in NVT units are greater than NPT units. Therefore, (Z)-phytol (Ligand 39) is predicted

<span id="page-12-0"></span>Table 11. Drug-likeness prediction and Physicochemical Properties (PC) through OSIRIS property explorer and the Swiss ADME online server of the best inhibitors.



MW: molecular weight, MLogP: logarithm of partition coefficient of the compound between water and n-octanol: log: solubility; TPSA or Topological Polar Surface Area: the surface belonging to polar atoms in the compound.

Refra: Molar Refractivity, Lipophi: Lipophilicity , Solub: Water solubility, Skin perm: skin permeation.

Table 12. Pharmacokinetic and toxicity evaluated parameters of best compounds.



Green = good, yellow = tolerable, red = bad.

MS: Moderately soluble, PS: Poorly soluble.

Active components: 39—(Z)-Phytol, 42—Eicosane. BBB: Blood-brain barrier.

ADMET: Absorption, distribution, metabolism, excretion and toxicity.

 $VD_{SS}$ : < -0.15 low, >0.45 high, BBB: >0.3 cross BBB, < -1 poorly distributed to the BBB, CNS: > -2 penetrate CNS, < -3 unable to penetrate CNS, Low skin permeability:  $> -2.5$ , Caco-2 permeability:  $> 0.9$ , Human intestinal absorption:  $> 90$ .

<sup>a</sup>Results from SwissADME tools.





A: Active, I: Inactive.

to be the most interactive system. These results are in total agreement with the docking prediction results (see [Tables 7](#page-8-0) and [8\)](#page-9-0). Thermodynamic parameters in agreement with molecular docking results demonstrated that schiff base complexes could combine with catalase spontaneously through hydrogen bonds and Van der Waals interactions.

<span id="page-13-0"></span>Table 14. Energy balance of complexes formed with Catalase (Cat) under potent clinical antioxidant, some species of Centaurea and our results for essential oils of the Sulphurea.

# Some species of Centaurea.



3.2.2.2. Structural dynamics properties. We have studied the evolution structural dynamics of the best test compound, (Z)-phytol (Ligand 39) (See [Table 5\)](#page-7-0) by IMODS. Results of structural molecular dynamics simulation are listed in [Figure](http://dx.doi.org/10.1080/07391102.2022.2090438) [S2](http://dx.doi.org/10.1080/07391102.2022.2090438) [\(Supplementary Materials](https://doi.org/10.1080/07391102.2022.2090438)).

The normal mode analysis (NMA) of the prepared, (Z)-phytol (Ligand 39)-catalase (Cat) complex was illustrated in [\(Figure](https://doi.org/10.1080/07391102.2022.2090438) [S2a\)](https://doi.org/10.1080/07391102.2022.2090438) From the molecular dynamics study of the prepared (Z) phytol (Ligand 39)—catalase (Cat) complex, it was clear that the prepared enzyme-ligand complex had quite high eigenvalue of  $1.927144e - 04$  the eigenvalue is illustrated in [Figure](https://doi.org/10.1080/07391102.2022.2090438) [S2\(b\)](https://doi.org/10.1080/07391102.2022.2090438). However, the variance map showed a higher degree of cumulative variances than individual variances [\(Figure S2c](https://doi.org/10.1080/07391102.2022.2090438)). The elastic network map and co-variance also produced quite satisfactory results [\(Figure S2d](https://doi.org/10.1080/07391102.2022.2090438) and [S2e](https://doi.org/10.1080/07391102.2022.2090438) respectively). The deformability graphs of the complex (Z)-phytol (Ligand 39) catalase (Cat) illustrate the peaks in the graphs correspond to the regions in the protein with deformability ([Figure S2f](https://doi.org/10.1080/07391102.2022.2090438)). The two selected ligand molecules can be used as potential agents to deplete DPPH and free radicals. Overall, in our study, (Z) phytol (Ligand 39) emerged as the most potent anti-catalase (Cat) agent. However, more in vitro and in vivo researches should be performed on the (Z)-phytol (Ligand 39) the best ligands to confirm the findings of this study.

# 3.2.3. The OSIRIS property explorer and Bioisosteric replacement

A computational study was carried out for the best compounds to assess their OSIRIS properties. The obtained value is depicted in [Table 9](#page-10-0) and the results of predicted toxicity risks of other compounds are summarized in [Table S8](http://dx.doi.org/10.1080/07391102.2022.2090438) [\(Supplementary Materials\)](https://doi.org/10.1080/07391102.2022.2090438). Prediction results are valued and color coded (Nalini et al., [2011](#page-21-0)). The predicted results of Bioisosteric replacement are presented in [Table 10](#page-11-0).

The results summarized in [Table 9](#page-10-0) ([Supplementary](https://doi.org/10.1080/07391102.2022.2090438) [Materials](https://doi.org/10.1080/07391102.2022.2090438) [Table S8\)](http://dx.doi.org/10.1080/07391102.2022.2090438) revealed that compounds L22, L23, L30, L33 and L39, L40, L42, L60 are the best ligands while L24, L36 have less affinity via the catalase target and L58 was predicted to cause irritation. Ligand L50 does not to possess druglikeness properties since it is predicted to be tumorigenic, mutagenic, irritant and moderately reproductive. Therefore, we are interested in the two compounds L39 and L42 with a remarkable interest in L39, because the former has good complementarity with the site of catalase and DNA sequence. Therefore, we thought to propose another molecule by using fragments of the compound-39. For this, we used, Molopt (A web server for drug design using bioisosteric transformation) which automatically generates analogs lists by replacing molecular substructures with chemical groups with similar biological properties. The resulting set of transforming analogs can be evaluated for future synthesis.

# 3.2.4. In silico assessment of the ADMET properties and drug-likeness

Poor pharmacokinetics Absorption, Distribution, Metabolism, Excretion and Toxicity (ADMET) is the major concern for the failure of drug candidates in clinical trials. So, knowing ADME features for the compound in advance is more important for drug discovery. The predicted results of drug-likeness,

<span id="page-14-0"></span>

Figure 3. Displaying the Catalase binding site cavity 3D interaction diagram of (Z)-Phytol with pocket (b) and without pocket (c); Binding mode of (Z)-Phytol as 2D diagram (d). The binding patterns (Z)-Phytol in the active site of Catalase, in which (Z)-Phytol is appeared in stick model with pink while the surface of Cat is shown in blue red green (a).



Figure 4. Displaying the Catalase binding site cavity 3D interaction diagram of Eicosane with pocket (b) and without pocket (c); Binding mode of Eicosane as 2D diagram (d). The binding patterns (Z)-Phytol in the active site of Catalase, in which Eicosane is appeared in stick model with pink while the surface of Cat is shown in blue red green (a).

pharmacokinetics and organ toxicity are presented in [Tables](#page-12-0) [11, 12](#page-12-0), [and](#page-12-0) 13, respectively.

3.2.4.1. Drug-likeness evaluation. A good drug candidate is absorbed in required time and well distributed throughout the system for its effective metabolism and action. [Table](#page-12-0) [11](#page-12-0) depicts the drug-likeness properties of test compounds with least binding energies predicted using OSIRIS Property Explorer.

Result of Drug-likeness prediction and Physicochemical Properties (PC) for other compounds is listed in [Tables S9](https://doi.org/10.1080/07391102.2022.2090438) and [S10](https://doi.org/10.1080/07391102.2022.2090438) [\(Supplementary Materials\)](https://doi.org/10.1080/07391102.2022.2090438) respectively.

The results listed in [Table 11](#page-12-0) revealed that ligand (Z)-phytol (Ligand 39), (E)-phytol (Ligand 60), eicosane (Ligand 42),

<span id="page-15-0"></span>

(a) Z-Phytol L39



(b) Eicosane L42

Figure 5. Molecular docked model of the most favorable binding site of compounds (a) L39 and (b) L42 with DNA dodecamer duplex of sequence d (CGCGAATTCGCG)2 (PDB ID: 1BNA).

heneicosane (Ligand 40), have high absorption with a low molecular weight of order 296.54. Also, we can note that these compounds comply with Lipinski's rule of 5 Veber's rules and Egan's rule. MW range 264.41 (<500), A log S value indicates solubility; the lesser the log S value, the higher the solubility, which would enhance the absorption log for (Z)-phytol (Ligand 39) and eicosane (Ligand 42) were  $-4.63$  and  $-5.84$ , respectively. A lower molecular weight would again enhance the absorption rate and thus most of the drugs were tried to be kept at the lowest possible molecular weight, suggesting that these compounds would not be expected to cause problems with oral bioavailability.

The ADME parameters were calculated for compounds under study, i.e. L22, L23, L30, L33, L39, L40, L42, and L60 by calculating the different Physico-chemical and bio-pharmaceutical highlights ([Table 11](#page-12-0); [Supplementary Table S10\)](https://doi.org/10.1080/07391102.2022.2090438).

The results indicated that the molecular refractivity was 69.04, 69.04, 70.46, 70.46, 80.48, 103.06, 98.25 and 98.94 for lead compounds, namely, L22, L23, L30, L33, L39, L40, L42, and L60, respectively. Water solubility properties were calculated through Log S ESOL Class  $(-3.56, -3.76, -3.29, -3.51,$  $-5.98, -7.41, -7.05$  and  $-5.98$ ), log S AliClass (-3.70, -4.02,  $-3.49, -3.86, -8.47, -10.96, -10.40$  and  $-8.47$ ), SILISCOS-ITClass  $(-3.07, -3.32, -3.41, -3.21, -5.51, -8.34, -7.94$  and 5.51) class. Lipophilicity is a key physicochemical property that plays a crucial role in determining ADMET (absorption, distribution, metabolism, excretion, and toxicity) properties and the overall suitability of drug candidates. The results were assessed for ILOGP and SILISCOS-IT which revealed that all compounds except (Z)-phytol (Ligand 39), (E)-phytol (Ligand 60), eicosane (Ligand 42), heneicosane (Ligand 40) (ILOGP4.78, 4.77, 5.64, 5.85 and SILISCOS-IT 6.57, 6.57, 7.98, 8.43), respectively showed a most favorable range, which describes a good balance between permeability and solubility and is expected to show good bioavailability upon oral drug administration. GI absorption predicted was low for each selected molecule. Drugs diffuse across a cell membrane in a concentration

<span id="page-16-0"></span>

Figure 6. The compound-39; docked (blue) into the binding site of Cat the final ligand pose and the docking pose after a molecular dynamics (MD) in NVT simulation.



Figure 7. The compound—39; docked (yellow) into the binding site of Cat the final ligand pose and the docking pose after a molecular dynamics (MD) in NPT simulation.

gradient, a region of high concentration (e.g. gastrointestinal fluids) to a region of low concentration (e.g. blood). This permeability foresight helps to understand the outcomes of ADMET and the cell-based bioassays. The results showed that the permeability over human skin was found to be  $-4.71$ ,  $-4.49$ ,  $-5.25$ ,  $-5.00$ ,  $-2.29$ ,  $-0.31$ ,  $-0.60$  and  $-2.29$  cm/s for compounds viz., L22, L23, L30, L33, L39, L40, L42, and L60, respectively. These compounds showed almost no possibility to cross the BBB except L30 and L33. All medicines intended to work on the body pass into the blood stream. In this way, the fate of the drug—or rather its active ingredient—is commonly divided into four main stages: ADME (absorption, distribution in the body, metabolism and elimination) (See [Table 12](#page-12-0)).

Apropos, the absorption parameters compound L39; and L42 presents a promising oral availability, due to the optimal Caco-2 cell permeability and HIA ( $>0.9$  and Human intestinal >90%, respectively) (See [Table 12](#page-12-0)).

3.2.4.2. ADME-T properties. Here, we evaluated the ADME properties of the selected L39–L42 and analogues compounds by using in silico SwissADME server to see the pharmacokinetic properties (Daina et al., [2017\)](#page-19-0). The Absorption, Distribution, Metabolism, Excretion and Toxicity properties of the selected and analogues compounds have shown in [Table 12](#page-12-0).

<span id="page-17-0"></span>

Figure 8. SMARTCyp results illustrating the metabolic sites for L39 and L42 which were predicted correctly with top-ranking atoms and ranked depending on the major metabolite.

All compounds passed the AMES tests. The volume of distribution (VDss) for our two best ligands (0.385 and 0.614 for L39 and L42, respectively) suggests that the drug will be distributed in the tissue as potent antioxidative agents. The control ligands, ethylenediaminetetraacetic acid (EDTA) and the Lref (NADPH) co-crystallized inhibitor are entirely unable to penetrate the central nervous system (CNS). The distribution and absorption parameters, respectively, have been graphically represented by the extended and renewed version of the Edan-Egg (Egg) model named Brain Or Intestinal EstimateD (BOILED) permeation predictive model (BOILED-Egg) ([Figure S3,](http://dx.doi.org/10.1080/07391102.2022.2090438) [Supplementary Materials\)](https://doi.org/10.1080/07391102.2022.2090438).

The graph ([Figure S3,](http://dx.doi.org/10.1080/07391102.2022.2090438) [Supplementary Materials\)](https://doi.org/10.1080/07391102.2022.2090438) showed that the ligands butyl hydroxyl toluene (BHT),  $\beta$ -eudesmol and Y-eudesmol, analogue-1 and analogue-2 are absorbed by the brain. The ligands Z-phytol E-phytol, analogue-3 and analogue-4 showed gastrointestinal absorption within acceptable limits, except for ligands ethylenediaminetetraacetic acid (EDTA) and the Lref (NADPH) (TPSA 155.68 and 393.56  $\AA^2$ , respectively.

3.2.4.3. Prediction toxicity risk. Studying the toxicity profile was necessary in order to access the safety profile of the desired compounds. All results of toxicological pathways, including organ toxicity, toxicity and stress response pathways are given in [Table 13.](#page-12-0) To identify the toxicity of the selected L39–L42, BHT, EDTA and analogues compounds, we used ProtoxII (Banerjee et al., [2018](#page-19-0)).

Organ Toxicity, Toxicity and Stress response pathways were also carried out for 10 biological activities. We note that butylated hydroxyltoluene (BHT) Predicted LD50 is 650 mg/kg and falls to Class 4 while 5000 mg/kg was Predicted for ethylene diaminetetraacetic and falls in class 2 of Toxicity Class. BHT falls to class 4 with range of 300 to 2000 mg/kg, these would be harmful in case of oral delivery. In addition, the compounds (Z)-phytol L39 was inactive for all toxic effects but eicosane L42 was active for androgen receptor (AR). (Z)-phytol L39 was in the toxicity class 5 and nontoxic, hence the best compound for our study. The toxicity class profile is in the order; (Z)-phytol L39

Predicted (Class: 5) >butyl hydroxyl toluene (BHT) (Class: 4 >eicosane) L42 (Class: 4>) ethylenediaminetetraacetic acid (EDTA) (Class: 2).

#### 3.2.5. Pharmacophore mapping

Metabolism presents an essential function in the drug-drug interaction and bioavailability of drugs. Only the free form of the drug can bind with drug-metabolizing enzymes. To study the metabolic behavior of lead compounds, it is very important to study the cytochrome P450 enzymes (CYPs) as they are the most notable class of enzymes.

The possible sites of a chemical compound are illustrated by the circles on the chemical structure of the compound (Zaretzki et al., [2013](#page-22-0)). Figure 8 showed the possible interaction of L39 and L42 with CYP450 (3A4). So, the Site of Metabolism (SOM) at C1, C2, and C3 sites was predicted, and the ability of the two ligands to activate/inhibit the cytochrome system was determined.

The P450 SOM predictions showed that Z-phytol L39 had 4 sites of metabolism (SOMs) for the CYP450 1A2, 450 2A6 enzyme, CYP450 2B6, CYP450 2C8, CYP450 2C19, CYP450 2D6, CYP450 2E1 and CYP450 3A4 and 5 sites for CYP450 2C9. Are given in [Table S11](http://dx.doi.org/10.1080/07391102.2022.2090438) [\(Supplementary Materials](https://doi.org/10.1080/07391102.2022.2090438)).

The Pharmacophore Mapping was carried out for the (Z) phytol best ligand of the oxygenated diterpene. (Z)-phytol showed 1 Hydrogen acceptor bonds, 12 Hydrophobic groups, one Aromatic rings and 2 Hydrogen donor bonds. It also generated a good number of good contacts with the Pharmacophore of catalase, [Figure 9](#page-18-0).

The Pharmacophore of Z-phytol generates a hypothesis which can be applied successfully in biological screening for further experiments (Dixon et al., [2006\)](#page-19-0).

Validation of our results, for essential oils of C. sulphurea, the synthetic antioxidant butyled hydroxyl toluene (BHT) and ethylenediaminetetraacetic acid (EDTA) and some species of Inula genuses are given in [Table 14.](#page-13-0)

According to the table above, we note also that the compound L39 and their analogues have a high value of energy score compared to other compounds.

<span id="page-18-0"></span>

Figure 9. (a) Pharmacophore Mapping of Z-phytol L39. (b) Asteric constriction (dark gray) was added to the pharmacophore model.

The Oxygenated diterpene compounds were the most dominant. The complex formed by the compound L39 (Z) phytol gives a low energy value of the score  $-7.148$  kcal mol<sup>-1</sup> that it is very close to the value of the clinical drugs (see [Table 14](#page-13-0)), this compound establishes one interaction LYS 237 with the residues of active sites of the catalase ([Figure 3\)](#page-14-0).

The results presented in [Table 11](#page-12-0) revealed that compound L39 has high lipophilicity and high coefficient of skin permeability. Therefore, we propose (Z)-phytol was the best ligand which allows the inhibition of three targets and ctDNA sequence. So, we suggest (Z)-phytol present in (oxygenated diterpene) with its validated activity score  $(-7.184, -3.993,$  $-4.413$ ,  $-6.978$ ); respectively for three targets and ctDNA sequence as a new oral ligand. According to its pharmacophore properties the compound 39 generated a hypothesis which can be applied successfully in biological screening for further experiments (Figure 9). In vivo, many studies were focused on the inhibitory effect of the sulphurea compounds, on key enzymes linked to investigate antioxidant activity; catalase and superoxide dismutase. The results of Souza et al. [\(2019\)](#page-21-0) have proved that extracts of C. sulphurea showed  $IC_{50}$  values of 103.9 at 24 and 48 h. Our results showed that essential oil of C. sulphurea showed  $IC_{50}$  values of 2.06 g/L and 1.29 g/L. Through these results, we can conclude that, our oil presented an excellent antioxidant activity.

In our research the software platform that integrates visualization and modeling detect the hydrophobic interactions between (Z)-phytol (constituent molecules of the aerial and root parts of essential oil of C. sulphure) and the three endogenous enzymes. The orientations of the docked ligands are consistent with a mechanism whereby these hydrophobic compounds dock into a hydrophobic pocket near the active site, there by blocking binding of the receptor. The results revealed inhibitory activities against novel three targets. Furthermore, compound-39 Z-phytol showed a high level of gastrointestinal adsorption, which contributes to good oral bioavailability. Consequently, the study carried out in this research reveals many secrets conveyed by the use of magic plants. At the end of our study, we propose that all biological activity depends on the presence of certain metabolites inside the tissues of the plant. The results obtained in this study reveal that (Z)-phytol and eicosane have potential antioxidant ability in three receptors via Reactive oxygen species (ROS) generation. Thus, (Z)-phytol and eicosane may be used for more analyses in order to further evaluate their efficiency in the reduction of oxidative stress and a possible antioxidant to be used in the pharmaceutical industry.

# 4. Conclusion

The present research aimed at the chemical and biological investigation of the essential oil of the aerial and root parts of the C. sulphurea species in hopes to find new natural products. The results showed that essential oil of C. sulphurea is a good source of caryophyllene oxide, aplotaxene and (Z) phytol. The essential oils demonstrated greater antioxidant activity. However, no information was found in the available literature about the biological in vivo and in vitro activities of C. sulphurea. It would be interesting to study the antioxidant activity of these essential oils to check whether they possess antioxidant activities. The inhibition of Catalase receptor was theoretically investigated by two methods of computational chemistry: molecular docking analyses, MD simulations, ADME properties and pharmacological knowledge. The results reveal that ligand natural inhibitor (Z)-phytol L39 and eicosane L42 of essential oils from aerial and root parts of C. sulphurea during its vegetative cycle has an affinity to interact with cDNA sequence and three receptors. Compound (Z) phytol L39 and their analogues showed better antioxidant, scavenging activity than other compounds. The results were also analysed computationally using the molecular dynamic and a molecular docking approach. From two analyses, it was also found that among all the tested compounds, compound 39 exhibited the best antioxidant activity. Moreover, the penetration through the Blood-Brain Barrier came out to be best for (Z)-phytol and their analogues than the control molecule and Lref. (Z)-phytol and their analogues were the best inhibitors for 1dgb, considering the pharmacokinetic

<span id="page-19-0"></span>and pharmacodynamic properties. (Z)-phytol (Oxygenated diterpene) has the highest binding affinity among all the inhibitors, it is proposed as a natural orally active drug, and it may also be a good candidate for further biological and pharmacological investigations. The results reveal that (Z) phytol L39 and their analogues have potential antioxidant ability in at least three endogenous receptors (catalase (CAT), superoxide dismutase (SODs) and glutathione peroxidase (GPX) and DNA sequence) via ROS generation. Thus, (Z)-phytol can be used as templates for further development of antioxidant therapeutic agents.

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#### Disclosure statement

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