



# *In silico* screening of anticholinesterase alkaloids for cyclooxygenase-2 (COX-2) and matrix metalloproteinase 8 (MMP-8) inhibitory potentials as multi-target inhibitors of Alzheimer's disease

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Received: 6 June 2019 / Accepted: 19 July 2019 / Published online: 27 July 2019  
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## Abstract

Alzheimer's disease (AD) is a progressive neurodegenerative disorder with yet no effective drug treatment; although several anticholinesterases are being used to offer relief from the symptoms of the disease. Recent studies have indicated that over-activation of cyclooxygenase-2 (COX-2) and matrix metalloproteinase-8 (MMP-8) may cause neuronal death in the brain of AD subjects, suggesting that inhibition of COX-2 and MMP-8 may be of therapeutic value in the management of AD. Therefore, it is important and rational to investigate new agents with anticholinesterase, COX-2 and MMP-8 inhibitory activities. In this study, molecular docking study was performed with earlier identified anticholinesterase alkaloids to search for compounds with high affinity for COX-2 and MMP-8. Molecular docking was done using Blind Docking Server while ligand-protein molecular interaction of compounds with remarkable inhibitory characteristics against COX-2 and MMP-8 were viewed with PyMOL. Alkaloids with high binding affinity and remarkable binding interaction with the target proteins were subjected to drug likeness investigation based on absorption-distribution-metabolism-excretion (ADME) properties using the Swiss online ADME web tool. Nine alkaloids (haloxysterol A, haloxysterol B, haloxysterol C, haloxysterol D, sarcodine, isosarcodine, axillaridine A, sarsaligenone and voacangine hydroxyindolenine) showed high affinities for both COX-2 and MMP-8. Thus, this *in silico* study identified 9 orally drugable, anticholinesterase alkaloids with COX-2 and MMP-8 multi-target activities that could be studied further as agents against AD.

**Keywords** Alkaloids · Anticholinesterase · Cyclooxygenase · Matrix metalloproteinase 8 · Molecular docking

## Introduction

Alzheimer's disease (AD) is a progressive neurodegenerative disorder named by Emil Kraepelin in honor of Alois Alzheimer, who first recognized the disease in 1906 (Möller and Graeber 1998). It is the most common neurodegenerative disorder that affects up to one-third of old individuals with the incidence doubling every 5 years among the elderly, where it is associated with memory impairment, excessive cholinesterase (ChE) activity, formation of neurotoxic

amyloid plaque, and tau protein aggregation (Möller and Graeber 1998; Ahmed et al. 2013; Song et al. 2015; Rasool et al. 2018). Pathogenesis of Alzheimer's disease is characterized by alterations in the activity of several proteins including the 2 sister Cholinesterase (ChE) enzymes; acetylcholinesterase (AChE) and butyrylcholinesterase (BChE), cyclooxygenase-2 (COX-2) and matrix metalloproteinase-8 (MMP-8), also called neutrophil collagenase. The 2 sister ChE enzymes, AChE and BChE hydrolyze acetylcholine and butyrylcholine respectively; thus, their inhibitors are the major drugs currently used in the treatment of the symptoms of Alzheimer's disease (Orhan et al. 2011). Apart from the ChE enzymes, COX-2 is another important protein implicated in the pathology of AD (Rasool et al. 2018); it is an important target for chemoprevention and its pharmacological modulation is being exploited as target in many inflammation-associated conditions including AD and cancer (Plummer et al. 1999; Rasool et al. 2018). In the brain, the expression of COX-2, which is induced in the neurons in

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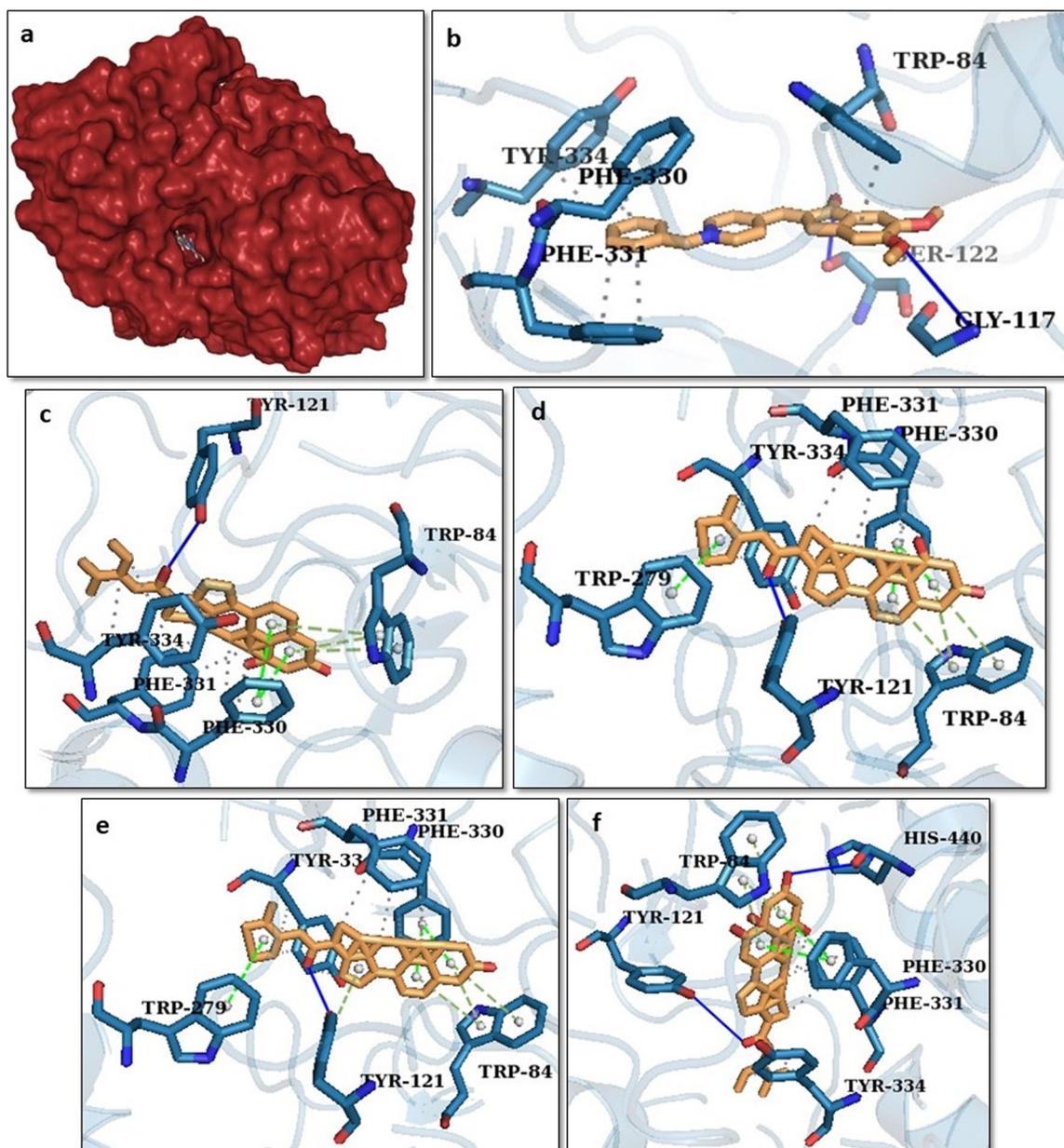
**Table 1** Binding affinity of potential donepezil and selected alkaloids acetylcholinesterase, butyrylcholinesterase, cyclooxygenase-2 and matrix metalloproteinase 8

S/N	Compounds	Binding Affinity (Kcal/mol)				Reported CHE-inhibitory activity IC <sub>50</sub> (μM)	Calculated pIC <sub>50</sub>	References
		AChE	BChE	COX-2	MMP-8			
S	Donepezil (inhibitor)	-15.1	-12.5	-13.7	-16.0	0.058	7.2	(Mohsen 2012)
1	Assoanine	-9.8	-8.8	-8.0	-7.5	3.87	5.4	(López et al. 2002)
2	Buxamine B	-10.0	-11.2	-8.8	-8.1	79.6	4.1	(Ata et al. 2010)
3	Coronaridine	-8.8	-10.3	-8.2	-8.8	-	NA	(Andrade et al. 2005)
4	Epinorgalantamine	-10.6	-9.7	-9.7	-7.9	9.6	5.0	(López et al. 2002)
5	Gаланthamine	-9.9	-9.2	-7.5	-7.1	1.07	6.0	(López et al. 2002)
6	Huperzine A	-9.4	-9.2	-7.3	-7.5	10 <sup>-4</sup>	10.0	(Orhan et al. 2004)
7	Oxoasooanine	-10.1	-9.2	-9.1	-7.7	47.2	4.3	(López et al. 2002)
8	Palmatine	-11.4	-9.6	-8.7	-8.7	5.8	5.2	(Kim et al. 2004)
9	Physostigmine	-9.5	-8.2	-7.0	-7.9	6 × 10 <sup>-4</sup>	9.2	(Karczmar 1998)
10	Protopine	-9.0	-10.3	-8.5	-9.7	16.1	4.8	(Kim et al. 2004)
11	Rivastigmine	-9.0	-7.7	-6.6	-6.6	501	3.3	(Krátký et al. 2016)
12	Rupicoline	-8.8	-11.4	-8.1	-9.3	-	-	(Andrade et al. 2005)
13	Sanguinine	-9.6	-9.4	-7.8	-8.1	0.10	7.0	López et al. 2002
14	Sarsalignone	-13.1	-10.9	-9.8	-9.6	7.02	5.2	(Choudhary 2001)
15	Vaganine A	-12.1	-11.2	-9.9	-9.8	8.59	5.1	(Choudhary 2001)
16	Vaganine D	-11.9	-11.4	-9.9	-9.8	46.89	4.3	(ul Haq and Uddin 2011)
17	Voacangine	-9.0	-10.8	-8.2	-8.1	-	NA	(Andrade et al. 2005)
18	1-O-Acetyllycorine	-12.6	-12.1	-12.6	-10.2	0.96	6.0	(Elgorashi et al. 2004)
19	Axillaridine A	<b>-17.7</b>	<b>-15.0</b>	<b>-16.2</b>	<b>-18.7</b>	5.21	5.3	(Atta-ur-Rahman et al. 2002)
20	Berberine	-12.4	-11.8	-12.5	-13.9	-	NA	(Howes and Houghton 2009)
21	Coptisine	-12.5	-12.4	-11.7	-13.7	-	NA	(Howes and Houghton 2009)
22	Dehydroevodiamine	-12.4	-12.4	-13.6	-13.3	37.8	4.4	(Park et al. 1996)
23	Crinine	-12.7	-12.3	-11.6	-12.9	461	3.3	(Elgorashi et al. 2004)
24	Haloxysterol A	<b>-18.7</b>	<b>-15.5</b>	<b>-15.9</b>	<b>-19.4</b>	8.3	5.1	(Ahmed et al. 2006)
25	Haloxysterol B	<b>-18.7</b>	<b>-15.4</b>	<b>-15.9</b>	<b>-19.4</b>	0.89	6.1	(Ahmed et al. 2006)
26	Haloxysterol C	<b>-18.4</b>	<b>-14.9</b>	<b>-15.6</b>	<b>-19.1</b>	1.0	6.0	(Ahmed et al. 2006)
27	Haloxysterol D	<b>-18.6</b>	<b>-15.3</b>	<b>-16.9</b>	<b>-20.2</b>	17.2	4.8	(Ahmed et al. 2006)
28	Sarcodine	<b>-16.1</b>	<b>-13.7</b>	<b>-14.6</b>	<b>-17.6</b>	18.3	4.7	(Khalid et al. 2004)
29	Isosarcodine	<b>-16.0</b>	<b>-13.4</b>	<b>-14.4</b>	<b>-17.6</b>	1.89	5.7	(Khalid et al. 2004)
30	Lycopodine A	-12.4	-12.0	-13.1	-13.4	-	NA	(Dall'Acqua 2013)
31	Methyl isoplatydesmine	-11.4	-10.7	-10.5	-12.0	74.5	4.1	(Sultana and Sultana 2009)
32	Sarsalignone	<b>-17.0</b>	<b>-14.2</b>	<b>-15.3</b>	<b>-18.3</b>	4.29	5.3	(ul Haq and Uddin 2011)
33	Voacangine hydroxyindolenine	-14.6	<b>-14.1</b>	<b>-13.8</b>	-14.2	-	NA	(Andrade et al. 2005)

AChE acetylcholinesterase, BChE butyrylcholinesterase, COX-2 cyclooxygenase-2, MMP-8 matrix metalloproteinase 8, NA not available

response to excitatory synaptic activity and glial cells in response to inflammation, is upregulated in AD subjects (Aisen 2002; Woodling et al. 2016). Studies have shown that the administration of selective COX-2 inhibitors attenuate inflammation and cholinergic hypofunction (Giovannini et al. 2003). Another important target protein implicated in the development of AD is MMP-8, which has been linked to the development of many diseases, including cancer metastasis, chronic inflammation and neurological disorders (Rasool et al. 2018). Matrix metalloproteinases (MMPs) are said to contribute to the formation and degradation of amyloid proteins in AD and cause death of dopaminergic neurons in Parkinson's disease (Rosenberg 2009). In normal physiological conditions, tissue inhibitors of matrix metalloproteinases (TIMPs) control the activity of MMPs; overexpression of MMP activity, or inadequate control by TIMPs, have been reported in a number of disease conditions, including

Alzheimer's disease (Peress et al. 1995; Pochetti et al. 2009). Although the major therapeutic strategies for AD is the use of anticholinesterase, such as donepezil, tacrine, galantamine, and ensaculin (Sugimoto et al. 2000; Hoerr and Noeldner 2002; Camps et al. 2010; Kavanagh et al. 2011); the employment of multi-target-directed molecules is now been considered to be a promising strategy for AD treatment, because of the multifactorial mechanisms implicated in the pathology of the disease, hence the global interest in finding new multi-target-directed ligands for the treatment of AD especially from phytochemicals since prolonged usage of the current synthetic drugs used to manage the symptoms of AD have been associated with some side effect (Lin et al. 2017; Hu et al. 2018). Interestingly, some studies and have considered the use of multi-target-directed ligands for AD; however, to the best of our knowledge, very few of such studies relate to the co-inhibition of important target proteins

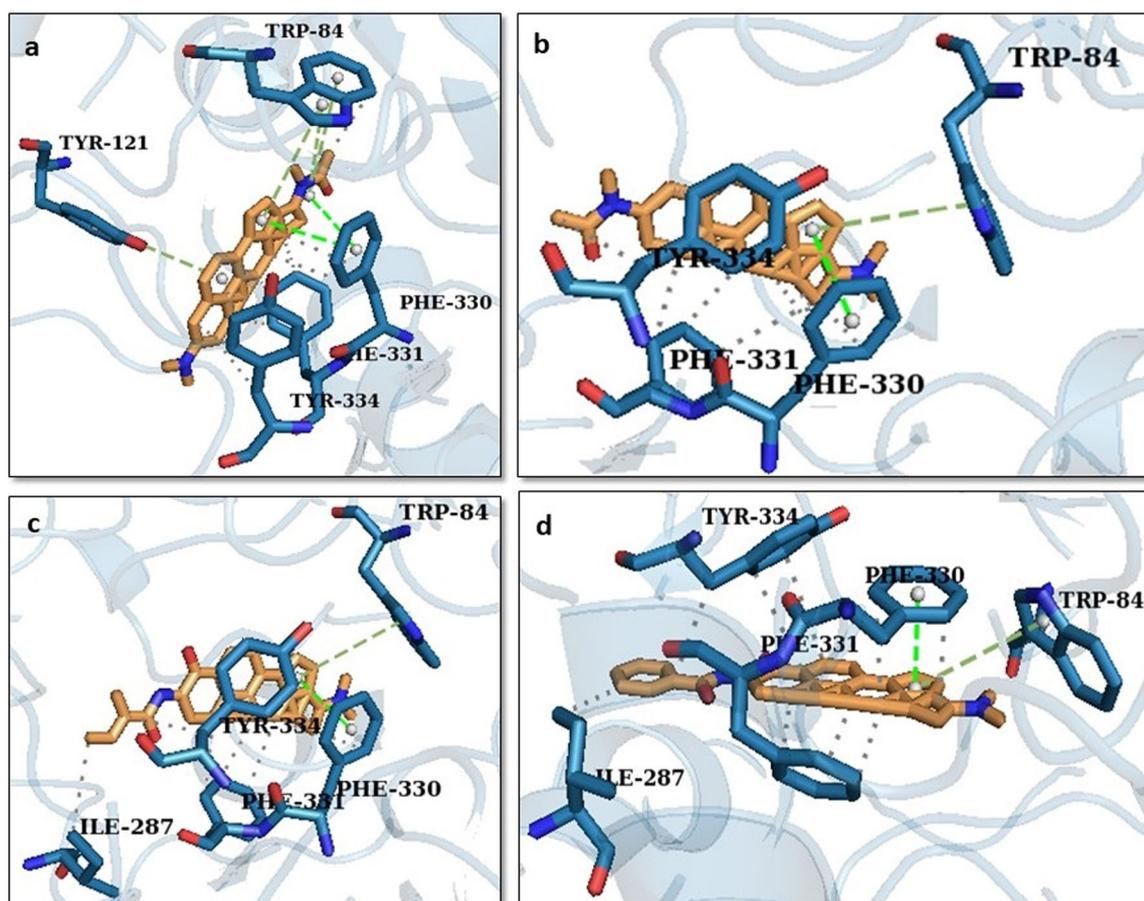


**Fig. 1 a–f** Interaction between acetylcholinesterase and potential inhibitors and **a** binding pocket occupied by donepezil and other ligands. Interaction between amino acids in the binding site of

acetylcholinesterase: **b** donepezil, **c** Haloxysterol A, **d** Haloxysterol B, **e** Haloxysterol C, **f** Haloxysterol D

(AChE, BChE, COX-2 and MMP-8) by alkaloids, a popular group of phytochemicals identified as the major constituents responsible for a variety of the bioactivities of most plant extracts, including anticholinesterase, antioxidant as well as inhibitory activity against many proteins (Ahmed et al. 2013; Hussain et al. 2018). Therefore, in an effort to identify potential drug agents against AD, we have decided to carry out a study into AChE, BChE, COX-2 and MMP-8 targeted alkaloids against AD, using *In silico* methods, since phytochemicals are not only less toxic relative to the synthetic drugs, they also have other beneficial effects like antioxidant

and antiinflammatory activities (Kumar and Khanum 2012; Kim et al. 2014; Venkatesan et al. 2015). To achieve this aim, 33 alkaloids were selected for molecular docking studies, based on literature search, to explore their binding modes with AChE, BChE, COX-2 and MMP-8, using donepezil, a standard neurological drug as the bench mark. Molecular docking was done using Blind Docking Server (Sánchez-Linares et al. 2012) while ligand-protein molecular interaction of compounds with remarkable inhibitory characteristics against the selected target proteins were viewed with PyMOL (PyMOL Molecular Graphics System, Version 2.0 Schrodinger LLC)



**Fig. 2 a–d** Interaction between amino acids in the binding site of acetylcholinesterase and **a** sarcosine, **b** isosarcosine, **c** sarsalignenone, **d** axillaridine A

to gain structural insight into the binding interaction, including the types of bonding interaction and the amino acids involved in such interactions, compared to the selected standard anticholinesterase inhibitor. Furthermore, alkaloids with high binding affinity and remarkable binding interaction with the target proteins were subjected to drug likeness investigation based on absorption-distribution-metabolism-excretion (ADME) properties using the Swiss online ADME web tool. This is in order identify orally drugable AChE, BChE, COX-2 and MMP-8 inhibitors that qualify for further drug development studies.

## Materials and methods

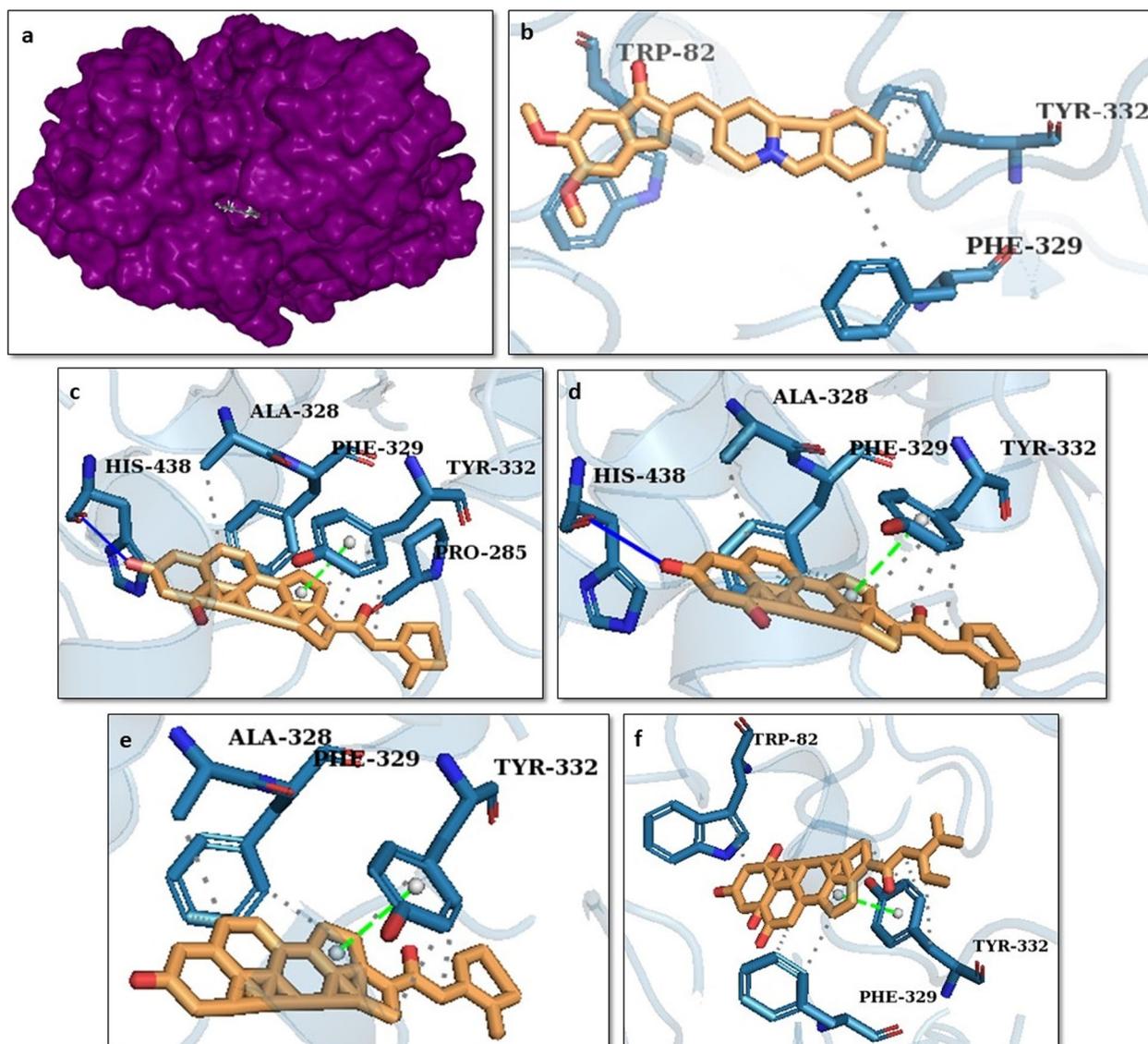
### Protein preparation

The crystal structures of acetylcholinesterase (AChE), butyrylcholinesterase (BChE), cyclooxygenase-2 (COX-2) and neutrophil collagenase (MMP-8) with PDB IDs 1QTL, 1POP, 5W58 and 3TT4 respectively were retrieved from the

protein databank ([www.rcsb.org](http://www.rcsb.org)). The crystal structures were prepared individually by removing existing ligands and water molecules while missing hydrogen atoms were added using Autodock v4.2 program, Scripps Research Institute. Thereafter, non-polar hydrogens were merged while polar hydrogen were added to each protein. The process was repeated for each protein and subsequently saved into dockable pdbqt format in preparation for molecular docking.

### Ligand preparation

SDF structures of the standard drug donepezil and 33 potential inhibitors of cholinesterase were retrieved from the PubChem database ([www.pubchem.ncbi.nlm.nih.gov](http://www.pubchem.ncbi.nlm.nih.gov)). The compounds were converted to mol2 chemical format using Open babel (O'Boyle et al. 2011). Polar hydrogen charges of the Gasteiger-type were assigned and the nonpolar hydrogens were merged with the carbons and the internal degrees of freedom and torsions were set to zero. The compounds were further converted to the dockable pdbqt format using Autodock tools.



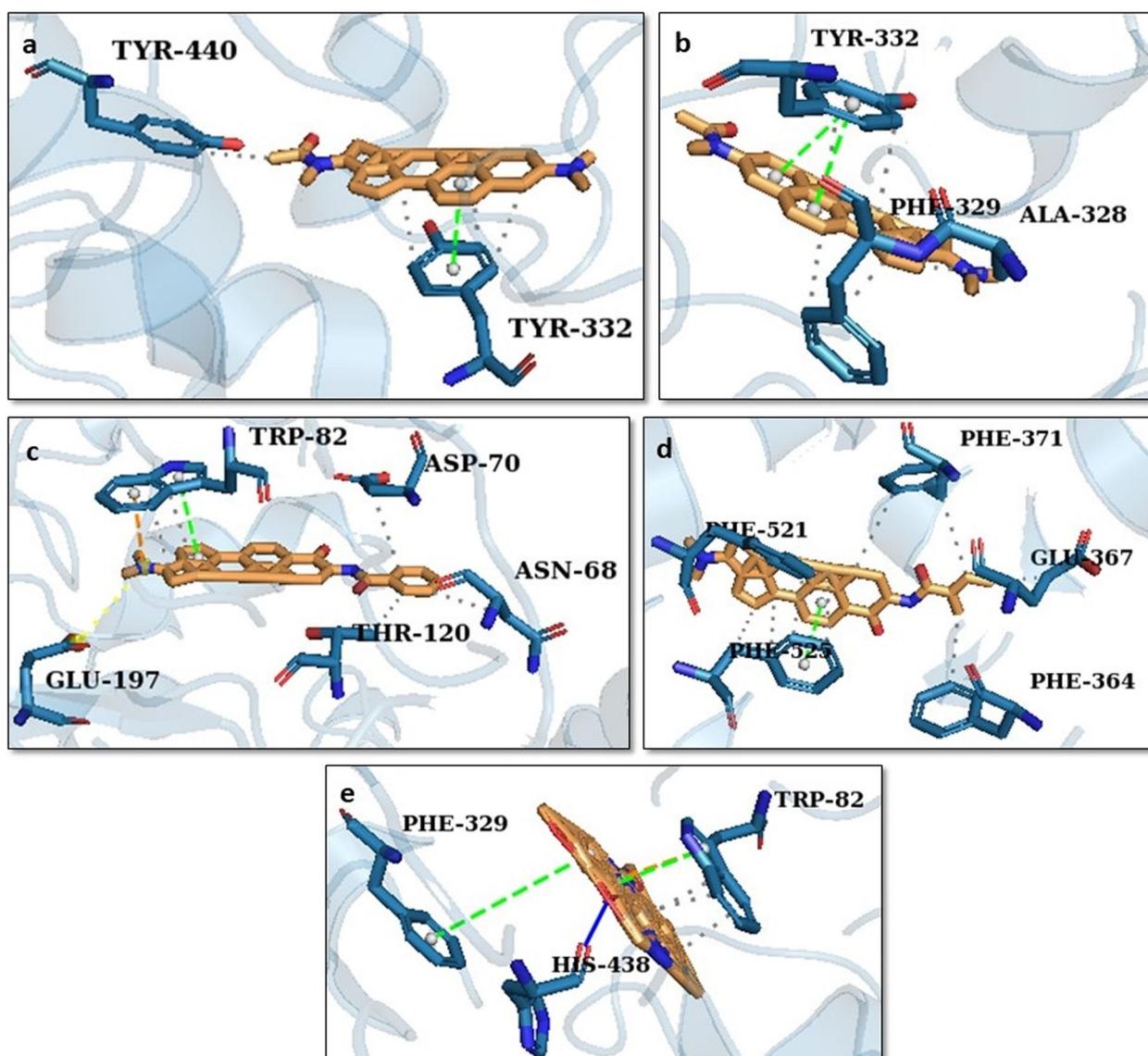
**Fig. 3** a–f Interaction between butyrylcholinesterase and potential inhibitors and **a** binding pocket occupied by donepezil and other ligands. Interaction between amino acids in the binding site of

acetylcholinesterase: **b** donepezil, **c** haloxysterol A, **d** haloxysterol B, **e** haloxysterol C, **f** haloxysterol D

## Molecular docking

Docking of the ligands to AChE, BChE, COX-2 and MMP-8, as well as determination of binding affinities was carried out using Blind Docking Server (Sánchez-Linares et al. 2012). The web base tool utilizes a modified version of Autodock Vina (Trott and Olson 2010) to sample across the whole protein surface to determine the best pose. Pdbqt form of individual protein and ligands were uploaded into their respective columns and the online tool was run. Blind Docking Server performs exhaustive docking simulations on each alpha carbon of the protein and uses its pose clustering

algorithm to detect new binding modes and calculate binding affinities. After the affinities were calculated, the tool clusters the results according to spatial overlapping of the resulting poses. For each cluster, the pose with the best affinity was taken as the representation of this cluster. The binding affinities of compounds for three proteins were calculated. The compounds were then ranked by their affinity scores. Thereafter, molecular interaction between AChE, BChE, COX-2 and MMP-8 and compounds with binding affinity higher than that of donepezil (standard inhibitor) were viewed with PyMOL (PyMOL Molecular Graphics System, Version 2.0 Schrodinger LLC).



**Fig. 4** a–e Interaction between amino acids in the binding site of butyrylcholinesterase and **a** Sarcodine, **b** isosarcodine, **c** axillaridine A, **d** sarsaligenone, **e** voacangine hydroxyindolenine

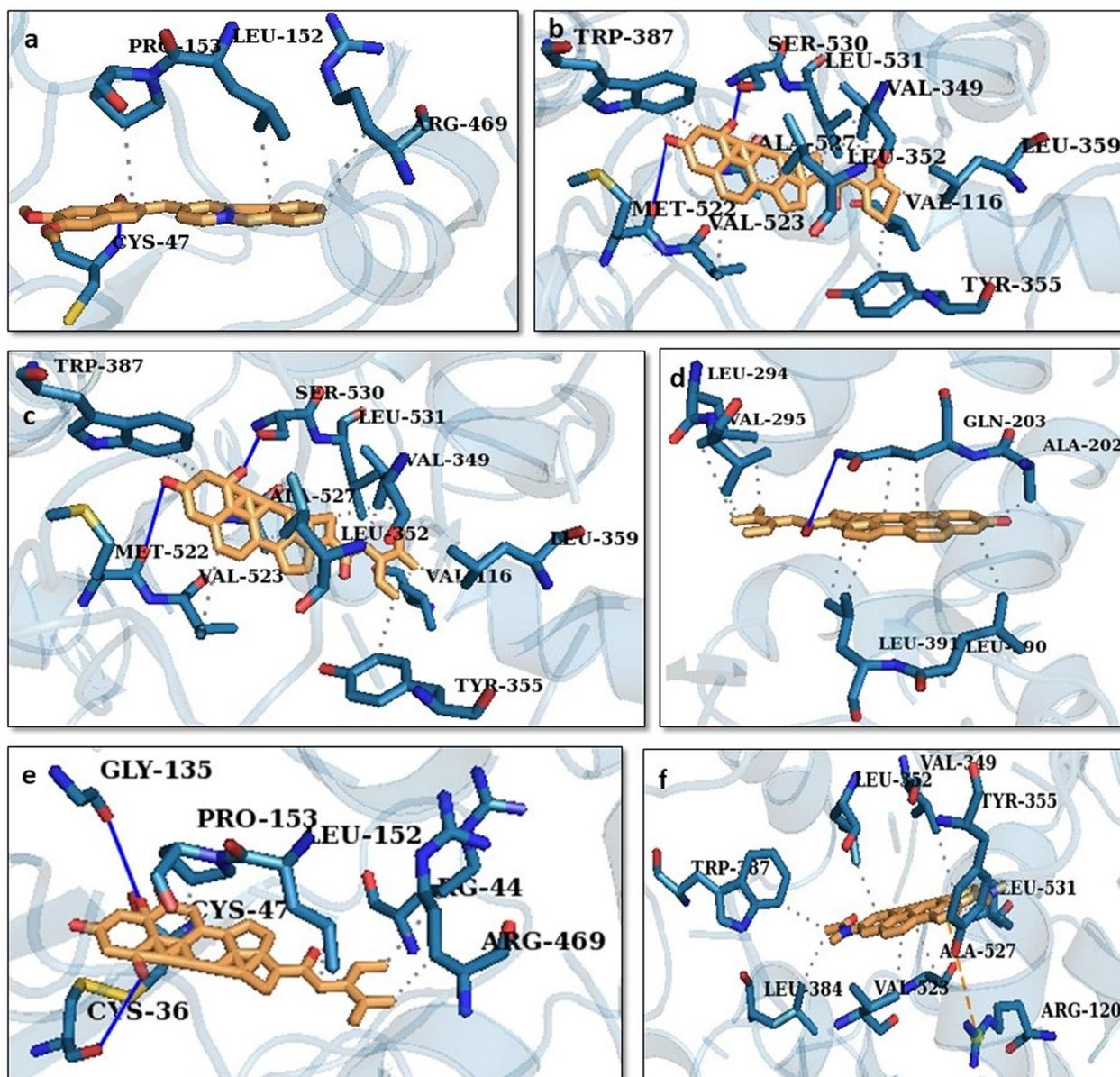
### Drug likeness and prediction of ADME

*In-silico* methods for the determination of Absorption-Distribution-Metabolism-Excretion (ADME) parameters rely on theoretically derived statistical models, which have been generated by relating the structural characteristics of compounds that have been measured in a given assay to their biological responses and is now widely used due to its low resource requirement (Gleeson et al. 2011). Therefore, nine of the compounds that showed reasonable binding modes with AChE, BChE, COX-2 and MMP-8 based on similar binding pattern to donepezil and higher negative binding affinity were subjected to physico-chemical studies. ADME studies were carried out using

the Swiss online ADME web tool (Daina et al. 2014; Daina and Zoete 2016; Daina et al. 2017) to evaluate the drug-likeness of the selected compounds. A graph of WLOGP against TPSA was plotted using GraphPad Prism 6 software (GraphPad Software, California, USA) to determine the blood brain barrier (BBB) properties of the compounds.

### Determination of $pIC_{50}$ value

$IC_{50}$  ( $\mu M$ ) value of the donepezil and the 33 anticholinesterase alkaloids used in this study were retrieved from literature.  $pIC_{50}$  values were calculated as  $-\log(IC_{50})$  (Selvaraj et al. 2011).



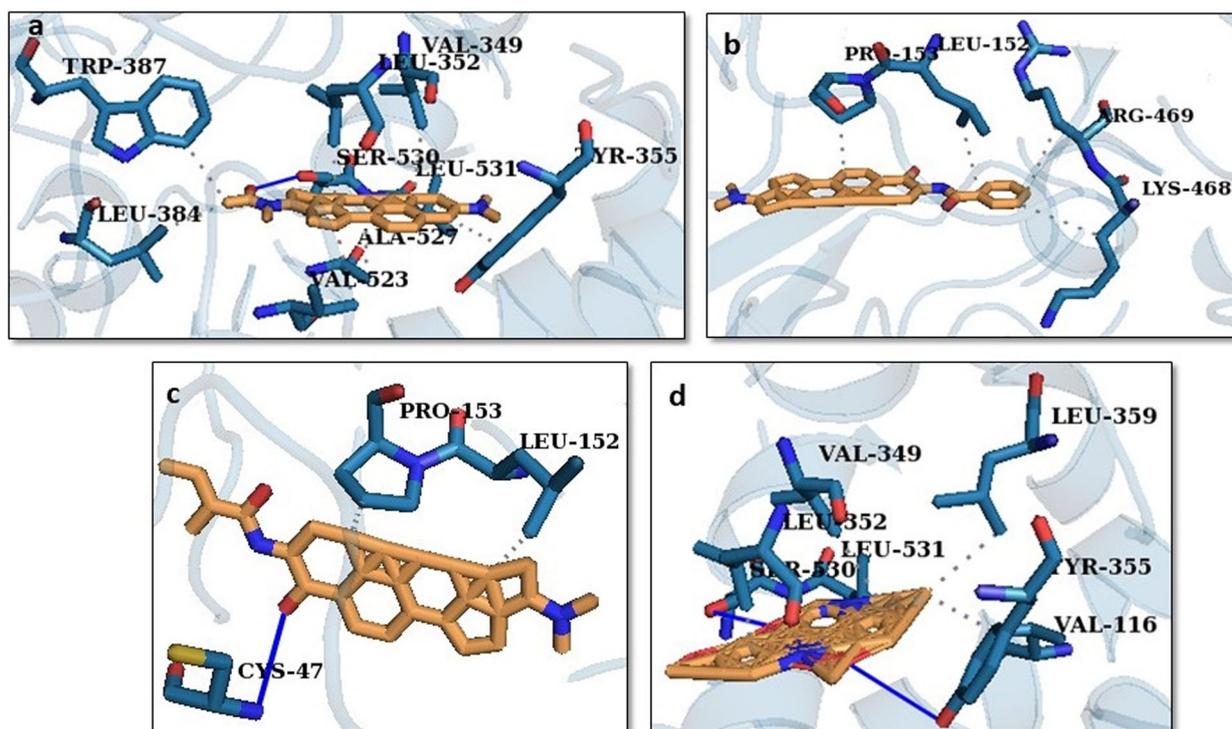
**Fig. 5** a–f Amino acid interaction between cyclooxygenase-2 and **a** donepezil, **b** haloxysterol A, **c** haloxysterol B, **d** haloxysterol C, **e** haloxysterol D, **f** isosarcodine

## Results and discussion

### Molecular docking

The result of the binding energy of the selected alkaloids to selected vital target proteins (AChE, BChE, COX2, and MMP8) implicated in the pathogenesis of AD from the molecular docking study is shown in Table 1, with the values for compounds having higher binding affinity for the target proteins indicated in bold face. The result revealed

that the standard inhibitor (donepezil) has a binding affinity of  $-15.1$  and  $-12.5$  Kcal/mol for AChE and BChE respectively. These Figures were surpassed by 9 out of the 33 alkaloids evaluated for anticholinesterase activity. The more negative the binding energy number, the higher the binding affinity of the alkaloid for the specific target protein. Thus, haloxysterols A, B, C and D have the most negative binding affinity for AChE ( $-18.7$ ,  $-18.7$ ,  $-18.4$ , and  $-18.6$  Kcal/mol, respectively) and BChE ( $-15.5$ ,  $-15.4$ ,  $-14.9$ , and  $-15.3$ , respectively) compared to

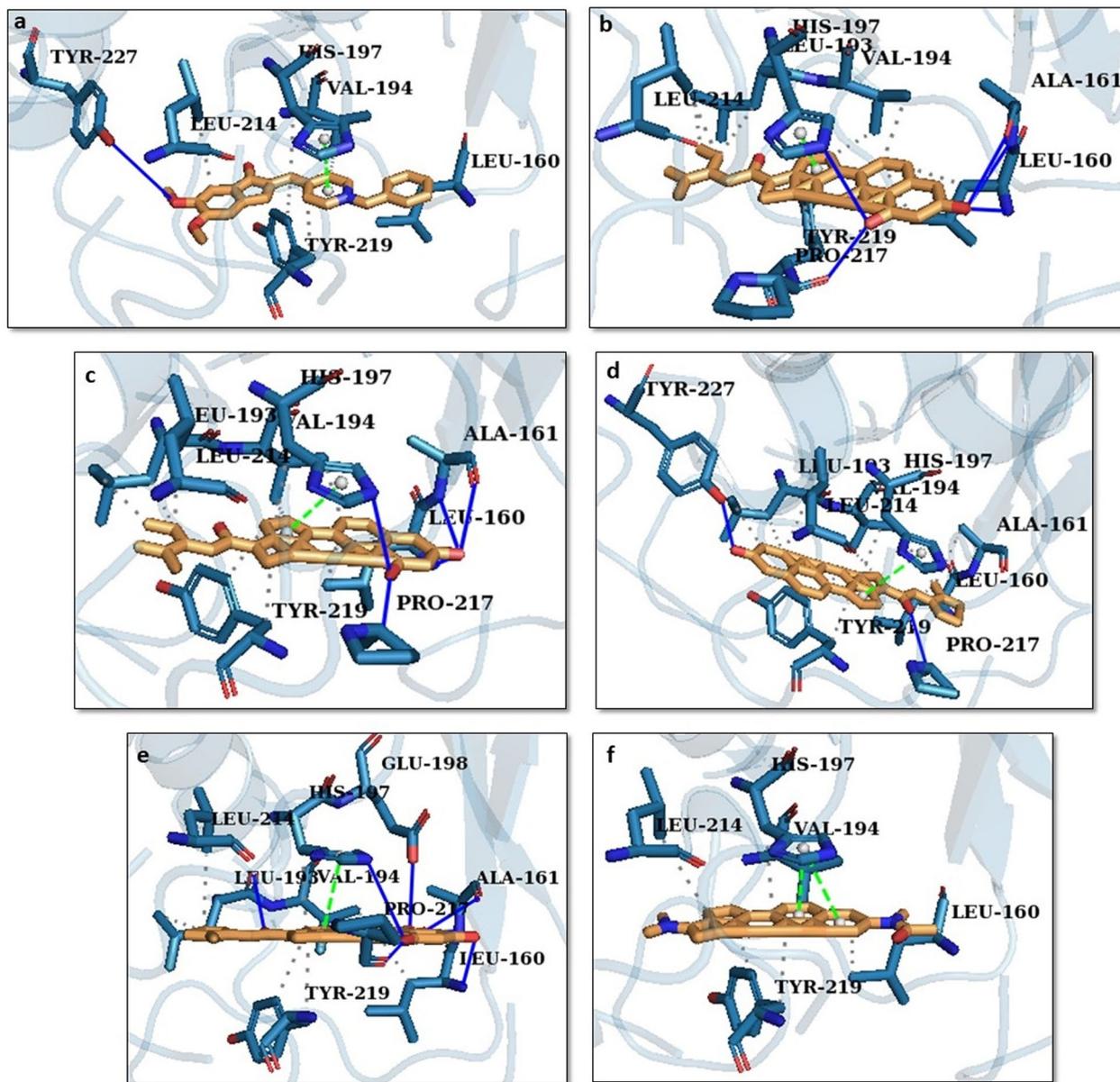


**Fig. 6** a–d Amino acid interaction between cyclooxygenase-2 and **a** sarcodine, **b** axillaridine A, **c** sarsalignenone, **d** voacangine hydroxyindolenine

donepezil. Axillaridine A, sarsalignenone, sarcodine and isosarcodine also have higher binding energy than donepezil, with binding energy of  $-17.7$ ,  $-17.0$ ,  $-16.1$ , and  $16.0$  Kcal/mol respectively for AChE and  $-15.0$ ,  $-14.2$ ,  $-13.7$ , and  $-13.4$  Kcal/mol, respectively for BChE. Voacangine hydroxyindolenine was selective for BChE with a binding affinity of  $-14.1$  Kcal/mol. The result obtained on the ligand-protein binding interaction showed that donepezil docked in a narrow gorge (Fig. 1a) composed of several conserved amino acids, with donepezil interacting with TRYP84 and PHE330 of the anionic site of AChE via hydrophobic interaction and TYR334 of the peripheral anionic site, PAS (Fig. 1b). Similarly, haloxysterol A, B, C and D interacted with TRYP84 via a  $\pi$ - $\pi$  stacking and PHE330 in the anionic site and a hydrophobic interaction with TYR334, and also hydrogen bond with TYR121 in the PAS region (Fig. 1c–f). However, only haloxysterol D has a hydrogen bond interaction with one of the catalytic triad residue (HIS440). Sarcodine, isosarcodine, sarsalignenone and axillaridine A exhibit similar binding pattern, creating a characteristic  $\pi$ - $\pi$  stacking interactions with TRP84 in the catalytic site and PHE330 in the anionic site of AChE, while interactions were also observed between the compounds and PHE331 of AChE (Fig. 2a–d). The ligand-BChE binding interaction showed that donepezil and the alkaloids docked in a narrow gorge, shown in Fig. 3a. The binding of donepezil to BChE revealed hydrophobic interaction with the conserved residue (TRP82) and a

hydrophobic interaction with PHE329 at the anionic site (Fig. 3b); a similar binding interaction was observed for haloxysterol D (Fig. 3f). Haloxysterols, A, B and C in addition to hydrophobic interaction with PHE329, interacted with ALA328 while an additional hydrogen bond was formed between haloxysterols B and C and HIS438 of the catalytic triad of BChE (Fig. 3c–e). A  $\pi$ - $\pi$  stacking was observed between sarcodine /isosarcodine and TYR322, with hydrophobic interaction with anionic site residue PHE329 in isosarcodine (Fig. 4a, b). Axillaridine A and voacangine hydroxyindolenine had a  $\pi$ - $\pi$  stacking with conserved residue TRP82, while an extra hydrophobic interaction with ASP70 in the case of the later was also observed (Fig. 4c, d). Voacangine hydroxyindolenine had a hydrogen bond interaction with catalytic histidine residue at position 438, while sarsalignenone a  $\pi$ - $\pi$  interaction with GLU325 in the catalytic triad of the enzyme.

The binding of various ligands to COX-2 also revealed 9 alkaloids with remarkable binding affinities, these include haloxysterols A, B, C, D, axillaridine A, sarcodine, isosarcodine, sarsalignenone and voacangine hydroxyindolenine having more negative binding energy ( $-15.9$ ,  $-15.9$ ,  $-15.5$ ,  $-16.9$ ,  $-16.2$ ,  $-14.6$ ,  $-14.4$ ,  $-15.3$  and  $-13.8$  Kcal/mol respectively) for this important protein, compared to donepezil with a binding energy of  $-13.7$  Kcal/mol (Table 1); whereas, from the results obtained for MMP-8. Eight, out of the 33 alkaloids exhibit higher binding affinity for the

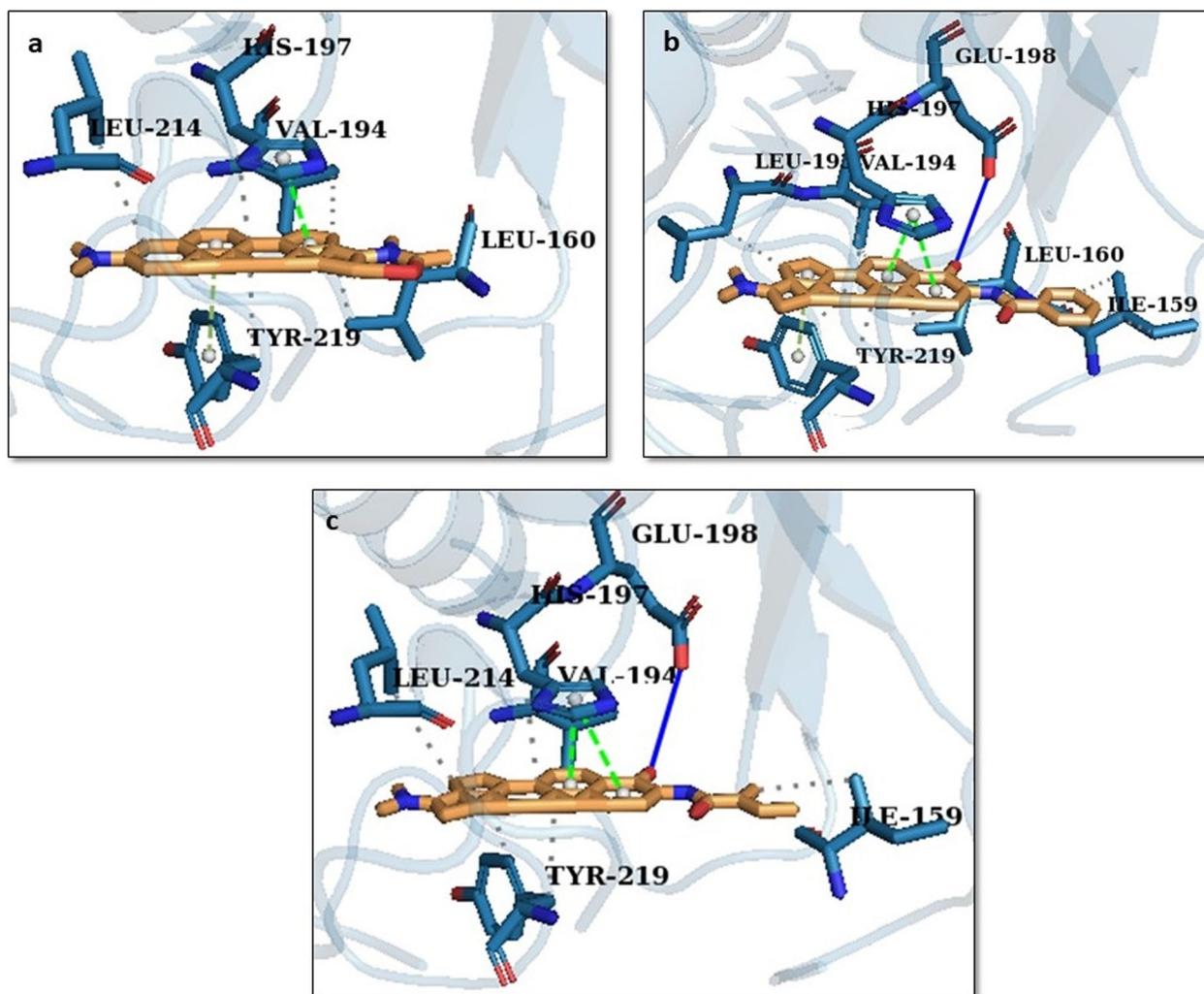


**Fig. 7** a–f Amino acid interaction between neutrophil collagenase and **a** donepezil, **b** haloxysterol A, **c** haloxysterol B, **d** haloxysterol C, **e** haloxysterol D, **f** isosarcodine

protein than donepezil, these include axillaridine A, haloxysterols A, B, C, D, sarcodine, isosarcodine and voacangine hydroxyindolenine with binding energy of  $-18.7$ ,  $-19.4$ ,  $-19.4$ ,  $-19.1$ ,  $-20.2$ ,  $-17.6$ ,  $-17.6$  and  $-18.3$  Kcal/mol compared to  $-16.0$  Kcal/mol for donepezil (Table 1). 29 of the 33 compounds have reported in vitro anticholinesterase inhibitory activity expressed in ( $\mu$ M). Huperzine A and physostigmine, have higher  $pIC_{50}$  values (10.0 and 9.2 respectively) compared to donepezil (7.2). Sanguinine, galanthamine, 1-O-Acetyllycorine, haloxysterol B and C also have notable  $pIC_{50}$  of 7.0, 6.0, 6.1 and 6.1 respectively. In vitro cholinesterase activity of alkaloids have been previously reported (Mukherjee et al. 2007; Howes and

Houghton 2009; Ahmed et al. 2013) making it ideal to explore possible role of the compounds in the treatment of other neurological disorders.

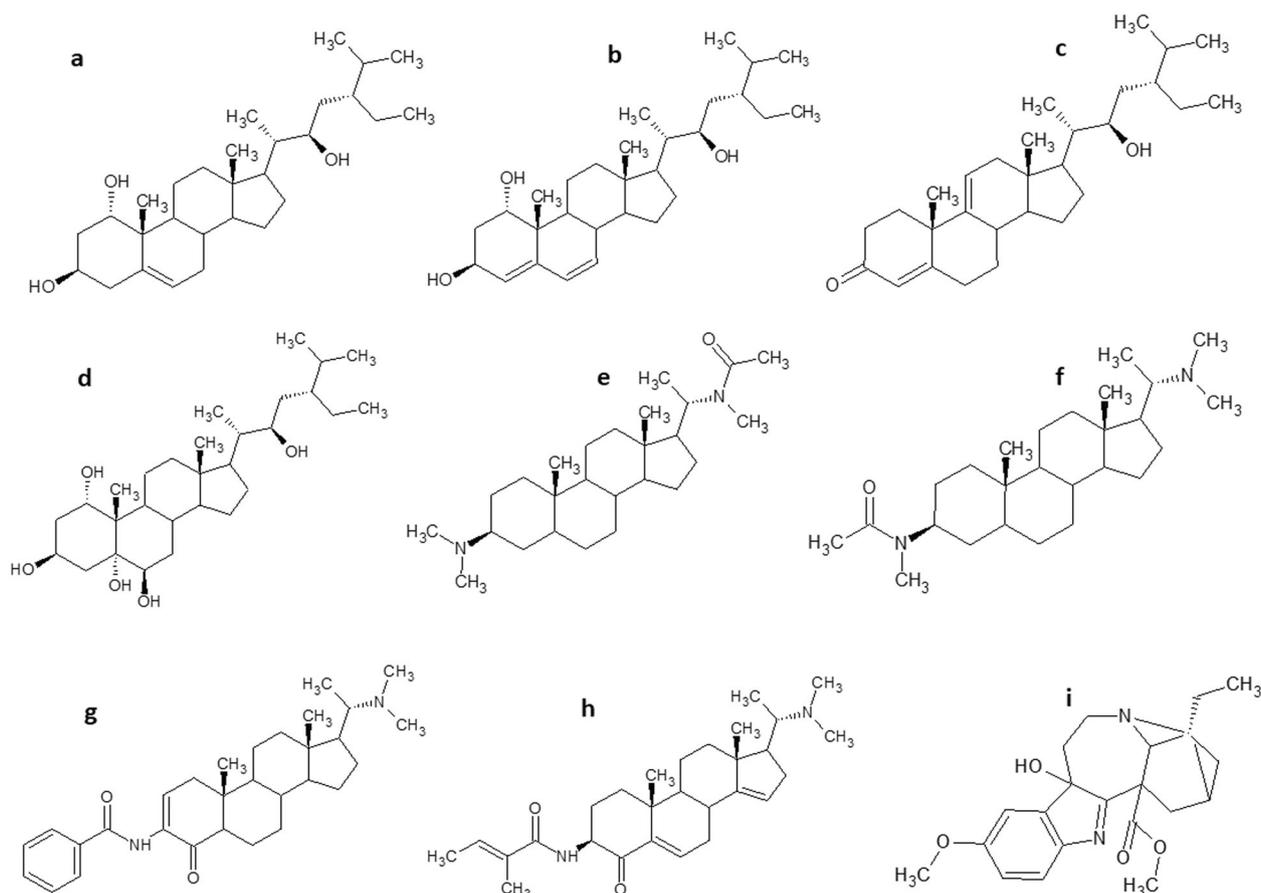
Evaluation of different binding poses of donepezil in COX-2 revealed a hydrophobic interaction with LEU152, PRO153, and ARG469 with an additional hydrogen bond with CYS47 (Fig. 5a). Haloxysterols A and B showed similar binding pattern, but with additional interaction with SER530 and MET522 via hydrogen bond and hydrophobic interaction with TRP387, TYR355, and VAL523 (Fig. 5b, c). A single hydrogen bond was formed between haloxysterol C and GLN203 of COX-2 while hydrophobic interaction was predominant between the compound and amino acids in COX-2



**Fig. 8** a–c Amino acid interaction between neutrophil collagenase and **a** sarcodine, **b** axillaridine A, **c** sarsaligenone

binding site (Fig. 5d). A total of two hydrogen bonds were formed between haloxysterol D and CYS36 and GLY35 (Fig. 5e) while isosarcodine (Fig. 5f) and sarcodine (Fig. 6a) have a similar binding pattern to haloxysterols A and B but with isosarcodine having an extra  $\pi$ -cation interaction with ARG120 of COX-2. Axillaridine A had only hydrophobic interaction with amino acids in COX-2, interacting with PRO153, LEU152, ARG469 and LYS468 (Fig. 6b). Of the 9 compounds, only sarsaligenone had a similar binding pattern with donepezil in COX-2, interacting with CYS47 via hydrogen bonding as well as hydrophobic interaction with LEU152 and PRO153 (Fig. 6c). SER530 and TYR355 were seen in a hydrogen bond interaction with voacangine hydroxyindolenine in the presence of other amino acids in the binding site of COX-2 (Fig. 6d). For, MMP-8,  $\pi$ - $\pi$  stacking exists between the compounds and HIS197 of the protein, as well as hydrophobic interactions with VAL194, and LEU214 (Figs. 7 and 8). Donepezil (Fig. 7a) and haloxysterol C (Fig. 7d) shared similar hydrogen bond interaction with

TYR227 while hydrogen bond interaction with LEU160, ALA161, HIS197 and PRO217 were observed in the case of haloxysterols A, B and D (Fig. 7b, c, e); axillaridine A (Fig. 8b) and sarsaligenone (Fig. 8c) formed hydrogen bond interaction with GLU198 of MMP-8 while sarcodine had an extra  $\pi$ -stacking with TYR219 (Fig. 8a). The structure of the 9 alkaloids with remarkable binding energy with acetylcholinesterase, butyrylcholinesterase, cyclooxygenase-2 and matrix metalloproteinase 8 are shown in Fig. 9. Multi-target-directed ligands for the management of AD is being explored as a viable strategy in the management of this neurodegenerative disease with phytochemicals as viable alternatives (Hu et al. 2018); since reasons such as side effects and low bioavailability limit the drugability and uses in medicine of the current drugs, necessitating a great demand to identify new inhibitors (Orhan et al. 2011; Paula et al. 2013). From the results obtained in this study, 9 anticholinesterase alkaloids (haloxysterol A, haloxysterol B, haloxysterol C, haloxysterol D, sarcodine, isosarcodine, axillaridine A, sarsaligenone and



**Fig. 9** a–i structures of alkaloids with remarkable binding energy with acetylcholinesterase, butyrylcholinesterase, cyclooxygenase-2 and matrix metalloproteinase 8: **a** haloxysterol A, **b** haloxysterol B, **c** haloxysterol C, **d** haloxysterol D, **e** sarcodine, **f** isosarcodine, **g** axillaridine A, **h** sarsalignenone, **i** voacangine hydroxyindolenine

voacangine hydroxyindolenine) with remarkable inhibitory tendency towards COX-2 and MMP-8 were identified from a set of 33 selected alkaloids. Studies have shown that COX-2 may have a central role in neurodegeneration, supporting clinical evaluation of selective COX-2 inhibitors as neuroprotective agents in AD (Aisen 2002). COX-2 expression is increased in frontal cortex of the brain of AD subjects (Pasinetti and Aisen 1998). Therefore, ability of the selected alkaloids to inhibit COX-2 may decrease the neurodegeneration observed in AD brain. Matrix metalloproteinases play a significant role in diseases of the central nervous system (CNS) because they mediate disruption of the blood brain barrier, regulate extracellular matrix protein destruction and remodeling as well as tissue inflammation in response to oxidative stress (Yong et al. 2001). Upregulation of MMPs has been reported in several neurological disorders including AD (Yong et al. 2001) prompting the search for new inhibitors of MMPs. The ability of haloxysterols A, B, C, D, sarcodine, isosarcodine, axillaridine A, sarsalignenone, voacangine hydroxyindolenine to inhibit MMP-8 with higher binding affinity compared to Donepezil (a standard drug) may prove significant in the quest for new treatments for AD.

### Pharmacokinetic properties of selected alkaloids

The results obtained for the ADME study on the 9 compounds with remarkable binding energy for the selected proteins are shown in Table 2. Interestingly, the result indicated that the 9 compounds are potential oral drug candidates. All but haloxysterol C has no Lipinski violation i.e., they all have molecular weight of less than 400 Daltons, less than 10 hydrogen bond acceptor, less than 5 hydrogen bond donor and octanol/water partition coefficient (MLogP) of less than 5 (haloxysterol C had an MLogP of 5.6). Also, all nine compounds have less than 10 rotatable bonds and topological surface area (TPSA) less than 140 Å<sup>2</sup> signifying that none of the compounds violated Veber's rule. Lipinski examined orally active compounds to define physicochemical ranges for high probability to be an oral drug (i.e., the drug-likeness). This popular *Rule-of-five* delineated the relationship between pharmacokinetic and physicochemical parameters (Lipinski 2000). Lipinski's rule states that, generally, an orally active drug has no more than one violation of the following criteria: (1) Not >5 hydrogen bond donors (nitrogen or oxygen atoms with one or more

**Table 2** Physicochemical properties of alkaloids with remarkable binding energy with acetylcholinesterase, butyrylcholinesterase, cyclooxygenase-2 and matrix metalloproteinase 8

S/N	Compounds	Molecular Weight	H-bond acceptor	H-bond donor	MLogP	Lipinski's violations	Rotatable bonds	TPSA ( $\text{\AA}^2$ )	Veber's violation	WLOGP	BBB permeation
1	Haloxysterol A	446.71	3	3	4.92	0	6	60.69	0	5.97	Yes
2	Haloxysterol B	444.69	3	3	4.82	0	6	60.69	0	5.74	Yes
3	Haloxysterol C	426.67	2	1	5.60	1	6	37.30	0	7.12	No
4	Haloxysterol D	480.72	5	5	3.39	0	6	101.15	0	4.13	No
5	Sarcodine	402.66	2	0	4.74	0	4	23.55	0	5.44	Yes
6	Isosarcodine	402.66	2	0	4.74	0	4	23.55	0	5.44	Yes
7	Axillaridine A	462.67	3	1	4.48	0	5	49.41	0	5.70	Yes
8	Sarsalignenone	438.65	3	1	3.90	0	5	49.41	0	5.07	Yes
9	Voacangine hydroxyindolenine	384.47	6	1	1.97	0	6	71.36	0	1.78	Yes

*MLOGP* Octanol/Water Partition Coefficient

*TPSA* Topological Polar Surface Area

*WLOGP* Lipophilicity

hydrogen atoms). (2) Not >10 hydrogen bond acceptors (nitrogen or oxygen atoms) (3) A molecular mass <500 Daltons and (4) An octanol-water partition coefficient log P not greater than 5. The nine compounds with higher negative binding affinity have all their parameters within the acceptable range stated by Lipinski i.e., none of the compounds have more than one violation of the Lipinski rule of five. Also, the compounds were evaluated using Veber's rule taking into account the polar surface area and the number of rotatable bonds (Veber et al. 2002). None, out of the 9 alkaloids violated the Veber's rule which further strengthen their potential as oral drug candidates.

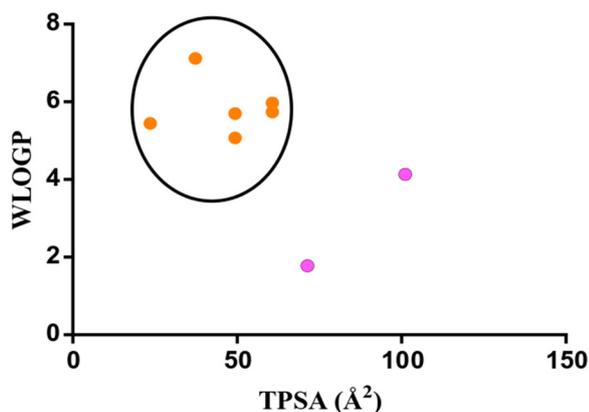
Moderately polar ( $TPSA < 79 \text{\AA}^2$ ) and relatively lipophilic (*WLOGP* from 0.4 to 6.0) compounds have a high probability to access the central nervous system (CNS) (Daina and Zoete 2016). Consequently, only haloxysterol C ( $TPSA = 101.15 \text{\AA}^2$ ) and haloxysterol D ( $WLOGP = 7.12$ ) (Table 2) violated this rule while the seven other compounds may transverse the BBB. This was depicted in an egg-yolk-like model where seven of the compounds aggregated in a sphere with the two non BBB permeant (BBB-) outside the sphere (Fig. 10). However, only six spheres are visible inside the box because sarcosine and isosarcosine appear as a single sphere since they have exactly the same *WLOGP*, *TPSA* and *MLogP*. The Blood Brain Barrier (BBB) can be regarded as a cover protecting the brain by a "physical" barrier and a "biochemical" barrier consisting of enzymatic activities and active efflux (Daina and Zoete 2016). Thus, BBB serves as the most important barrier between CNS and systemic circulation (Goodwin 2005). Despite the massive effort in CNS drug research in both academia and industry, there has been no parallel effort

in CNS drug delivery, which is peculiar owing to the existence of the BBB (Pardridge 2009); therefore, the ability of the selected alkaloids to cross the blood brain barrier may prove significant in the treatment of Alzheimer's disease.

Based on the remarkable binding affinity of the anticholinesterase alkaloids for both COX-2 and MMP-8 (indicated by their high negative binding energies relative to donepezil), their properties of oral drug likeness (no violation of Lipinski's and Veber's rules) and their blood brain barrier crossing potentials, they qualify for further study as drug candidates for AD.

## Conclusion

Alzheimer's disease is a neurodegenerative disorder wherein the death of neuronal cells in the brain causes loss of memory and cognitive decline that negatively affect quality of life and expectancy. Due to the complexity of the causes of AD, new agents that are based on different mechanisms are needed. Computer-based study and drug design has now become an important approach for the discovery of novel drugs. Results obtained from this study revealed that 9 alkaloids, earlier identified as having anticholinesterase activity have now been identified as orally drugable, COX-2 and MMP-8 multi-target inhibitors and also possess the ability to cross the blood brain barrier, with the exception of haloxysterols C and D. This study highlighted alkaloids that should be examined further, using different experimental models, to validate their promising potential as lead compounds in the management of AD and other related neurodegenerative diseases.



**Fig. 10** Blood brain barrier properties of anticholinesterase alkaloids with significant remarkable binding affinity to cyclooxygenase-2 and matrix metalloproteinase 8. 7 permeants (BBB<sup>+</sup>, orange dots inside black sphere), 2 non permeants (BBB<sup>-</sup>, purple dots)

## Compliance with ethical standards

**Conflict of interest** The authors declare that they have no conflict of interest.

**Ethical approval** This article does not contain any studies with human participants or animals performed by any of the authors.

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