

1182-2014-1-PB.pdf

by Istyastono_18 Enade

Submission date: 30-Aug-2017 04:24PM (UTC+0700)

Submission ID: 841203809

File name: 1182-2014-1-PB.pdf (876.08K)

Word count: 5969

Character count: 33711

COMPUTER-AIDED DESIGN OF CHALCONE DERIVATIVES AS LEAD COMPOUNDS TARGETING ACETYLCHOLINESTERASE

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Submitted: 27-12-2016

Revised: 25-01-2017

Accepted: 25-02-2017

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ABSTRACT

One of well-established biological activities for chalcone derivatives is as acetylcholinesterase inhibitors, which can be developed for the therapy of Alzheimer's disease. Assisted by retrospectively validated structure-based virtual screening (SBVS) protocol to identify potent acetylcholinesterase inhibitors, 80 chalcone derivatives were designed and virtually screened. The *F*-measure value as the parameter of the predictive ability of the SBVS protocol developed in the research presented in this article was 0.413, which was considerably better than the original SBVS protocol (*F*-measure=0.226). Among the screened chalcone derivatives two were selected as potential lead compounds to design potent inhibitors for acetylcholinesterase: 3-[4-(benzyloxy)-3-methoxyphenyl]-1-(4-hydroxy-3-methoxy-phenyl)prop-2-en-1-one (**3k**) and 3-[4-(benzyloxy)-3-methoxyphenyl]-1-(4-hydroxyphenyl)prop-2-en-1-one (**4k**).

Key words: Computer-aided drug design, virtual screening, chalcone derivatives, acetylcholinesterase, Alzheimer's disease

INTRODUCTION

Alzheimer's disease (AD), a progressive brain disorder, is a neurodegenerative disease which becomes symptomatic after brain changing happened over the years (Aggarwal *et al.*, 2015). The prevalence of dementia, as AD symptom were varied (Rizzi *et al.*, 2014) and the number of people living with AD have been predicted to be increased two times every two decades from 46.8 million by 2015 to 74.7 million people by 2030 (Prince *et al.*, 2015). The deficiency of the brain neurotransmitter acetylcholine (ACh) is often associated with pathogenesis of AD (Tabet, 2006). Acetylcholine plays important roles in the nervous system such as increasing neurotransmitter release, supporting synaptic transmission, inducing synaptic plasticity, and coordinating firing of groups of neurons (Picciotto *et al.*, 2012; Tsuda, 2012). The hydrolysis of ACh into choline and acetic acid, a reaction needed to allow the returning of cholinergic neuron to the resting state, was catalyzed by a family of enzymes called cholinesterase (Colovic *et al.*, 2013). Acetylcholinesterase (AChE), one of cholinesterase types found in many types of

conducting tissue, is a highly possible therapeutic target of Alzheimer disease (Mehta *et al.*, 2012).

Recently, research on AChE inhibitor has been rapidly developed due to the availability of supporting facilities for designing AChE inhibitor compounds in the treatment of AD (Singh *et al.*, 2013). Promising compounds to be developed as AChE inhibitor were chalcone derivatives (Sukumaran *et al.*, 2016; Tran *et al.*, 2016). Chalcones or 1,3-diphenyl-2-propene-1-one can be obtained both from the plants (Abdelwahab, 2013; Adewusi *et al.*, 2010) and from the synthetic way due to condensation reaction between substituted aromatic aldehyde with substituted acetophenones in alkaline condition (Jayapal and Sreedhar, 2010). Nevertheless, it is important to consider the structure-activity relationship and computational approach in designing more active AChE inhibitors (Andersson *et al.*, 2013; Ece *et al.*, 2015).

Some strategies to optimize predictive abilities of Structure-based Virtual Screening (SBVS) protocols have been developed (de Graaf *et al.*, 2011; Istyastono, 2015; Istyastono *et al.*, 2015^a; Istyastono and Setyaningsih, 2015;

Radifar *et al.*, 2013^b; Sirci *et al.*, 2012). Some of the strategies have been employed successfully in the prospective screenings to discover novel potent fragments for histamine H₁ (de Graaf *et al.*, 2011), H₃ (Sirci *et al.*, 2012) and H₄ receptors (Istyastono *et al.*, 2015^a), and in the repurposing selective cyclooxygenase-2 inhibitor celecoxib as a potent ligand for estrogen α receptor (Istyastono *et al.*, 2015^b; Radifar *et al.*, 2013^b). In 2011, by combining ChemPLP score (Korb *et al.*, 2009) and the post-docking scoring functions of the interaction fingerprint (IFP) program (Marcou and Rognan, 2007) as the cutoff values, de Graaf *et al.* could reach *F*-measure value of about 0.515 and discover 19 novel fragments with Ki ranging from 10 μ M to 6 nM for histamine H₁ receptor after virtually screened about 13 million compounds and tested only 26 hits resulted from the prospective virtual screening (de Graaf *et al.*, 2011). In 2012, employing Fingerprint for Ligand and Protein (FLAP) software as the post-docking modeling strategy to identify active histamine H₃ fragments Sirci *et al.* could discover 18 novel fragments out of 29 tested hits resulted from prospective virtual screening of 156,090 compounds (Sirci *et al.*, 2012). In 2015, by employing several homology models with different reference ligands, using post-docking scoring functions of the IFP program (Marcou and Rognan, 2007), Istyastono *et al.* could optimize the *F*-measure value from 0.018 to 0.553 and discover 9 novel histamine H₄ fragments after virtually screen 43,326 fragments and tested 37 hits resulted from the prospective virtual screening (Istyastono *et al.*, 2015^a). Fortunately the structure of histamine receptors was well-studied, which established ASP^{3.32} as the anchor of the receptor-ligand binding (Istyastono *et al.*, 2011^a; Jongejan *et al.*, 2008). These success stories employed the anchor interaction to filter the docking poses before proceeding to the subsequent step in the SBVS protocols (de Graaf *et al.*, 2011; Istyastono *et al.*, 2015^a; Sirci *et al.*, 2012). However, the information of the anchor interaction is still rare for other targets in drug discovery. Moreover, instead of having anchor interaction, some targets accept more poses for their potent ligands (Istyastono, 2015). Several attempts to optimize SBVS protocols by taking

into account several poses of active ligands (Istyastono *et al.*, 2011^b; Wang *et al.*, 2015) by decision trees construction have been performed targeting estrogen α receptor and could optimize the *F*-measure value from 0.215 to 0.642 (Istyastono, 2015; Setiawati *et al.*, 2014). Notably, the same strategy could not be applied in this research since no decision tree could be constructed. Another strategy to optimize the predictive ability of the SBVS protocol in this research should be developed and tested.

The research presented in this paper was aimed to design chalcone derivatives as potent AChE inhibitors by utilizing retrospectively validated SBVS protocols constructed by employing PLANTS1.2 as the molecular docking software (Korb *et al.*, 2009, 2007) and PyPLIF as the Protein-Ligand Interaction Fingerprints (PLIF) identification software for re-scoring (Radifar *et al.*, 2013^a; Radifar *et al.*, 2013^b). New post PLIF identification descriptor or employing ensemble PLIF (abbreviated here to *ensplif*) was introduced and employed here to construct and optimize SBVS protocols (Istyastono *et al.*, 2017), which was then assessed (Cannon *et al.*, 2007; de Graaf *et al.*, 2011; Desaphy *et al.*, 2013; Powers, 2011) and compared to the original SBVS accompanying the release of DUD-E (Mysinger *et al.*, 2012). The best SBVS protocol constructed in this research could outperform the predictive ability of the SBVS protocol of DUD-E. The protocol was subsequently employed to assist the selection of chalcone derivatives as lead compounds in the development of acetylcholinesterase inhibitors

MATERIALS AND METHODS

The crystal structure of AChE obtained from the protein data bank (PDB) with PDB id of 1E66 was used as the reference structure (Dvir *et al.*, 2002; Mysinger *et al.*, 2012). Active AChE inhibitors (453) and the decoys (26,350) from DUD-E (Mysinger *et al.*, 2012) were employed to perform retrospective validations for the SBVS protocol. Chalcone derivatives inspired from Imran *et al.* (Imran *et al.*, 2015) which were designed manually (Table I) were used as entry points for lead compounds selection. All calculations and computational

simulations were performed on a Linux (Ubuntu 12.04 LTS Precise Pangolin) machine with Intel[®] Xeon[®] CPU E31220 (@ 3.10GHz) as the processors and 8.00GB of RAM. Computational medicinal chemistry applications employed in this research were SPORES (ten Brink and Exner, 2009), PLANTS1.2 (Korb *et al.*, 2009; Korb *et al.*, 2007), Open Babel 2.2.3 (O'Boyle *et al.*, 2011), PyPLIF0.1.1 (Radifar *et al.*, 2013^a; Radifar *et al.*, 2013^b), MarvinSketch 14.11.10.0 (ChemAxon, 2014) and PyMOL 1.2r1 (Lill and Danielson, 2011). Statistical analysis was performed by using R 3.3.0 (R Core Team, 2016).

Computational methods

Virtual molecular target preparation

Previously published method to prepare cyclooxygenase-2 as virtual target (Istyastono, 2016) was adopted to prepare virtual target AChE. The crystal structure of AChE was downloaded from <http://www.rcsb.org/pdb/explore.do?structureId=1e66>. Then, the module *splitpdb* in SPORES was subsequently used to split the pdb file and to convert the splitted files into *mol2* files the virtual AChE (*protein.mol2*), the co-crystal ligand3-chloro-9-ethyl-6,7,8,9,10,11-hexahydro-7,11-methanocycloocta[B]quinolin-12amine (*ligand_HUX803_0.mol2*), and the water molecules. The *mol2* files were then ready to be employed in molecular docking simulation employing PLANTS1.2 docking software.

Ligands preparation for retrospective virtual screening

Similar to virtual target preparation, previously published methods for ligands preparation (Istyastono, 2016; Istyastono and Yuniarti, 2016) were adopted and modified. Known AChE active inhibitors and their decoys were downloaded in their SMILES format from DUD-E (Mysinger *et al.*, 2012). They were stored locally as *actives_final.ism*, and *decoys_final.ism*. Each compound in the files was then subjected to Open Babel 2.2.3 conversion software to be converted in its three dimensional (3D) format as a *mol2* file. The *reprot* module in SPORES was subsequently employed to properly check and assign the

protonation state of the *mol2* file into a proper *mol2* file ready to be docked by using PLANTS1.2 docking software.

Automated molecular docking and virtual screening

Similar to previously published procedures (Istyastono *et al.*, 2015^b; Istyastono and Setyaningsih, 2015; Setiawati *et al.*, 2014), all virtual screenings were performed by docking program PLANTS1.2. For each compound, 50 poses were produced and clustered at root mean square deviation (RMSD) of 1.0 Å. The ChemPLP scoring function was used at speed setting 2. The binding pocket was defined by the coordinates of the center of the co-crystal *ligand_HUX803_0.mol2* and a radius of 5 Å. All other options of PLANTS1.2 were left at their default setting. Every compound was virtually screened five times independently. Seven different interaction types (negatively charged, positively charged, hydrogen bond (H-bond) acceptor, H-bond donor, aromatic face-to-edge, aromatic face-to-face, and hydrophobic interactions) were subsequently identified by employing PyPLIF for each docking pose (Radifar *et al.*, 2013^a; Radifar *et al.*, 2013^b).

Predictive ability of the SBVS protocols

The predictive ability of the SBVS protocols was determined by their *F*-measure value of the retrospective validation (Cannon *et al.*, 2007; Desaphy *et al.*, 2013). The SBVS protocols predict screened compound as active or inactive. Since the biology activity as AChE inhibitor of the compounds in the retrospective validation attempts using DUD-E has already known (Mysinger *et al.*, 2012), the confusion matrix could be constructed (Cannon *et al.*, 2007): (i) Active compounds which were predicted as active were assigned as true positives (TP); (ii) Active compounds which were predicted as inactive were assigned as false negatives (FN); (iii) Decoys which were predicted as active were assigned as false positives (FP); and (iv) Decoys which were predicted as inactive were assigned as true negatives (TN). The *F*-measure value (Cannon *et al.*, 2007; Desaphy *et al.*, 2013) was calculated as follows: $(2 \times TP) / ((2 \times TP) + FN + FP)$.

Predictive ability optimization of the SBVS protocols

For comparison as the standard, the compounds in the retrospective SBVS were ranked based on the best ChemPLP score and the ChemPLP score of the 1% identified FP was used as the cutoff to predict as active or inactive (de Graaf *et al.*, 2011; Istyastono *et al.*, 2015; Korb *et al.*, 2009; Mysinger *et al.*, 2012). The optimization of the SBVS protocols was performed by optimizing the post SBVS decision trees constructed in RPART package (Istyastono, 2015; R Core Team, 2016; Therneau *et al.*, 2015) by using *ensplif* as the descriptors. Besides considering all poses resulted in the SBVS, *ensplif* as descriptors were calculated by selecting poses by using ChemPLP scores systematically from -125 to 0. The algorithm of the *ensplif* calculation was as follows: (i) Poses selection based on the ChemPLP score as the cutoff; (ii) In every PLIF bitstring, all "on" interactions were counted; (iii) The numbers resulted from point (ii) were divided by 250 since the molecular docking resulted in 50 docking poses in each run and every compound was screened 5 times (see subsection Automated molecular docking and virtual screening).

Computer-aided identification of chalcone derivatives as lead compounds to discover potent AChE inhibitors

Eighty chalcone derivatives were designed (Table I). Every structure in table I was built and converted to SMILES format by using module *Copy as smiles* in Marvin Sketch 14.11.10.0 (ChemAxon, 2014). The structure was then undergone ligand preparation process as presented in the subsection Ligands preparation for retrospective virtual screening. The best SBVS protocol to identify potent AChE inhibitors resulted from the subsection Predictive ability optimization of the SBVS protocols was used to virtually screen the designed compound. Based on the results of the virtual screening, some lead compounds were selected. The synthesis feasibility of the selected lead compounds was subsequently analyzed.

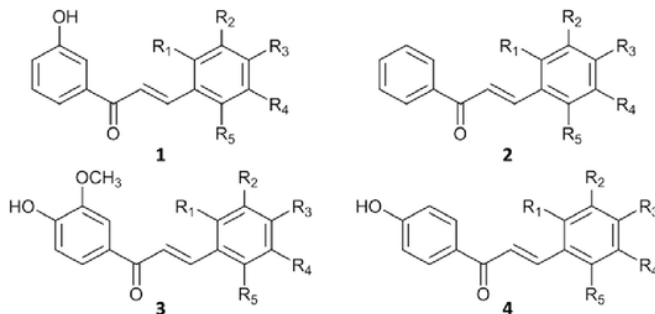
RESULTS AND DISCUSSION

Aimed to initiate the discovery and development of potent AChE inhibitors, this research constructed and optimized the predictive ability of SBVS protocol to identify potent AChE inhibitors and employed the best protocol to select best potential inhibitors from 80 chalcone derivatives presented in Table I as lead compounds. The construction and optimization of the SBVS protocol to identify potent AChE inhibitors employed potent AChE inhibitors with IC_{50} value of less than 1 μ M and their decoys organized and stored in DUD-E (Mysinger *et al.*, 2012) as the retrospective compounds for the validation. Chalcone derivatives were selected since the synthesis expertise in the field is accessible for further investigation in the subsequent discovery and development process (Imran *et al.*, 2015).

Construction and Predictive Ability Optimization of the SBVS Protocol

During molecular docking and PLIF identification phases in the retrospective SBVS campaign, nineteen ligands and 1,735 decoys could not pass the protocol, which were then predicted as inactive compounds. Therefore, the protocol has resulted in 19 FN and 1735 TN during the molecular docking and the PLIF identification phases. In every remaining result, the docking pose with the best ChemPLP score was collected and ranked based on the ChemPLP score. In this ranked database, at 1% FP (263 compounds) there were 52 TP, 401 FN, and 25,987 TN. Therefore the *F*-measure value of this ranked database was 0.135, which was corresponded to the enrichment factor value of 11.46. This predictive ability of the SBVS protocol by using 1% FP as the cutoff to predict the activity was much worse than the original protocol accompanying the release of DUD-E, which showed *F*-measure and enrichment factor values of 0.226 and 20.1, respectively (Mysinger *et al.*, 2012). Moreover, with this predictive ability, the SBVS protocol is not suggested to be used for prospective virtual screening campaigns (Chen, 2015; de Graaf *et al.*, 2011; Istyastono *et al.*, 2015; Sirci *et al.*, 2012). Predictive ability optimization of this SBVS protocol was therefore required.

Table I. Designed and virtually screened chalcone derivatives in this research.



Code	R ₁	R ₂	R ₃	R ₄	R ₅
a	-H	-OH	-H	-OH	-H
b	-H	-H	-F	-H	-H
c	-H	-NO ₂	-H	-H	-H
d	-H	-OCH ₃	-OH	-H	-H
e	-H	-H	-OH	-H	-H
f	-H	-H	-OCH ₃	-H	-H
g	-H	-OCH ₃	-OCH ₃	-OH	-H
h	-OCH ₃	-OCH ₃	-OCH ₃	-H	-H
i	-OCH ₃	-H	-OCH ₃	-OCH ₃	-H
j	-H	-H	-O-(CH ₂) ₃ -CH ₃	-H	-H
k	-H	-OCH ₃	-O-CH ₂ -C ₆ H ₅	-H	-H
l	-NO ₂	-OH	-H	-H	-H
m	-OCH ₃	-H	-OCH ₃	-H	-H
n	-OCH ₃	-H	-OCH ₃	-H	-OCH ₃
o	-OCH ₃	-CH ₃	-OCH ₃	-H	-H
p	-OCH ₃	-H	-OCH ₃	-H	-CH ₃
q	-OCH ₃	-H	-OCH ₃	-OCH ₃	-H
r	-H	-OCH ₃	-OCH ₃	-OCH ₃	-H
s	-H	-OH	-OH	-H	-H
t	-OH	-OH	-H	-H	-H

Equipped with the facts that some ligands could interact with their protein targets in more than one pose (Istyastono *et al.*, 2011^b; Wang *et al.*, 2015) and inspired by the lock-and-key theory (Koshland, 1994; Stoddard and Koshland, 1992), we introduce a novel post PLIF identification technique to optimize the predictive ability of the SBVS protocol by using *ensplif*. This strategy was successfully utilized to slightly increase the SBVS protocol to identify potent ligands for estrogen α receptor (Istyastono, 2015; Istyastono *et al.*, 2017). Therefore, we were tempted to apply the same technique in this research since employing the

technique used by Istyastono (2015) could not result in any constructed decision tree in this research. Taking into account all docking poses in every retrospective screened compound in this research resulted in a post SBVS decision tree using *ensplif* as the descriptors with *F*-measure value of 0.371, which was better than the ChemPLP-based ranked database at 1% FP and to the original protocol accompanying the release of DUD-E (*F*-measure = 0.226; Mysinger *et al.*, 2012). Notably, with this *F*-measure value the SBVS protocol has already accepted for further prospective virtual screening. However, the protocol could still be

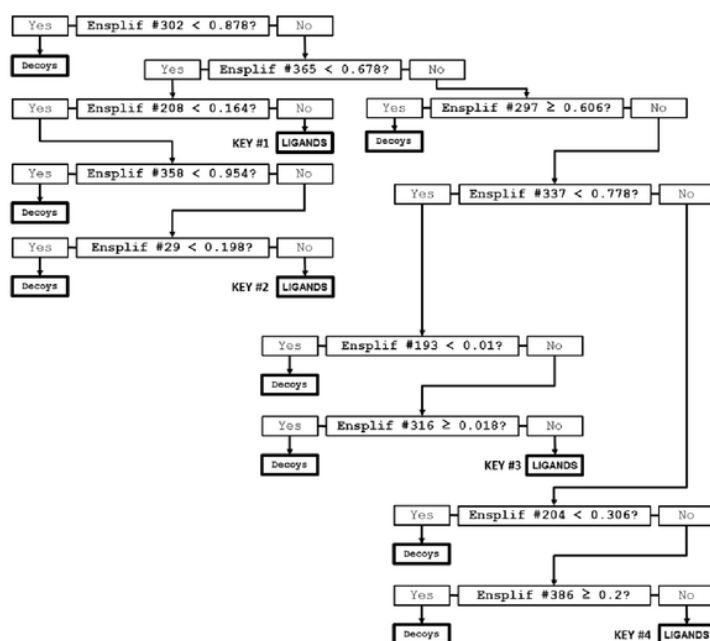


Figure 1. The best decision tree employing ensplif as descriptors to identify potent ligands for AChE. Four types of how ligands bind to AChE or “key” are identified.

optimized by selecting the more plausible docking poses with a certain ChemPLP score as the cutoff (de Graaf *et al.*, 2011).

The optimization by systematically assessing the predictive ability of employing ChemPLP scores from -125 to 0 as the cutoff for pose selection resulted in F -measure values ranging from 0.103 to 0.413. The best SBVS protocol with F -measure value of 0.413 was comprised of molecular docking simulation using PLANTS1.2 (Korb *et al.*, 2009), PLIF identification of the docking poses using PyPLIF (Radifar *et al.*, 2013^a; Radifar *et al.*, 2013^b), and the decision tree constructed using RPART (Therneau *et al.*, 2015) with ensplif calculated from PLIF of docking poses with ChemPLP score ≤ -33 (Figure 1).

The RPART method to construct decision trees used in the research is one of supervised machine learning methods which are susceptible for overfitting (Cannon *et al.*, 2007; Gabel *et al.*, 2014) and chance correlation (Lim *et*

al., 2009; Tarcsay *et al.*, 2013; Zambre *et al.*, 2007). A model is overfitting if the ratio of the cross-validation error rate over the training error rate is more than 1.5 (Cappel *et al.*, 2015; Istyastono, 2016). Since the ratio of the cross-validation error rate over the training error rate of the best decision tree (Figure 1) was 1.158, this model was not overfitting. In order to ensure if the best decision tree was not a chance correlation, 1000 times y -randomization were performed (Lim *et al.*, 2009; Smits *et al.*, 2010) and there was no y -randomized model with F -measure higher than the F -measure of the best decision tree (Figure 1). Therefore, there was no evidence of overfitting and chance correlation of the SBVS protocol comprising the best decision tree constructed using RPART with ensplif calculated from PLIF of docking poses with ChemPLP score ≤ -33 as the descriptors.

There are 11 selected ensplif in the decision tree (Table II). Notably, hydrophobic

Table II. The ensplif as selected descriptors in the decision tree (Figure 1) and their corresponding interactions in the AChE binding pocket

Ensplif No.	Corresponding Interactions in the AChE Binding Pocket	
	Amino Acid Residue	Interaction Type ^{a)}
29	GLN ⁷⁴	hydrophobic interaction
193	TYR ¹³⁰	hydrogen bond (protein as the donor)
204	SER ²⁰⁰	hydrophobic interaction
208	SER ²⁰⁰	hydrogen bond (protein as the acceptor)
297	PHE ³³⁰	aromatic edge-to-face interaction
302	PHE ³³¹	hydrophobic interaction
316	LEU ³³³	hydrophobic interaction
337	TRP ⁴³²	hydrophobic interaction
358	HIS ⁴⁴⁰	hydrophobic interaction
365	GLY ⁴⁴¹	hydrophobic interaction
386	ILE ⁴⁴⁴	hydrophobic interaction

^{a)}Ref: (Radifar *et al.*, 2013b)

interaction to PHE³³¹ is essential for AChE ligand since the ligand should have ensplif #302 \geq 0.878 to be predicted active as potent ligand for AChE, otherwise it will be predicted as inactive (Figure 1). Hydrophobic interactions dominate the selected interactions. This interaction type is however responsible only for the affinity but not for the selectivity because of its lack of directionality (Bissantz *et al.*, 2010; Desaphy *et al.*, 2013; Marcou and Rognan, 2007). Only three out of these 11 interactions have directionality (Bissantz *et al.*, 2010; Desaphy *et al.*, 2013; Marcou and Rognan, 2007; Radifar *et al.*, 2013b): (i) Ensplif#193 (hydrogen bond to TYR¹³⁰ with tyrosine as the donor); (ii) Ensplif#208 (hydrogen bond to SER²⁰⁰ with serine as the acceptor); and (iii) Ensplif#297 (aromatic edge-to-face interaction to PHE³³⁰). These three interactions are responsible not only for the ligand affinity but also for the ligand selectivity (Bissantz *et al.*, 2010; Istyastono *et al.*, 2011a, 2011b). Hydrogen bond and aromatic interaction have been identified as the main factors in activity cliffs with at least 100-fold activity increase (Furtmann *et al.*, 2015). Based on the decision tree presented in Figure 1, there are 4 types of “key” that can bind to the “lock” AChE. Notably, all branches leading to active compound in the decision tree (Figure 1) or the “keys” involve either the hydrogen bond (ensplif#208 or #193) or the aromatic interaction (ensplif#297). Oddly, in

contrary with the hydrogen bonds, which are favorable, the aromatic interaction here is unfavorable.

In the retrospective attempts, the optimized protocol resulted in *F*-measure value of 0.413 from 124 TP; 329 FN; 26,226 TN and 24 FP. By employing the retrospective results, the sensitivity (true positive rate) and the specificity (true negative rate) can be calculated (Cannon *et al.*, 2007) and get the following results: 0.274 and 0.999, respectively. This indicates that the optimized protocol tends to correctly predict inactive compounds. A predicted active compound using the optimized protocol is therefore highly probable to be an active AChE inhibitors but it is highly suggested to further investigate a predicted inactive compound especially the one that has ensplif number 302 of more than or equal to 0.878 (Figure 1).

Virtual Screening on Designed Chalcone Derivatives Employing the Optimized Protocol

Eighty chalcone derivatives presented in Table I were virtually screened employing the optimized SBVS protocol (Figure 1). However, none of these compounds were predicted as active. Therefore, selection of lead compounds instead of identification of potent AChE inhibitors from the chalcone derivatives (Table I) was the subsequent step. As mentioned in the previous subsection,

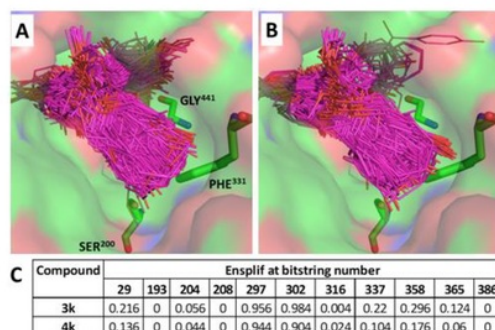


Figure 2. Docking poses of **3k**(A) and **4k**(B) which show hydrophobic interaction to PHE³³¹ but do not show hydrophobic interaction to GLY⁴⁴¹ and the corresponding important ensplif values (C). Carbon atoms of compounds **3k** and **4k** are presented in magenta. Carbon atoms of AChE are presented in green. Oxygen and nitrogen atoms are presented in red and blue, respectively. Hydrogen atoms are not shown for clarity. The ligands are in lines mode, while the enzyme is in surface mode with 0.5 transparencies. Important residues following path of key #1 in Figure 1 are also shown in stick mode.

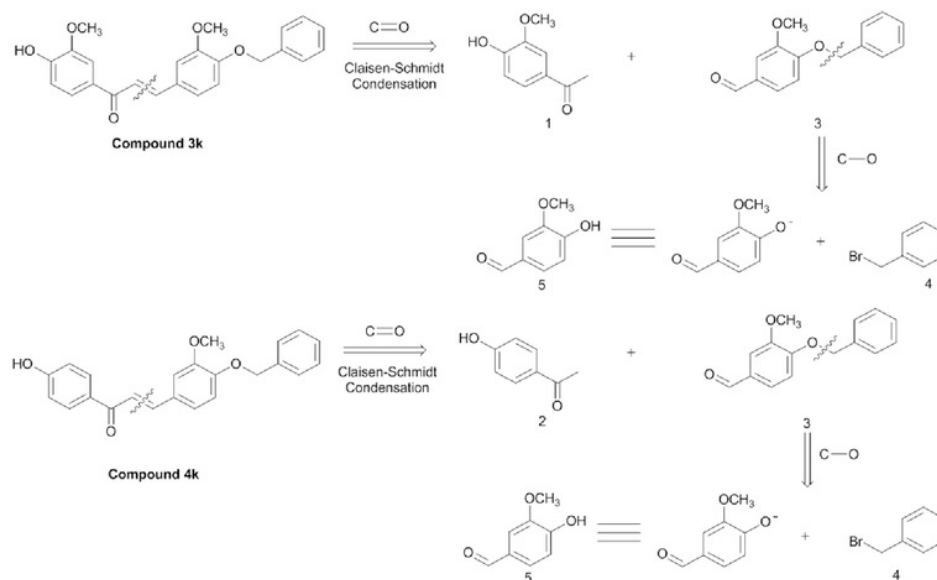


Figure 3. Retrosynthetic analysis of compound **3k** and **4k**. Reagents: (1) acetovanillone; (2) 3'-hydroxyacetophenone; (3) o-benzylvanillin; (4) benzyl bromide; (5) vanillin.

all predicted active compounds must have ensplif #302 \geq 0.878 (Figure 1). Among the virtually screened chalcone derivatives (Table I), only compounds **3k** and **4k** showed ensplif

#302 \geq 0.878. The ensplif #302 of compounds **3k** and **4k** were 0.956 and 0.944 (Figure 2). Therefore, compounds **3k** and **4k** were selected as lead compounds for further investigation in

this quest to discover potent AChE inhibitors. Since compounds **3k** and **4k** showed ensplif #365 < 0.678 (Figure 2), the shortest path to design potent AChE inhibitor by employing these lead compounds is the path of key #1 (Figure 1). Additional hydrogen bond to SER²⁰⁰ is therefore required (Figures 1 and 2). Based on visual inspection using PyMOL in docking poses of **3k** and **4k** which show hydrophobic interaction to PHE³³¹ but do not show hydrophobic interaction to GLY⁴⁴¹ (Figure 2), this could be achieved by appending or substituting the R₂ part of the selected lead compounds (Table I) with functional groups which have potential to be hydrogen bond donors, e.g., guanidine, amide and isothiourea.

Synthesis and further verification using *in vitro* analysis should be done in the near future to provide evidences that compounds **3k** and **4k** could serve as lead compounds. Retrosynthetic analysis or synthon disconnection approaches of compounds **3k** and **4k** (Figure 3). We propose here *o*-benzylvanillin (4-(benzyloxy)-3-methoxybenzaldehyde) to be used as starting material which could be synthesized using vanillin(4-hydroxy-3-methoxybenzaldehyde) and benzylbromide (bromomethylbenzene). Further, *o*-benzylvanillin could be reacted with acetovanillone (1-(4-hydroxy-3-methoxyphenyl) ethanone) for yielding compound **3k** and 3'-hydroxyacetophenone (1-(4-hydroxyphenyl) ethanone) for yielding compound **4k**.

CONCLUSIONS

Compounds **3k** and **4k** have been identified as potent lead compounds in the drug discovery and development for AD therapy targeting AChE. The identification of these lead compounds employed a retrospectively validated SBVS protocol with a decision tree employing ensplif resulted from molecular docking PLANTS1.2 and PLIF identification PyPLIF. In the retrospective validation, the SBVS protocol showed *F*-measure value of 0.413, which outperformed the original SBVS accompanying the database used for the retrospective validation.

ACKNOWLEDGEMENT

This research was financially supported by the Internship Grant for Lecturer 2016,

Faculty of Pharmacy Sanata Dharma University (No. Far/079/X/2016/ST/D).

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