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Screening of Bioactive Compounds of *Spirulina platensis* as Potential Antioxidants: An In-silico Approach

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Abstract

Oxidative stress is a significant trigger of degenerative diseases, caused by an imbalance between free radicals and the body's antioxidant defenses. This study aims to identify bioactive compounds from Spirulina platensis and to evaluate their antioxidant potential using an in-silico approach. Candidate screening was conducted using Gas Chromatography-Mass Spectrometry (GC-MS) analysis, antioxidant activity prediction, pharmacokinetic evaluation (Lipinski's Rule of Five), and ligand–receptor interaction analysis (molecular docking). GC-MS analysis identified 30 bioactive compounds across various classes, including hydrocarbons, alcohols, phenols, aldehydes, and steroids. Activity prediction showed that all compounds exhibited antioxidant potential with Pa > 0.7 and Pi > 0.3, meeting both Lipinski's criteria and drug-likeness requirements. Among them, phytol and ethyl iso-allocholate were demonstrated binding energies (ΔG) of –5.0 and –7.3 kcal/mol, respectively, which were lower than the natural ligand 3-[(1R)-1-(2,6-dichloro-3-fluorophenyl) ethoxy]-5-(1-piperidin-4-yl-1H-pyrazol-4-yl) pyridin-2-amine with –8.3 kcal/mol, suggesting their potential as free radical inhibitors. The microalga S. platensis thus contains antioxidant-active compounds with promising potential for further development. However, additional evaluations through active compound isolation as well as in vitro and in vivo studies are required.

Keywords: antioxidant, ligand, molecular docking, receptors.

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Introduction

Oxidative stress is an important issue in biomedicine because it plays a role in various chronic and degenerative diseases, including cancer, diabetes mellitus, atherosclerosis, and Alzheimer's disease (Maharan et al., 2025). This condition arises when the body's antioxidant system is overwhelmed by free radical production, leading to damage to DNA, proteins, and lipids. Antioxidants function to neutralize free radicals, but the body's natural mechanisms, both enzymatic (superoxide dismutase, catalase, glutathione peroxidase) and non-enzymatic (vitamin C, vitamin E, glutathione), are not always optimal, especially under conditions of stress, pollution, UV radiation, or chronic disease (Nursifa et al., 2025).

The limitations of synthetic antioxidants, such as Butylated Hydroxyanisole (BHA) and BHT, include their long-term side effects, which further drive the search for natural antioxidant sources (Nusaibah et al., 2023). One potential natural antioxidant candidate is Spirulina platensis, a photosynthetic microalga that produces bioactive metabolites, including chlorophyll pigments, carotenoids, and phycobiliproteins, which contribute to antioxidant activity (Aryono et al., 2022). This microalga also has enzymes that counteract Reactive Oxygen Species (ROS), such as Superoxide dismutase (SOD), Glutathione peroxidase (GPX), Catalase (CAT), and Peroxiredoxin oxidoreductase (PrxR). However, their production in the body decreases with age (Mu'Arifah, 2021). The antioxidant activity of active compounds can be observed by their inhibition of free radicals, nitric oxide, and superoxide radicals (Gonçalves et al., 2024).

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Analysis of the bioactive compounds in Spirulina platensis can be performed using Gas Chromatography-Mass Spectrometry (GC-MS) for molecular identification (Darmapatni et al., 2016), as well as an in-silico approach that can predict compound activity virtually with high efficiency (Maghfiroh et al., 2025). Previous studies have reported that GC-MS analysis of commercial spirulina identified 155 compounds whose biological activities have not yet been studied (Prasetiyo et al., 2024). Procedures for predicting the biological activity of compounds can be performed using the PASSonline application. Biological activity analysis using PASSonline can predict the wound-healing potential of plant-derived active compounds (Rathinavel et al., 2023). The results of bioactive compound screening in spirulina using GC-MS and in silico studies identified 13 compounds with potential as active ingredients for antidiuretic and anti-inflammatory agents (Riyadi et al., 2023). Exploration of active compounds and optimization of antioxidant activity potential using PASSonline are necessary to improve prediction and accuracy in molecular docking.

Molecular docking is an in-silico method that models interactions between proteins and ligands using databases such as PDB and PubChem. This technique enables the prediction of the mechanisms of action of bioactive compounds, which supports the search for new drug candidates (Syahputra, 2014). In-silico methods have advantages, including their speed and low cost. However, they have the disadvantage that the precision and accuracy of their predictions have yet to be demonstrated through in vitro and in vivo assays (Vijh & Gupta, 2024). Before performing in silico procedures, it can be combined with pharmacokinetic evaluation of candidate compounds, such as drug-likeness profiles (Lipinski's rules) from the SwissADME online database, to predict the potential of compounds as drug candidates (Riyadi et al., 2021). The exploration of antioxidant compounds from natural sources, such as Spirulina, has not been widely conducted using an in-silico approach. An evaluation of the pharmacokinetic properties of candidate antioxidant compounds derived from Spirulina is needed to predict their potential for development as drugs.

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This study explores the active compounds of spirulina, selects the most promising antioxidants, evaluates their pharmacokinetic properties, and conducts molecular docking to optimize prediction and precision. Exploring the active components of Spirulina platensis as a candidate for natural antioxidants in silico is important to identify potential compounds with potent antioxidant activity, safety, and the potential to be developed as basic ingredients for supplements or natural medicines. The urgency of this research lies not only in its contribution to the development of natural antioxidant sources but also in the application of efficient and sustainable modern computational methods in biotechnology and pharmacy (Pannindriya et al., 2021).

Method

Materials and equipment

The primary research materials were Spirulina platensis powder (PT. Algaepark, Klaten, Indonesia), the structure of Human ROS1 Kinase (ID: 3ZBF) as the target protein obtained from the PDB protein database, ethanol (Merck), PTFE syringe filter (0.45 µm), and 2 mL amber GC vials. The equipment used in this study included: GC-MS (Agilent 7890B & 7000), incubator, oven, rotary evaporator, 10 ml measuring flask, and microtube. The hardware used was an AMD Athlon Silver 3050U processor laptop with 8 GB of RAM, meeting the analysis requirements. The software and online tools used were PyRx, PyMOL, BIOVIA: Discovery Studio Visualizer, PASS Online, Protox II, PubChem, and Protein Data Bank (PDB).

GC-MS analysis

Approximately 10 g of spirulina powder was extracted with ethanol, sonicated for 15 minutes, filtered through a 0.45 µm syringe filter, and placed in a 2 mL amber vial before injection into the GC-MS system (Agilent 7890B & 7000). Gas chromatography was performed using an Agilent HP-5MS column (30 m × 0.25 mm × 0.25 µm) with helium as the carrier gas, at 1.987 psi, 0.438 mL/min, 100 °C oven temperature, and 310 °C injector temperature. The MS system used Electron Ionisation (EI), source temperature 250 °C, interface temperature 305 °C, and a m/z range of 28–600. Peaks on the chromatogram were then identified as compound types using the National Institute of Standards and Technology (NIST) and National Institutes of Health (NHI) databases.

Analysis of antioxidant potential and pharmacokinetic Lipinski's Rule (Rules of five)

Compounds identified by GC-MS were selected as ligands used in molecular docking analysis. Potential ligands were selected based on their antioxidant activity online at the PASS website https://way2drug.com/PassOnline/. Next, their pharmacokinetic properties were predicted using Lipinski's Rule of Five to assess their suitability as drug candidates online at https://tox.charite.de/protox3/.

Molecular docking

The molecular docking steps are as follows: prepare the protein-ligand by downloading it in 3D *SDF format from https://www.rcsb.org/. Then, find the protein code to be used using the 3ZBF code for Human ROS1 (Reactive Oxygen Species) Kinase on the website https://pubchem.ncbi.nlm.nih.gov/, and download it in *PDB format (Fadillah et al., 2024). The results of protein and ligand preparation were visualized in Pymol to remove water, ions, and native ligands, then to add polar hydrogen and Gasteiger charges. Next, the Pymol results were docked using PyRx to predict the ligand's position in the protein's active site and calculate the binding affinity. The results of molecular docking were visualized using BIOVIA software: Discovery Studio Visualizer to observe the types of bonds and amino acid residues involved in the interaction.

 E-ISSN: 2303-0720

Analysis data

The data obtained were analysed descriptively by reviewing the binding affinity values, protein-ligand residue interaction patterns, and pharmacological activity predictions (Anandhy, 2021) (Anandhy, 2021). This stage enabled the identification of bioactive compound candidates from Spirulina platensis with the potential to be developed as natural antioxidant sources.

Result and Discussion

Analysis of GC-MS and potential antioxidant

Gas Chromatography-Mass Spectrometry (GC-MS) analysis was performed to identify volatile bioactive compounds contained in Spirulina platensis. GC-MS analysis shows that spirulina contains more than 100 compounds, of which the antioxidant potential remains unknown. Phytol is a volatile ester compound commonly found in spirulina supplements (Paraskevopoulou et al., 2024). Other compounds include benzene, 1,4-dimethylheptadecane, phenylethyl alcohol, hexadecenoic acid, methylinoleate, and ethylhexadecanoate (Justus & Baraza, 2019). The results of other studies also indicate that spirulina has a relatively high abundance of volatile compounds, suggesting it is more selective in its volatile production.

The probability of activity (Pa) results indicate that 30 compounds exhibit antioxidant potential, including 1,4-Benzenediol, 2,6-bis(1,1-dimethylethyl)-, Phytol, Heptadecane, Citronellol, and others, as shown in **Table 1**. Compounds identified using the PASS online application showed positive activity with a probability of activity (Pa) > probability of inactivity (Pi). The most potential compounds based on Pa values are 1,4-Benzenediol, 2,6-bis (1,1-dimethylethyl)- (Pa = 0.729; Pi = 0.044) and Citronellol (Pa = 0.589; Pi = 0.005), shows in **Table 1**. Several spirulina compounds with antioxidant potential have also been reported to have anti-inflammatory properties, such as octadecane, hexadecane, methyl ester, and cyclohexane (Riyadi et al., 2023).

Pharmacokinetic Lipinski's Rule of Five

The Lipinski rules are used to assess the pharmacokinetic potential of compounds as drugs, with the following criteria: molecular mass <500 Da, HBD ≤ 5, HBA ≤ 10, LogP ≤ 5, and MR 40–130. The target protein ROS (PDB ID 3ZBF, Homo sapiens, resolution 2.20 Å) and natural ligands were separated for binding site identification. Molecular docking showed variations in binding affinity. The results of screening using Lipinski's Rule of Five can be seen in **Table 2**. Analysis of Lipinski's Rule of Five on 30 compounds from Spirulina platensis resulted in 24 compounds that passed and met the basic pharmacokinetic criteria with a molecular mass <500 Da, HBD ≤5, HBA ≤10, and MR in the range of 40-130. Small compounds such as Glyceraldehyde and compounds with balanced polarity such as Phytol are expected to have the best absorption, while long-chain hydrocarbons with high LogP values (>5) have the potential for limited solubility and bioavailability. GC-MS identification, with most meeting Lipinski's Rule of Five criteria and having an antioxidant activity probability (Pa) between 0.3 and 0.7. Other studies mention that based on drug-likeness criteria, spirulina has 24 active compounds that have the potential to be sources of bioactive compounds, one of which acts as an antioxidant (Riyadi et al., 2021).

 E-ISSN: 2303-0720

Table 1. Screening of bioactive compounds with antioxidant potential

No.	Compounds	RT (s)	Peak %	Antioxidant activity	Pa[1)]	Pi[2)]
1.	Phytol	21.372	65.5	Positive	0.475	0.008
2.	3.7.11.15-Tetramethy l-2-hexadecen-1-ol (phytol)	18.446	31.9	Positive	0.475	0.008
3.	3,7,11-Trimethyl-1-dodecanol	18.546	24.1	Positive	0,444	0,009
4.	2(4H)Benzofuranone,5,6,7,7atetrahydro-4,4,7a-trimethyl-, (R)-	14.906	19.9	Positive	0.051	0.101
5.	13-Heptadecyn-1-ol	18.73	14.8	Positive	0.155	0.097
6.	Heptadecane	16.78	14.4	Positive	0.170	0.079
7.	Octadecane	16.78	9.13	Positive	0.170	0.079
8.	4,4-Dimethyl-3-(2-nitro-phenyl) -2 oxaspiro[5,5]undecane-1,5-dione	8.863	6.71	Positive	0.177	0.072
9.	3,4,4-Trimethyl-3-(3-oxo-but-1-enyl) -bicyclo[4.1.0]heptan-2-one	14.1	5.48	Positive	0.200	0.055
10.	2-Butyl-5-methyl-3-(2-methylprop-2-enyl) cyclohexanone	14.906	4.54	Positive	0.136	0.119
11.	Ethyl iso-allocholate	19.398	4.29	Positive	0.181	0.068
12.	Pregan-20-one,2-hydroxy-5.6-epoxy-15-methyl-	14.092	4.13	Positive	0.215	0.048
13.	(R)-(-)-(Z)-14-Methyl-8-hexadecen-1-ol	18.446	4.07	Positive	0.383	0.014
14.	2-Butoxy-6-[(dimethylamino) methyl]phenol	8.863	4.3	Positive	0.197	0.057
15.	2-Buten-1-one,1-(2,6,6-trimethyl-1-cyclohexen-1-yl)-	14.092	3.17	Positive	0.405	0.012
16.	2-Butoxy-6-[(dimethylamino) methyl]phenol	8.863	4.3	Positive	0.197	0.057
17.	3,7,7-Trimethyl-8-(2-methyl-1-propenyl)bicyclo[4.2.0]oct-2-ene	8.863	3.08	Positive	0.195	0.058
18.	1,4-Benzenediol, 2,6-bis(1,1 dimethylethyl)-	24.981	2.92	Positive	0.729	0.044
19.	1,8(2H,5H)-Naphthalenedione, hexahydro-8a-methyl-, cis-	14.906	2.75	Positive	0.134	0.122
20.	Hexadecane, 7-methyl-	16.78	2.44	Positive	0.392	0.013
21.	2,2,6,7-Tetramethyl-10-oxatricyclo [4.3.0.1(1.7)]decan-5-one	14.914	2.44	Positive	0.164	0.086
22.	9,17-Octadecadienal. (Z)-	21.556	2.36	Positive	0.181	0.069
23.	3-Hydroxymethylene-1,7,7-trimethylbicyclo[2.2.1]heptan-2-one	14.914	1.78	Positive	0.183	0.067
24.	Citronellol	21.372	1.76	Positive	0.589	0.005
25.	Oxirane, hexadecyl-	21.372	1.76	Positive	0.145	0.109
26.	1,2,4-Cyclopentanetrione. 3-(2-pentenyl)-	14.906	1.68	Positive	0.136	0.119
27.	Z-4-Octadecen-1-ol acetate	18.73	1.59	Positive	0.262	0.032
28.	Isophytol, acetate	21.372	1.495	Positive	0.295	0.024
29.	1,2-15,16-Diepoxyhexadecane	21.372	0.585	Positive	0.144	0.11
30.	Glyceraldehyde	4.171	0.14	Positive	0.146	0.108

Notes: [1)]A Pa value < 0.7 predicts vigorous antioxidant activity, while compounds with a Pa < 0.7 are considered to have sufficient potential (Pa > 0.7). [2)] A Pi value < 0.3, weak prediction means that there is little chance that the compound is inactive, thus supporting its potential antioxidant activity.

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Table 2. Screening pharmacokinetic properties using Lipinski's Rule of Five

No.	Compounds	Mass (<500 Da)	HBD (<5)	HBA (<10)	LogP (<5)	MR (40-130)	Lipinski's criteria[1]
1.	**Phytol**	296.53	1	1	6.36	98.94	√
2.	3.7.11.15-Tetramethy l-2-hexadecen-1-ol (phytol)	371.52	0	2	6	119.72	√
3.	3,7,11-Trimethyl-1-dodecanol	228.41	1	1	4.64	75.38	√
4.	2(4H) Benzofuranone, 5,6,7,7atetrahydro-4,4,7a-trimethyl-, (R)-	180.24	0	2	2.44	51.35	√
5.	13-Heptadecyn-1-ol	252.44	1	1	5.07	83.16	√
6.	**Heptadecane**	240.47	0	0	6.88	83.83	√
7.	Octadecane	254.49	0	0	7.27	88.64	√
8.	3,4,4-Trimethyl-3-(3-oxo-but-1-enyl) -bicyclo[4.1.0]heptan-2-one	220.31	0	2	2.77	64.59	√
9.	2-Butyl-5-methyl-3-(2-methylprop -2-enyl) cyclohexanone	222.37	0	1	4.37	71.83	√
10.	**Ethyl iso-allocholate**	436.63	3	5	3.93	122.89	√
11.	(R)-(-)-(Z)-14-Methyl-8-hexadecen-1-ol	254.45	1	1	5.48	84.52	√
12.	2-Buten-1-one,1-(2,6,6 trimethyl-1-cyclohexen-1-yl)-	192.3	0	1	3.66	61.48	√
13.	1,4-Benzenediol, 2,6-bis(1,1 dimethylethyl)-	222.32	2	2	3.63	69.03	√
14.	1,8(2H,5H)Naphthalenedione, hexahydro-8a methyl-, cis-	180.204	0	2	2.11	50.9	√
15.	Hexadecane, 7-methyl-	240.47	0	0	6.73	83.83	√
16.	**2,2,6,7-Tetramethyl-10-oxatricyclo [4.3.0.1(1.7)] decan-5-one**	371.52	0	2	6	119.72	√
17.	**9,17-Octadecadienal. (Z)-**	371.52	0	2	6	119.72	√
18.	3-Hydroxymethylene-1,7,7-trimethylbicyclo[2.2.1]heptan-2-one	180.24	1	2	2.45	51.54	√
19.	Oxirane, hexadecyl-	264.48	0	1	6.26	87.61	√
20.	1,2,4-Cyclopentanetrione. 3-(2-pentenyl)-	371.52	0	2	6	119.72	√
21.	Z-4-Octadecen-1-ol acetate	338.57	0	2	6.93	108.72	√
22.	Isophytol, acetate	156.27	1	1	2.75	50.87	√
23.	1,2-15,16-Diepoxyhexadecane	254.41	0	2	4.47	76.97	√
24.	Glyceraldehyde	90.08	2	3	1.46	18.06	√

Noted: [1] √ meets Lipinski's rules, provided that no more than two rules are violated, it can still be considered to have passed the criteria (Sari et al., 2022).

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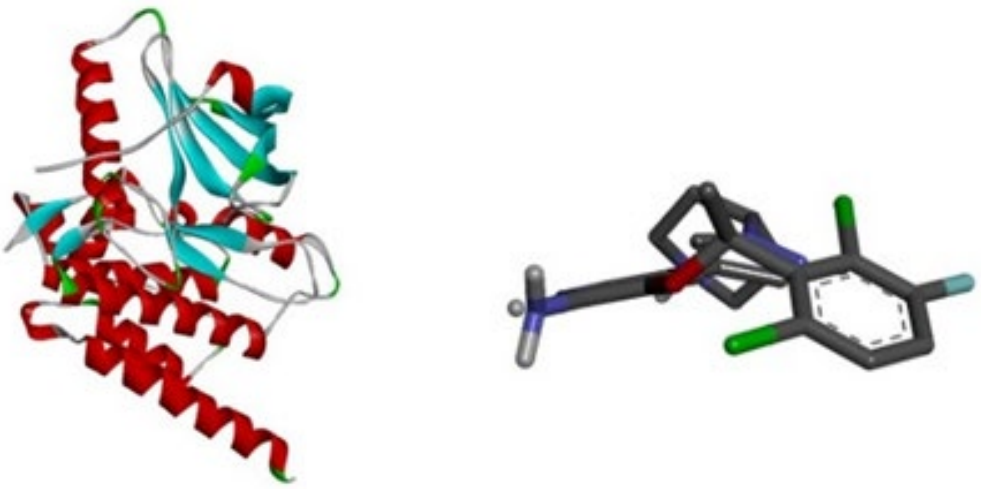
Protein Receptors and Native Ligands

Figure 1 shows the three-dimensional (3D) structure of the Human ROS1 Kinase 3ZBF protein and the native ligand 3-[(1R)-1-(2,6-dichloro-3-fluorophenyl) ethoxy]-5-(1-piperidin-4-yl -1H-pyrazol-4-yl) pyridin-2-amine or crizotinib which is a small compound with an aromatic skeleton and substituents in the form of halogen atoms and heteroatom groups that can inhibit ROS (Cen et al., 2024). The presence of aromatic rings plays an important role in providing hydrophobic stability. At the same time, oxygen and nitrogen atoms enable the formation of hydrogen bond interactions with amino acid residues in the target protein (Fadillah et al., 2024). Halogen substitution in aromatic rings can also increase ligand affinity through hydrophobic and electrostatic interactions. The protein structure shown in the second image is displayed as a ribbon to emphasize its secondary structural elements. Alpha helices (red), beta sheets (blue-cyan), and loops (grey/white) are the main structures that form the protein framework—the active site (binding pocket) of the protein functions as the ligand binding site.



(a) (b)

Figure 1. (a) Macromolecular structure of Human ROS1 Kinase 3ZBF Protein and (b) Natural Ligand 3-[(1R)-1-(2,6-dichloro-3-fluorophenyl)ethoxy]-5-(1-piperidin-4-yl-1H-pyrazol-4-yl)pyridin-2-amine

Ligand–receptor interaction (Molecular docking)

Docking results show that the ligand can orient well at the active site of the protein (Fig 1 and Fig 2). This orientation is determined by binding affinity, where the lower the binding energy value, the more stable the ligand-protein complex formed. The interactions identified include hydrogen bonds between the polar groups of the ligand and the polar residues of the protein, hydrophobic interactions between the aromatic ring of the ligand and nonpolar residues, and possible interactions with specific aromatic residues (Fadillah et al., 2024). The results of molecular docking visualization of natural ligands and ligands from active compounds in spirulina can be seen in **Figure 2** and **Table 3**. The visualization results show that ligands can bind to the active site of the receptor protein. Visualization was performed to see the changes that occurred after the docking process, such as bond position, conformation, and new interactions between molecules (Sari et al., 2022).

The docking results show that the ligand can orient well within the protein's active site (Fig. 1 and Fig. 2). This orientation is determined by binding affinity: the lower the binding energy, the more stable the ligand-protein complex. The interactions identified include hydrogen bonds between the ligand's polar groups and the protein's polar residues, hydrophobic interactions between the ligand's aromatic ring and nonpolar residues, and possible interactions with specific aromatic residues (Fadillah et al., 2024). The results of molecular docking visualisation of natural ligands and ligands from active compounds in spirulina are shown in **Figure 2** and **Table 3**. The visualisation results show that ligands

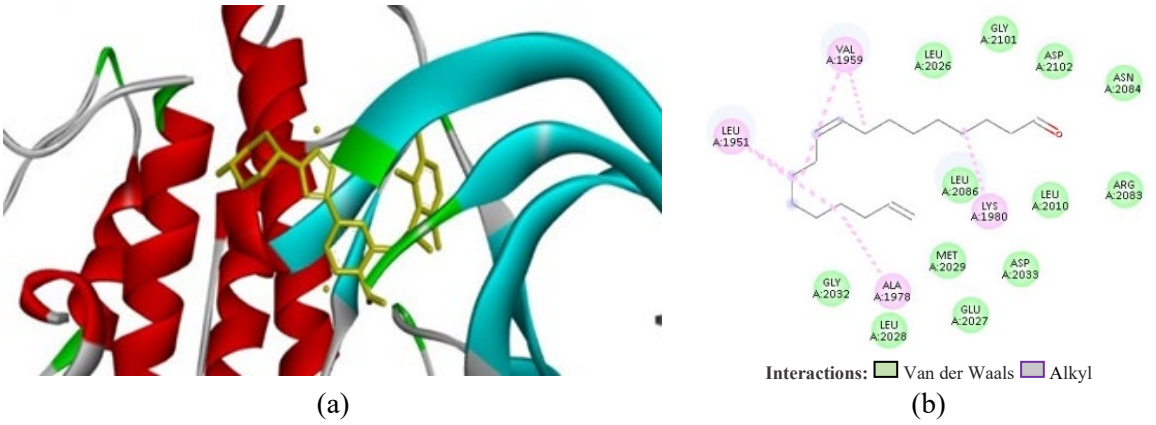
 E-ISSN: 2303-0720

bind to the receptor protein's active site. Visualisation was performed to observe changes after docking, including bond positions, conformations, and new intermolecular interactions (Sari et al., 2022).

In-silico molecular docking results revealed that several compounds, such as Phytol and Ethyl iso-allocholate, exhibit stronger binding affinities than the control ligands, suggesting strong potential as free radical inhibitors. The level of bond stability is reflected in the shorter bond distance. This is related to the receptor binding site: the shorter the bond distance between the ligand and the receptor, the less energy is required (Hindami et al., 2024). Overall, almost all compounds have the potential to be bioactive, although those with high lipophilicity still require further evaluation. Spirulina platensis has the potential to serve as a source of natural antioxidant candidates for functional foods and herbal medicines to counteract oxidative stress.

The molecular docking results show that the native ligand 3[(1R) 1 (2,6-dichloro-3-fluorophenyl) ethoxy]- (1-piperidin-4-yl-1H-pyrazol-4-yl) pyridin-2-amine has the lowest binding energy (-8.3 kcal/mol), indicating the strongest binding affinity to the target protein (**Table 4**). The more negative the binding affinity value, the more stable the configuration and the more stable the ligand will be in binding to the receptor (Hindami et al., 2024). This ligand interaction involves hydrophobic, conserved amino acid such as Leucine at residue sequence 1951 (Leu:1951), Valine at residue sequence 1959 (Val:1959), Alanine at residue sequence 1978 (Ala:1978), Lysine at residue sequence 1980 (Lys:1980), and Aspartic at residue sequence 2102 (Asp:2102), which form a stable binding pocket, as well as polar residues (Asp and Gly) that strengthen the bond through hydrogen and electrostatic interactions (Rahayu et al., 2024). Other ligands such as Heptadecane, Phytol, and 9,17-Octadecadienal have higher binding energies (-4.3 to -5.0 kcal/mol), indicating relatively weaker binding affinity. However, all three still interact with the identical conservative residues, indicating a consistent protein active-site character. Ethyl iso-allocholate (-7.3 kcal/mol) forms hydrophobic contacts with Methionine at residue sequence 2029 (Met:2029), which potentially increases the stability of the ligand complex (Rahayu et al., 2024).

Overall, ligands with more negative bond energies tend to be more stable and have the potential to be antioxidant candidates. The involvement of hydrophobic and polar residues indicates a binding mechanism involving van der Waals forces, hydrogen bonds, and electrostatic interactions. The consistency of residue interactions confirms the biological validity of the docking results, making Spirulina platensis, the natural ligand, a promising candidate for further development through in vitro and in vivo studies (Fadillah et al., 2024).



(a) (b)

Figure 2. (a) 3D Visualisation of the binding between the native ligand and the Human ROS1 3ZBF receptor protein, and (b) 2D interaction between the target protein and the native ligand

 E-ISSN: 2303-0720

Table 3. 2D visualization of 5 Spirulina compounds with the 3ZBF receptor protein

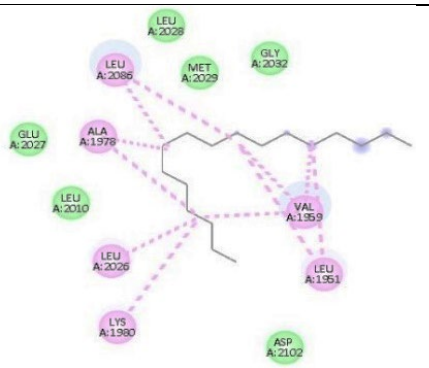
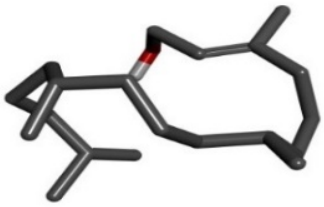
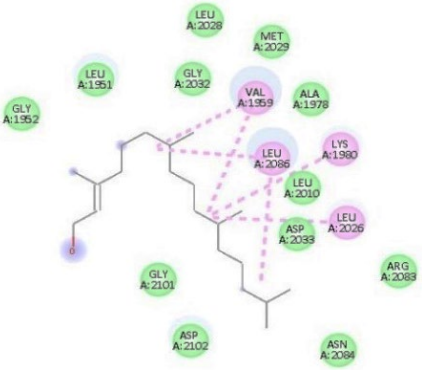
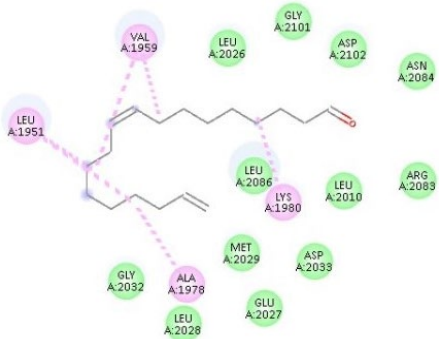
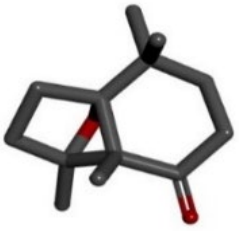
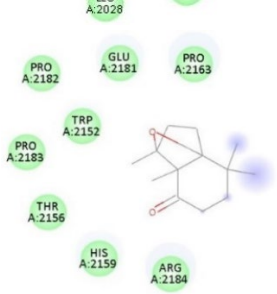
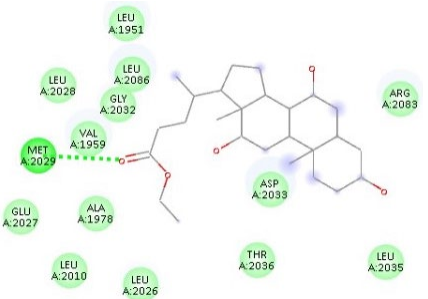
Ligand structure	2D Visualization of the binding
 Heptadecane	
 Phytol	
 9,17 Octadecadienal (Z)-	
 2,2,6,7-Tetramethyl-10 oxatricyclo [4.3.0.1(1.7)] decan-5-one	
 Ethyl iso-allocholate	

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Table 4. The results of molecular docking and amino acid residue interactions

No.	Ligand	Amino acid residues*	Binding Distances (Å)	Binding affinity (kkal/mol)
1.	3-[(1R)-1-(2,6-dichloro-3- fluorophenyl) ethoxy]-5-(1-piperidin-4-yl 1H-pyrazol-4-yl) pyridin-2-amine (ligan native)	**Leu:1951** **Leu: 2086** **Leu: 2026** Leu: 2010 **Val: 1959** **Lys:1980** Gly:2101 **Ala1978** **Asp:2102** Asn:2084 Arg:2083	4.5	-8.3
2.	Heptadecane	**Leu: 2086** **Leu: 1951** **Leu: 2026** **Lys: 1980** **Val: 1959** **Ala: 1978**	3.6	-4.3
3.	Phytol	**Val: 1959** **Leu: 2086** **Leu:2026** **Lys: 1980**	3.5	-5.0
4.	9,17-Octadecadienal (Z)-	**Leu: 1951** **Lys: 1980** **Val: 1959** **Ala: 1978**	3.6	-4.8
5.	2,2,6,7-Tetramethyl-10 oxatricyclo [4.3.0.1(1.7)] decan-5-one	Pro: 2182 Glu: 2181 Trp: 2152 Thr: 2156 His: 2159 Arg: 2184	3,6	-5.7
6.	Ethyl iso-allocholate	Met:2029	3.6	-7.3

Noted: * The amino acid residues in bold are interrelated bonds; the more interrelated they are, the better they are as drug candidates.

Conclusion

This study shows that Spirulina platensis contains approximately 30 bioactive compounds identified, with most of them meeting Lipinski's Rule of Five criteria (24 compounds) and having a probability of antioxidant activity (Pa 0.3–0.7). In silico analysis using molecular docking revealed that several compounds, such as Phytol and Ethyl iso-allocholate, exhibit stronger binding affinities than control ligands, suggesting strong potential as free radical inhibitors. Overall, these results confirm the potential of Spirulina platensis as a source of natural antioxidant candidates that might be developed for functional foods and herbal medicines to counteract oxidative stress.

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