Assessment on the Antiviral Properties Of Sulphated and Non-Sulphated Polysaccharides from Marine Seaweeds

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**Abstract:**This study investigates the potential antiviral properties of two seaweed-derived polysaccharides, laminarin and ulvan, against key proteins of Dengue Virus 2 (DENV2) and Human Immunodeficiency Virus 1 (HIV-1) using molecular docking techniques. The research aims to explore the interactions between these natural compounds and viral proteins crucial for infection: the Envelope protein E of DENV2 and the gp120 glycoprotein of HIV-1 YU2. Molecular structures of laminarin and ulvan were obtained from PubChem, while protein structures were retrieved from the RCSB Protein Data Bank. Molecular docking was performed using virtual screening software with AutoDock Vina as the docking engine. The best-fit models were selected based on binding affinity scores, and interactions were visualized and analyzed. Results showed promising binding affinities for both polysaccharides. Laminarin exhibited binding affinities of -7.1 kcal/mol with DENV2 Envelope protein E and -6.6 kcal/mol with HIV-1 gp120. Ulvan demonstrated binding affinities of -7.1 kcal/mol with DENV2 Envelope protein E and -8.3 kcal/mol with HIV-1 gp120. Detailed analysis revealed multiple interactions, including hydrogen bonds and Van der Waals forces, with key residues in functional regions of the viral proteins. These findings suggest that laminarin and ulvan may have potential as antiviral agents, possibly by interfering with viral entry mechanisms. The study provides a molecular basis for understanding the antiviral properties of these seaweed-derived compounds and highlights the value of marine natural products in drug discovery. While further experimental validation is necessary, this research contributes to the growing body of knowledge on natural product-based antiviral strategies and opens avenues for future investigations in this field.

**Keywords:** Molecular docking; Antiviral agents; Seaweed polysaccharides; Laminarin; Ulvan; Viral envelope proteins

# Introduction

Seaweeds have long been recognized as a rich source of bioactive compounds with potential therapeutic applications[(Ramsundar et al., 2023; Rieshy et al., 2023; Singh et al., 2023)](https://paperpile.com/c/DD4kRy/xW7mm+CSEXn+xpn7k). This study focuses on two polysaccharides derived from seaweeds: laminarin and ulvan. Laminarin, a non-sulphated polysaccharide found in brown seaweeds, has a molecular formula of C18H32O16 and a molecular weight of 504.4 g/mol [(Kadam et al., 2015)](https://paperpile.com/c/DD4kRy/QQFE). Ulvan, on the other hand, is a sulphated polysaccharide extracted from green seaweeds [(Kidgell et al., 2019)](https://paperpile.com/c/DD4kRy/4hoJ). Both compounds have attracted scientific interest due to their diverse biological activities, including potential antiviral properties [(Pereira et al., 2009)](https://paperpile.com/c/DD4kRy/jswa). The research aims to investigate the interactions between these seaweed-derived polysaccharides and two critical viral proteins: the Envelope protein E of Dengue Virus 2 (DENV2) and the glycoprotein 120 (gp120) of Human Immunodeficiency Virus 1 (HIV-1 YU2). These proteins play crucial roles in their respective viral life cycles and are prime targets for antiviral strategies [(Modis et al., 2004)](https://paperpile.com/c/DD4kRy/42BG).The Envelope protein E of DENV2 is essential for viral entry into host cells. It mediates the fusion of the viral and host cell membranes, allowing the virus to release its genetic material into the cell[(Pavithra et al., 2023; Shenoy et al., 2023; Thomas & Jain, 2023)](https://paperpile.com/c/DD4kRy/O1dwm+p3guS+B1CBJ). This protein is also a major target for neutralizing antibodies, making it an important focus for vaccine and antiviral drug development [(Rey, 2003)](https://paperpile.com/c/DD4kRy/ZK7H). Similarly, gp120 of HIV-1 is vital for the virus's interaction with host cells. It binds to the CD4 receptor on T cells, initiating the process of viral entry[(Doshi et al., 2023; Lampl et al., 2023; Pandiyan et al., 2023)](https://paperpile.com/c/DD4kRy/3uWRP+GPp53+GHpbo). Due to its critical role in HIV infection, gp120 has been extensively studied as a target for antiretroviral therapies and vaccine design [(Kwong et al., 1998)](https://paperpile.com/c/DD4kRy/cnsK).The study employs molecular docking, a computational method used to predict the binding orientation and affinity of small molecules to target proteins[(Janani et al., 2021; Kachhara et al., 2021; Subramanian et al., 2023)](https://paperpile.com/c/DD4kRy/xYKoo+FxPXy+dPED3). This approach allows for the rapid screening of potential interactions between the seaweed polysaccharides and the viral proteins [(Kitchen et al., 2004)](https://paperpile.com/c/DD4kRy/r1ai). By simulating these interactions, researchers can gain insights into how laminarin and ulvan might interfere with viral processes at the molecular level[(Gandhi et al., 2021; Katyal et al., 2023; Priyadharshini et al., 2023)](https://paperpile.com/c/DD4kRy/UP2gV+Qhxjb+P4SUO). The docking process involves several key steps, including obtaining three-dimensional structures of the ligands and target proteins, preparing these structures for docking, defining a search space within the protein structure, and generating numerous possible orientations of the ligand within this space [(Trott & Olson, 2010)](https://paperpile.com/c/DD4kRy/9iPO). Each of these poses is evaluated based on its predicted binding affinity, which is calculated using scoring functions that consider various types of molecular interactions[(Chokkattu et al., 2023; Dharman et al., 2023; Govindaraj & Shanmugam, 2023)](https://paperpile.com/c/DD4kRy/NTl23+cLj0t+sWDSu).Following the docking simulations, the resulting protein-ligand complexes are analyzed in detail. This analysis focuses on identifying specific interactions between the ligands and the viral proteins, such as hydrogen bonds, hydrophobic interactions, and other non-covalent forces that contribute to the stability of the complex [(Du et al., 2016)](https://paperpile.com/c/DD4kRy/vjXG). This computational approach offers several advantages in the study of potential antiviral compounds. It allows for the rapid screening of multiple compounds against various targets, provides atomic-level insights into binding mechanisms, and can guide the design of more focused experimental studies. Moreover, by exploring natural products as potential antiviral agents, this research aligns with the growing interest in identifying novel, sustainable sources of bioactive compounds [(Karthikeyan et al., 2022)](https://paperpile.com/c/DD4kRy/Z9s8).The findings from this study could have significant implications for antiviral drug discovery. If laminarin and ulvan show promising interactions with these viral proteins, they could serve as lead compounds for the development of new antiviral drugs. Additionally, understanding how these natural polysaccharides interact with viral proteins could inform the design of synthetic compounds that mimic or improve upon these interactions.

# Materials and Methods

Laminarin (C18H32O16) is a non-sulphated polysaccharide found in the cell walls of brown seaweeds, with a molecular weight of 504.4 g/mol. Ulvan, a sulphated polysaccharide derived from green seaweeds, is also studied as a ligand. The structures of laminarin and ulvan were obtained from PubChem (CID: 439306 and 405234592, respectively), hosted by the National Library of Medicine, NCBI, NIH.In this study, two key viral marker proteins were selected for docking experiments: Envelope protein E of Dengue Virus 2 (DENV2) (PDB: 3C5X) [(Li et al., 2008)](https://paperpile.com/c/DD4kRy/t9Vf) and HIV-1 YU2 glycoprotein (gp120) (PDB: 3TGQ) [(Kwon et al., 2012)](https://paperpile.com/c/DD4kRy/2xhz). Their molecular structures were sourced from the Protein Data Bank (RCSB PDB). Both protein structures were processed using BIOVIA Discovery Studio Visualizer 2024 (v24.1.0.23298) by Dassault Systems Biovia Corp, where unnecessary ligands, chains, and water molecules were removed, and polar charges were added.Molecular docking simulations were performed between the ligands (laminarin and ulvan) and the viral proteins (Envelope protein E of DENV2 and HIV-1 YU2 glycoprotein) using PyRx-Python Prescription 0.8 and Autodoc Vina as the molecular docking engine [(Akshatha et al., 2021; Dallakyan & Olson, 2015)](https://paperpile.com/c/DD4kRy/3Hpa+fZzg). The grid center and dimension coordinates for docking were adjusted and recorded in Tables 1 and 2. The best-fit models were selected based on the lowest binding affinity. Interactions between the ligands and proteins were visualized, analyzed, and documented using BIOVIA Discovery Studio Visualizer 2024.

**Table 1.** The grid centre and dimension parameters set for EP of DENV2 and gp120 of HIV-1 for the ligand laminarin

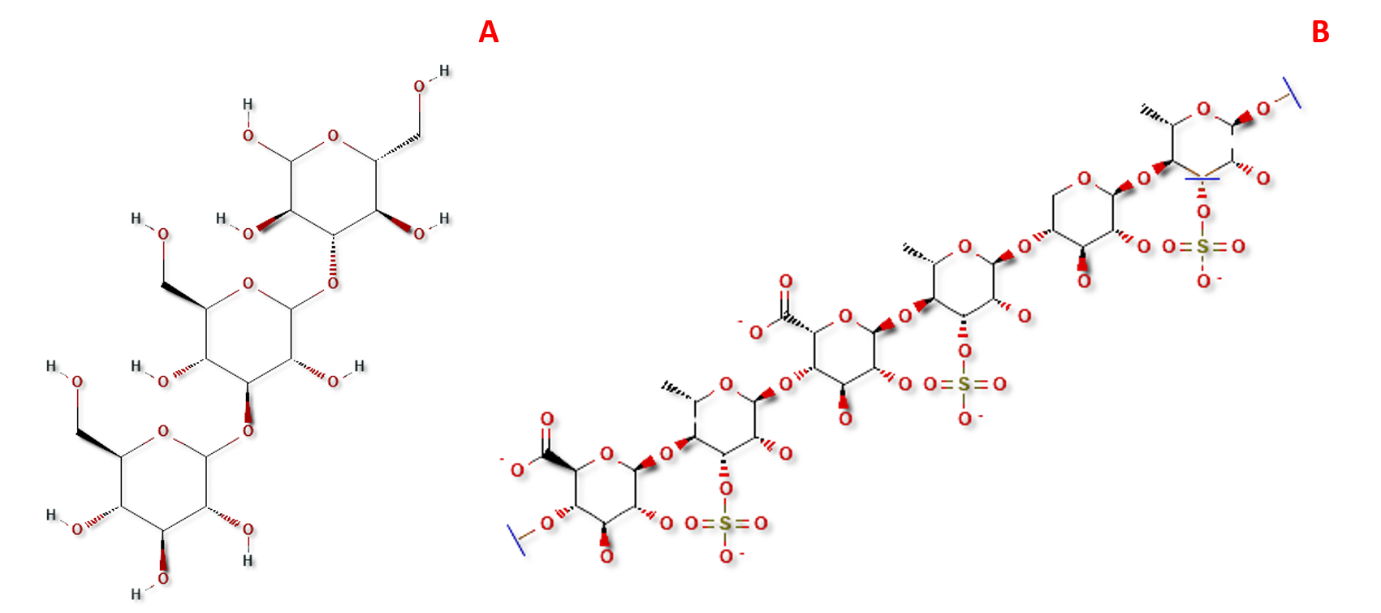
|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | **Grid Centre** | |  | **Dimensions (Å)** | | |
| **Protein** | **PDB** | **X** | **Y** | **Z** | **X** | **Y** | **Z** |
| Envelope protein E of Dengue Virus 2 | 3C5X | 11.09 | -23.94 | -18.84 | 85.24 | 91.23 | 163.26 |
| HIV-1 YU2 glycoprotein (gp120) | 3TGQ | -61.45 | -64.89 | 2.64 | 78.02 | 80.29 | 73 |

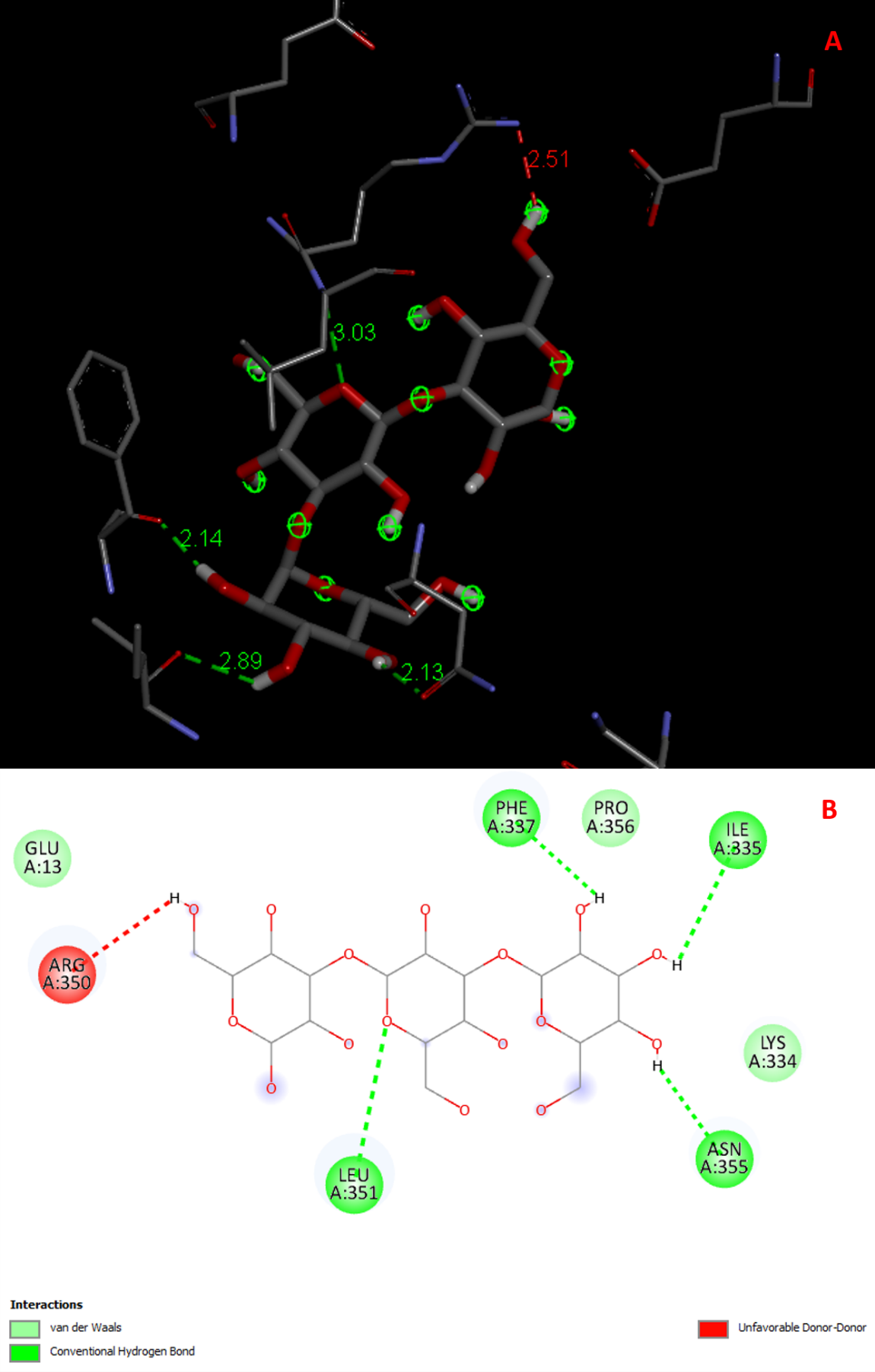
**Table 2.** The grid centre and dimension parameters set for MCP-1 and NFκB

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | **Grid Centre** | |  | **Dimensions (Å)** | | |
| **Protein** | **PDB** | **X** | **Y** | **Z** | **X** | **Y** | **Z** |
| Envelope protein E of Dengue Virus 2 | 3C5X | 7.99 | 22.97 | 21.33 | 85.24 | 91.23 | 163.26 |
| HIV-1 YU2 glycoprotein (gp120) | 3TGQ | -57.6 | 68.819 | 0.17 | 81.54 | 80.29 | 73 |

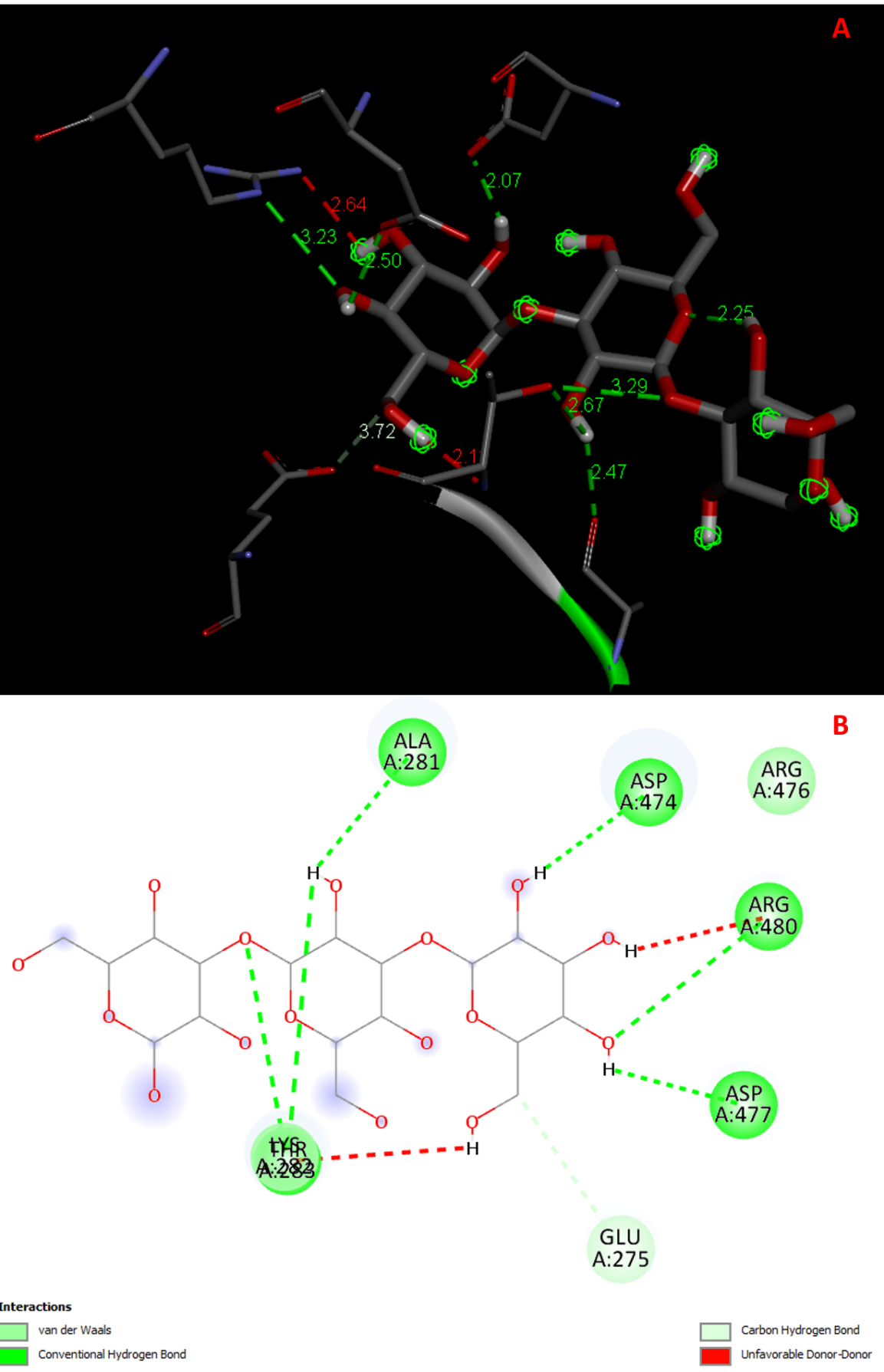
# Results and Discussion

The molecular structures of laminarin and ulvan are shown in Figure 1. The lowest binding affinity for laminarin with Envelope protein E of Dengue Virus 2 was -7.1 kcal/mol (Table 3). Molecular docking revealed that laminarin interacts with Envelope protein E of Dengue Virus 2 through three Van der Waals interactions (GLU13, PRO356, LYS334), four conventional hydrogen bonds (ASN355, ILE335, PHE337, LEU351), and one unfavorable donor-donor interaction (ARG350) (Fig. 2 and Table 7).For the interaction between laminarin and HIV-1 YU2 glycoprotein (gp120), the binding affinity was -6.6 kcal/mol (Table 4). This interaction includes two Van der Waals interactions (ARG476, LYS282), six conventional hydrogen bonds (ASP474, ALA281, ARG480, ASP477, two with THR283), and two unfavorable donor-donor interactions (THR283, ARG480) (Fig. 3 and Table 8).The lowest binding affinity for ulvan with Envelope protein E of Dengue Virus 2 was -7.1 kcal/mol (Table 5). Ulvan interacts with Envelope protein E of Dengue Virus 2 via three Van der Waals interactions (THR165, GLU136, LEU175), nine conventional hydrogen bonds (two with SER168, LYS163, GLU172, HIS158, THR176, two with GLU174, LYS160), and one carbon-hydrogen bond (LYS157) (Fig. 4 and Table 9).The binding affinity between ulvan and HIV-1 YU2 glycoprotein (gp120) was -8.3 kcal/mol (Table 6). This interaction includes seven Van der Waals interactions (GLU275, ASP474, ASP477, ARG469, GLY471, ILE371, VAL101), thirteen conventional hydrogen bonds (THR49, ASN99, LYS282, THR283, ASN280, two with ASP457, two with SER365, THR455, SER364, GLY472, ASN98), two carbon-hydrogen bonds (GLU102, GLY471), one unfavorable donor-donor interaction (ARG480), and one attractive charge (LYS282) (Fig. 5 and Table 10).

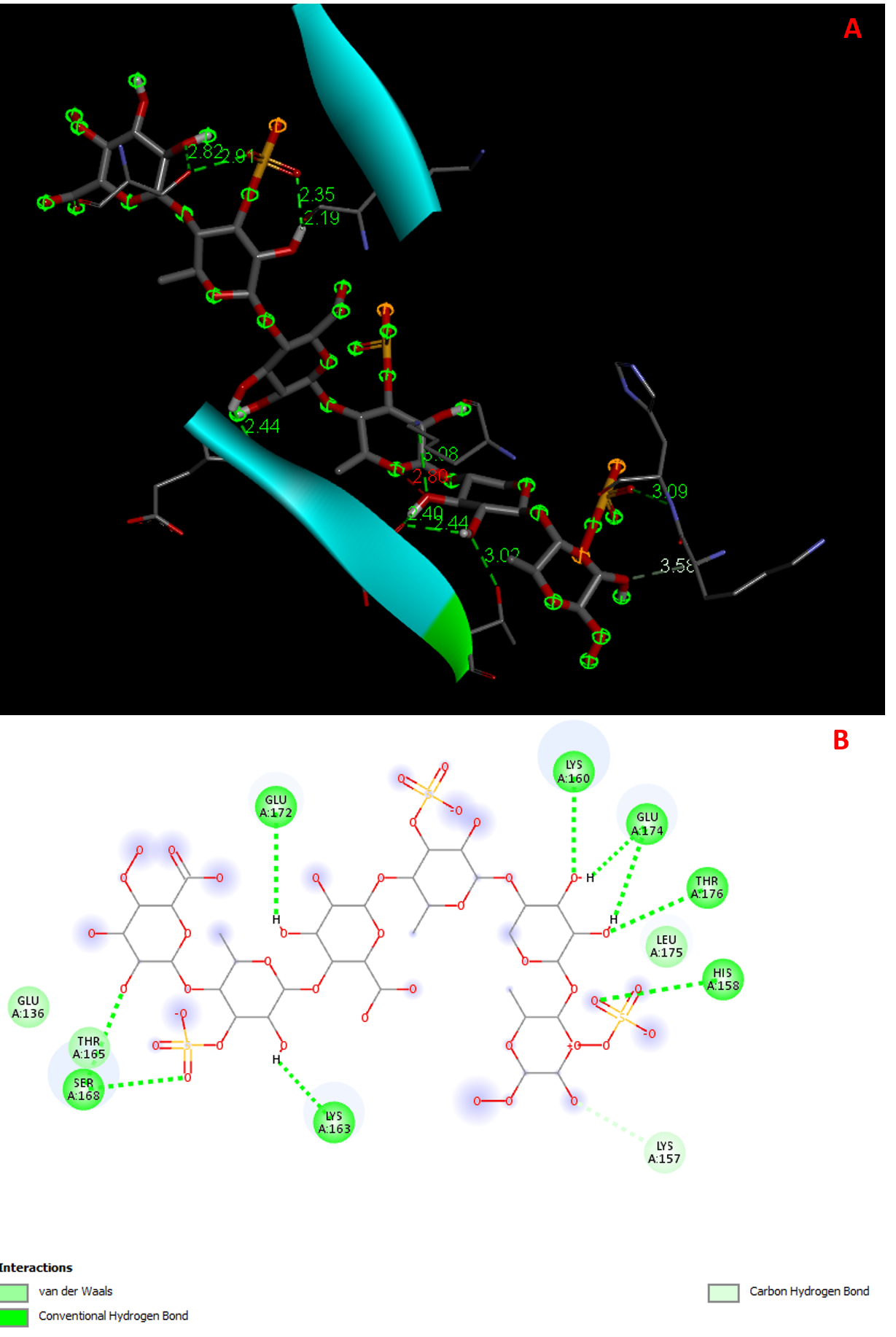


**Figure 1.** Molecular structure of a Laminarin and Ulvan, in which ulvan showing sulphate groups

**Figure 2.** Molecular interactions between the ligand Laminarin and Envelope protein E of Dengue Virus 2 showing three Van der Waals interactions (GLU13; PRO356; LYS334), four conventional hydrogen bonds (ASN355; ILE335; PHE337; LEU351), and one unfavourable donor-donor interactions (ARG350); A) Three-dimensional view, B) Two-dimensional view.



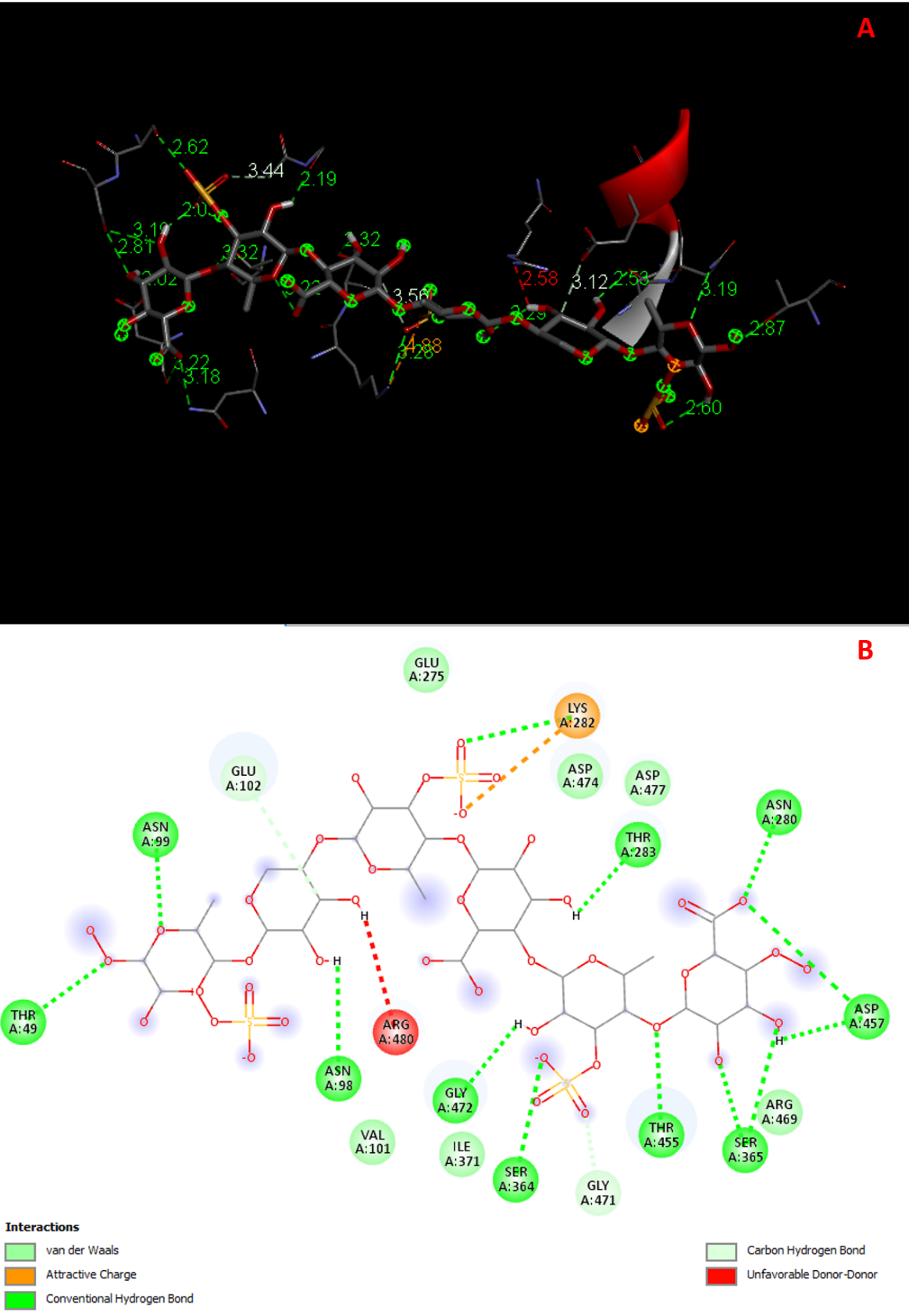
**Figure 3.** Molecular interactions between the ligand Laminarin and HIV-1 YU2 glycoprotein (gp120) showing two Van der Waals interactions (ARG476; LYS282), six conventional hydrogen bonds (ASP474; ALA281; ARG480; ASP477; two THR283), two unfavourable donor-donor interactions (THR283; ARG480); A) Three-dimensional view, B) Two-dimensional view.



**Figure 4.** Molecular interactions between the ligand Ulvan and Envelope protein E of Dengue Virus 2 showing three Van der Waals interactions (THR165; GLU136; LEU175), nine conventional hydrogen bonds (two SER168; LYS163; GLU172; HIS158; THR176; two GLU174; LYS160), one carbon-hydrogen bond (LYS157); A) Three-dimensional view, B) Two-dimensional view.

**Table 3.** The table retrieved after molecular docking between Laminarin and Envelope protein E of Dengue Virus 2 showing binding affinity.

|  |  |  |  |
| --- | --- | --- | --- |
| **Ligand** | **Binding Affinity** | **rmsd/ub** | **rmsd/lb** |
| 3tgq\_439306\_uff\_E=583.99 | -6.6 | 0 | 0 |
| 3tgq\_439306\_uff\_E=583.99 | -6.5 | 10.168 | 7.126 |
| 3tgq\_439306\_uff\_E=583.99 | -6.4 | 12.634 | 6.893 |
| 3tgq\_439306\_uff\_E=583.99 | -6.4 | 11.359 | 6.41 |
| 3tgq\_439306\_uff\_E=583.99 | -6.3 | 9.145 | 1.828 |
| 3tgq\_439306\_uff\_E=583.99 | -6.2 | 9.308 | 4.498 |
| 3tgq\_439306\_uff\_E=583.99 | -6.1 | 7.534 | 3.747 |
| 3tgq\_439306\_uff\_E=583.99 | -6 | 21.609 | 19.539 |
| 3tgq\_439306\_uff\_E=583.99 | -6 | 7.827 | 4.056 |



**Figure 5.** Molecular interactions between the ligand Ulvan and HIV-1 YU2 glycoprotein (gp120) showing seven Van der Waals interactions (GLU275; ASP474; ASP477; ARG469; GLY471; ILE371; VAL101), thirteen conventional hydrogen bonds (THR49; ASN99; LYS282; THR283; ASN280; two ASP457; two SER365; THR455; SER364; GLY472, ASN98), two carbon-hydrogen bonds (GLU102; GLY471), one unfavourable donor-donor (ARG480), one attractive charge (LYS282); A) Three-dimensional view, B) Two-dimensional view.

**Table 4.** The table retrieved after molecular docking between Ulvan and HIV-1 YU2 glycoprotein (gp120) showing binding affinity.

|  |  |  |  |
| --- | --- | --- | --- |
| **Ligand** | **Binding Affinity** | **rmsd/ub** | **rmsd/lb** |
| 3tgq\_405234592\_ghemical\_E=8567.53 | -8.3 | 0 | 0 |
| 3tgq\_405234592\_ghemical\_E=8567.53 | -8.2 | 11.795 | 5.017 |
| 3tgq\_405234592\_ghemical\_E=8567.53 | -8.2 | 5.339 | 3.688 |
| 3tgq\_405234592\_ghemical\_E=8567.53 | -8 | 3.067 | 2.231 |
| 3tgq\_405234592\_ghemical\_E=8567.53 | -7.9 | 3.071 | 2.099 |
| 3tgq\_405234592\_ghemical\_E=8567.53 | -7.8 | 15.008 | 10.97 |
| 3tgq\_405234592\_ghemical\_E=8567.53 | -7.7 | 14.596 | 10.898 |
| 3tgq\_405234592\_ghemical\_E=8567.53 | -7.6 | 4.088 | 2.925 |
| 3tgq\_405234592\_ghemical\_E=8567.53 | -7.5 | 8.121 | 5.506 |

**Table 5.** The table retrieved after molecular docking between Ulvan and Envelope protein E of Dengue Virus 2 showing binding affinity.

|  |  |  |  |
| --- | --- | --- | --- |
| **Ligand** | **Binding Affinity** | **rmsd/ub** | **rmsd/lb** |
| 3c5x\_405234592\_ghemical\_E=8567.53 | -7.1 | 0 | 0 |
| 3c5x\_405234592\_ghemical\_E=8567.53 | -7 | 27.777 | 33.809 |
| 3c5x\_405234592\_ghemical\_E=8567.53 | -7 | 52.068 | 61.64 |
| 3c5x\_405234592\_ghemical\_E=8567.53 | -7 | 28.357 | 33.704 |
| 3c5x\_405234592\_ghemical\_E=8567.53 | -6.9 | 48.235 | 54.198 |
| 3c5x\_405234592\_ghemical\_E=8567.53 | -6.8 | 52.65 | 62.229 |
| |  |  |  |  | | --- | --- | --- | --- | | **Ligand** | **Binding Affinity** | **rmsd/ub** | **rmsd/lb** | | 3c5x\_439306\_uff\_E=583.99 | -7.1 | 0 | 0 | | 3c5x\_439306\_uff\_E=583.99 | -6.7 | 8.084 | 1.785 | | 3c5x\_439306\_uff\_E=583.99 | -6.5 | 22.677 | 21.096 | | 3c5x\_439306\_uff\_E=583.99 | -6.5 | 4.928 | 2.263 | | 3c5x\_439306\_uff\_E=583.99 | -6.2 | 24.652 | 23.023 | | 3c5x\_439306\_uff\_E=583.99 | -6.2 | 2.304 | 1.046 | | 3c5x\_439306\_uff\_E=583.99 | -6.2 | 52.088 | 48.292 | | 3c5x\_439306\_uff\_E=583.99 | -6.1 | 58.206 | 54.791 | | 3c5x\_439306\_uff\_E=583.99 | -6 | 3.533 | 1.864 |   3c5x\_405234592\_ghemical\_E=8567.53 | -6.8 | 44.617 | 52.888 |
| 3c5x\_405234592\_ghemical\_E=8567.53 | -6.7 | 48.421 | 54.45 |
| 3c5x\_405234592\_ghemical\_E=8567.53 | -6.7 | 17.865 | 25.469 |

**Table 6.** The table showing bond interactions and its length between Laminarin and Envelope protein E of Dengue Virus 2 showing amino acid residues involves in it

|  |  |  |  |
| --- | --- | --- | --- |
| **Bond Interactions** | **No. of bonds** | **Bond length (Å)** | **Amino acid residue** |
| Van der Waals interactions | 3 |  | GLU13  PRO356  LYS334 |
| Conventional hydrogen bonds | 4 | 2.13 | ASN355 |
| 2.89 | ILE335 |
| 2.14 | PHE337 |
| 3.03 | LEU351 |
| Unfavourable donor-donor | 1 | 2.51 | ARG350 |
| Total number of interactions | 8 |  |  |

**Table 8.** The table showing bond interactions and its length between Laminarin and HIV-1 YU2 glycoprotein (gp120) showing amino acid residues involves in it

|  |  |  |  |
| --- | --- | --- | --- |
| **Bond Interactions** | **No. of bonds** | **Bond length (Å)** | **Amino acid residue** |
| Van der Waals interactions | 2 |  | ARG476  LYS282 |
| Conventional hydrogen bonds | 6 | 2.07 | ASP474 |
| 2.47 | ALA281 |
| 3.23 | ARG480 |
| 2.50 | ASP477 |
| 3.29 | THR283 |
| 2.67 | THR283 |
| Unfavourable donor-donor | 2 | 2.12 | THR283 |
| 2.64 | ARG480 |
| Total number of interactions | 10 |  |  |

**Table 9.** The table showing bond interactions and its length between Ulvan and Envelope protein E of Dengue Virus 2 showing amino acid residues involves in it

|  |  |  |  |
| --- | --- | --- | --- |
| **Bond Interactions** | **No. of bonds** | **Bond length (Å)** | **Amino acid residue** |
| Van der Waals interactions | 3 |  | THR165  GLU136  LEU175 |
| Conventional hydrogen bonds | 9 | 2.82 | SER168 |
| 2.91 | SER168 |
| 2.19 | LYS163 |
| 2.44 | GLU172 |
| 3.09 | HIS158 |
| 3.02 | THR176 |
| 2.44 | GLU174 |
| 2.40 | GLU174 |
| 3.08 | LYS160 |
| Carbon-hydrogen bonds | 1 | 3.58 | LYS157 |
| Total number of interactions | 13 |  |  |

# Discussion

The molecular docking study of laminarin and ulvan against key viral proteins of Dengue Virus 2 (DENV2) and Human Immunodeficiency Virus 1 (HIV-1) provides valuable insights into the potential antiviral properties of these seaweed-derived polysaccharides. The results reveal promising interactions between these natural compounds and the viral proteins, suggesting their potential as lead compounds for antiviral drug development[(Rajeshkumar & Lakshmi, 2021; Sivakumar et al., 2021)](https://paperpile.com/c/DD4kRy/jDYA6+pifWH).Laminarin, a β-glucan found in brown seaweeds, demonstrated significant binding affinity to both the Envelope protein E of DENV2 and the gp120 glycoprotein of HIV-1 YU2. The binding affinity of -7.1 kcal/mol with the DENV2 Envelope protein E indicates a strong interaction, comparable to many small molecule inhibitors [(Lim et al., 2013)](https://paperpile.com/c/DD4kRy/RljO). The multiple interactions observed, including Van der Waals forces and conventional hydrogen bonds, suggest a stable binding mode. Of particular interest is the interaction with LYS334, which has been identified as a key residue in the fusion loop of the DENV2 Envelope protein [(Modis et al., 2004)](https://paperpile.com/c/DD4kRy/42BG). This interaction could potentially interfere with the virus's ability to fuse with host cell membranes, a critical step in viral entry.The interaction of laminarin with HIV-1 gp120, while slightly weaker at -6.6 kcal/mol, still represents a significant binding event. The multiple hydrogen bonds formed with residues such as ASP474 and ARG480 are particularly noteworthy, as these residues are located in regions of gp120 known to be important for CD4 binding [(Kwong et al., 1998)](https://paperpile.com/c/DD4kRy/cnsK). By interacting with these residues, laminarin could potentially interfere with the virus's ability to attach to host cells, thereby inhibiting the initial stages of HIV infection.Ulvan, a sulphated polysaccharide from green seaweeds, showed equally promising results. Its binding affinity of -7.1 kcal/mol to the DENV2 Envelope protein E matches that of laminarin, suggesting that both polysaccharides have similar potential against DENV2. The extensive network of hydrogen bonds formed by ulvan, particularly with residues in the domain III of the Envelope protein (e.g., THR165, SER168), is significant. Domain III is involved in receptor binding, and interactions in this region could disrupt the virus's ability to recognize and attach to host cells [(Rey, 2003)](https://paperpile.com/c/DD4kRy/ZK7H). Most notably, ulvan demonstrated the strongest binding affinity of all tested interactions with HIV-1 gp120, at -8.3 kcal/mol. This strong affinity, coupled with the extensive network of interactions including thirteen conventional hydrogen bonds and an attractive charge interaction, suggests that ulvan could be a particularly promising candidate for HIV-1 inhibition. The interactions with residues such as LYS282 and THR283 are especially interesting, as these are part of the CD4 binding site on gp120 [(Pancera et al., 2014)](https://paperpile.com/c/DD4kRy/pkCR). However, murrayanol, a compound from Murraya koengii showed a binding energy of -7.21 kcal/mol Epstein-Barr virus nuclear antigen (EBNA-1) [(Mathivadani et al., 2020)](https://paperpile.com/c/DD4kRy/eE3H).The observed binding modes of both laminarin and ulvan to these viral proteins provide a molecular basis for understanding their potential antiviral mechanisms(Saadh et al., 2024). The polysaccharides appear to interact with key functional regions of the viral proteins, potentially interfering with processes crucial for viral entry and infection. This is consistent with previous studies that have reported antiviral activities of seaweed-derived polysaccharides, although the exact mechanisms were not always clear [(Wang et al., 2012)](https://paperpile.com/c/DD4kRy/UVqD).It's important to note that while these computational results are promising, they represent only the first step in the drug discovery process(Almatrafi et al., 2024).

**Table 10.** The table showing bond interactions and its length between Ulvan and HIV-1 YU2 glycoprotein (gp120) amino acid residues involves in it

|  |  |  |  |
| --- | --- | --- | --- |
| **Bond Interactions** | **No. of bonds** | **Bond length (Å)** | **Amino acid residue** |
| Van der Waals interactions | 7 |  | GLU275  ASP474  ASP477  ARG469  GLY471  ILE371  VAL101 |
| Conventional hydrogen bonds | 13 | 2.87 | THR49 |
| 3.19 | ASN99 |
| 3.28 | LYS282 |
| 2.32 | THR283 |
| 3.18 | ASN280 |
| 3.22 | ASP457 |
| 2.02 | ASP457 |
| 2.81 | SER365 |
| 3.19 | SER365 |
| 3.32 | THR455 |
| 2.62 | SER364 |
| 2.19 | GLY472 |
| 2.53 | ASN98 |
| Carbon-hydrogen bonds | 2 | 3.12 | GLU102 |
| 3.44 | GLY471 |
| Unfavourable donor-donor | 1 | 2.58 | ARG480 |
| Attractive charge | 1 | 4.88 | LYS282 |
| Total number of interactions | 24 |  |  |

The binding affinities and interaction patterns observed in silico need to be validated through experimental studies. Furthermore, factors such as bioavailability, stability, and potential toxicity of these polysaccharides need to be thoroughly investigated before they can be considered as viable drug candidates.The similar binding affinities of laminarin to both DENV2 and HIV-1 proteins suggest that it might have broad-spectrum antiviral potential. This is particularly interesting from a drug development perspective, as compounds with activity against multiple viral targets are highly desirable. Ulvan, with its stronger affinity for HIV-1 gp120, might be more promising as a specific anti-HIV agent.The sulphated nature of ulvan versus the non-sulphated structure of laminarin may contribute to their different binding profiles. Sulphated polysaccharides have been shown to have enhanced antiviral activities in many cases, possibly due to their ability to mimic heparan sulfate, a cell surface molecule often involved in viral attachment. The stronger binding of ulvan to HIV-1 gp120 could be partly attributed to this structural feature. There have been reports of microalgae chemicals having therapeutic potential for a number of neurological disorders [(Parameswari & Lakshmi, 2022)](https://paperpile.com/c/DD4kRy/VcFh). While plant sources of antimicrobial compounds have been extensively studied [(Monica et al., 2022)](https://paperpile.com/c/DD4kRy/QM0B) microalgae are found close to plants that contain a number of as-yet-undiscovered antimicrobial metabolites. These findings also highlight the potential of marine-derived compounds as a source of novel antiviral agents. Seaweeds, being abundant and sustainable resources, could provide a rich pipeline of bioactive compounds for pharmaceutical development. The structural diversity of seaweed polysaccharides, as exemplified by laminarin and ulvan, offers opportunities for discovering compounds with varied mechanisms of action against different viral targets.

# Conclusion

In conclusion, this molecular docking study provides compelling evidence for the potential antiviral activities of laminarin and ulvan against DENV2 and HIV-1. The observed interactions with key viral proteins suggest mechanisms by which these compounds might interfere with viral entry and infection processes. While further experimental validation is necessary, these results lay a foundation for future research into seaweed-derived polysaccharides as antiviral agents. The study not only contributes to our understanding of how these natural compounds might exert their antiviral effects but also underscores the value of computational approaches in the initial stages of drug discovery. As we continue to face challenges in combating viral diseases, exploring natural products like these seaweed polysaccharides could open new avenues in antiviral drug development.

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