NanoLAS 2.0: A Comprehensive Update on a Nanobody-Focused Platform with Advanced Visualization and Docking Simulation Features

Xin Wang[†‡]
Shenzhen Technology University[*]
Shenzhen, 518118, China
wangxin@sztu.edu.cn

Zebiao Zheng[†]
Shenzhen Technology University[*]
Shenzhen, 518118, China
me@brookezb.com

Wei Qin[†]
Shenzhen Technology University[*]
Shenzhen, 518118, China
2767457074@qq.com

Kangrui Yu[†]
Shenzhen Technology University[*]
Shenzhen, 518118, China
yukangruicn@163.com

Yangqi Hong
Shenzhen Technology University[*]
Shenzhen, 518118, China
zshyydyx@163.com

Yongqi Tang
Shenzhen Technology University[*]
Shenzhen, 518118, China
1390962598@qq.com

Tiantai Wang
Shenzhen Technology University[*]
Shenzhen, 518118, China
3253239994@qq.com

Lixin Liang[‡]
Shenzhen Technology University[*]
Shenzhen, 518118, China
lianglixin@sztu.edu.cn

Bingding Huang[‡]
Shenzhen Technology University[*]
Shenzhen, 518118, China
huangbingding@sztu.edu.cn

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***Abstract*—Nanobodies are a unique class of antibodies with significant therapeutic potential. However, existing nanobody databases often lack standardized data, advanced search capabilities, and integrated analysis tools. We previously developed NanoLAS to address data integration. Here, we present NanoLAS 2.0, a comprehensive update that introduces a multi-condition associative search, an enhanced 3D viewer with molecular docking simulation, an improved sequence viewer, and integrated binding site prediction via NanoBERTa-ASP. The platform features an updated database backend and a redesigned user interface. NanoLAS 2.0 (available at https://www.nanolas2.online) provides a powerful all-in-one platform to accelerate nanobody research.**

***Index Terms*—Nanobody, Database, Structural Biology, Molecular Docking**

I. Introduction

Nanobodies, derived from camelid heavy-chain antibodies, offer unique advantages in therapeutics due to their stability and size [1]–[3]. Their application has accelerated, notably in SARS-CoV-2 research [4]–[6]. However, the proliferation of nanobody data across disparate databases (e.g., PDB, INDI, SdAb-DB) [7]–[10] creates challenges in data integration, standardized search, and analysis. While specialized tools like PyMol [11] exist, they require offline data handling and lack integration.

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[*]School of Artificial Intelligence, Shenzhen Technology University.

[†]Xin Wang, Zebiao Zheng, Wei Qin, and Kangrui Yu contributed equally to this work.

[‡]Corresponding authors.

To address this, we previously developed NanoLAS [12], a platform for integrated nanobody data. Building on this foundation, we present NanoLAS 2.0, which introduces four major upgrades:

1) **Data and Search:** Comprehensively updated data with a new multi-condition associative search.
2) **3D Visualization:** An optimized 3D viewer supporting dynamic molecular docking simulation and precise distance measurement.
3) **Sequence Analysis:** A new sequence viewer integrated with the NanoBERTa-ASP [13] binding site prediction model.
4) **UI/UX:** A fully redesigned, user-friendly interface with detailed documentation.

These enhancements aim to provide a streamlined, powerful platform for nanobody research.

II. Implementation

A. Molecular Docking Simulation

NanoLAS 2.0 integrates the Mol* Viewer [14], a WebGL-based tool, for high-performance 3D molecular visualization. We extended its UI using ReactJS to include advanced features like molecular overlay and distance measurement.

A key update is the web-based molecular docking simulation. While Mol* Viewer lacks native docking, we implemented functionality allowing users to load multiple molecules into the same canvas and manipulate their translation and rotation in real-time. NanoLAS 2.0 3D Viewer implements its own matrix operation library. By calculating the appropriate

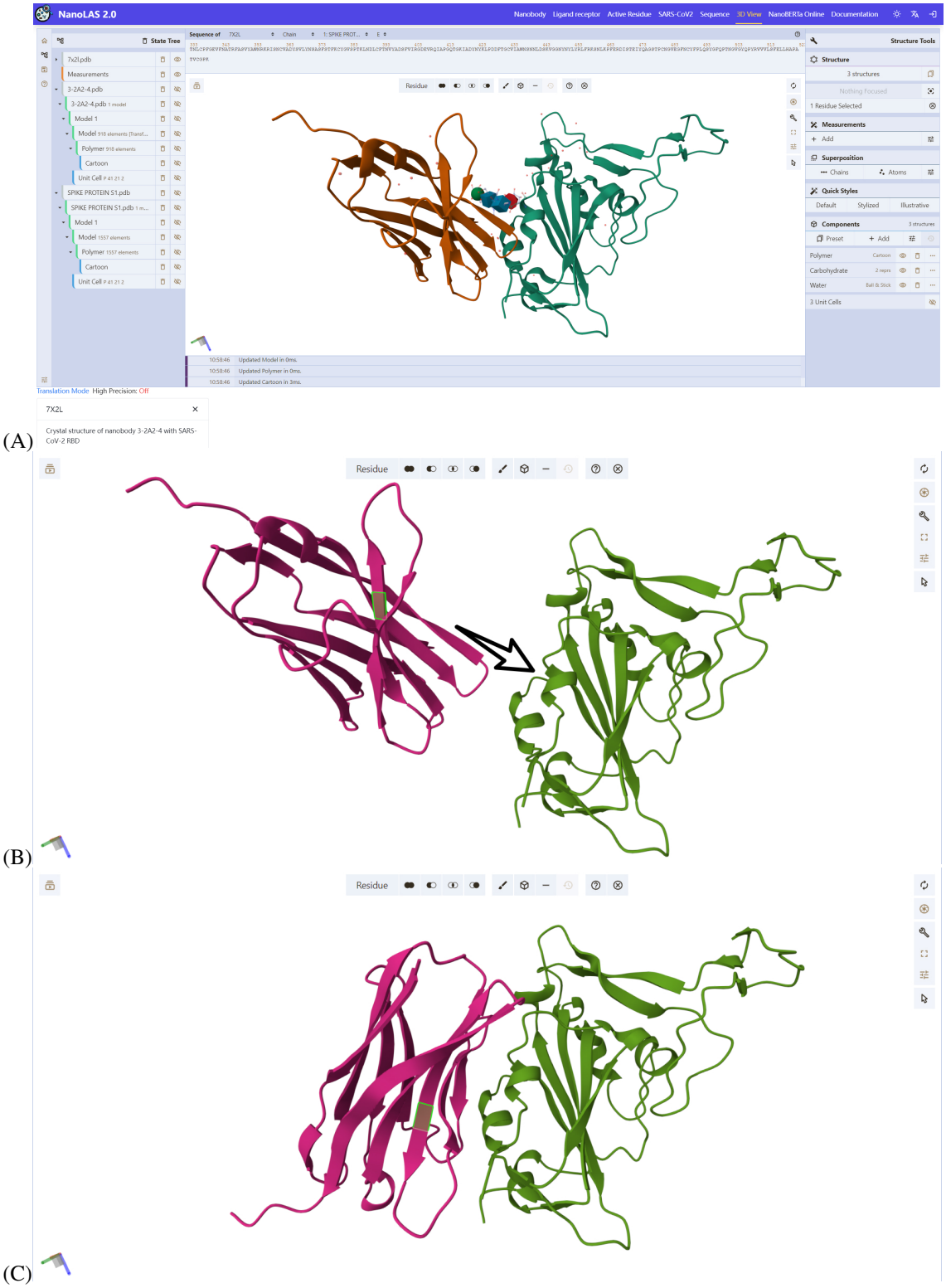

Fig. 1. 3D viewer and demonstration of molecular docking simulation. (A) 3D presentation of complex "7X2L". (B) The isolated nanobody 3-2A2-4 and spike protein S1 were put into the same canvas. (C) Simulating molecular docking via user-controlled rotation and translation.

transformation matrices, spatial transformation operations on molecules can be performed. With JavaScript's keyboard event listeners, users can interactively control the spatial transformation of the molecular model. This, combined with a Euclidean distance measurement tool, enables interactive simulation of binding interactions (Fig. 1).

For example, the complex "7X2L" (nanobody 3-2A2-4 and SARS-CoV-2 RBD) [4] can be split, and its components repositioned to simulate the binding (Fig. 1(B-C)). This integration streamlines research by removing the need to download data for use in offline viewers.

B. Sequence Viewer Enhancements

Inspired by RCSB Saguaro [15], we redesigned the sequence viewer. The new viewer clearly marks binding sites and active residues and supports interactive features like mouse-controlled zooming and residue highlighting.

The new viewer also boasts performance optimizations. Constructed using SVG technology, it leverages the 'letter-spacing' attribute to control text spacing. In the 1.0 version, displaying a sequence of length N required N DOM(Document Object Model) nodes, whereas in the 2.0 version, we have optimized it to create just a single DOM node. This improvement significantly reduces the computational load on the browser, allowing the viewer to maintain smooth performance.

C. Integration of NanoBERTa-ASP for Binding Site Prediction

We integrated NanoBERTa-ASP, a RoBERTa-based model for nanobody binding site prediction [13]. We constructed a web service for the model using the Flask framework, providing a RESTful API interface. From any nanobody detail page, users can run predictions on its sequence. The prediction outcomes are displayed on the enhanced sequence viewer, with segments surpassing a user-adjustable binding probability threshold highlighted in green (see Supplementary Figure 1). This integration creates a seamless sequence-to-prediction workflow.

D. Advanced Search

NanoLAS 2.0 features a new multi-condition advanced search mechanism. Users can combine multiple fields (e.g., PDB ID, keyword, release date) with 'AND'/'OR' logic. This allows for complex, precise queries, such as finding all "SARS"-related antibodies released in "2023-2024".

This functionality benefits from the powerful customization capabilities of the MyBatis framework and the high flexibility of the MyBatisFlex plugin. In response to the significant increase in sequence data volume, we have implemented cursor pagination techniques to optimize paginated queries, enhancing the efficiency of SQL query execution. Search results link to detailed pages with 3D structures, sequences, and links to the analysis tools.

E. Optimization of System Kernel and Interface

The kernel architecture of NanoLAS 2.0 has been meticulously designed for modularity and high availability. The backend technology stack continues to use the Java language and the Spring Boot framework. Furthermore, the introduction of the Spring Security framework has enhanced user authentication mechanisms and data protection measures.

In terms of interface optimization, we have continued to use Vue.js for its reactive state management. To meet the needs of researchers worldwide, we have implemented internationalization support for both frontend text and backend API messages. The website also features a responsive user interface and has been completely redesigned to enhance user experience, supplemented by comprehensive documentation.

III. Data Collection and Database Refinement

NanoLAS 2.0 features a comprehensive data update from PDB, Opig-SAbDab, and NCBI [10], [16]. A key refinement was restructuring the database. Instead of counting by *protein* (which could have multiple sites), the data is now organized by *binding site* for greater precision.

The database schema (Supplementary Figure 4) was redesigned to mirror the PDB hierarchy. This new structure, which retrieves PDB files on-the-fly from RCSB/PDBe rather than storing them locally, improves response time and enables the advanced multi-condition search.

IV. Discussion

Several platforms compile nanobody data, but NanoLAS 2.0 offers a more comprehensive feature set (Supplementary Table 1). For example, INDI [8] has a large sequence collection but lacks 3D visualization. SAbDab-nano [10] and sdAb-DB [9] provide simpler 3D displays but lack integrated docking and advanced sequence search.

While professional offline tools like PyMol [11] are powerful, they require installation and manual data loading. PyMol can import and display 3D structures and allows users to edit them, measure distances, and perform other operations. Although NanoLAS 2.0 is a website platform, it also has these essential functions and is faster to start. However, for functions like Python scripts, command line operations, and molecular dynamics simulation analysis, PyMol is even more powerful. NanoLAS 2.0 provides the most essential visualization, measurement, and simulation docking capabilities directly in the browser, significantly accelerating the research workflow for the most common tasks.

In addition, we are also contemplating the incorporation of support for WebVR/AR in future iterations. WebVR/AR technologies have the potential to integrate virtual reality and augmented reality within a web environment, thereby providing users with an immersive interactive experience. Utilizing WebAR technology, we can project 3D molecular structure models onto a fixed location in the real world. Users can then view and manipulate these molecular models through their mobile devices, without the need for costly VR equipment.

Furthermore, we recognize that while nanobodies represent an emerging segment of the antibody field, traditional antibodies also have substantial demand in areas such as data collection and 3D molecular structure presentation. In future work, we plan to develop a comprehensive database for various types of antibodies, adding specific functionalities tailored to different antibody categories. Our goal is to achieve seamless connectivity and data interoperability between databases of different antibody types, further promoting research and applications in the field of antibodies. We sincerely hope that

users will provide valuable feedback and suggestions to assist us in enhancing and refining the database.

V. Conclusion

We presented NanoLAS 2.0, a major update featuring an expanded database, advanced multi-condition search, an integrated sequence-to-prediction pipeline with NanoBERTa-ASP, and an in-browser 3D viewer with molecular docking simulation. These enhancements (Supplementary Table 1) provide a powerful, unified platform for nanobody analysis, streamlining data retrieval, visualization, and predictive analysis for researchers. We believe these enhancements will provide a robust impetus for the future development of nanobodies.

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