



Universidad Nacional de San Agustín

Tópicos en Computación Gráfica

ArgosMol: A web tool for protein visualization

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Proteomics is the large-scale study of proteins [1]

Proteins are large, complex molecules that play many critical roles in the body. They do most of the work in cells. [1]

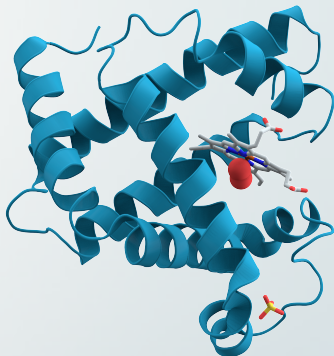


Figure: A representation of the 3D structure of the protein myoglobin.
Source: [PDB](#).

Protein structure

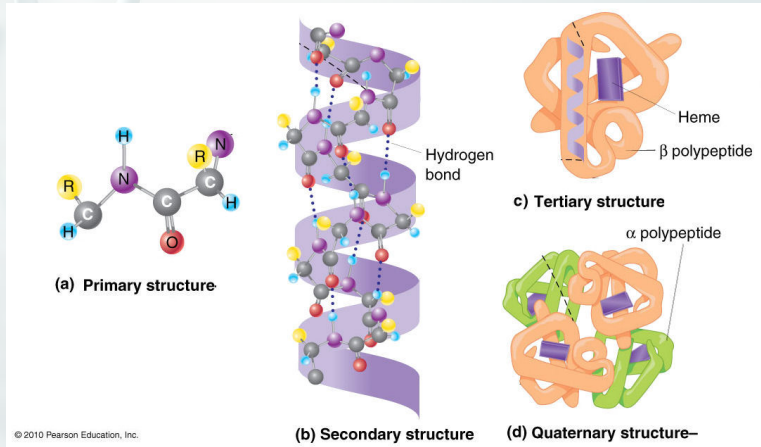


Figure: Types of protein structures. Source: [2].



Protein structures are complex systems with several tens, hundreds and **thousand** of residues (amino acids).

Only about **1%** of the total number of sequenced proteins has experimentally determined [3].

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Is one of the most used task in Bioinformatics [4, 5].

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Ligand-binding pockets or other details in macromolecular assemblies helps to elucidate the relationship between protein structure and function [6].



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Interactive visualization of large molecular structures can now be achieved via web-based 3D, It is not restricted to stand alone applications [7].

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There is not a robust Web-based tool for protein visualization. The current applications are in development:

- ▶ They have bugs.
- ▶ They doesn't have all the functionality like stand-alone applications.
- ▶ They are not easy to use.



Figure: Web page of Jolecule.

NGL@2.0.0-dev.32 gallery

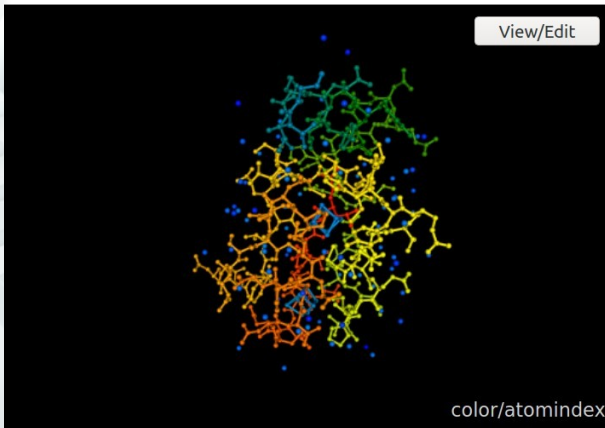
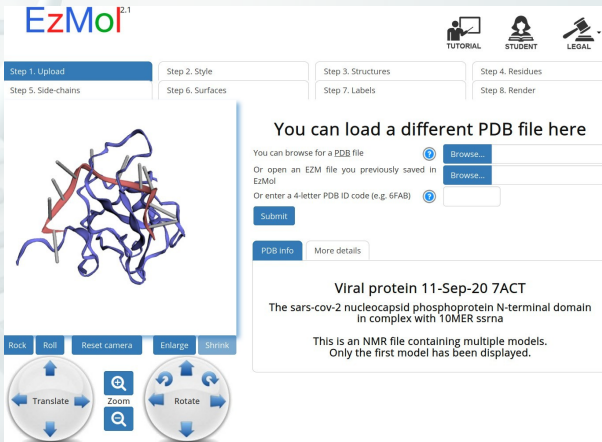


Figure: Web page of NGL [8].



EzMol^{2.1}

TUTORIAL STUDENT LEGAL

Step 1. Upload
Step 5. Side-chains
Step 2. Style
Step 6. Surfaces
Step 3. Structures
Step 7. Labels
Step 4. Residues
Step 8. Render

You can load a different PDB file here

You can browse for a PDB file

Or open an EZM file you previously saved in EzMol

Or enter a 4-letter PDB ID code (e.g. 6FAB)

Viral protein 11-Sep-20 7ACT
The sars-cov-2 nucleocapsid phosphoprotein N-terminal domain
in complex with 10MER ssrna

This is an NMR file containing multiple models.
Only the first model has been displayed.

Rock Roll Reset camera Enlarge Shrink

Translate Zoom Rotate

Figure: Web page of EzMol [6].



Figure: Web page of iCn3D [7].

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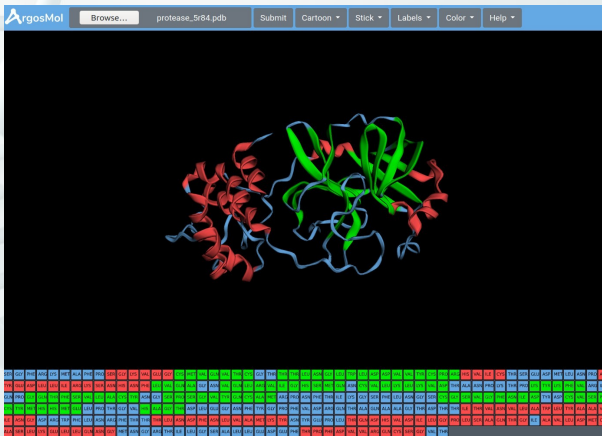


Figure: Web page of ArgosMol [Enlace](#).

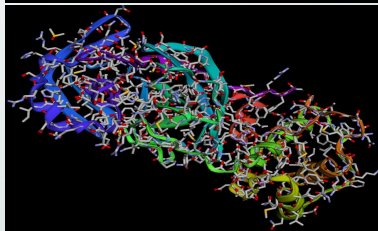
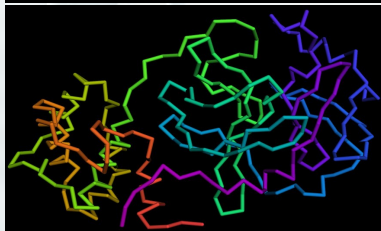
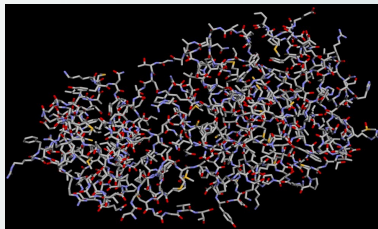
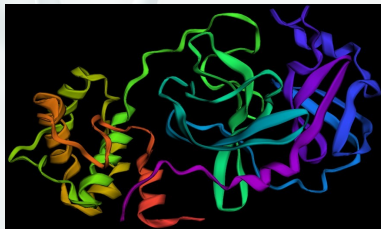


Figure: Visualization in ArgosMol.

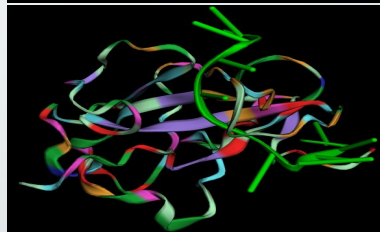
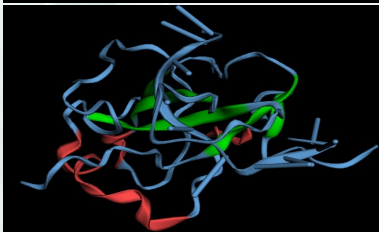
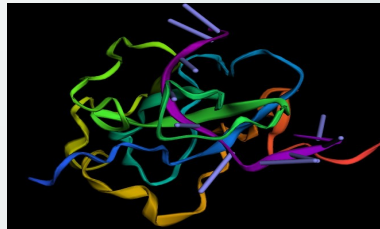
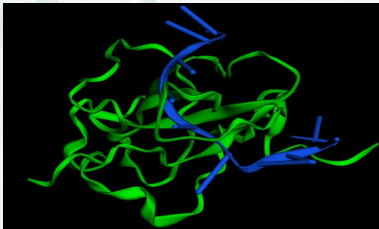


Figure: Colors in ArgosMol.

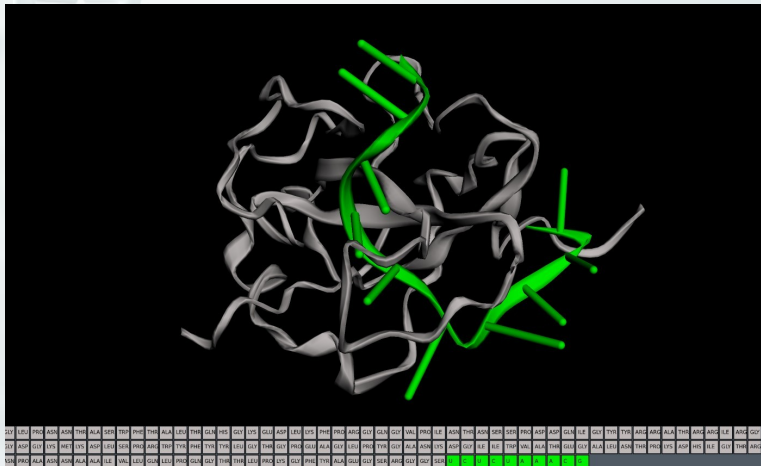


Figure: Relation between the model and the sequence in ArgosMol.

Conclusions



ArgosMol is an alternative to stand-alone applications that require installation.

ArgosMol is part of a small number of Web-based tools for protein visualization. Nevertheless, ArgosMol improves the usability and the relation between the model and sequence.

In future version of ArgosMol, we will include protein structure prediction.



- [1] N. L. Anderson and N. G. Anderson, “Proteome and proteomics: new technologies, new concepts, and new words,” *Electrophoresis*, vol. 19, no. 11, pp. 1853–1861, 1998.
- [2] P. J. Russell and K. Gordey, *IGenetics*. Benjamin Cummings San Francisco, 2002, no. QH430 R87.
- [3] H. Rangwala and G. Karypis, *Introduction to protein structure prediction: methods and algorithms*. John Wiley & Sons, 2011, vol. 18.
- [4] S. I. O’donoghue, D. S. Goodsell, A. S. Frangakis, F. Jossinet, R. A. Laskowski, M. Nilges, H. R. Saibil, A. Schafferhans, R. C. Wade, E. Westhof *et al.*, “Visualization of macromolecular structures,” *Nature methods*, vol. 7, no. 3, pp. S42–S55, 2010.
- [5] C. Mura, C. M. McCrimmon, J. Vertrees, and M. R. Sawaya, “An introduction to biomolecular graphics,” *PLoS Comput Biol*, vol. 6, no. 8, p. e1000918, 2010.



- [6] C. R. Reynolds, S. A. Islam, and M. J. Sternberg, “Ezmol: a web server wizard for the rapid visualization and image production of protein and nucleic acid structures,” *Journal of molecular biology*, vol. 430, no. 15, pp. 2244–2248, 2018.
- [7] J. Wang, P. Youkharibache, D. Zhang, C. J. Lanczycki, R. C. Geer, T. Madej, L. Phan, M. Ward, S. Lu, G. H. Marchler *et al.*, “icn3d, a web-based 3d viewer for sharing 1d/2d/3d representations of biomolecular structures,” *Bioinformatics*, vol. 36, no. 1, pp. 131–135, 2020.
- [8] A. S. Rose and P. W. Hildebrand, “Ngl viewer: a web application for molecular visualization,” *Nucleic acids research*, vol. 43, no. W1, pp. W576–W579, 2015.

