

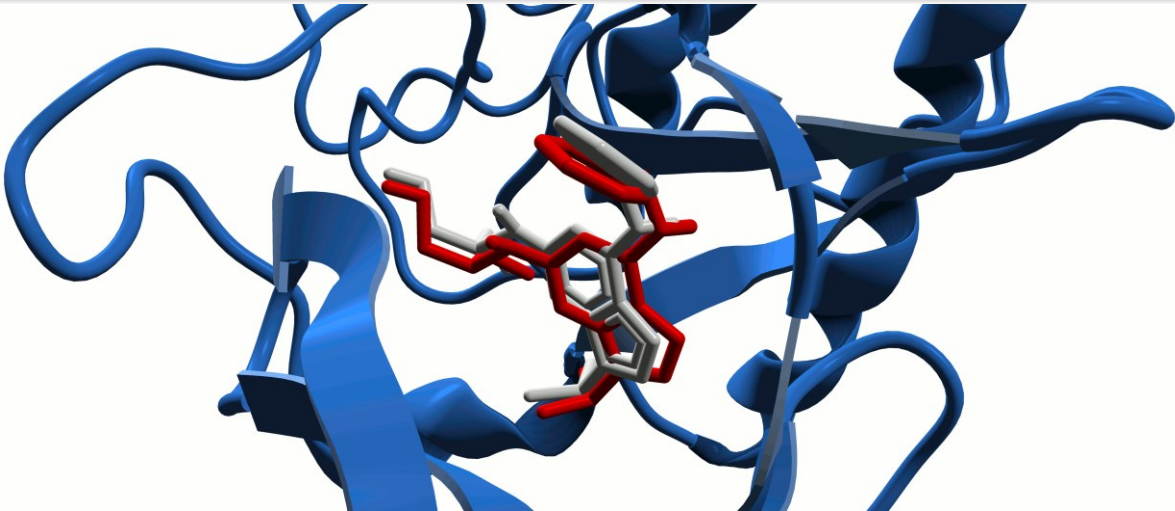
Aprendizado de Máquina Supervisionado II



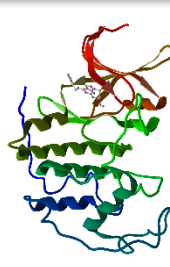
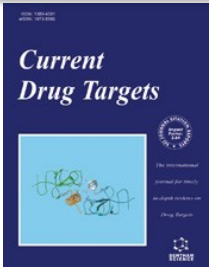
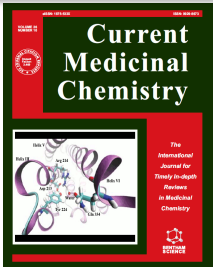
Prof. Dr. Walter F. de Azevedo, Jr.

walter@azevedolab.net

- [Biography 01](#) ♥
- [Biography 02](#) ♥
- [Biography 03](#) ♥
- [Biography 04](#) ♥

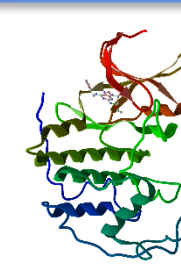
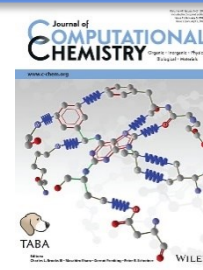
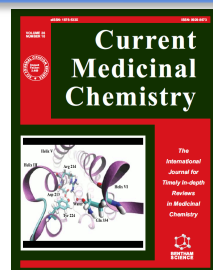
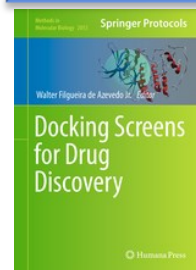


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 Section Editor (Bioinformatics in Drug Design and Discovery) for the [Current Medicinal Chemistry](#) ISSN: 1875-533X

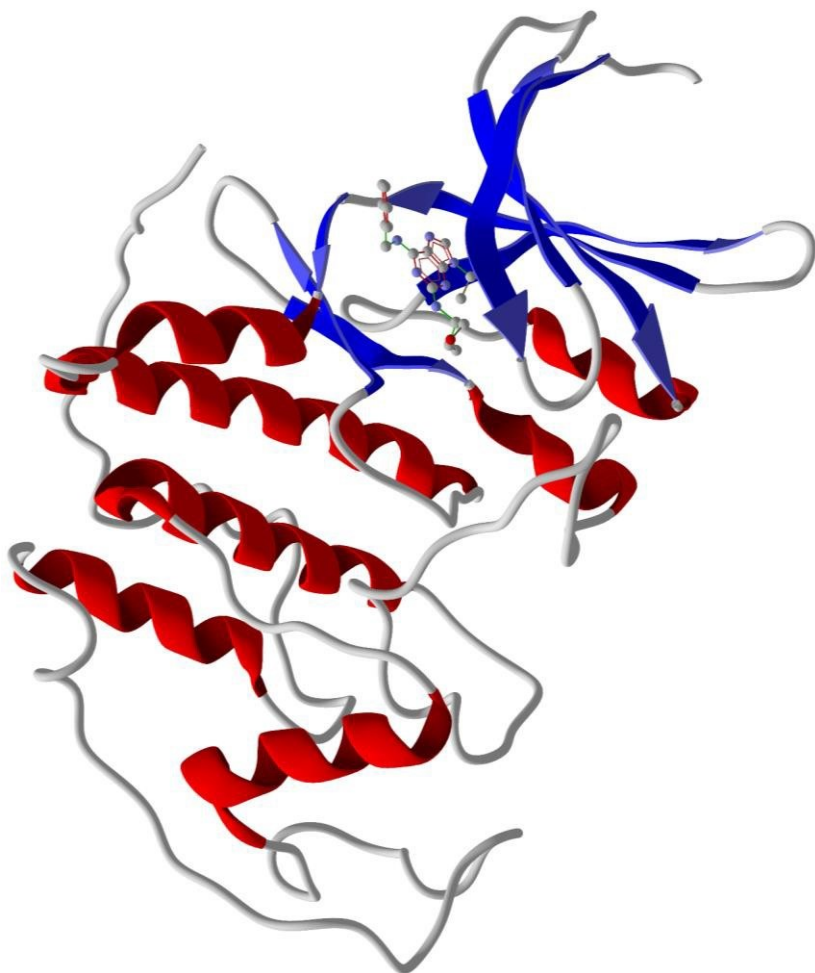


Conteúdo

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- [CDK2](#)
- [Download da Estrutura do Protein Data Bank](#)
- [Docagem Molecular com o MVD](#)
- [Espaço Luz da Ciência](#)
- [Referências](#)

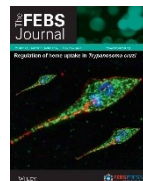


Resumo



A quinase dependente de ciclina 2 (*cyclin-dependent kinase 2*, CDK2) está envolvida no ciclo celular. Foi identificada em aproximadamente 50 % dos tumores cancerígenos uma mutação no gene que codifica a proteína p53. Esta proteína é um fator de transcrição da proteína p21, uma proteína inibidora de CDK2. A inibição da CDK2 suspende a progressão do ciclo celular e pode levar à apoptose. No caso de células cancerígenas, a inibição da CDK2 evita a propagação do tumor. A partir desse conhecimento, começou-se a investigar a interação da CDK2 com inibidores não proteicos, como a molécula de roscovitina mostrada em complexo com a CDK2 na figura ao lado. Na aula de hoje, veremos simulações de docagem molecular contra essa proteína.

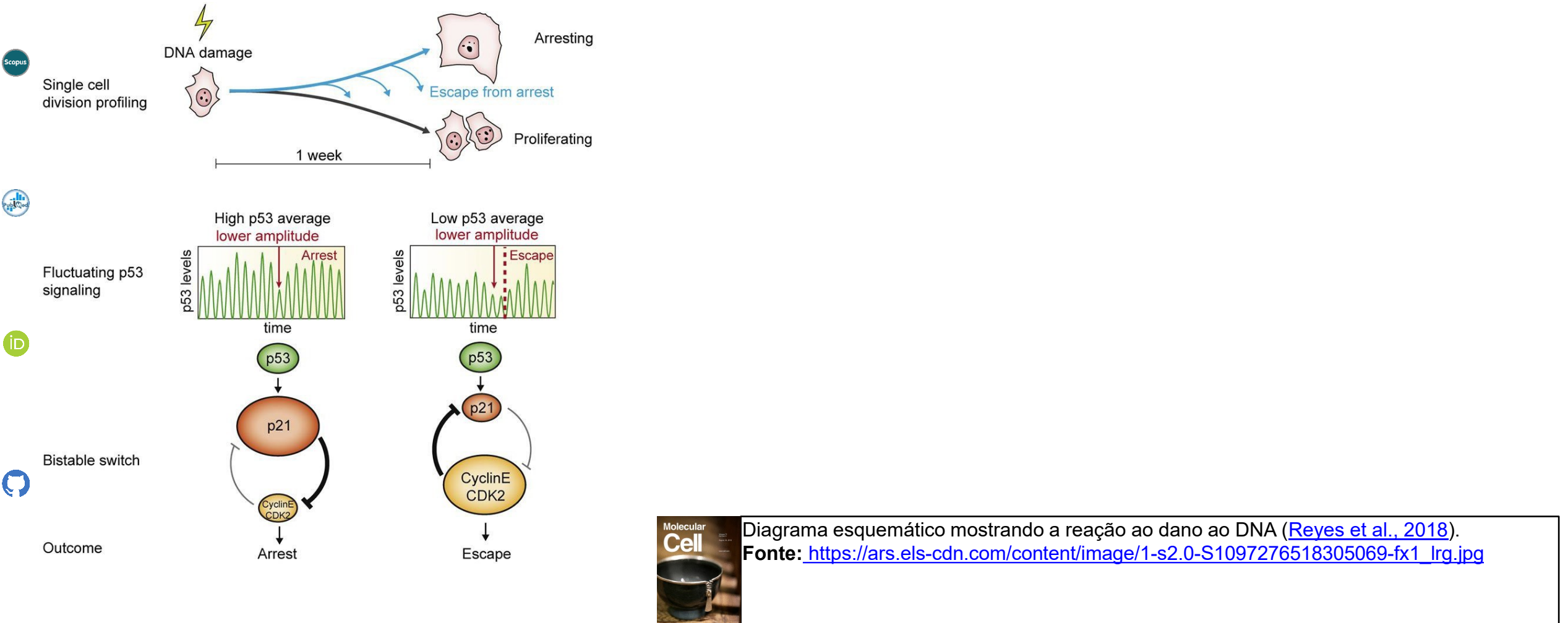
Palavras-chave: *Docking*, *molecular Docking*, docagem, docagem molecular, p53, p21, *cyclin-dependent kinase 2*, CDK2, roscovitina, câncer, fármacos, inibidores, bolsão de ligação de ATP, Molegro Virtual Docker.



Estrutura da CDK2 em complexo com Roscovitina. **Referência:** De Azevedo WF, Leclerc S, Meijer L, Havlicek L, Strnad M, Kim SH. Inhibition of cyclin-dependent kinases by purine analogues: crystal structure of human cdk2 complexed with roscovitine. Eur J Biochem. 1997;243(1-2):518-26. [doi: 10.1111/j.1432-1033.1997.0518a.x](https://doi.org/10.1111/j.1432-1033.1997.0518a.x).

CDK2

Dano ao DNA (como aquele devido à exposição à radiação ultravioleta) leva à expressão da proteína p53 que ativa a produção da proteína p21. A CDK2 é inibida pela p21.



 A partir da identificação da importância da inibição da CDK2 para a indução da apoptose, houve um grande interesse no estudo de inibidores químicos desta enzima, com o objetivo de identificar um novo fármaco contra câncer.

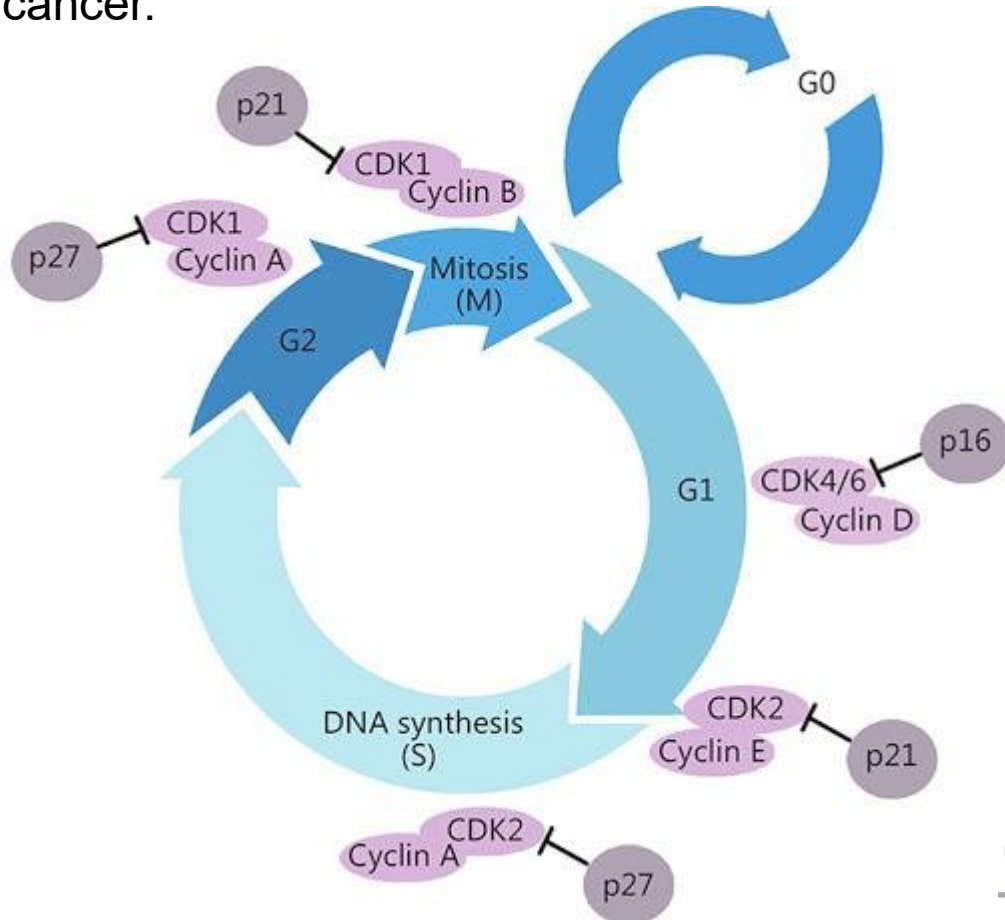
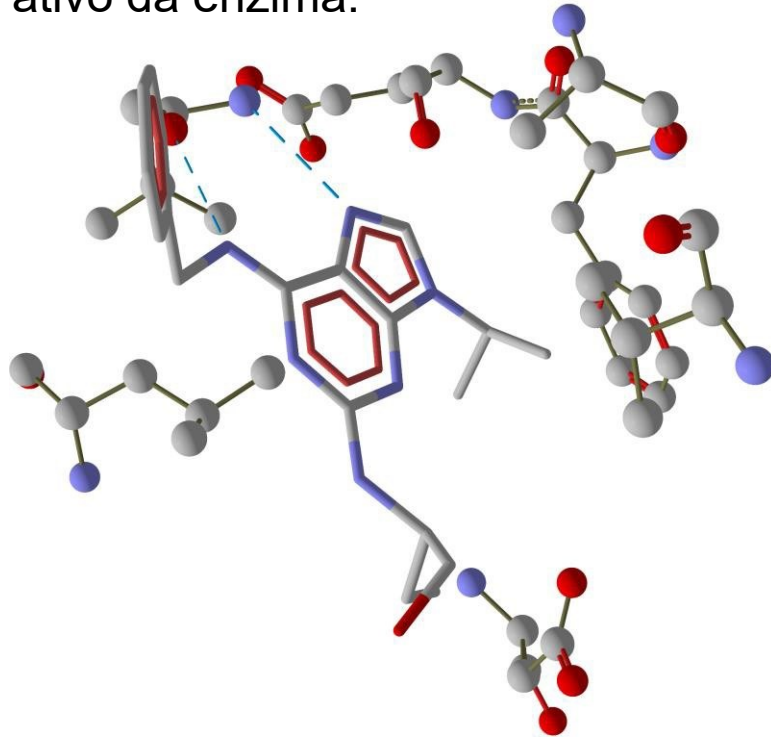


Diagrama esquemático mostrando a participação da CDK2 no ciclo celular (Bai *et al.*, 2017).
Fonte: <http://www.cancerbiomed.org/index.php/cocr/article/viewFile/1070/1194/3235>

CDK2

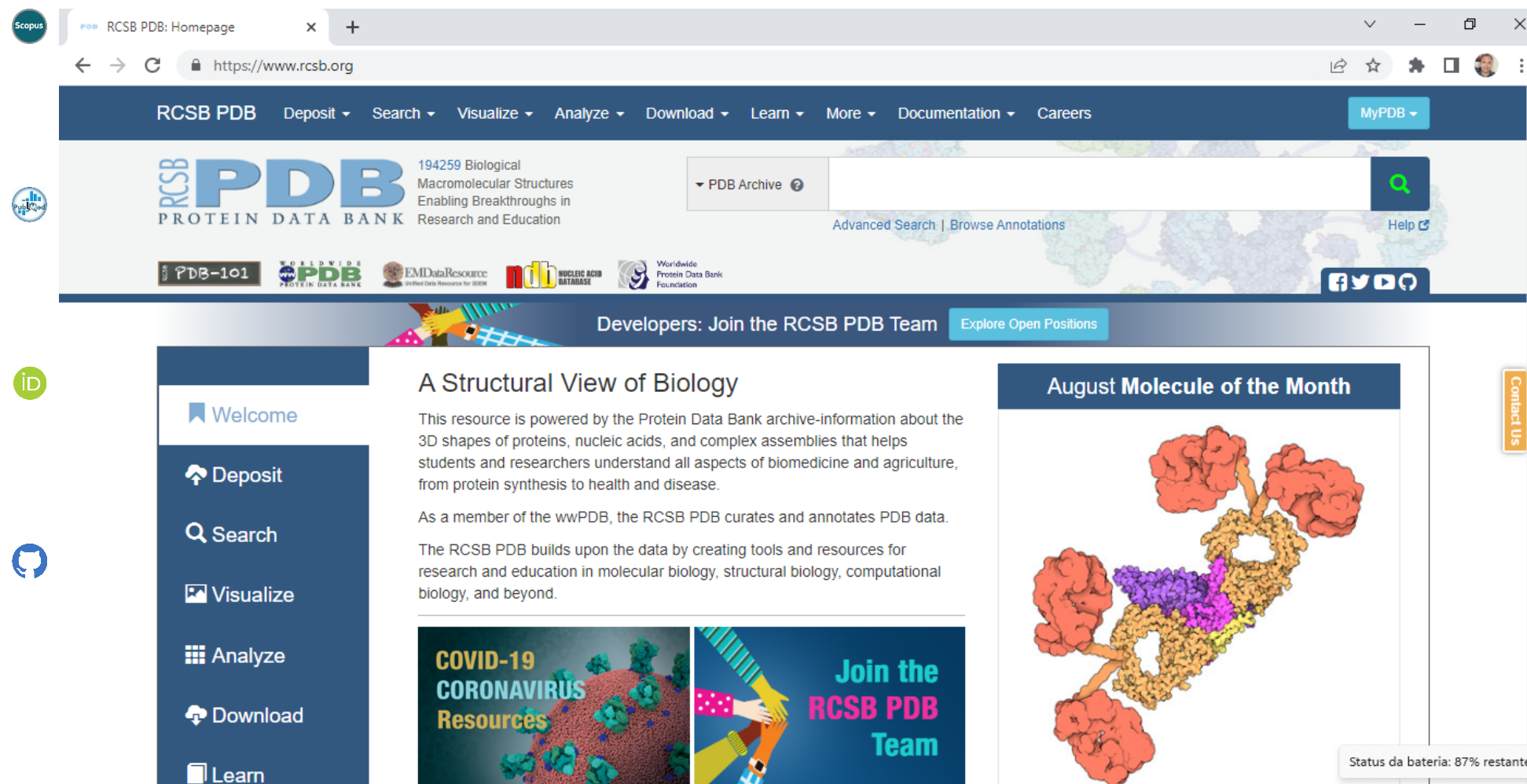
- Inibidores competitivos com ATP impendem a ligação desta ao sítio ativo da CDK2, levando à sua inibição química. A molécula de roscovitine é um inibidor de CDK2, abaixo vemos sua interação intermolecular com o sítio ativo da enzima.



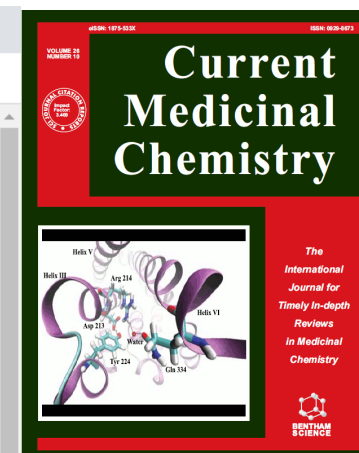
Zoom do sítio ativo da CDK2 em complexo com Roscovitina. **Referência:** De Azevedo WF, Leclerc S, Meijer L, Havlicek L, Strnad M, Kim SH. Inhibition of cyclin-dependent kinases by purine analogues: crystal structure of human cdk2 complexed with roscovitine. Eur J Biochem. 1997;243(1-2):518-26. [doi: 10.1111/j.1432-1033.1997.0518a.x](https://doi.org/10.1111/j.1432-1033.1997.0518a.x).

Download da Estrutura do Protein Data Bank

- 
 Abaixo temos a página de entrada do site do Protein Data Bank (PDB). Esta base de dados disponibiliza a informação estrutural sobre todas biomoléculas que tiveram sua estrutura tridimensional resolvida, o que permite seu uso para busca de fármacos.



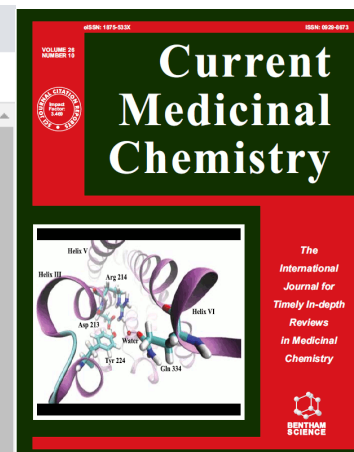
The screenshot shows the RCSB PDB homepage. The header includes navigation links: RCSB PDB, Deposit, Search, Visualize, Analyze, Download, Learn, More, Documentation, Careers, and a MyPDB button. The main content area features the RCSB PDB logo, the text '194259 Biological Macromolecular Structures Enabling Breakthroughs in Research and Education', a search bar, and a PDB Archive dropdown. Below this are logos for PDB-101, OPDB, EMDatResource, NUCLEIC ACID DATABASE, and Worldwide Protein Data Bank Foundation. A banner at the bottom encourages developers to join the RCSB PDB Team and explore open positions. The left sidebar contains a 'Welcome' message and links to Deposit, Search, Visualize, Analyze, Download, and Learn. The main content area is divided into two sections: 'A Structural View of Biology' and 'August Molecule of the Month'.



Referência: Veit-Acosta M, de Azevedo Junior WF. The Impact of Crystallographic Data for the Development of Machine Learning Models to Predict Protein-Ligand Binding Affinity. *Curr Med Chem.* 2021; 28(34):7006-7022. doi: [10.2174/0929867328666210210121320](https://doi.org/10.2174/0929867328666210210121320)

Download da Estrutura do Protein Data Bank

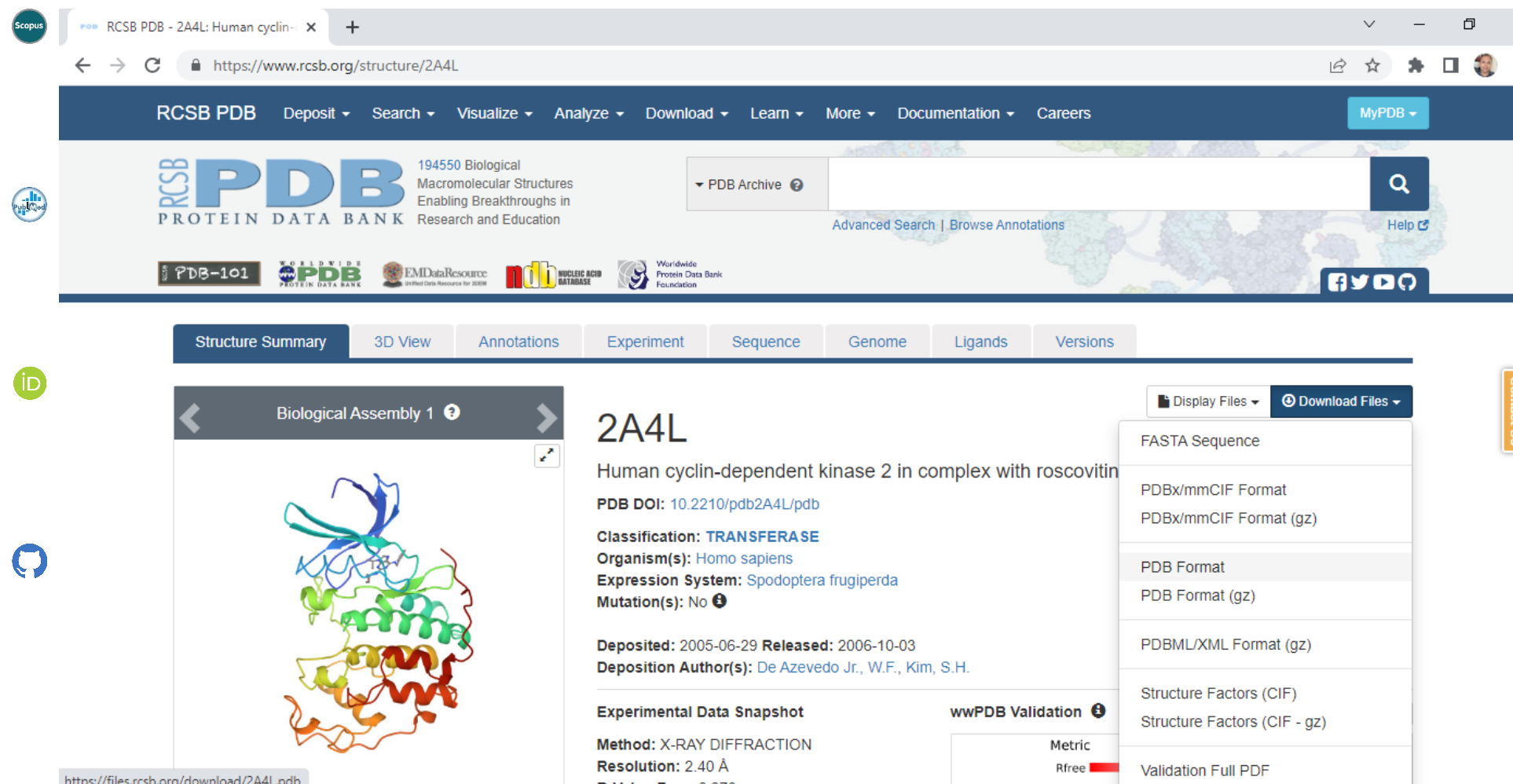
Podemos baixar as coordenadas atômicas (código de acesso PDB [2A4L](https://www.rcsb.org/entry/2A4L)).



Referência: Veit-Acosta M, de Azevedo Junior WF. The Impact of Crystallographic Data for the Development of Machine Learning Models to Predict Protein-Ligand Binding Affinity. Curr Med Chem. 2021; 28(34):7006-7022. doi: [10.2174/0929867328666210210121320](https://doi.org/10.2174/0929867328666210210121320)

Download da Estrutura do Protein Data Bank

- Na página da estrutura [2A4L](#) clicamos em *Download Files->PDB Format*, como mostrado abaixo. Depois escolhemos a pasta onde será salvo o arquivo PDB.



RCSB PDB - 2A4L: Human cyclin- x +

https://www.rcsb.org/structure/2A4L

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RCSB PDB 194550 Biological Macromolecular Structures Enabling Breakthroughs in Research and Education

PDB Archive ?

Advanced Search | Browse Annotations

Help

PDB-101 WORLDWIDE PDB EMDDataResource NUCLEIC ACID DATABASE Worldwide Protein Data Bank Foundation

Structure Summary 3D View Annotations Experiment Sequence Genome Ligands Versions

Biological Assembly 1 ?

2A4L

Human cyclin-dependent kinase 2 in complex with roscovitine

PDB DOI: [10.2210/pdb2A4L/pdb](#)

Classification: **TRANSFERASE**

Organism(s): [Homo sapiens](#)

Expression System: [Spodoptera frugiperda](#)

Mutation(s): No

Deposited: 2005-06-29 Released: 2006-10-03

Deposition Author(s): [De Azevedo Jr., W.F., Kim, S.H.](#)

Experimental Data Snapshot

Method: X-RAY DIFFRACTION

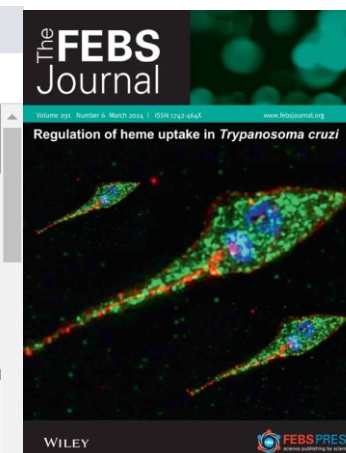
Resolution: 2.40 Å

wwPDB Validation

Metric Rfree

Display Files Download Files

- FASTA Sequence
- PDBx/mmCIF Format
- PDBx/mmCIF Format (gz)
- PDB Format
- PDB Format (gz)
- PDBML/XML Format (gz)
- Structure Factors (CIF)
- Structure Factors (CIF - gz)
- Validation Full PDF



Referência: De Azevedo WF, Leclerc S, Meijer L, Havlicek L, Strnad M, Kim SH. Inhibition of cyclin-dependent kinases by purine analogues: crystal structure of human cdk2 complexed with roscovitine. Eur J Biochem. 1997;243(1-2):518-26. [doi: 10.1111/j.1432-1033.1997.0518a.x.](#)

Download da Estrutura do Protein Data Bank

- Antes de proceder com a simulação de docagem molecular, podemos verificar na página do PDB as informações do ligante, basta rolarmos a página. O ligante que usaremos na simulação é o RRC, mostrado abaixo.





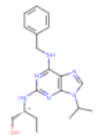

RCSB PDB - 2A4L: Human cyclin- x

https://www.rcsb.org/structure/2A4L

RCSB PDB Deposit Search Visualize Analyze Download Learn More Documentation Careers MyPDB

Small Molecules

Ligands 1 Unique

ID	Chains	Name / Formula / InChI Key	2D Diagram	3D Interactions
RRC Query on RRC Download Ideal Coordinates CCD File Download Instance Coordinates	B [auth A]	R-ROSCOVITINE C₁₉ H₂₆ N₆ O BTIHMVBBUGXLCJ-OAHLLOKOSA-N		Ligand Interaction

Binding Affinity Annotations

ID	Source	Binding Affinity
RRC		Ki: 250 (nM) from 1 assay(s)
	BindingDB: 2A4L	Kd: min: 2900, max: 3400 (nM) from 2 assay(s)
		IC50: min: 0.1, max: 708 (nM) from 19 assay(s)
	Binding MOAD: 2A4L	IC50: 400 (nM) from 1 assay(s)
	PDBBind: 2A4L	IC50: 400 (nM) from 1 assay(s)

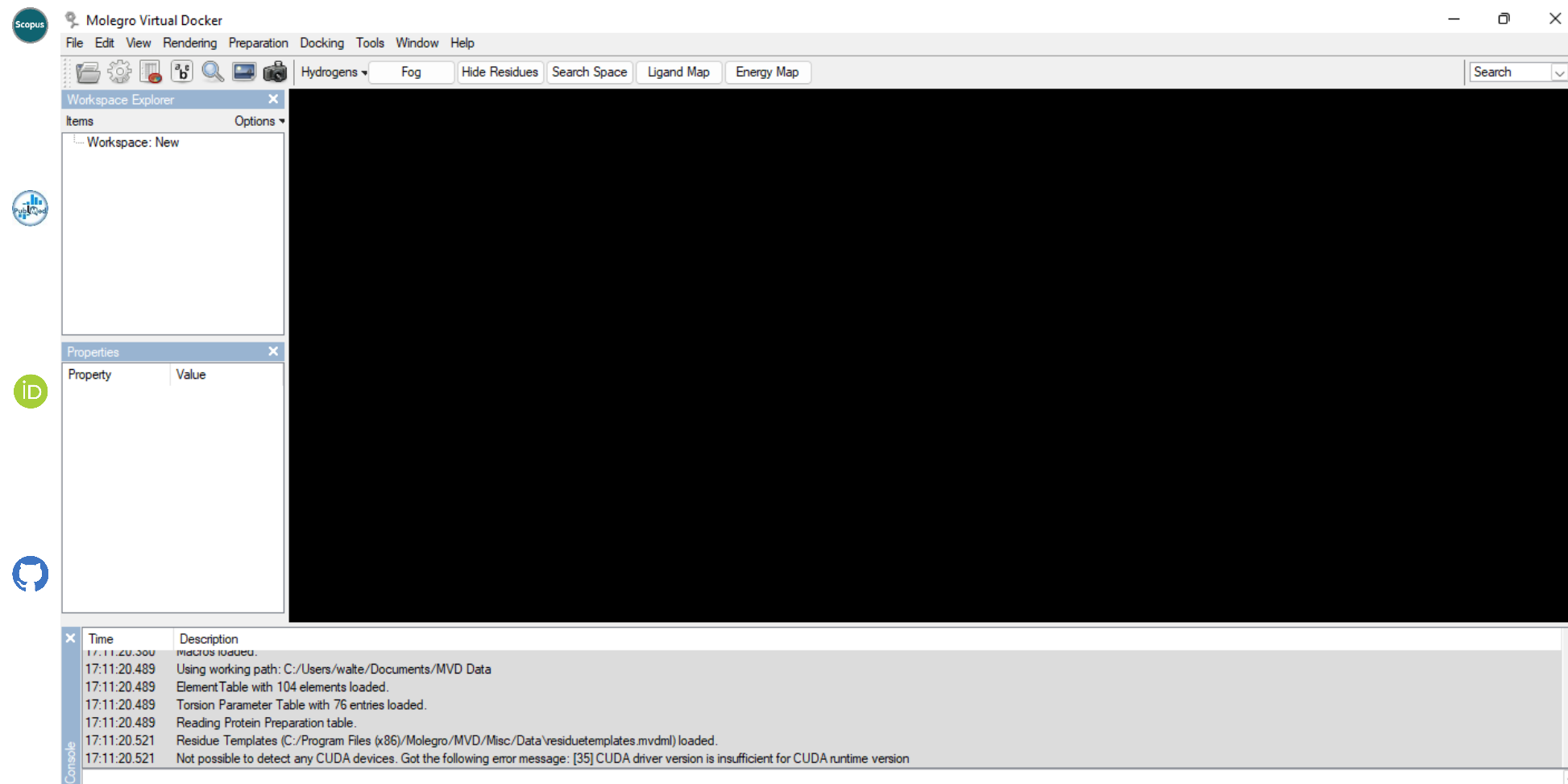
Experimental Data & Validation



Referência: De Azevedo WF, Leclerc S, Meijer L, Havlicek L, Strnad M, Kim SH. Inhibition of cyclin-dependent kinases by purine analogues: crystal structure of human cdk2 complexed with roscovitrine. Eur J Biochem. 1997;243(1-2):518-26. [doi: 10.1111/j.1432-1033.1997.0518a.x](https://doi.org/10.1111/j.1432-1033.1997.0518a.x).

Docagem Molecular com o MVD

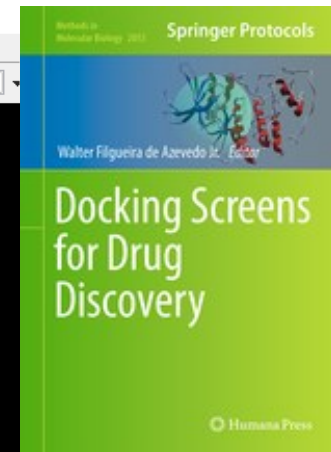
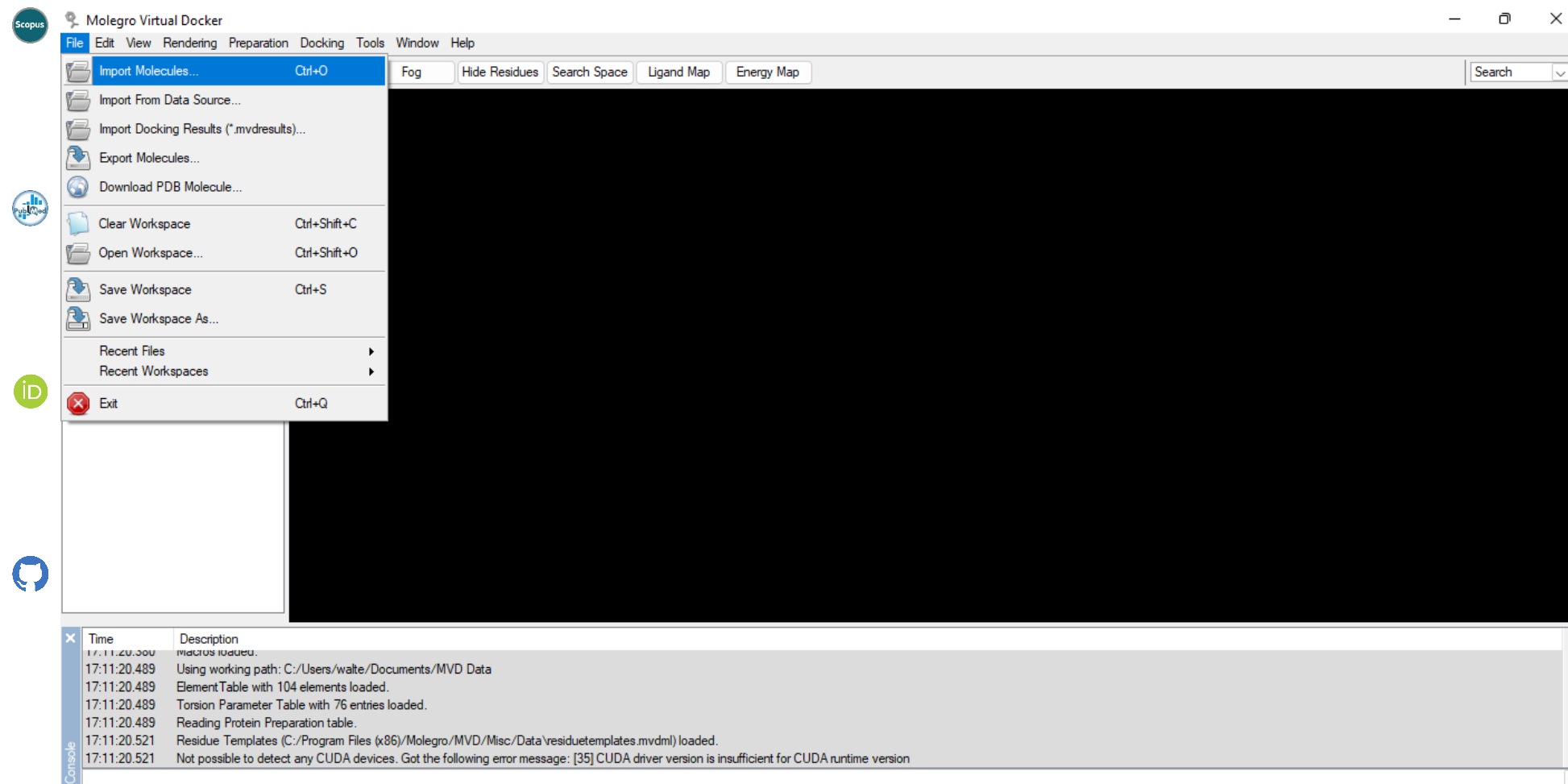
- Supondo que você tem o programa MVD (*Molegro Virtual Docker*) instalado e rodando no seu computador. Depois de clicar no ícone do MVD, você terá a janela aberta abaixo.



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

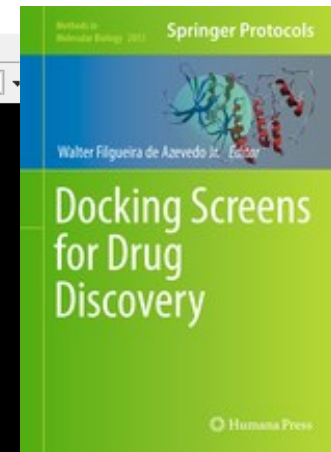
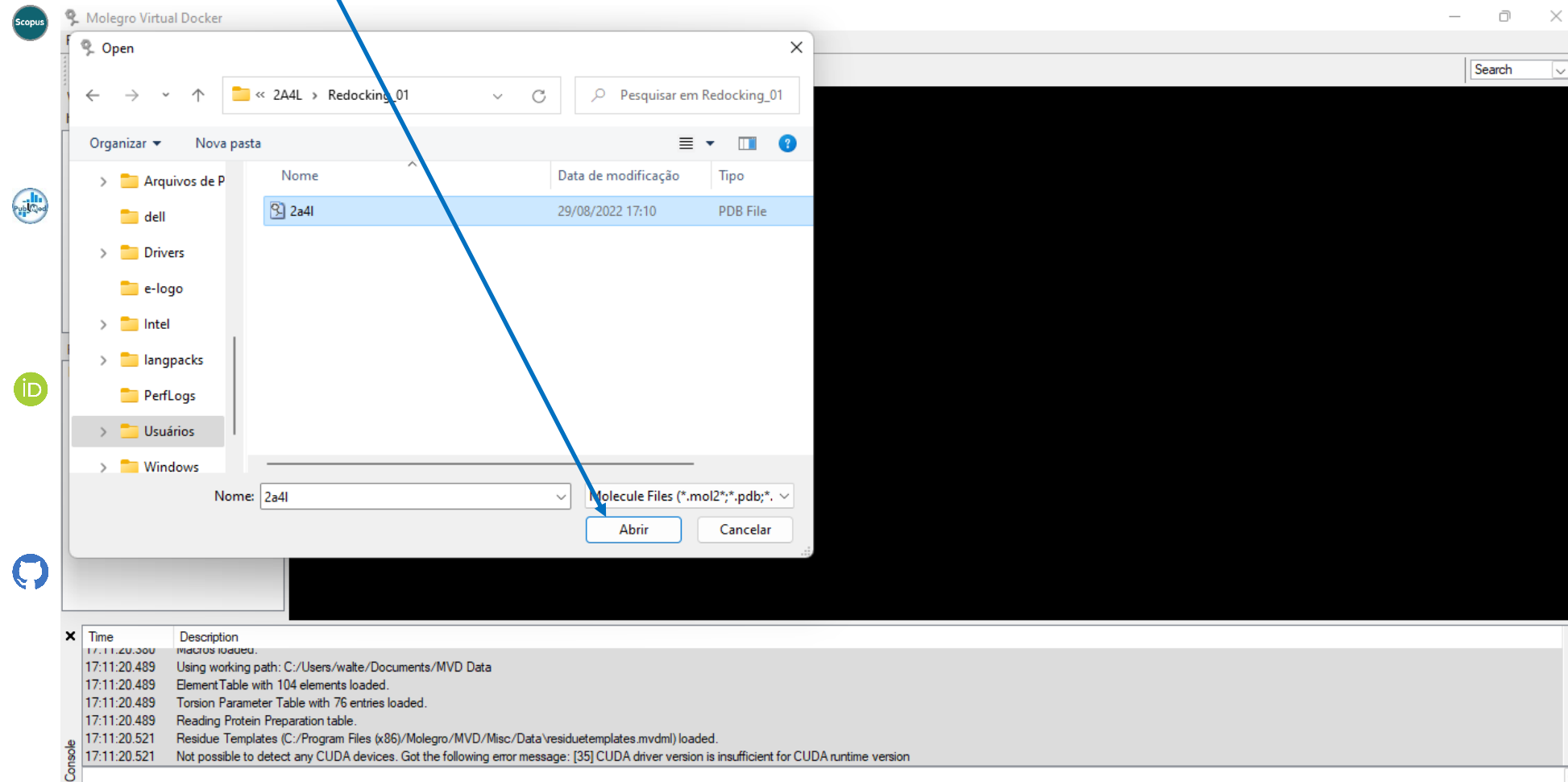
- Procederemos com a verificação do protocolo de docagem, ou seja, veremos se o programa MVD é capaz de recuperar a posição do ligante. Para carregar o PDB, clicamos em *File->Import Molecules...*



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

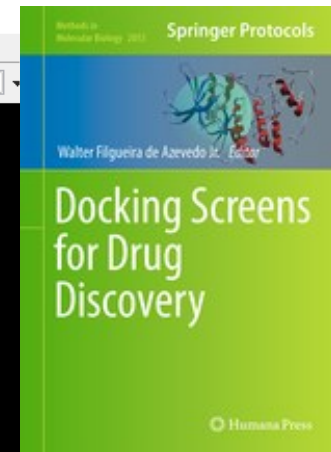
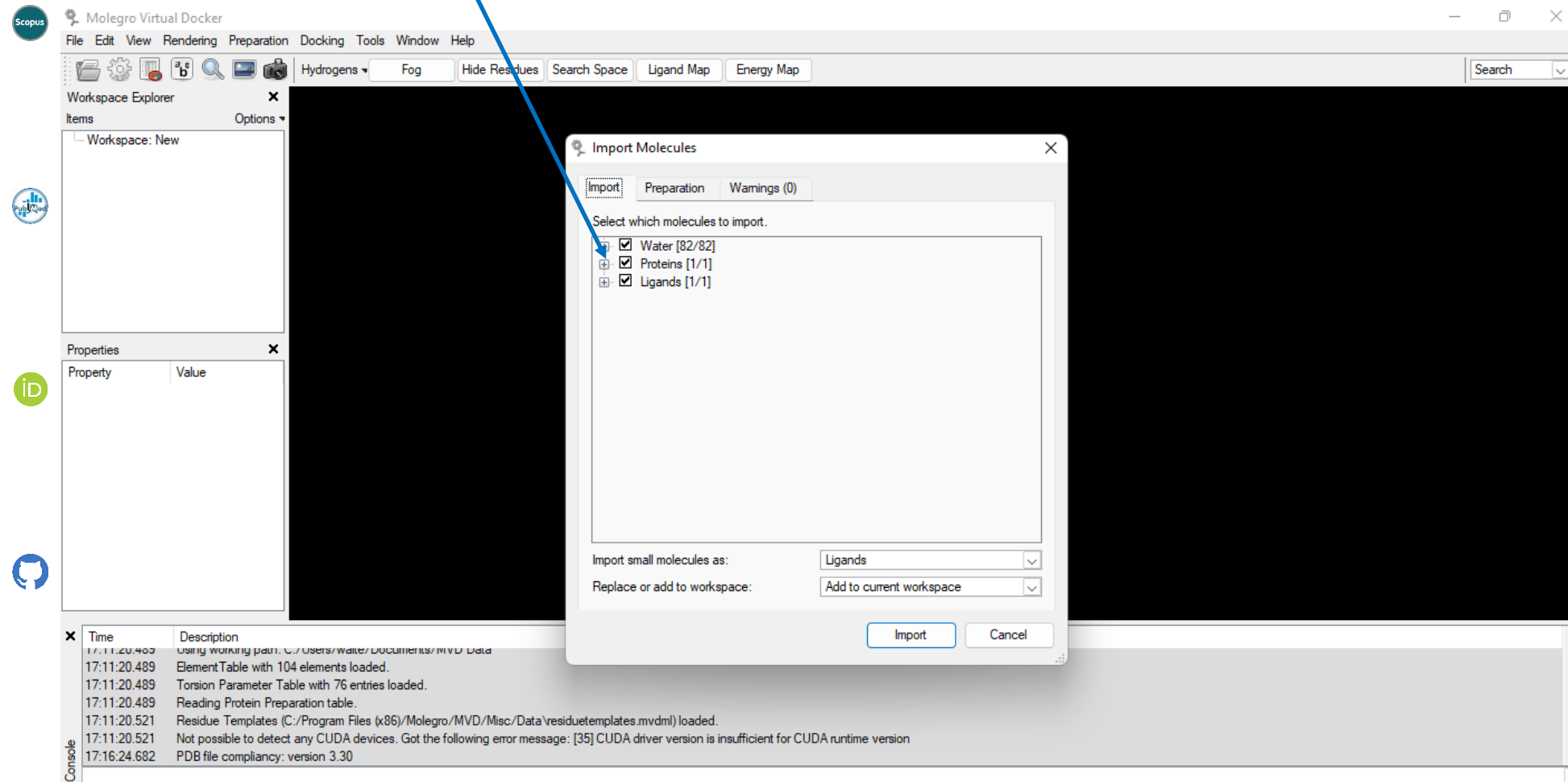
- Em seguida procuramos a pasta onde temos o arquivo PDB da estrutura ([2A4L](#)) e clicamos no arquivo PDB e no botão Abrir.



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](#).

Docagem Molecular com o MVD

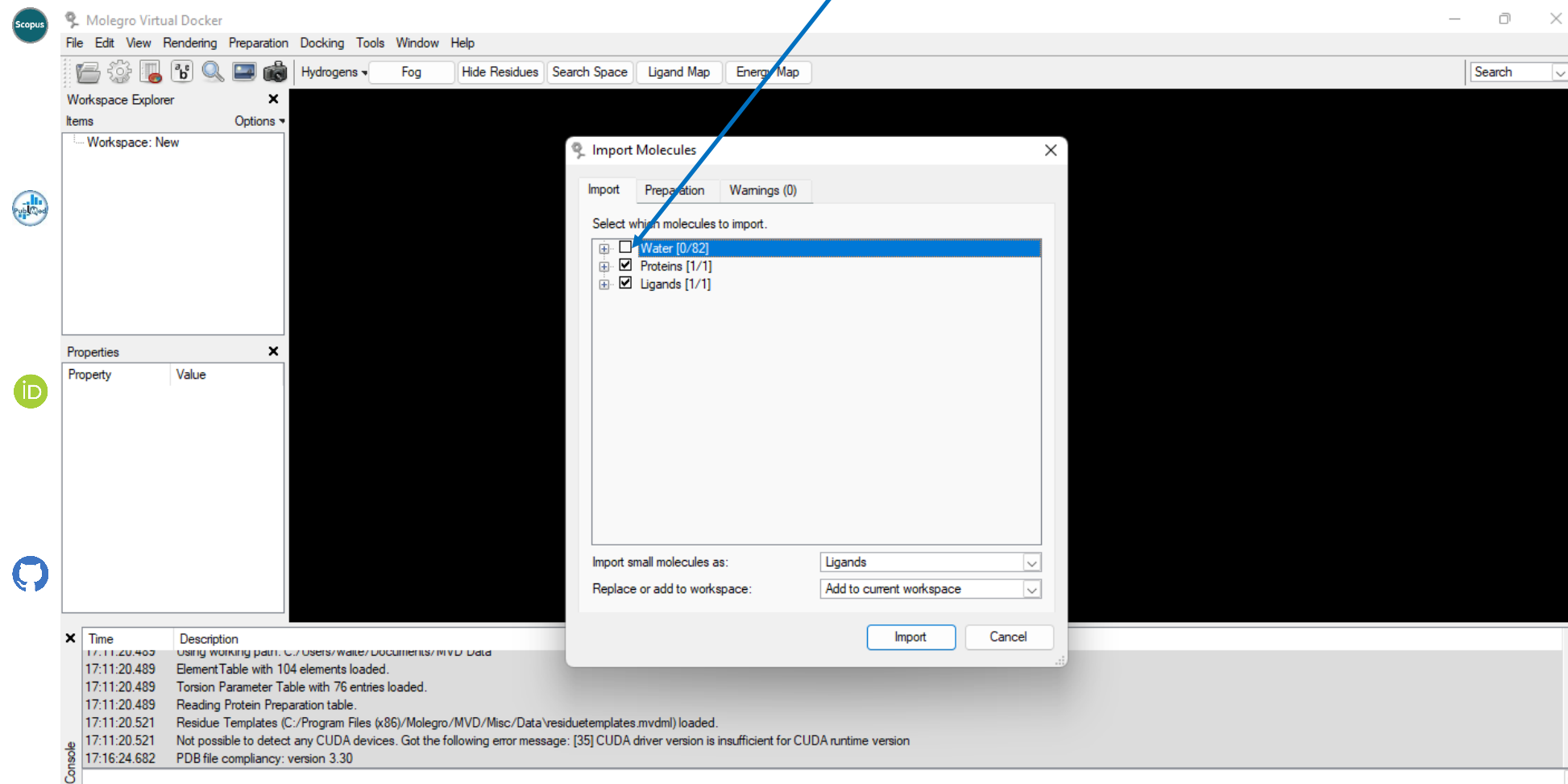
- Na nova janela, temos o conteúdo do arquivo PDB, neste caso 82 moléculas de água, uma proteína (cadeia polipeptídica ou trecho) e um ligante (RRC).



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

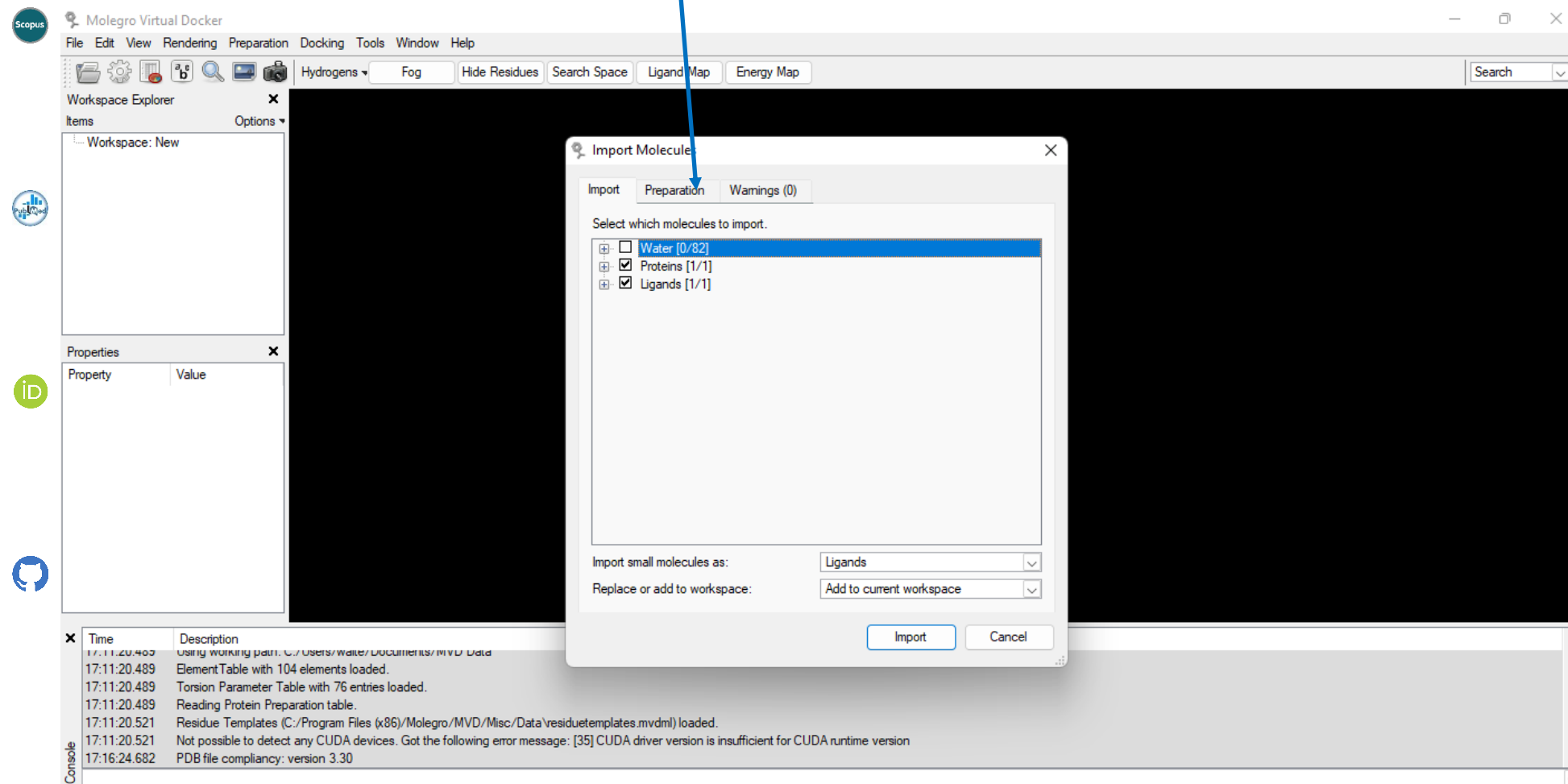
- Desabilitamos a caixa relacionada às moléculas de água.



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

Em seguida clicamos na opção *Preparation*.



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

- 🔗 No campo *Assign All Below*, escolhemos *Always*.

Import Molecules

Import Preparation Warnings (0)

Assign All Below

Assign bonds Custom

Assign bond orders and hybridization If Missing

Create explicit hydrogens Always

Assign charges (calculated by MVD) Always

Detect flexible torsions in ligands Always

Assign Tripos atom types If Missing

Notice:

The preparation options (If Missing, Always, Never, Remove) applies to each individual molecule (not each individual bond or atom).

For instance, setting 'Assign bonds' to 'If Missing' results in covalent bonds being created for molecules not containing any bonds at all while molecules with bond information will preserve their bond assignments.

Likewise, setting 'Create explicit hydrogens' to 'If Missing' will not add additional hydrogens to molecules containing e.g. polar hydrogens only. In this case, 'Always' should be used if all hydrogens should be created.

Import Cancel

Console

Time	Description
17:11:20.465	Using working path: C:/Users/walter/Documents/MVD/Data
17:11:20.489	Element Table with 104 elements loaded.
17:11:20.489	Torsion Parameter Table with 76 entries loaded.
17:11:20.489	Reading Protein Preparation table.
17:11:20.521	Residue Templates (C:/Program Files (x86)/Molegro/MVD/Misc/Data/residuotemplates.mvdm) loaded.
17:11:20.521	Not possible to detect any CUDA devices. Got the following error message: [35] CUDA driver version is insufficient for CUDA runtime version
17:16:24.682	PDB file compliancy: version 3.30



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

Clique no botão *Import*.

Molegro Virtual Docker

File Edit View Rendering Preparation Docking Tools Window Help

Hydrogens Fog Hide Residues Search Space Ligand Map Energy Map

Workspace Explorer

Items Options

Workspace: New

Properties

Property Value

Console

Time Description

17:11:20.465 Using working path: C:/Users/walter/Documents/MVD/Data

17:11:20.489 Element Table with 104 elements loaded.

17:11:20.489 Torsion Parameter Table with 76 entries loaded.

17:11:20.489 Reading Protein Preparation table.

17:11:20.521 Residue Templates (C:/Program Files (x86)/Molegro/MVD/Misc/Data/residue templates.mvdm) loaded.

17:11:20.521 Not possible to detect any CUDA devices. Got the following error message: [35] CUDA driver version is insufficient for CUDA runtime version

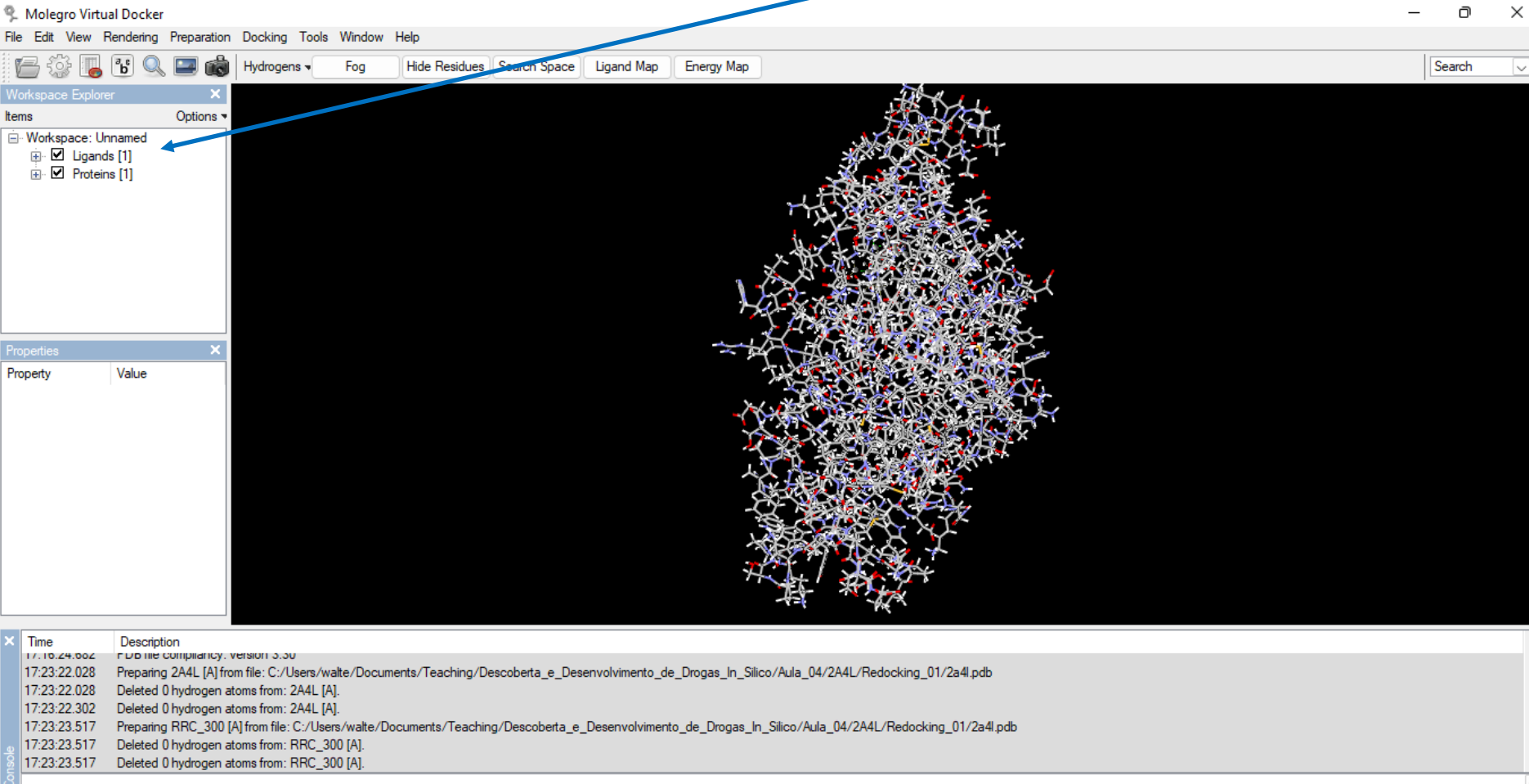
17:16:24.682 PDB file compliancy: version 3.30



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

- O programa carrega a estrutura da CDK2 em complexo com o inibidor. No *Workspace* está listado o conteúdo do arquivo PDB.



Workspace Explorer

- Workspace: Unnamed
 - Ligands [1]
 - Proteins [1]

Properties

Property	Value

Console

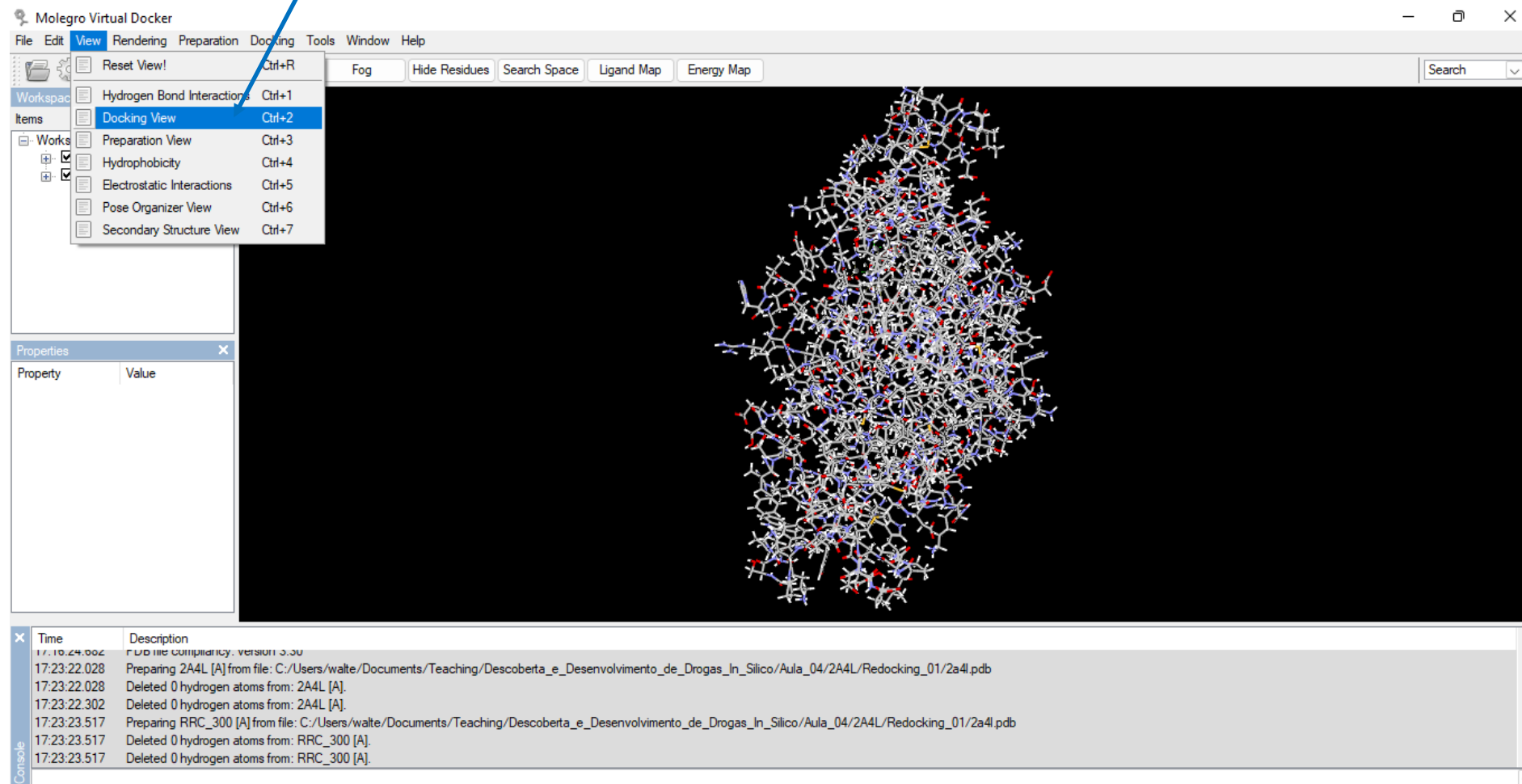
Time	Description
17:16:24.602	File compliance: version 3.30
17:23:22.028	Preparing 2A4L [A] from file: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/2a4l.pdb
17:23:22.028	Deleted 0 hydrogen atoms from: 2A4L [A].
17:23:22.302	Deleted 0 hydrogen atoms from: 2A4L [A].
17:23:23.517	Preparing RRC_300 [A] from file: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/2a4l.pdb
17:23:23.517	Deleted 0 hydrogen atoms from: RRC_300 [A].
17:23:23.517	Deleted 0 hydrogen atoms from: RRC_300 [A].



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

Agora clicamos em *View->Docking View*.



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

- No *Workspace*, podemos selecionar o que mostrar na tela gráfica, desmarcamos a proteína.

Molegro Virtual Docker

File Edit View Rendering Preparation Docking Tools Window Help

Hydrogens Fog Hide Residues Search Space Ligand Map Energy Map

Workspace Explorer

Items Options

Workspace: Unnamed

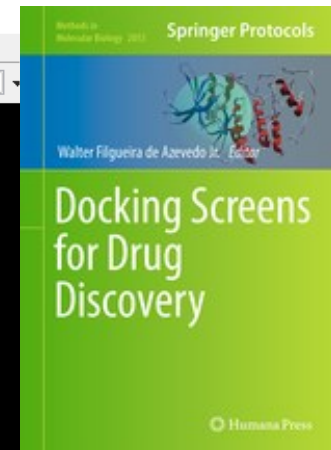
- Ligands [1]
- Proteins [1]

Properties

Property	Value
----------	-------

Console

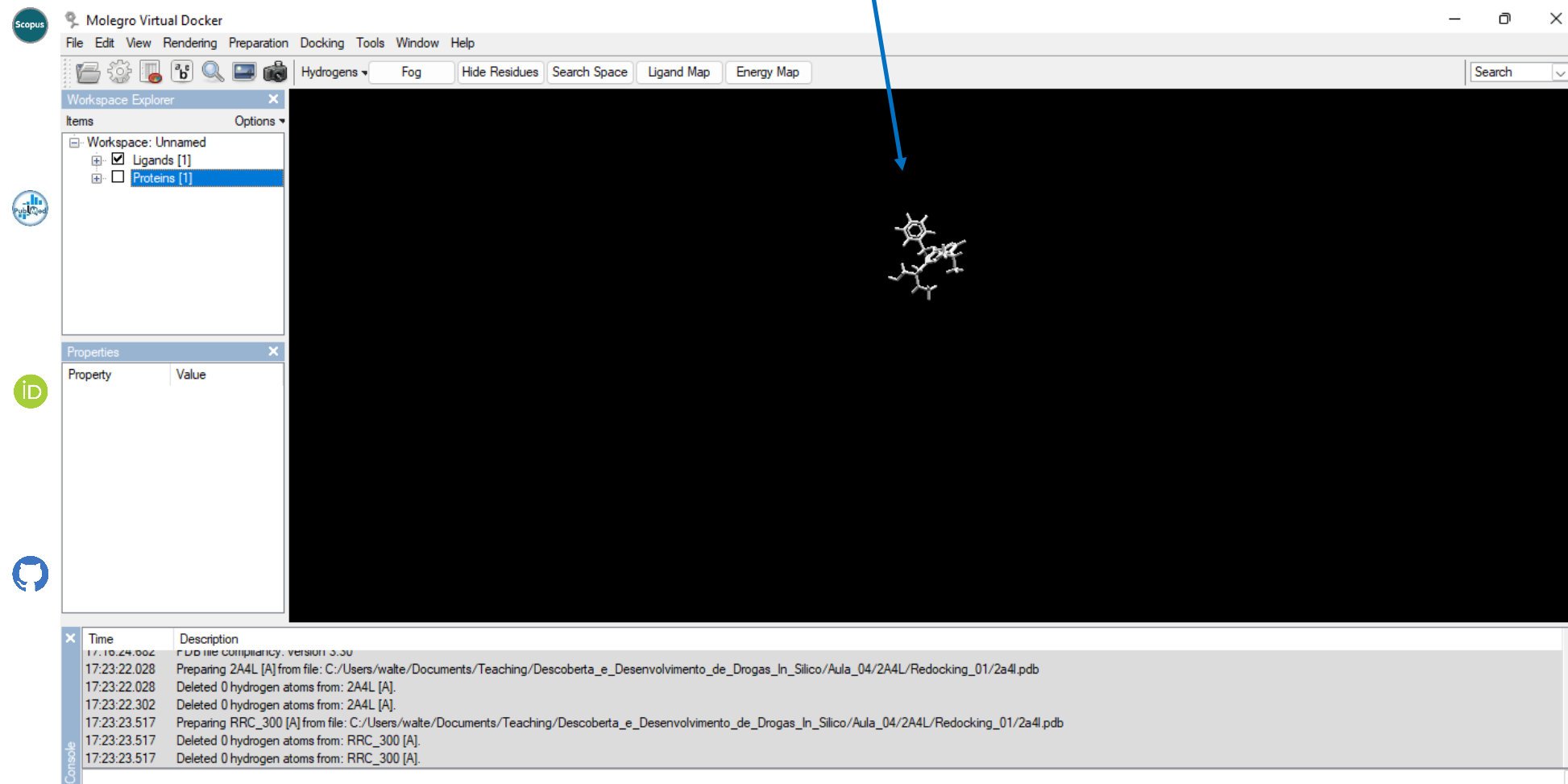
Time	Description
17:16:24.602	Preparing 2A4L [A] from file: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/2a4l.pdb
17:23:22.028	Deleted 0 hydrogen atoms from: 2A4L [A].
17:23:22.302	Deleted 0 hydrogen atoms from: 2A4L [A].
17:23:23.517	Preparing RRC_300 [A] from file: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/2a4l.pdb
17:23:23.517	Deleted 0 hydrogen atoms from: RRC_300 [A].
17:23:23.517	Deleted 0 hydrogen atoms from: RRC_300 [A].



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

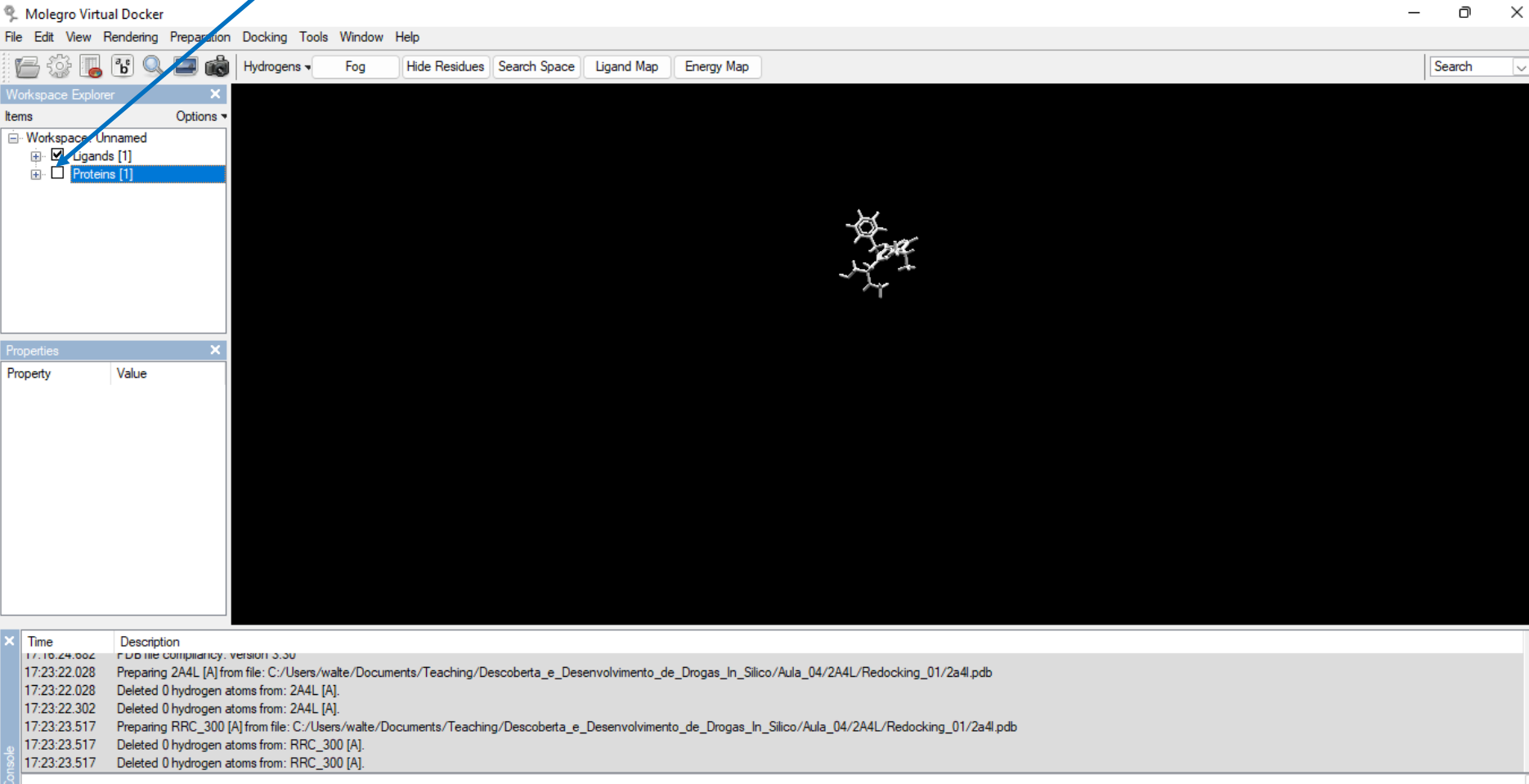
- Na tela gráfica temos a posição do ligante RRC.



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

- Clicamos na opção *Protein* do *Workspace* para retornar a visualização da proteína.



Molegro Virtual Docker

File Edit View Rendering Preparation Docking Tools Window Help

Hydrogens Fog Hide Residues Search Space Ligand Map Energy Map Search

Workspace Explorer

Items Options

Workspace: Unnamed

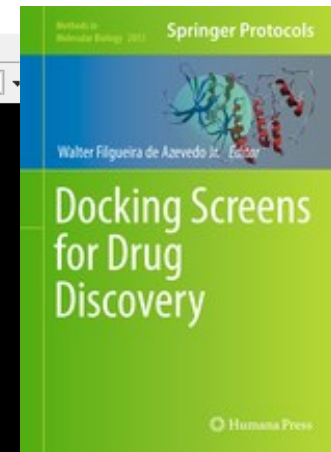
- ☒ Ligands [1]
- ☐ Proteins [1]

Properties

Property	Value
----------	-------

Console

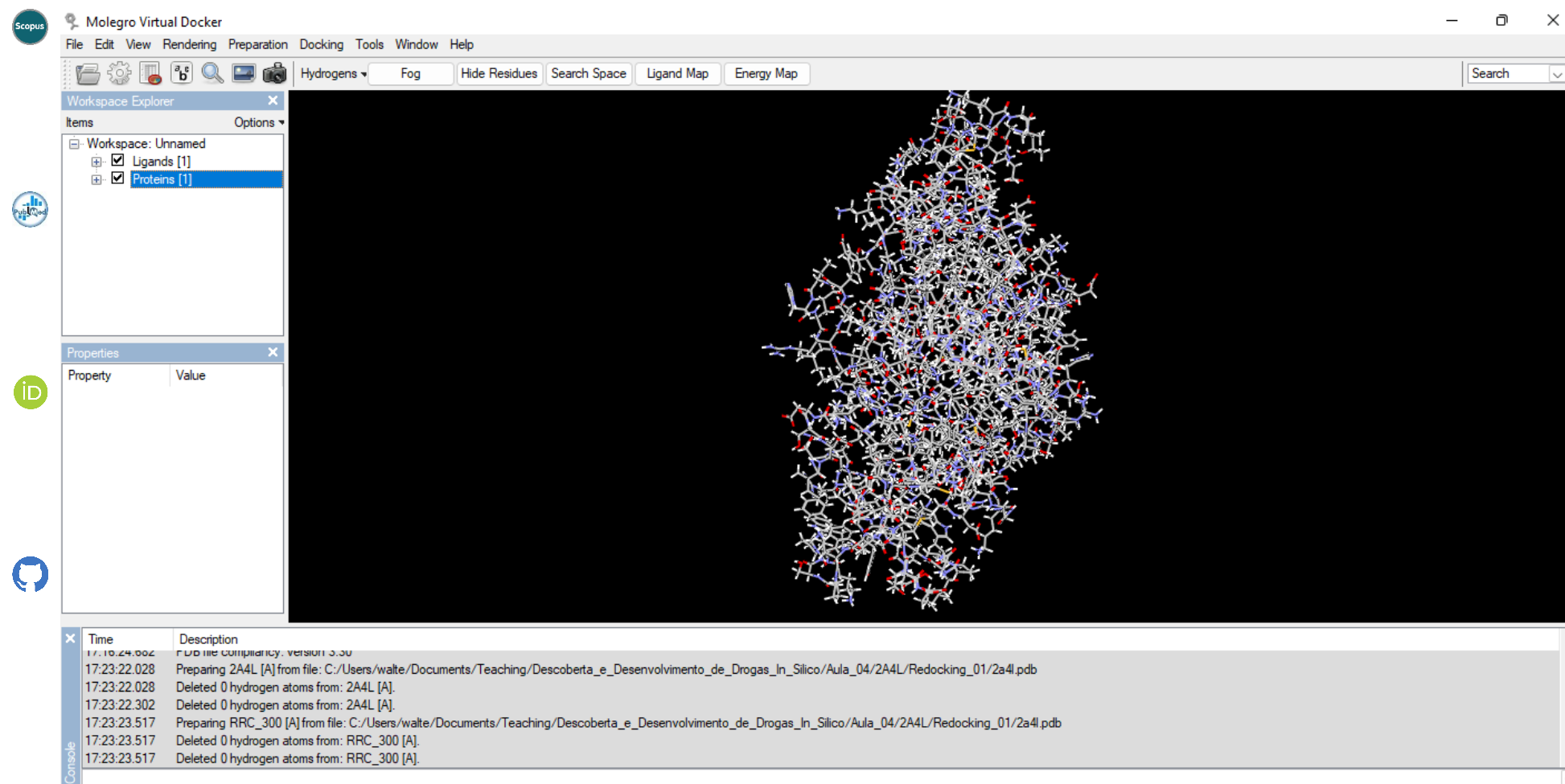
Time	Description
17:16:24.662	PDH file compliance: version 3.30
17:23:22.028	Preparing 2A4L [A] from file: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/2a4l.pdb
17:23:22.028	Deleted 0 hydrogen atoms from: 2A4L [A].
17:23:22.302	Deleted 0 hydrogen atoms from: 2A4L [A].
17:23:23.517	Preparing RRC_300 [A] from file: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/2a4l.pdb
17:23:23.517	Deleted 0 hydrogen atoms from: RRC_300 [A].
17:23:23.517	Deleted 0 hydrogen atoms from: RRC_300 [A].



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

 Agora temos a proteína de volta à tela gráfica.



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

- Em seguida, procedemos a simulação de docagem molecular. Clicamos em *Docking->Docking Wizard*, como mostrado abaixo.

Molegro Virtual Docker

File Edit View Rendering Preparation Docking Tools Window Help

Search Space Ligand Map Energy Map

Workspace Explorer

Items Options

Workspace: Unnamed

Items

Options

Workspace: Unnamed

Items

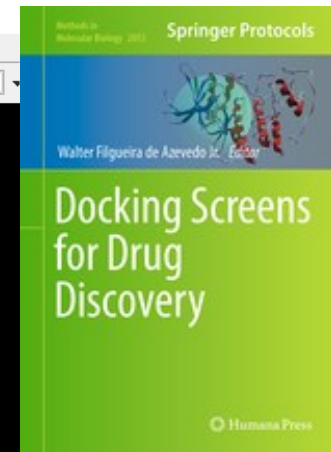
Options

Properties

Property	Value
Position	91.247 66.53 84...
Residue	Phe 240
Internal residue ...	227
Atom ID	1832
Element	C (6)
PDB atom name	CD2
PDB atom ID	1833
Tripos atom type	C.2
Plants atom type	Not Defined
Hydrogens	1
VdW radius	1.7 Å
Covalent radius	0.68 Å
Hydrogen bondi	Nonpolar

Console

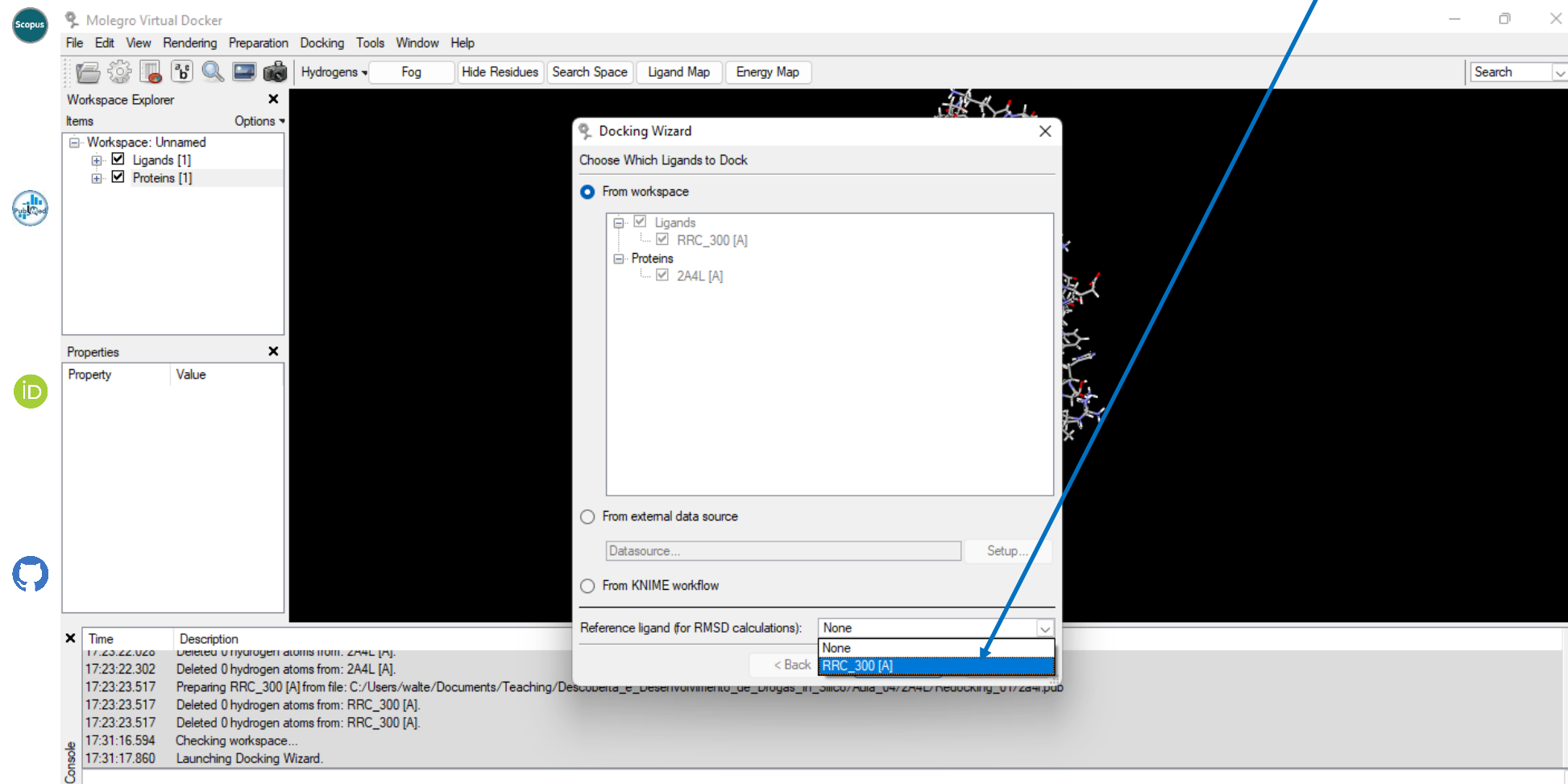
Time	Description
17:16:24.602	Preparing 2A4L [A] from file: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/2a4l.pdb
17:23:22.028	Preparing 2A4L [A] from file: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/2a4l.pdb
17:23:22.028	Deleted 0 hydrogen atoms from: 2A4L [A].
17:23:22.302	Deleted 0 hydrogen atoms from: 2A4L [A].
17:23:23.517	Preparing RRC_300 [A] from file: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/2a4l.pdb
17:23:23.517	Deleted 0 hydrogen atoms from: RRC_300 [A].
17:23:23.517	Deleted 0 hydrogen atoms from: RRC_300 [A].



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

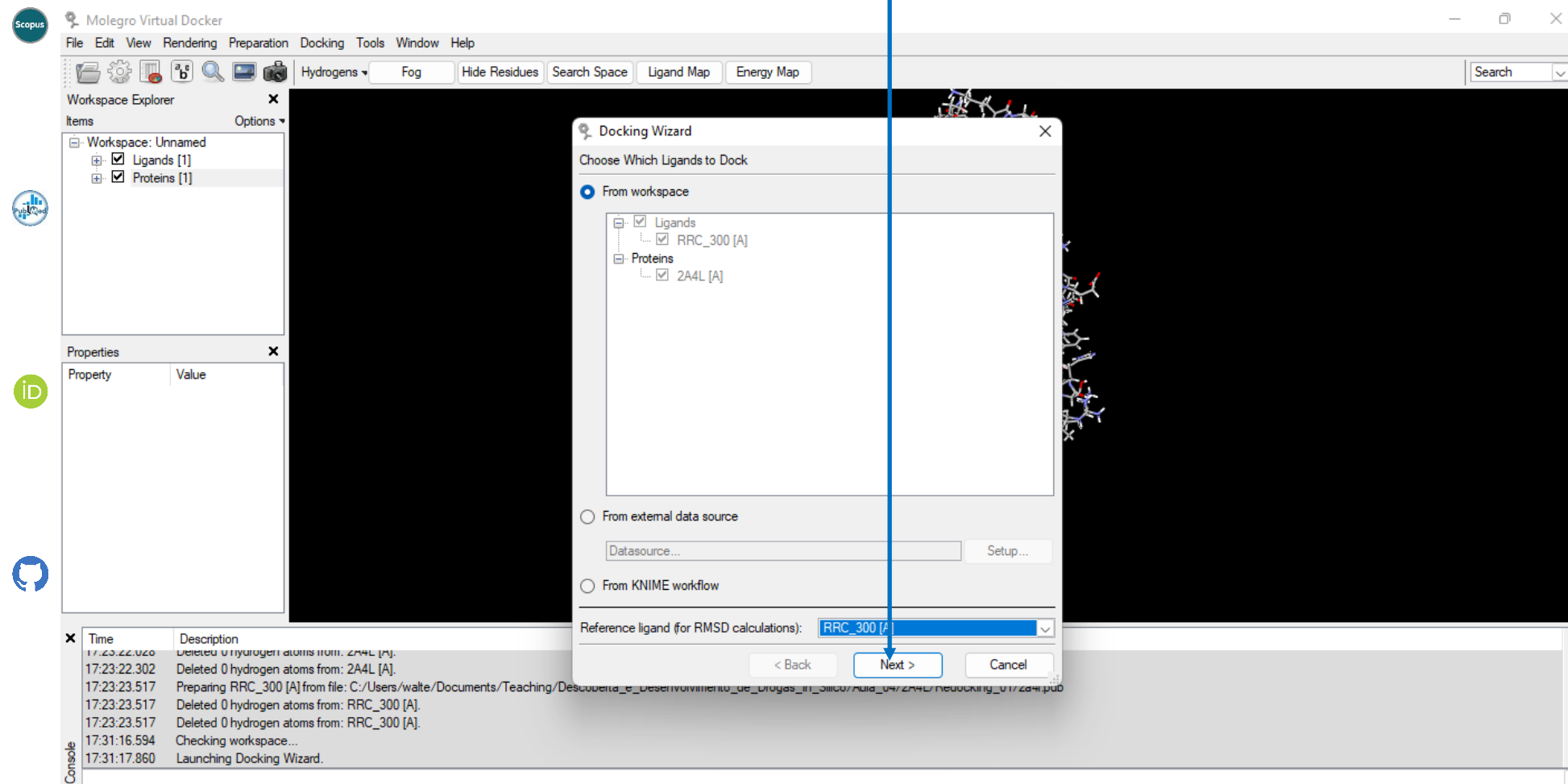
- Na nova janela, na opção *Reference ligand*, escolhemos o ligante, o RRC, como indicado abaixo.



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

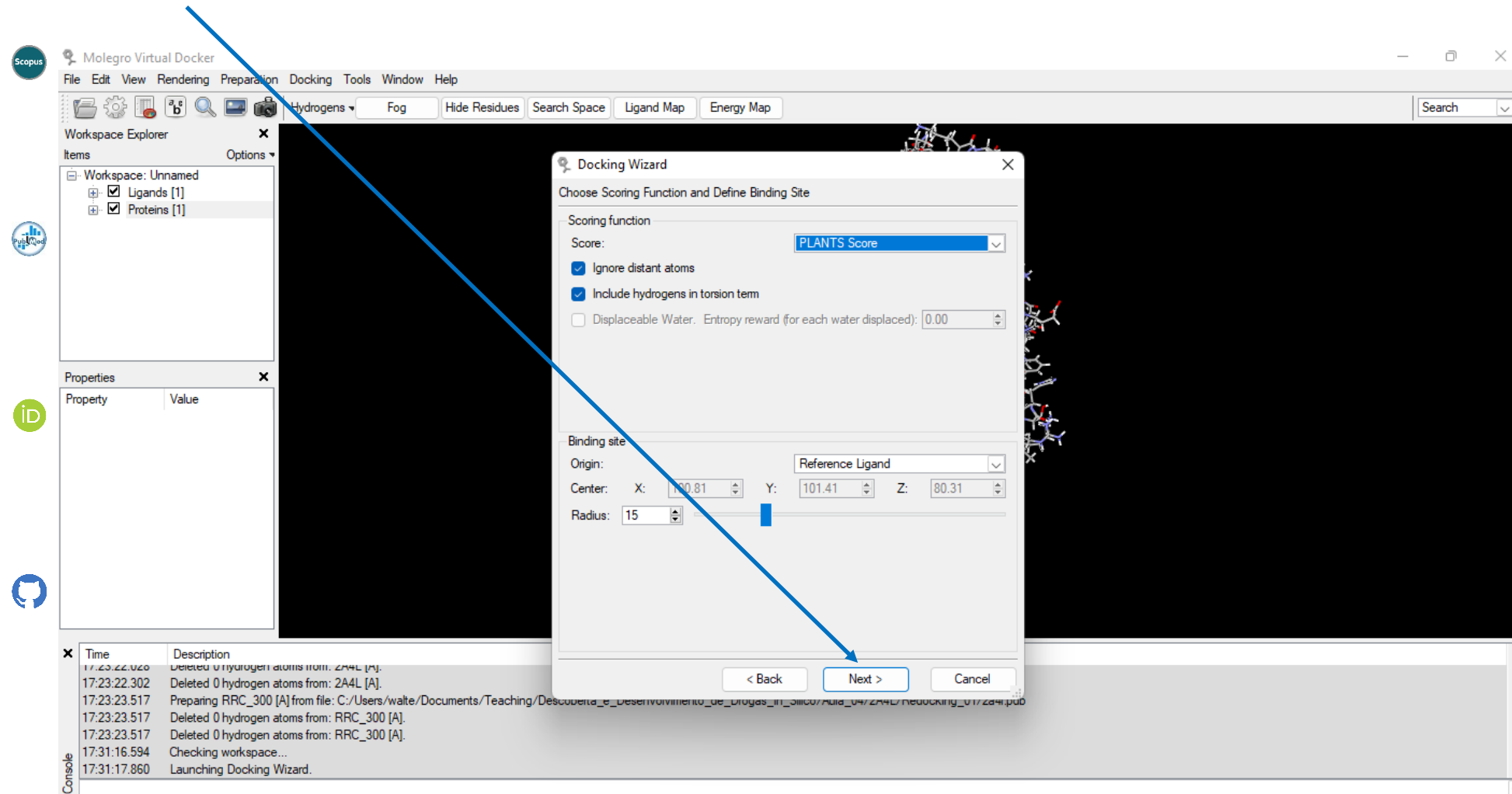
Com o ligante selecionado, clicamos no botão *Next*.



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

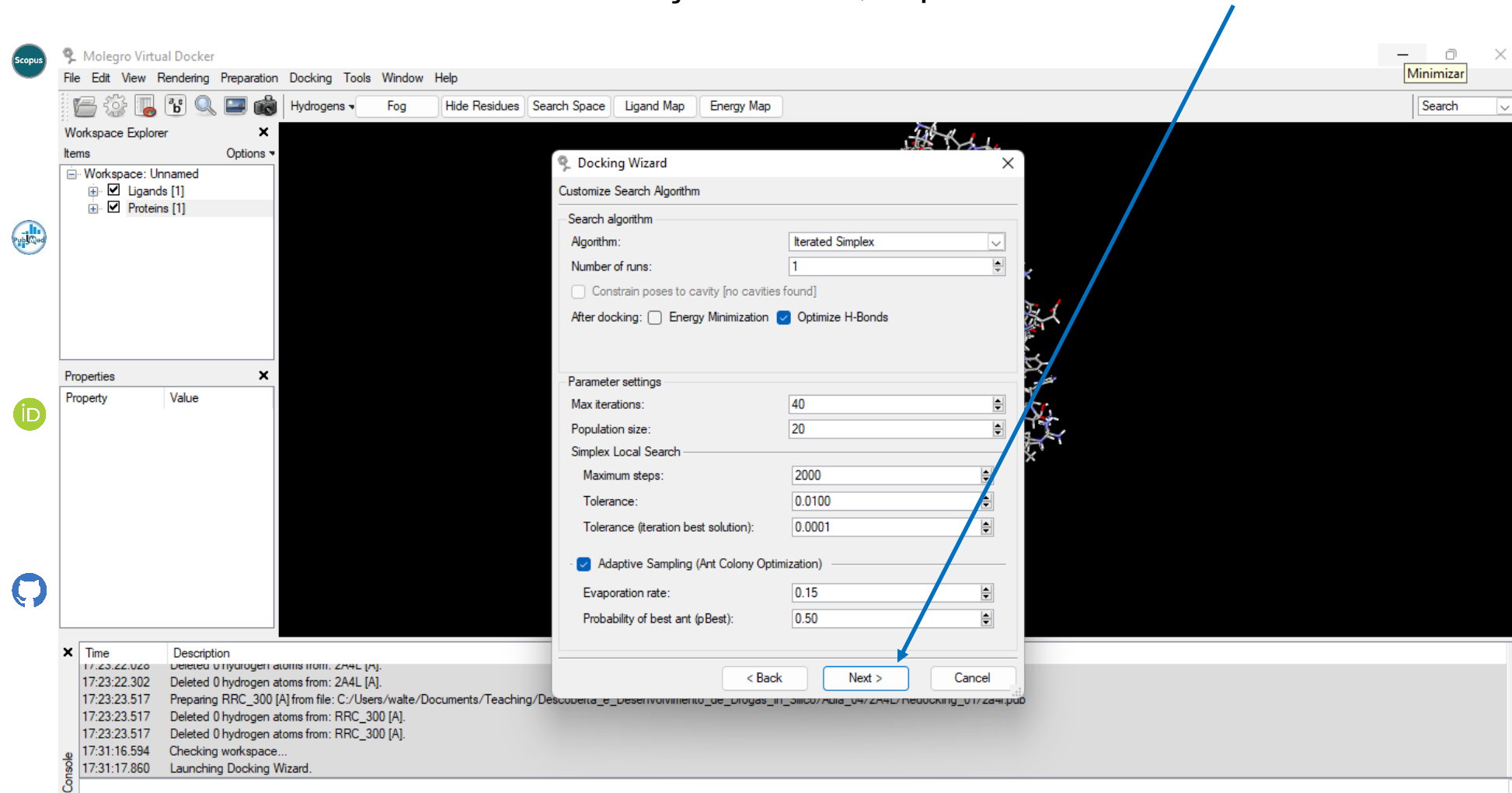
- Na nova janela, escolhemos a função escore (Score) *PLANTS Score* e definimos o raio (*Radius*) como 15 Å. O raio define a região da proteína onde procuraremos posicionar o ligante na proteína. Em seguida clicamos no botão *Next*.



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

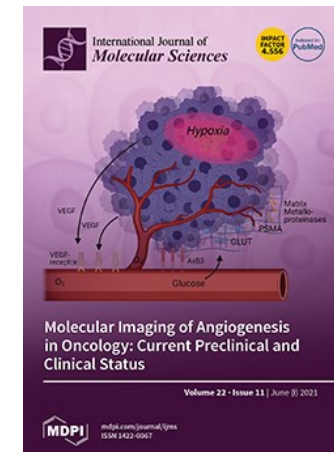
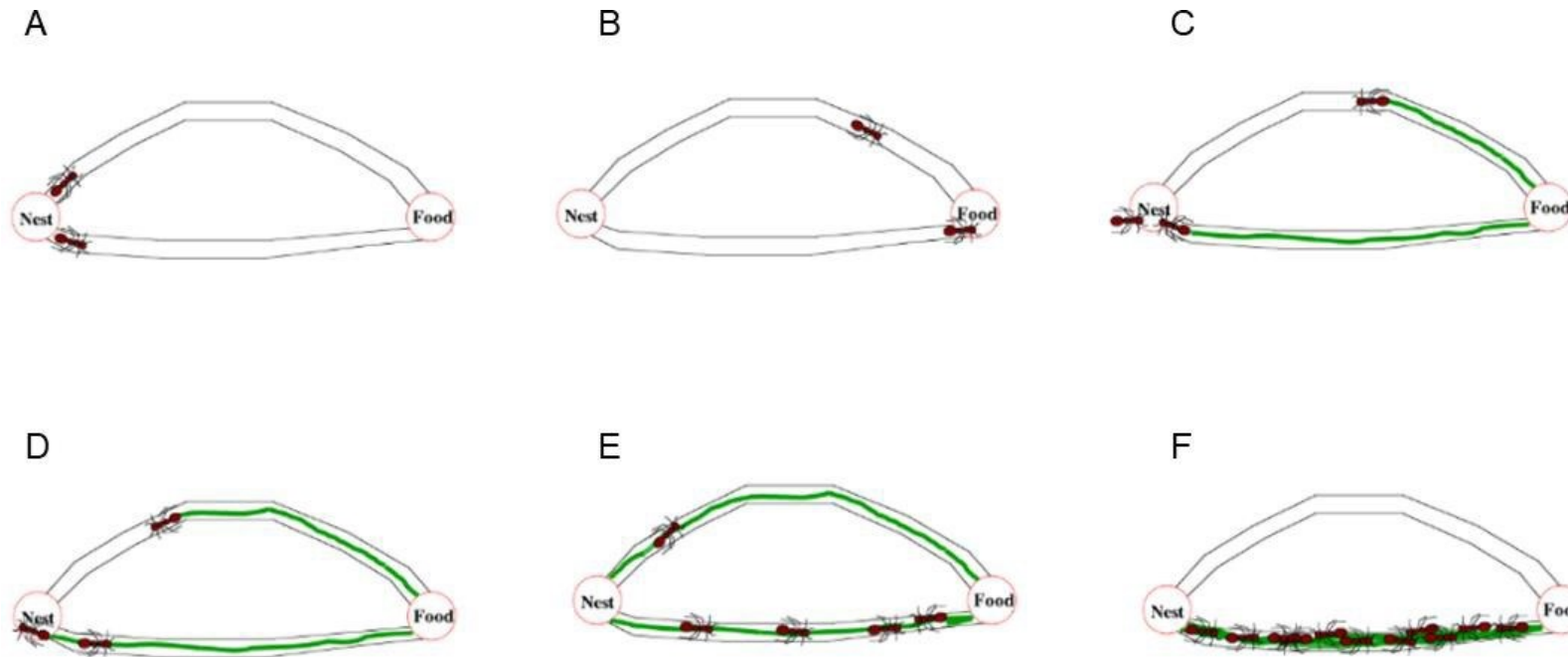
- Nesta etapa definimos o algoritmo de busca (*Search algorithm*), ou seja, como o programa irá procurar a posição do ligante no sítio ativo da enzima. Escolhemos o algoritmo de otimização das formigas (*Ant Colony Optimization*). Definimos o número máximo de iterações em 40, depois clicamos no *Next*.



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

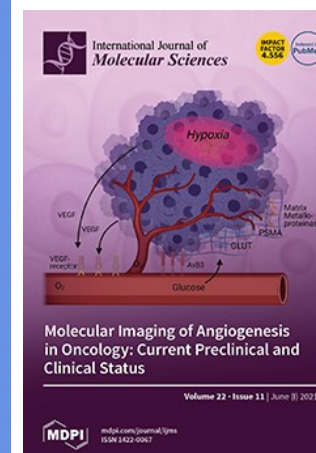
- Na figura abaixo temos dois caminhos possíveis para ligar o formigueiro à fonte de alimento, o caminho mais curto recebe um reforço por ter maior número de formigas passando por ele.



Gorgulla C, Çınaroğlu SS, Fischer PD, Fackeldey K, Wagner G, Arthanari H. VirtualFlow Ants-Ultra-Large Virtual Screenings with Artificial Intelligence Driven Docking Algorithm Based on Ant Colony Optimization. Int J Mol Sci. 2021; 22(11):5807.
DOI: [10.3390/ijms22115807](https://doi.org/10.3390/ijms22115807)

Docagem Molecular com o MVD

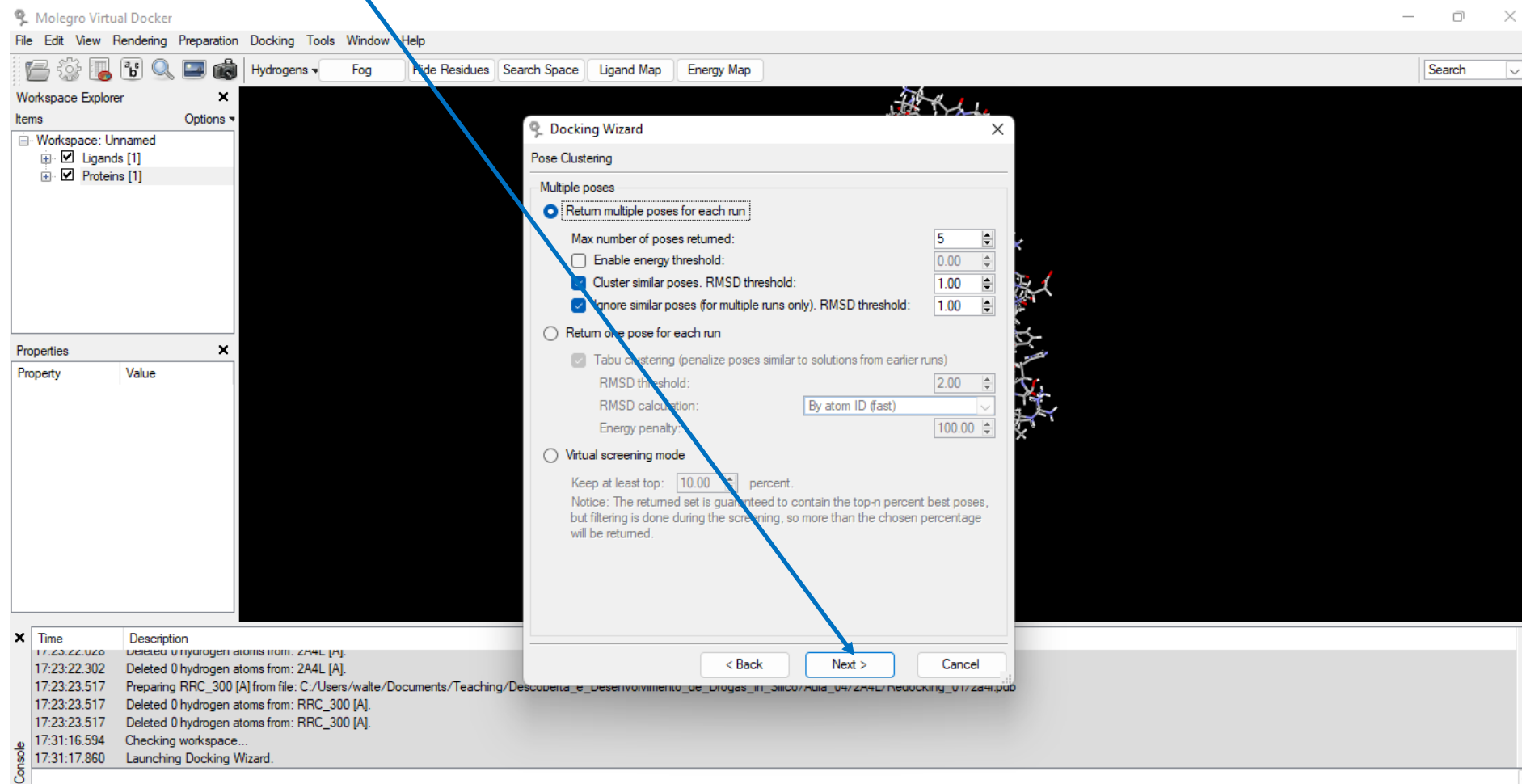
- O algoritmo da otimização da colônia de formigas acha posições possíveis para o encaixe do ligante na proteína.



Gorgulla C, Çınaroğlu SS, Fischer PD, Fackeldey K, Wagner G, Arthanari H. VirtualFlow Ants-Ultra-Large Virtual Screenings with Artificial Intelligence Driven Docking Algorithm Based on Ant Colony Optimization. Int J Mol Sci. 2021; 22(11):5807.
DOI: [10.3390/ijms22115807](https://doi.org/10.3390/ijms22115807)

Docagem Molecular com o MVD

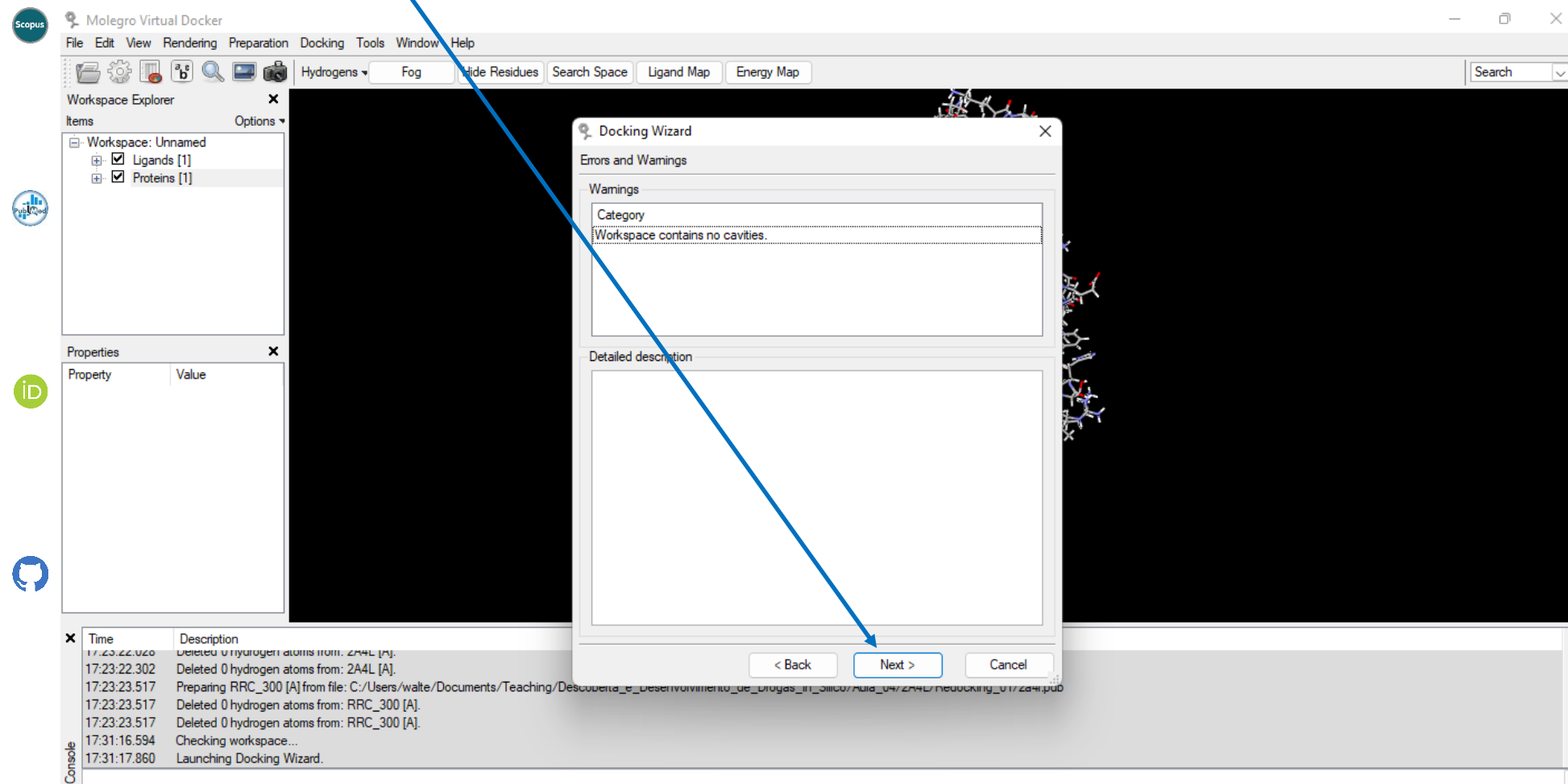
Clicamos no *Next*.



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

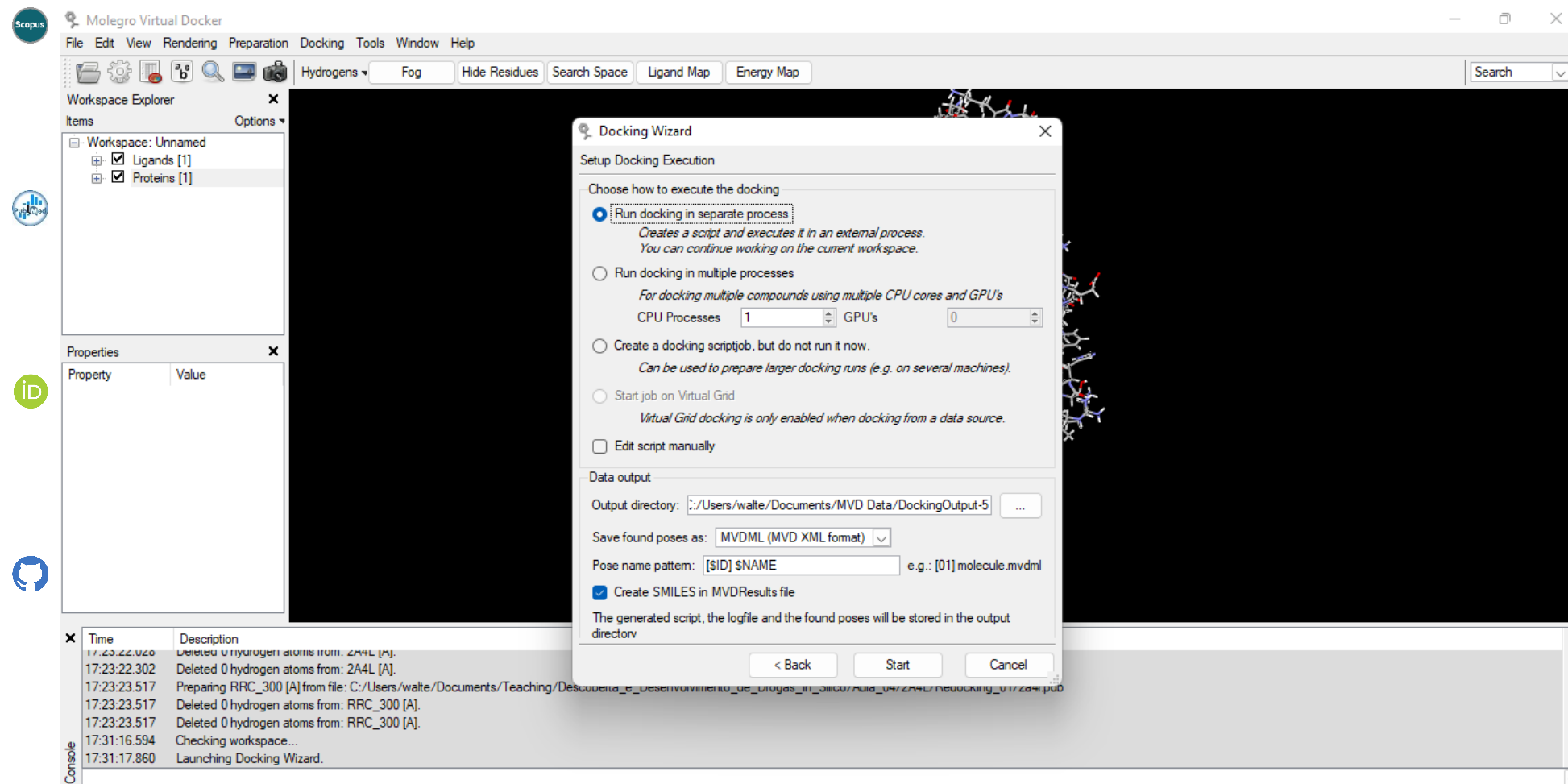
Clicamos no *Next*.



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

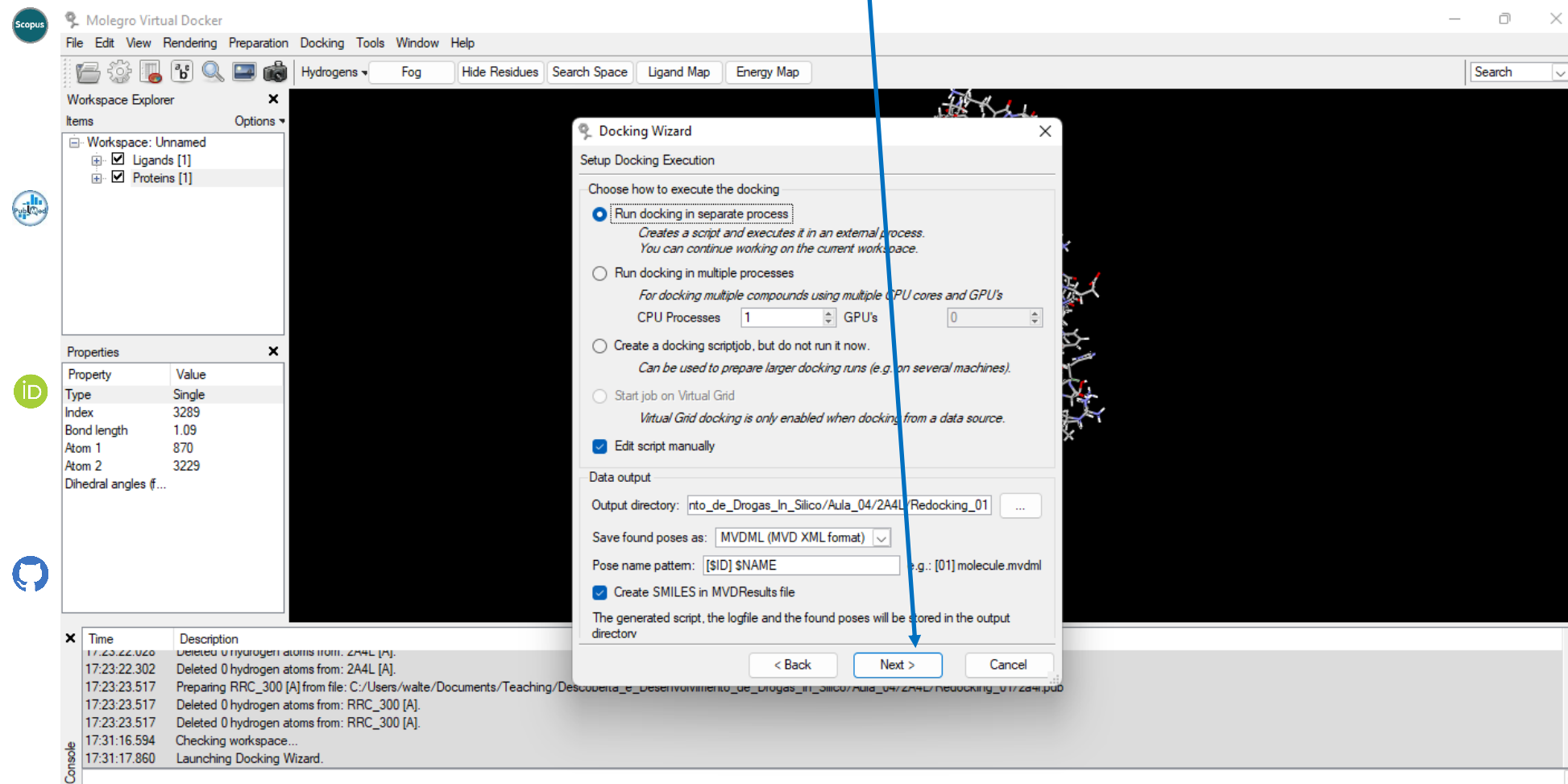
Clicamos na opção *Edit script manually* e no campo *Output directory*. Depois escolhemos a pasta onde serão salvos os resultados (*Output directory*).



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

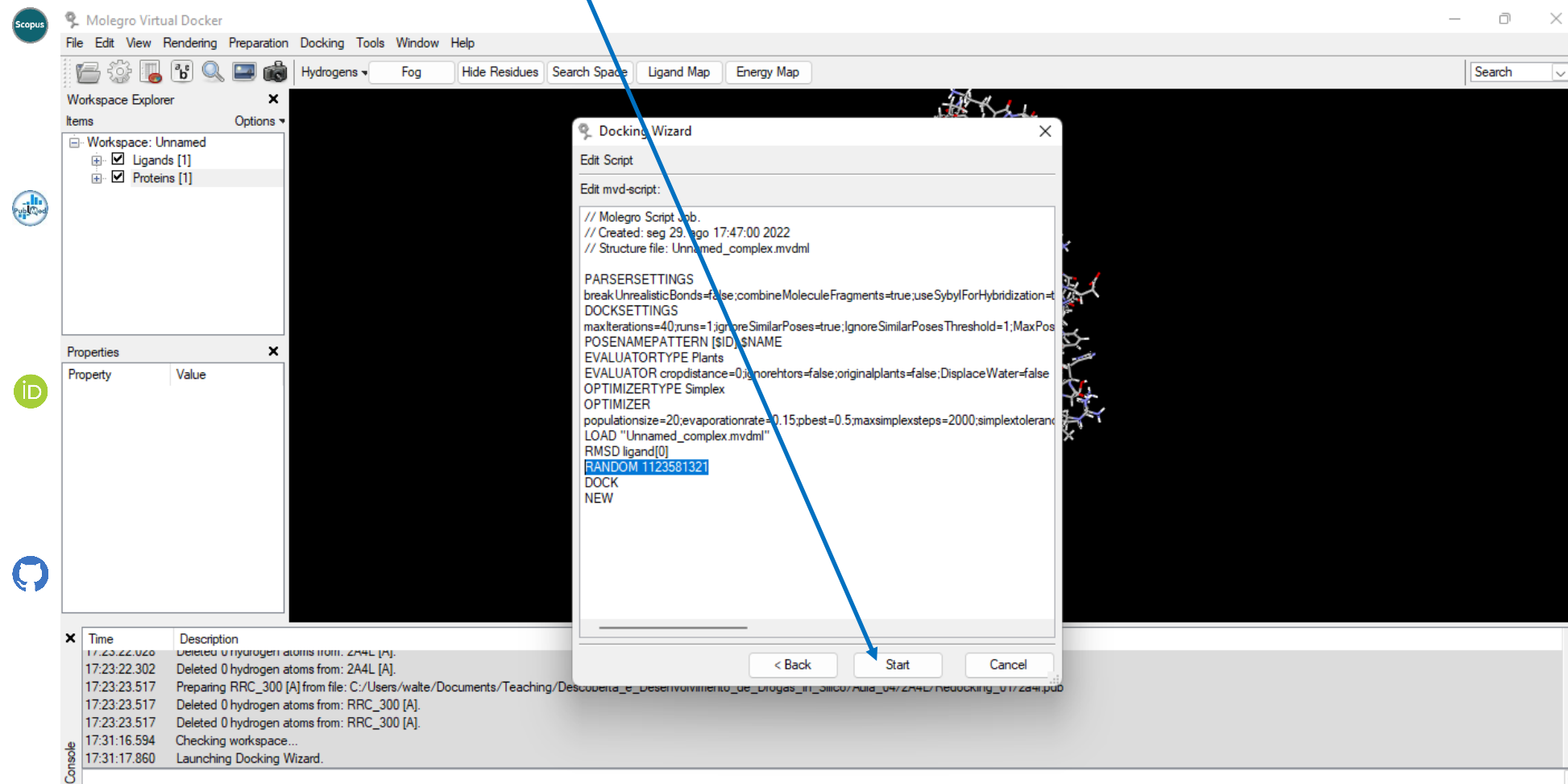
Temos a situação mostrada abaixo. Clicamos *Next*.



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

- No editor de texto, adicionamos uma linha e digitamos ***RANDOM 1123581321***, como em destaque abaixo. Depois clicamos no botão ***Start*** para começarmos a simulação de docagem molecular.



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

Podemos acompanhar a evolução da simulação com a barra verde.

Molegro Virtual Docker Batchjob (Running...)

Batchjob started: seg 29. ago 17:47:59 2022. Elapsed: 00:00:01

Finish (estimated): ?

Working path: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01

Current ligand (1 / 1 runs) 7%

Log Poses (current ligand) Poses (all) Graph Current script

Time	Description
17:47:59.198	Script successfully parsed.
17:47:59.198	Setting Parser Settings: ignoreBonds: false combineFragments: true useSybylForHybridization: true
17:47:59.455	Loaded workspace C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/...
17:47:59.455	Workspace C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocki...
17:47:59.455	Found grid in workspace.
17:47:59.455	Setting evaluator init string: cropdistance=0;ignoretors=false;originalplants=false;DisplaceWater=false
17:47:59.455	You are using Iterated Simplex optimizer
17:47:59.455	Setting optimizer init string: populationSize=20;evaporationRate=0.15;pbest=0.5;maxsimplexSteps=2000;simplextolerance=0.01;simplext...
17:47:59.455	The random seed used for this session is: 1123581321
17:47:59.455	Optimizer: Iterated Simplex params: populationSize=20, cavity=No, evaporationRate=0.15, pBest=0.5, iterationsDBupdate=5, maxSim...
17:47:59.471	Evaluator: Version: PLP CropDistance: 0 Ignore hydrogens in torsion term: No Use original Plants setup: No Energy offset: -20Evalua...
17:47:59.471	Creating Docking Results file: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_...
17:47:59.487	Docking ligand: RRC_300 [A]
17:47:59.503	Beginning run 1 out of 1.
17:47:59.503	Source Ligand was randomized. This will destroy its original orientation.
17:48:00.268	Found 4 automorphism(s) for RRC_300 [A]

Status: Docking 'RRC_300 [A]' from 'Unnamed_complex.mvdm1'

Pause Stop batchjob

Console

17:31:10.394 C
17:31:17.860 L
17:47:58.599 Preparing docking.
17:47:58.941 Saved copy of current workspace as: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/Unnamed_complex.mvdm1
17:47:58.941 Docking in separate process.
17:47:58.957 Spawning process...
17:47:58.957 Process spawned...

VIVOFIBRA-CBAB
Internet access



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

🌀 Ao final da simulação computacional de docagem molecular, temos a mensagem “Status: Finished”.

Molegro Virtual Docker Batchjob (Finished)

Batchjob started: seg 29. ago 17:47:59 2022. Elapsed: 00:01:11
 Finish (estimated): 17:49:09. Remaining: 23:59:59

Working path: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01
 Current ligand (1 / 1 runs) 100%

Log Poses (current ligand) [5] Poses (all) [5] Graph Current script

Time	Description
17:49:10.970	Saving file: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/...
17:49:10.970	Saved ligand: [03]RRC_300 [A].mvdml RRC_300 [A] -82.6636 -114.888 -94.9819 7.23543 8
17:49:10.986	Saving pose: [04]RRC_300 [A].mvdml
17:49:10.986	Saving file: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/...
17:49:10.986	Saved ligand: [04]RRC_300 [A].mvdml RRC_300 [A] -82.1965 -110.703 -89.1836 2.05504 8
17:49:10.986	Adding output file: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/...
17:49:11.003	Script finished.
17:49:11.020	Import the results file into MVD by:
17:49:11.020	1) selecting "Import Docking Results (*.mvdresults)..." from the file menu
17:49:11.020	2) or dragging and dropping the results file onto the MVD application
17:49:11.020	(Hint: you can drag the icon below onto the main application to inspect the results.)
17:49:11.020	It is safe to close this window now

Results: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/DockingResults.mvdresults

Status: Finished.

Pause Close



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

Agora arrastamos o ícone *Results* para a tela gráfica (tela preta).

Molegro Virtual Docker Batchjob (Finished)

Batchjob started: seg 29. ago 17:47:59 2022. Elapsed: 00:01:11
Finish (estimated): 17:49:09. Remaining: 23:59:59

Working path: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01
Current ligand (1 / 1 runs) 100%

Log Poses (current ligand) [5] Poses (all) [5] Graph Current script

Time	Description
17:49:10.970	Saving file: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/Results.mvdresults
17:49:10.970	Saved ligand: [03]RRC_300 [A].mvdml RRC_300 [A] -82.6636 -114.888 -94.9819 7.23543 8
17:49:10.986	Saving poses: [04]RRC_300 [A].mvdml
17:49:10.986	Saving file: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/Results.mvdresults
17:49:10.986	Saved ligand: [04]RRC_300 [A].mvdml RRC_300 [A] -82.1965 -110.703 -89.1836 2.05504 8
17:49:10.986	Adding output file: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/Results.mvdresults
17:49:11.003	Script finished.
17:49:11.020	Import the results file into MVD by:
17:49:11.020	1) selecting "Import Docking Results (*.mvdresults)..." from the file menu
17:49:11.020	2) or dragging and dropping the results file onto the MVD application
17:49:11.020	(Hint: you can drag the icon below onto the main application to inspect the results.)
17:49:11.020	It is safe to close this window now

Results: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/DockingResults.mvdresults

Status: Finished.

Pause Close

Console

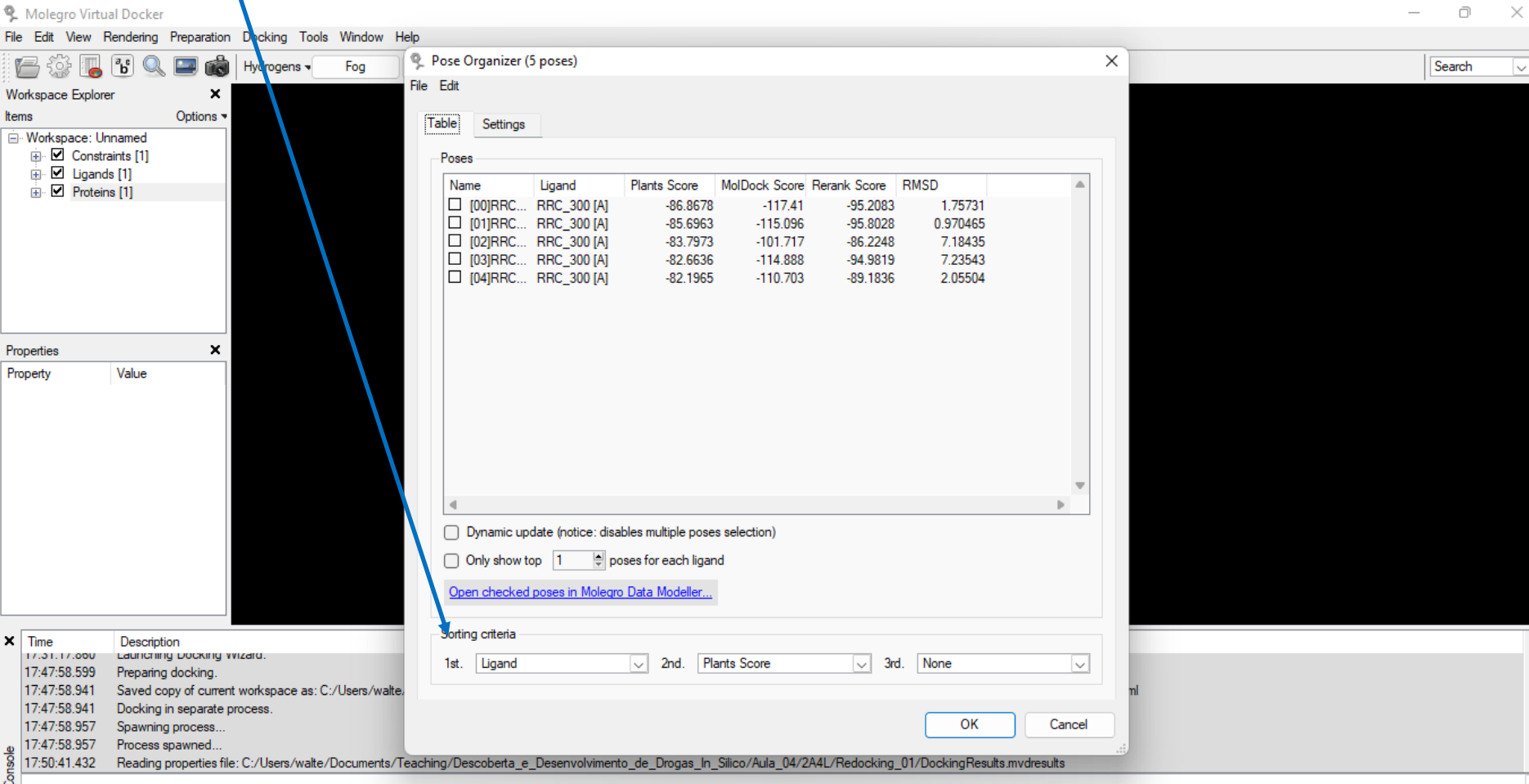
17:31:10.994 C
17:31:17.860 L
17:47:58.599 Preparing docking.
17:47:58.941 Saved copy of current workspace as: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/Unnamed_complex.mvdml
17:47:58.941 Docking in separate process.
17:47:58.957 Spawning process...
17:47:58.957 Process spawned...



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

-  O MVD gera uma planilha com os melhores resultados. Ordenamos os resultados mudando o campo *Sorting criteria* para *PLANTS Score*.



Workspace Explorer

- Workspace: Unnamed
 - Constraints [1]
 - Ligands [1]
 - Proteins [1]

Properties

Property	Value

Console

```

17:51:17.000 Launching Docking wizard.
17:47:58.599 Preparing docking.
17:47:58.941 Saved copy of current workspace as: C:/Users/walte...
17:47:58.941 Docking in separate process.
17:47:58.957 Spawning process...
17:47:58.957 Process spawned...
17:50:41.432 Reading properties file: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/DockingResults.mvd/results
    
```

Pose Organizer (5 poses)

File Edit

Table Settings

Poses

Name	Ligand	Plants Score	MolDock Score	Rerank Score	RMSD
[00]RRC...	RRC_300 [A]	-86.8678	-117.41	-95.2083	1.75731
[01]RRC...	RRC_300 [A]	-85.6963	-115.096	-95.8028	0.970465
[02]RRC...	RRC_300 [A]	-83.7973	-101.717	-86.2248	7.18435
[03]RRC...	RRC_300 [A]	-82.6636	-114.888	-94.9819	7.23543
[04]RRC...	RRC_300 [A]	-82.1965	-110.703	-89.1836	2.05504

☐ Dynamic update (notice: disables multiple poses selection)
☐ Only show top 1 poses for each ligand
[Open checked poses in Molegro Data Modeller...](#)

Sorting criteria

1st. Ligand 2nd. Plants Score 3rd. None

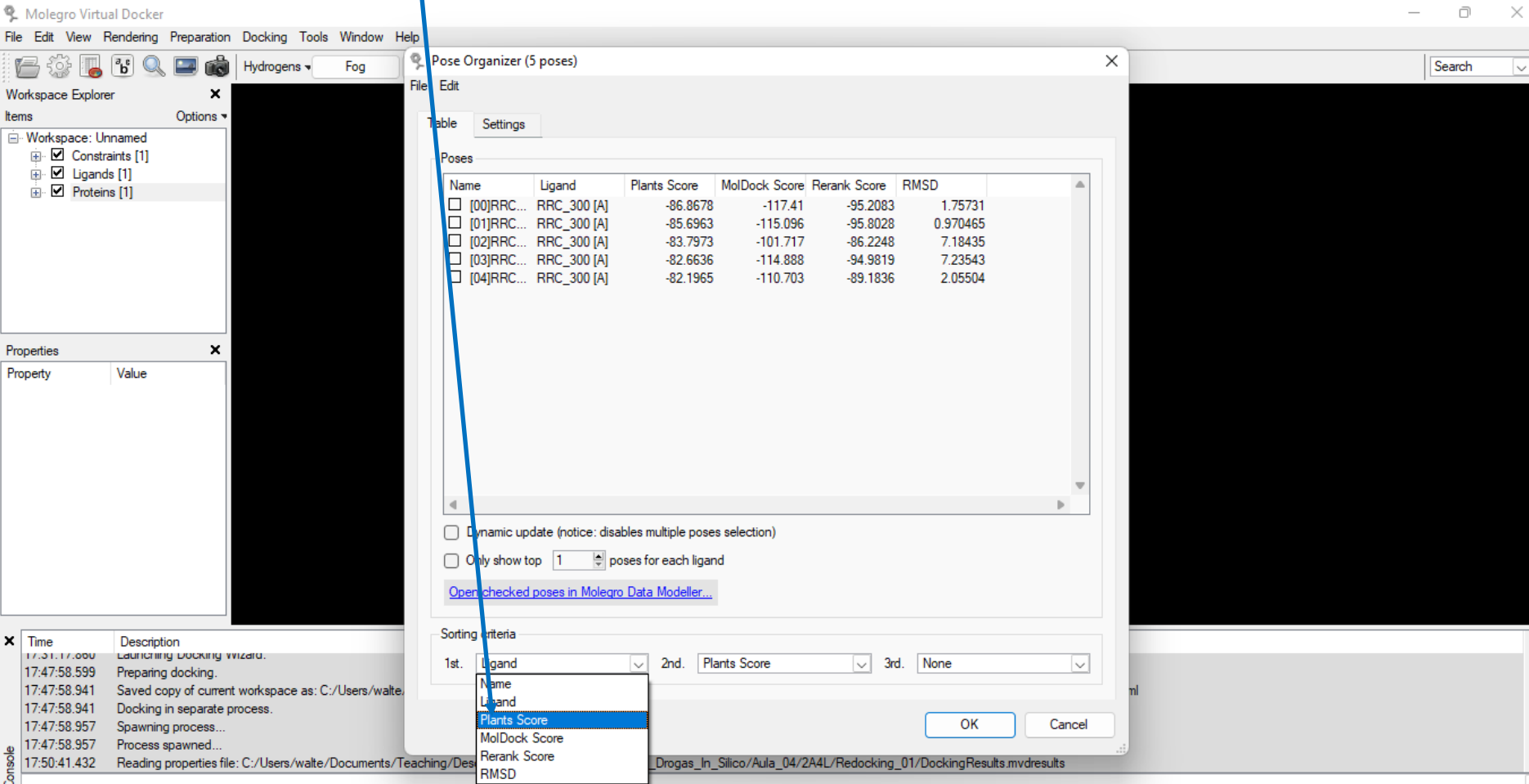
OK Cancel



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

Clicamos na opção *PLANTS Score*.



Workspace Explorer

- Workspace: Unnamed
 - Constraints [1]
 - Ligands [1]
 - Proteins [1]

Properties

Property	Value

Console

Time	Description
17:51:17.000	Launching Docking wizard.
17:47:58.599	Preparing docking.
17:47:58.941	Saved copy of current workspace as: C:/Users/walte...
17:47:58.941	Docking in separate process.
17:47:58.957	Spawning process...
17:47:58.957	Process spawned...
17:50:41.432	Reading properties file: C:/Users/walte/Documents/Teaching/Des...

Pose Organizer (5 poses)

Name	Ligand	Plants Score	MolDock Score	Rerank Score	RMSD
[00]RRC...	RRC_300 [A]	-86.8678	-117.41	-95.2083	1.75731
[01]RRC...	RRC_300 [A]	-85.6963	-115.096	-95.8028	0.970465
[02]RRC...	RRC_300 [A]	-83.7973	-101.717	-86.2248	7.18435
[03]RRC...	RRC_300 [A]	-82.6636	-114.888	-94.9819	7.23543
[04]RRC...	RRC_300 [A]	-82.1965	-110.703	-89.1836	2.05504

Sorting criteria

1st. **Ligand** 2nd. **Plants Score** 3rd. **None**

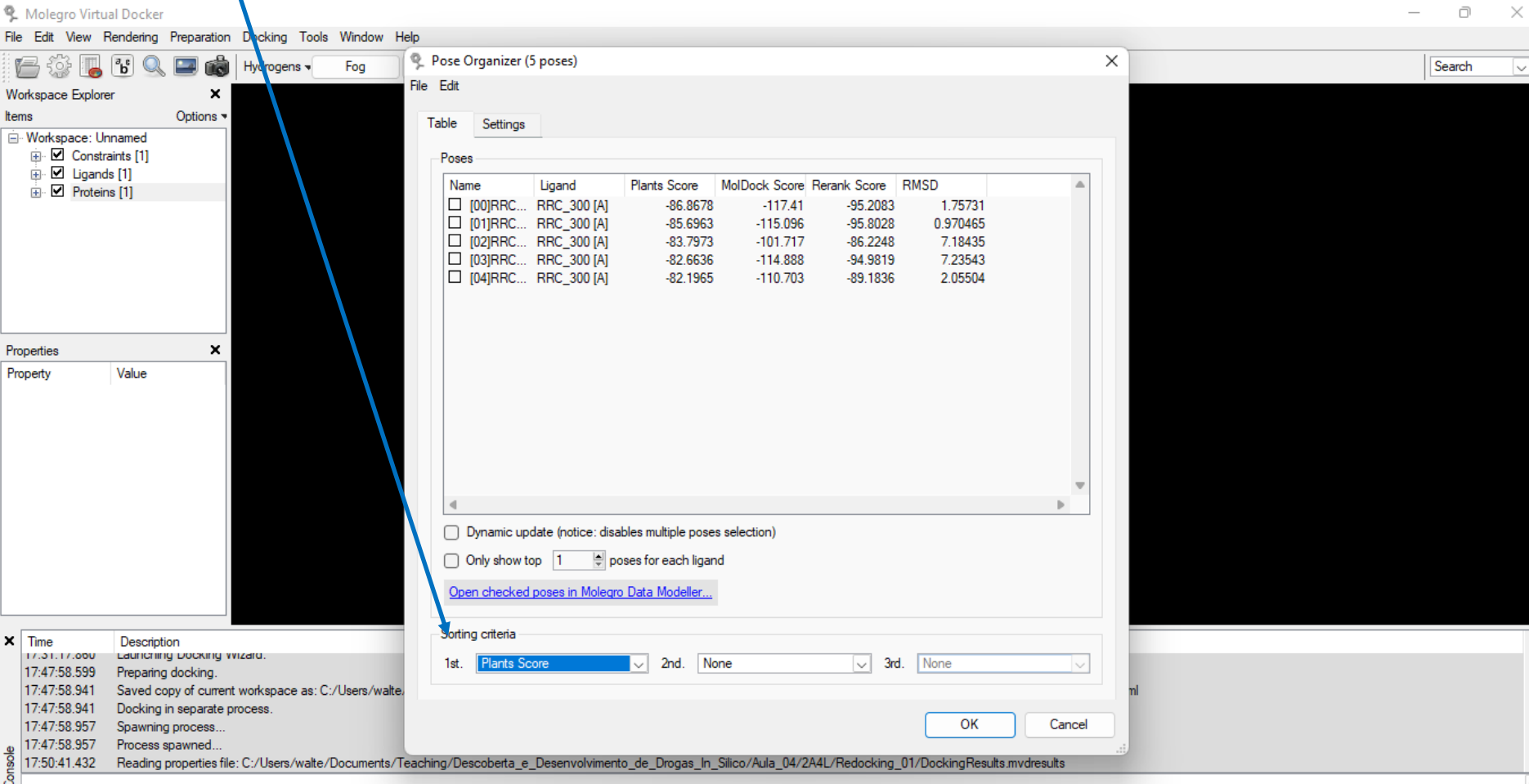
Buttons: OK, Cancel



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

-  O MVD gera uma planilha com os melhores resultados. Ordenamos os resultados mudando o campo *Sorting criteria* para *PLANTS Score*.



Molegro Virtual Docker

File Edit View Rendering Preparation Docking Tools Window Help

Workspace Explorer

Items Options

Workspace: Unnamed

- ☒ Constraints [1]
- ☒ Ligands [1]
- ☒ Proteins [1]

Properties

Property Value

Console

Time Description

17:51:17.000 Launching Docking wizard.

17:47:58.599 Preparing docking.

17:47:58.941 Saved copy of current workspace as: C:/Users/walte/

17:47:58.941 Docking in separate process.

17:47:58.957 Spawning process...

17:47:58.957 Process spawned...

17:50:41.432 Reading properties file: C:/Users/walte/Documents/Teaching/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/DockingResults.mvd/results

Pose Organizer (5 poses)

File Edit

Table Settings

Poses

Name	Ligand	Plants Score	MolDock Score	Rerank Score	RMSD
☐ [00]RRC...	RRC_300 [A]	-86.8678	-117.41	-95.2083	1.75731
☐ [01]RRC...	RRC_300 [A]	-85.6963	-115.096	-95.8028	0.970465
☐ [02]RRC...	RRC_300 [A]	-83.7973	-101.717	-86.2248	7.18435
☐ [03]RRC...	RRC_300 [A]	-82.6636	-114.888	-94.9819	7.23543
☐ [04]RRC...	RRC_300 [A]	-82.1965	-110.703	-89.1836	2.05504

☐ Dynamic update (notice: disables multiple poses selection)

☐ Only show top 1 poses for each ligand

[Open checked poses in Molegro Data Modeller...](#)

Sorting criteria

1st. **Plants Score** 2nd. None 3rd. None

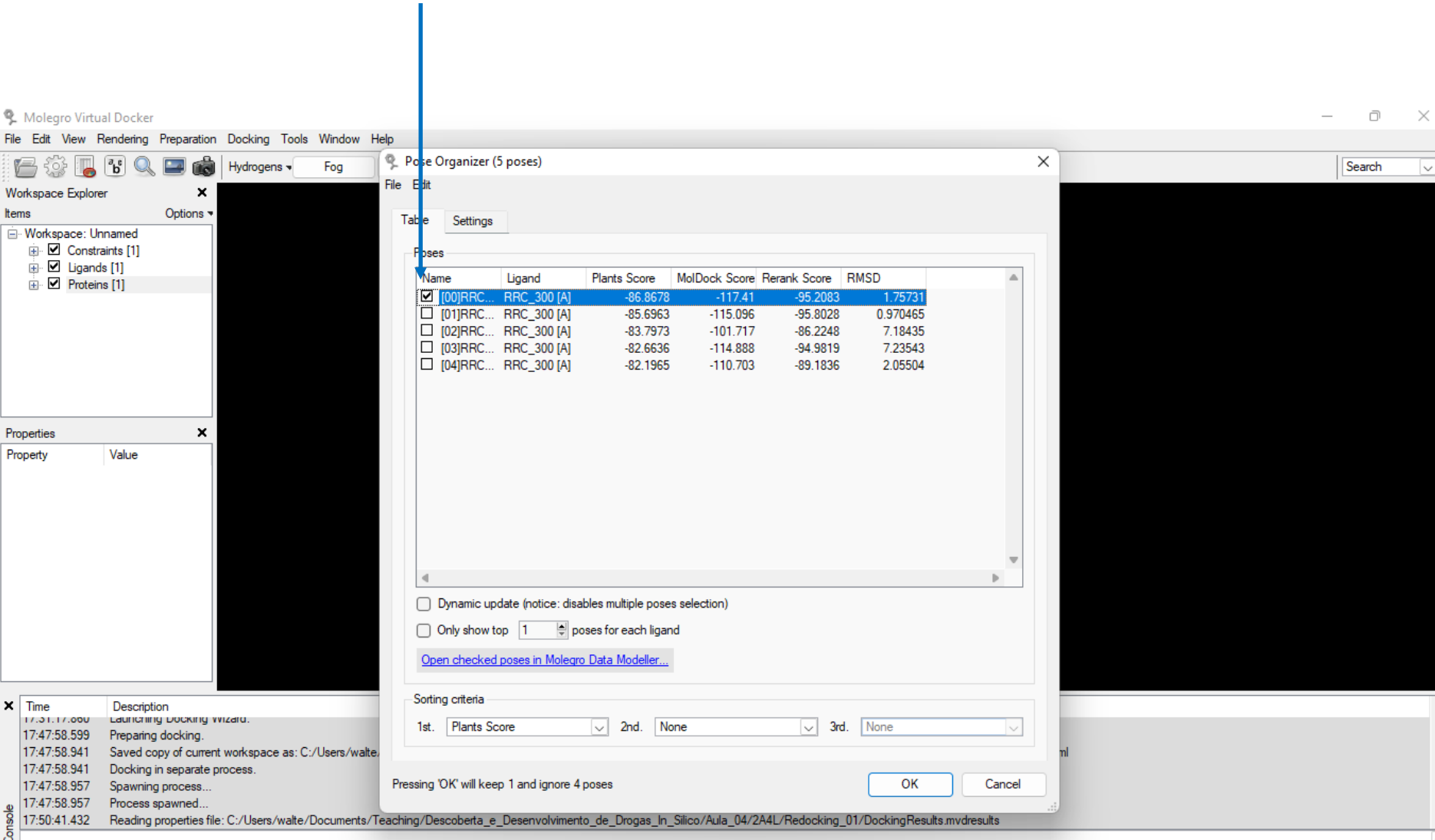
OK Cancel



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

Selecionamos o primeiro resultado.



Molegro Virtual Docker

File Edit View Rendering Preparation Docking Tools Window Help

Hydrogens Fog

Workspace Explorer

Items Options

Workspace: Unnamed

- ☒ Constraints [1]
- ☒ Ligands [1]
- ☒ Proteins [1]

Properties

Property	Value

Console

Time	Description
17:51:17.000	Launching Docking wizard.
17:47:58.599	Preparing docking.
17:47:58.941	Saved copy of current workspace as: C:/Users/walte...
17:47:58.941	Docking in separate process.
17:47:58.957	Spawning process...
17:47:58.957	Process spawned...
17:50:41.432	Reading properties file: C:/Users/walte/Documents/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/DockingResults.mvd/results

Pose Organizer (5 poses)

File Edit

Table Settings

Poses

Name	Ligand	Plants Score	MolDock Score	Rerank Score	RMSD
☒ [00]RRC...	RRC_300 [A]	-86.8678	-117.41	-95.2083	1.75731
☐ [01]RRC...	RRC_300 [A]	-85.6963	-115.096	-95.8028	0.970465
☐ [02]RRC...	RRC_300 [A]	-83.7973	-101.717	-86.2248	7.18435
☐ [03]RRC...	RRC_300 [A]	-82.6636	-114.888	-94.9819	7.23543
☐ [04]RRC...	RRC_300 [A]	-82.1965	-110.703	-89.1836	2.05504

☐ Dynamic update (notice: disables multiple poses selection)

☐ Only show top 1 poses for each ligand

[Open checked poses in Molegro Data Modeller...](#)

Sorting criteria

1st. Plants Score 2nd. None 3rd. None

Pressing 'OK' will keep 1 and ignore 4 poses

OK Cancel



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

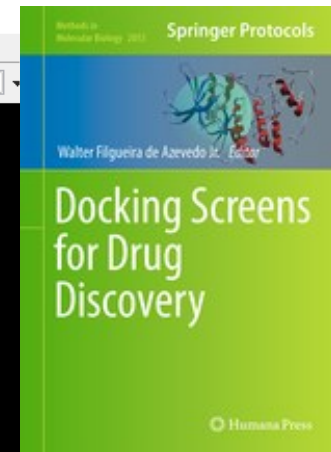
Docagem Molecular com o MVD

O melhor resultado apresenta um RMSD de 1,75731 Å. O RMSD é o *root mean square deviation* (desvio médio quadrático) que indica a distância da posição gerada pelo programa (chamada pose) e a posição experimental. Aceitamos $\text{RMSD} < 2\text{\AA}$.

The screenshot shows the Molegro Virtual Docker (MVD) software interface. The main window displays a 3D molecular model of a protein-ligand complex. Overlaid on this is the 'Pose Organizer (5 poses)' dialog box, which contains a table of docking results. The table lists five poses, with the first pose ([00]RRC... RRC_300 [A]) selected, showing an RMSD of 1.75731 Å. The table also includes columns for Plants Score, MolDock Score, Rerank Score, and RMSD. Below the table, there are checkboxes for 'Dynamic update' and 'Only show top 1 poses for each ligand', and a button to 'Open checked poses in Molegro Data Modeller...'. At the bottom, there are sorting criteria dropdowns and 'OK' and 'Cancel' buttons.

Name	Ligand	Plants Score	MolDock Score	Rerank Score	RMSD
[00]RRC... RRC_300 [A]	RRC_300 [A]	-86.8678	-117.41	-95.2083	1.75731
[01]RRC... RRC_300 [A]	RRC_300 [A]	-85.6963	-115.096	-95.8028	0.970465
[02]RRC... RRC_300 [A]	RRC_300 [A]	-83.7973	-101.717	-86.2248	7.18435
[03]RRC... RRC_300 [A]	RRC_300 [A]	-82.6636	-114.888	-94.9819	7.23543
[04]RRC... RRC_300 [A]	RRC_300 [A]	-82.1965	-110.703	-89.1836	2.05504

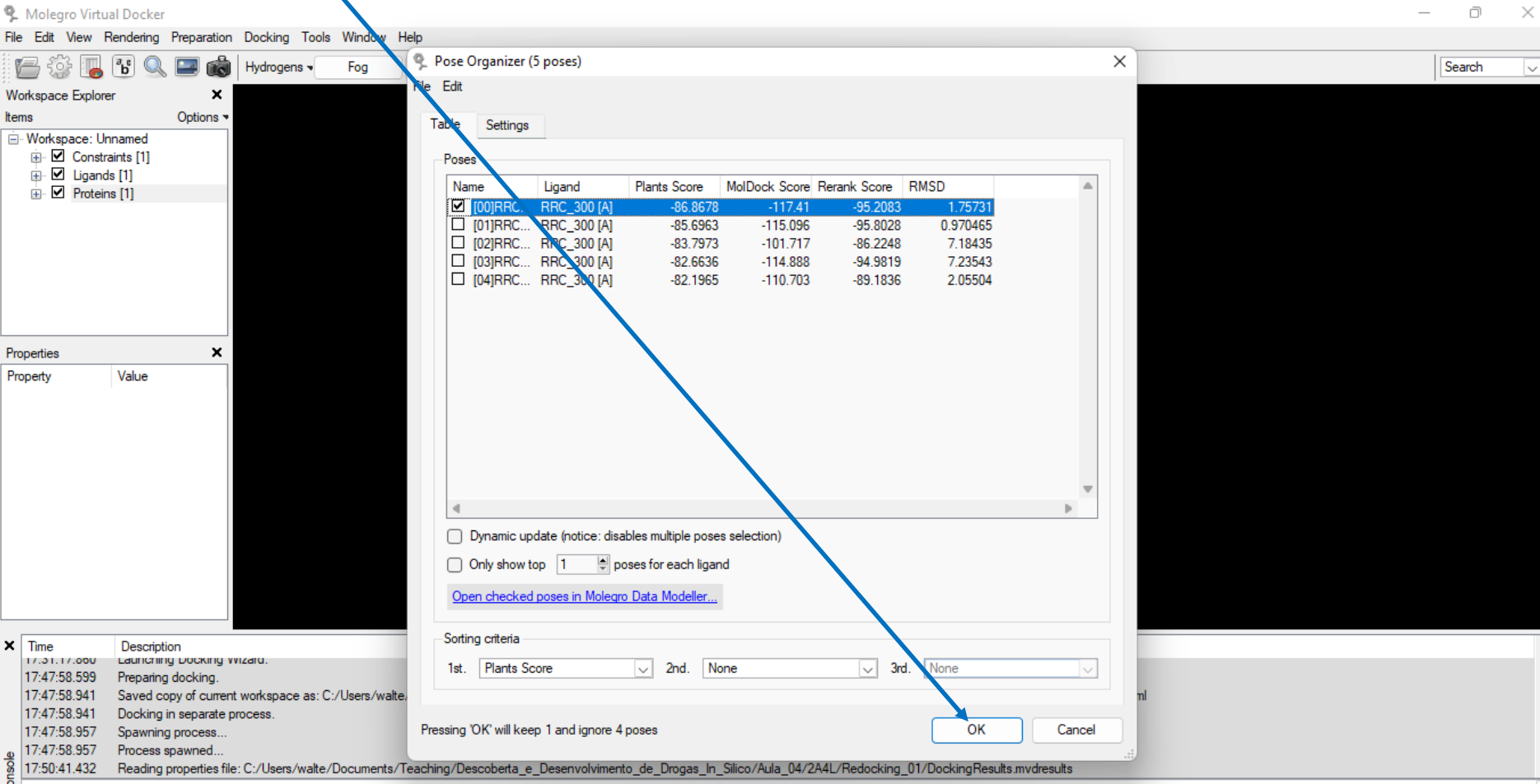
Pressing 'OK' will keep 1 and ignore 4 poses



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. *Methods Mol Biol.* 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

Clicamos OK para visualizar o resultado.



Molegro Virtual Docker

File Edit View Rendering Preparation Docking Tools Window Help

Hydrogens Fog Pose Organizer (5 poses)

Workspace Explorer

Items Options

Workspace: Unnamed

- ☒ Constraints [1]
- ☒ Ligands [1]
- ☒ Proteins [1]

Properties

Property Value

Console

Time Description

17:51:17.000 Launching Docking wizard.

17:47:58.599 Preparing docking.

17:47:58.941 Saved copy of current workspace as: C:/Users/walte...

17:47:58.941 Docking in separate process.

17:47:58.957 Spawning process...

17:47:58.957 Process spawned...

17:50:41.432 Reading properties file: C:/Users/walte/Documents/Descoberta_e_Desenvolvimento_de_Drogas_In_Silico/Aula_04/2A4L/Redocking_01/DockingResults.mvd/results

Poses

Name	Ligand	Plants Score	MolDock Score	Rerank Score	RMSD
☒ [00]RRC...	RRC_300 [A]	-86.8678	-117.41	-95.2083	1.75731
☐ [01]RRC...	RRC_300 [A]	-85.6963	-115.096	-95.8028	0.970465
☐ [02]RRC...	RRC_300 [A]	-83.7973	-101.717	-86.2248	7.18435
☐ [03]RRC...	RRC_300 [A]	-82.6636	-114.888	-94.9819	7.23543
☐ [04]RRC...	RRC_300 [A]	-82.1965	-110.703	-89.1836	2.05504

☐ Dynamic update (notice: disables multiple poses selection)

☐ Only show top 1 poses for each ligand

[Open checked poses in Molegro Data Modeller...](#)

Sorting criteria

1st. Plants Score 2nd. None 3rd. None

Pressing 'OK' will keep 1 and ignore 4 poses

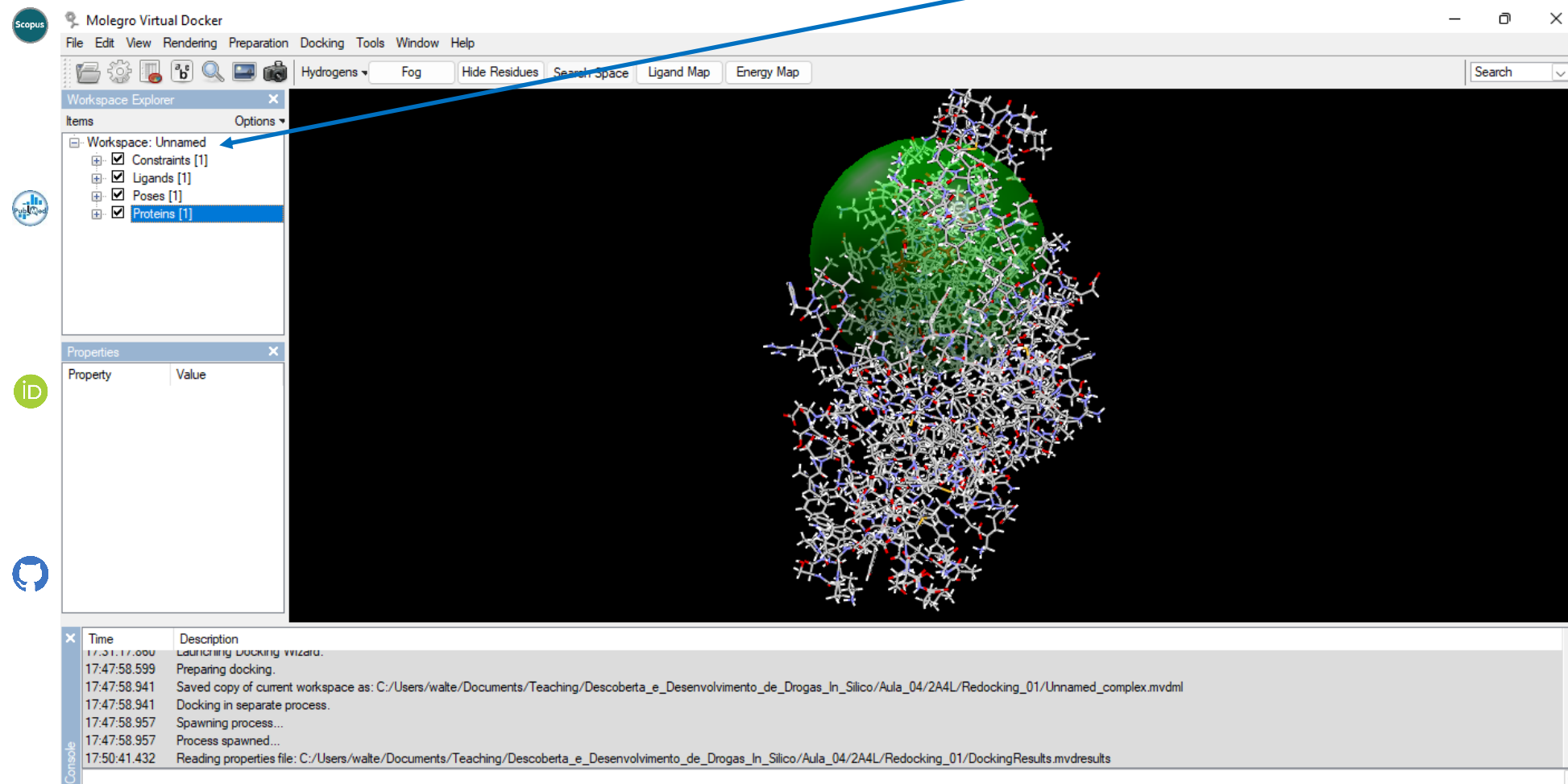
OK Cancel



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

- 
 Temos o resultado da simulação de docagem molecular na tela gráfica. Para facilitar a visualização dos resultados de docagem molecular, deixamos só selecionados o ligante e a pose no *Workspace*.



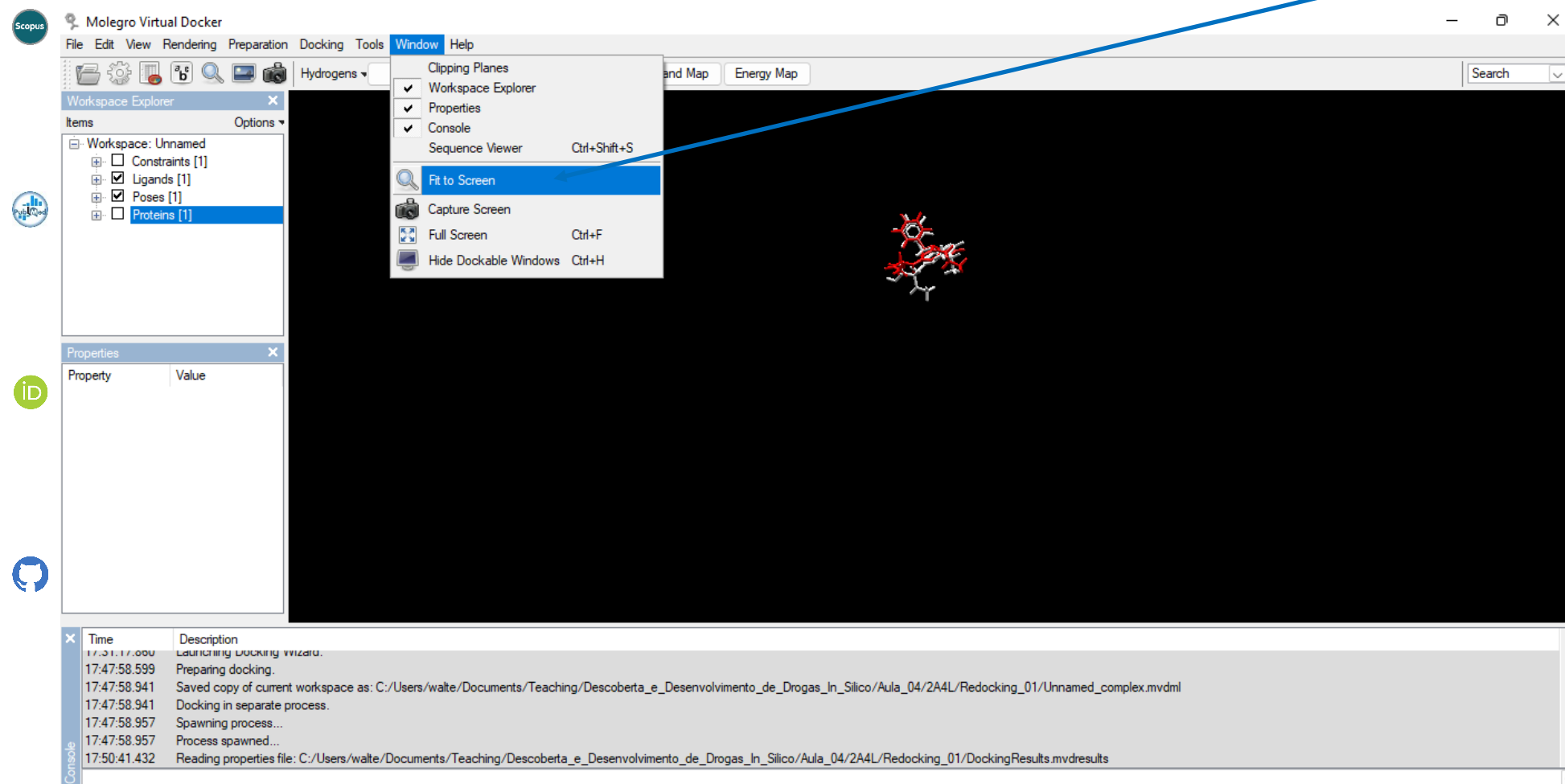
Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

- 



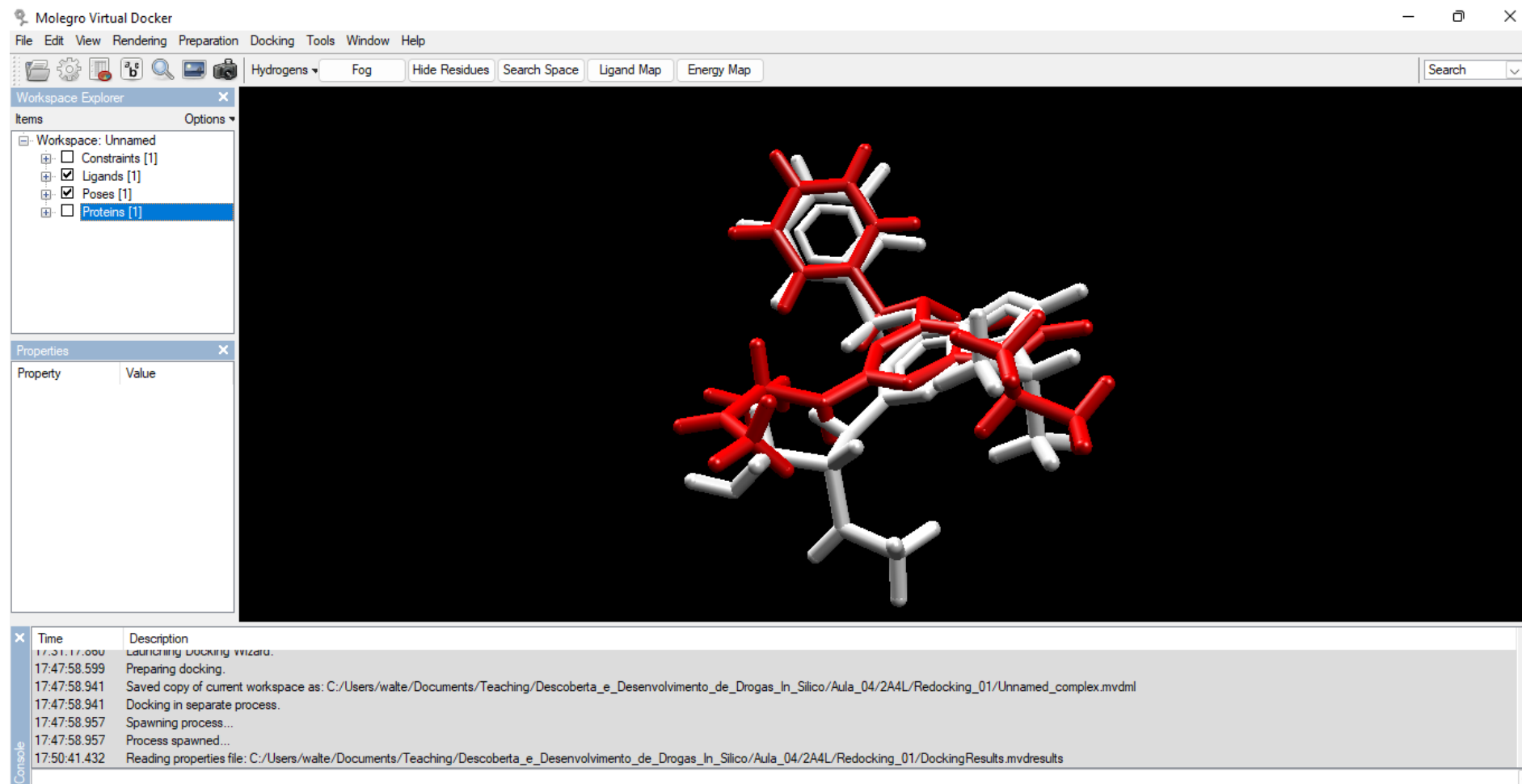
 O resultado da docagem está na tela gráfica. Para centralizar a visualização, clicamos em *Window->Fit to Screen*, como indicado abaixo.



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD

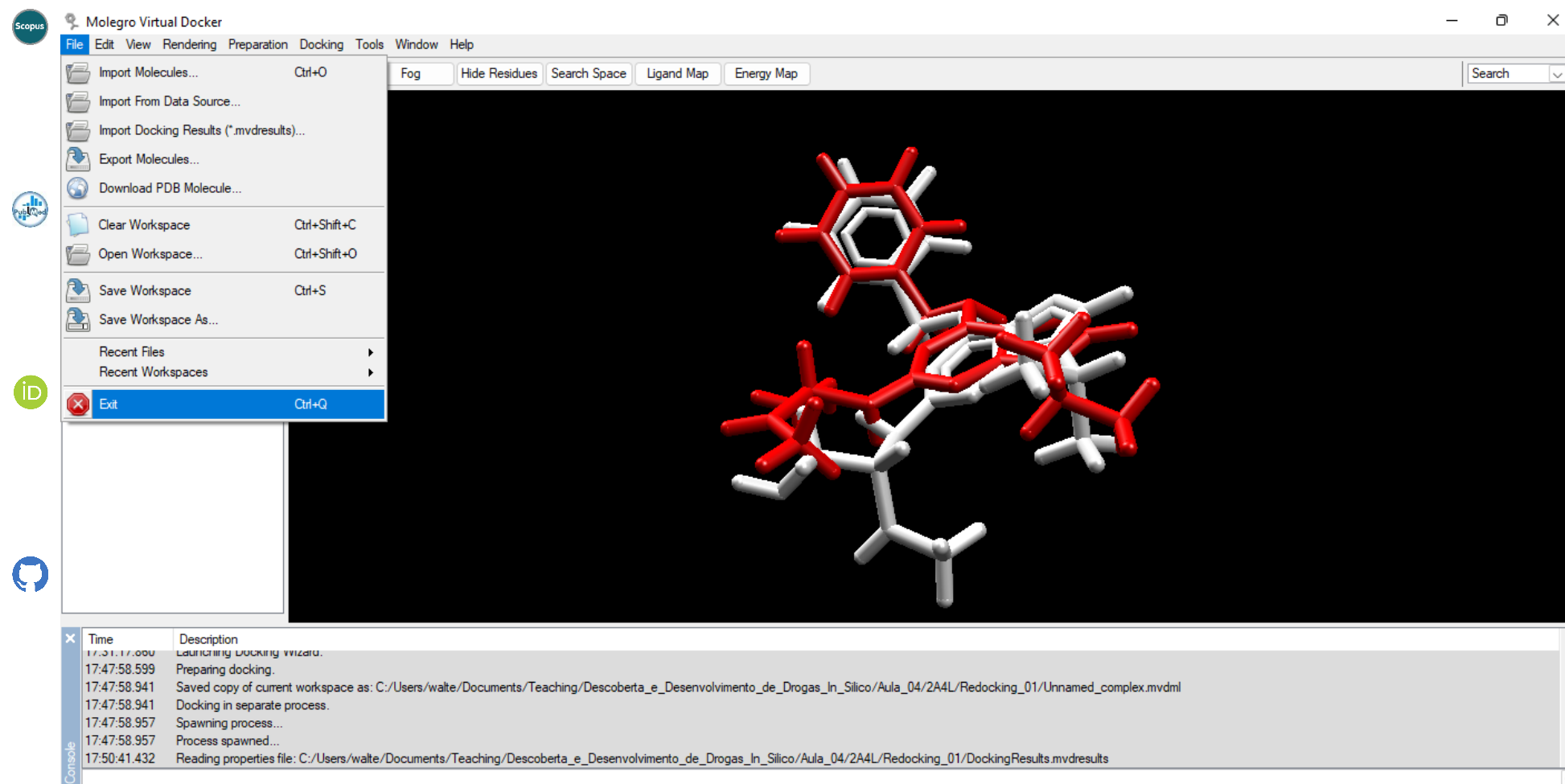
Em branco temos a posição experimental do ligante e em vermelho a pose (gerado pelo programa). Vemos a concordância entre as duas posições. Assim, podemos usar este protocolo de docagem molecular para buscar um novo ligante.



Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

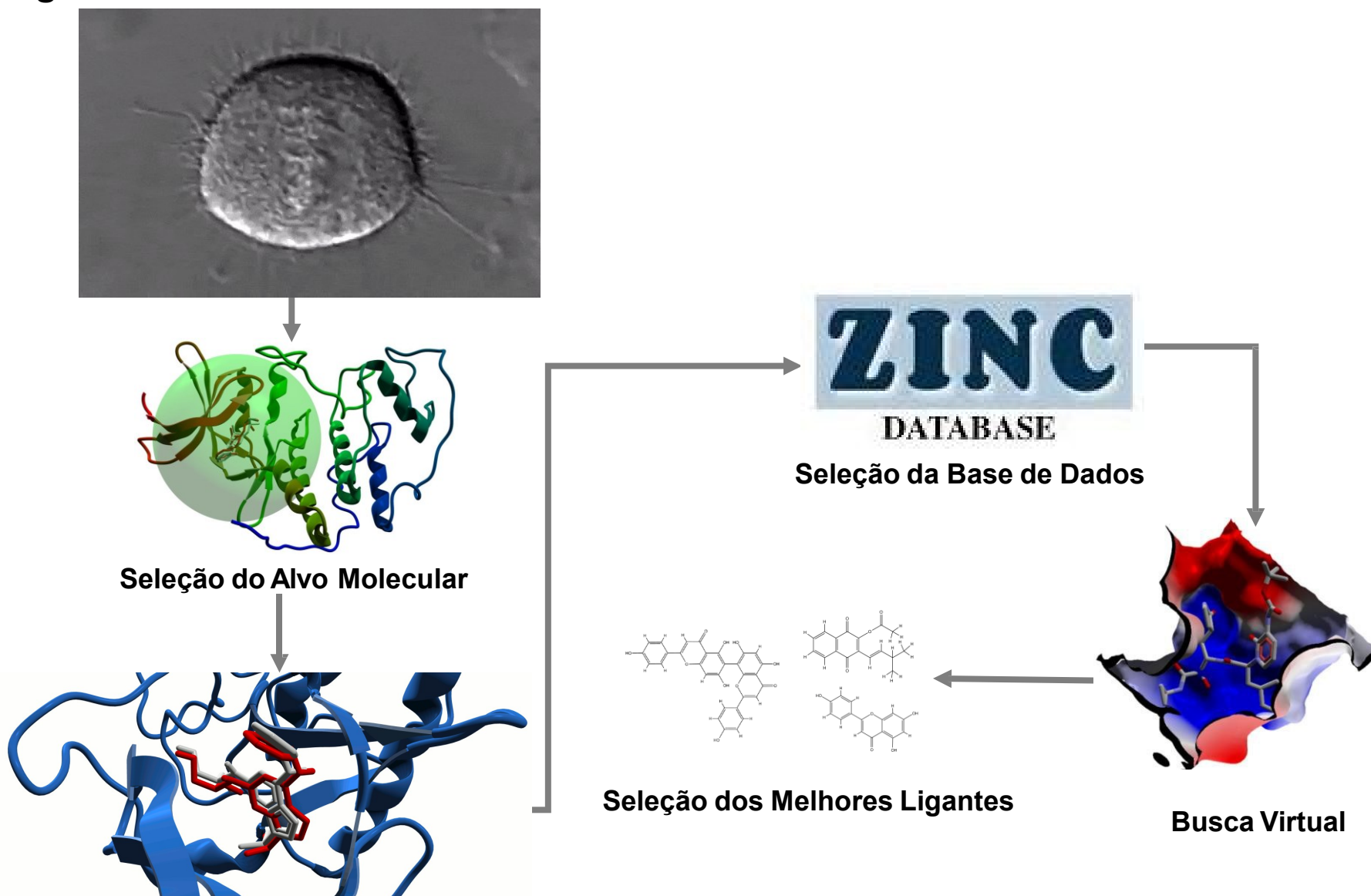
Docagem Molecular com o MVD

Para encerrar a sessão, clicamos em *File->Exit*, como indicado abaixo. Depois clicamos na opção Yes.

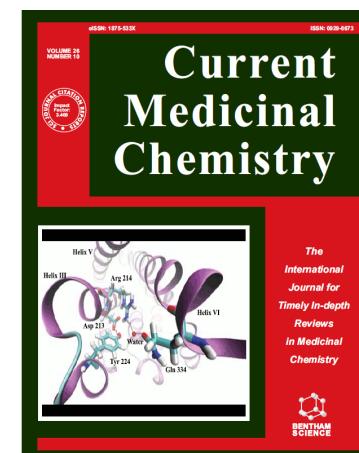


Referência: Bitencourt-Ferreira G, de Azevedo WF Jr. Molegro Virtual Docker for Docking. Methods Mol Biol. 2019;2053:149-167. doi: [10.1007/978-1-4939-9752-7_10](https://doi.org/10.1007/978-1-4939-9752-7_10).

Docagem Molecular com o MVD



Docagem Molecular com o MVD



Referência: Veit-Acosta M, de Azevedo Junior WF. The Impact of Crystallographic Data for the Development of Machine Learning Models to Predict Protein-Ligand Binding Affinity. *Curr Med Chem.* 2021; 28(34):7006-7022. [doi: 10.2174/0929867328666210210121320](https://doi.org/10.2174/0929867328666210210121320)

Docagem Molecular com o MVD

ZINC20

Welcome to ZINC, a free database of commercially-available compounds for virtual screening. ZINC contains over 230 million purchasable compounds in ready-to-dock, 3D formats. ZINC also contains over 750 million purchasable compounds you can search for analogs in under a minute.

ZINC is provided by the [Irwin](#) and [Shoichet](#) Laboratories in the Department of Pharmaceutical Chemistry at the University of California, San Francisco (UCSF). We thank [NIGMS](#) for financial support (GM71896).

To cite ZINC, please reference: Irwin, Tang, Young, Dandarchuluun, Wong, Khurelbaatar, Moroz, Mayfield, Sayle, *J. Chem. Inf. Model* 2020, in press. <https://pubs.acs.org/doi/10.1021/acs.jcim.0c00675>. You may also wish to cite our previous papers: Sterling and Irwin, *J. Chem. Inf. Model*, 2015 <http://pubs.acs.org/doi/abs/10.1021/acs.jcim.5b00559>. Irwin, Sterling, Mysinger, Bolstad and Coleman, *J. Chem. Inf. Model*, 2012 DOI: [10.1021/ci3001277](https://doi.org/10.1021/ci3001277) or Irwin and Shoichet, *J. Chem. Inf. Model*, 2005;45(1):177-82 PDF, DOI.

Getting Started

- Getting Started
- What's New
- About ZINC 20 Resources
- Current Status / In Progress
- Why are ZINC results "estimates"?

Ask Questions

You can use ZINC for **general** questions such as

- How many substances in current clinical trials have PAINS patterns? (150)
- How many natural products have names in ZINC and are not for sale? (9296) get them as SMILES, names and calculated logP

ZINC20 News

- ZINC20 has been released

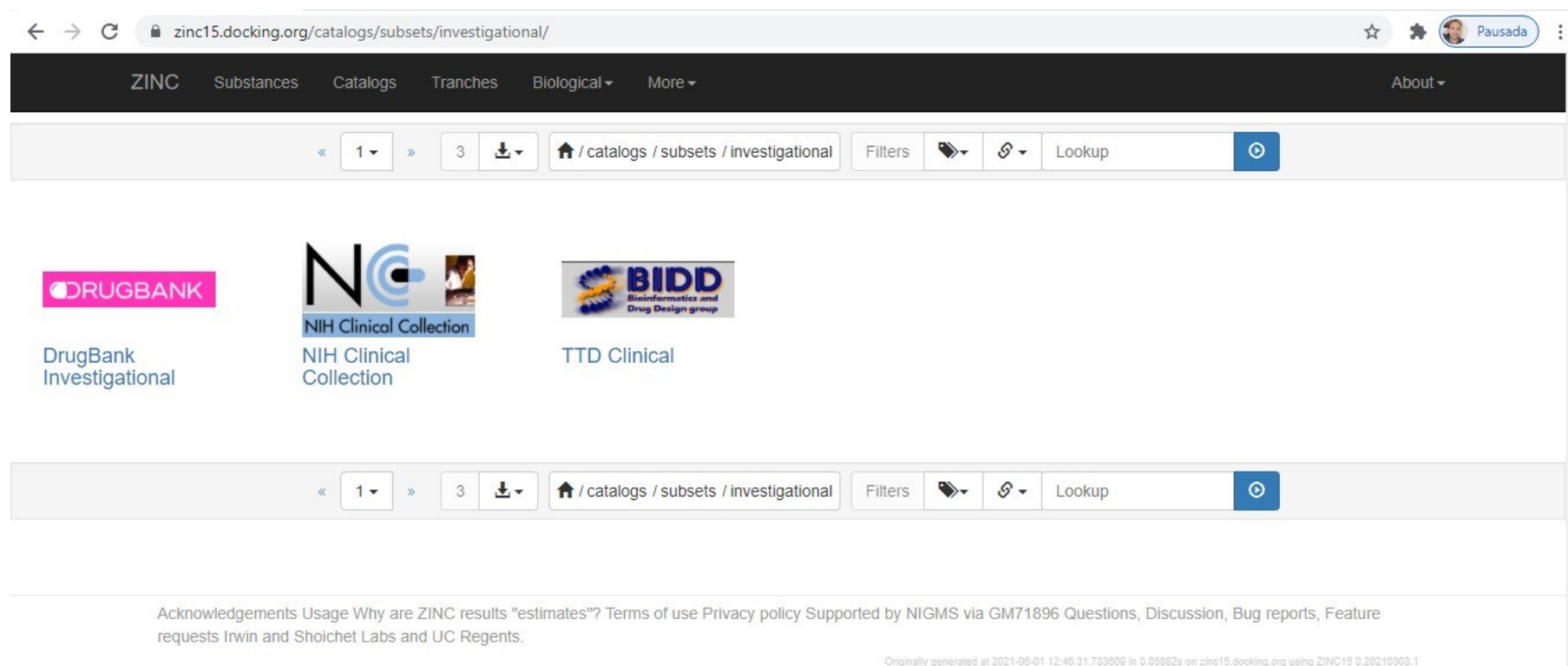
Caveat Emptor: We do not guarantee the quality of any molecule for any purpose and take no responsibility for errors arising from the use of this database. ZINC is provided to the best of our knowledge.



Referência: Irwin JJ, Shoichet BK. ZINC--a free database of commercially available compounds for virtual screening. *J Chem Inf Model*. 2005; 45(1):177-82. doi: [10.1021/ci049714+](https://doi.org/10.1021/ci049714+).

Fonte: <https://zinc.docking.org/>

Docagem Molecular com o MVD



zinc15.docking.org/catalogs/subsets/investigational/

ZINC Substances Catalogs Tranches Biological More About

« 1 » 3 [download icon] / catalogs / subsets / investigational Filters [filter icon] [link icon] Lookup [search icon]

DrugBank Investigational NIH Clinical Collection TTD Clinical

« 1 » 3 [download icon] / catalogs / subsets / investigational Filters [filter icon] [link icon] Lookup [search icon]

Acknowledgements Usage Why are ZINC results "estimates"? Terms of use Privacy policy Supported by NIGMS via GM71896 Questions, Discussion, Bug reports, Feature requests Irwin and Shoichet Labs and UC Regents.

Originally generated at 2021-06-01 12:48:31.733609 in 0.05882s on zinc15.docking.org using ZINC15 0.20210303.1



Referência: Irwin JJ, Shoichet BK. ZINC--a free database of commercially available compounds for virtual screening. J Chem Inf Model. 2005; 45(1):177-82. doi: [10.1021/ci049714+](https://doi.org/10.1021/ci049714+).

Espaço Luz da Ciência



~~Fake News~~

~~Negativismo~~

Espaço Luz da Ciência

Como destacamos, a web é um mar rico de informação científica relevante. Vamos destacar hoje a entrevista do brilhante pesquisador Prof. Miguel Nicolelis. Segue link para um entrevista do Prof. Nicolelis sobre um projeto educacional focado numa escola sem provas e com visão para formação de cidadãos.



Fonte: <https://youtu.be/fhgMGrZK0SU> (Pode assistir toda a entrevista, mas destaco o trecho a partir de 1h28min.

Espaço Luz da Ciência

Os cientistas são considerados influentes se apresentam índice h igual ou maior a 45 (<https://www.sciencenews.org/article/rating-researchers>). Nos EUA e em países que valorizam a educação e a pesquisa, cientistas que atingem índice h de 45 ou acima são convidados para fazer parte da Academia de Ciências do país, este é o caso dos Estados Unidos.

SN Rating Researchers | Science News x +

← → ↺ https://www.sciencenews.org/article/rating-researchers

MATH TREK MATH

Rating Researchers

By Ivars Peterson

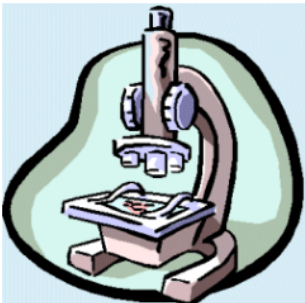
DECEMBER 2, 2005 AT 3:12 PM

✉ f t p v s i

For baseball pitchers, it's the earned run average. For National Football League passers, it's the quarterback rating. In each case, a single number gives some sense of a player's value.

How would you quantify the cumulative impact and relevance of a researcher's scientific work? Furthermore, is there a single number that would usefully characterize a scientist's output?

"In a world of limited resources, such quantification (even if potentially distasteful) is often needed for evaluation and comparison purposes," physicist Jorge E. Hirsch of the University of California, San Diego argues in the Nov. 15 *Proceedings of the National Academy of*



Espaço Luz da Ciência

O [Prof. Nicolelis](#) é um neurocientista que vem revolucionando a ciência com suas descobertas. Eles tem centenas de artigos científicos e um índice h de 7.

SC Nicolelis, Miguel A.L. - Author d

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Duke University School of Medicine, Durham, United States

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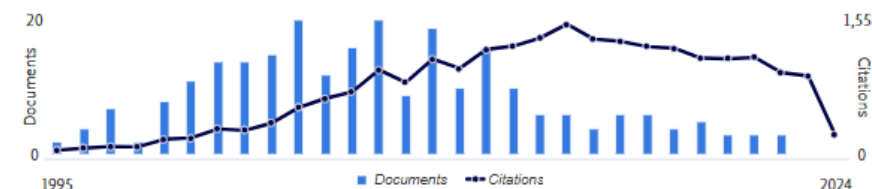
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Year	Documents	Citations
1995	1	0
2000	5	10
2005	15	40
2010	20	80
2015	18	120
2020	10	1500
2024	5	1558

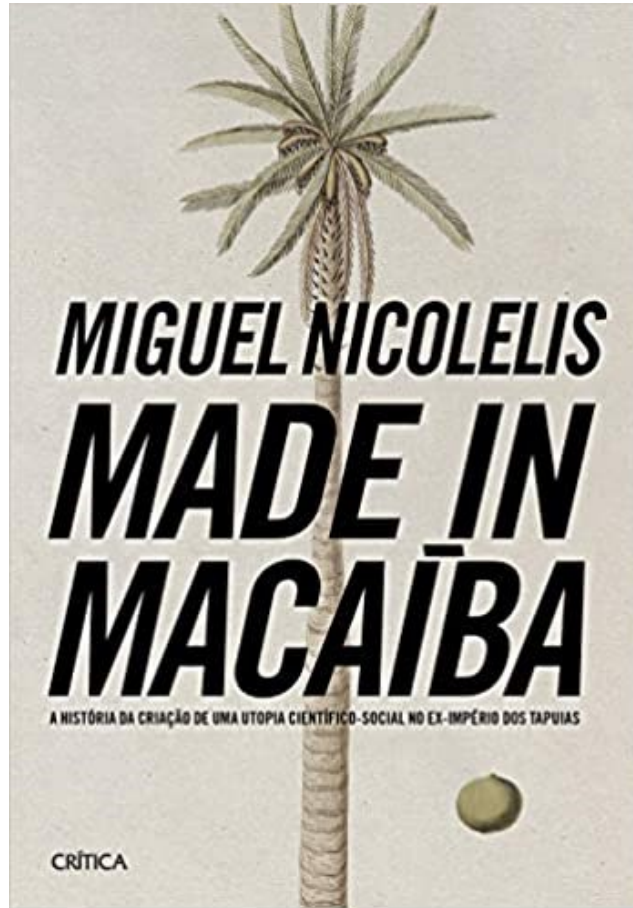
Scopus Preview

Scopus Preview users can only view a limited set of features. Check your institution's access to view all documents and features.

Check access

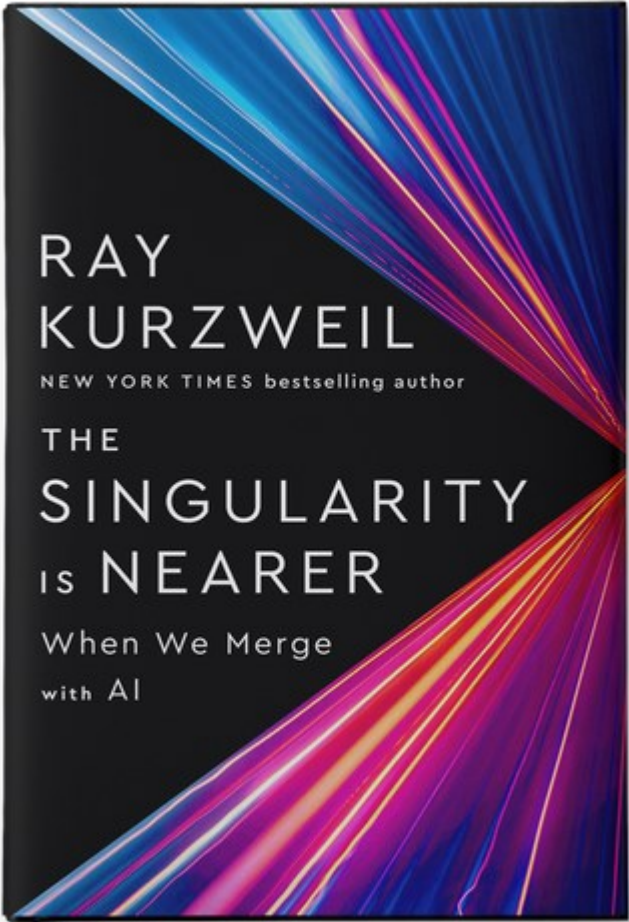
Espaço Luz da Ciência

O Prof. Nicolelis tem diversos livros de divulgação científica, entre eles o indicado abaixo.



Espaço Luz da Ciência

Visitem o site do futurista Ray Kurzweil sobre o livro *The Singularity is Nearer*.



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- Veit-Acosta M, de Azevedo Junior WF. The Impact of Crystallographic Data for the Development of Machine Learning Models to Predict Protein-Ligand Binding Affinity. *Curr Med Chem*. 2021; 28(34):7006-7022.





Que a luz da ciência acabe com
as trevas do negacionismo.