

分子動力學模擬簡介

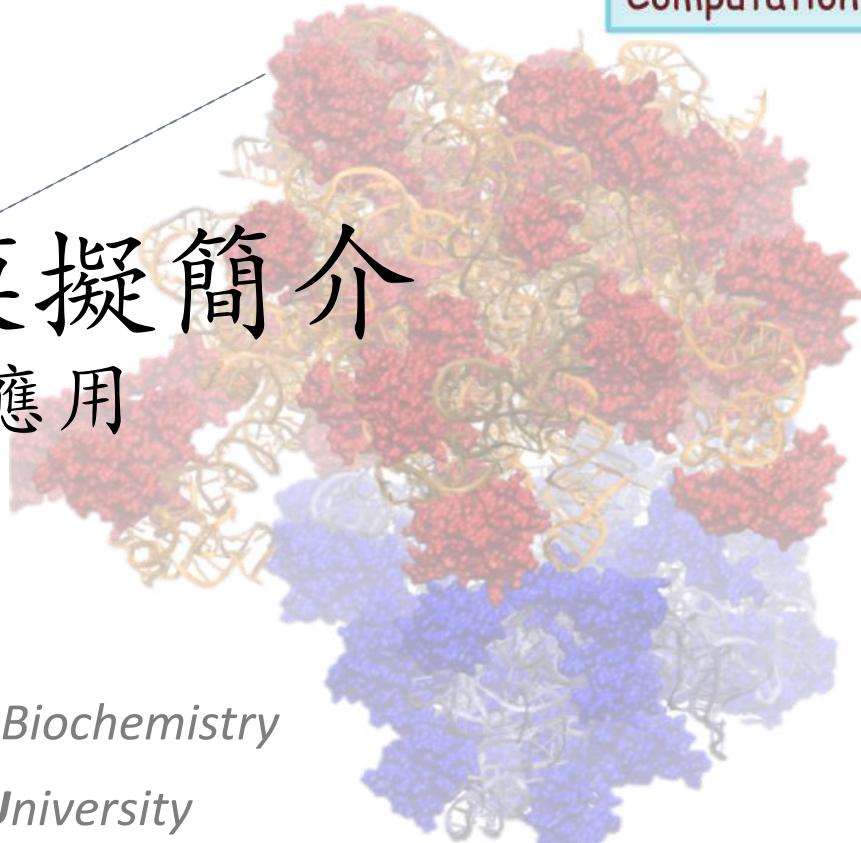
理論與實務應用

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National Chung Cheng University

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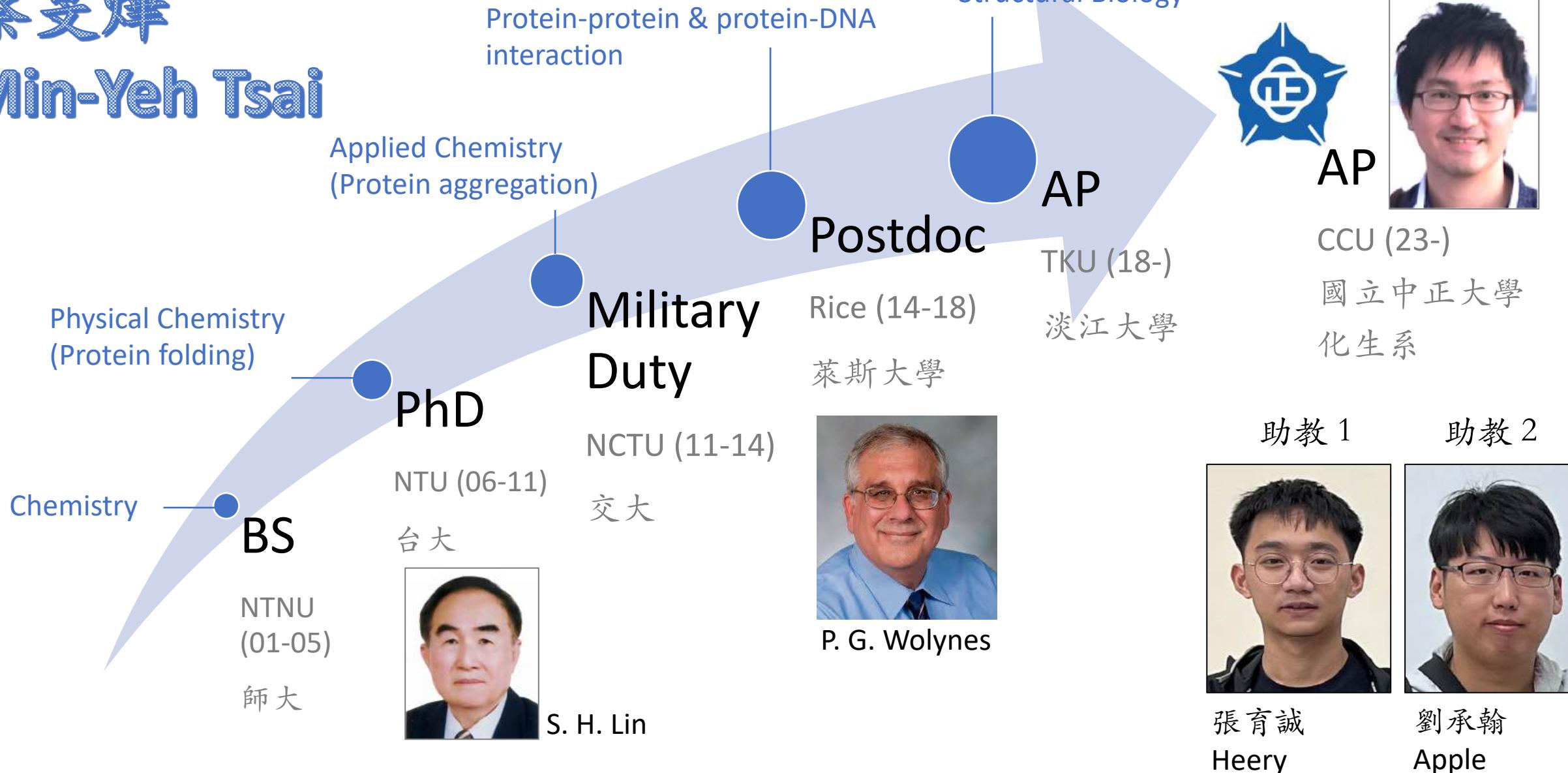


Aug. 26, 2024
@臺大計中

請注意！

此投影片僅用於教學使用，其授權許可證屬於 CC BY-NC（非商業性使用）。

蔡曼燁 Min-Yeh Tsai



這六個小時會學些什麼?

You will learn

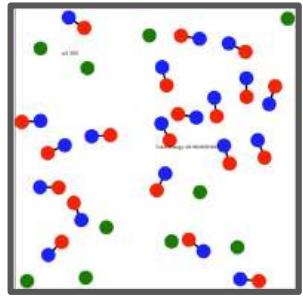
- 分子動力學模擬的ABC
- 從頭快速建立一簡單之粒子模型
- 使用軟體VMD視覺化複雜分子系統
- 使用VMD建立模型以及使用 NAMD 進行動力學模擬
- 模擬設定的輸入/輸出 (I/O)
- 快速建立應用於生物分子、奈米材料體系的 MD 模擬
- 對模擬軌跡進行簡單結構與能量分析
- 了解MD模擬的整個流程，快速找到參考資料

You will NOT learn

- 進階的MD理論
- 分子力場開發
- 建立完全符合您研究上的模擬系統
(一天是不夠的…)
- 成為MD的專家
(Rome wasn't built in a day…)

讓各位對於建立模型與設定動態模擬的工具有初步的認識
→激勵學習分子模擬的種子

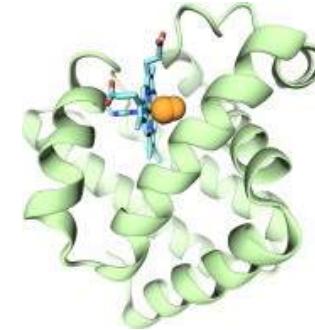
Outline



- I. Simple MD**
- Python
 - JupyterLab

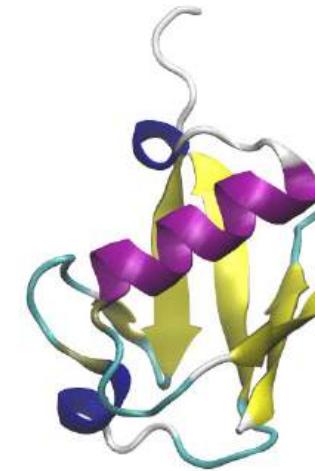


JupyterLab

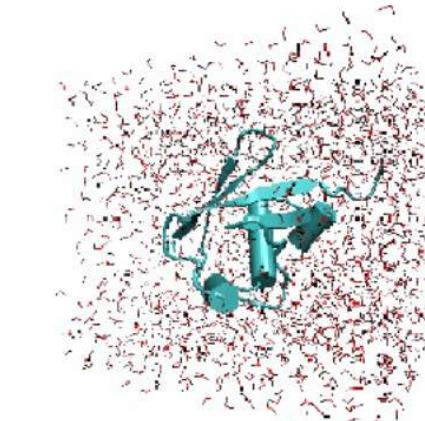


- II. Visualization**
- MolView
 - VMD

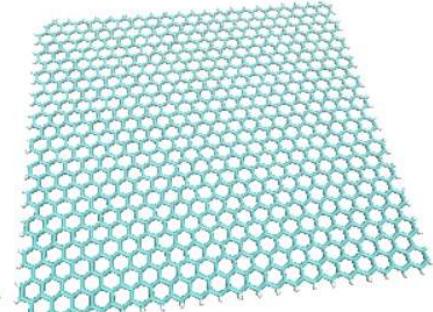
VMD
Visual Molecular Dynamics



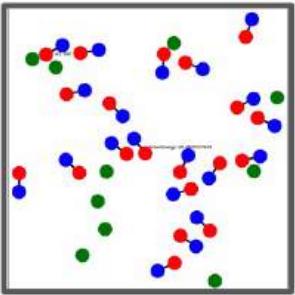
- III. MD (Bio)**
- NAMD/VMD
 - Protein
 - Water



- IV. MD (Nano)**
- NAMD/VMD
 - Graphene
 - Small molecules



NAMD
Scalable Molecular Dynamics



I. Simple MD

- Python
- JupyterLab



JupyterLab

II. Visualization

- MolView
- VMD

Part I (分子動力學模擬ABC)

III. MD (Bio)

- NAMD/VMD

IV. MD (Nano)

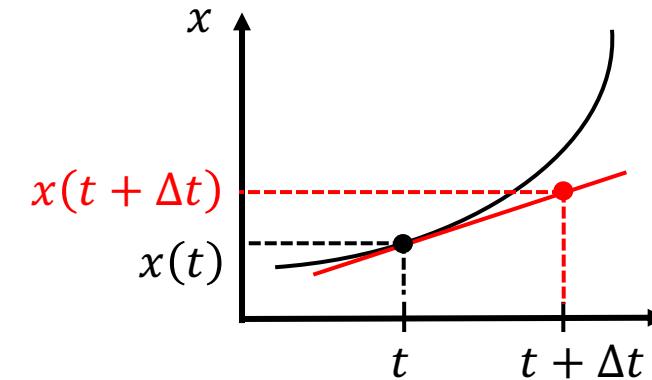
- NAMD/VMD
- Graphene
- Small molecules

預測運動軌跡好比預測未來發生的事

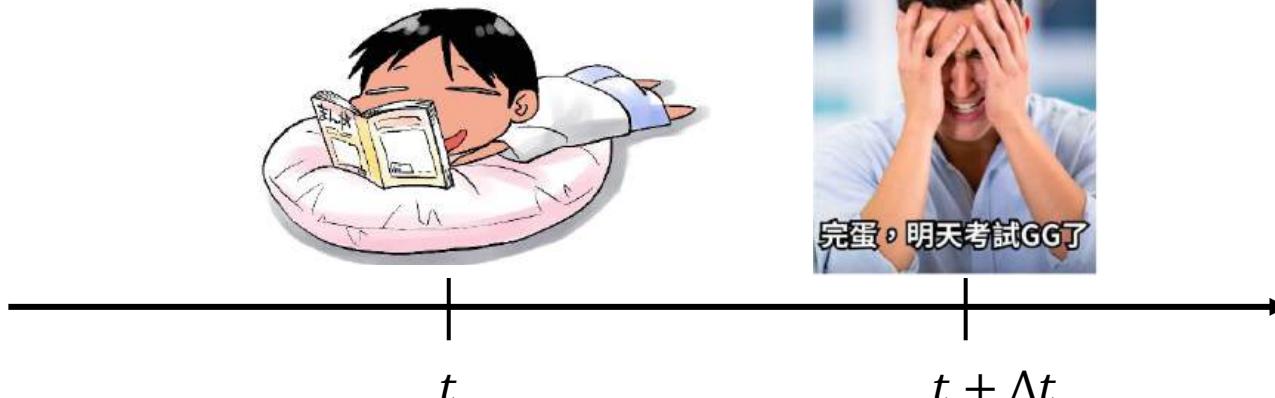
- 位置與時間關係 $x(t)$ 的一階線性關係

$$x(t + \Delta t) = x(t) + \dot{x}\Delta t \quad \dot{x} = \frac{dx}{dt} = v \text{ (velocity)}$$

粒子現在位於 $x(t)$, 經過 Δt 之後到達 $x(t + \Delta t)$



- 線性思維



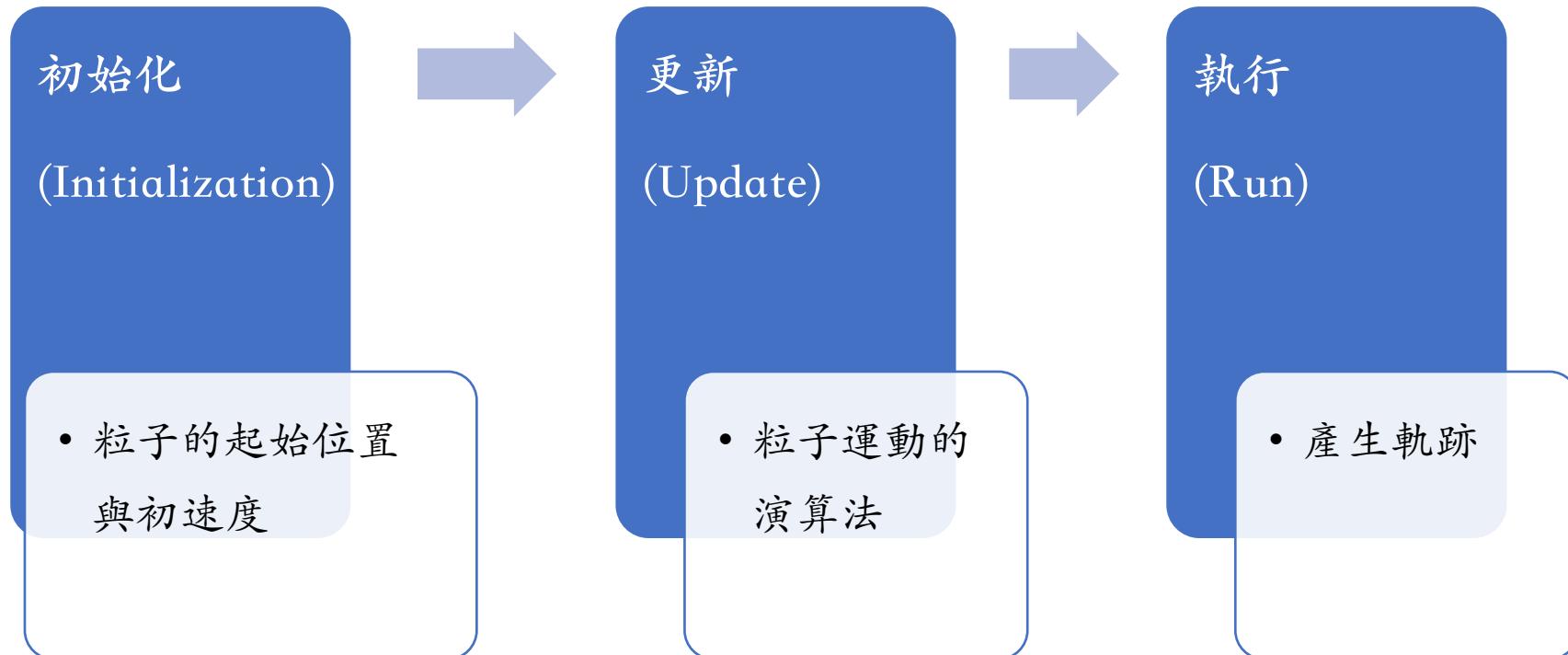
今日(t)不讀書

明日($t + \Delta t$)考試就GG囉

$$\text{考試表現} = \underline{\text{目前能力}} + \underline{\text{用功程度}} \times \underline{\text{時間}}$$

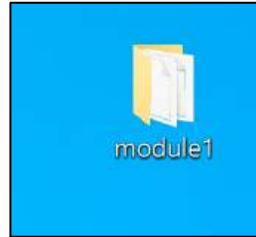
$x(t + \Delta t)$ $x(t)$ \dot{x} Δt

讓粒子動起來的三部曲



→ 視覺化 (Visualization) & 分析 (Analysis)

1. 從Dropbox下載 112.2 MD workshop.zip



2. 解壓縮檔案至 112.2 MD workshop\



JupyterLab

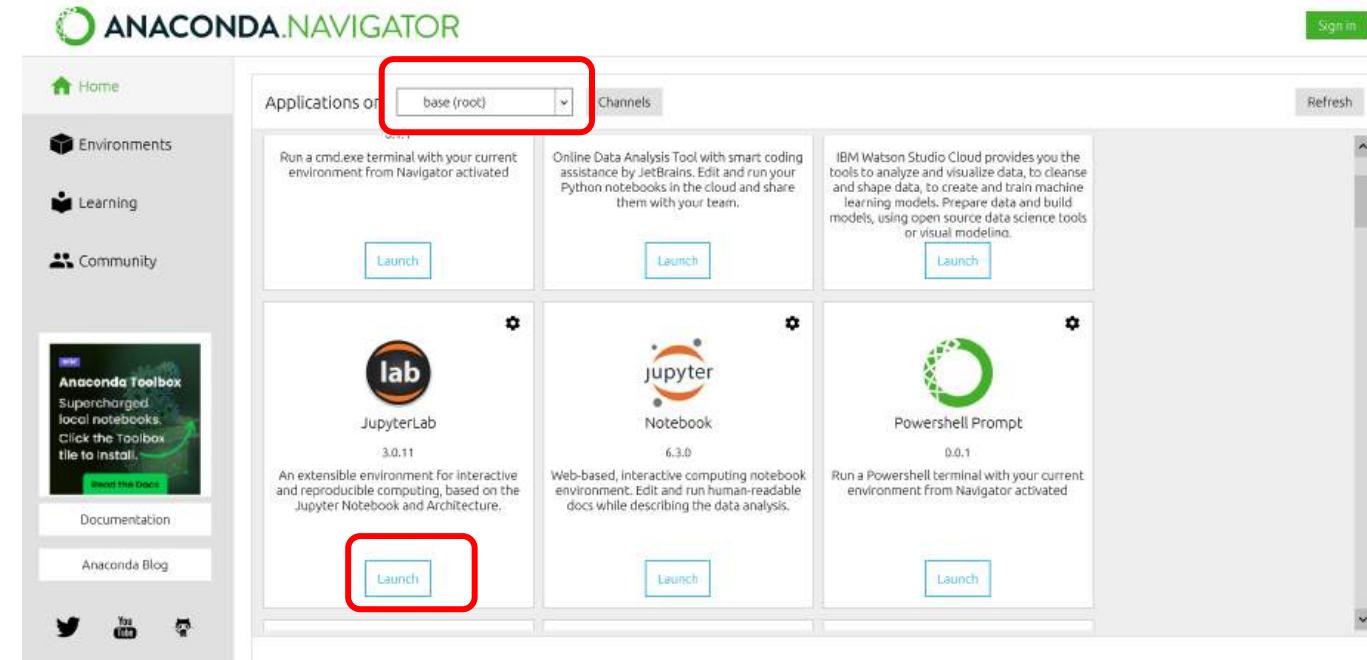
3. 進入112.2 MD workshop\ 資料夾，將 **module1** 移至桌面 (Desktop)

4. 開啟 Anaconda → (稍等一下) → 在 **base (root)** 環境下開啟 JupyterLab → 點 **Launch**

5. JupyterLab將開啟於瀏覽器新分頁

將左側之目錄切換至『桌面』

→ 進入 **module1**。



將左側之目錄切換至『桌面』→進入 module1

→開啟 pythonIntro_ntu.ipynb

The screenshot shows a Jupyter Notebook interface. On the left, there is a file browser sidebar with a search bar and a list of files in the 'module1' directory. The file 'pythonIntro_ntu.ipynb' is highlighted with a blue selection bar. The main notebook area displays the content of the selected file:

Python basics

This Notebook is used to introduce python basics, including Basic Math, Data Type, Function, Array, and Plotting 此份Notebook 介紹基本的python指令與使用，包含【基本運算】、【資料型態】、【函式】、【陣列】與【繪圖】。

Created by Min-Yeh Tsai (MYTLab)

Nov 23, 2022 updated (MYT)

參考資料

- J.R. Johansson, Intro to Python Programming
- J.R. Johansson, Numpy

此文件僅供教學使用

All rights reserved.

The python world (初探python的世界)

```
[ ]: print("hello world!") #印出字串 "hello world!"
```

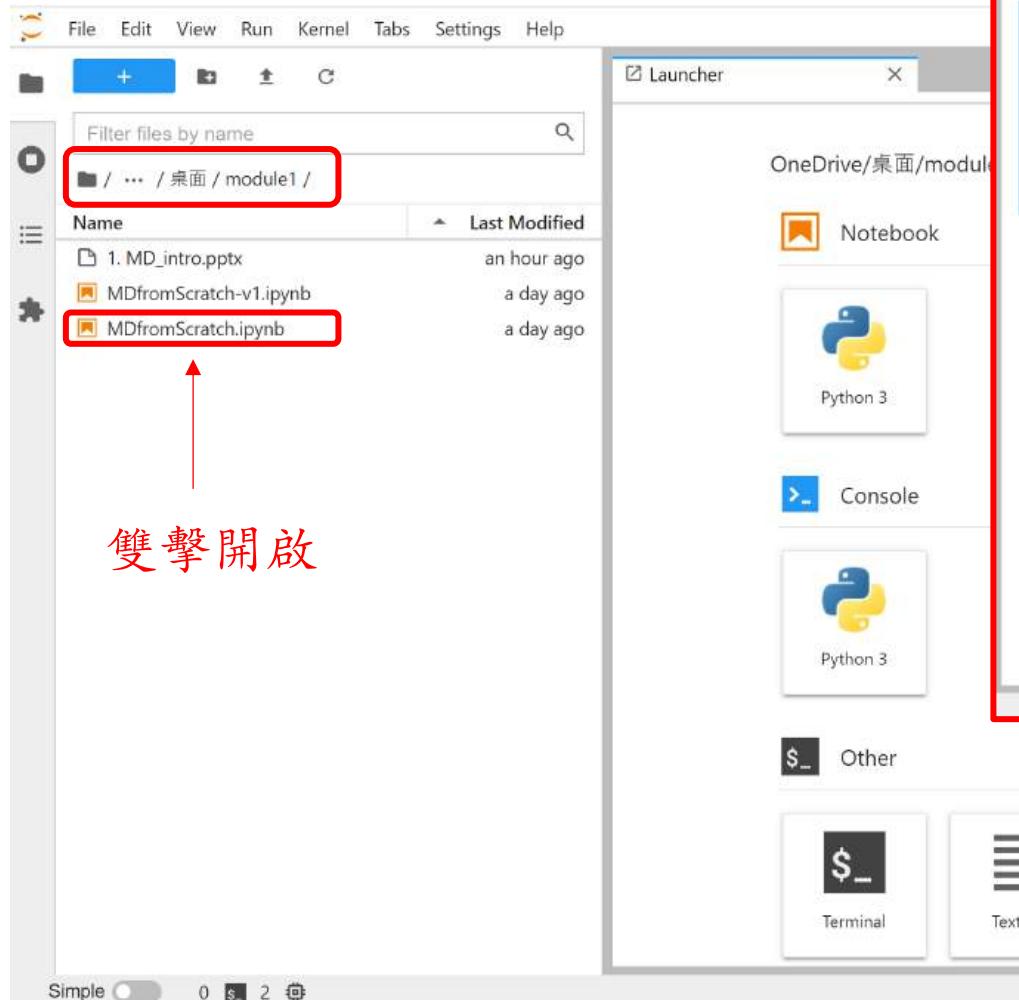
```
[ ]: "test" #字串以 "" 包覆表示
```

```
[ ]: seq_1="hello " #宣告一變數 seq_1 指派成為一字串 "hello"
```

Simple 0 s 3 Python 3 | Idle Saving completed Mode: Command ↵ Ln 1, Col 1 pythonIntro_ntu.ipynb

將左側之目錄切換至『桌面』→進入 module1

→開啟 MDfromScratch.ipynb



The screenshot shows a Jupyter Notebook cell with a red border. The title of the cell is '讓粒子動起來!'. The content of the cell is as follows:

```
[1]: #import numerical library (匯入函式庫)
import numpy as np

[14]: #parameters
n = 10 # number of particles (粒子的數量)
D = 3 # dimensions (維度)
dt = 0.01 # time interval (時間的間隔)
t_steps = 100 # time steps (時間步數)
#arrays of variables
r = 100*np.random.rand(n,D) # initialize random positions for n particles in D dimensions
v = 100*(np.random.rand(n,D)-0.5) # initialize random velocities for n particles in D dimensions
```

Mode: Command ⚙ Ln 1, Col 1 MDfromScratch.ipynb

將左側之目錄切換至『桌面』→進入 **module1**

→ 開啟 **MDfromScratch-v1.ipynb**

The screenshot shows a Jupyter Notebook interface with a red border around the main content area. The title bar says 'MDfromScratch-v1.ipynb'. The notebook contains the following content:

"看見"粒子動起來!

1. 初始化 (準備粒子的起始位置、初速度+盒子大小+週期邊界條件)
2. 更新 (粒子運動的演算法+週期邊界條件)
3. 執行 (反覆迭代產生軌跡+3D繪圖)

參考資料 [PolymerTheory](#)

Visualization version

1. 初始化

```
[4]: #import numerical library (匯入函式庫)
      import numpy as np

[18]: #parameters
      n = 5 # number of particles (粒子的數量)
      D = 3 # dimensions (維度)

      #---- new addition ----#
      LL = 100 # box size (盒子大小)
      BC = 1 # PBC switch; on/off=1/0
      #-----#
      dt = 0.1 # time interval (時間的間隔)
      t_steps = 100 # time steps (時間步數)
```

Mode: Command Ln 1, Col 1 MDfromScratch-v1.ipynb

預測的品質與採取的策略有關

- **Verlet algorithm**

(韋爾萊算法)

$$x(t + \Delta t) = 2x(t) - x(t - \Delta t) + \ddot{x}\Delta t^2$$

↑ ↑ ↑ ↙
表現 目前 實力 過去 實力 有效努力 \times 時間 2

實際表現是根據過去與目前的差異，透過一定時間內有效的努力所達成

了解歷史，掌握當下，加上持續的努力 → 成功

[補充] 運用數值方法解運動方程式

**Position and dynamic properties can be approximated as
Taylor series expansions**

$$\text{Position} \rightarrow \mathbf{r}(t + \delta t) = \mathbf{r}(t) + \delta t \mathbf{v}(t) + \frac{1}{2} \delta t^2 \mathbf{a}(t) + \frac{1}{6} \delta t^3 \mathbf{b}(t) + \frac{1}{24} \delta t^4 \mathbf{c}(t) + \dots$$

$$\text{Velocity} \rightarrow \mathbf{v}(t + \delta t) = \mathbf{v}(t) + \delta t \mathbf{a}(t) + \frac{1}{2} \delta t^2 \mathbf{b}(t) + \frac{1}{6} \delta t^3 \mathbf{c}(t) + \dots$$

$$\begin{aligned}\text{Acceleration} \rightarrow \mathbf{a}(t + \delta t) &= \mathbf{a}(t) + \delta t \mathbf{b}(t) + \frac{1}{2} \delta t^2 \mathbf{c}(t) \dots \\ \mathbf{b}(t + \delta t) &= \mathbf{b}(t) + \delta t \mathbf{c}(t) + \dots\end{aligned}$$

Truncated

Verlet algorithm

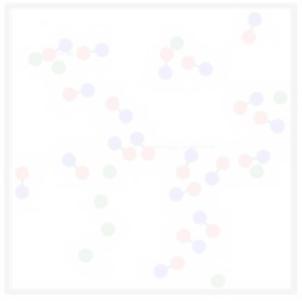
$$\mathbf{r}(t + \delta t) = \mathbf{r}(t) + \delta t \mathbf{v}(t) + \frac{1}{2} \delta t^2 \mathbf{a}(t) + \dots$$

$$\mathbf{r}(t - \delta t) = \mathbf{r}(t) - \delta t \mathbf{v}(t) + \frac{1}{2} \delta t^2 \mathbf{a}(t) - \dots$$

↓ Summation

**Truncated at $O(\delta t^4)$
→Fourth-order method**

$$\mathbf{r}(t + \delta t) = 2\mathbf{r}(t) - \mathbf{r}(t - \delta t) + \delta t^2 \mathbf{a}(t)$$

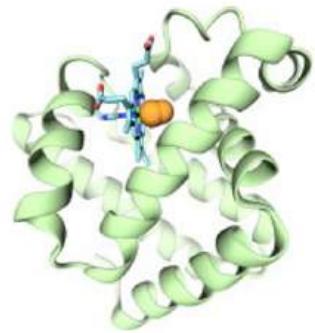


I. Simple MD

- Python
- JupyterLab



JupyterLab



II. Visualization

- MolView
- VMD



Part II

III. MD (分子結構 & 視覺化)

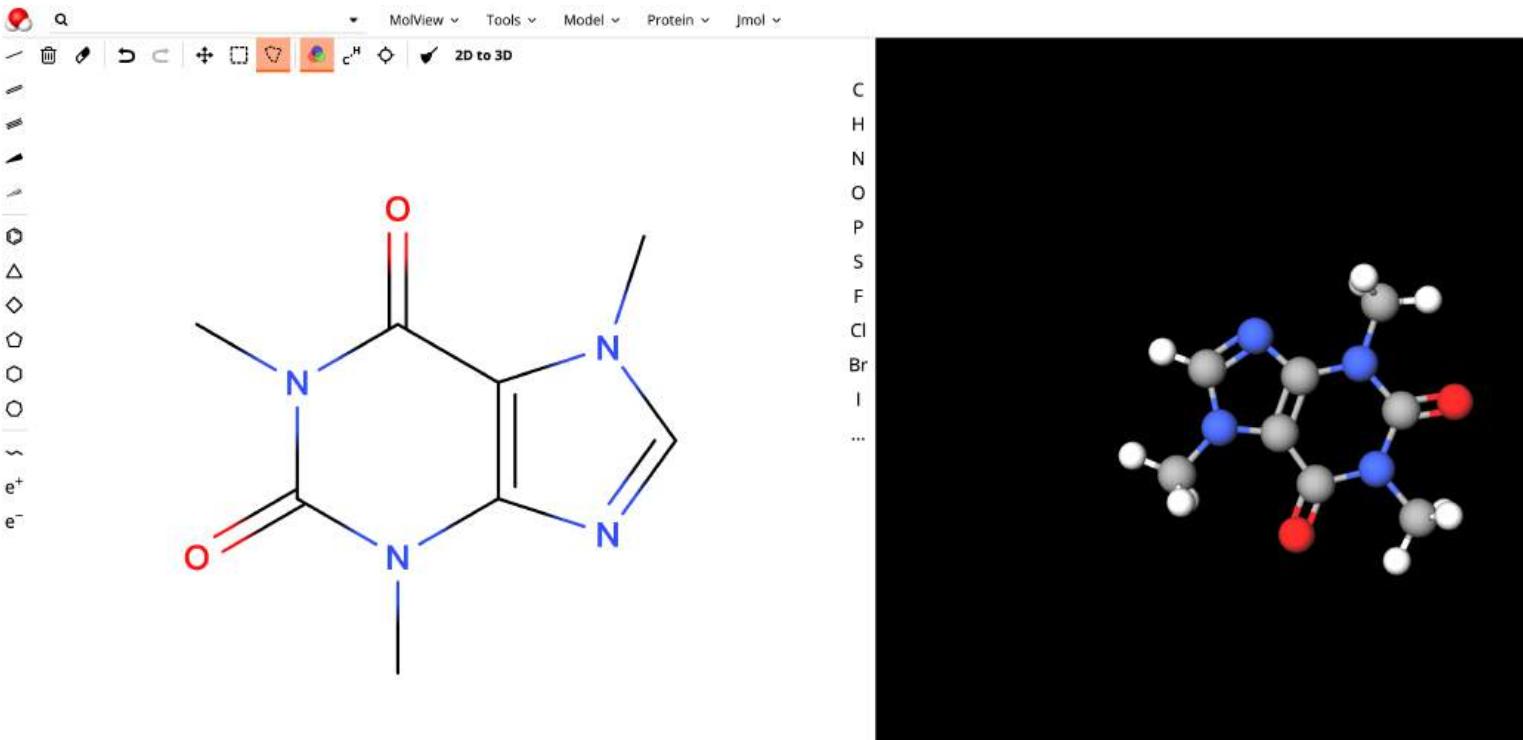
- NAMD/VMD
- Protein
- Water

IV. MD (Nano)

- NAMD/VMD
- Graphene
- Small molecules



MolView

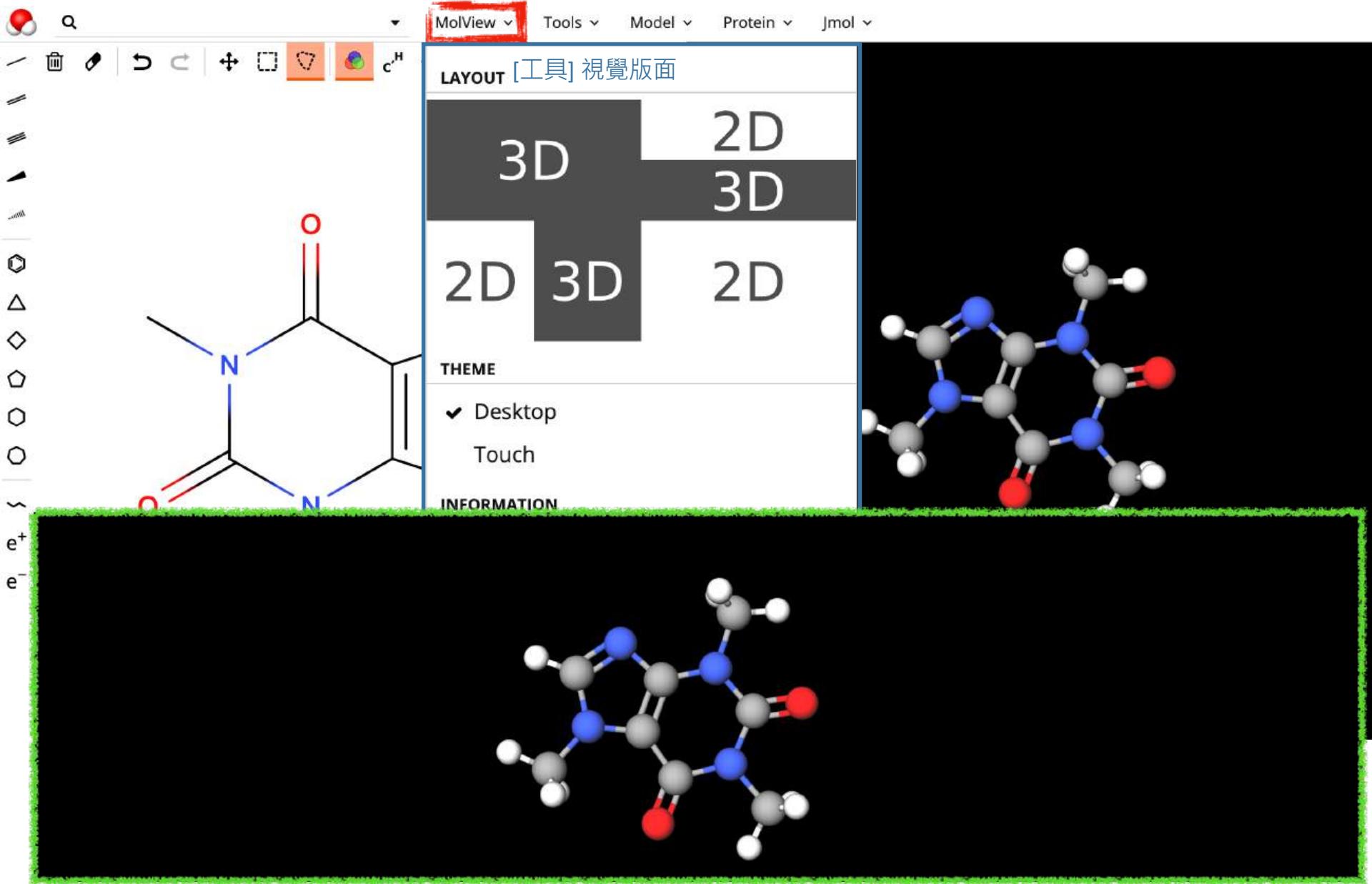


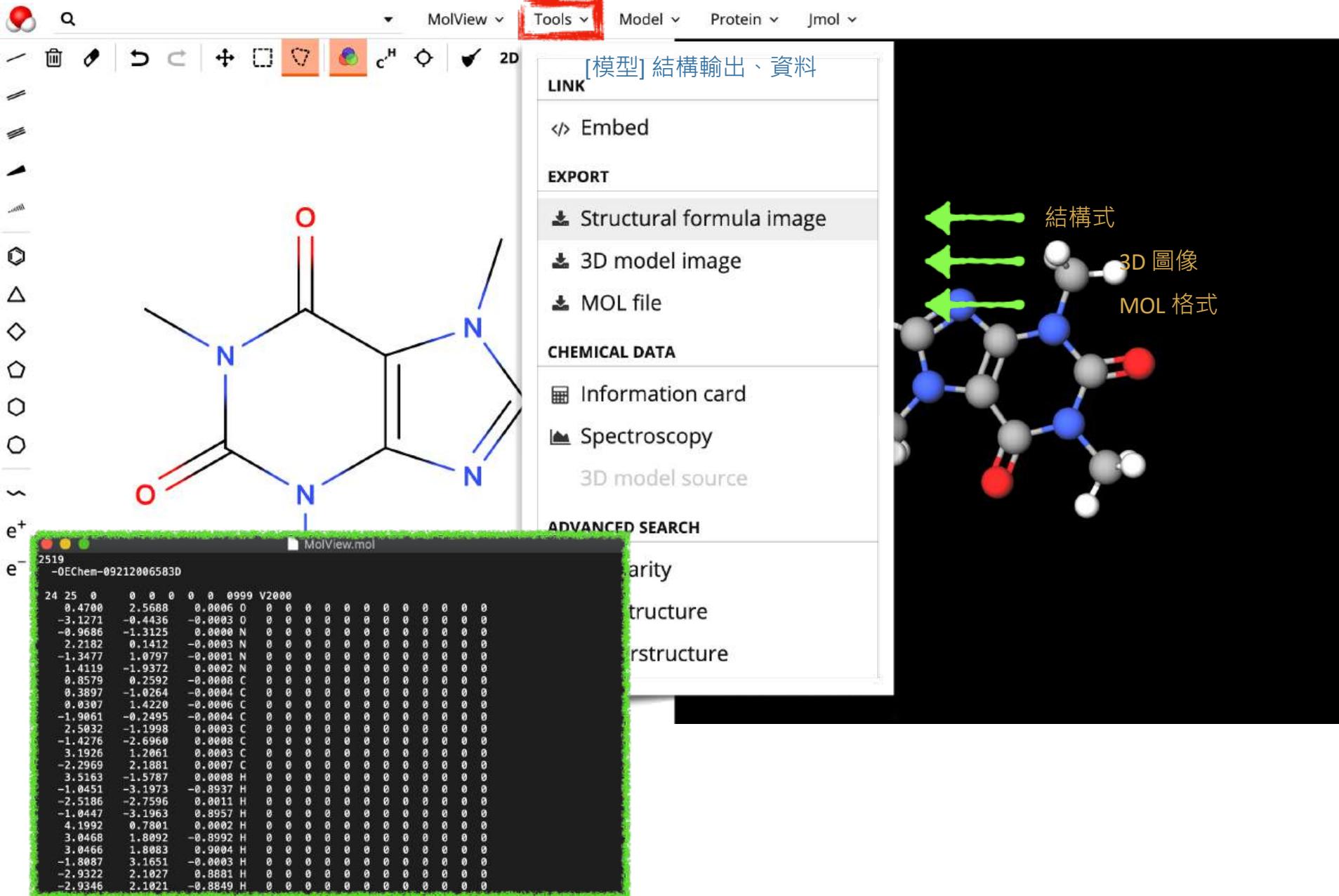
<https://molview.org/>

- Video tutorial:

<https://www.youtube.com/watch?v=ZesFyuFj30s>

<https://www.youtube.com/watch?v=af6PAAfVpRc>







Q

MolView

Tools

Model

Protein

Jmol

c^H

2D

**Systematic name**

1,3,7-trimethylpurine-2,6-dione

Canonical SMILES

CN1C=NC2=C1C(=O)N(C(=O)N2C)C

Isomeric SMILES

CN1C=NC2=C1C(=O)N(C(=O)N2C)C

InChIKey

RYYVLZVUVIJVGH-UHFFFAOYSA-N

InChI

InChI=1S/C8H10N4O2/c1-10-4-9-6-5(10)7(13)12(3)8(14)11(6)2/h4H,1-3H3

CAS Number

58-08-2

PubChem Compound ID

2519

[模型] 結構輸出、資料

LINK

</> Embed

EXPORT

Structural formula image

3D model image

MOL file

CHEMICAL DATA

Information card

Spectroscopy

3D model source

ADVANCED SEARCH

≈ Similarity

▫ Substructure

▫ Superstructure

Caffeine

Caffeine is a trimethylxanthine in which the three methyl groups are located at positions 1, 3, and 7. A purine alkaloid that occurs naturally in tea and coffee. It has a role as a central nervous system stimulant, an EC 3.1.4.* (phosphoric diester hydrolase) inhibitor, an adenosine receptor antagonist, an EC 2.7.11.1 (non-specific serine/threonine protein kinase) inhibitor, a ryanodine receptor agonist, a fungal metabolite, an adenosine A2A receptor antagonist, a psychotropic drug, a diuretic, a food additive, an adjuvant, a plant metabolite, an environmental contaminant, a xenobiotic, a human blood serum metabolite, a mouse metabolite and a mutagen. It is a purine alkaloid and a trimethylxanthine.

Formula	C ₈ H ₁₀ N ₄ O ₂
---------	--

Molecular weight	194.19 u
------------------	----------

Hydrogen bond donors	0
----------------------	---

Hydrogen bond acceptors	3
-------------------------	---

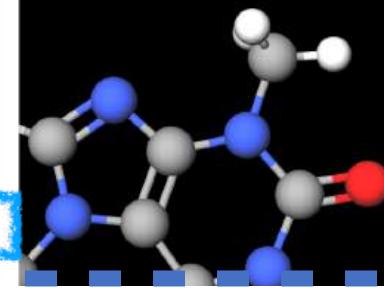
Percent composition

C	12.0107 u × 8	49.480 %
---	---------------	----------

H	1.00794 u × 10	5.1905 %
---	----------------	----------

N	14.0067 u × 4	28.851 %
---	---------------	----------

O	15.9994 u × 2	16.478 %
---	---------------	----------





Q

▼

MolView ▾

Tools ▾

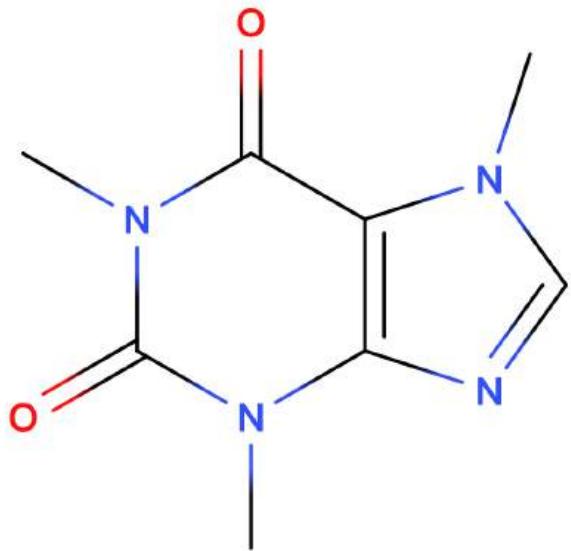
Model ▾

Protein ▾

Imol ▾

c^H

2D to 3D



Model ▾

Reset

REPRESENTATION

✓ Ball and Stick

Stick

van der Waals Spheres

Wireframe

Line

BACKGROUND

✓ Black

Gray

White

ENGINE

✓ GLmol

Jmol

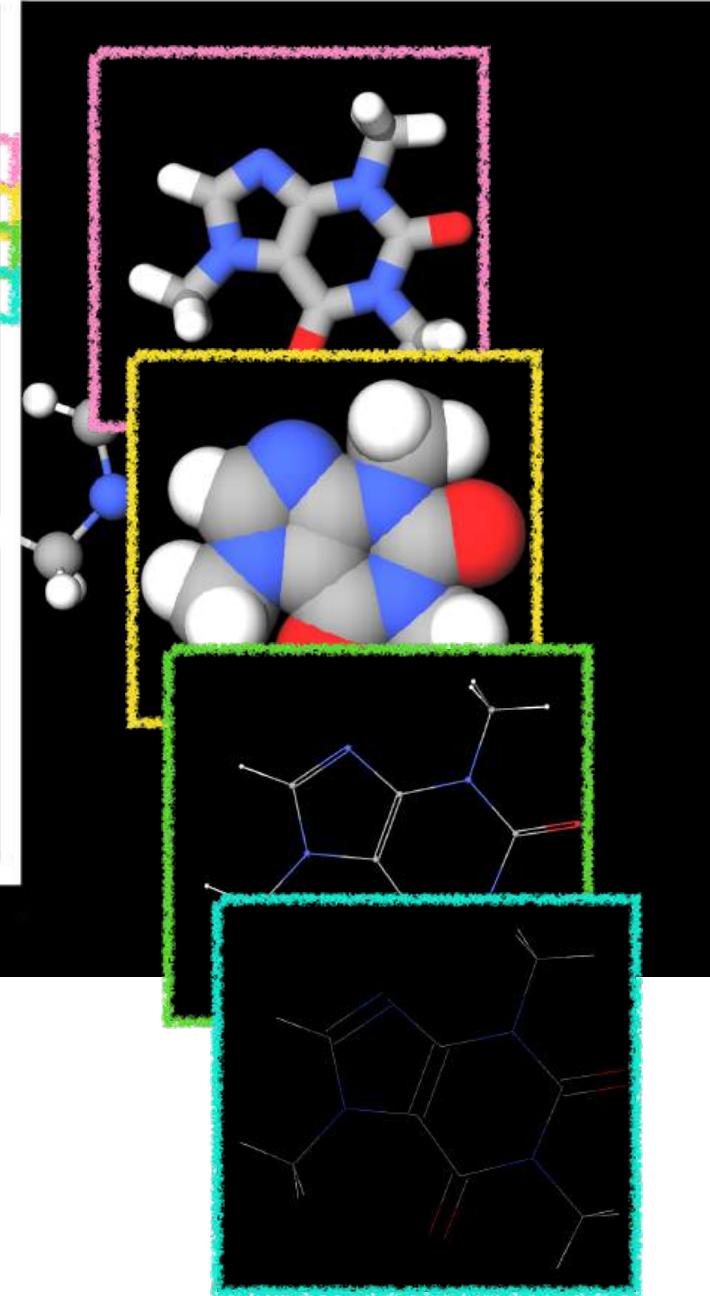
ChemDoodle

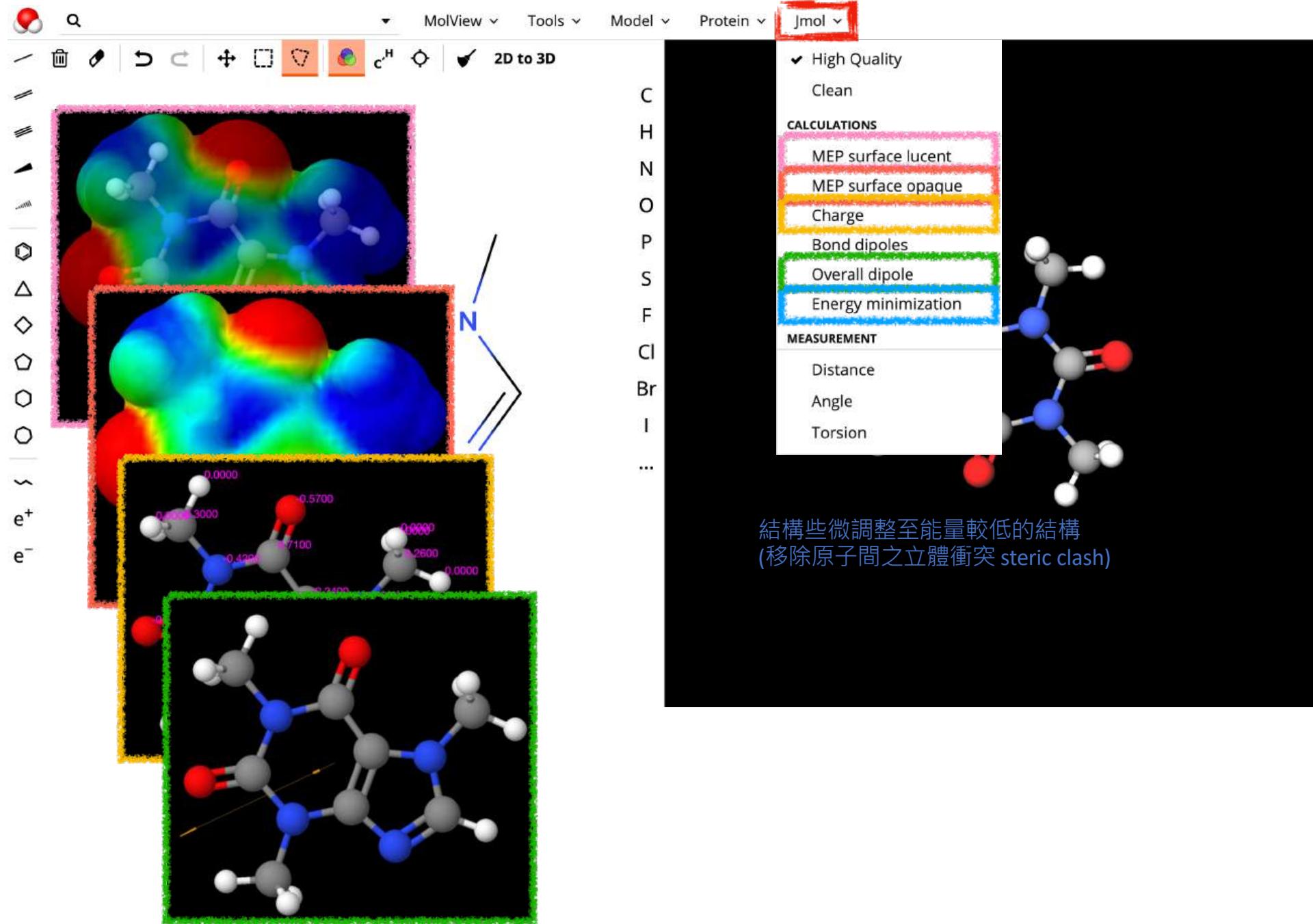
CRYSTALLOGRAPHY

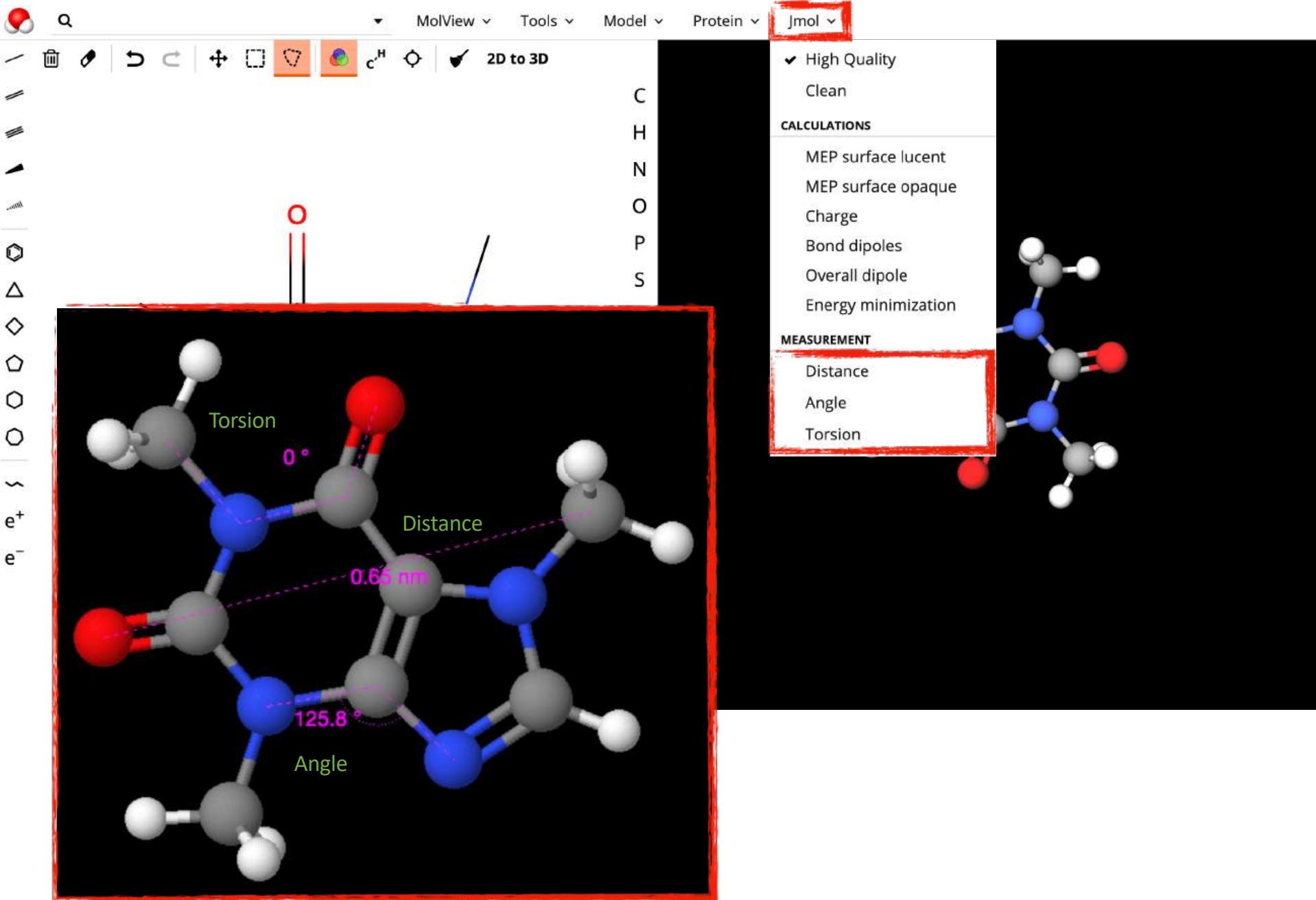
Load unit cell

Load 2×2×2 supercell

Load 1×3×3 supercell









Q Catechin

MolView ▾

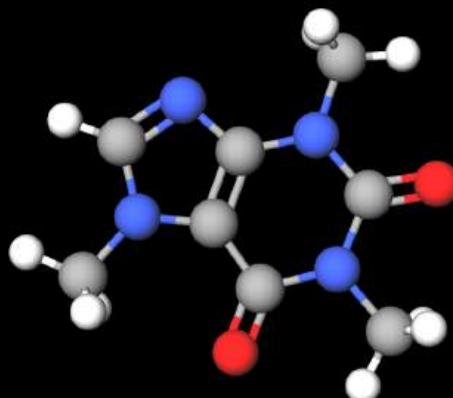
Tools ▾

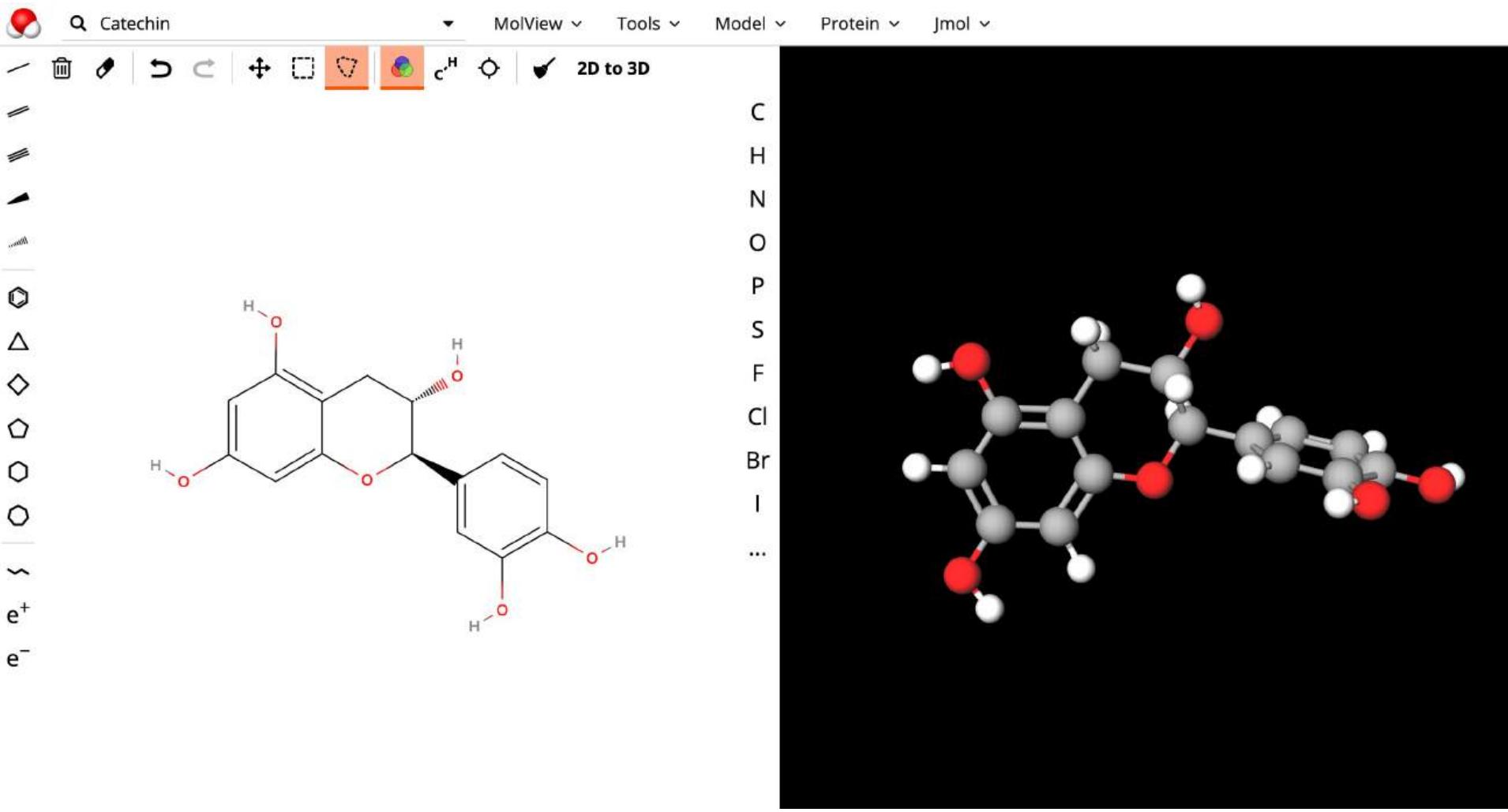
Model ▾

Protein ▾

Jmol ▾

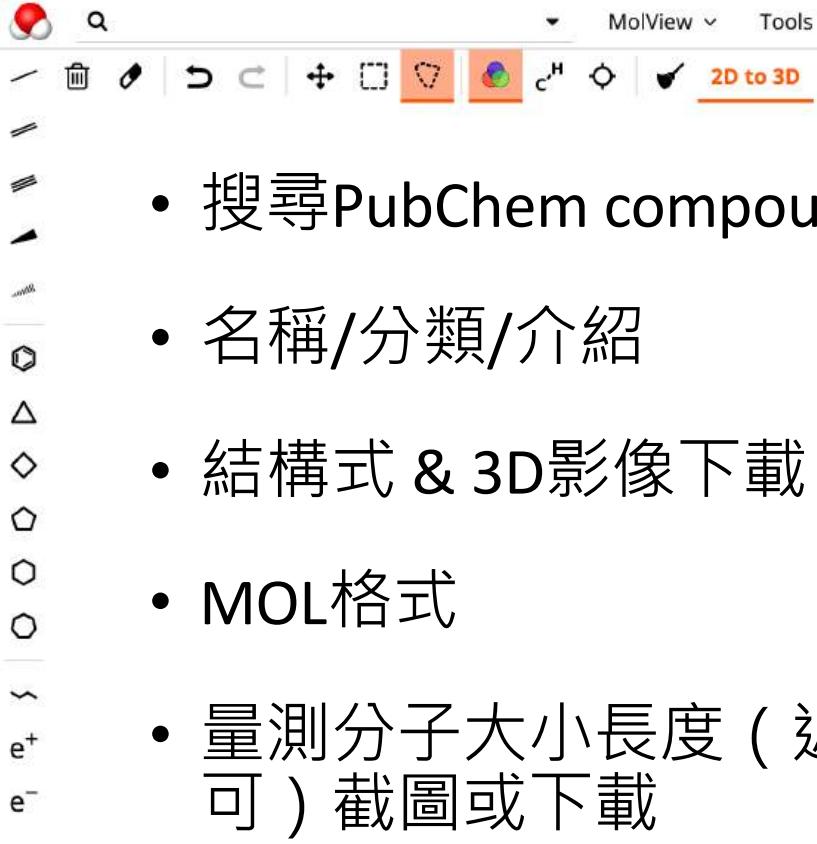
Catechol	Compound
Catechin	Compound
Catecholborane	Compound
Catechuic acid	Compound
Catechinic acid	Compound
Catechol violet	Compound
Catechol diacetate	Compound
Catechol diethyl ether	Compound
Catechol dimethyl ether	Compound
Catechol Dimethylether-d6	Compound
Cahnite	Mineral
Calcite	Mineral
Caoxite	Mineral
Cavoite	Mineral
Catalase	Enzymes
Arcanite	Mineral
Cafetite	Mineral
Caminite	Mineral
Canasite	Mineral
Cattiite	Mineral
Cejkaite	Mineral
Cytochrome c	Energy Production
Collagen	Infrastructure

C
H
N
O
P
S
F
Cl
Br
I
...



Your Turn!

找尋日常生活會用到的小分子藥物



MolView Tools Model Protein Jmol

2D to 3D

- 搜尋PubChem compounds
- 名稱/分類/介紹
- 結構式 & 3D影像下載
- MOL格式
- 量測分子大小長度（近似即可）截圖或下載
- 將分子用surface表示後截圖或下載

PubChem Classification Browser

Browse PubChem data using a classification of interest, or search for PubChem records annotated with DNA repair). More...

Select classification Search selected classification by

MeSH Keyword Enter desired search term

Classification description (from MeSH)
MeSH (Medical Subject Headings) is the NLM controlled vocabulary thesaurus used for indexing articles for PubMed.

Data type counts to display Display zero count nodes?

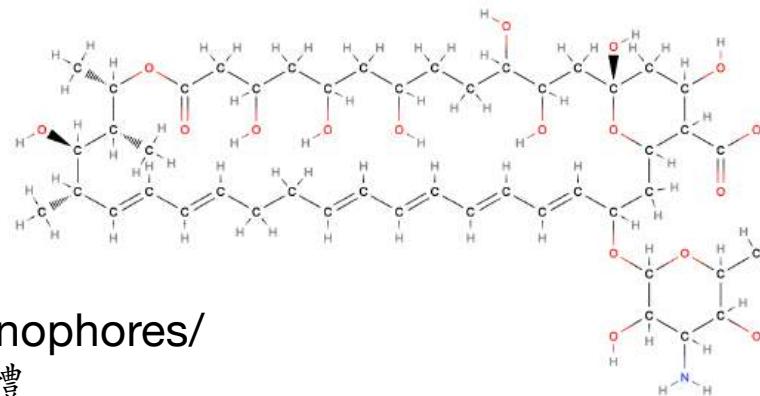
None Compound Substance PubMed Yes No

Browse MeSH Tree

- MeSH Tree 130,583
 - Analytical, Diagnostic and Therapeutic Techniques and Equipment Category
 - Anatomy Category
 - Anthropology, Education, Sociology and Social Phenomena Category
 - Chemicals and Drugs Category 130,583
 - Amino Acids, Peptides, and Proteins 13,015
 - Biological Factors 4,089
 - Biomedical and Dental Materials 596
 - Carbohydrates 10,185
 - Chemical Actions and Uses 17,199
 - Complex Mixtures 366
 - Enzymes and Coenzymes 993
 - Heterocyclic Compounds 51,578
 - Hormones, Hormone Substitutes, and Hormone Antagonists 3,182
 - Inorganic Chemicals 4,802
 - Lipids 7,917
 - Macromolecular Substances 775
 - Nucleic Acids, Nucleotides, and Nucleosides 4,347
 - Organic Chemicals 67,528
 - Pharmaceutical Preparations 280
 - Polycyclic Compounds 20,358

Nystatine as an example

- 名稱/分類/介紹
Nystatine/Antibiotics, antifungal, Macrolide, Ionophores/
抗黴菌素/抗生素, 抗真菌, 大環內酯類, 離子載體



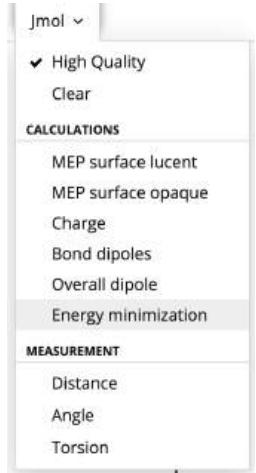
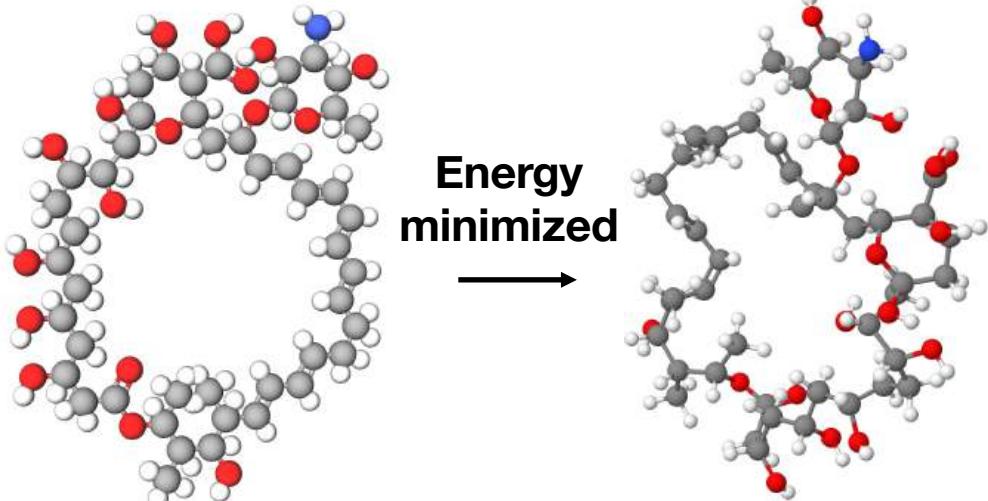
Macrolide antifungal antibiotic complex produced by Streptomyces noursei, S. aureus, and other Streptomyces species. The biologically active components of the complex are nystatin A1, A2, and A3.

由諾氏鏈黴菌、金黃色葡萄球菌和其他鏈黴菌產生的大環內酯類抗真菌抗生素複合物。該複合物的生物活性成分是製黴菌素 A1、A2 和 A3。

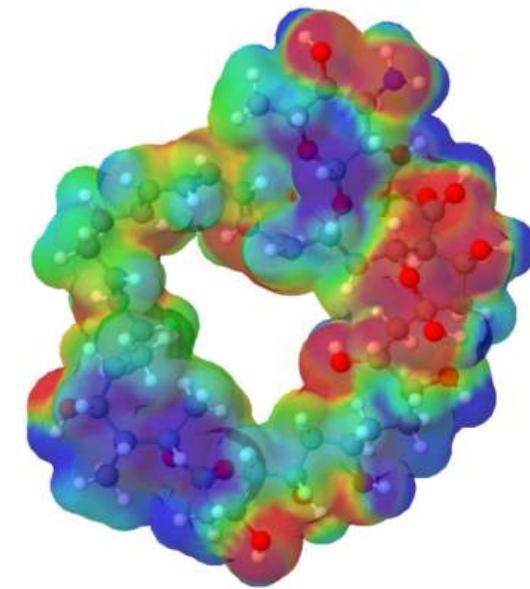
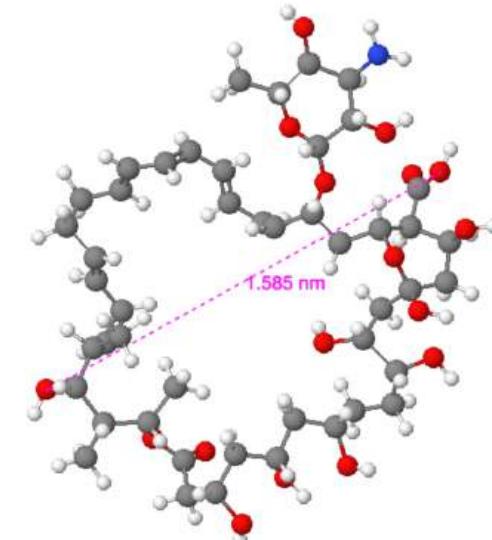
- 結構式 & 3D影像下載
- MOL格式
- 量測分子大小長度（近似即可）截圖或下載
- 將分子用surface表示後截圖或下載

C47H75N017									
APtclcactv10122200512D 0 0.00000 0.00000									
140142	0	0	1	0	0	0	0	0.999	V2000
12.3100		0.6569		0.0000	0	0	0	0	0
12.3100		1.6569		0.0000	C	0	0	0	0
12.1495		2.2558		0.0000	H	0	0	0	0
11.3100		1.6569		0.0000	C	0	0	0	0
10.7274		1.4449		0.0000	H	0	0	0	0
11.4177		1.0463		0.0000	H	0	0	0	0
10.8100		2.5230		0.0000	C	0	0	0	0
11.4300		2.5230		0.0000	H	0	0	0	0
9.8100		2.5230		0.0000	C	0	0	0	0
9.5000		1.9860		0.0000	H	0	0	0	0
9.3100		3.3890		0.0000	C	0	0	0	0
9.4177		3.9996		0.0000	H	0	0	0	0
8.3100		3.3890		0.0000	C	0	0	0	0
8.0000		2.8520		0.0000	H	0	0	0	0
7.8100		4.2550		0.0000	C	0	0	0	0
8.1200		4.7919		0.0000	H	0	0	0	0
6.8100		4.2550		0.0000	C	0	0	0	0
6.5000		4.7919		0.0000	H	0	0	0	0
6.3100		3.3890		0.0000	C	0	0	0	0
6.6200		2.8520		0.0000	H	0	0	0	0
5.3100		3.3890		0.0000	C	0	0	0	0
5.0000		3.9259		0.0000	H	0	0	0	0

Nystatin as an example

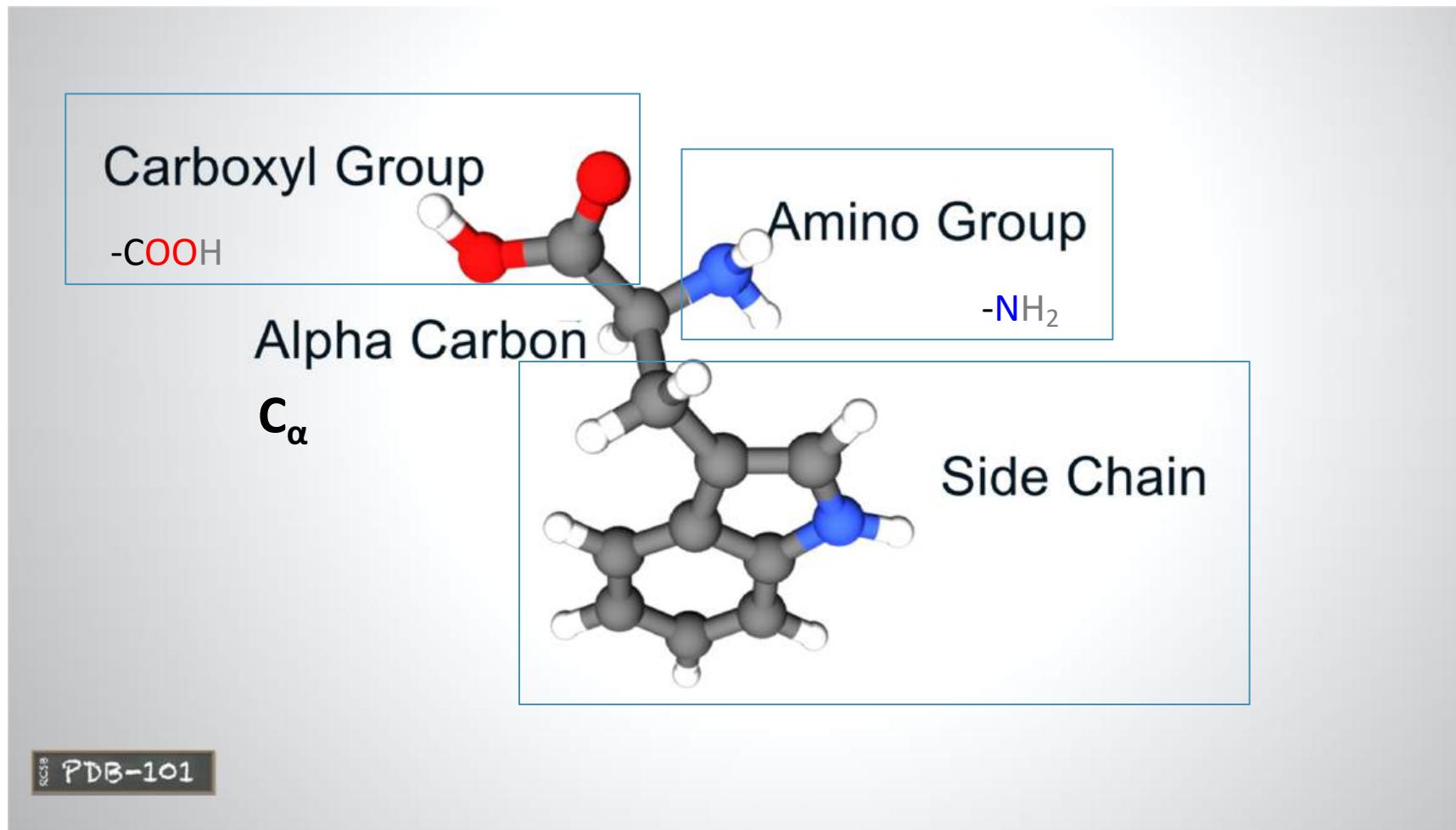


注意分子結構會動!



The Building Blocks of Proteins

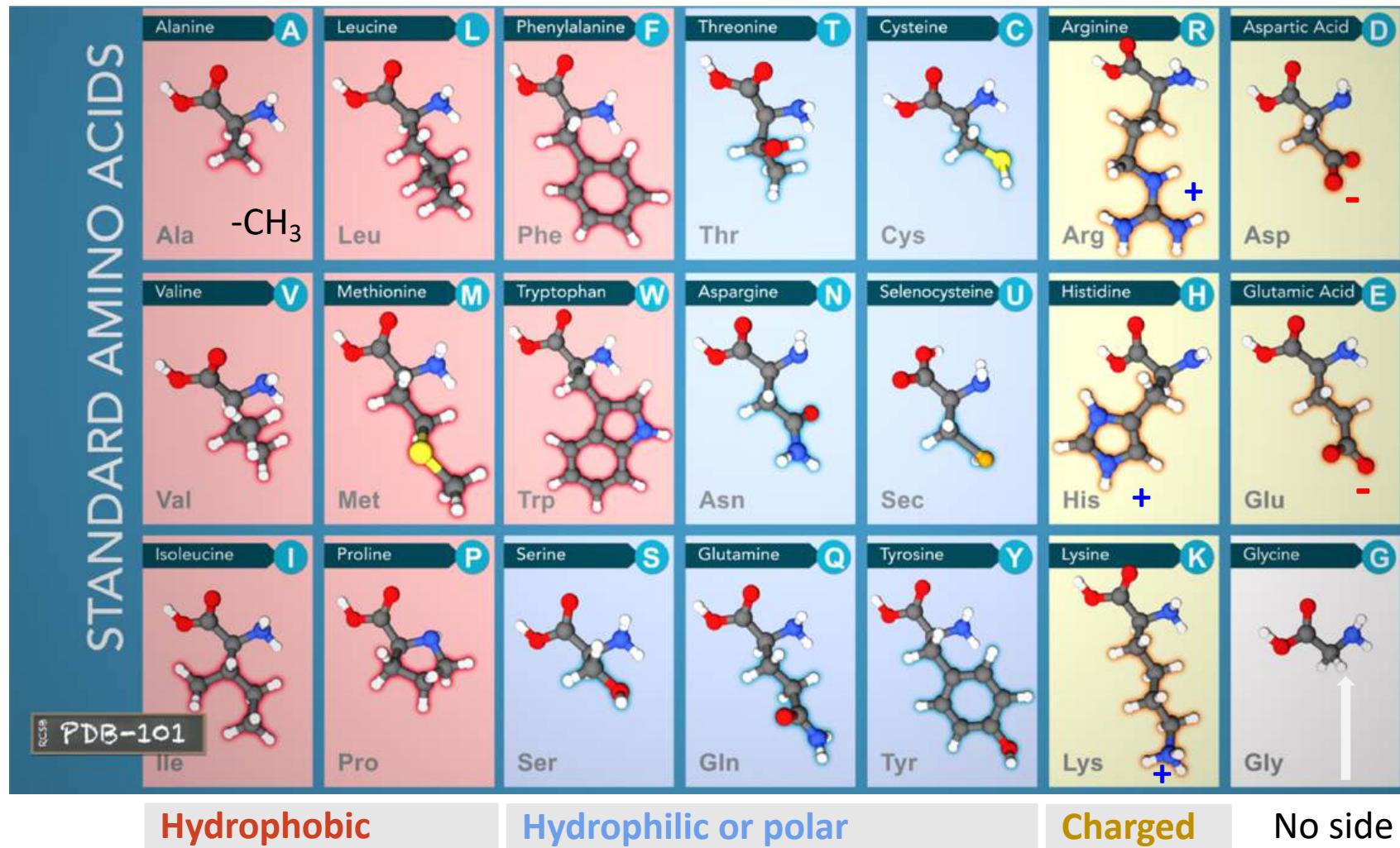
[pdb101.rcsb.org](https://www.rcsb.org/pdb101)



The atoms of each amino acid form an **amino group**, a **carboxyl group**, and a **side chain** attached to a central carbon atom.

The Building Blocks of Proteins

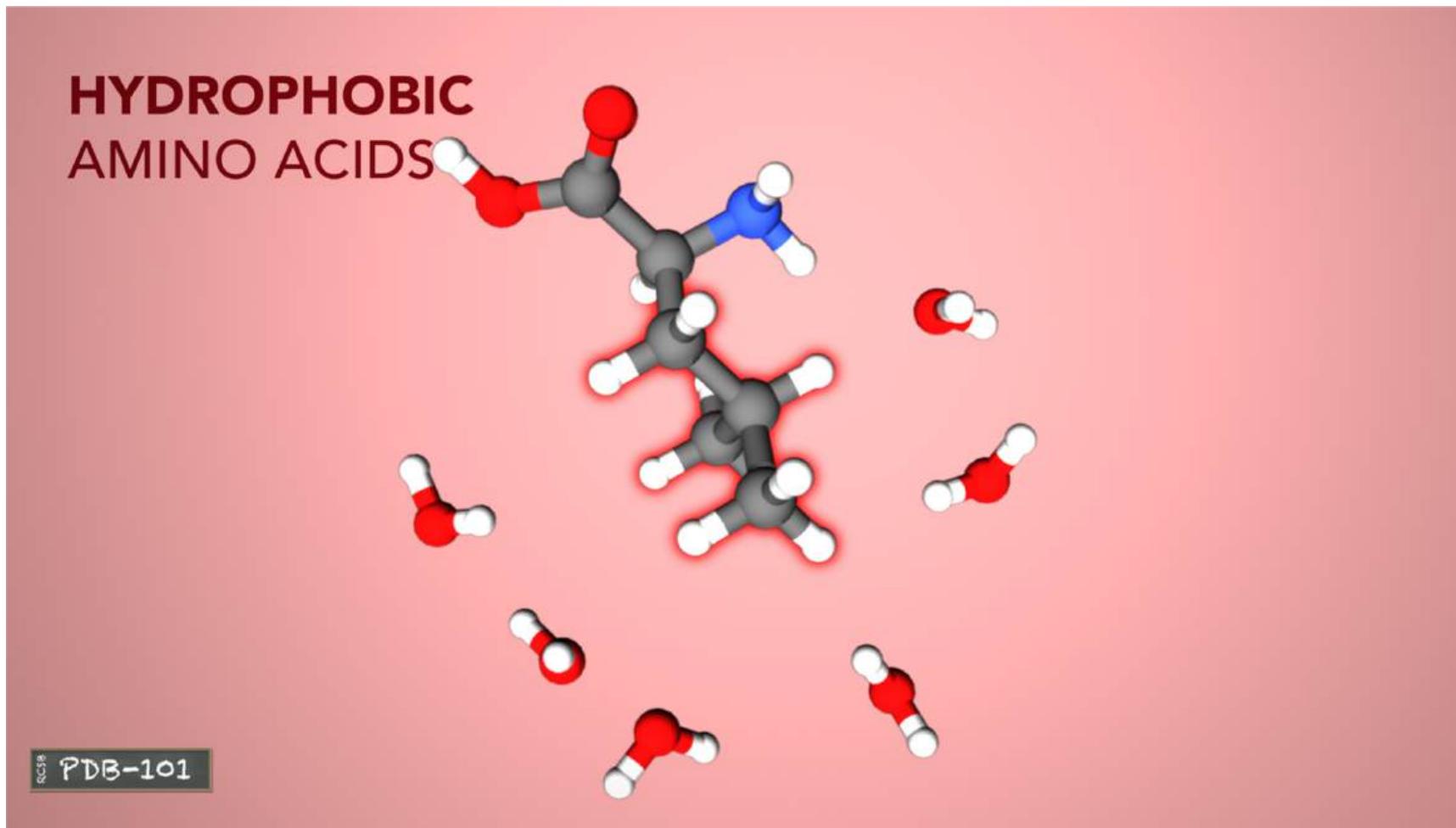
[pdb101.rcsb.org](https://www.rcsb.org/pdb101)



The side chain is the only part that varies from amino acid to amino acid and determines its chemical properties.

The Building Blocks of Proteins

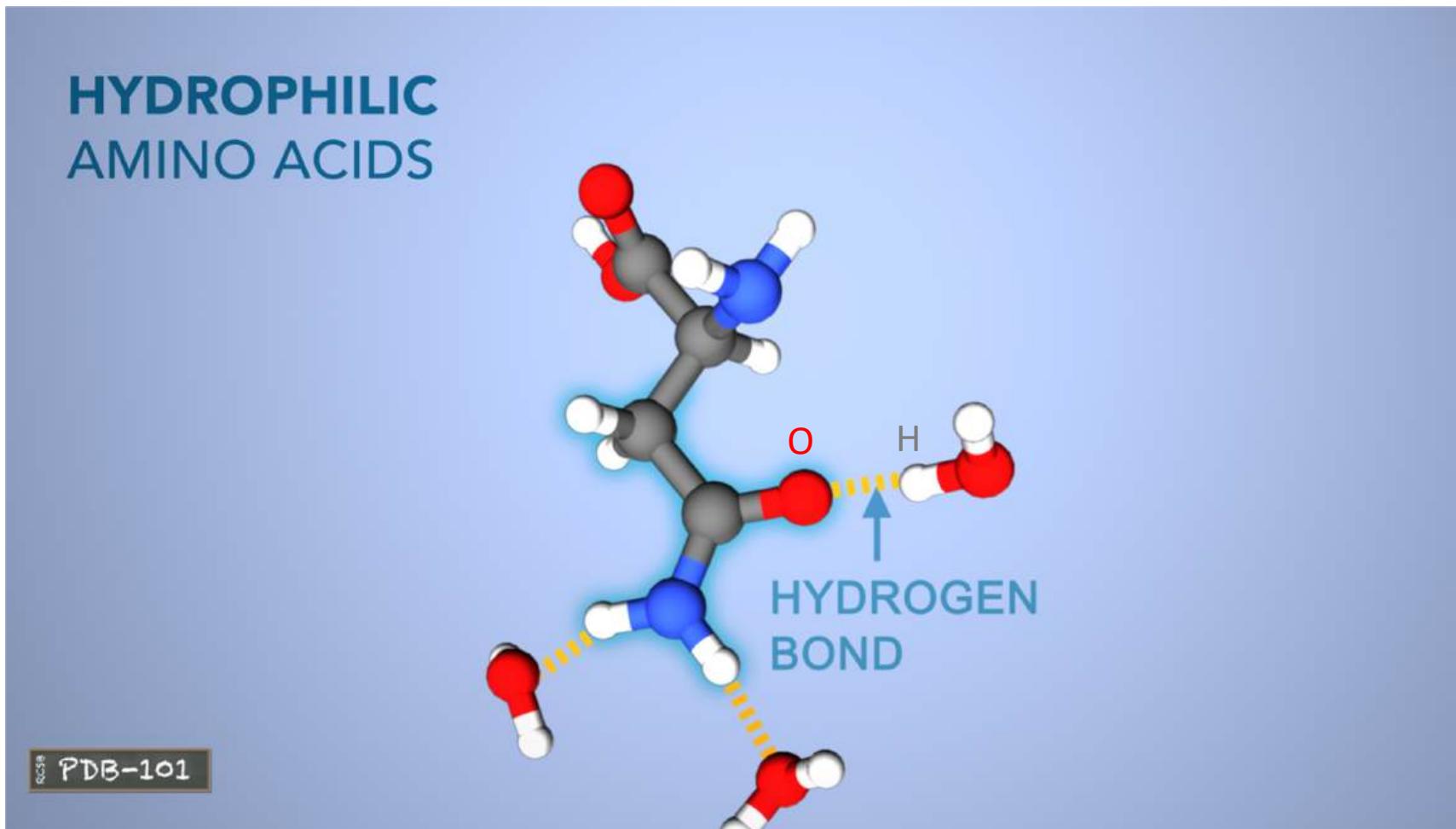
[pdb101.rcsb.org](https://www.rcsb.org/pdb101)



Hydrophobic amino acids have carbon-rich side chains, which don't interact well with water.

The Building Blocks of Proteins

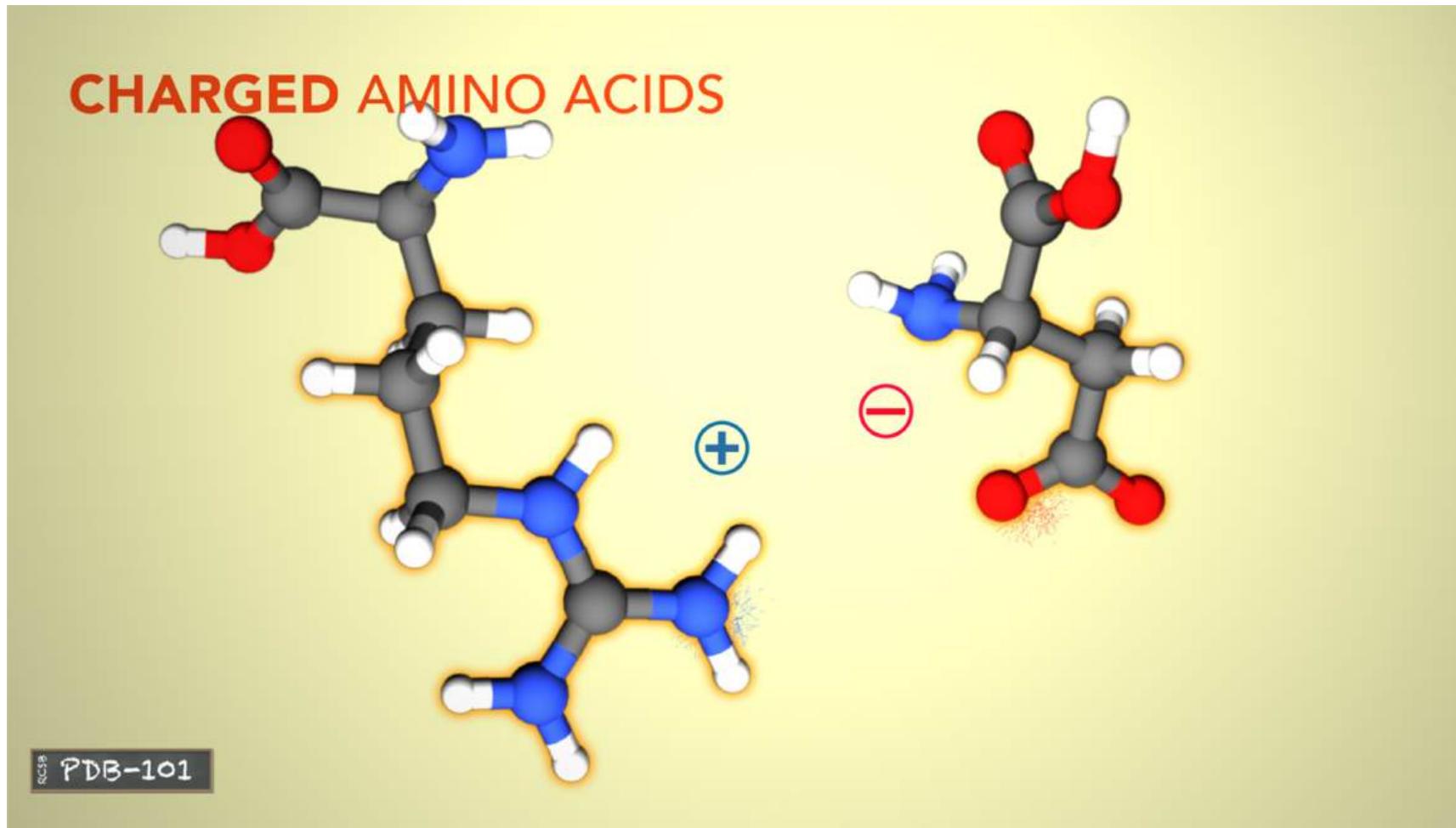
[pdb101.rcsb.org](https://www.rcsb.org/pdb101)



Hydrophilic or polar amino acids interact well with water.

The Building Blocks of Proteins

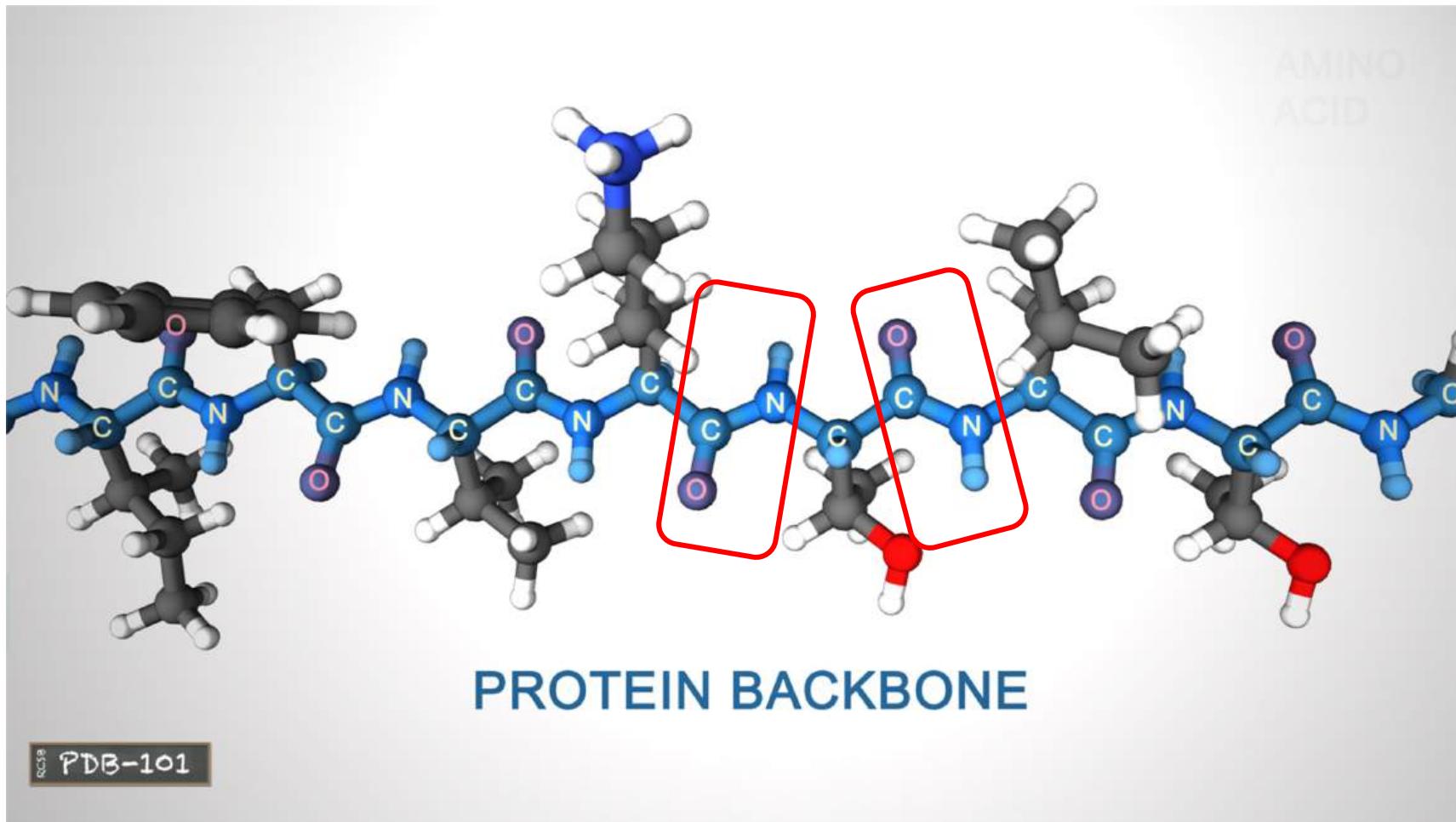
[pdb101.rcsb.org](https://www.rcsb.org/pdb101)



Charged amino acids interact with oppositely charged amino acids or other molecules.

Protein Structure: Primary Structure

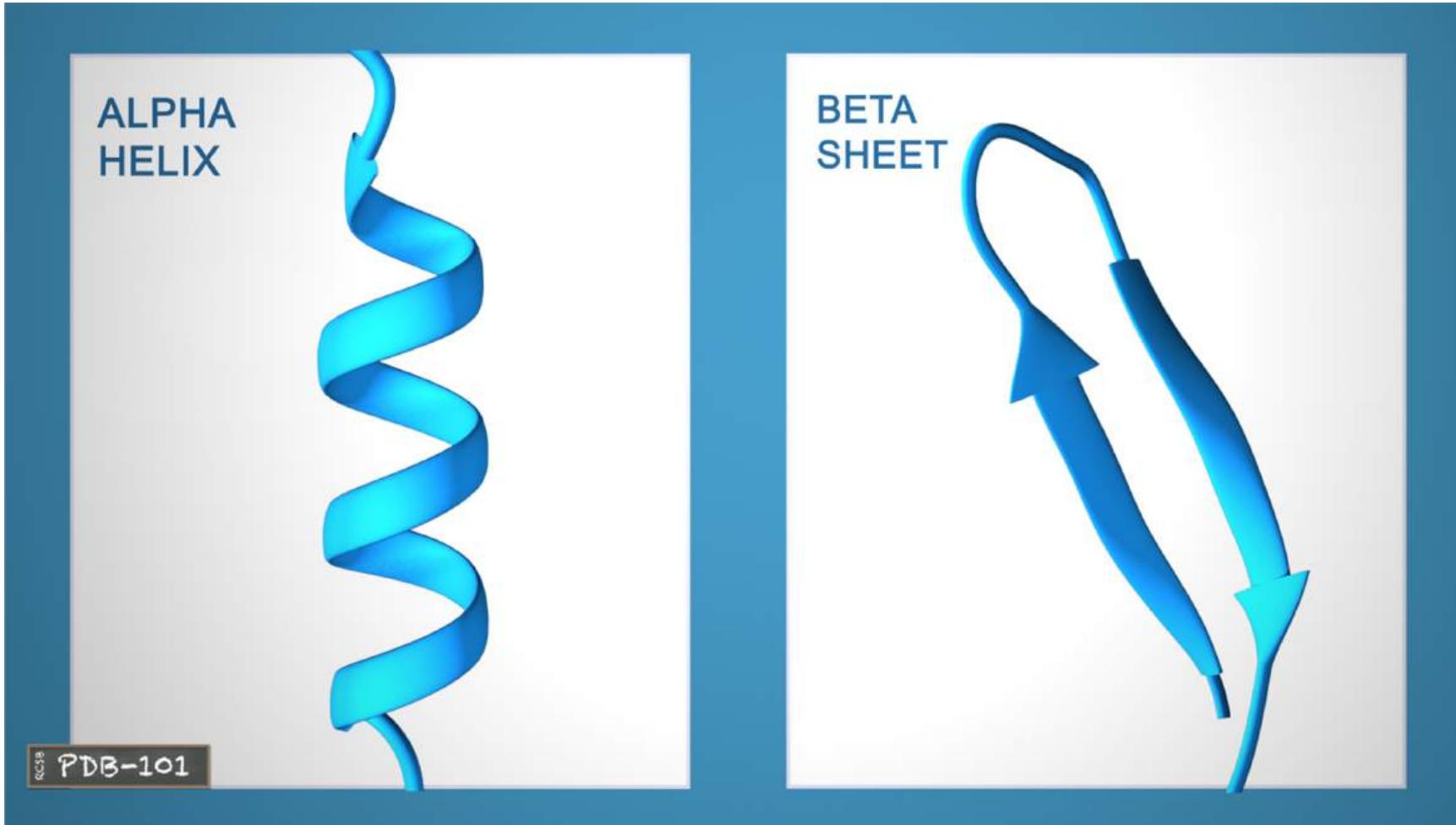
[pdb101.rcsb.org](https://www.rcsb.org/pdb101)



The linked series of carbon, nitrogen, and oxygen atoms make up the **protein backbone**.

Protein Structure: Secondary Structure

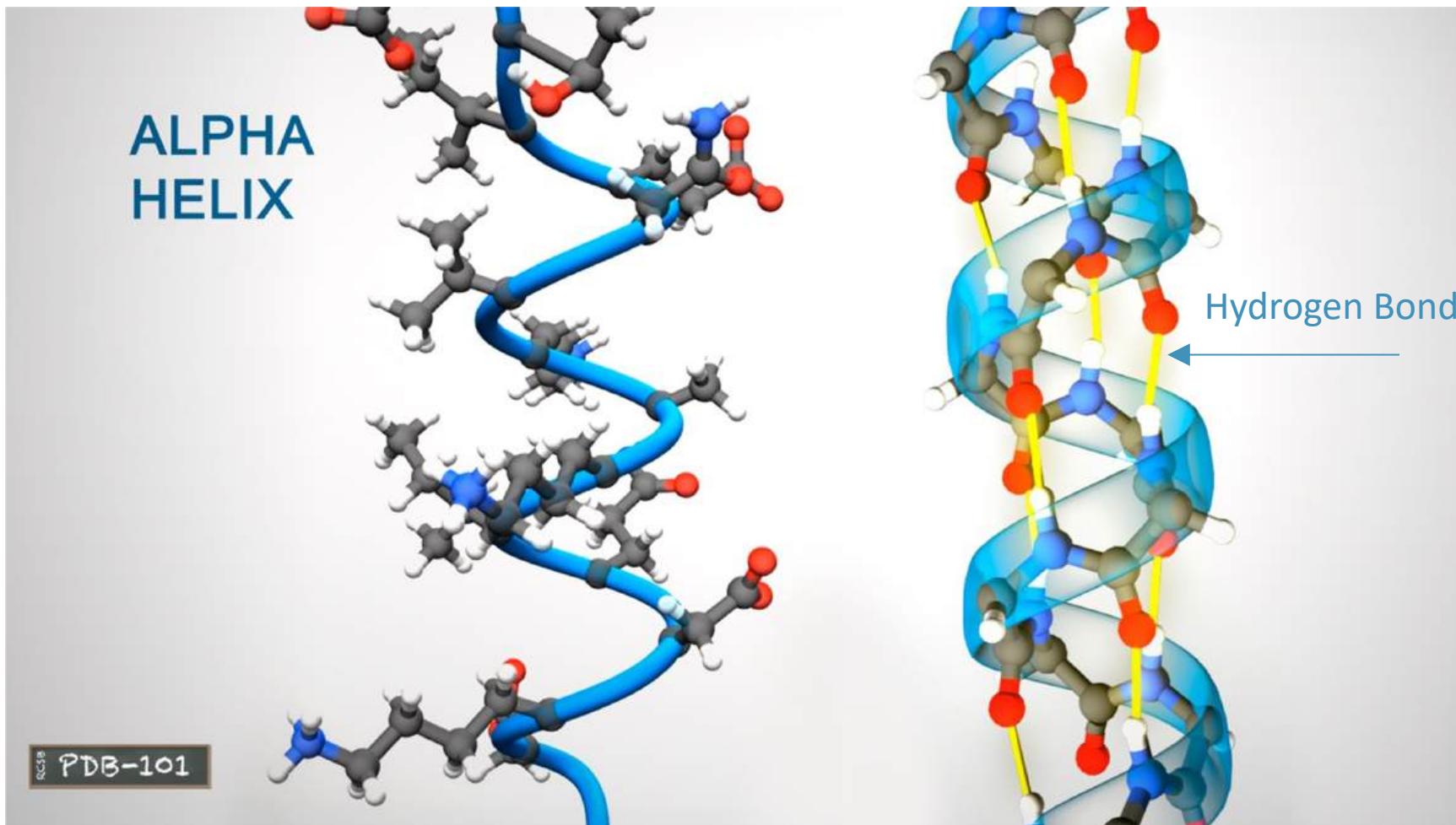
[pdb101.rcsb.org](https://www.rcsb.org/pdb101)



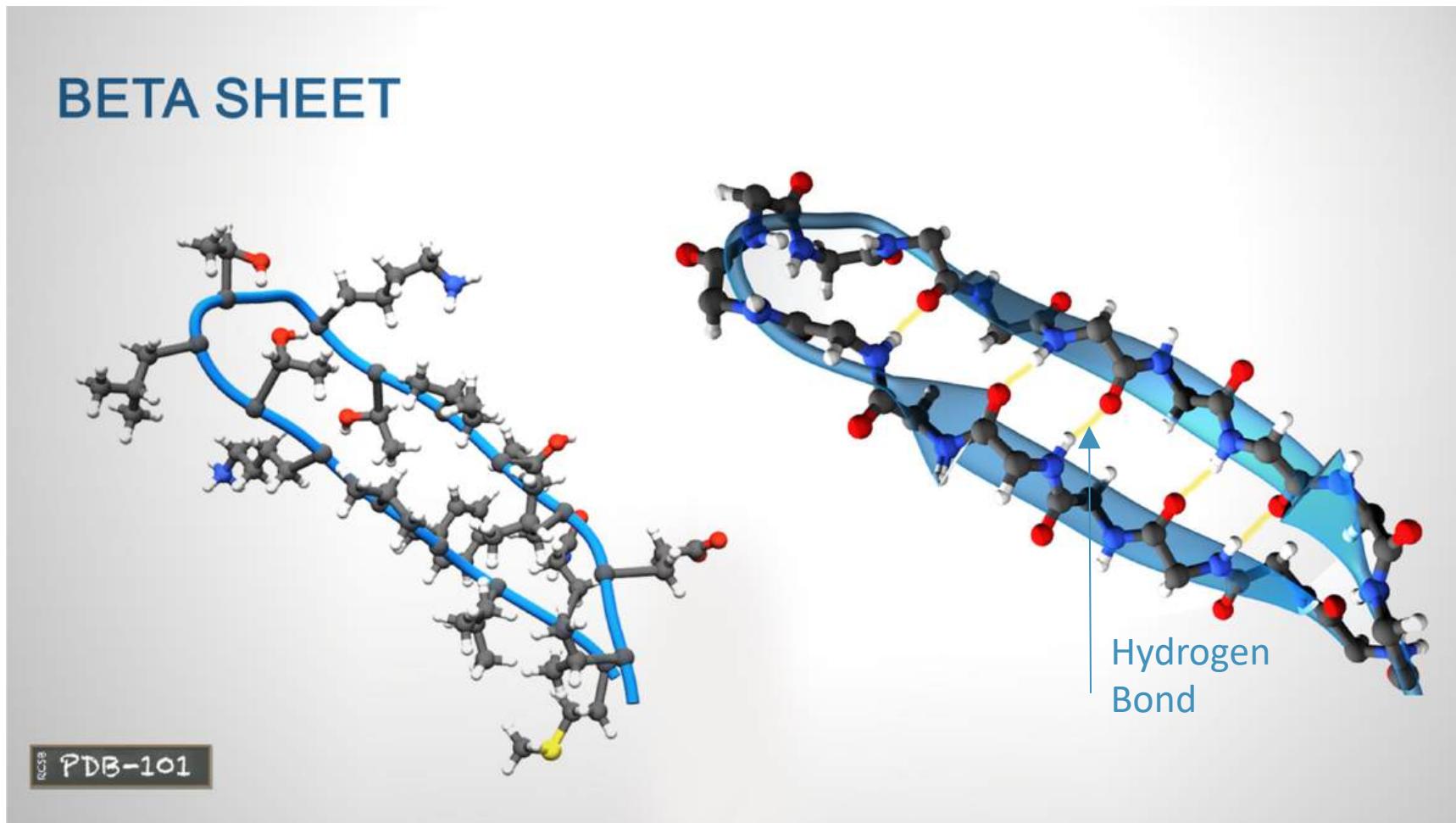
The protein chains often fold into two types of secondary structures: **alpha helices**, or **beta sheets**.

Protein Structure: Secondary Structure

[pdb101.rcsb.org](https://www.rcsb.org/pdb101)



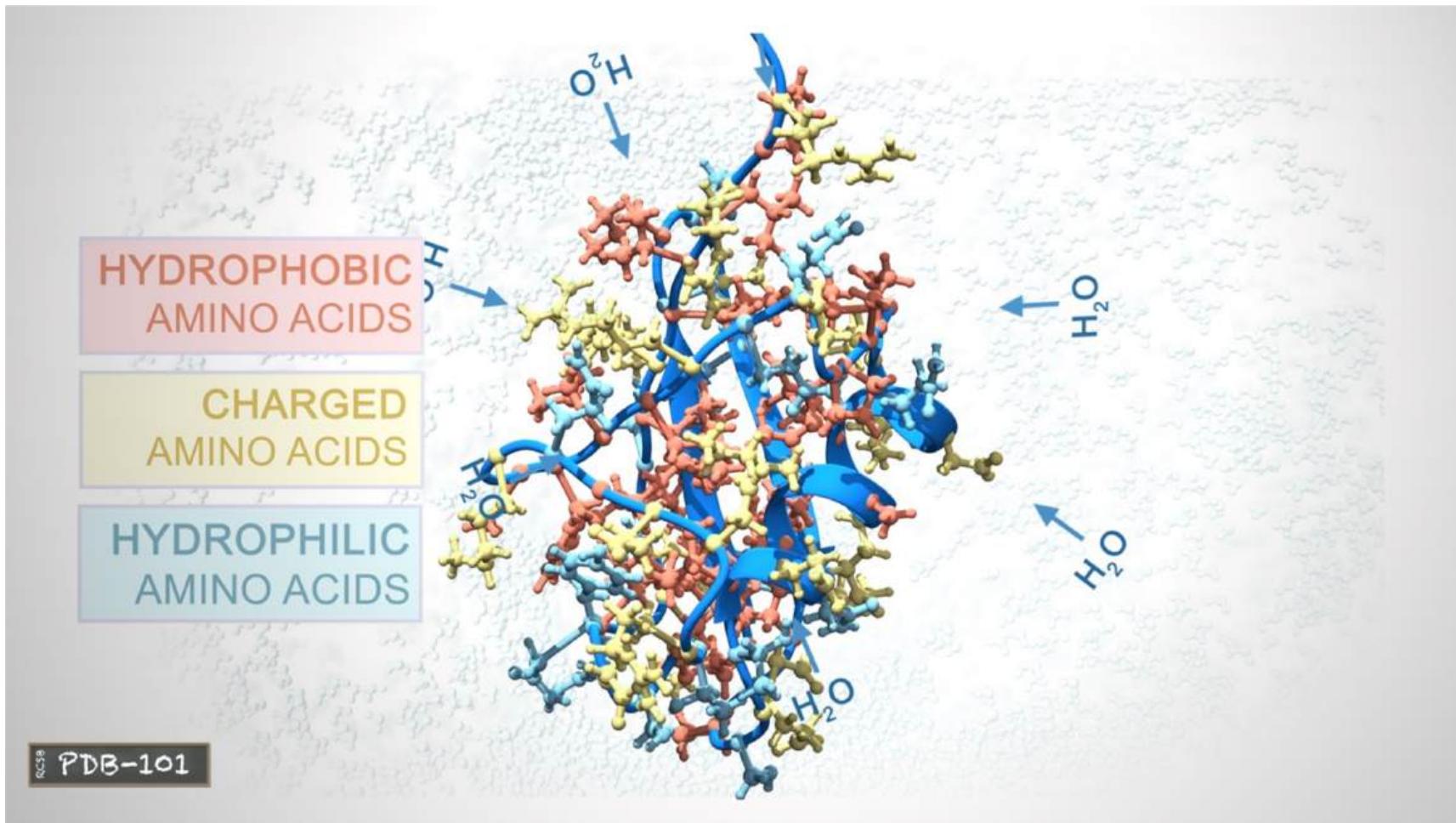
An alpha helix is a **right-handed coil** stabilized by **hydrogen bonds** between the amine and carboxyl groups of nearby amino acids



Beta-sheets are formed when hydrogen bonds stabilize **two or more adjacent strands**.

Protein Structure: Tertiary Structure

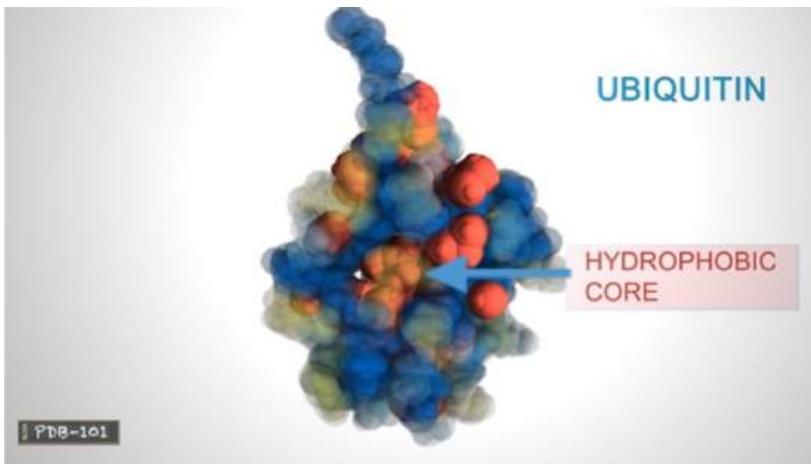
[pdb101.rcsb.org](https://www.rcsb.org/pdb101)



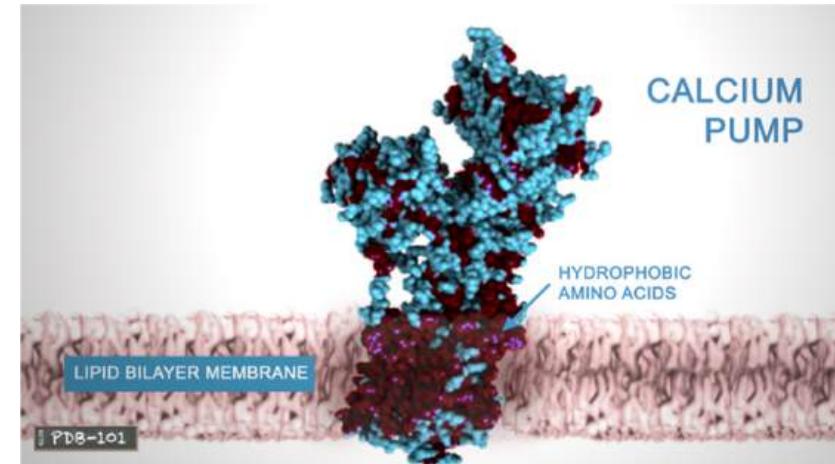
The tertiary structure of a protein is the **three-dimensional shape of the protein chain**. This shape is determined by the characteristics of the amino acids making up the chain.

Protein Structure: Tertiary Structure

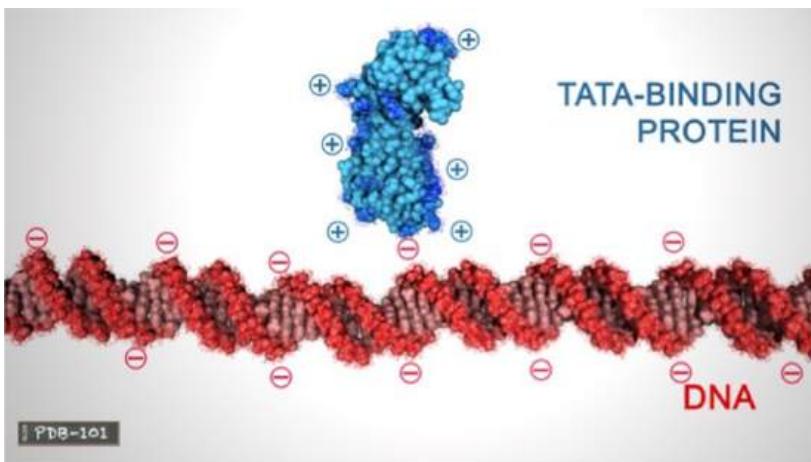
[pdb101.rcsb.org](https://www.rcsb.org/pdb101)



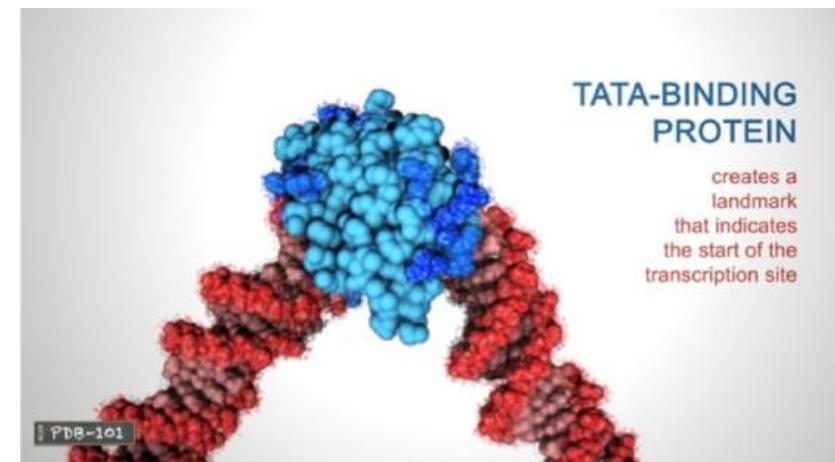
Many proteins form globular shapes with hydrophobic side chains sheltered inside, away from the surrounding water.



Membrane-bound proteins have hydrophobic residues clustered together on the outside, so that they can interact with the lipids in the membrane.

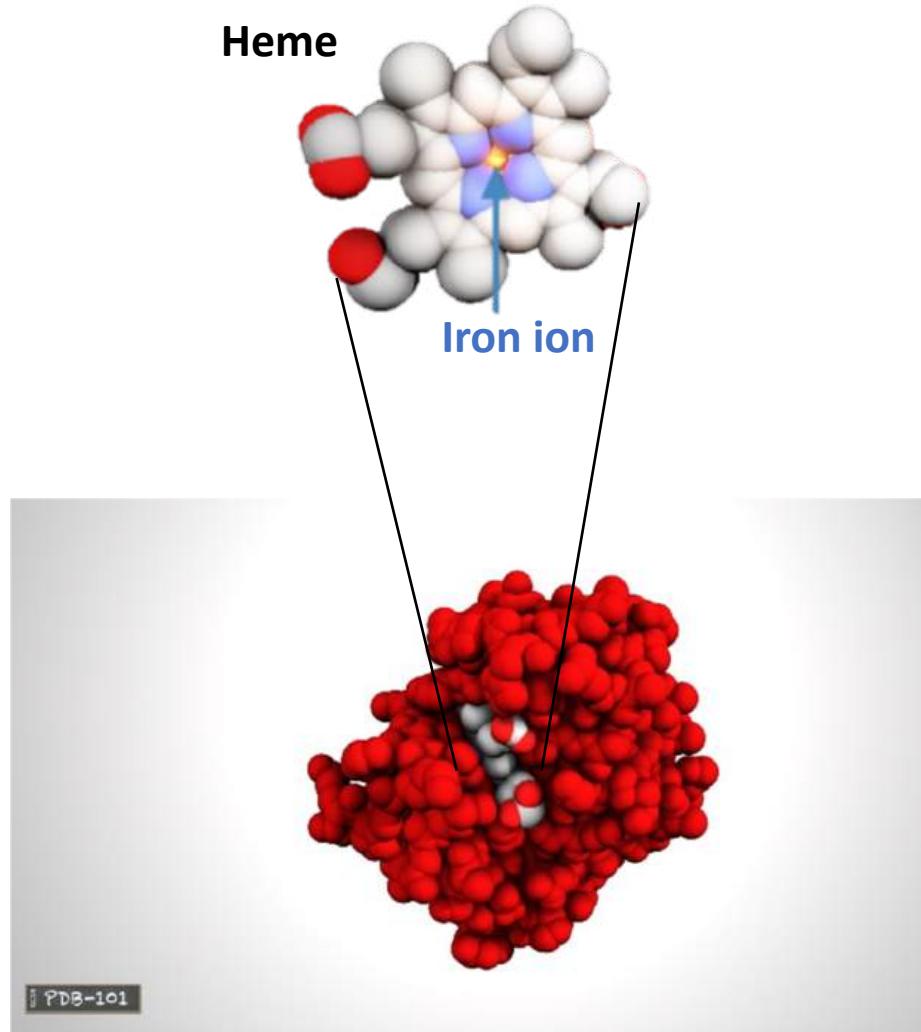


Charged amino acids allow proteins to interact with molecules that have complementary charges.



Protein Structure: Tertiary Structure

[pdb101.rcsb.org](https://www.rcsb.org/pdb101)

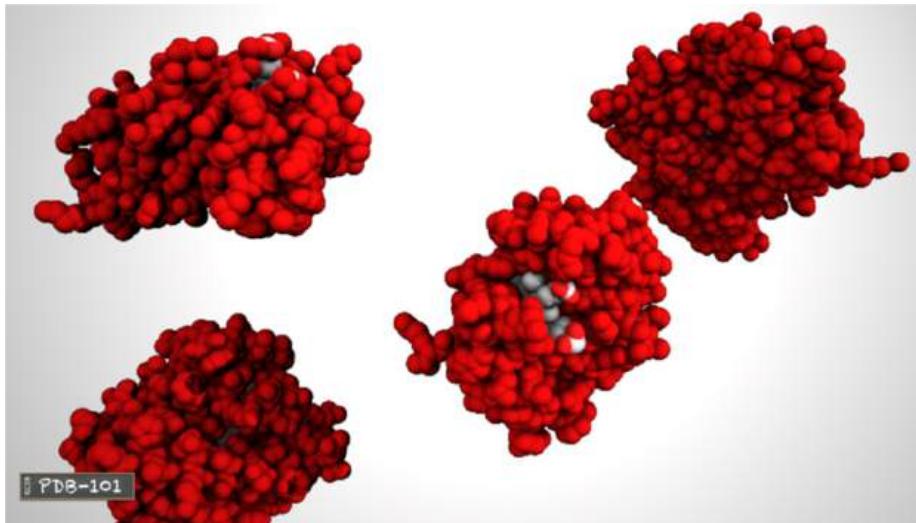


The functions of many proteins rely on their three-dimensional shapes.

For example, **hemoglobin** forms a pocket to hold **heme**, a small molecule with an **iron** atom in the center that binds oxygen.

Protein Structure: Quaternary Structure

[pdb101.rcsb.org](https://www.rcsb.org/pdb101)



Two or more polypeptide chains can come together to form one functional molecule with several subunits.



For example, the four subunits of hemoglobin cooperate so that the complex can pick up more oxygen in the lungs and release it in the body.

Protein Data Bank (PDB)

The screenshot shows the homepage of the RCSB Protein Data Bank (PDB). At the top left is the RCSB PDB logo with the text "PROTEIN DATA BANK". To its right is a banner stating "138464 Biological Macromolecular Structures Enabling Breakthroughs in Research and Education". A search bar at the top right contains the placeholder "Search by PDB ID, author, macromolecule, sequence, or ligands" with a "Go" button. Below the search bar are links for "Advanced Search" and "Browse by Annotations". The header also features a map of the world and social media icons for Facebook, Twitter, YouTube, and GitHub.

Welcome

- Deposit**
- Search**
- Visualize**
- Analyze**
- Download**
- Learn**

A Structural View of Biology

This resource is powered by the Protein Data Bank archive-information about the 3D shapes of proteins, nucleic acids, and complex assemblies that helps students and researchers understand all aspects of biomedicine and agriculture, from protein synthesis to health and disease.

As a member of the wwPDB, the RCSB PDB curates and annotates PDB data. The RCSB PDB builds upon the data by creating tools and resources for research and education in molecular biology, structural biology, computational biology, and beyond.

New Video: What is a Protein?

PDB-101
VIDEO
WHAT IS A
PROTEIN?

March Molecule of the Month

Vacuolar ATPase

Protein Data Bank (PDB)

The screenshot shows the RCSB PDB homepage on the left and a detailed search result page for 'Hemoglobin' on the right.

RCSB PDB PROTEIN DATA BANK
138878 Biological Macromolecular Structures Enabling Breakthroughs in Research and Education

A Structural View of Bi
This resource is powered by the Protein Data Bank. It provides access to the 3D shapes of proteins, nucleic acids, and carbohydrates, enabling students and researchers understand all aspects of molecular biology from protein synthesis to health and disease.

As a member of the wwPDB, the RCSB PDB builds upon the data by providing a single, integrated resource for the research and education in molecular biology, and beyond.

New Video: What is a Protein?

Hemoglobin Go

UniProt Molecule Name

- Hemoglobin beta chain (330)
- Hemoglobin alpha chain (326)
- Hemoglobin subunit beta (325)
- Dimeric hemoglobin (64)
- Hemoglobin (19)
- Neural hemoglobin (17)

[More](#) [Find all](#)

Structural Domains

- Hemoglobin... (245)
- Alpha-hemoglobin... (8)
- Hemoglobin... (237)
- Hemoglobin [SCOP] (1)
- Hemoglobin I [SCOP] (20)
- Protozoan... hemoglobin... (15)

[More](#)

Membrane Proteins

- Hbp (hemoglobin... (2))

[close](#)

Sequence Cluster Name

- GLOBIN LI637

[Find all](#)

Ontology Terms

- hemoglobin... (33)
- hemoglobin... (427)
- hemoglobin... (265)
- AT : HEMOGLOBIN... (2)
- D12.776.124.400.405: Hemog... [... (36)
- hemoglobin... (4)

[More](#)

Vacuolar ATPase

Protein Data Bank (PDB)

Search Parameter:

Refinements

Currently showing 1 - 25 of 710 Page: 1 of 29 ← Previous Next → Displaying 25 Results

View: Reports: Sort: Download Files

Organism: Homo sapiens (270) Scapharca inaequivalvis (66) Amphitrite ornata (26) Equus caballus (18) Lupinus luteus (17) Cerebratulus lacteus (17) Physeter catodon (14) Other (282)

UNIPROT MOLECULE NAME: Hemoglobin subunit alpha (326) Hemoglobin subunit beta (325) Globin-1 (64) Dehaloperoxidase A (24) Leghemoglobin-2 (17) Neural hemoglobin (17) Hemoglobin subunit alpha-A (16) Refine Query

1FN3

CRYSTAL STRUCTURE OF NICKEL RECONSTITUTED HEMOGLOBIN-A CASE FOR PERMANENT, T-STATE HEMOGLOBIN

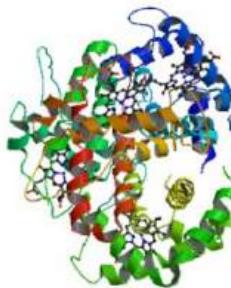
Venkateshrao, S., Deepthi, S., Pattabhi, V., Manoharan, P.T.

PubMed ID is not available.

Released: 10/7/2003 Method: X-ray Diffraction Resolution: 2.48 Å Residue Count: 574

Macromolecule: HEMOGLOBIN ALPHA CHAIN (protein) HEMOGLOBIN BETA CHAIN (protein) Unique Ligands: HNI Search term match score: 268.69

Matched fields in 1FN3.cif:

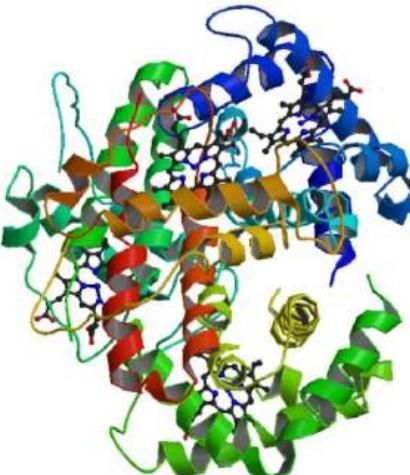


3D View

Protein Data Bank (PDB)

Structure Summary 3D View Annotations Sequence Sequence Similarity Structure Similarity Experiment

Biological Assembly 1 ?



1FN3

CRYSTAL STRUCTURE OF NICKEL RECONSTITUTED HEMOGLOBIN-A CASE FOR PERMANENT, T-STATE HEMOGLOBIN

DOI: [10.22110/pdb1FN3/pdb](https://doi.org/10.22110/pdb1FN3/pdb)

Classification: [OXYGEN STORAGE/TRANSPORT](#)

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

Deposited: 2000-08-20 Released: 2003-10-07

Deposition Author(s): [Venkateshrao, S., Deepthi, S., Patabhi, V., Manoharan, P.T.](#)

Experimental Data Snapshot

Method: X-RAY DIFFRACTION
Resolution: 2.48 Å

R-Value Free: 0.324
R-Value Work: 0.242

wwPDB Validation

Metric	Percentile Ranks	Value
Clashscore	66	
Ramachandran outliers	5.5%	
Sidechain outliers	35.7%	
RSRZ outliers	15.3%	

Worse Better
Percentile relative to all X-ray structures
Percentile relative to X-ray structures of similar resolution

Literature

Crystal Structure of Nickel Reconstituted Hemoglobin - A Case for Permanent, T-State Hemoglobin

[Venkateshrao, S., Deepthi, S., Patabhi, V., Manoharan, P.T.](#)
(2003) CURR.SCI. 84: 179-187

Download Primary Citation ▾

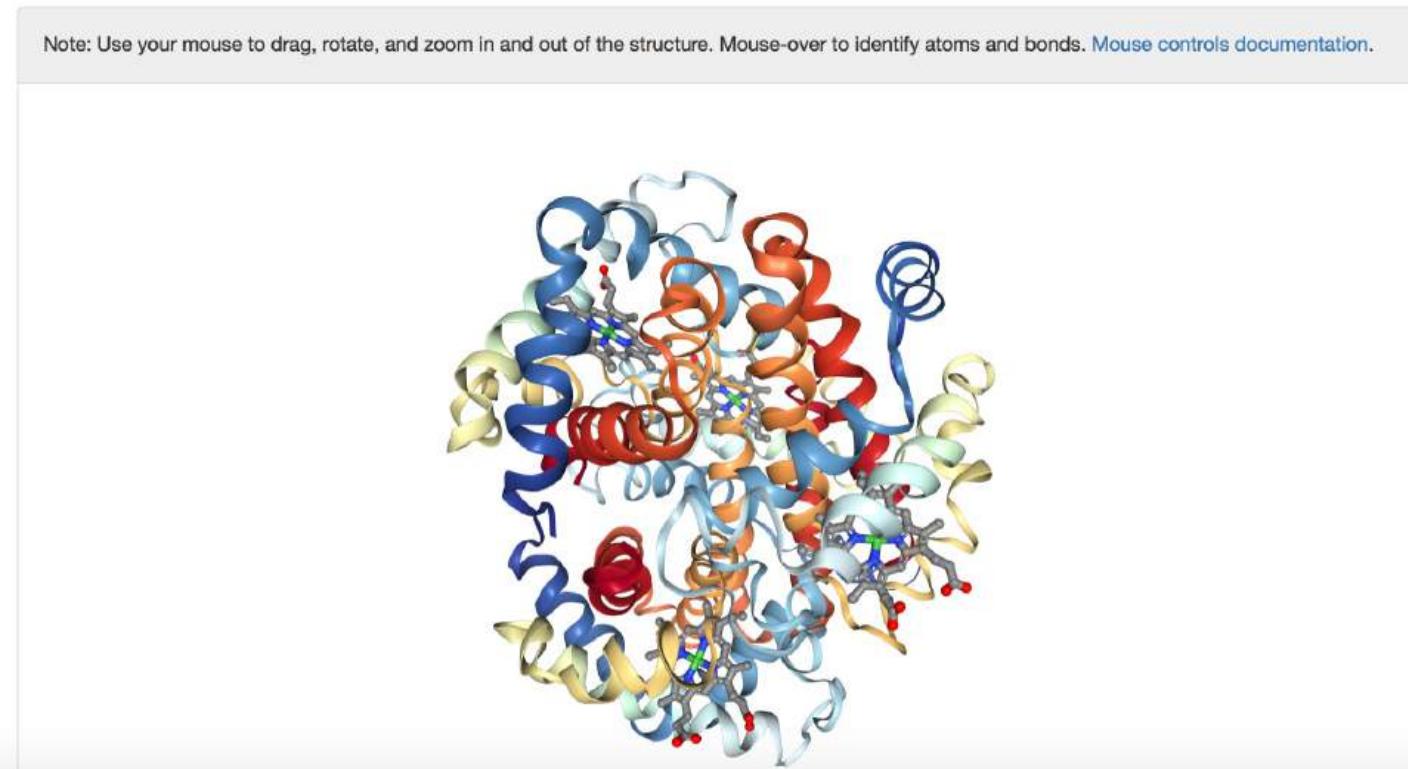
Protein Data Bank (PDB)

Structure Summary 3D View Annotations Sequence Sequence Similarity Structure Similarity Experiment

1FN3

CRYSTAL STRUCTURE OF NICKEL RECONSTITUTED HEMOGLOBIN-A CASE FOR PERMANENT, T-STATE

Note: Use your mouse to drag, rotate, and zoom in and out of the structure. Mouse-over to identify atoms and bonds. [Mouse controls documentation.](#)



Sequence format

Display Files Download Files

FASTA Sequence

PDB Format

PDB Format (gz)

PDBx/mmCIF Format

PDBx/mmCIF Format (gz)

PDBML/XML Format (gz)

Biological Assembly 1

Structure Factors (CIF)

Structure Factors (CIF - gz)

2fo-fc Map (DSN6)

fo-fc Map (DSN6)

Water ? Ions ?

Hydrogens ? Clashes ?

Default Structure View ?

HEADER

OXYGEN STORAGE/TRANSPORT

20-AUG-00

1FN3

TITLE

CRYSTAL STRUCTURE OF NICKEL RECONSTITUTED HEMOGLOBIN-A CASE FOR

TITLE

2 PERMANENT, T-STATE HEMOGLOBIN

SOURCE MOL_ID: 1;

SOURCE 2 ORGANISM_SCIENTIFIC: HOMO SAPIENS;

SOURCE 3 ORGANISM_COMMON: HUMAN;

SOURCE 4 ORGANISM_TAXID: 9606;

KEYWDS PERMANENT T-STATE, METAL ION COORDINATION, SUBUNIT INEQUIVALENCE,

KEYWDS 2 SPECTROSCOPY, CRYSTALLOGRAPHY., OXYGEN STORAGE-TRANSPORT COMPLEX

EXPDAT X-RAY DIFFRACTION

AUTHOR S.VENKATESHRAO,S.DEEPITHI,V.PATTABHI,P.T.MANOHARAN

REMARK 2 RESOLUTION. 2.48 ANGSTROMS

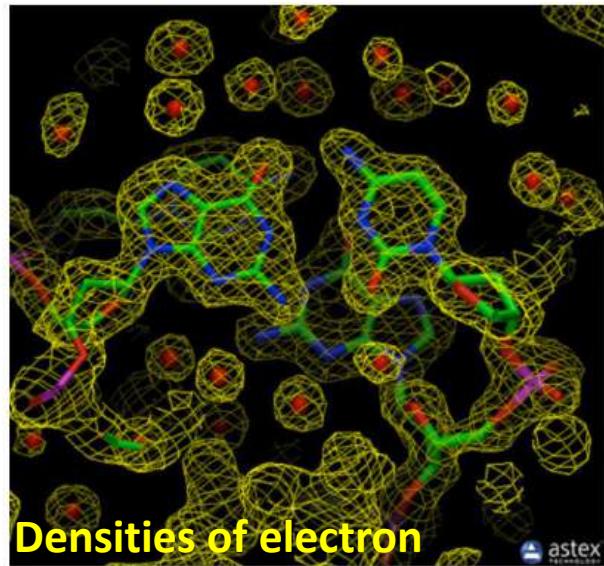
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ATOM	2	CA	VAL A	1	43.152	19.932	2.662	1.00	30.16	C
ATOM	3	C	VAL A	1	42.742	20.917	1.574	1.00	26.03	C
ATOM	4	O	VAL A	1	41.698	20.768	0.947	1.00	29.47	O
ATOM	5	CB	VAL A	1	43.197	18.504	2.062	1.00	33.08	C
ATOM	6	CG1	VAL A	1	41.808	18.088	1.572	1.00	36.44	C
ATOM	7	CG2	VAL A	1	44.230	18.448	0.938	1.00	34.80	C
ATOM	8	N	LEU A	2	43.570	21.931	1.360	1.00	23.04	N
ATOM	9	CA	LEU A	2	43.289	22.947	0.349	1.00	17.29	C
ATOM	10	C	LEU A	2	44.042	22.680	-0.952	1.00	12.46	C

: Atomic coordinates

Methods for Determining Atomic Structures

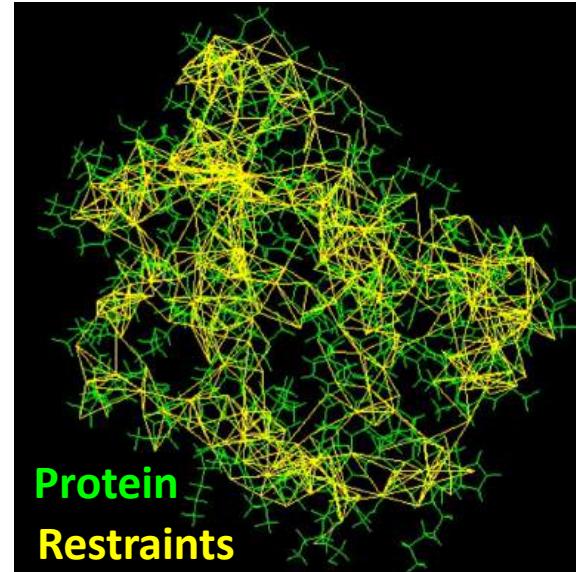
X-ray Crystallography

diffraction pattern



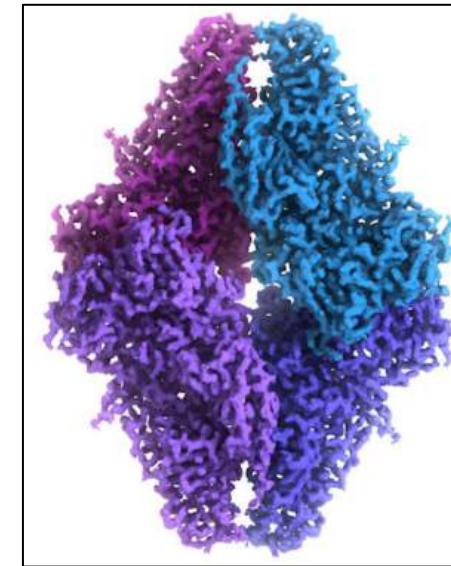
NMR Spectroscopy

distance between atoms



cryo-Electron Microscopy

image of the overall shape



- 需要純化與結晶
- 只能解析重原子
- PDB 資料最多!
- 誤差 1-2 埃

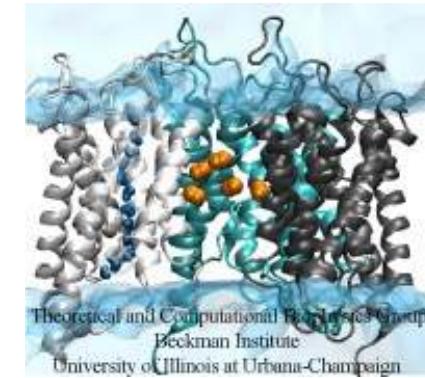
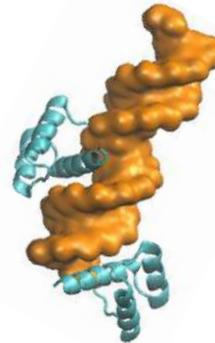
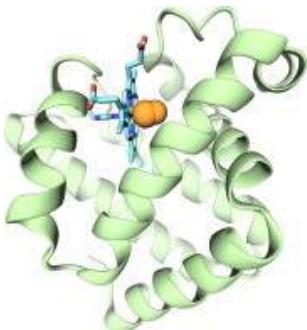
- 溶液或固態 (無需結晶)
- 多種結構(系綜)
- 誤差2-4埃

- 專解巨型大分子
- 解析度稍低
- 多種方法混搭使用能完善
解析度
- 誤差2-9埃



<http://www.ks.uiuc.edu/Research/vmd/>

VMD is designed for **visualization, analysis, and modeling** of biological systems such as proteins, nucleic acids, lipid bilayer assemblies, etc. VMD can read standard Protein Data Bank (**PDB**) files and display the contained structure.

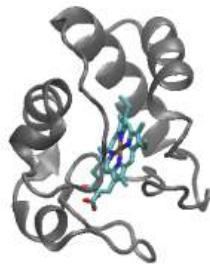


Theoretical and Computational Biophysics Group
Beckman Institute
University of Illinois at Urbana-Champaign

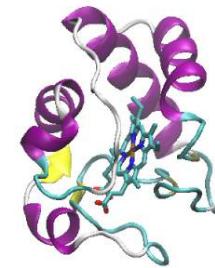
- Support all major computer platforms (ex. MacOS X, Windows, Linux)
- Many molecular rendering and coloring methods

What Can We Do with VMD?

- Visualize the structures that have been solved and reported

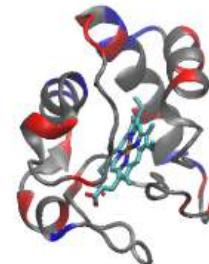


Cartoon
diagram

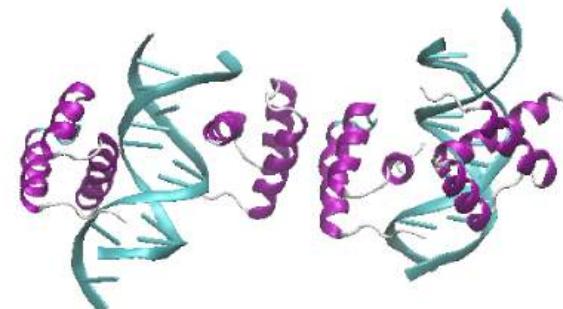


Secondary structure

PDB: 1hrc



Positively charged
Negatively charged

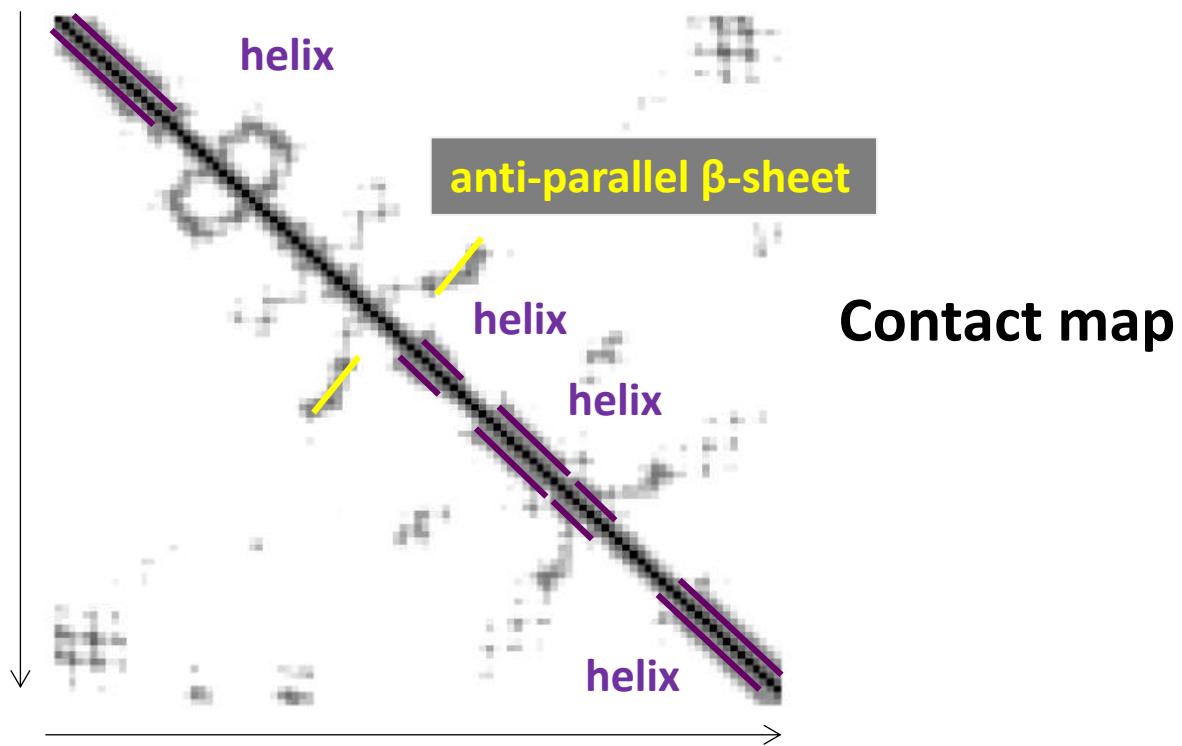
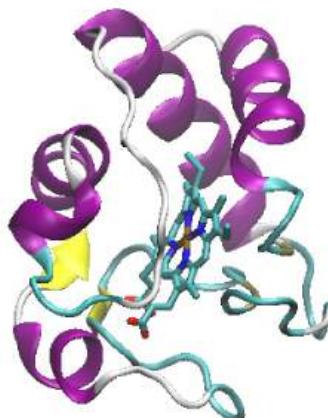


PDB: 4qtr

Multiple protein assembly

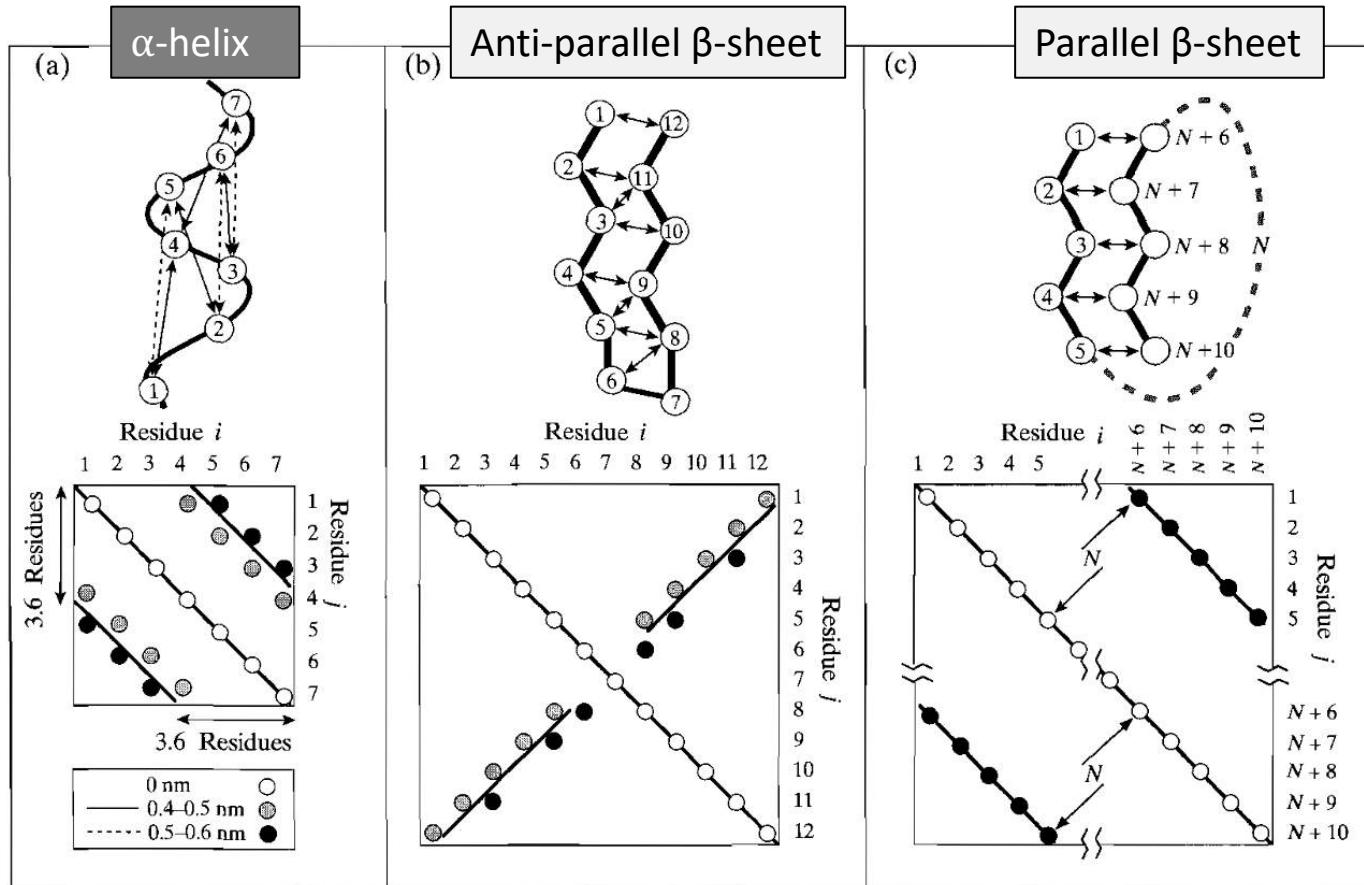
What Can We Do with VMD?

- Structural analysis (Contact map)



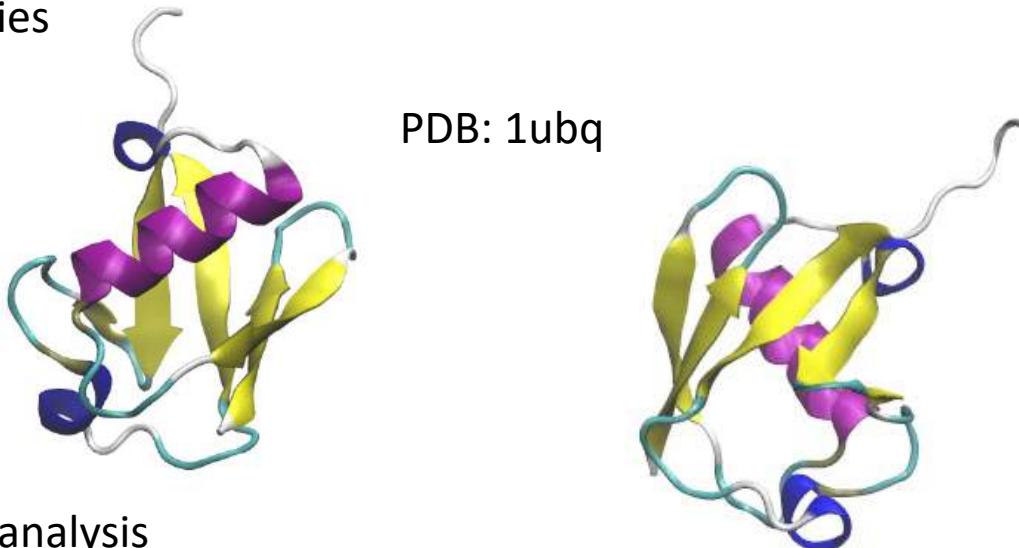
What Can We Do with VMD?

- Structural analysis (Contact plots for α -helix and β -sheets)

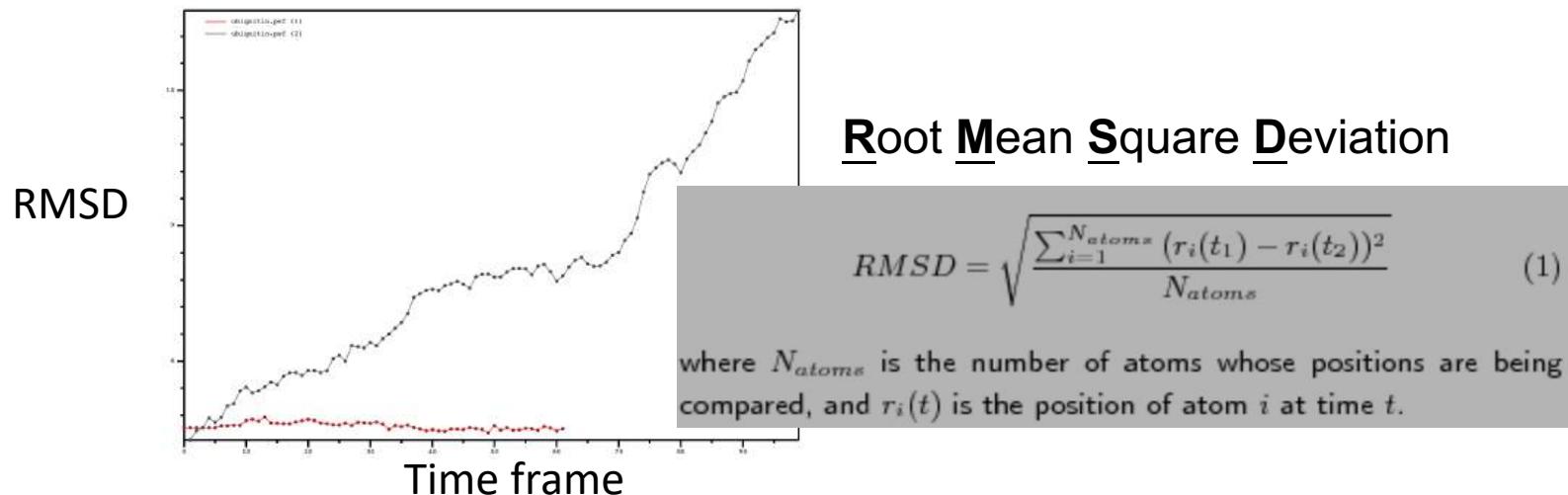


What Can We Do with VMD?

- Make movies

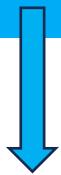
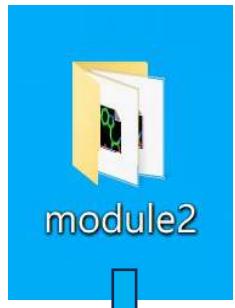


- Trajectory analysis



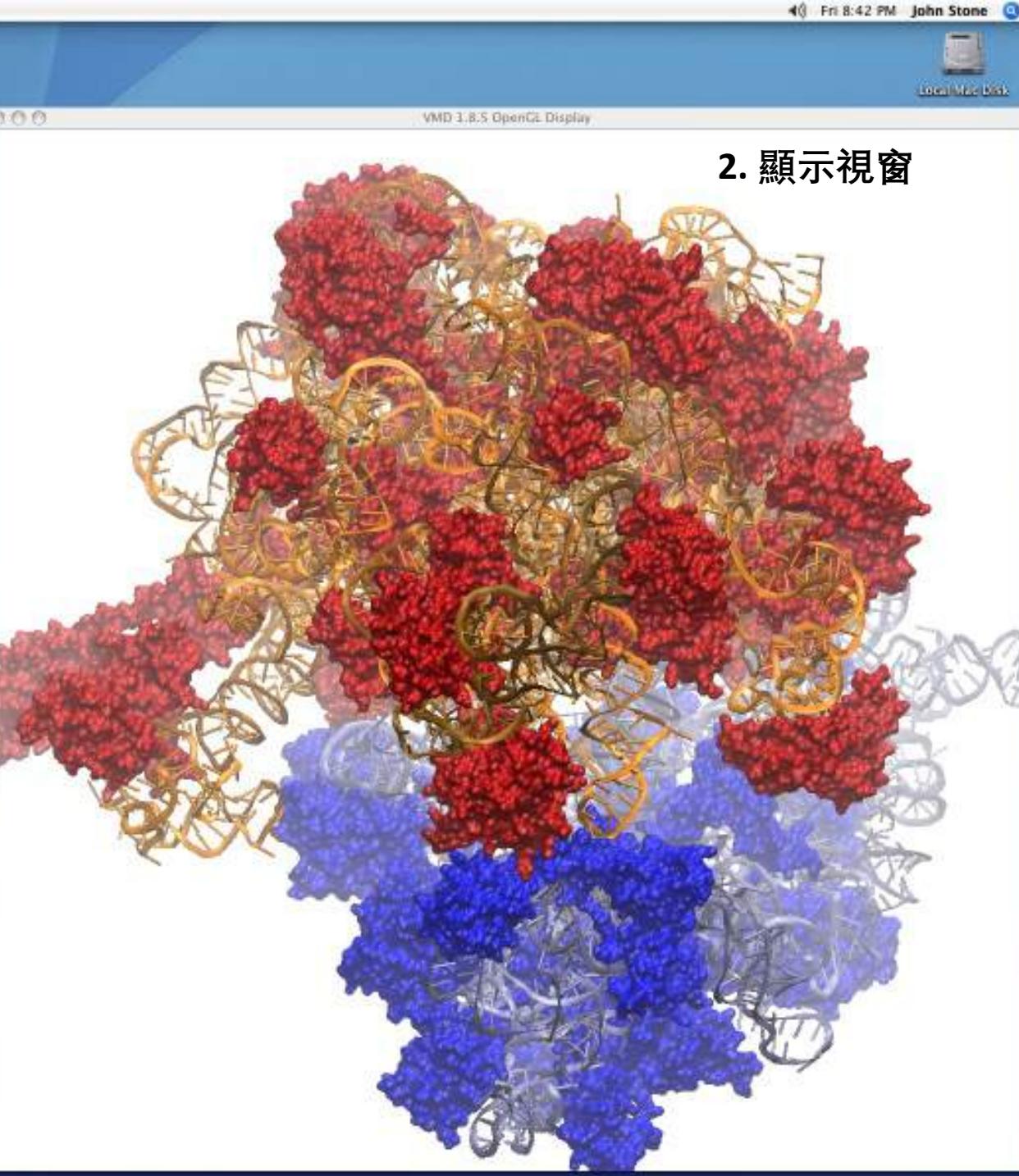
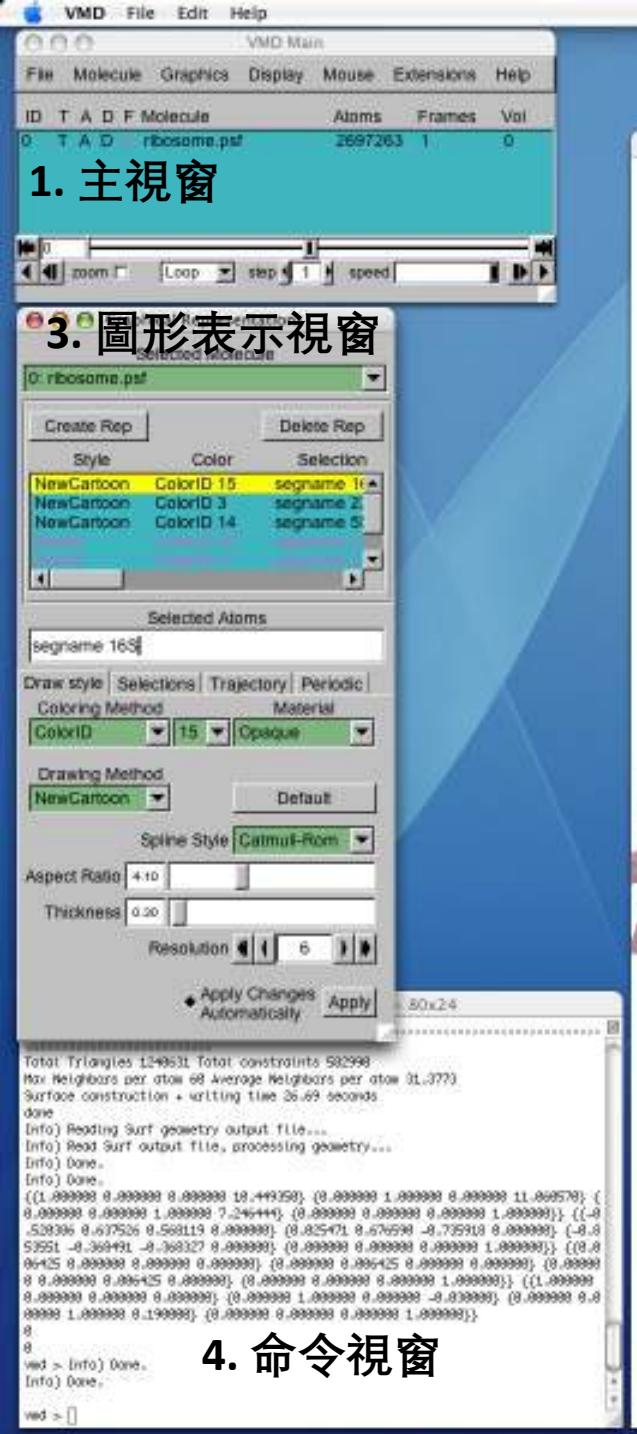
Now You Can Try to Launch VMD

桌面

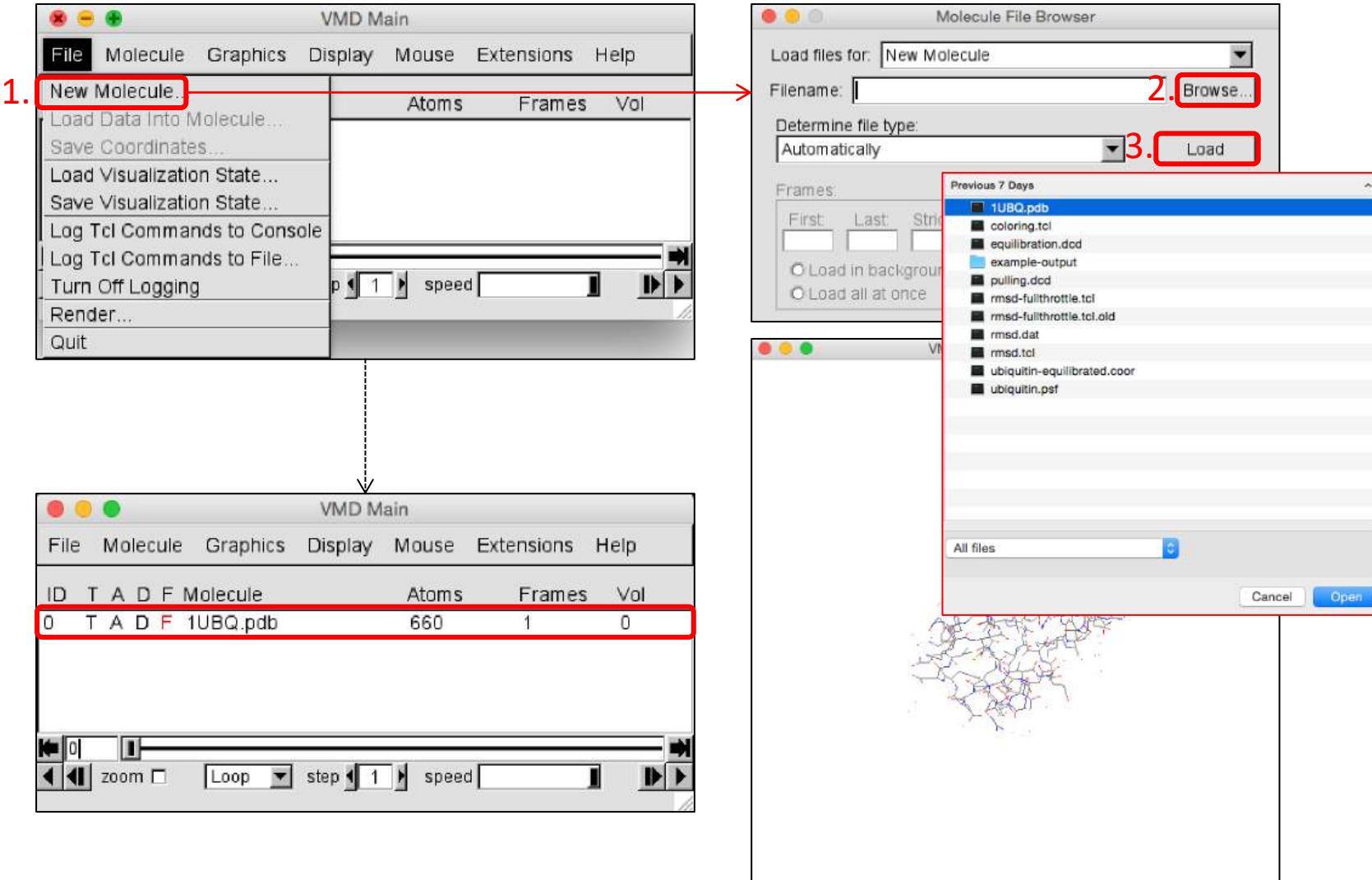


See *VMD-Installation-Guide.pdf* if you want to install it on your computer

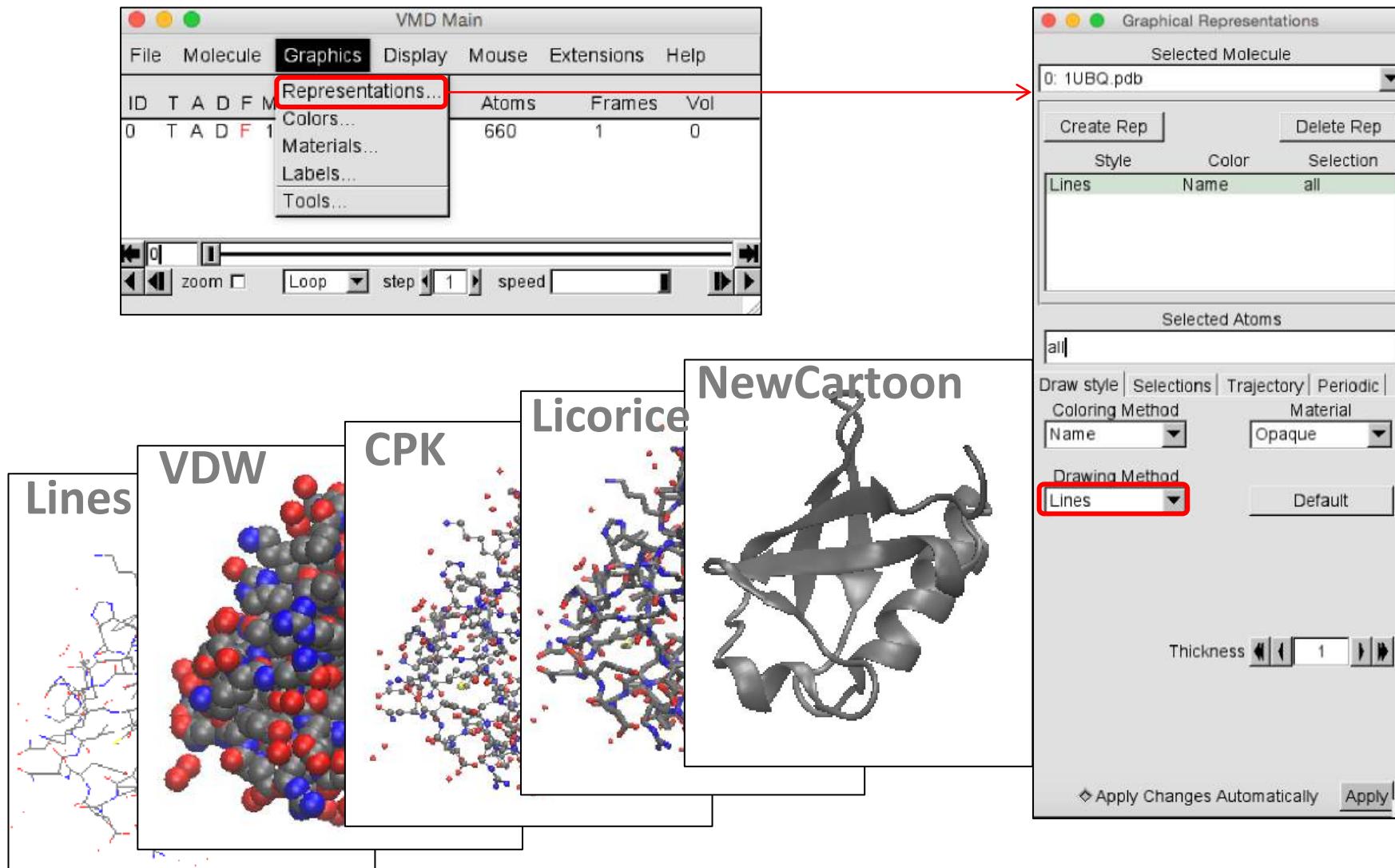
名稱	修改日期
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1ubq	2021/8/16
4qtr	2021/8/16
par_all36_prot.prm	2021/3/12
VMD-Installation-Guide	2018/3/15



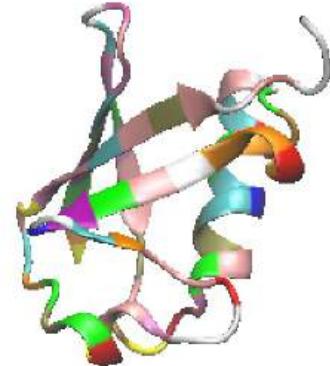
Loading a Molecule, Exploring it and Choosing Representations



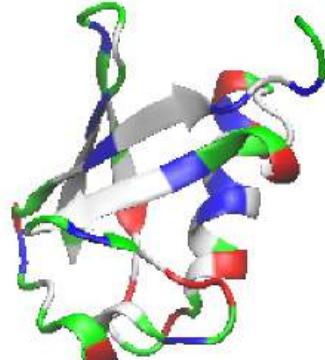
Loading a Molecule, Exploring it and Choosing Representations



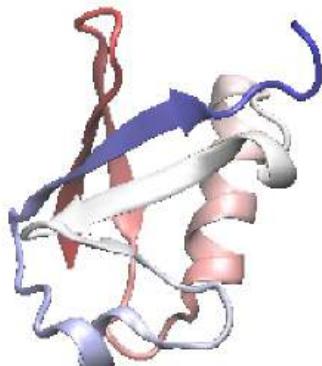
Loading a Molecule, Exploring it and Choosing Representations



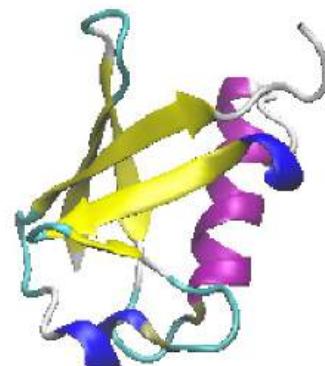
ResName



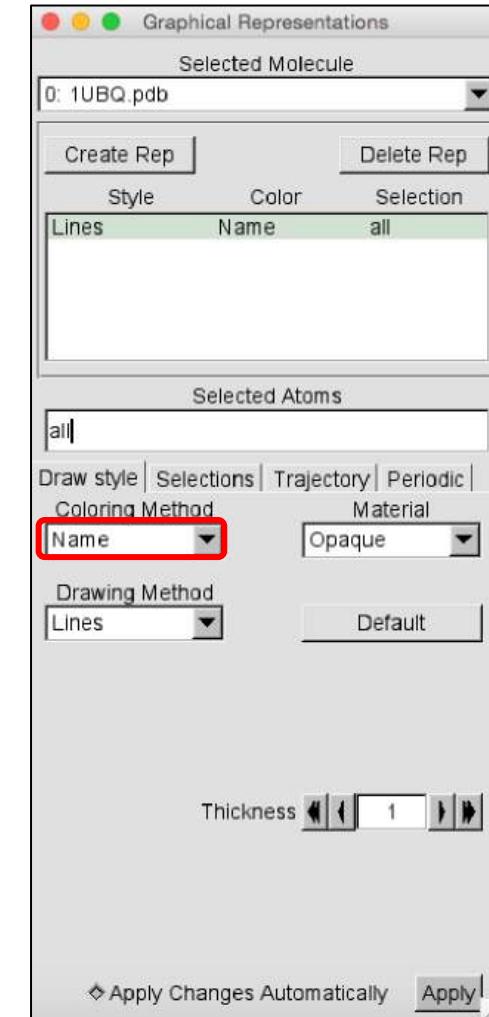
ResType



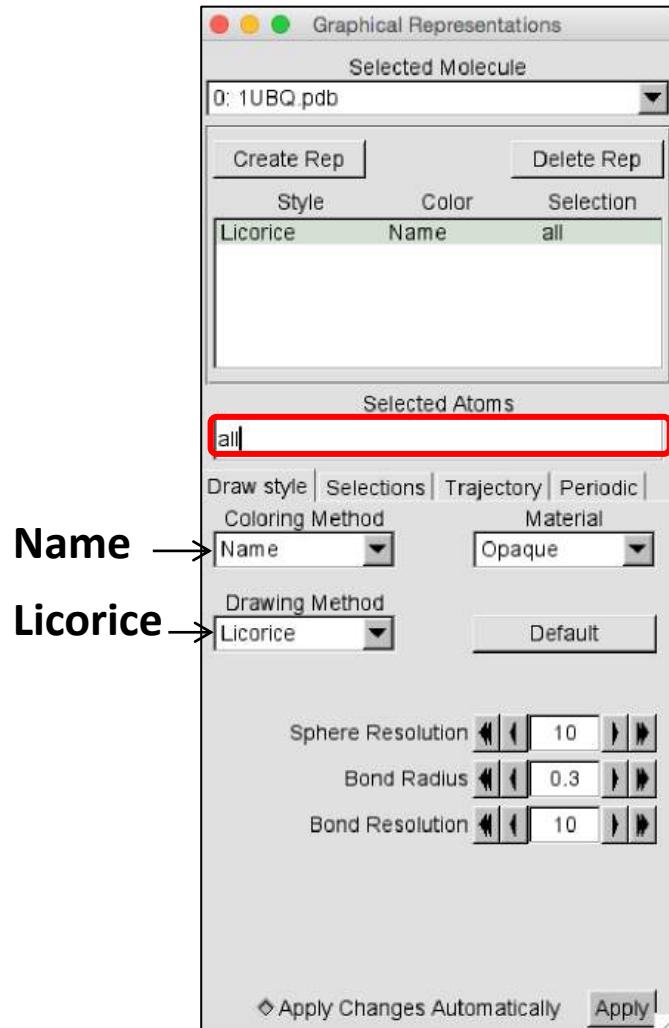
Index



Secondary Structure



Exercise: Selected Atoms

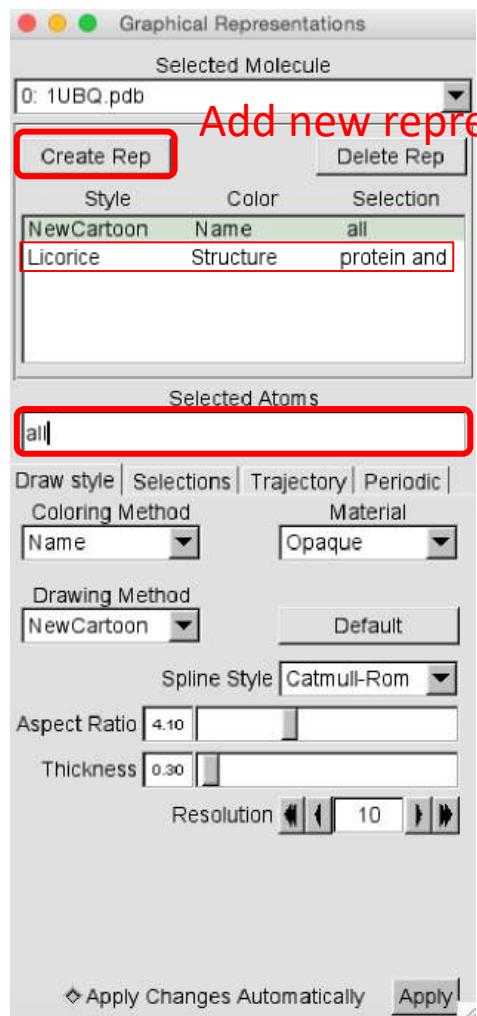


Selection	Action
protein	Shows the Protein
resid 1	The first residue
(resid 1 76) and (not water)	The first and last residues
(resid 23 to 34) and (protein)	The α -helix

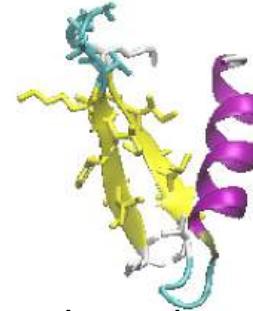
In **Drawing Method**, switch to “NewCartoon” to see the helix

Also try,
protein and resname LYS ARG
protein and resname GLU ASP

Displaying Different Selections



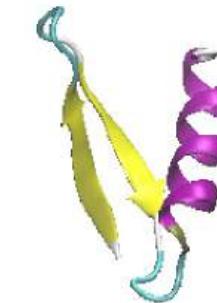
Add new representation



"protein and *resid 1 to 17*" with **Licorice**

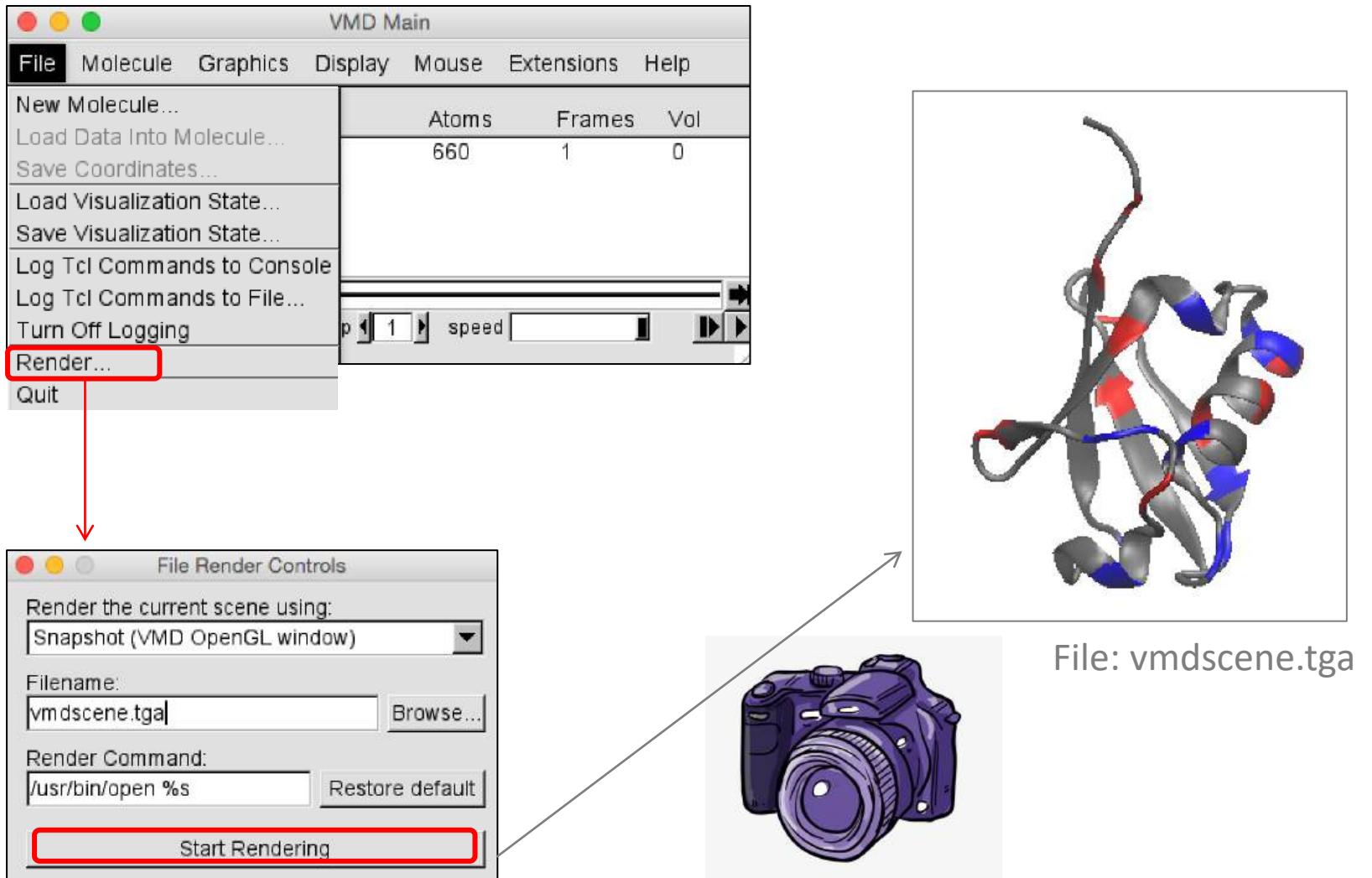


"protein and *resid 1 to 17*"



"protein and *resid 1 to 36*"

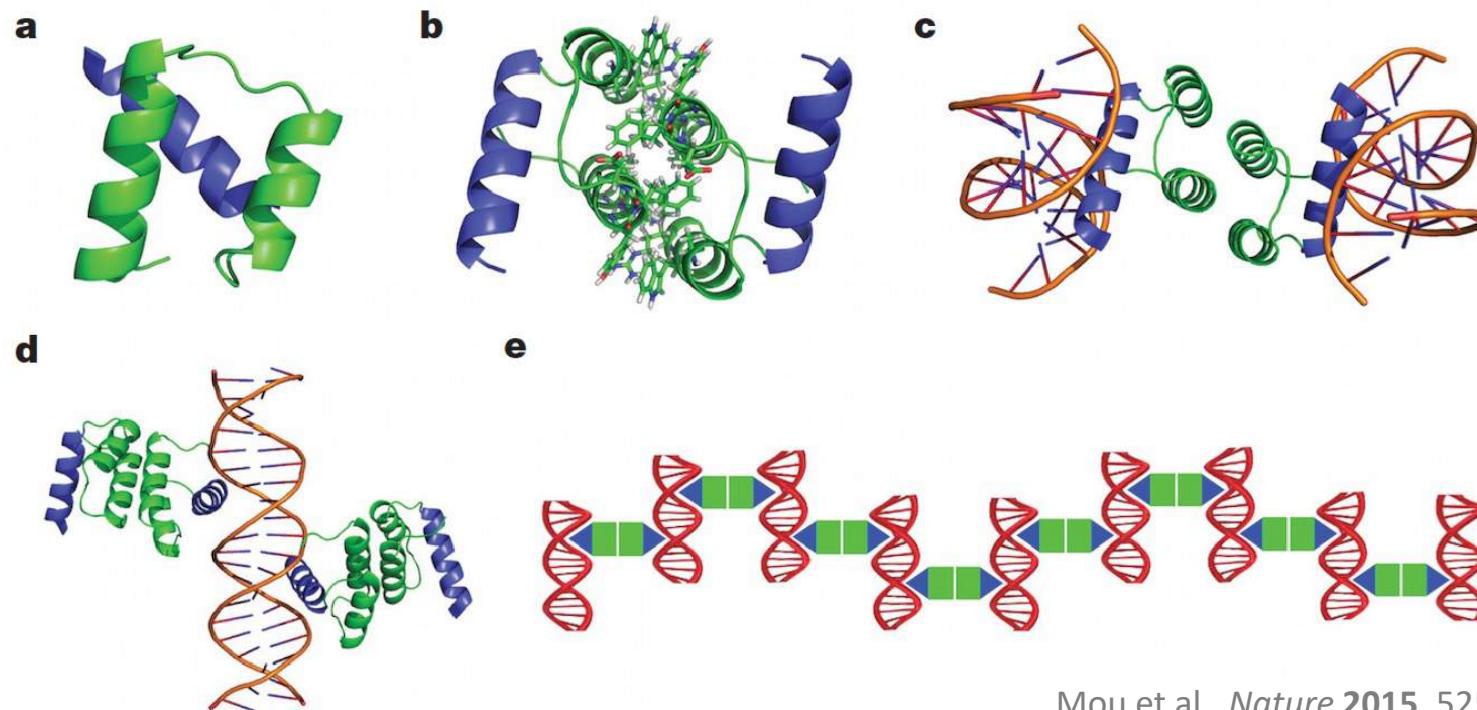
Rendering an Image

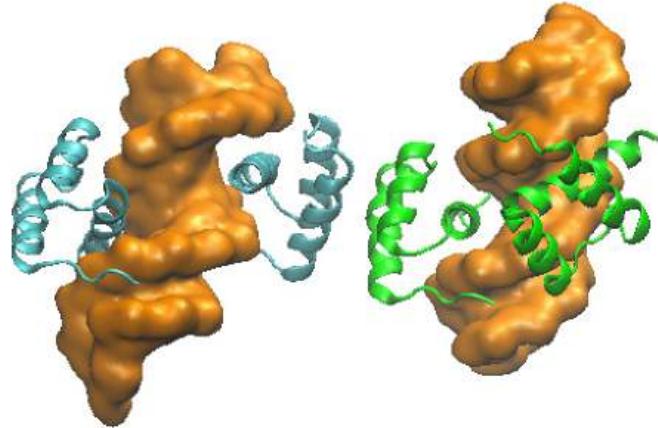


Computational design of co-assembling protein–DNA nanowires

Yun Mou¹, Jiun-Yann Yu², Timothy M. Wannier², Chin-Lin Guo³ & Stephen L. Mayo^{1,2}

230 | NATURE | VOL 525 | 10 SEPTEMBER 2015





Co-crystal structure for dualENH complexed with dsDNA
(PDB ID: 4QTR)

Demo

- Measure the distance between two atoms (Dimension of the molecular assembly)
- Visualize the distribution of charged residues on proteins
- Extract the structure of protein binding interface
- Calculate the total energy of the binding interface

Extended Data Table 1 | Sequences of wild-type ENH and dualENH

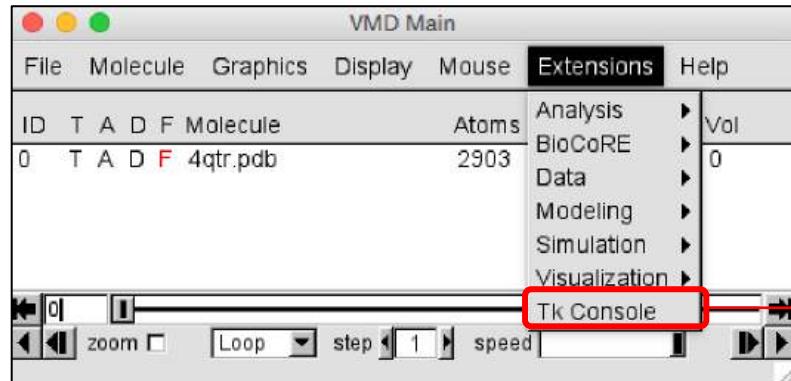
ENH (WT)	EKRPR TAF SSEQ LAR LKREF NRY LTER RR QQL SSEL GLNE A Q I KI WF QN KRA KIK KST
dualENH	----- E -- KKA - DLA - YFD ----- PEW - RY -- QR -----

Change Directory to Home “Desktop”

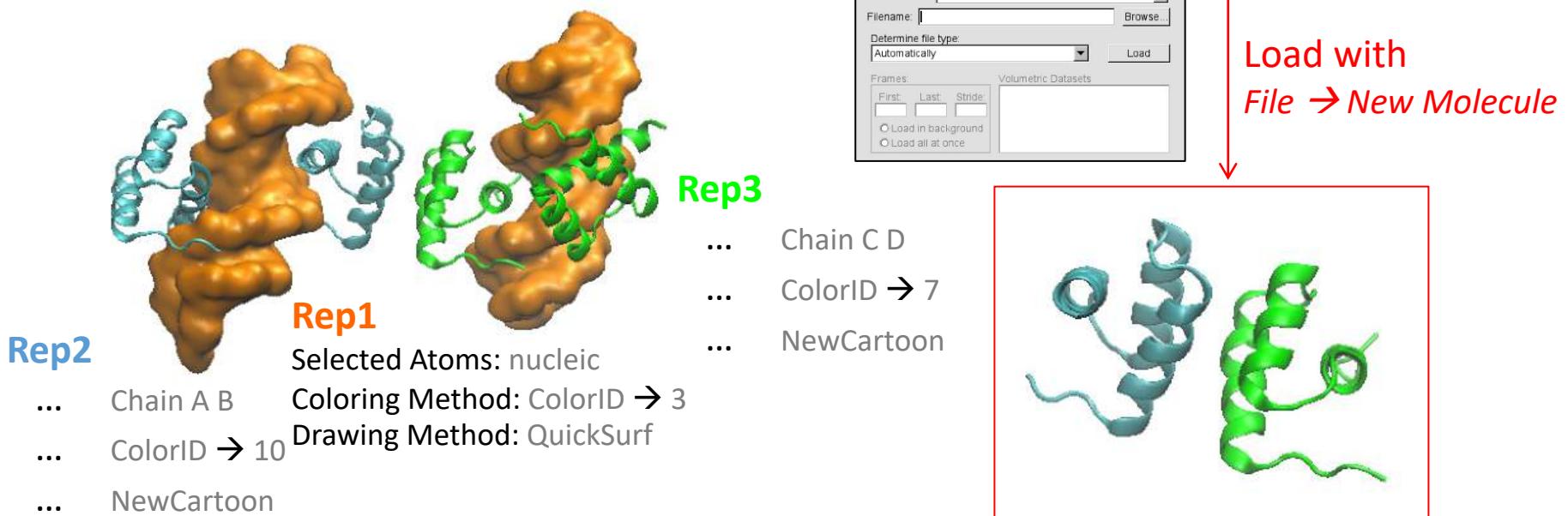
```
( ) 32 % pwd          → Check where you are in the path  
/  
( ) 33 % cd ~         → Change to ‘home’ directory  
(mytsai) 34 % pwd     → Check the path again  
/Users/mytsai  
(mytsai) 35 % cd Desktop/ → Change to ‘home’ Desktop  
(Desktop) 36 % pwd      → Check the path again  
/Users/mytsai/Desktop    → OK!  
(Desktop) 37 % |
```

“~” (curly brace): SHIFT + the key next to “1”

Extract the Structure at Binding Interface



```
loading history file ... 48 events added
Main console display active (Tcl8.5.6 / Tk8.5.6)
(MYTsa) 49 % set sel [atomselect top "chain B C"]
atomselect0
>Main< (MYTsai) 50 % $sel num
838
>Main< (MYTsai) 51 % $sel writepdb dimer.pdb
>Main< (MYTsai) 52 % pwd
/Users/MYTsa
>Main< (MYTsai) 53 %
```



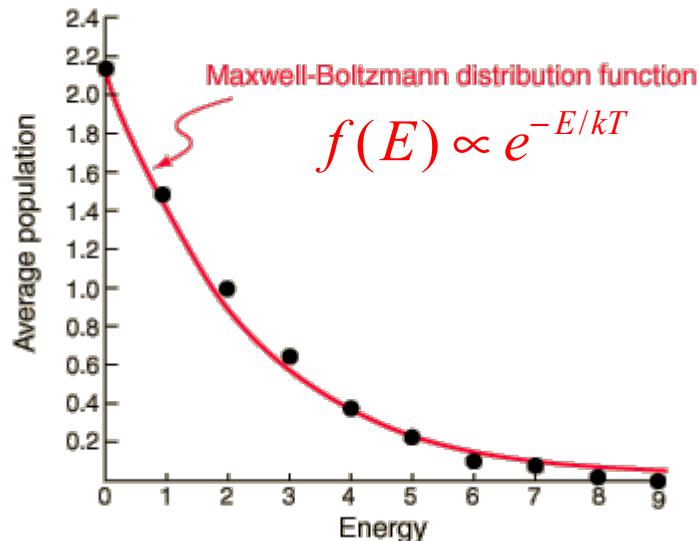
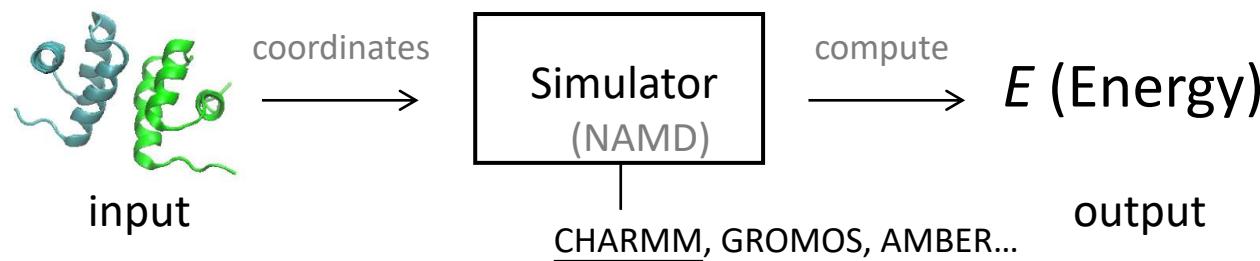
Use PSF Builder to Generate All-Atom Model

The image displays three windows illustrating the process of generating an all-atom model using VMD and AutoPSF.

- VMD Main Window:** Shows a list of molecules. The second molecule, "dimer.pdb", is highlighted with a green border. The "Extensions" menu is open, showing options like Analysis, BioCore, Data, Modeling, Simulation, Visualization, Tk Console, and "Automatic PSF Builder".
- AutoPSF Window:** A configuration window for "Step 1: Input and Output Files". It shows the "Molecule" dropdown set to "1: dimer.pdb" and the "Output basename" field set to "dimer_autopsf". Below it, "Topology files" are listed with a path to a VMD plugin directory. Buttons for "Add" and "Delete" are present. A red box highlights the "dimer_autopsf" output basename field.
- VMD OpenGL Display Window:** A 3D molecular visualization showing a complex protein dimer structure composed of grey sticks and red/purple spheres (representing atoms).
- Bottom Text:** The text "Add all hydrogen atoms back" is displayed in bold black font at the bottom right of the image.

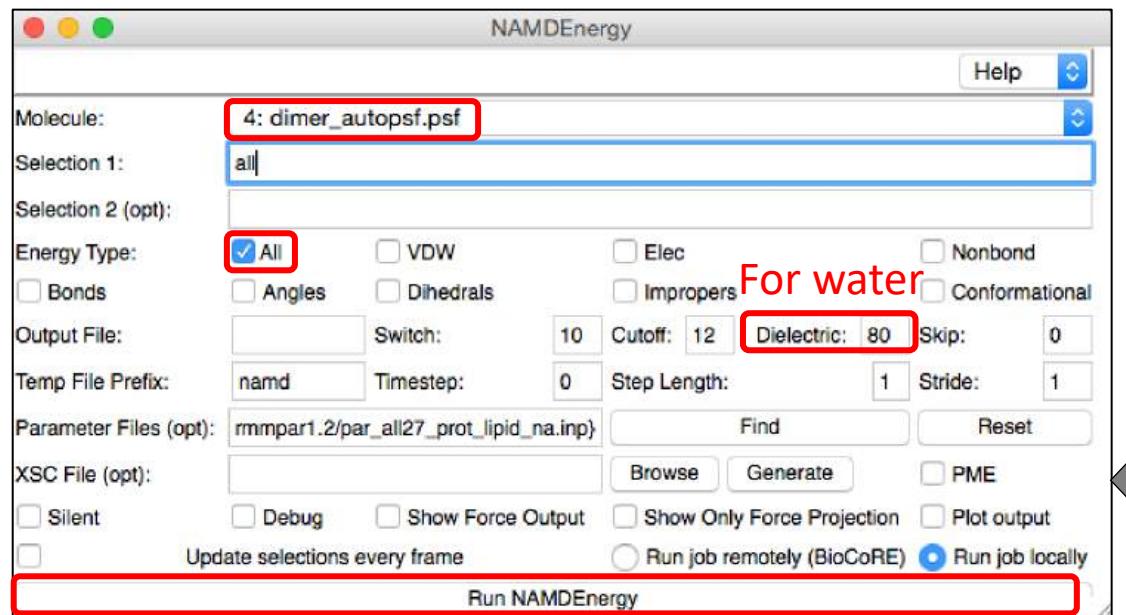
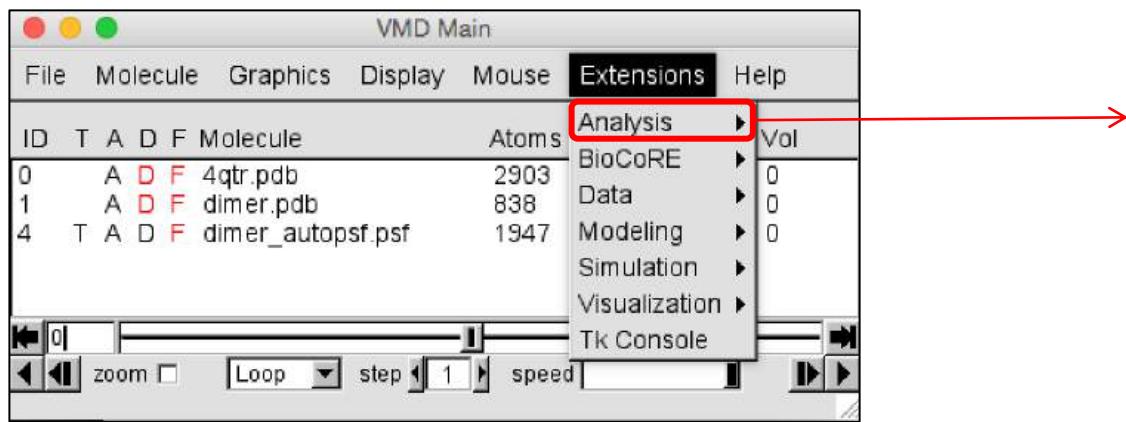
NAMD Energy Plug-in

The **NAMD Energy** plugin provides an interface for evaluating energies using **NAMD**. **NAMD Energy** will apply the desired energy calculations to each frame of the selected molecule.



The energy of the system correlates with the system's population through **Boltzmann distribution**.

NAMD Energy Plug-in



Analyze FEP Simulation
APBS Electrostatics
Collective variable analysis (PLUMED)
Contact Map
Heat Mapper
Hydrogen Bonds
Implicit Ligand Sampling
IR Spectral Density Calculator
MultiSeq
NAMD Energy
NAMD Plot
NetworkView
Normal Mode Wizard
PME Electrostatics
PropKa
Radial Pair Distribution Function $g(r)$
Ramachandran Plot
RMSD Calculator
RMSD Trajectory Tool
RMSD Visualizer Tool
Salt Bridges
Symmetry Tool
Sequence Viewer
Timeline
VolMap Tool

For water

NAMD Energy Plug-in

The figure illustrates the workflow for running NAMD energy calculations using the NAMD Energy Plug-in.

Top Left: Screenshot of the NAMD Energy application interface. The "Molecule" dropdown shows "0: dimer_automsf.pdb". The "Selection 1" field contains "protein". Under "Energy Type", the "All" checkbox is selected. The "Output File" section includes fields for "Switch", "Cutoff", "Dielectric", and "Skip". The "Parameter Files (opt)" field is set to "Downloads/par_all36m_prot.prm C:/U". A red box highlights the "Find" button. The "Run NAMD Energy" button at the bottom is also highlighted with a red box.

Top Right: Screenshot of a Windows File Explorer window showing the file path "本机 > Data (D) >". Inside the "Data (D)" folder, there is a subfolder "VMD" containing several files. One file, "par_all36m_prot.prm", is highlighted with a red box and has its full path displayed in the address bar: "D:\Data (D)\VMD\par_all36m_prot.prm".

Bottom: Screenshot of the VMD TkConsole window showing the command-line output of the NAMD energy calculation. The output includes the selection ("protein"), the command to run ("namd2.exe namd-temp.namd"), and the resulting energy data table. A red box highlights the energy data table at the bottom of the console window.

Frame	Time	Bond	Angle	Dihed	Impr	Elec	VdW	Conf	Nonbond	Total
0	0	+317.717	+352.285	+1090.87	+13.8173	-2584.28	+1e+011	+1774.69	+1e+011	+1e+011

CHARMM Force Field Files (if necessary)

Code Issues 7 Pull requests 1 Actions Projects Wiki Security Insights

master 2 branches 0 tags Go to file Code About

jamesmkrieger Merge pull request #74 from prody/revert-71-master ... 74c3d78 on Aug 11, 2020 266 commits

LICENSE	Initial commit	8 years ago
README.md	Updated README because homepage is case sensitive	6 years ago
anmmc.py	Merge branch 'master' of github.com:jamesmkrieger/coMD	4 years ago
comd.tcl	Revert "added pbc unwrap in case of pbc problems"	3 years ago
par_all36_prot.prm	Updated top and par files, and sorted out commandline args	5 years ago
par_all36m_prot.prm	Updated top and par files, and sorted out commandline args	5 years ago
pkgIndex.tcl	initial commit - Force	7 years ago
top_all36_carb.rtf	added modified carb forcefield that works with autopsf	5 years ago
top_all36_prot.rtf	Updated top and par files, and sorted out commandline args	5 years ago
toppar_water_ions.str	Updated top and par files, and sorted out commandline args	5 years ago

Download →

simulations pathway-analysis sampling-methods ann comd

Readme MIT license 1 star 6 watching 6 forks Report repository

Releases No releases published

Packages No packages published

README.md

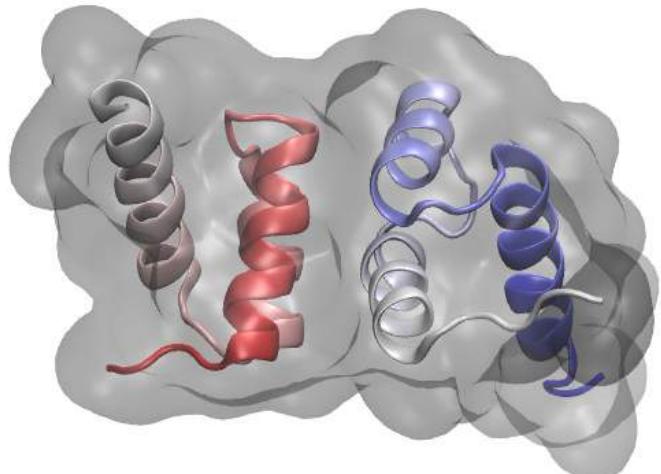
coMD

coMD is a VMD plugin GUI and a Python module developed for setup and analysis of simulations described in Gur et al., 2013.

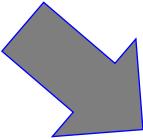
Homepage

<https://github.com/prody/coMD>

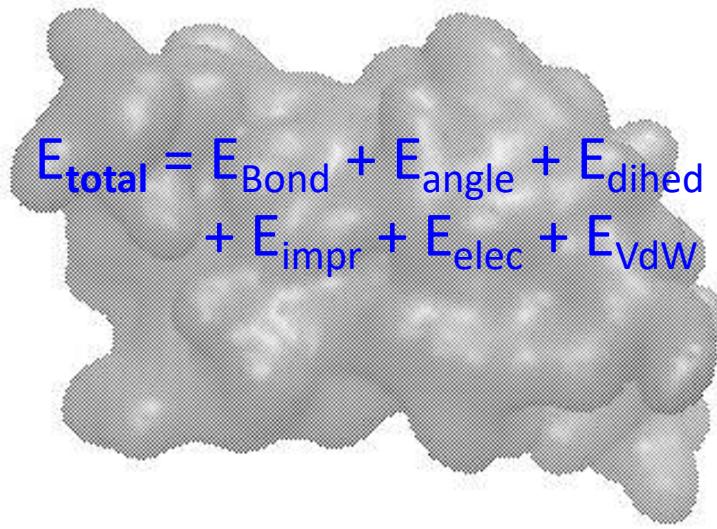
NAMD Energy Plug-in



Total Energy



Electronic energy as the
effective potential
experienced by the nuclei
→ Molecular Mechanics



NAMD Energy Plug-in

Check the result with

Extensions → Tk console

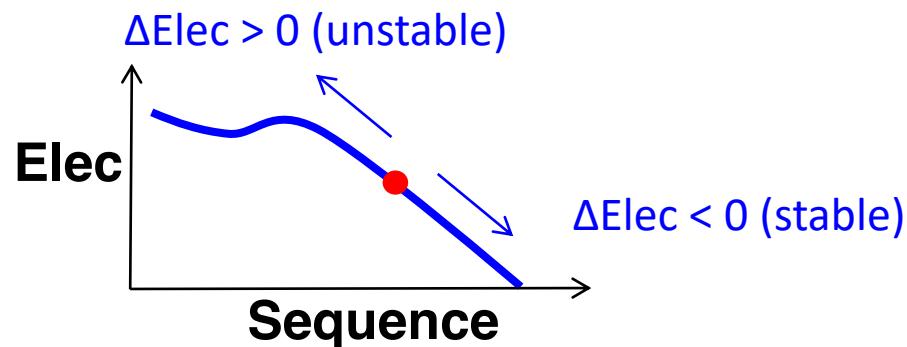
```
VMD TkConsole
PARS: (/Applications/VMD 1.9.1.app/Contents/vmd/plugins/noarch/tcl/readcharmmpar1.2/par_all27_prot_lipid_na.inp)
/Applications/VMD 1.9.1.app/Contents/vmd/plugins/noarch/tcl/readcharmmpar1.2/par_all27_prot_lipid_na.inp
namdEnergy) Computing energy for selection:
namdEnergy) all

namdEnergy) Running:
namdEnergy) /Users/MYTsaibin/namd2 namd-temp.namd

Frame      Time      Bond      Angle      Dihed      Impr      Elec      VdW      Conf      Nonbond      Total
0          0       +315.622    +435.294   +334.634   +13.8106   -32.9165   +1e+10   +1099.36   +1e+10   +1e+10
>Main< (MYTsai) 54 %
```

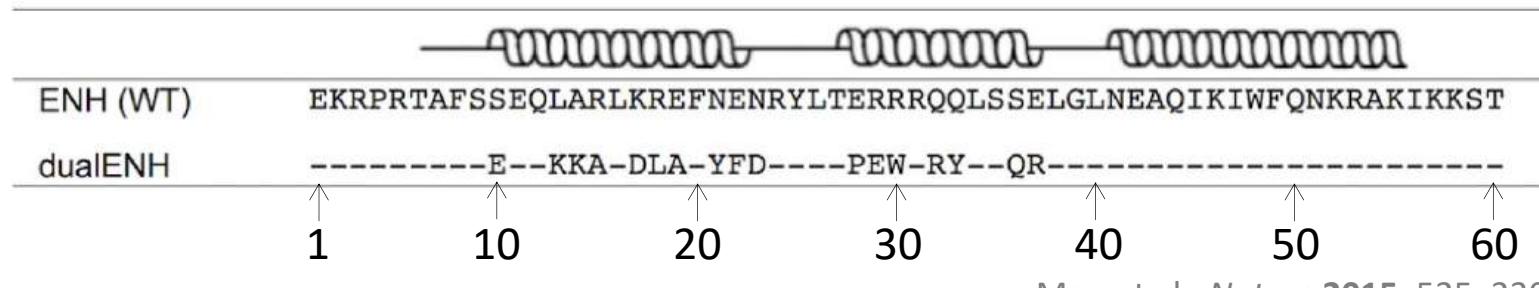
In kcal/mol

Evaluate the contribution of electrostatic energy from all the charged residues in the molecule.



Homework

- Given the wild type sequence in the same engineered dimer structure, calculate its energy using the *NAMD energy* plug-in and compare it with that of the engineered one. Which of the sequences is electrostatically more favorable? (Use *wt_dimer_autopsf.pdb* and *wt_dimer_autopsf.psf*)
- Use NAMD electrostatic energy to evaluate the effect of stabilization of a collection of mutations (S10E, K17D, and E37R; see the table below) on the wild type sequence. Then use *VMD* to render an image with these residues highlighted.
[Hint] Use the *NAMD energy* plug-in to compute the electrostatic energy. Use *VMD* to add a new representation with selected residues highlighted using coloring methods of interest and then render the resulting image.
- What do you think the disadvantage of using this approach in engineering a new protein dimer? Please provide your comment on it.



Mutator Plug-in

The *mutator* plugin provides a very simple method for mutating a target residue selected by its id, and the three character residue code for the mutant amino acid.

The image shows two windows related to the Mutator plug-in:

- VMD Main Window:** Shows the VMD interface with a menu bar. The "Extensions" menu is open, revealing a list of modules. The "Modeling" module is highlighted with a red box, and the "Mutate Residue" option under it is also highlighted with a red box. A red arrow points from the "Mutate Residue" option in the VMD menu to the corresponding option in the Mutator window.
- Mutator Window:** A separate window titled "Mutator". It contains the following fields:
 - Input:** PSF: (with a **Browse** button), PDB: (with a **Browse** button).
 - MUTATED_S10E:** A text input field containing "MUTATED_S10E", which is highlighted with a red box.
 - Target Residue:** Segment name of target residue (optional): (highlighted with a red box), ID of target residue: (highlighted with a red box).
 - Mutation (three letter residue name):** (highlighted with a red box).
 - Generate Free Energy Perturbation (FEP) files:** (unchecked).
 - FEP Prefix:** (empty), **Browse** button.

At the bottom of the Mutator window, there is a note: "Mutator does not support DNA. It is strongly recommended to perform a minimization on the resulting structure." Below this note is a large red box highlighting the "Run Mutator" button.

Resources

VMD Tutorials

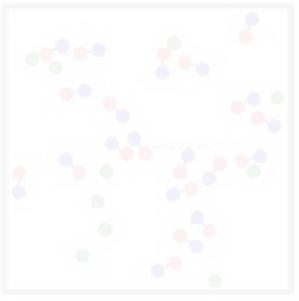
<http://www.ks.uiuc.edu/Research/vmd/current/docs.html#tutorials>

VMD plugins

<http://www.ks.uiuc.edu/Research/vmd/plugins/>

Tutorials and Scientific Case Studies

<http://www.ks.uiuc.edu/Training/Tutorials/>



I. Simple MD

- Python
- JupyterLab

Part III

(MD in Bio)



JupyterLab



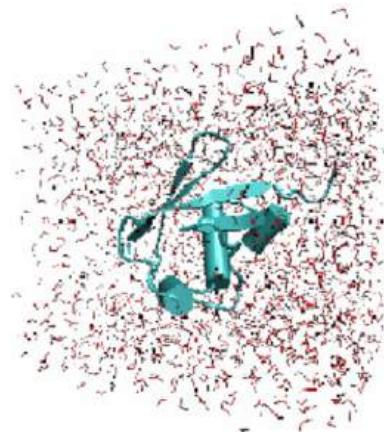
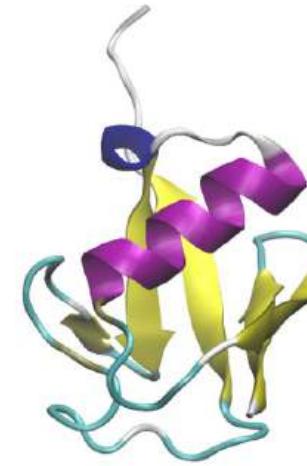
II. Visualization

- MolView
- VMD



III. MD (Bio)

- NAMD/VMD
 - Protein
 - Water



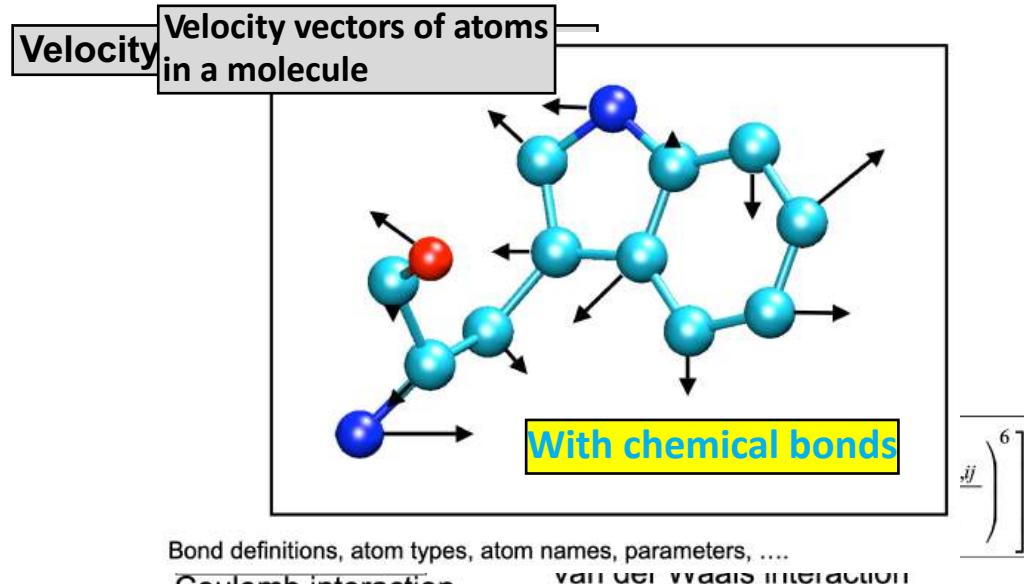
IV. MD (Nano)

- NAMD/VMD
 - Graphene
 - Small molecules



NAMD
Scalable Molecular Dynamics

分子力場/Molecular Force Fields



Electronic energy as the effective potential experienced by the nuclei

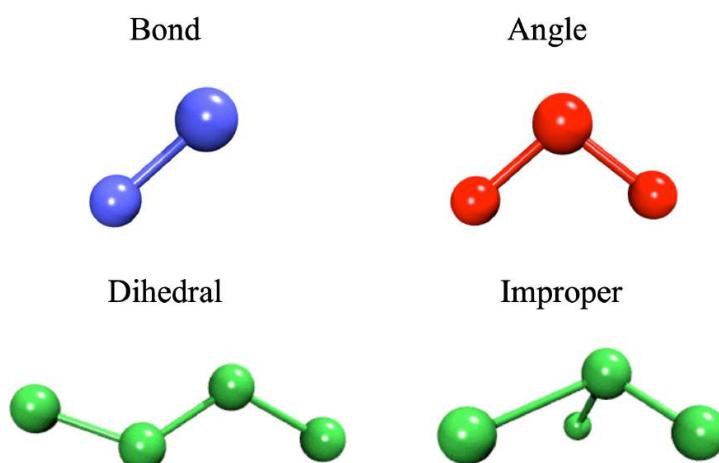
$$U(\vec{R}) = \underbrace{\sum_{bonds} k_i^{bond}(r_i - r_0)^2}_{U_{bond}} + \underbrace{\sum_{angles} k_i^{angle}(\theta_i - \theta_0)^2}_{U_{angle}} + \underbrace{\sum_{dihedrals} k_i^{dihed}[1 + \cos(n_i\phi_i + \delta_i)]}_{U_{dihedral}} + \underbrace{\sum_i \sum_{j \neq i} 4\epsilon_{ij} \left[\left(\frac{\sigma_{ij}}{r_{ij}} \right)^{12} - \left(\frac{\sigma_{ij}}{r_{ij}} \right)^6 \right]}_{U_{nonbond}} + \sum_i \sum_{j \neq i} \frac{q_i q_j}{\epsilon r_{ij}}$$

U_{bond} = oscillations about the equilibrium bond length

U_{angle} = oscillations of 3 atoms about an equilibrium bond angle

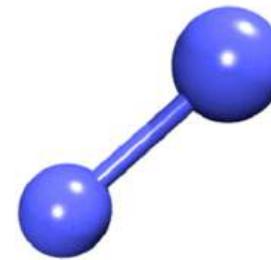
$U_{dihedral}$ = torsional rotation of 4 atoms about a central bond

$U_{nonbond}$ = non-bonded energy terms (electrostatics and Lenard-Jones)

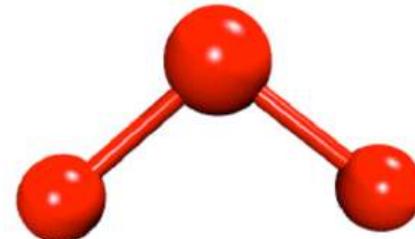


能量項/CHARMm Force Field

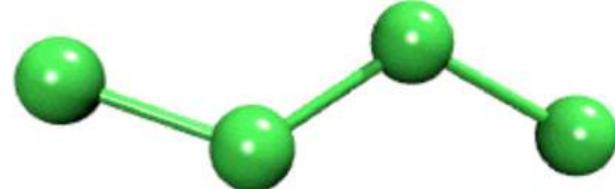
Bond



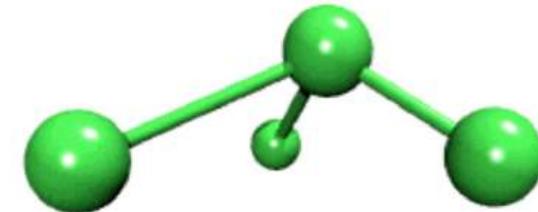
Angle



Dihedral

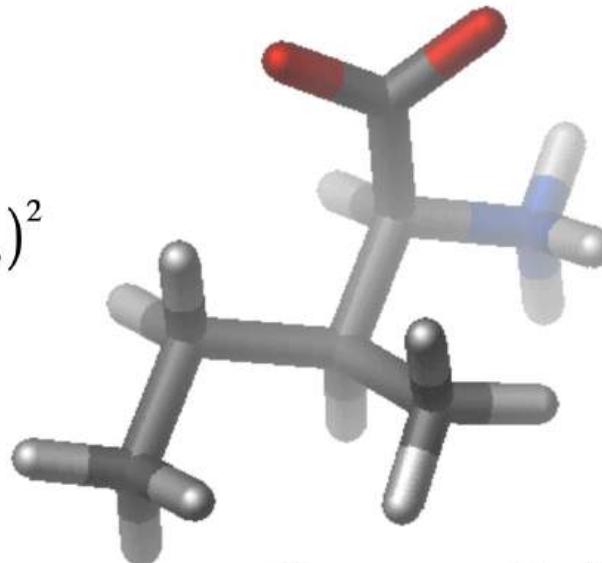


Improper



透過化學鍵的作用力/Bonded Interactions

$$V_{angle} = K_\theta (\theta - \theta_o)^2$$



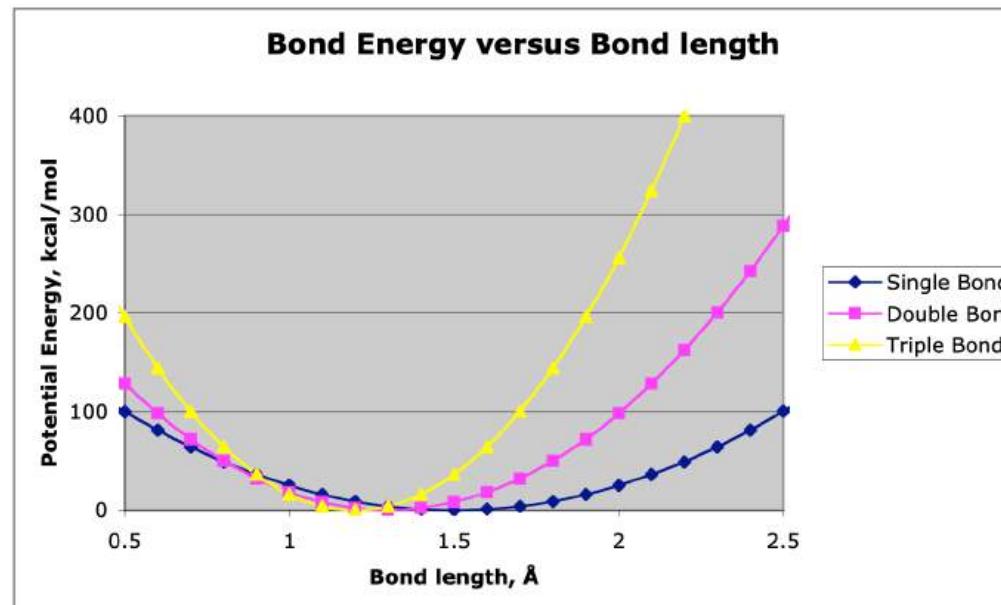
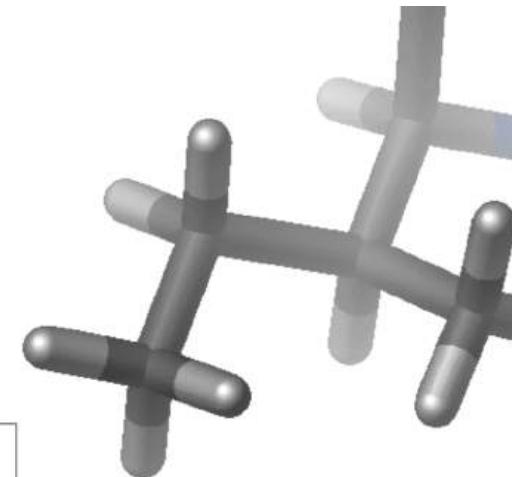
$$V_{bond} = K_b (b - b_o)^2$$

$$V_{dihedral} = K_\phi (1 + \cos(n\phi - \delta))$$

鍵長 / Bond Length

$$V_{bond} = K_b(b - b_o)^2$$

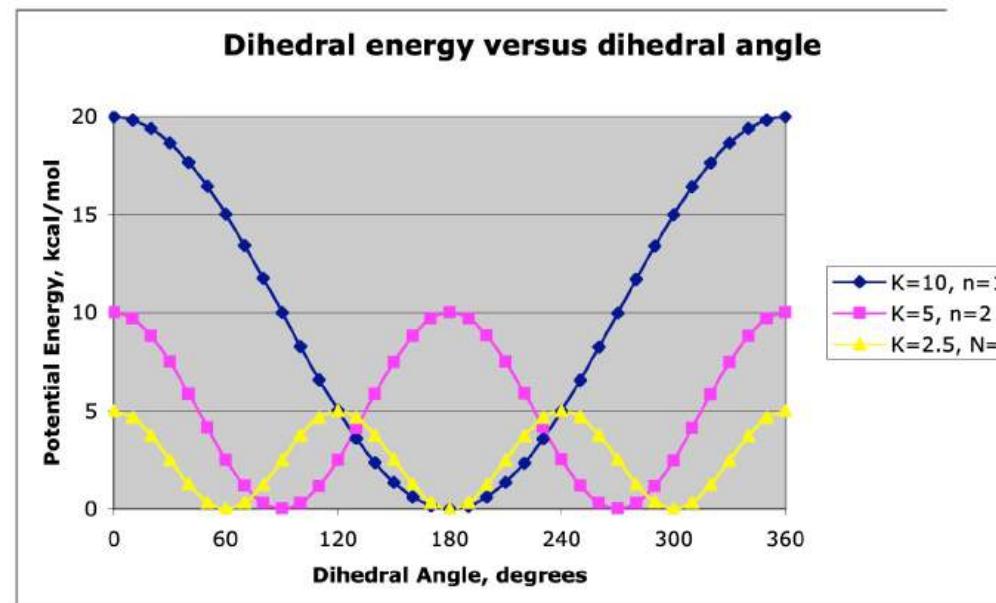
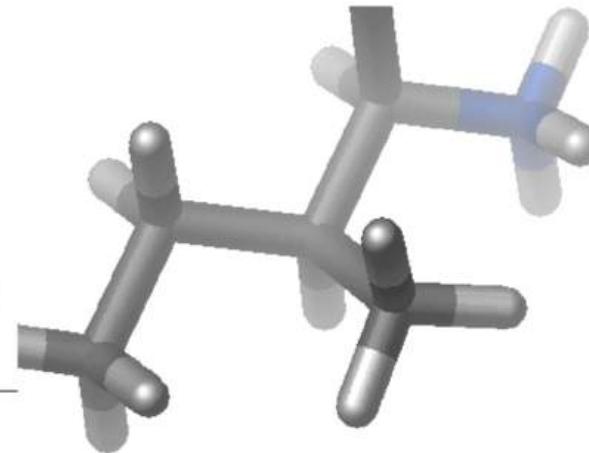
Chemical type	K _{bond}	b _o
C-C	100 kcal/mole/Å ⁻²	1.5 Å
C=C	200 kcal/mole/Å ⁻²	1.3 Å
C≡C	400 kcal/mole/Å ⁻²	1.2 Å



Bond angles and improper terms have similar quadratic forms, but with softer spring constants. The force constants can be obtained from vibrational analysis of the molecule (experimentally or theoretically).

Dihedral Potential

$$V_{dihedral} = K_\phi (1 + \cos(n\phi - \delta))$$



$$\delta = 0^\circ$$

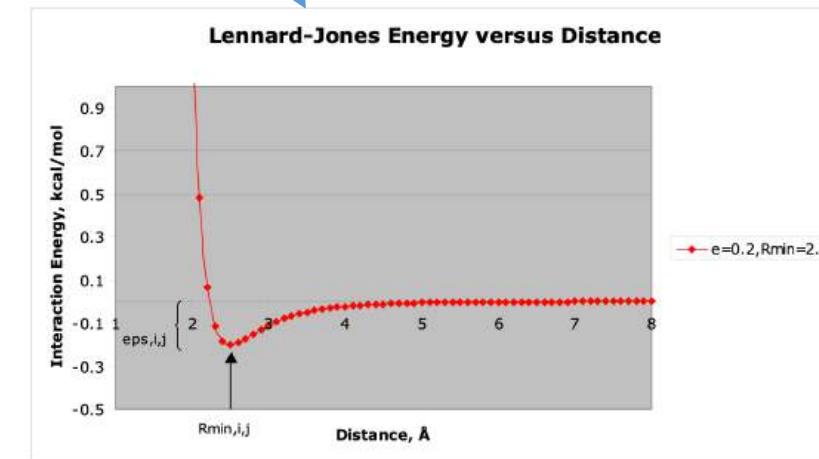
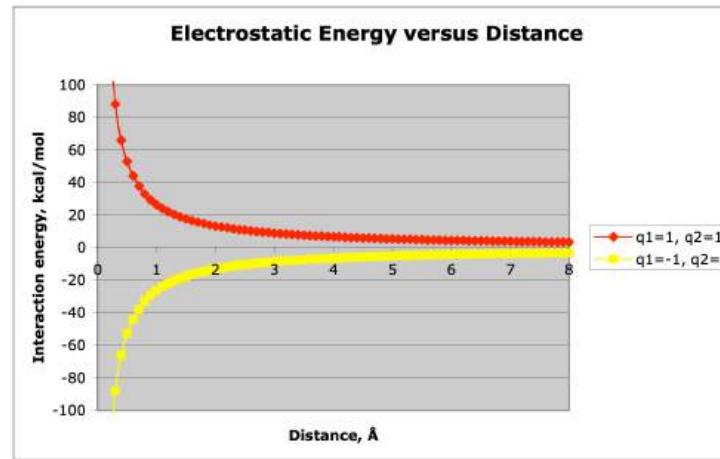
非鍵結作用力/Non-bonded Interactions

靜電作用力

$$\sum_{\text{nonbonded}} \frac{q_i q_j}{4\pi D r_{ij}}$$

$$+ \epsilon_{ij} \left[\left(\frac{R_{\min,ij}}{r_{ij}} \right)^{12} - 2 \left(\frac{R_{\min,ij}}{r_{ij}} \right)^6 \right]$$

凡德瓦力



Note that the effect is long range.

$\epsilon_{i,j}$: Lennard-Jones (LJ), van der Waals well-depth

$$\epsilon_{i,j} = \sqrt{\epsilon_i \cdot \epsilon_j}$$

D: dielectric constant

q_i : partial atomic charge

R_{\min} : LJ radius($R_{\min,ij}/2$ in CHARMM)

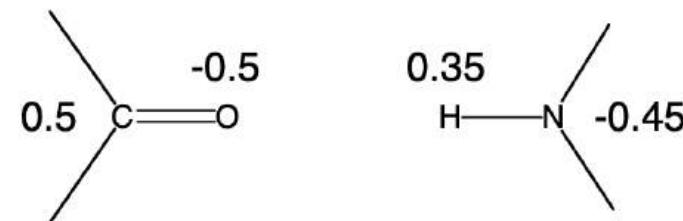
$$R_{\min,ij} = R_{\min,i} + R_{\min,j}$$

電荷擬合方法/Charge Fitting Strategy

CHARMM- Mulliken*

AMBER(ESP/RESP)

Partial atomic charges



*Modifications based on interactions with TIP3 water

主流生物分子力場/Popular Force Fields



<https://www.charmm.org/>

CHARMM是一種用於分子動力學的分子力場，同時，採用這種力場的分子動力學軟體包也採用了這個名稱。

CHARMM開發項目包括一個與馬丁·卡普拉斯及其在哈佛大學的研究小組合作的開發者網絡，這個網絡包含了美國等地的開發者，協同開發及維護CHARMM軟體包。這個軟體允許進行學術研究的個人及小組在支付一定費用之後得到使用許可。



<https://ambermd.org/>



<http://www.gromacs.org/>

GROMACS是一套分子動力學模擬程序包，主要用來模擬研究蛋白質、脂質、核酸等生物分子的性質。它起初由荷蘭格羅寧根大學生物化學系開發，目前由來自世界各地的大學和研究機構維護。GROMACS是開源免費的軟體，4.6版之前的版本使用GNU通用公共許可證發行，而4.6版之後使用GNU寬通用公共許可證發行。

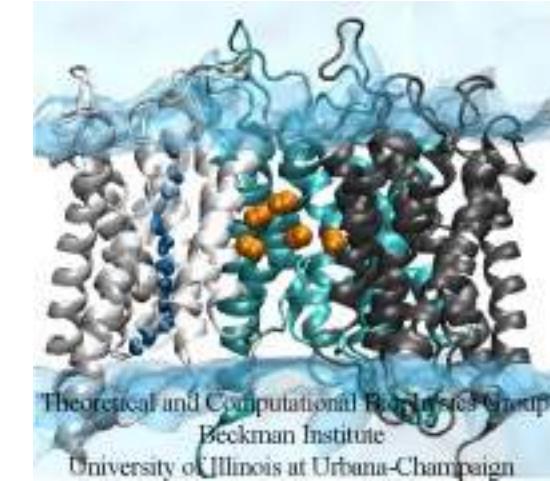
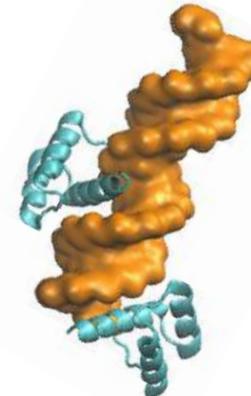
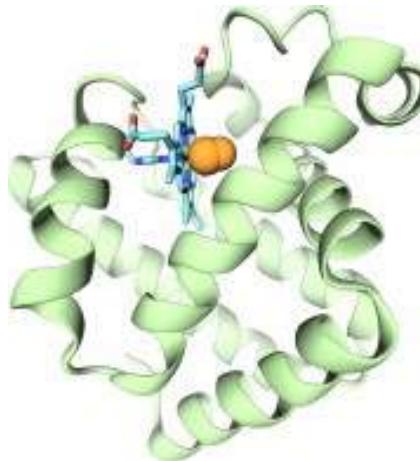
Visual Molecular Dynamics



<http://www.ks.uiuc.edu/Research/vmd/>

VMD is designed for **visualization, analysis, and modeling** of biological systems such as proteins, nucleic acids, lipid bilayer assemblies, etc.

VMD can read standard Protein Data Bank (**PDB**) files and display the contained structure.



- Support all major computer platforms (ex. MacOS X, Windows, Linux)
- Many molecular rendering and coloring methods

CHARMM Potential Function

$$U(\vec{R}) = \underbrace{\sum_{bonds} k_i^{bond} (r_i - r_0)^2}_{U_{bond}} + \underbrace{\sum_{angles} k_i^{angle} (\theta_i - \theta_0)^2}_{U_{angle}} + \underbrace{\sum_{dihedrals} k_i^{dih} [1 + \cos(n_i \phi_i + \delta_i)]}_{U_{dihedral}} + \underbrace{\sum_i \sum_{j \neq i} 4\epsilon_{ij} \left[\left(\frac{\sigma_{ij}}{r_{ij}} \right)^{12} - \left(\frac{\sigma_{ij}}{r_{ij}} \right)^6 \right]}_{U_{nonbond}} + \underbrace{\sum_i \sum_{j \neq i} \frac{q_i q_j}{\epsilon r_{ij}}}_{U_{electrostatic}}$$

幾何構型

PDB file → **geometry**

Topology PSF file

parameters ← **Parameter file** → **參數**

File Format/Structure

- The structure of a pdb file
- The structure of a psf file
- The topology file
- The parameter file
- Connection to potential energy terms

Structure of a PDB File

>>> It is an ascii, fixed-format file <<<

“No connectivity information”

Topology File

From top_all22_model.inp

```

RESI PHEN      0.00 ! phenol, adm jr.
GROUP
ATOM CG  CA   -0.115 !
ATOM HG  HP    0.115 !
                HD1   HE1
GROUP
ATOM CD1 CA   -0.115 !
                |     |
                CD1--CE1
ATOM HD1 HP    0.115 !
                //    \\
GROUP
ATOM CD2 CA   -0.115 !
                HG--CG   CZ--OH
ATOM CD2 HP    0.115 !
                \     /
                CD2==CE2   HH
GROUP
ATOM CE1 CA   -0.115 !
                |     |
ATOM HE1 HP    0.115
                HD2   HE2
GROUP
ATOM CE2 CA   -0.115
ATOM HE2 HP    0.115
GROUP
ATOM CZ  CA    0.110
ATOM OH  OH1   -0.540
ATOM HH  H     0.430
BOND CD2 CG CE1 CD1 CZ CE2 CG HG CD1 HD1
BOND CD2 HD2 CE1 HE1 CE2 HE2 CZ OH OH HH
DOUBLE CD1 CG CE2 CD2  CZ CE1

```

Top_all22_model.inp contains all protein model compounds. Lipid, nucleic acid and carbohydrate model compounds are in the full topology files.

HG will ultimately be deleted. Therefore, move HG (hydrogen) charge into CG, such that the CG charge becomes 0.00 in the final compound.

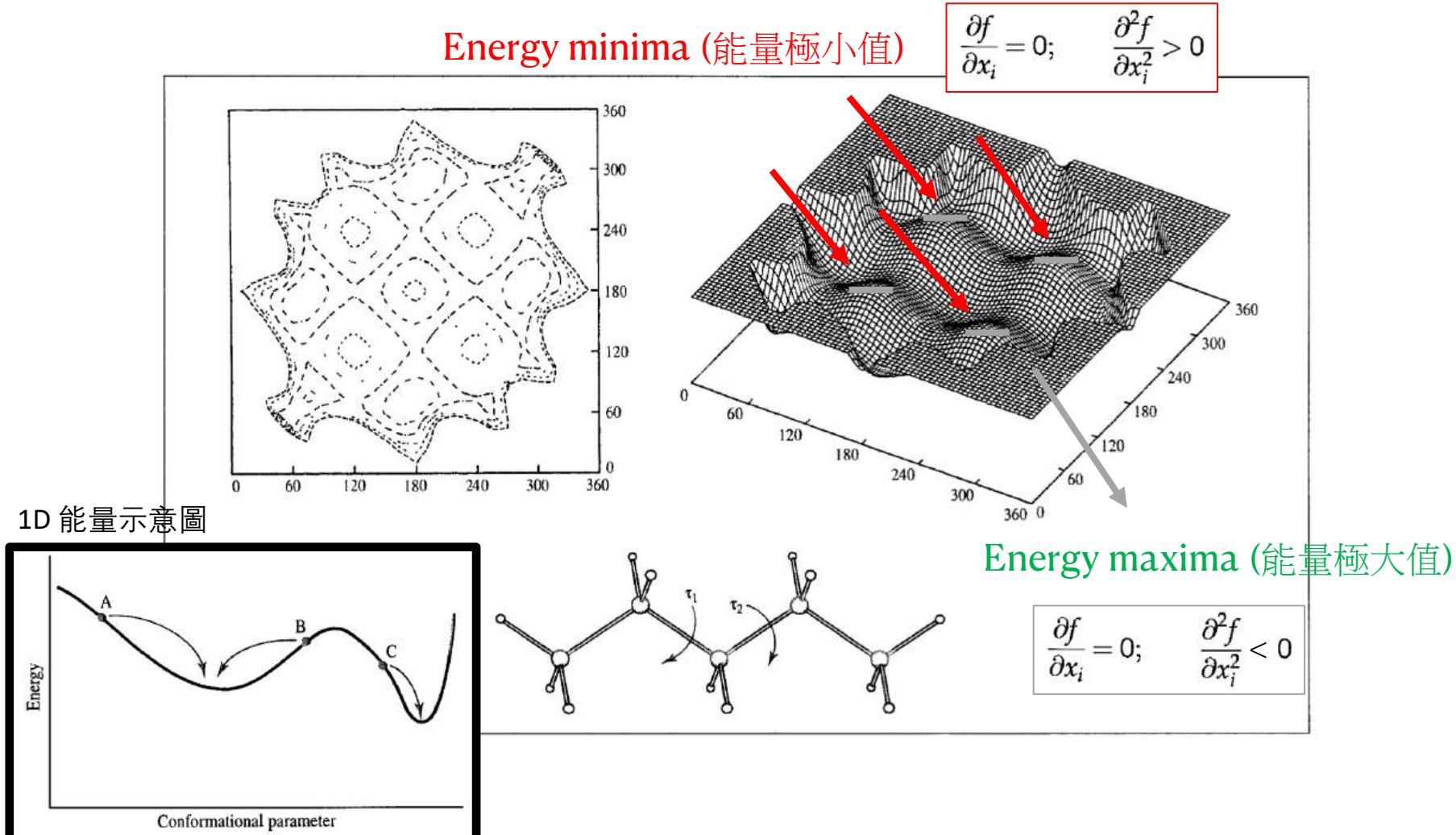
Use remaining charges/atom types without any changes.

Do the same with indole

From MacKerell

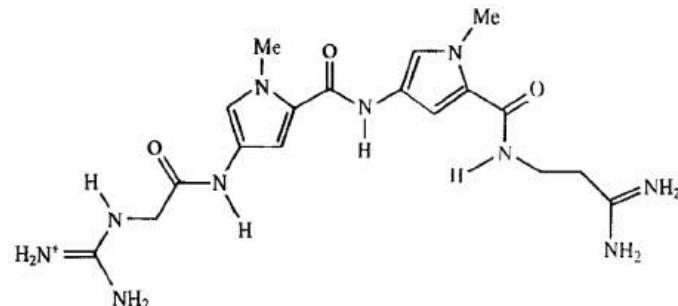
Energy Minimization

- Energy landscape of pentane with two torsion angles



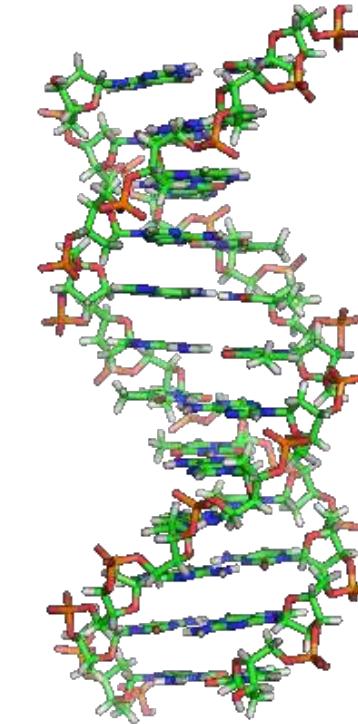
Energy Minimization

- Compare two different methods



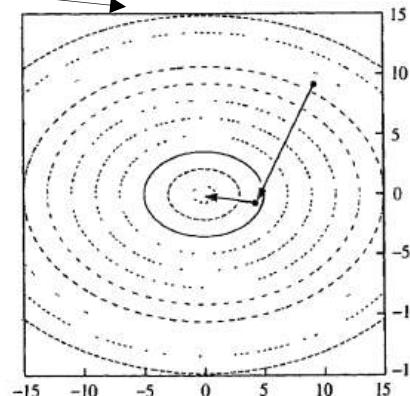
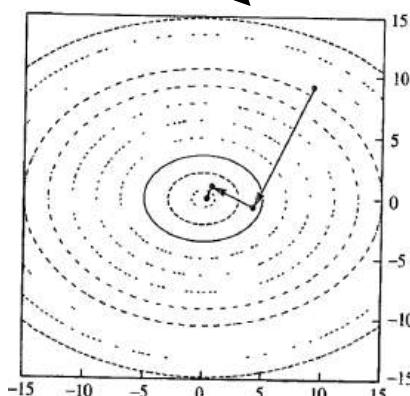
DNA inhibitor Netropsin
(紡錘黴素)

Docking
(對接/結合)



[WikiWand:DNA](#)

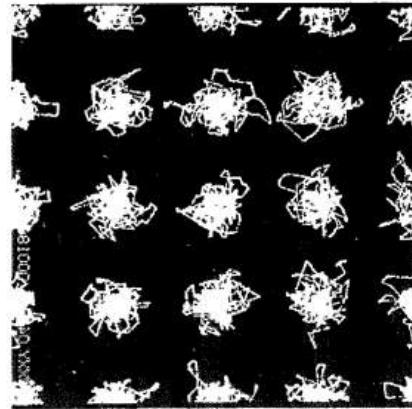
Method	Initial refinement (Av. gradient <1 kcal Å ⁻²)		Stringent minimisation (Av. gradient <0.1 kcal Å ⁻²)	
	CPU time (s)	Number of iterations	CPU time (s)	Number of iterations
Steepest descents	67	98	1405	1893
Conjugate gradients	149	213	257	367



Molecular Dynamics Simulation Method

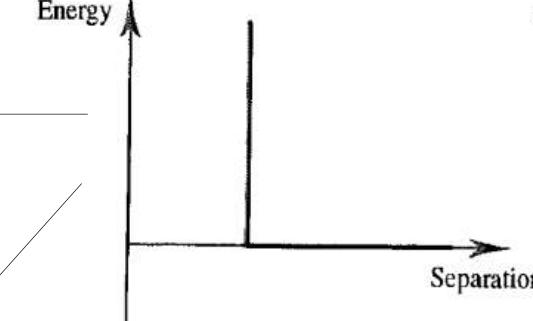
- Integrating Newton's law of motion

固態 Hard-sphere 模擬

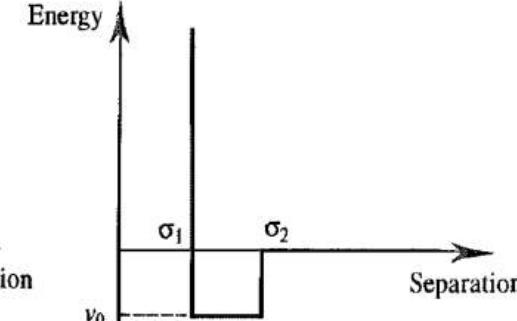


$$\frac{d^2x_i}{dt^2} = \frac{F_{x_i}}{m_i}$$

Hard-sphere (硬球) potential

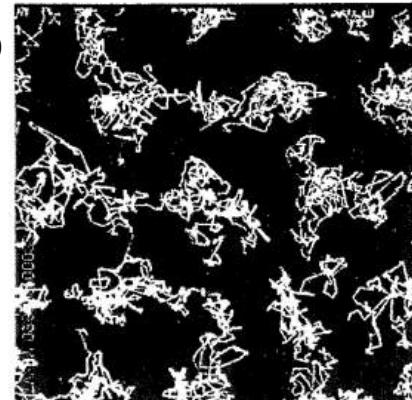


Square-well (方井) potential



液態 Hard-sphere 模擬

Alder and Wainwright, JCP 1959



Molecular Dynamics Simulation Method

- Position and dynamic properties can be approximated as Taylor series expansions
(位置以及動態性質可用泰勒展開式近似)

Position(位置) $\rightarrow \mathbf{r}(t + \delta t) = \mathbf{r}(t) + \delta t \mathbf{v}(t) + \frac{1}{2} \delta t^2 \mathbf{a}(t) + \frac{1}{6} \delta t^3 \mathbf{b}(t) + \frac{1}{24} \delta t^4 \mathbf{c}(t) + \dots$

Velocity(速度) $\rightarrow \mathbf{v}(t + \delta t) = \mathbf{v}(t) + \delta t \mathbf{a}(t) + \frac{1}{2} \delta t^2 \mathbf{b}(t) + \frac{1}{6} \delta t^3 \mathbf{c}(t) + \dots$ Truncated
(截斷)

Acceleration(加速度) $\rightarrow \mathbf{a}(t + \delta t) = \mathbf{a}(t) + \delta t \mathbf{b}(t) + \frac{1}{2} \delta t^2 \mathbf{c}(t) \dots$
 $\mathbf{b}(t + \delta t) = \mathbf{b}(t) + \delta t \mathbf{c}(t) + \dots$ 越高次項越準喔~

Verlet algorithm

$$\mathbf{r}(t + \delta t) = \mathbf{r}(t) + \delta t \mathbf{v}(t) + \frac{1}{2} \delta t^2 \mathbf{a}(t) + \dots$$

$$\mathbf{r}(t - \delta t) = \mathbf{r}(t) - \delta t \mathbf{v}(t) + \frac{1}{2} \delta t^2 \mathbf{a}(t) - \dots$$

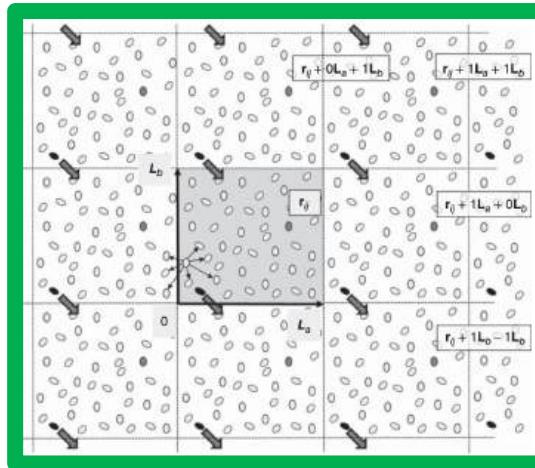
↓ 相加

Truncated at $O(\delta t^4)$
→Fourth-order method, Why?
(仍準確至三次項)

$$\mathbf{r}(t + \delta t) = 2\mathbf{r}(t) - \mathbf{r}(t - \delta t) + \delta t^2 \mathbf{a}(t)$$

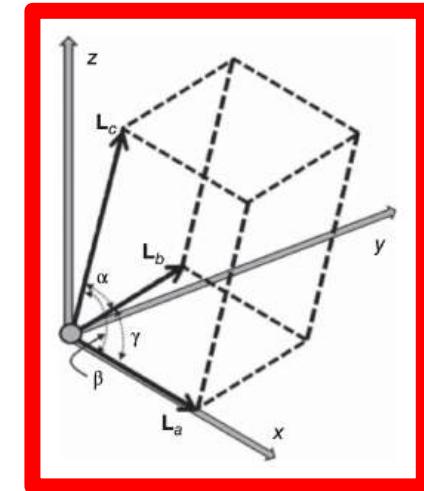
1. Initial Setup of the System

- Determining the shape and size of the container to confine the molecules of interest
- Defining the initial positions and velocities of the atoms
- Creating the **simulation cell**



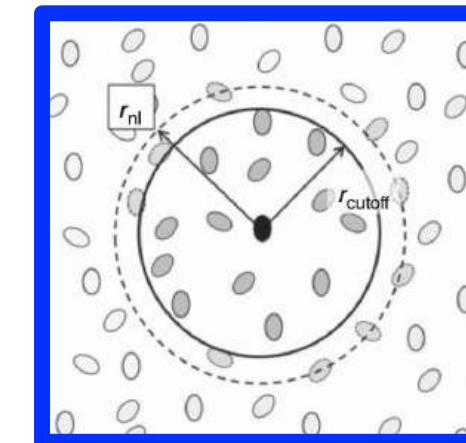
2. Boundary Conditions

- Modeling a macroscopic (bulk) system with a single *simulation cell* (10^6 instead of 10^{23})
- Applying **Periodic boundary conditions (PBC)** to simulate an infinite system

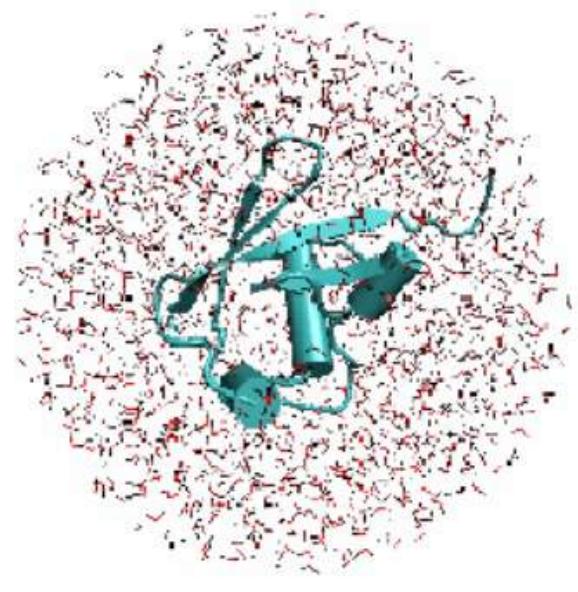


3. Treatment of Short-Range and Long-Range Forces

- Handling short-range forces between nearby atoms using cutoff distances or **neighbor lists**
- Accounting for long-range forces through methods like Ewald summation or *particle mesh Ewald (PME)*

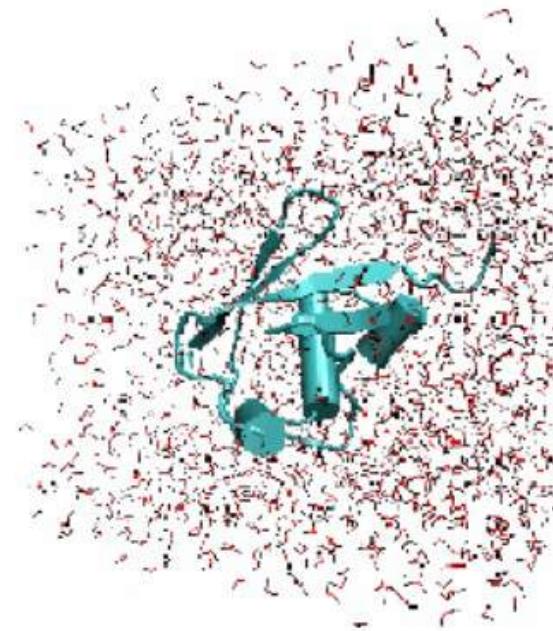


[補充] 表面張力 & 週期邊界條件



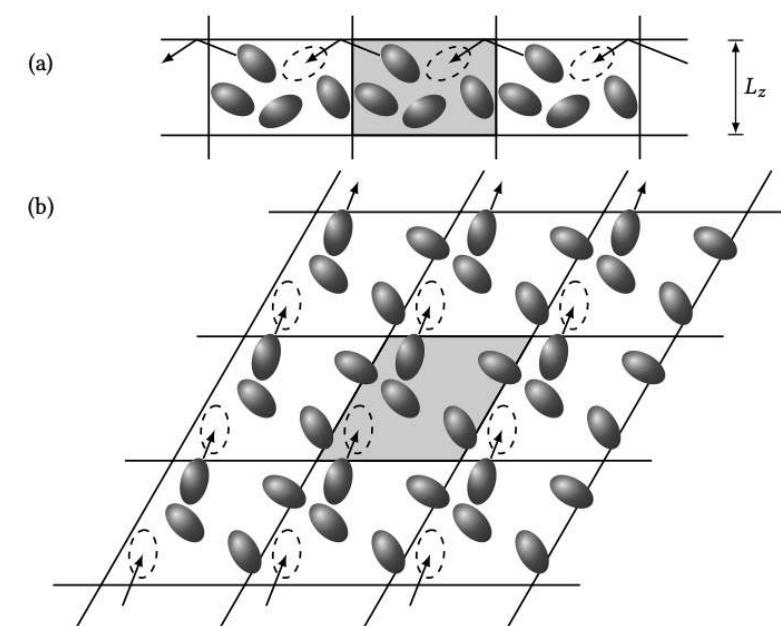
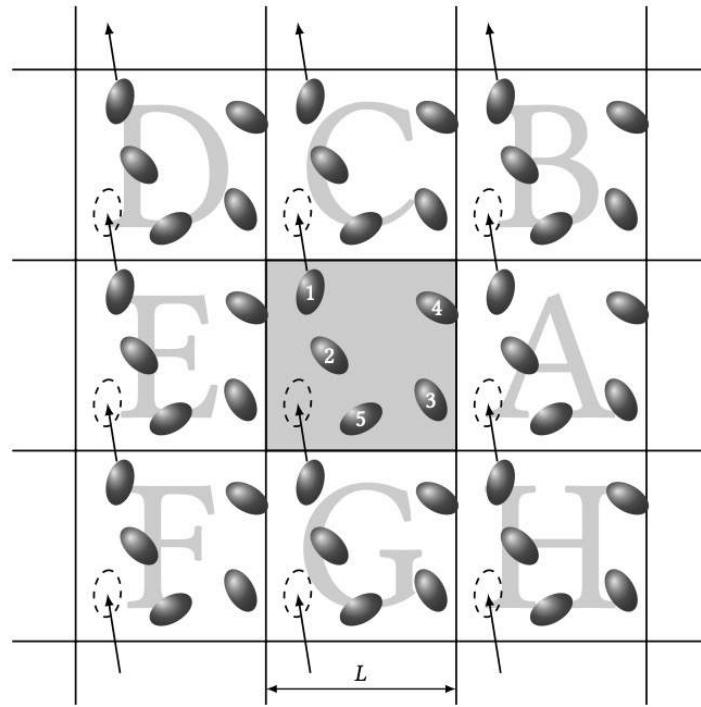
Water sphere

vs



Water box

[補充] 表面張力 & 週期邊界條件



Tutorial: 蛋白質模擬 (Protein)

方法一:

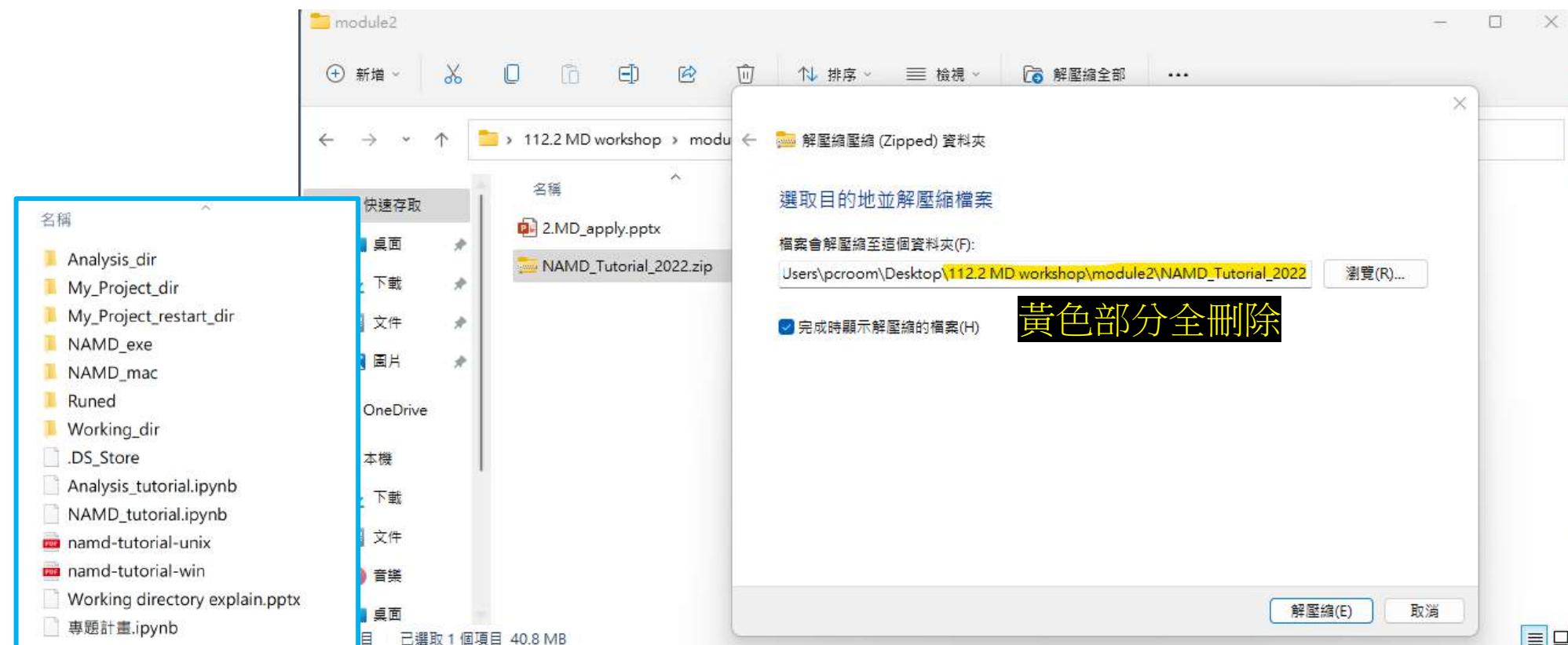
1. 從 112.2 MD workshop/module3 中，將 **NAMD_Tutorial_2022.zip** 資料夾拖曳至桌面
2. 按滑鼠右鍵 → 解壓縮檔案... → 目的地路徑 \.....\.....\Desktop\(**此處全刪除**)
3. 解壓縮

桌面



方法二:

或是直接從 **NAMD_Tutorial_2022.zip** 上按右鍵 → 解壓縮檔案...



Tutorial: 蛋白質模擬 (Protein)

開啟 JupyterLab

The screenshot shows the JupyterLab interface. On the left, a file browser displays a directory structure under '/ 桌面 / NAMD_Tutorial_2022 /'. A red box highlights the path '/ 桌面 / NAMD_Tutorial_2022 /' with the text '注意路徑' (Note the path) overlaid. The 'NAMDTutorial.ipynb' file is selected. On the right, a notebook editor shows the content of 'NAMDTutorial.ipynb'. The content includes:

NAMD tutorial

- Created : 2020/10/03
- Created by Yoyo, Jeff @MYTLab
- Last update: 2024/8/24 by MYT

MYTLab website: <https://mytsai.cc>

參考資料：

- NAMD tutorial ver.2017

此教程僅供教學用途

All rights reserved.

縮寫：

VMD TkCon = Tk Console

(必讀) 解壓縮注意事項：

> 課程下載：檔名為：NAMD Tutorial 2022.zip 的壓縮檔。

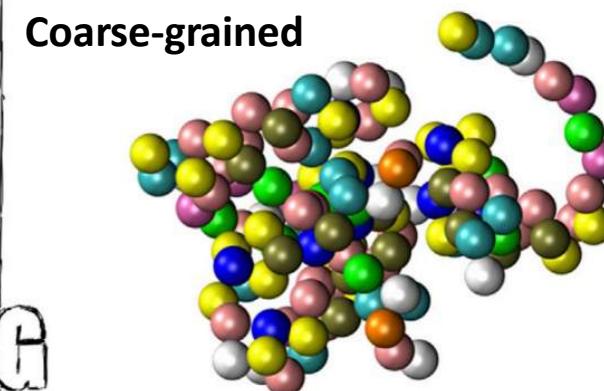
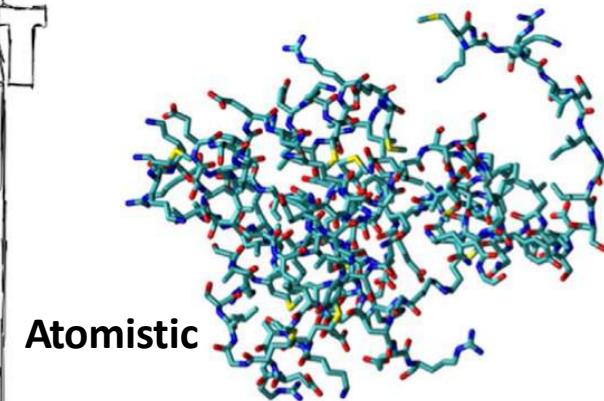
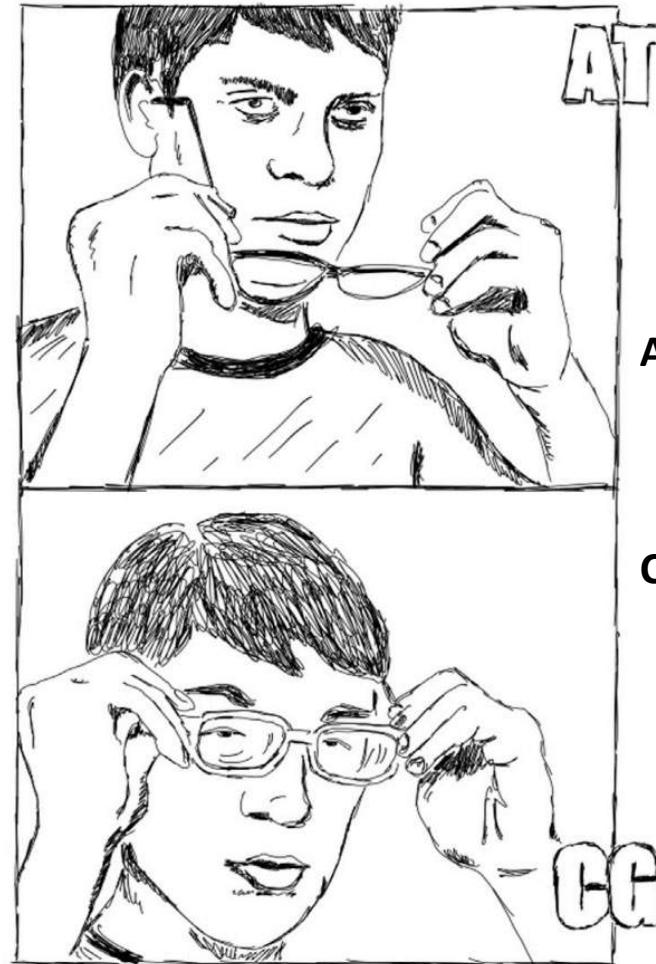
Simple 0 Python 3 | Idle

Saving completed

Mode: Command ⚙ Ln 1, Col 1 NAMDTutorial.ipynb

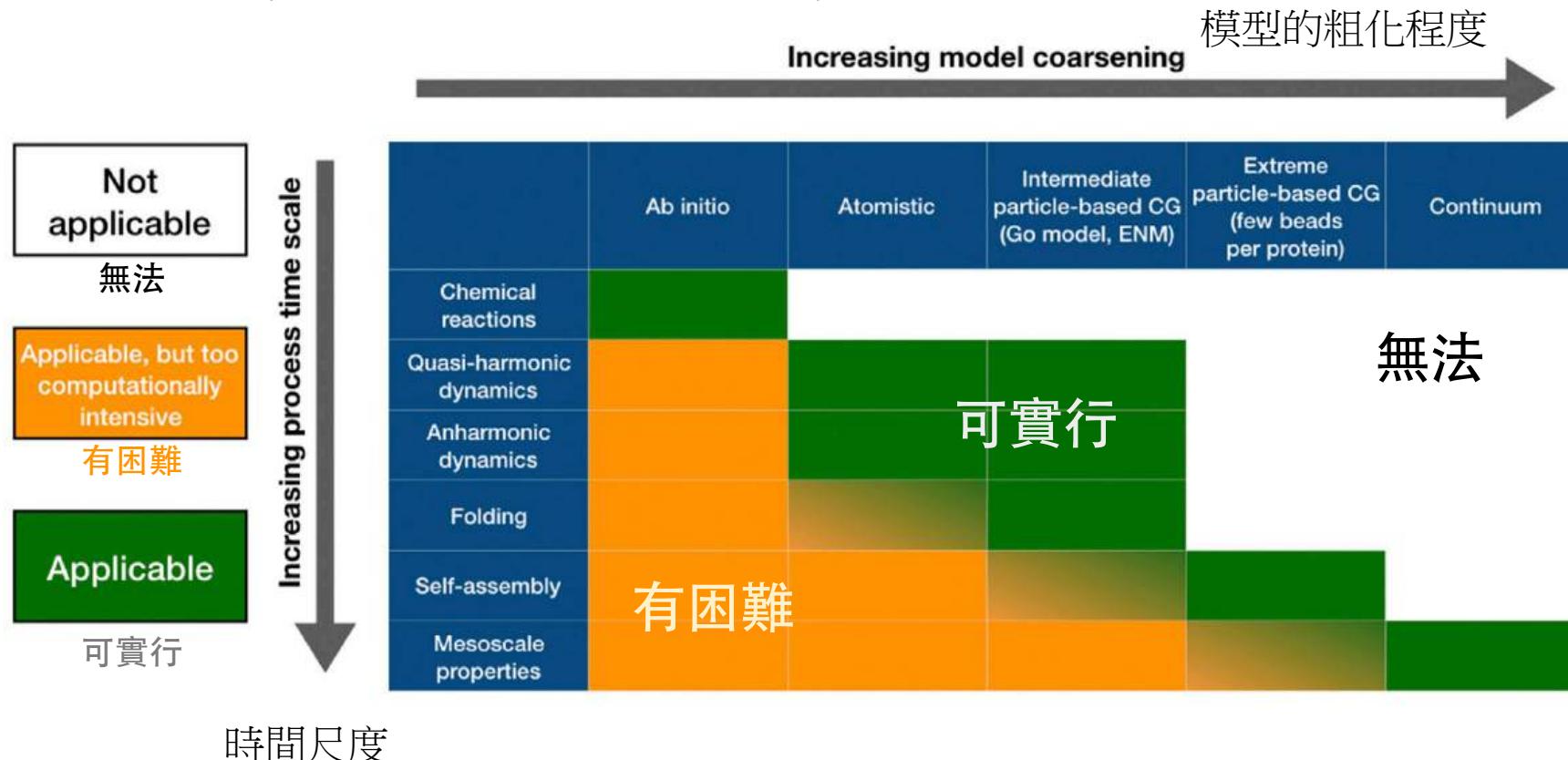
[補充] 粗粒化模型

- The loss of detail is a defect, however, it does have the advantage of simplicity and parsimony
(粗粒化有缺點，但也具有簡化後的優勢)



[補充] 時間尺度與解析程度

- (時間尺度的相關性與現象之間的關係)



[補充] 實驗、理論與模擬之間的連結

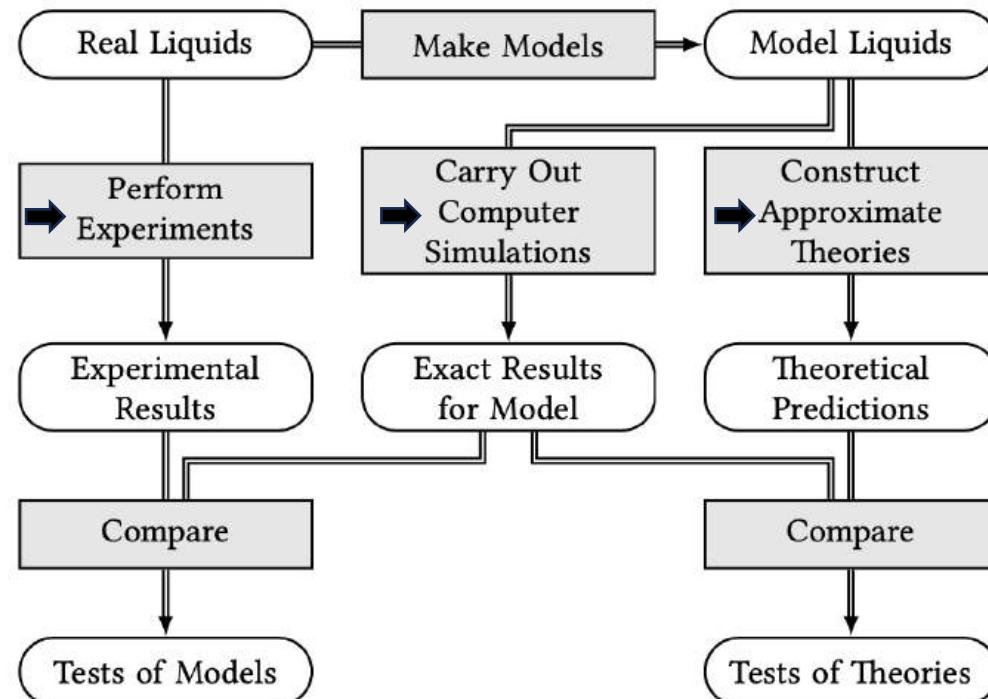


Fig. 1.2 The connection between experiment, theory, and computer simulation.

Tutorial: 水盒模擬 (Water Box)

桌面



開啟 JupyterLab

The JupyterLab interface is shown, displaying a notebook titled "Water Heat Capacity Tutorial". The notebook was completed on 2022/12 by Heery@MYTLab. It includes a reference section with links to NAMD tutorial ver.2017 and Levitt et al., J. Phys. Chem. B 1997. The notebook also contains text about the purpose of the tutorial and copyright information.

透過實際創建水盒並運行分子動力學模擬，以計算出與參考文獻實驗值相近的水的熱容量值

A. 水盒創建

A.0 打開 VMD (預設路徑應為: C:/Program Files (x86)/University of Illinois/VMD)

A.1 點選VMD Main的【 Extensions 】→【 Tk Console 】→鍵入:

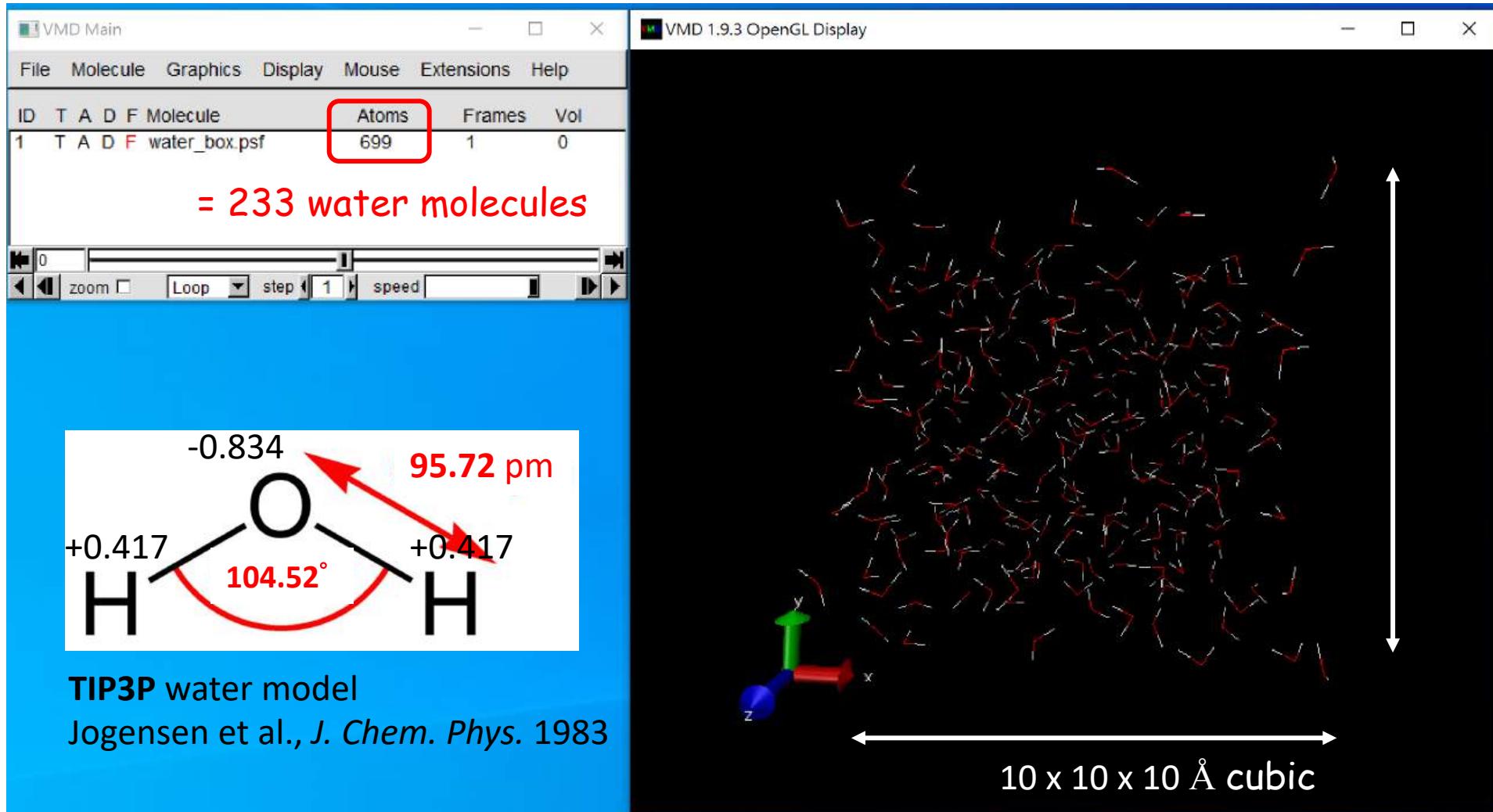
```
cd ~/Desktop/water_heat_capacity/    (更改為目標路徑)
```

A.2 再鍵入:

```
solvate -minmax {{0 0 0} {0 0 0}} -t 10 -o water_box
```

Simple 0 1 Python 3 (ipykernel) | Idle Mode: Command 0 Ln 1, Col 1 water_heat_capacityTutorial.ipynb 1

Tutorial: 水盒模擬 (Water Box)



從水盒分子能量變化計算水的熱容量/比熱

[補充] 統計熱力學

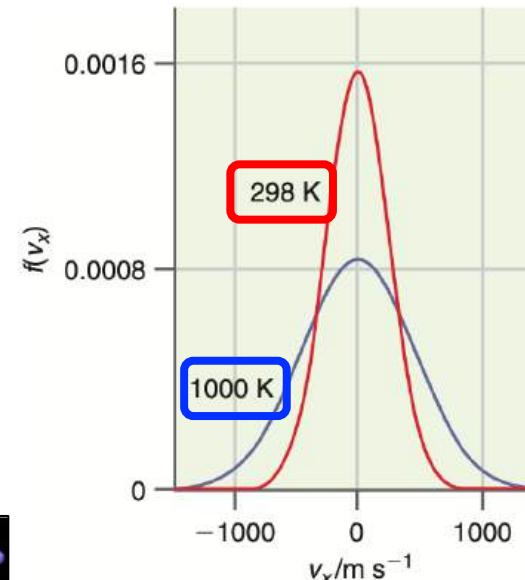


Ludwig E. Boltzmann
(1844-1906) from wiki

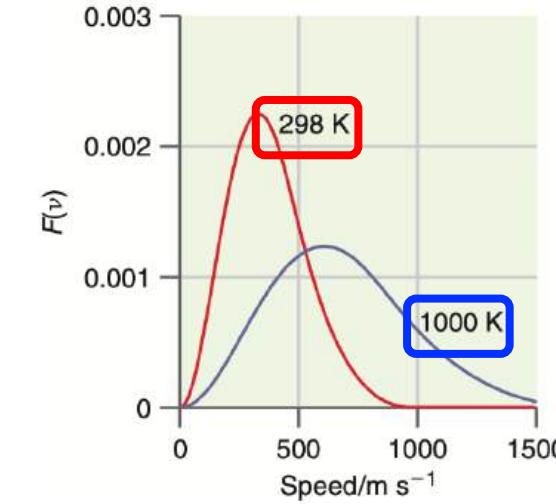


https://phet.colorado.edu/sims/html/gases-intro/latest/gases-intro_en.html

Distribution function (分佈函數)



$$f(v_j) = \left(\frac{M}{2\pi RT}\right)^{1/2} e^{(-Mv_j^2/2RT)}$$



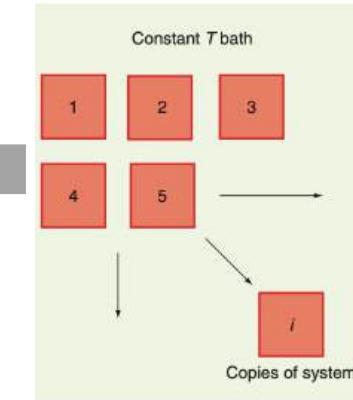
$$F(v) dv = 4\pi \left(\frac{M}{2\pi RT}\right)^{3/2} v^2 e^{-Mv^2/2RT} dv$$

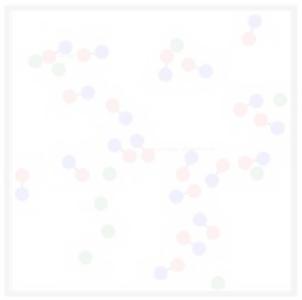
巨觀
(macro)

微觀(micro)

$$Q = \sum_n e^{-\beta E_n}$$

Canonical partition function
(正則配分函數)





I. Simple MD

- Python
- JupyterLab



JupyterLab

II. Visualization

- MolView
- VMD

VMD
Visual-Molecular Dynamics

Part IV

(MD in Nano)



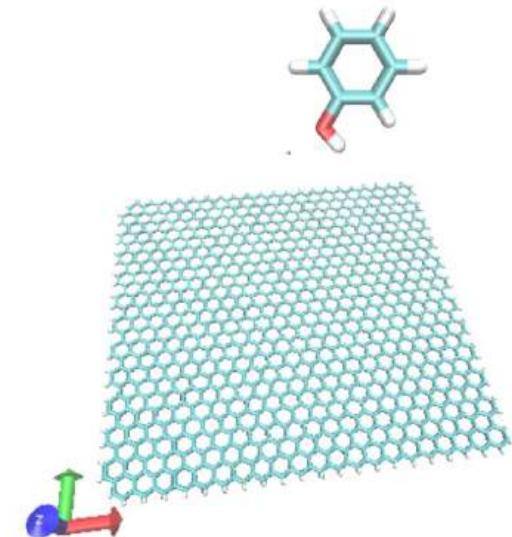
III. MD (Bio)

- NAMD/VMD
- Protein



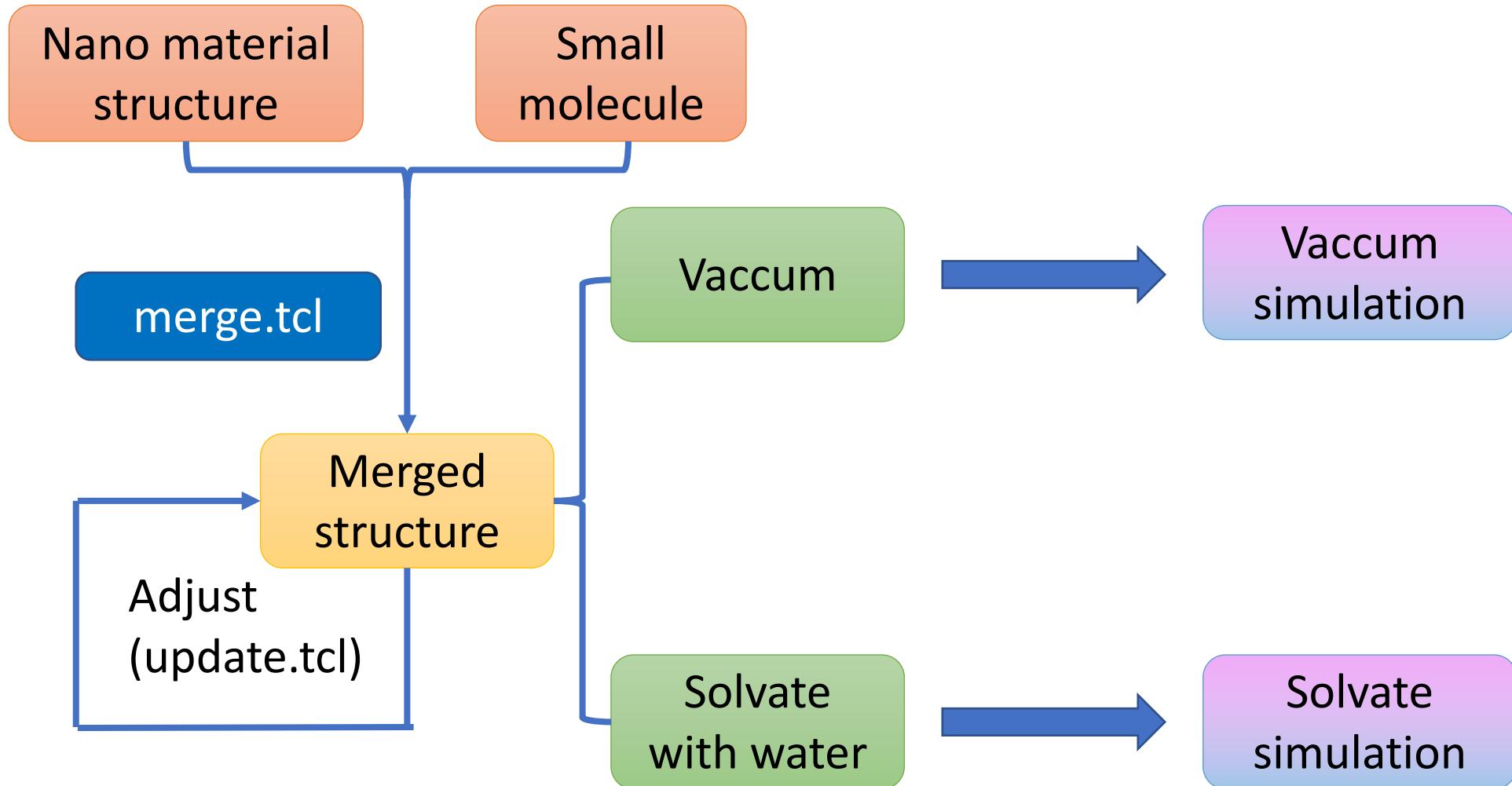
IV. MD (Nano)

- NAMD/VMD
- Graphene
- Small molecules



NAMD
Scalable Molecular Dynamics

Roadmap



<https://www.charmm-gui.org/> → 需要 User account registration

CHARMM-GUI

Effective Simulation Input Generator and More

CHARMM is a versatile program for atomic-level simulation of many-particle systems, particularly macromolecules of biological interest. - M. Karplus

[about us](#) :: [input generator](#) :: [Q&A](#) :: [forum](#) :: [archive](#) :: [lectures](#) :: [movie gallery](#) :: [video demo](#) :: [citations](#) :: [update log](#) :: [jobs & events](#) :: [giving](#)

Some [lectures](#), [job postings](#), and [FAQ](#) are now available. See [update log](#) for update history and [giving](#) for donation. [Contact](#) info is given below.

[Logout](#)

Input Generator

- Job Retriever
- Force Field Converter
- PDB Reader & Manipulator
- Glycan Reader & Modeler
- Ligand Reader & Modeler
- Glycolipid Modeler
- LPS Modeler

Nanomaterial Modeler

- Multicomponent Assembler
- Solution Builder
- Membrane Builder
- Martini Maker
- PACE CG Builder
- Polymer Builder
- Drude Prepper
- Enhanced Sampler
- Free Energy Calculator
- LBS Finder & Refiner

Nanomaterial Modeler

User Profile

Nanomaterial Modeler helps users generate a series of CHARMM inputs necessary to build nanomaterial structures for molecular dynamics simulations. Currently supported nanomaterials are given below.

Nanomaterial Modeler has been developed in collaboration with the [INTERFACE FF](#) development team and the [OpenKIM](#) development team.

- **Fcc metals:** Ac, Ag, Al, Au, Ca(α), Ce(γ), Cu, Es(β), Fe, Ir, Ni, Pb, Pd, Pt, Rh, Sr(α), Th(α), Yb(β), bulk minerals, including different cleavage planes (up to 3), a variety of shapes (i.e., sphere, cylinder, rod, polygon, and box), and Wulff construction. In particular, ligand-protected Au nanocluster/nanoparticle/surface are also provided.
- **Metal Oxides:** Al_2O_3 , Fe_2O_3 , Cr_2O_3 , CaO , MgO , and NiO with a box shape.

Metal Hydroxides: $\text{Ca}(\text{OH})_2$, $\text{Mg}(\text{OH})_2$, and $\text{Ni}(\text{OH})_2$ with a box shape.

Other Materials: Lithium Cobalt Oxide (LiCoO_2) with a box shape.

- **Clay Minerals:** Kaolinite ($\text{Al}_2\text{Si}_2\text{O}_5(\text{OH})_4$), Pyrophyllite ($\text{Al}_2\text{Si}_4\text{O}_{10}(\text{OH})_2$), and Montmorillonite ($\text{K}, \text{Na})_n[\text{Si}_4\text{O}_8][\text{Al}_{2-n}\text{Mg}_n\text{O}_2(\text{OH})_2]$). In the case of Montmorillonite, users can control the contents of Mg defect and ion types.

• **Mica:** Muscovite ($\text{KAl}_2(\text{AlSi}_3)\text{O}_{10}(\text{OH})_2$).

• **Calcium Sulfates:** Gypsum ($\text{CaSO}_4 \cdot 2\text{H}_2\text{O}$), Hemihydrate ($\text{CaSO}_4 \cdot 1/2\text{H}_2\text{O}$), and Anhydrite (CaSO_4) with different cleavage planes and Wulff construction.

• **Cement Minerals:** Tricalcium Silicate (Ca_3SiO_5) and Tricalcium Aluminate ($\text{Ca}_3\text{Al}_2\text{O}_6$) with different cleavage planes and Wulff construction.

• **Calcium Silicate Hydrate:** Tobermorite ($\text{Ca}_4\text{Si}_6\text{O}_{15}(\text{OH})_2 \cdot 5\text{H}_2\text{O}$).

• **Silica:** bulk minerals (α -quartz, α -cristobalite) as well as surfaces of different degree of ionization for specific pH values and particle sizes

• **Phosphate Minerals:** bulk mineral of Hydroxyapatite ($\text{Ca}_5(\text{PO}_4)_3(\text{OH})$), different cleavage planes and Wulff construction for various pH.

• **Transition Metal Dichalcogenides (TMDC):** Molybdenum Disulfide (MoS_2), Tungsten Disulfide (WS_2).

• **Carbonaceous Materials:** Carbon Nanotube, Graphene, and Graphite.



奈米材料模型建立

- The generated structure can be used in [Multicomponent Assembler](#) to model a nano-bio system.

GCMC/BD Ion Simulator

References for Nanomaterial Modeler:

S. Jo, T. Kim, V.G. Iyer, and W. Im (2008)

CHARMM-GUI: A Web-based Graphical User Interface for CHARMM. *J. Comput. Chem.* 29:1859-1865

Y.K. Choi, N.R. Kern, S. Kim, K. Kanhaiya, S.H. Jeon, Y. Afshar, S. Jo, B.R. Brooks, J. Lee, E.B. Tadmor, H. Heinz, and W. Im (2022)

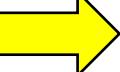
CHARMM-GUI Nanomaterial Modeler for Modeling and Simulation of Nanomaterial Systems. *J. Chem. Theory Comput.* 18:479-493

Download our initial systems and inputs [here](#).

Select a material from the list below. Currently selected material: **None**

1. 

Nanomaterial Type	Metals
	Metal Oxides
	Metal Hydroxides
	Battery Materials
	Clay Minerals
	Mica
	Calcium Sulfates
	Cement Minerals
	Calcium Silicate Hydrates
	Silica
	Phosphate minerals
	Transition Metal Dichalcogenides
Nanomaterial Shape	Carbonaceous Materials
Sphere Options	
Radius	
Material Volume	
System Volume	
System Type	
<input checked="" type="radio"/> Solvated	Carbon Nanotube (CNT)
<input type="radio"/> Vacuum	Graphene
	Graphite

2. 

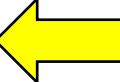
References for Nanomaterial Force Fields:

F. S. Emami, V. Puddu, R. J. Berry, V. Varshney, S. V. Patwardhan, C. C. Perry and H. Heinz (2014)

Force Field and a Surface Model Database for Silica to Simulate Interfacial Properties in Atomic Resolution. *Chem. Mater.* 26:2647-2658

H. Heinz, T.-J. Lin, R. Kishore Mishra and F. S. Emami (2013)

Thermodynamically consistent force fields for the assembly of inorganic, organic, and biological nanostructures: the INTERFACE force field. *Langmuir* 29:1751-1765

3. 

Next Step:
Build Nanomaterial 

奈米材料模型建立

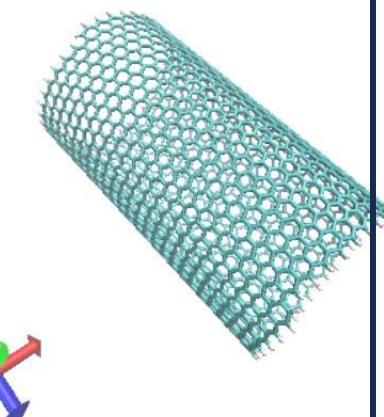
Select a material from the list below. Currently selected material: **Carbon Nanotube (CNT)**

Nanomaterial Type

Chirality (n, m) , Cell Copies Use virtual electron model

Calculated Tube Info

Tube Length	17.8 Å
Tube Diameter	29.4 Å
Tube Conductivity	Metallic
System Volume	62,927.2 Å ³



Periodic Options

 X Y Z

System Type

- Solvated
- Vacuum

Select a material from the list below. Currently selected material: **Graphene**

Nanomaterial Shape: Percent Defect Use virtual electron model

Box Options

Miller Index

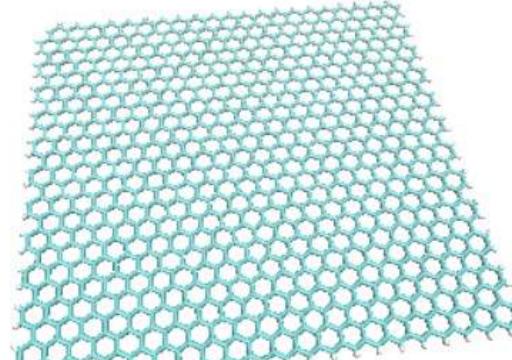
X length (Å) (54.3)

Y length (Å) (51.3)

Z length (Å) (3.3)

Material Volume (Å³) 9,317.3

System Volume (Å³) 9,317.3



Unit Cell Info

Unit Cell X 4.934 Å

Unit Cell Y 4.273 Å

Unit Cell Z 3.348 Å

Layer Dimension Z

Number of Layers 1

Periodic Options

 X Y Z

System Type

- Solvated
- Vacuum



奈米材料模型建立

Building Size Determination PBC Setup Input Generator

JOB ID: 2449995467

Building Input: [step1_nanomaterial.inp](#)
Building Output: [step1_nanomaterial.out](#)
Building PSF: [step1_nanomaterial.psf](#)
Image Patch PSF: [step1_nanomaterial_imc.psf](#)
Building PDB: [step1_nanomaterial.pdb \(view structure\)](#)
Building Info: [step1_nanomaterial.str](#)

點擊下載

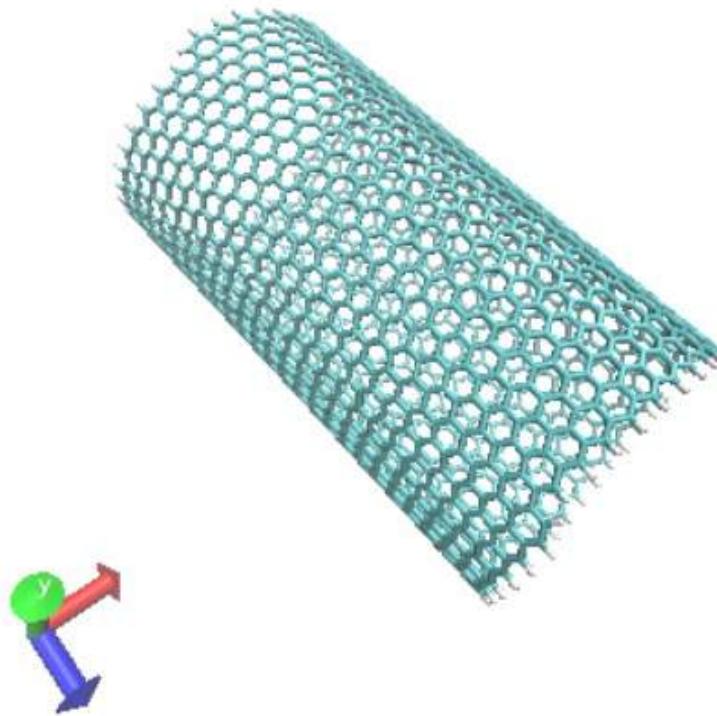
download.tgz



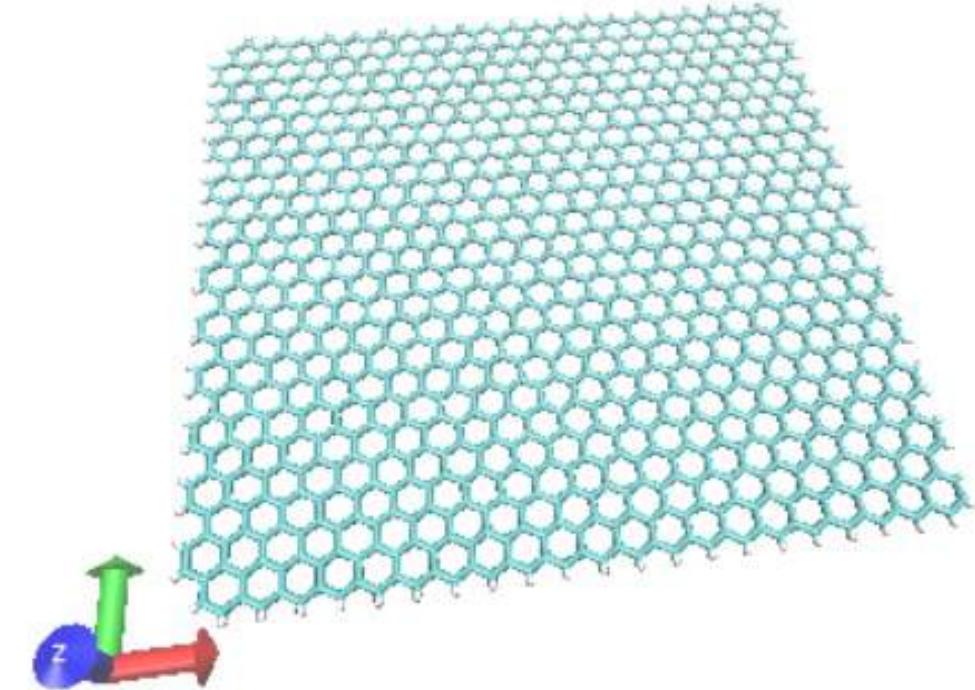
glycam.yml	4
molecule.py	9,508
molecule.pyc	10,183
rmimg_info.py	10,489
step1.1_user_input.str	150
step1_nanomaterial.crd	274,340
step1_nanomaterial.inp	2,992
step1_nanomaterial.out	129,153
step1_nanomaterial.pdb	149,981
step1_nanomaterial.psf	928,180
step1_nanomaterial.str	415
step1_nanotube.crd	274,134
step1_nanotube.pdb	157,492
step1_nanotube.rtf	98,373
toppar.str	3,670

: TdIII 模板檔案
? Python 來源檔案
? PYC 檔案
? Python 來源檔案
? STR 檔案
? CRD 檔案
? INP 檔案
? OUT 檔案
? PDB 檔案
? PSF 檔案
? STR 檔案
? CRD 檔案
? PDB 檔案
? RTF 格式
? STR 檔案

奈米材料模型建立

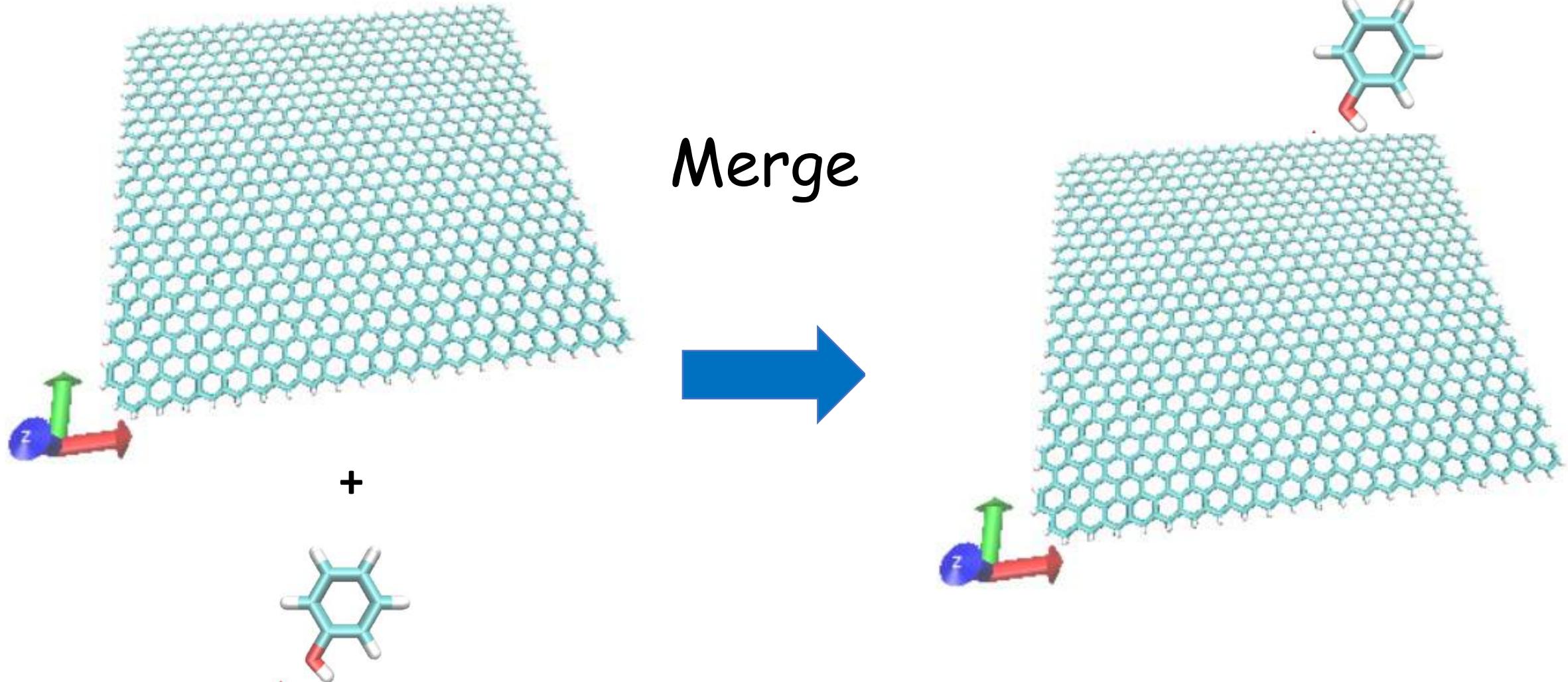


Nanotube



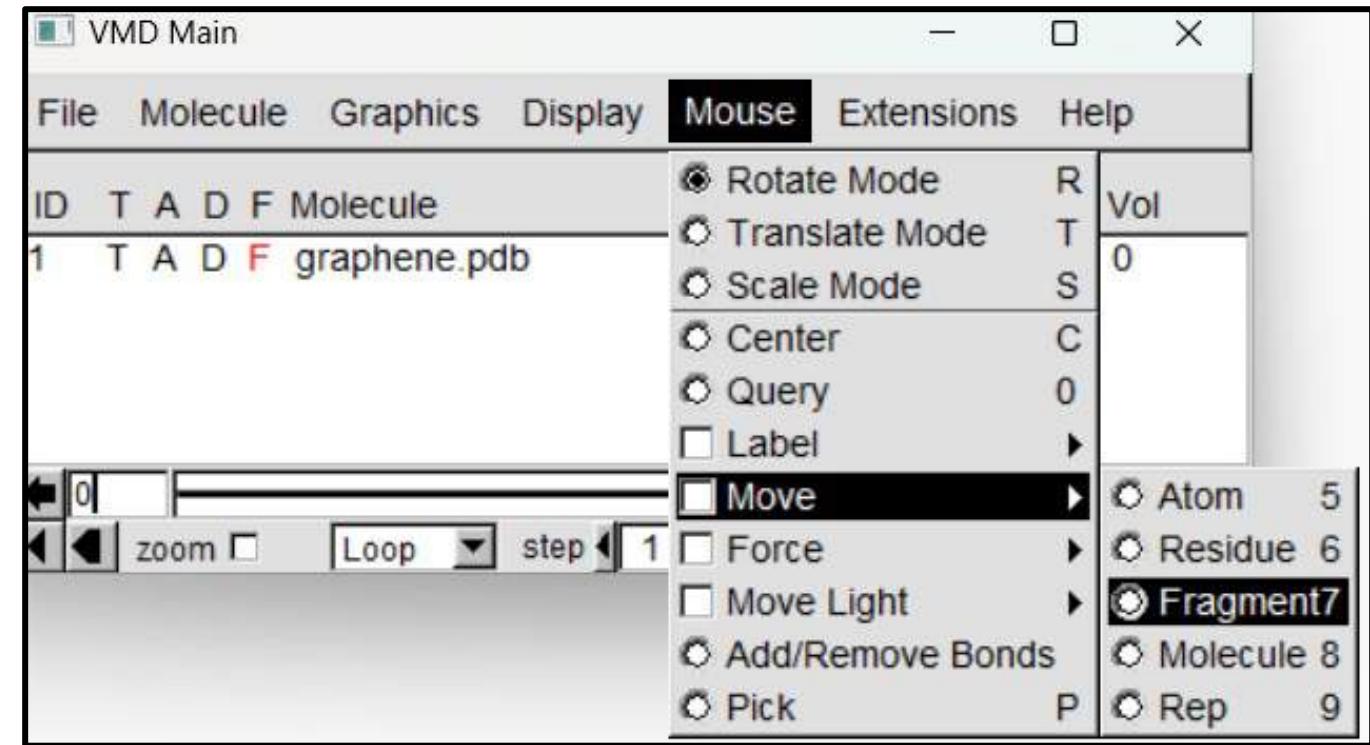
Graphene sheet

奈米材料模型建立 (1. Merge)



Adjustment

按住**shift**與左鍵可以
旋轉分子



完成旋轉與調整後，在 tk console 輸入
source update.tcl