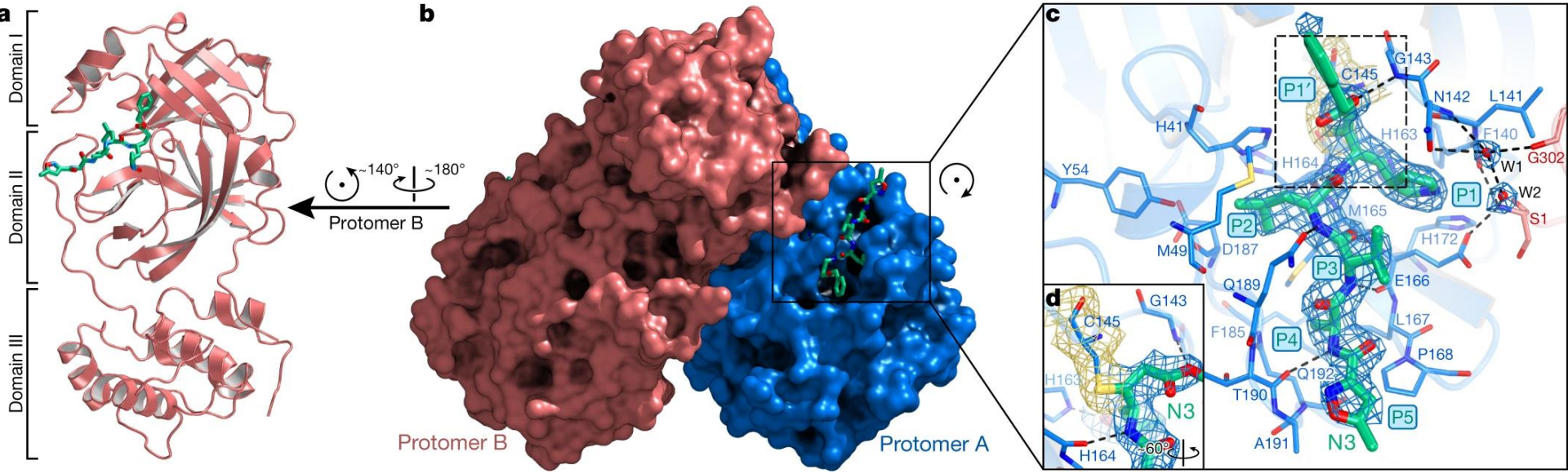
PDB数据库的使用

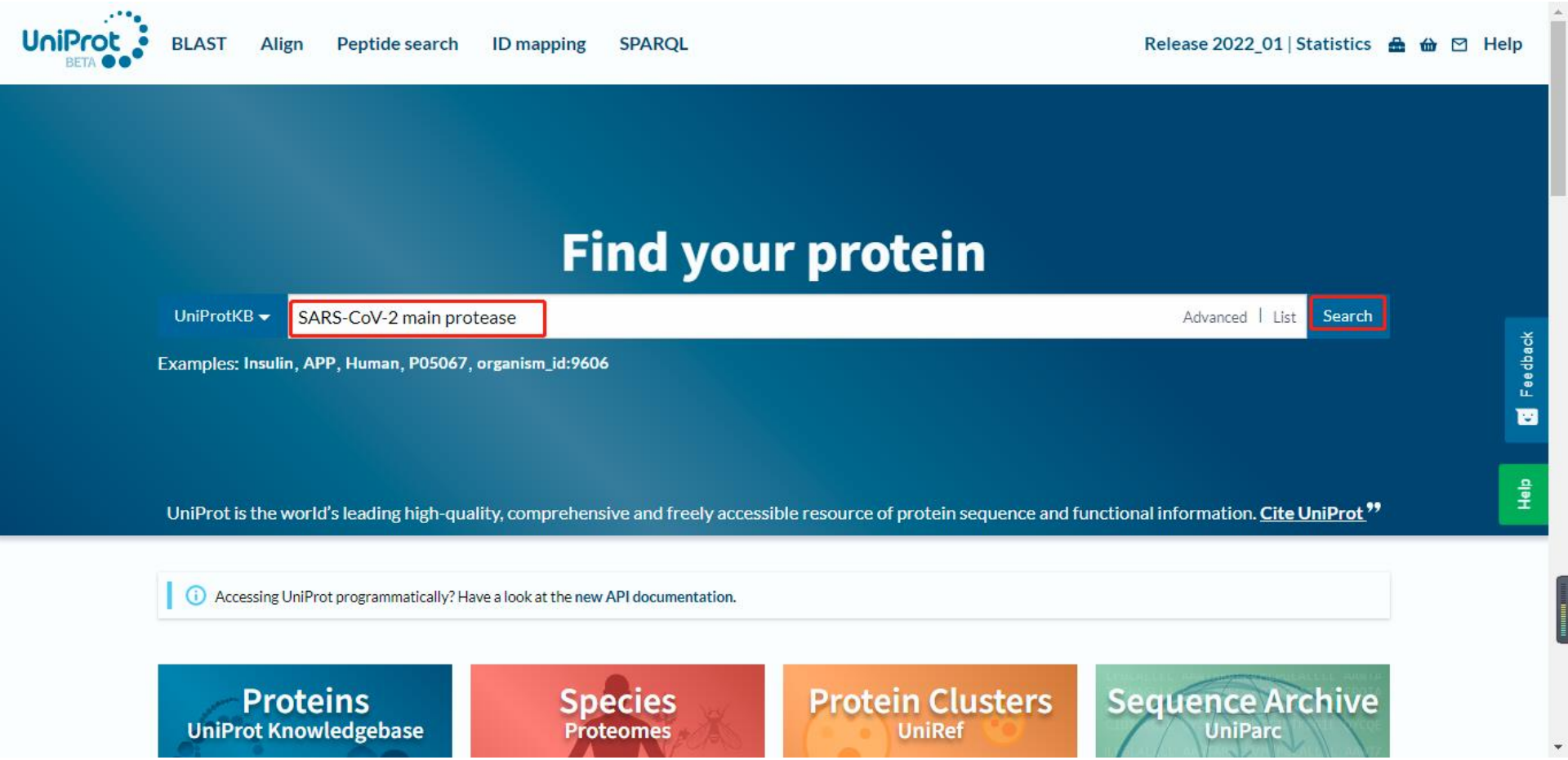
检索靶点结构



新冠SARS-CoV-2主蛋白酶和抑制剂PF-07321332

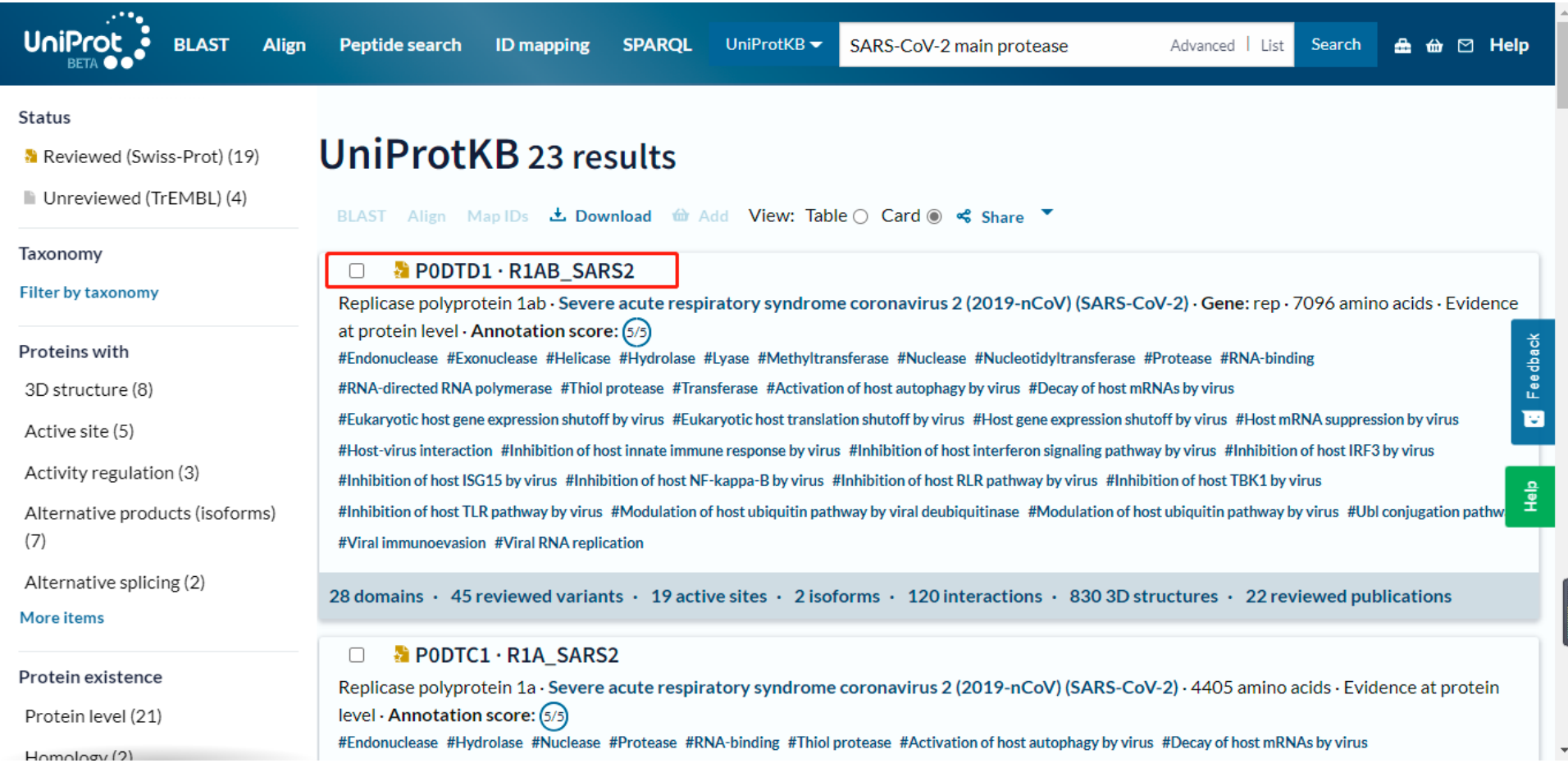
检 索 靶 点 结 构

旧网址：https://www.uniprot.org/ 新网址：https://beta.uniprot.org/



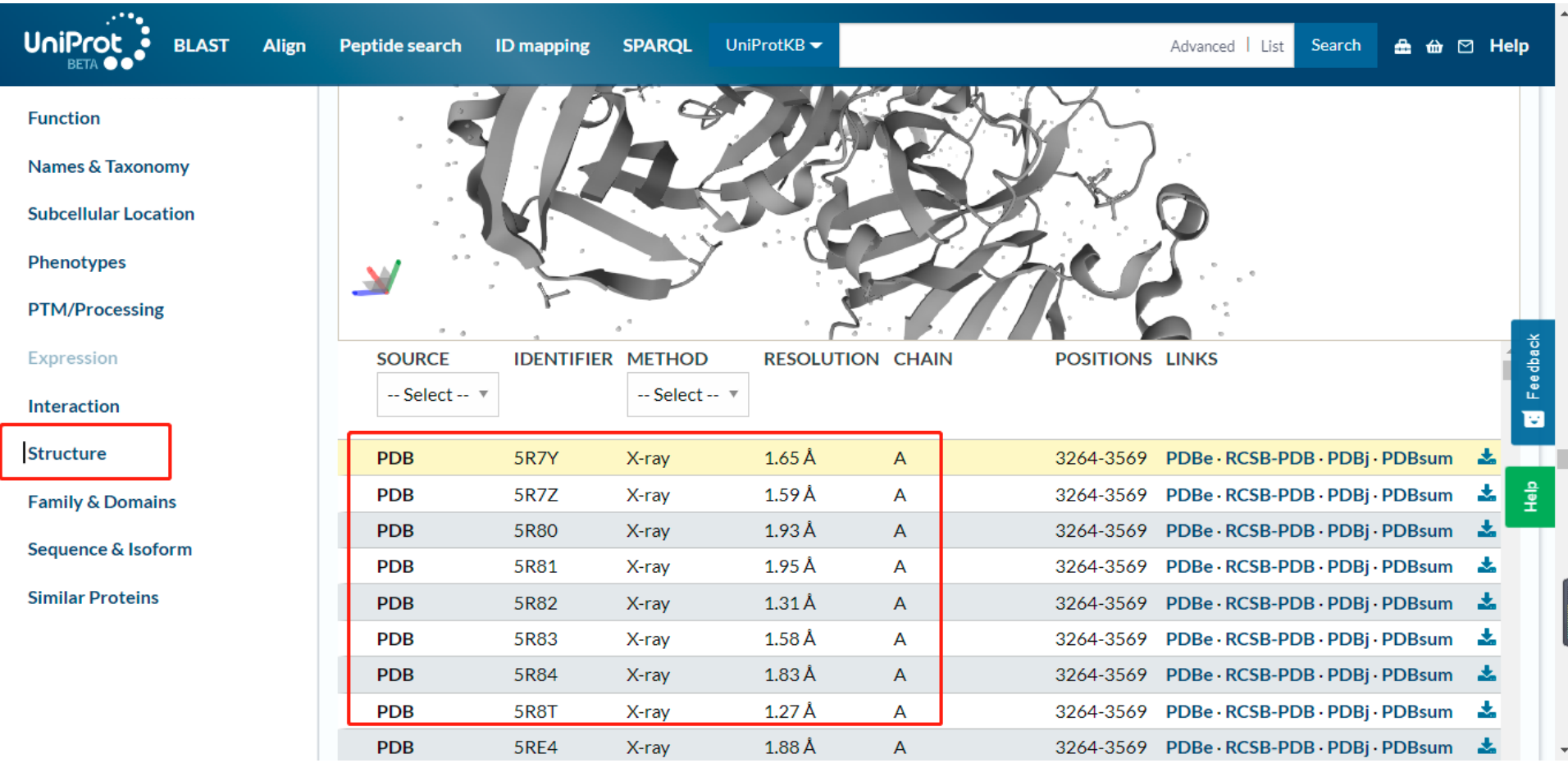
在不知道靶点其他信息的情况下，可以用靶点名称用此方法检索靶点的所有结构物

检 索 靶 点 结 构



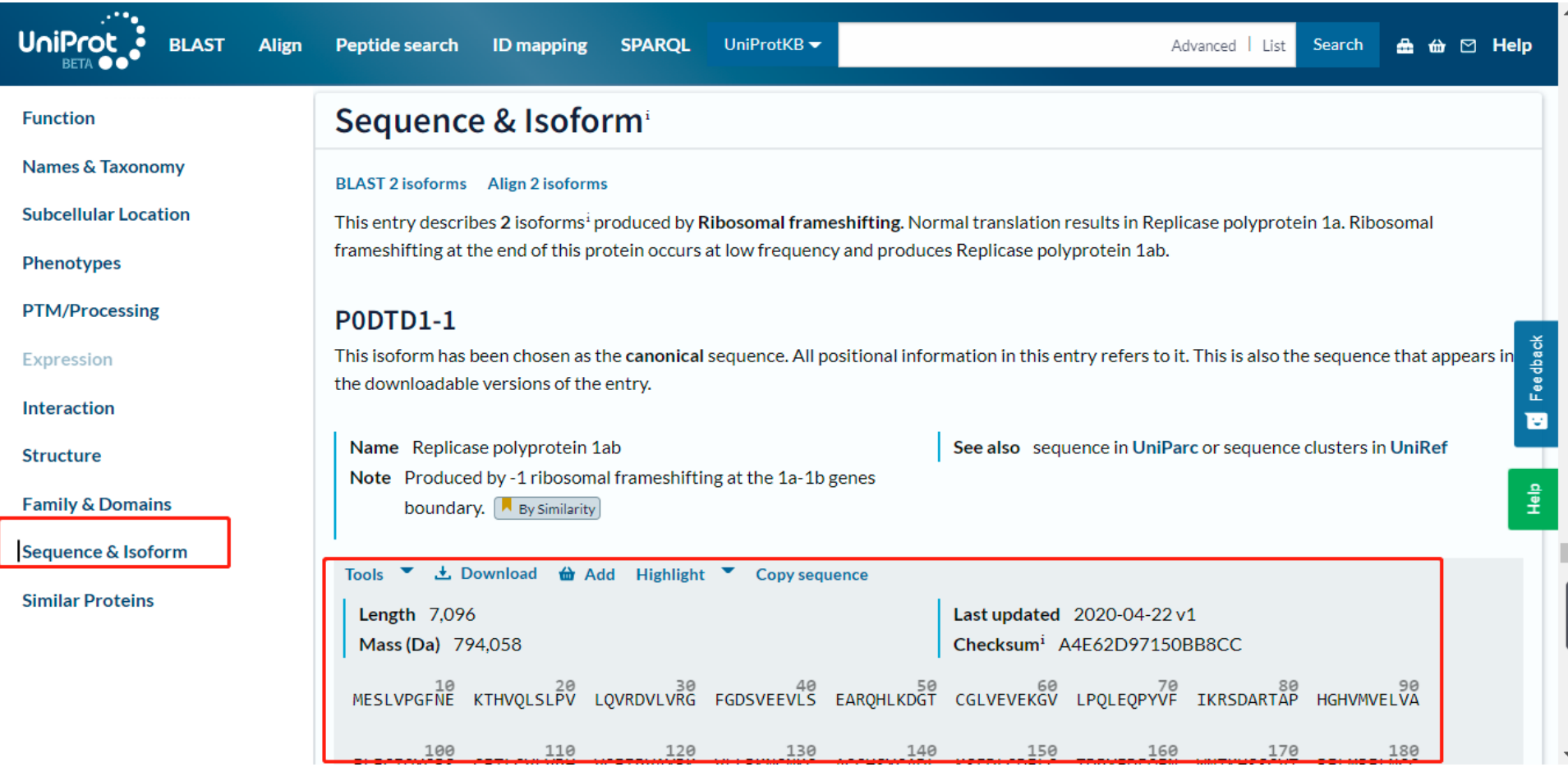
根据描述，选择第一个即可

检 索 靶 点 结 构



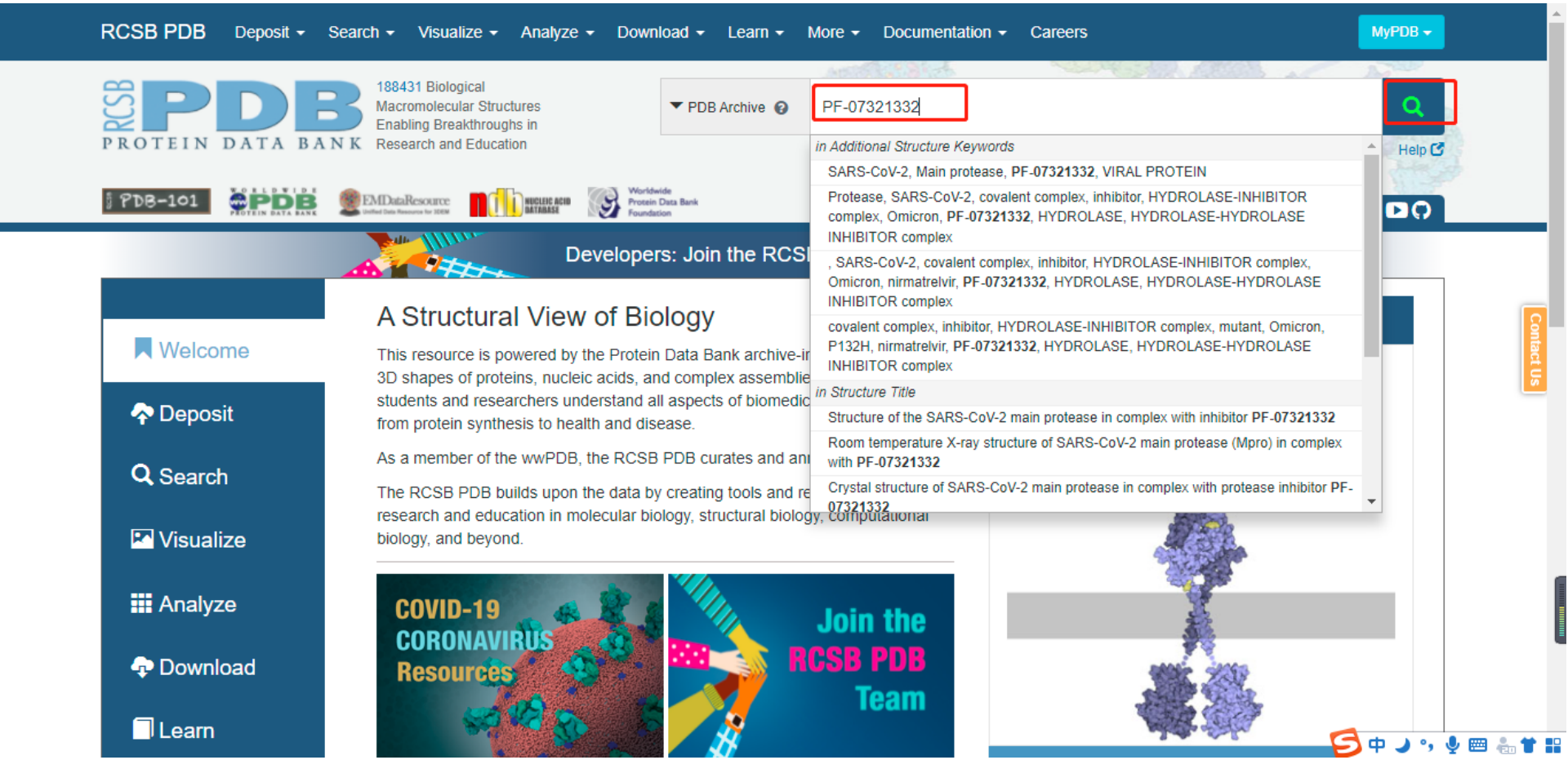
点击左侧“Structure”可以看到所有存在的pdb结构及其信息

检 索 靶 点 结 构



点击左侧“Sequence”可以看到靶点序列

检 索 靶 点 结 构



可以利用已知的靶点信息在PDB数据库检索（PDB ID、作者、配体等）

检 索 靶 点 结 构

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

SCIENTIFIC NAME OF SOURCE ORGANISM
- Severe acute respiratory syndrome coronavirus 2 (11)

TAXONOMY
- Riboviria (11)

EXPERIMENTAL METHOD
- X-RAY DIFFRACTION (11)
- NEUTRON DIFFRACTION (1)

POLYMER ENTITY TYPE
- Protein (11)

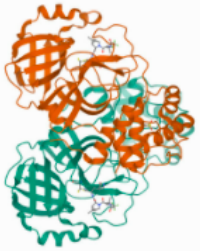
REFINEMENT RESOLUTION (Å)
- 1.5 - 2.0 (8)
- 2.0 - 2.5 (4)

RELEASE DATE
- 2020 - 2024 (11)

ENZYME CLASSIFICATION NAME
- Hydrolases (11)
- Transferases (7)

SYMMETRY TYPE

1 to 11 of 11 **Structures** Page 1 of 1 25 Sort by ↓ Score



3D View

7VH8

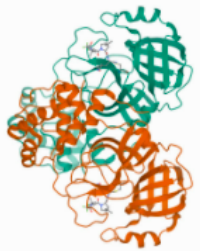
Download File View File

Crystal structure of SARS-CoV-2 main protease in complex with protease inhibitor PF-07321332

Zhao, Y., Zhang, Q., Yang, H., Rao, Z.

(2021) Protein Cell

Released	2021-11-03
Method	X-RAY DIFFRACTION 1.59 Å
Organisms	Severe acute respiratory syndrome coronavirus 2
Macromolecule	3C-like proteinase (protein)
Unique Ligands	4WI, DMS, H2S



3D View

7SI9

Download File View File

Room temperature X-ray structure of SARS-CoV-2 main protease (Mpro) in complex with PF-07321332

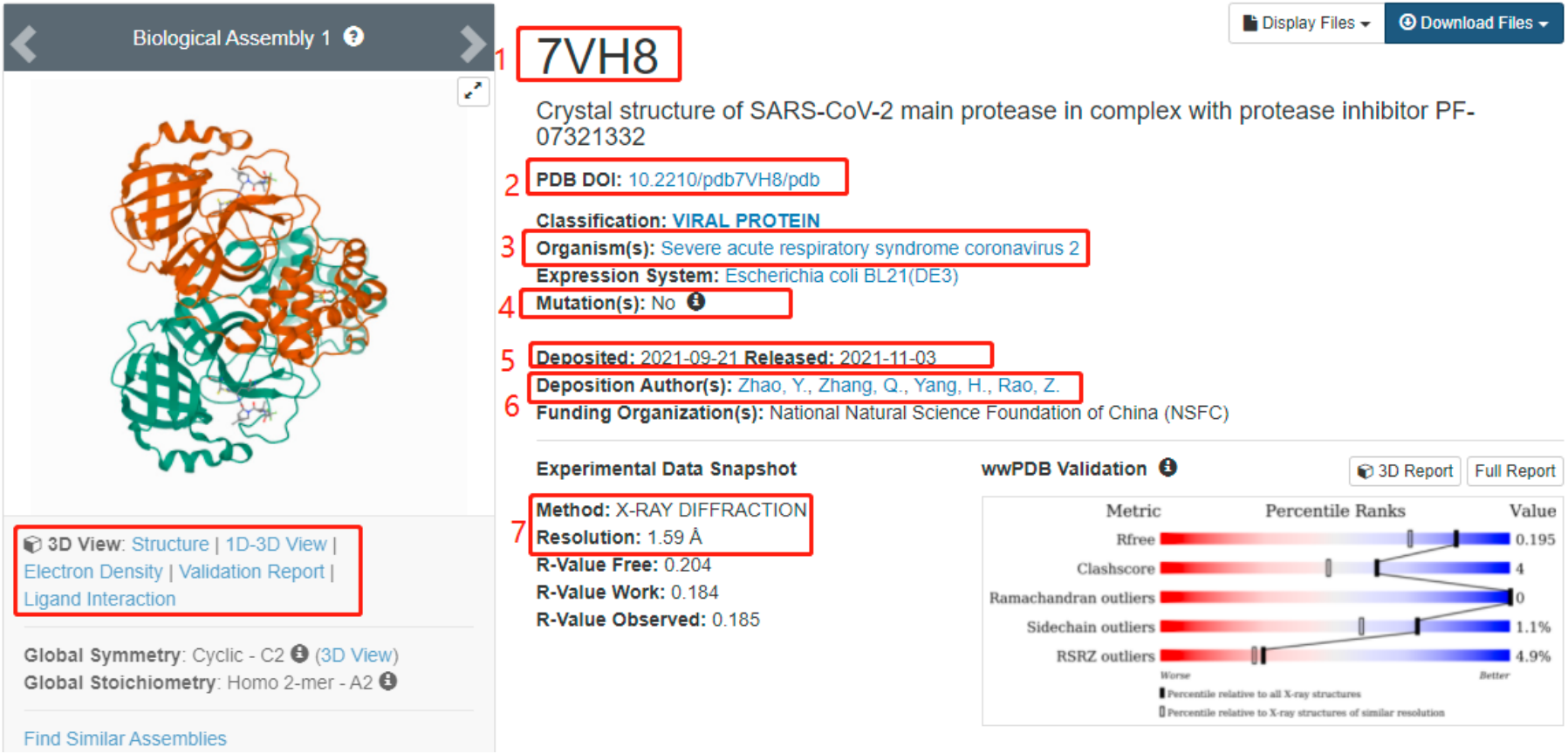
Kovalevsky, A., Kneller, D.W., Coates, L.

(2022) Res Sq

Released	2021-10-20
Method	X-RAY DIFFRACTION 2 Å
Organisms	Severe acute respiratory syndrome coronavirus 2
Macromolecule	3C-like proteinase (protein)
Unique Ligands	4WI

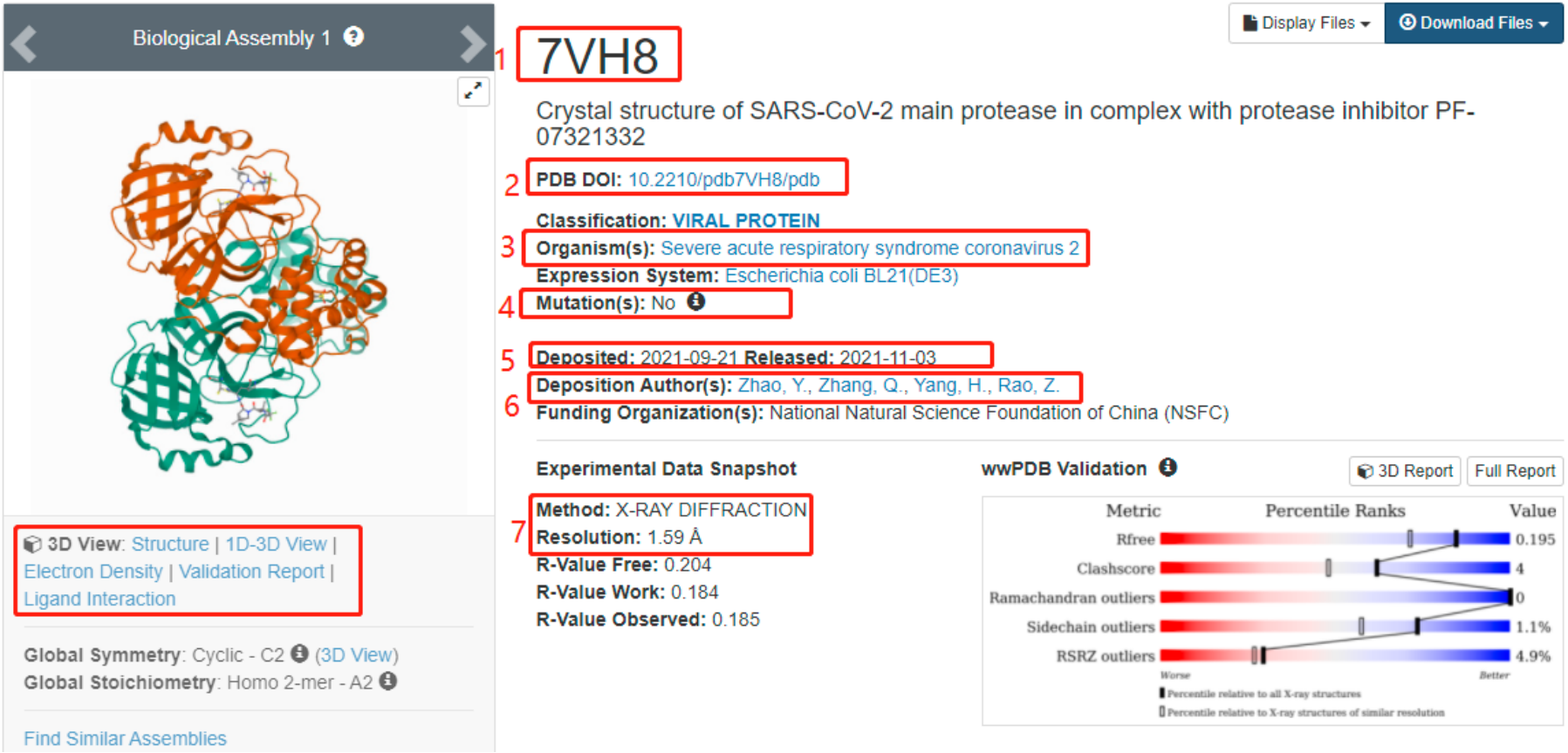
Contact Us

检 索 靶 点 结 构



I.PDB ID，4位：0-9数字+A-Z字母组合，每个蛋白序列唯一，因解析方法、实验条件、实验操作等不同可有不同ID

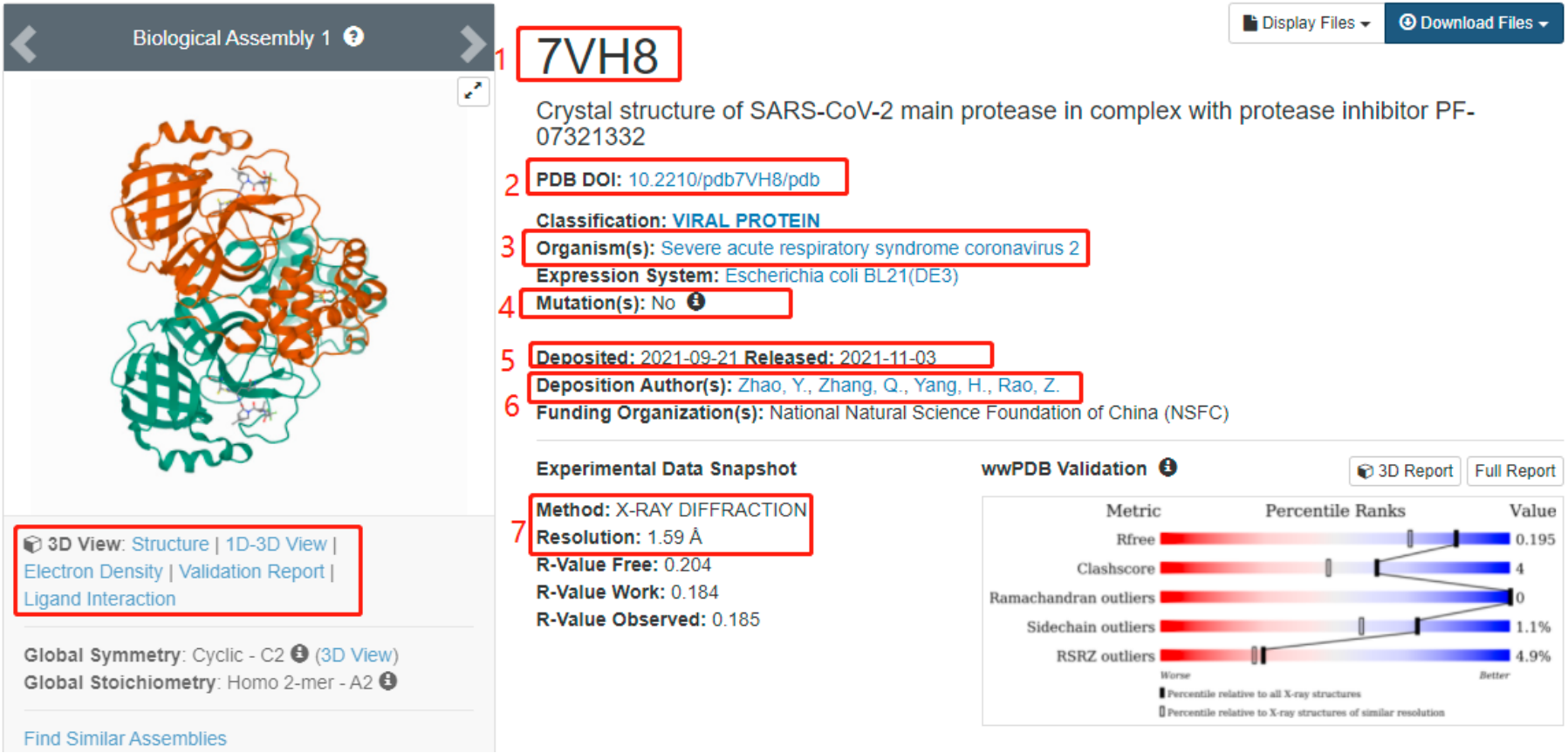
检 索 靶 点 结 构



2.关于该结构文献的doi　　3.物种来源

4.该结构是否有突变　　5.解析日期

检 索 靶 点 结 构

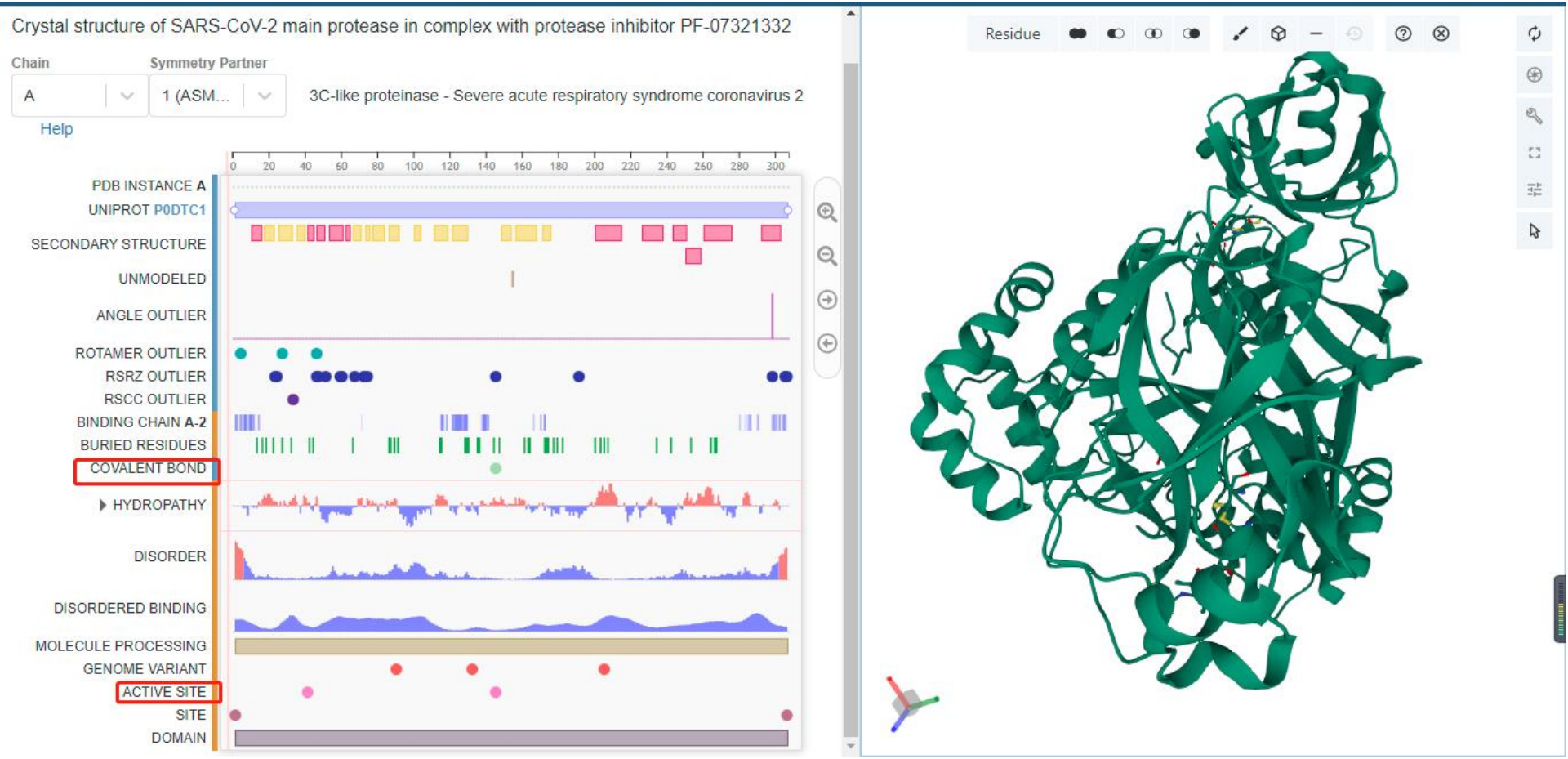


6.解析作者

7.解析方法和分辨率：2.5 Å以下，越小解析结构越精确

8.查看三维结构

检 索 靶 点 结 构


Crystal structure of SARS-CoV-2 main protease in complex with protease inhibitor PF-07321332
Chain
A
Symmetry Partner
1 (ASM...
3C-like proteinase - Severe acute respiratory syndrome coronavirus 2
Help
0 20 40 60 80 100 120 140 160 180 200 220 240 260 280 300
PDB INSTANCE A
UNIPROT P0DTC1
SECONDARY STRUCTURE
UNMODELED
ANGLE OUTLIER
ROTAMER OUTLIER
RSRZ OUTLIER
RSCC OUTLIER
BINDING CHAIN A-2
BURIED RESIDUES
COVALENT BOND
HYDROPATHY
DISORDER
DISORDERED BINDING
MOLECULE PROCESSING
GENOME VARIANT
ACTIVE SITE
SITE
DOMAIN
Residue

检 索 靶 点 结 构

Literature

Download Primary Citation

Crystal structure of SARS-CoV-2 main protease in complex with protease inhibitor PF-07321332.

Zhao, Y., Fang, C., Zhang, Q., Zhang, R., Zhao, X., Duan, Y., Wang, H., Zhu, Y., Feng, L., Zhao, J., Shao, M., Yang, X., Zhang, L., Peng, C., Yang, K., Ma, D., Rao, Z., Yang, H. (2021) Protein Cell

PubMed: 34687004 Search on PubMed Search on PubMed Central

DOI: 10.1007/s13238-021-00883-2

Primary Citation of Related Structures:

7VH8

关于该结构文献的信息显示

检 索 靶 点 结 构

Macromolecules

Find similar proteins by: Sequence (by identity cutoff) | 3D Structure

Entity ID: 1

Molecule	Chains	Sequence Length	Organism	Details	Image
3C-like proteinase	A	306	Severe acute respiratory syndrome coronavirus 2	**Mutation(s)**: 0 **EC:** 3.4.22.69 (PDB Primary Data), 3.4.19.12 (UniProt), 3.4.22 (UniProt)	

UniProt

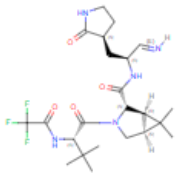
Find proteins for P0DTC1 *(Severe acute respiratory syndrome coronavirus 2)* Explore P0DTC1 Go to UniProtKB: P0DTC1

该蛋白的信息，分子名称，链，序列长度，突变信息等

每个蛋白质的氨基酸序列唯一，序列号唯一，可因科学家和实验条件等不同，解析出不同PDB ID 的蛋白结构，两个网站可互通访问。

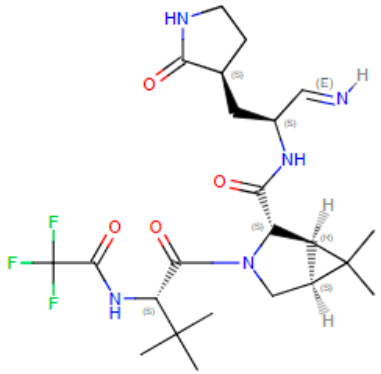
检 索 靶 点 结 构

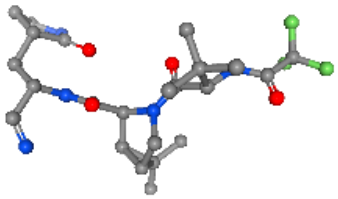
Ligands 3 Unique

ID	Chains	Name / Formula / InChI Key	2D Diagram	3D Interactions
4WI (Subject of Investigation/LOI) **Query on 4WI** Download Ideal Coordinates CCD File Download Instance Coordinates	B [auth A]	**(1R,2S,5S)-N-{(1E,2S)-1-imino-3-[(3S)-2-oxopyrrolidin-3-yl]propan-2-yl}-6,6-dimethyl-3-[3-methyl-N-(trifluoroacetyl)-L-valyl]-3-azabicyclo[3.1.0]hexane-2-carboxamide** $C_{23}H_{34}F_3N_5O_4$ WDVIRQQKRMIXGS-XIFHJVQQSA-N		Ligand Interaction
DMS **Query on DMS** Download Ideal Coordinates CCD File Download Instance Coordinates	C [auth A]	**DIMETHYL SULFOXIDE** C_2H_6OS IAZDPXIOMUYVGZ-UHFFFAOYSA-N		Ligand Interaction
H2S **Query on H2S** Download Ideal Coordinates CCD File Download Instance Coordinates	D [auth A]	**HYDROSULFURIC ACID** H_2S RWSOTUBLDIXVET-UHFFFAOYSA-N	H_2S	Ligand Interaction

该结构所含配体分子的信息

检 索 靶 点 结 构





View / Download Files

4WI

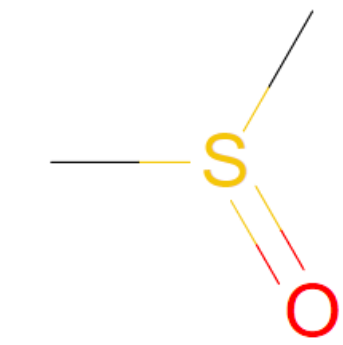
(1R,2S,5S)-N-{(1E,2S)-1-imino-3-[(3S)-2-oxopyrrolidin-3-yl]propan-2-yl}-6,6-dimethyl-3-[3-methyl-N-(trifluoroacetyl)-L-valyl]-3-azabicyclo[3.1.0]hexane-2-carboxamide

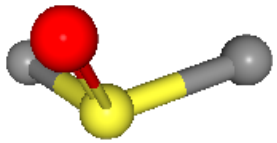
Find entries where: 4WI

☑ as a non-polymer is covalently linked to polymer or other heterogen groups 8 entries

search

Find related ligands:





View / Download Files

DMS

DIMETHYL SULFOXIDE

Find entries where: DMS

☑ is present as a standalone ligand in 3211 entries

☑ as a non-polymer is covalently linked to polymer or other heterogen groups 3 entries

search

Find related ligands:

Similar Ligands (Stereospecific)

Similar Ligands (including Stereoisomers)

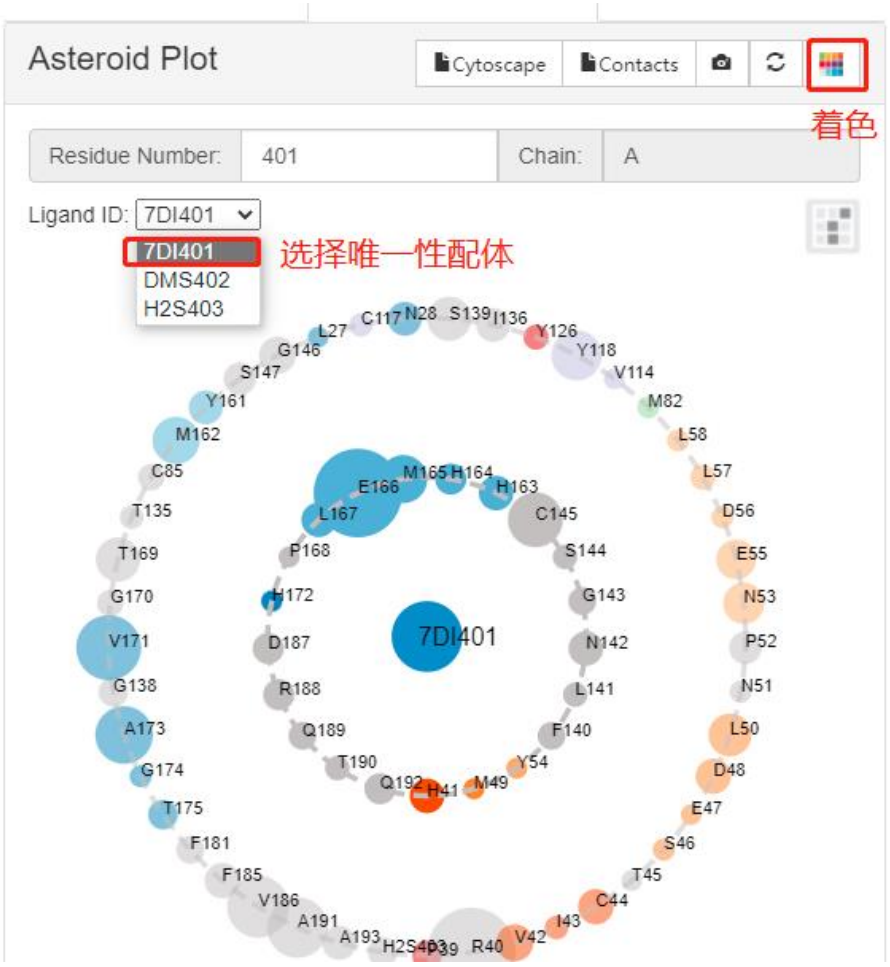
活 性 残 基 分 析

活性位点关键氨基酸残基分析

https://www.mrc-lmb.cam.ac.uk/rajini/index.html

以主蛋白酶为例，7VH8、7QBB、5RHC

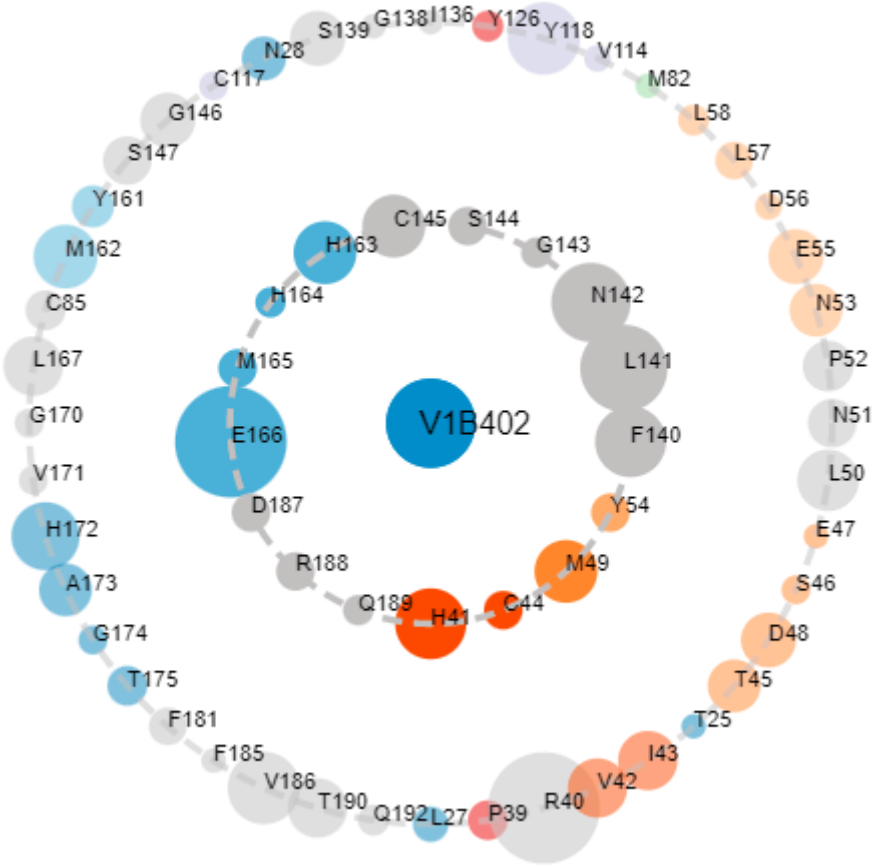
活 性 残 基 分 析


Asteroid Plot
Cytoscape
Contacts
着色
Residue Number:
401
Chain:
A
Ligand ID:
7DI401
7DI401
DMS402
H2S403
选择唯一性配体
7DI401
C117
N28
S139
I136
Y126
Y118
V114
M82
L58
L57
D56
E55
N53
P52
N51
L50
D48
E47
S46
T45
C44
I43
V42
R40
H2S403
A193
A191
V186
F185
F181
T175
G174
A173
G138
V171
G170
T169
T135
C85
M162
Y161
S147
G146
L27
E166
M165
H164
H163
L167
C145
P168
S144
H172
G143
D187
N142
R188
L141
Q189
F140
T190
Y54
Q192
H41
M49

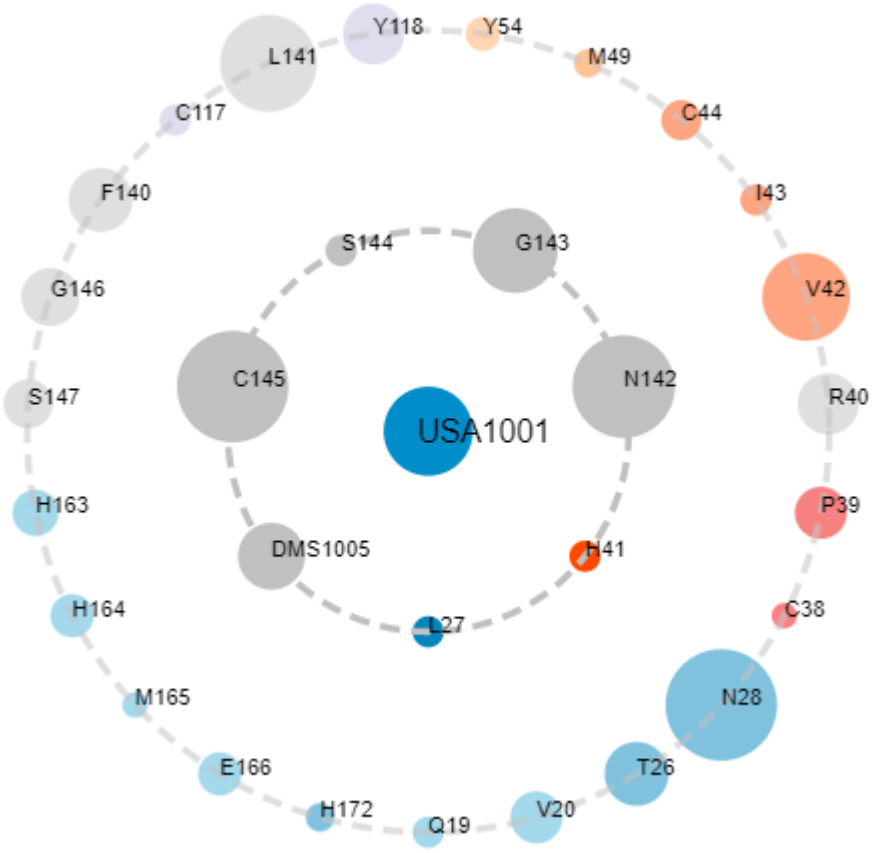

HOH
HETATM
Pymol

7VH8

活 性 残 基 分 析



7QBB

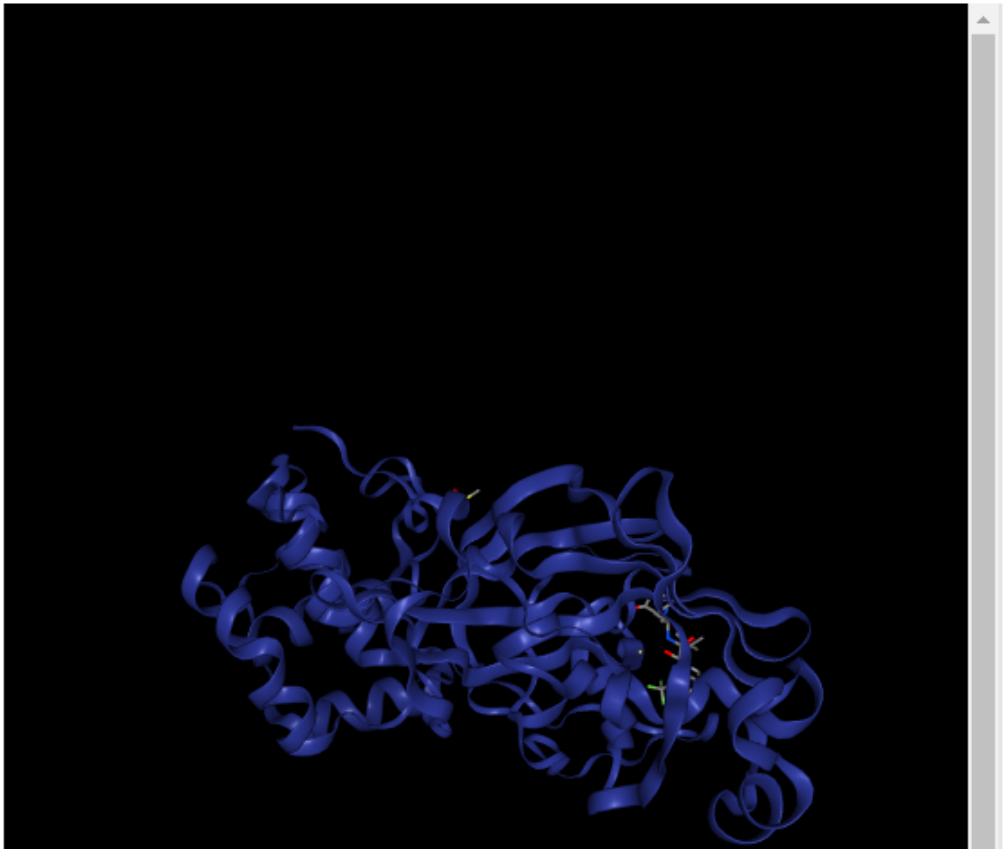


5RHC

靶点蛋白的活性位点预测

PROTEINS PLUS

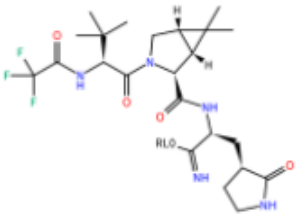
活 性 位 点 检 测



Ligands Pockets

Ligands

7DI_A_401



create pocket

DMS_A_402

Protoss Hydrogen prediction

DoGSiteScorer Binding site detection

DoGSiteScorer is a grid-based method which u
tial binding pockets - solely based on the 3D st
ckets. Global properties, describing the size, sh
(sub)pockets are calculated. Per default, a simp
(sub)pocket, based on a linear combination of
bicity and enclosure. Furthermore, a subset of
port vector machine (libsvm) to predict the (su
zero and one). The higher the score the more d

1. A. Volkamer, D. Kuhn, T. Grombacher, F. Rippm
res for structure-based druggability prediction

DoGSiteScorer

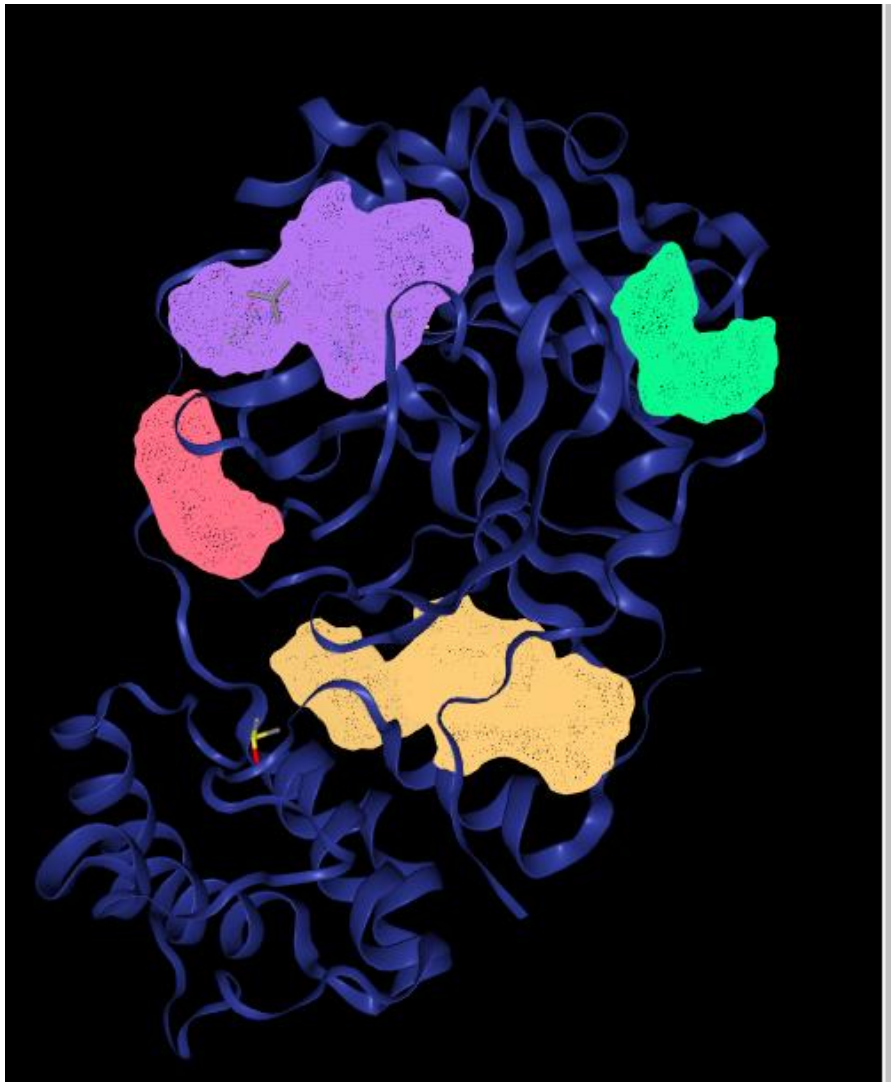
PoseView 2D interaction diagrams

SIENA Structure ensemble assembly

HyPPI Protein–protein interactions class

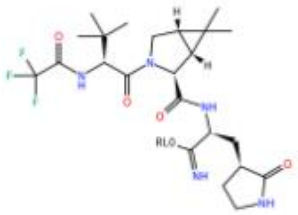
点击calculate

活 性 位 点 检 测



Ligands

7DI_A_401



create pocket

DMS_A_402

create pocket

DoGSiteScorer is a grid-based method which uses a Difference
binding pockets - solely based on the 3D structure of the prote

Result

Click on the plus to see your selected parameters:

Show 25 entries Searc

		Name	Volume Å³	Sur-face Å²	D Sc
		P_0	736.0	1120.98	0.
		P_1	630.53	675.28	0.
		P_2	240.19	442.82	0.
		P_3	160.26	380.18	0.
		P_4	143.04	243.73	0.

PyMol的介绍与使用

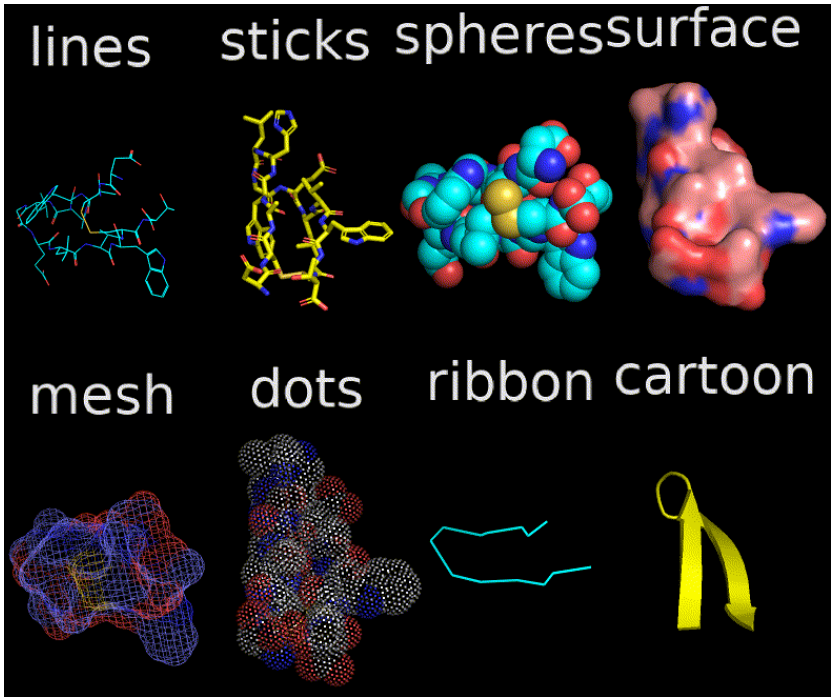
PyMol介绍

“Py”----python，该软件基于此计算机语言

“Mol”----molecule，该软件是用来显示分子结构

主要功能：创作高品质的小分子或是生物大分子（特别是蛋白质）的三维结构图像

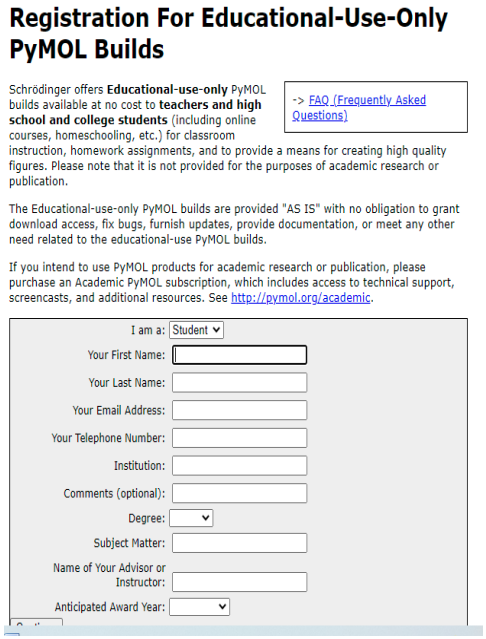
比对结构、光线追踪，探测静电力学、测距、动画制作等



PyMol下载

网址：https://pymol.org/edu/

Schrödinger为教师、高中生和大学生免费提供仅供教育使用的PyMOL构建



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-> FAQ (Frequently Asked Questions)

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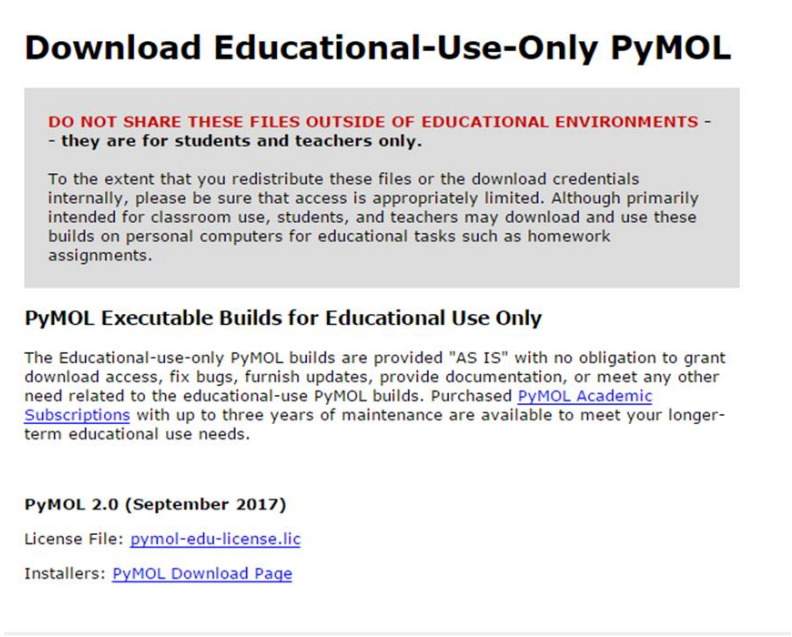
I am a: Student
Your First Name:
Your Last Name:
Your Email Address:
Your Telephone Number:
Institution:
Comments (optional):
Degree:
Subject Matter:
Name of Your Advisor or Instructor:
Anticipated Award Year:



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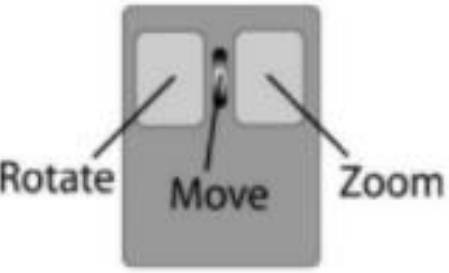
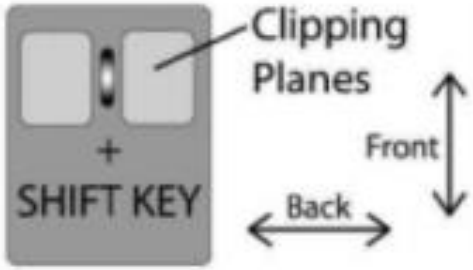
PyMOL 2.0 (September 2017)

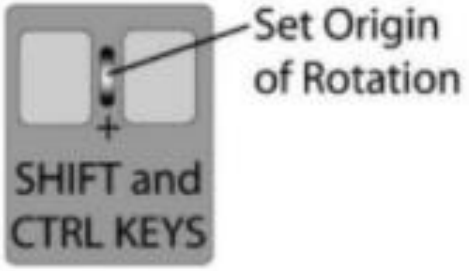
License File: pymol-edu-license.lic

Installers: PyMOL Download Page

PyMol基本操作

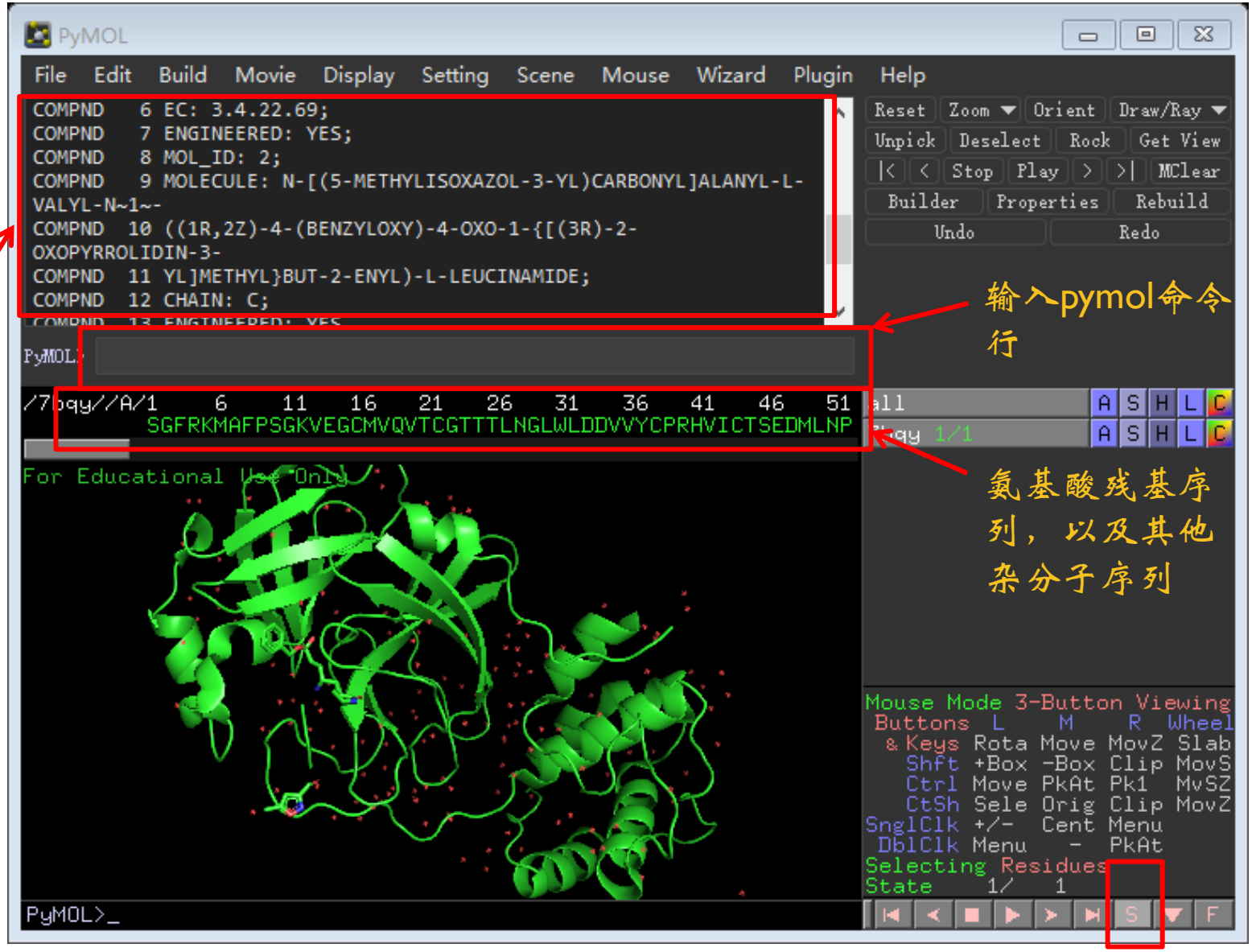

Rotate
Move
Zoom


Clipping Planes
+
SHIFT KEY
Front
Back


Set Origin of Rotation
+
SHIFT and CTRL KEYS


PyMOL
File Edit Build Movie Display Setting Scene Mouse Wizard Plugin Help
Detected GLSL version 4.60.
License Expiry date: 01-oct-2022
Detected 4 CPU cores. Enabled multithreaded rendering.
Reset Zoom Orient Draw/Ray
Unpick Deselect Rock Get View
Stop Play MClear
Builder Properties Rebuild
Undo Redo
PyMOL>
For Educational Use Only
Edu PyMOL
http://pymol.org/educational
v2.x
Schrödinger offers Educational-use-only PyMOL builds available at no cost to teachers and high school and college students for classroom instruction, homework assignments, and to provide a means for creating high quality figures. It is not provided for the purposes of academic research or publication.
There is no technical support from Schrödinger for "Edu" PyMOL, please use the pymol-users mailing list if you need help.
Licenses for academic: http://pymol.org/academic
Licenses for industry: http://pymol.org/contact
SCHRÖDINGER.
PyMOL>_
all
Mouse Mode 3-Button Viewing
Selecting Residues
State 1/ 1
External GUI
Viewer
Internal GUI

PyMol界面介绍

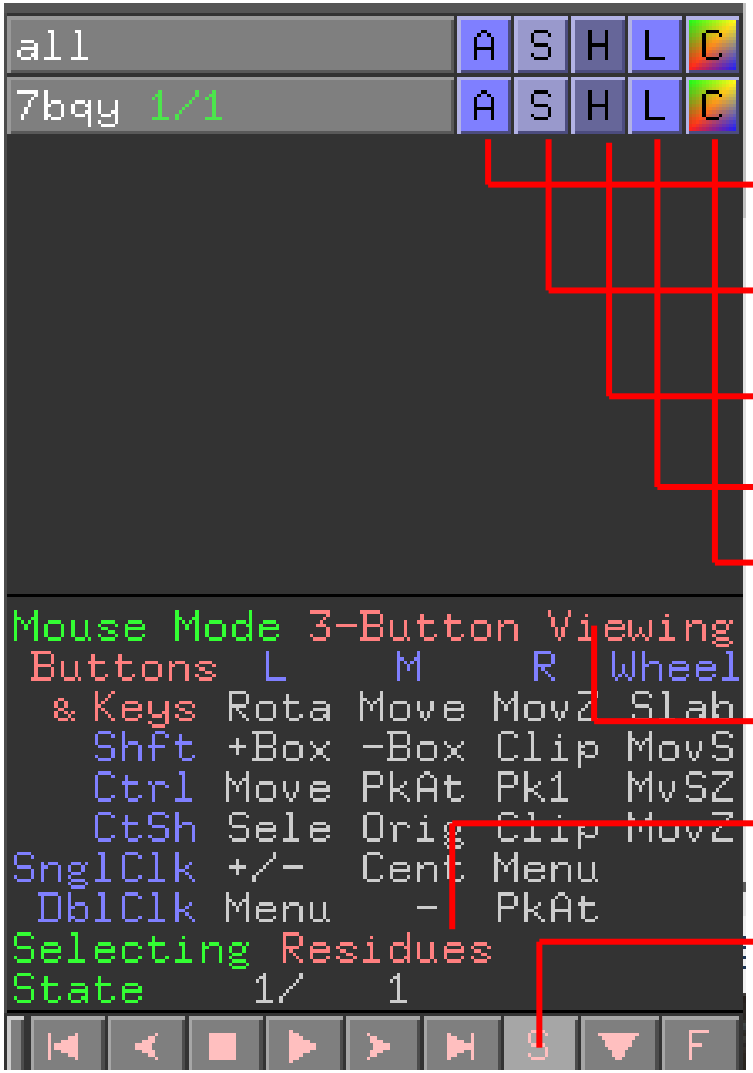


命令行或其他控制操作的进程显示屏幕

输入pymol命令行

氨基酸残基序列，以及其他杂分子序列

PyMol界面介绍



Action:对目标对象进行特定操作

Show:显示目标对象的特定样式

Hide:隐藏目标对象的特定样式

Label:调整目标对象的标注

Color:调整目标对象的颜色

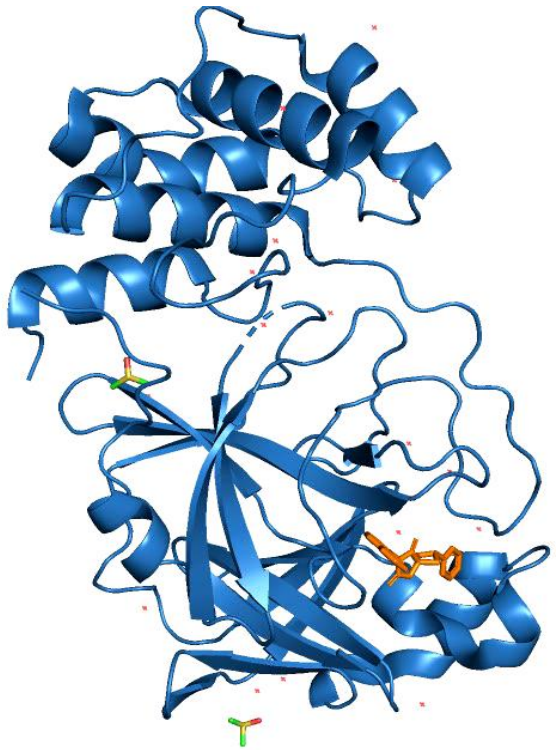
单击可变换鼠标模式：viewing/editing

单击可切换选择模式

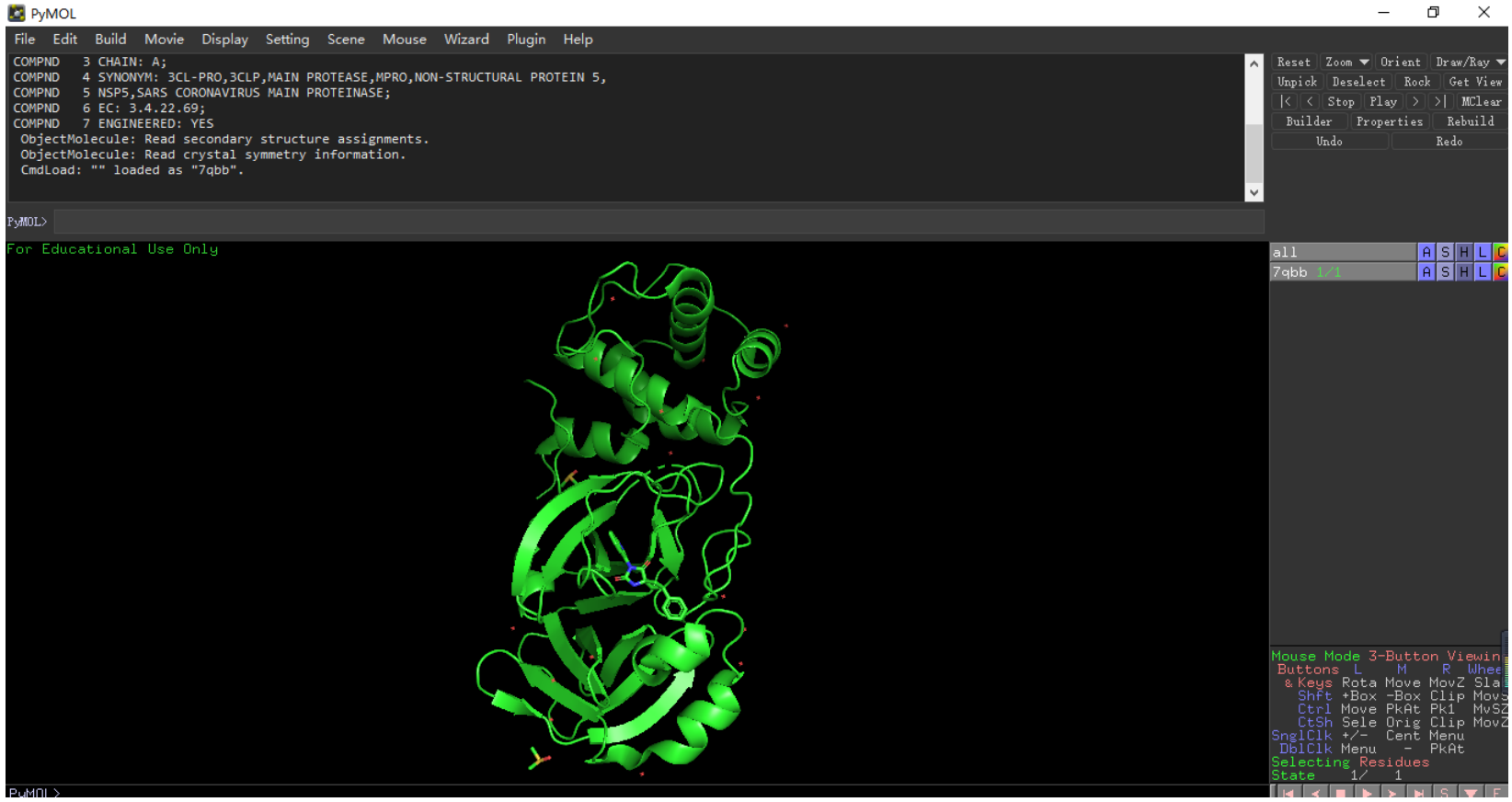
单击显示序列信息

PyMol实践一

简易动画制作



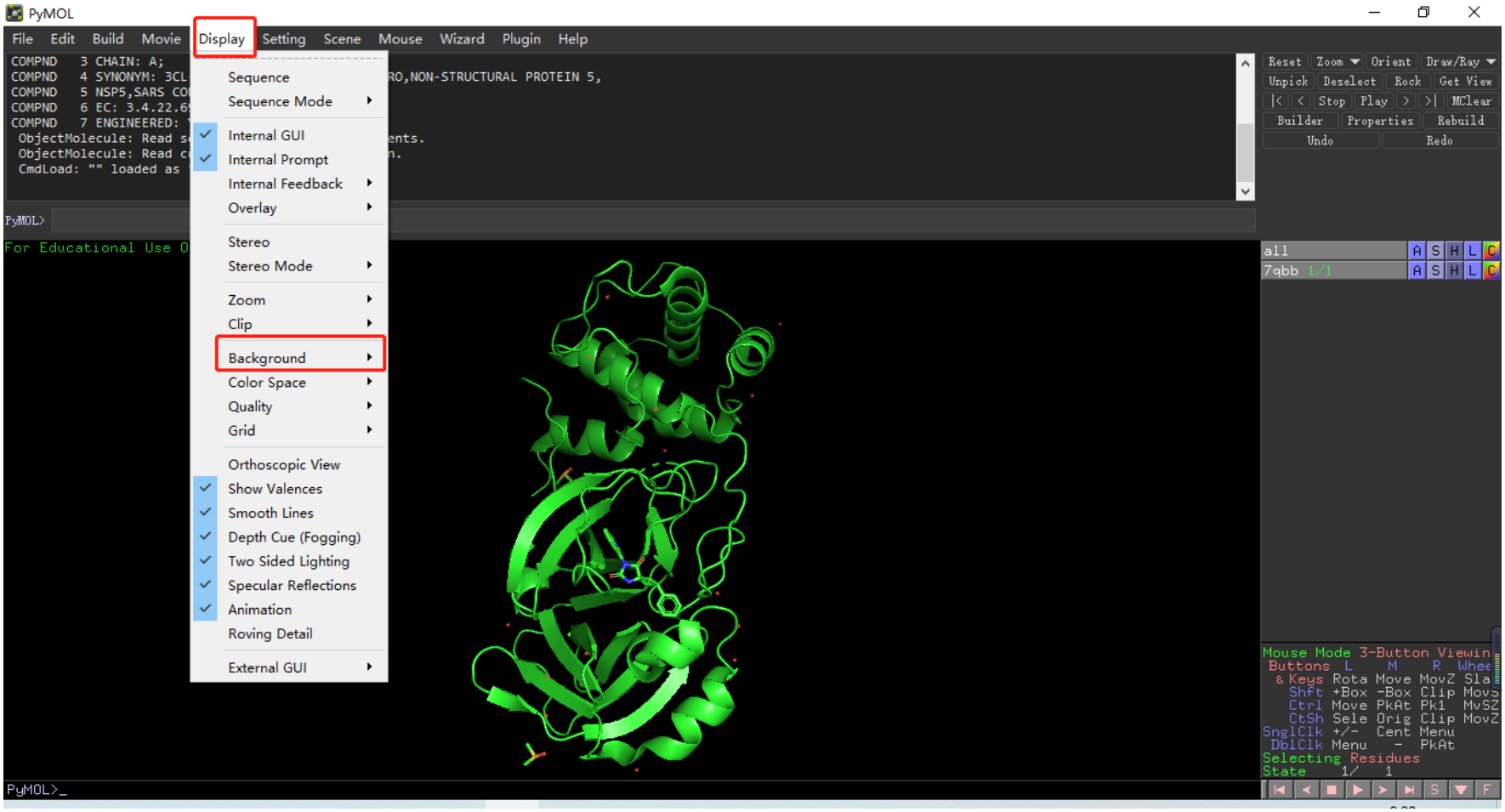
简 易 动 画 制 作



①用pymol打开SARS-CoV-2酶的晶体结构7qbb.pdb

或者直接在pymol的命令框中输入 fetch 7qbb

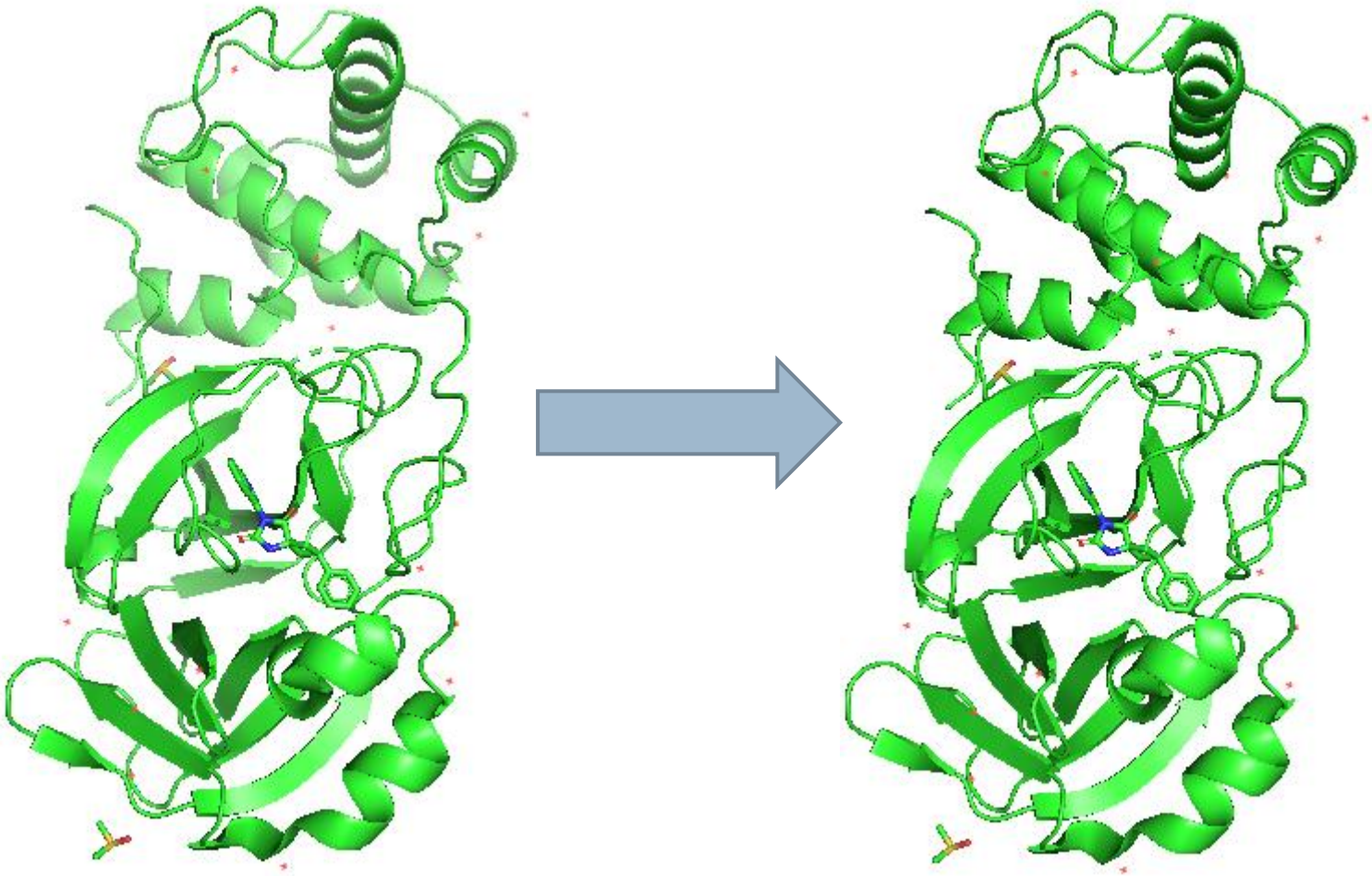
简 易 动 画 制 作



②将背景设置为白色，Display>Background>white

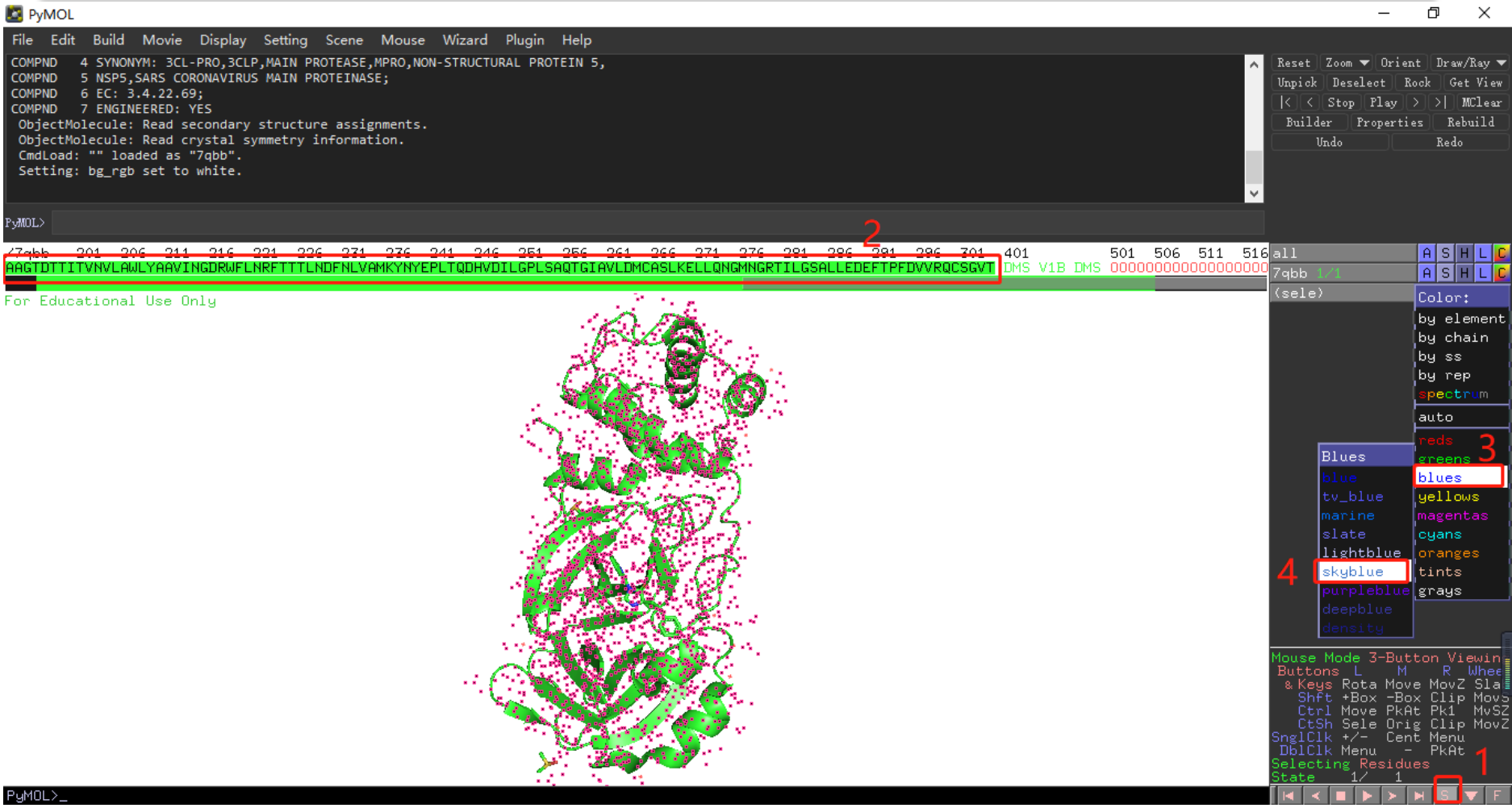
或者在命令行输入　　bg white

简 易 动 画 制 作



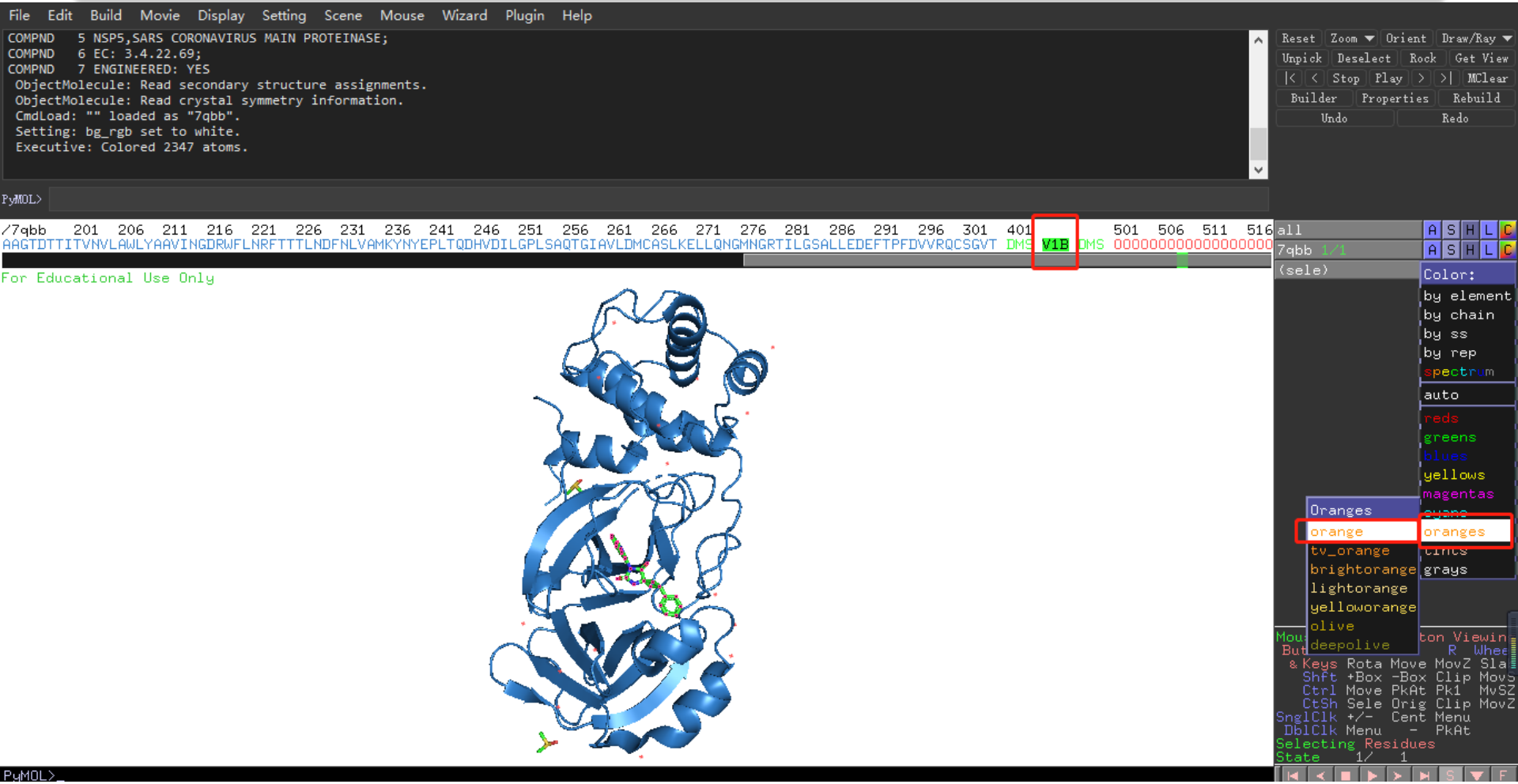
③滚动鼠标滑轮，关闭景深效果，可以看到上图的变化

简 易 动 画 制 作



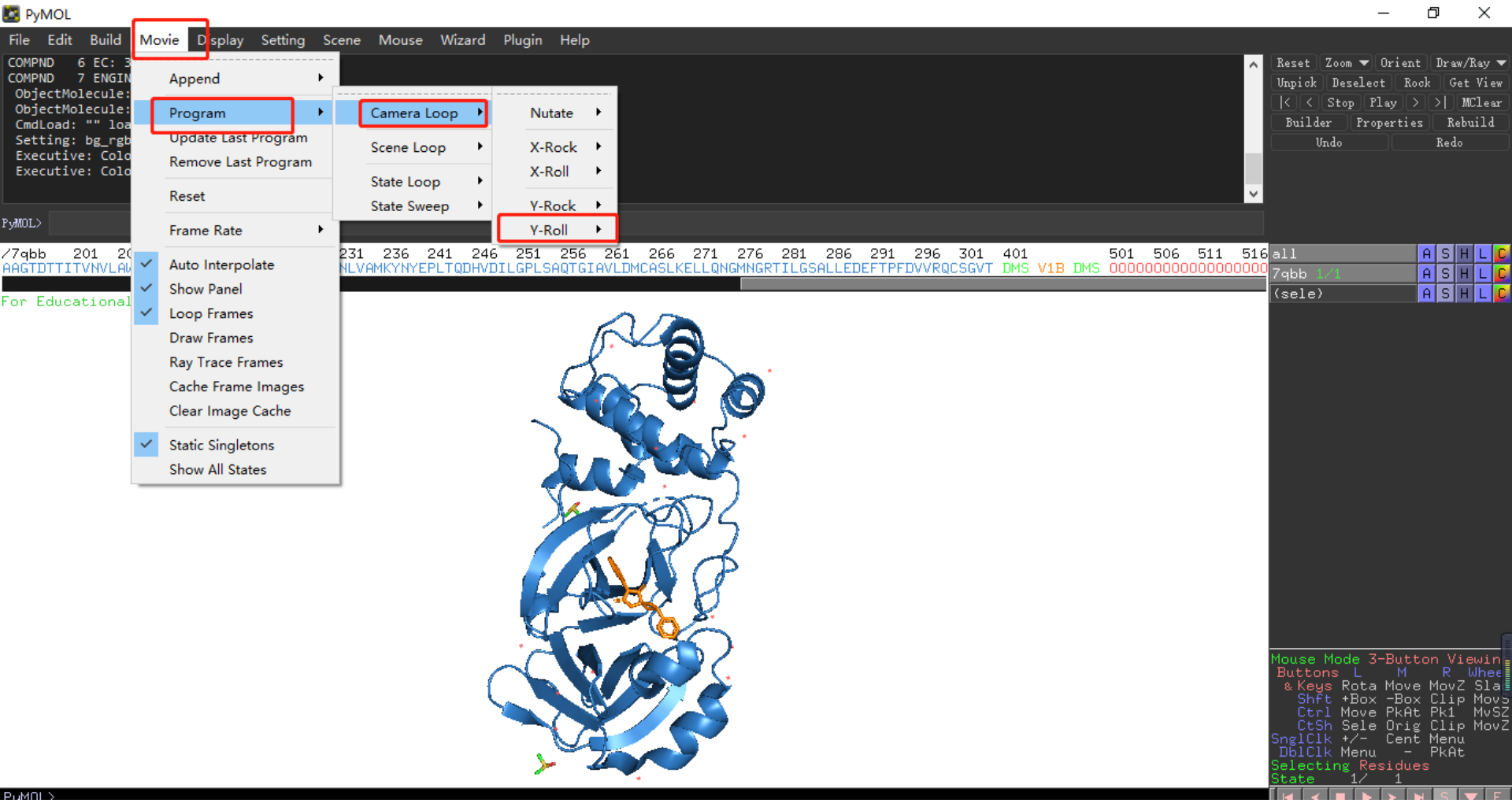
④打开序列（S）选中所有氨基酸残基序列（不包括溶剂和其他小分子），将颜色设置为skyblue

简 易 动 画 制 作



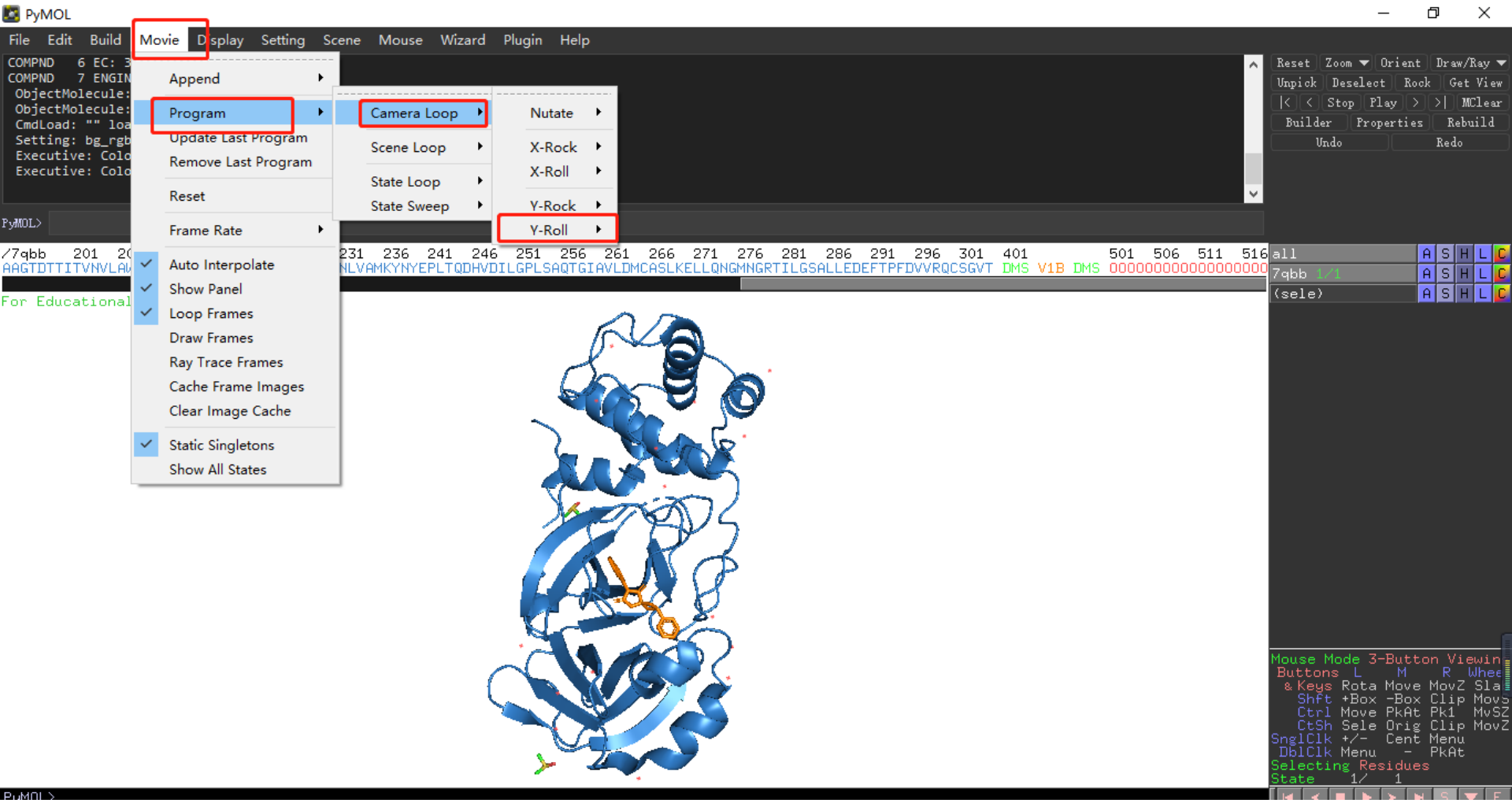
⑤点击空白处，取消上一步的选择，然后在序列上仅选择抑制剂配体VBI，将颜色设置为orange

简 易 动 画 制 作



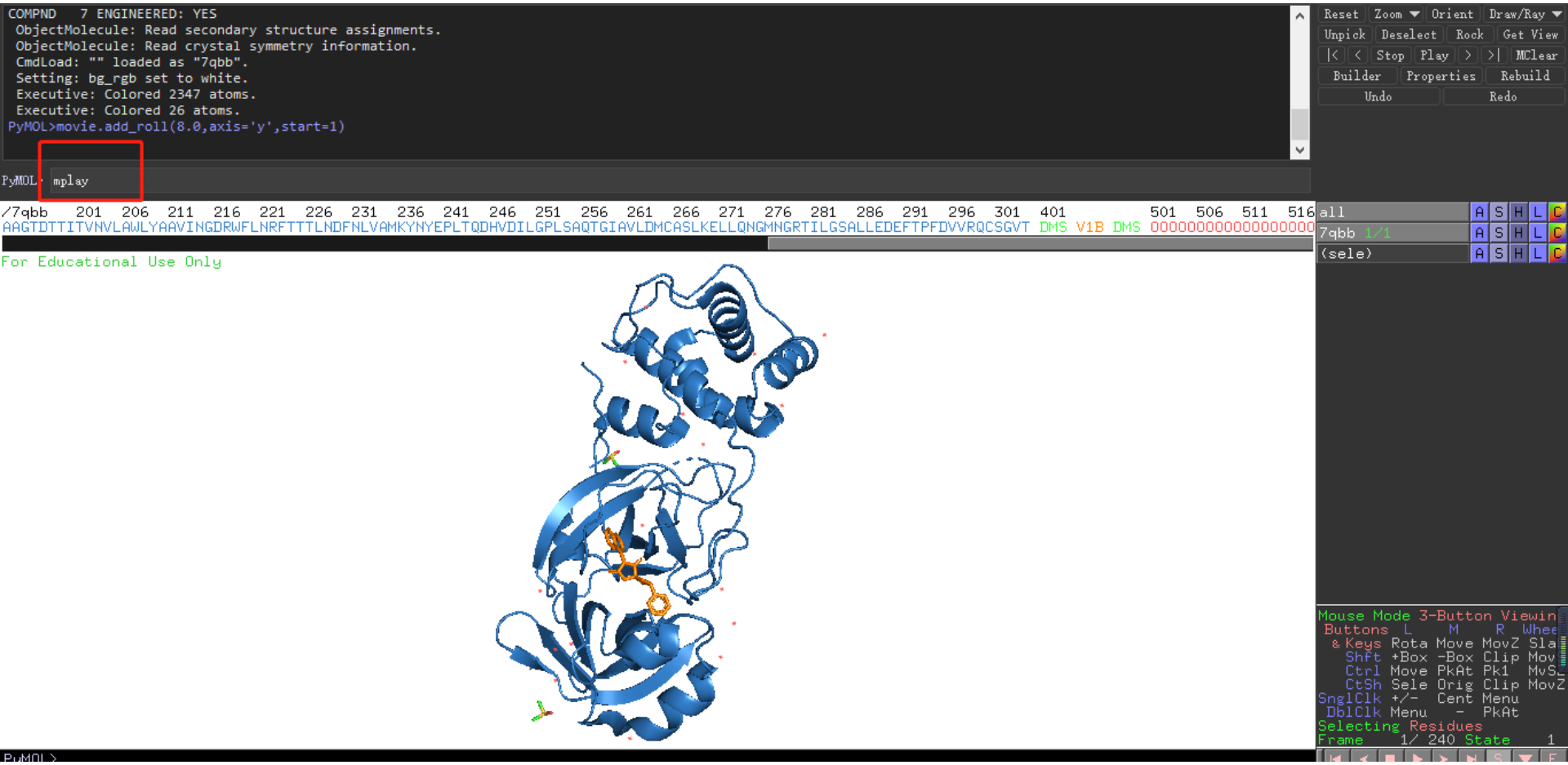
⑥制作动画，Movie>Program>Camera Loop>Y-Roll>8 seconds

简 易 动 画 制 作



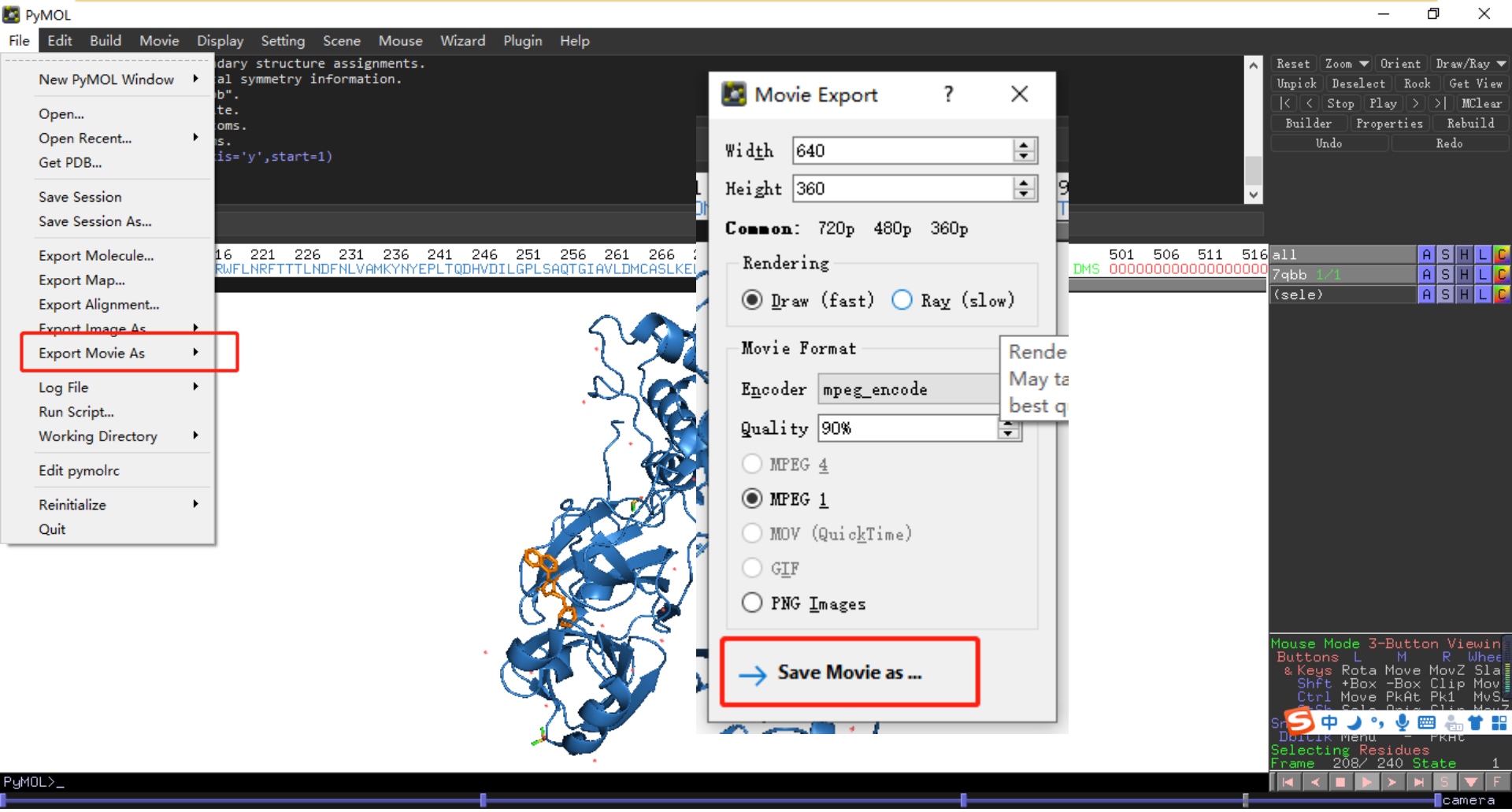
⑥制作动画，Movie>Program>Camera Loop>Y-Roll>8 seconds

简 易 动 画 制 作



⑦播放动画，在命令框中输入mplay 回车，即可以预看动画

简 易 动 画 制 作

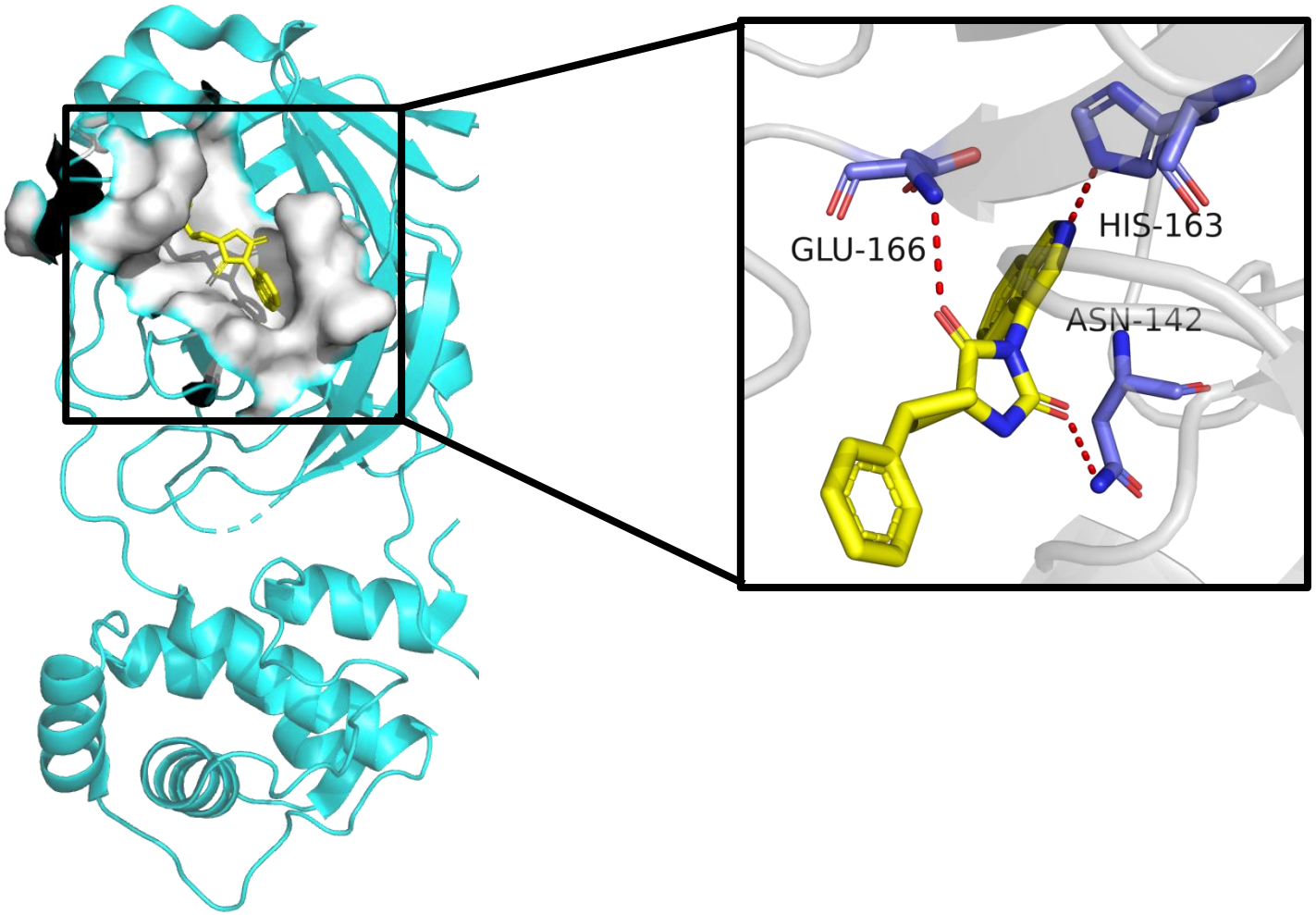


⑧保存动画，File>Export Movie As>MPEG

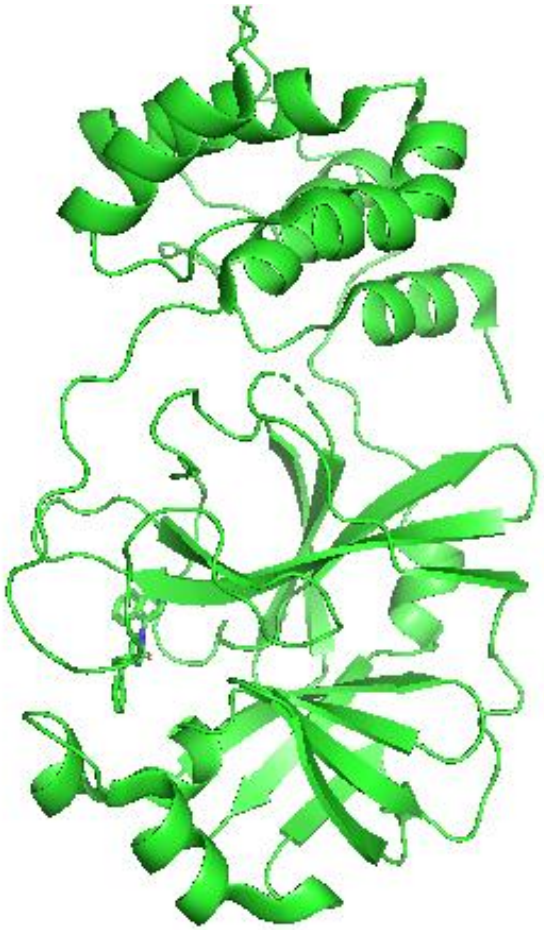
出现的对话框做简单调整，点击Save Movie as即可

PyMol实践二

精美图片制作

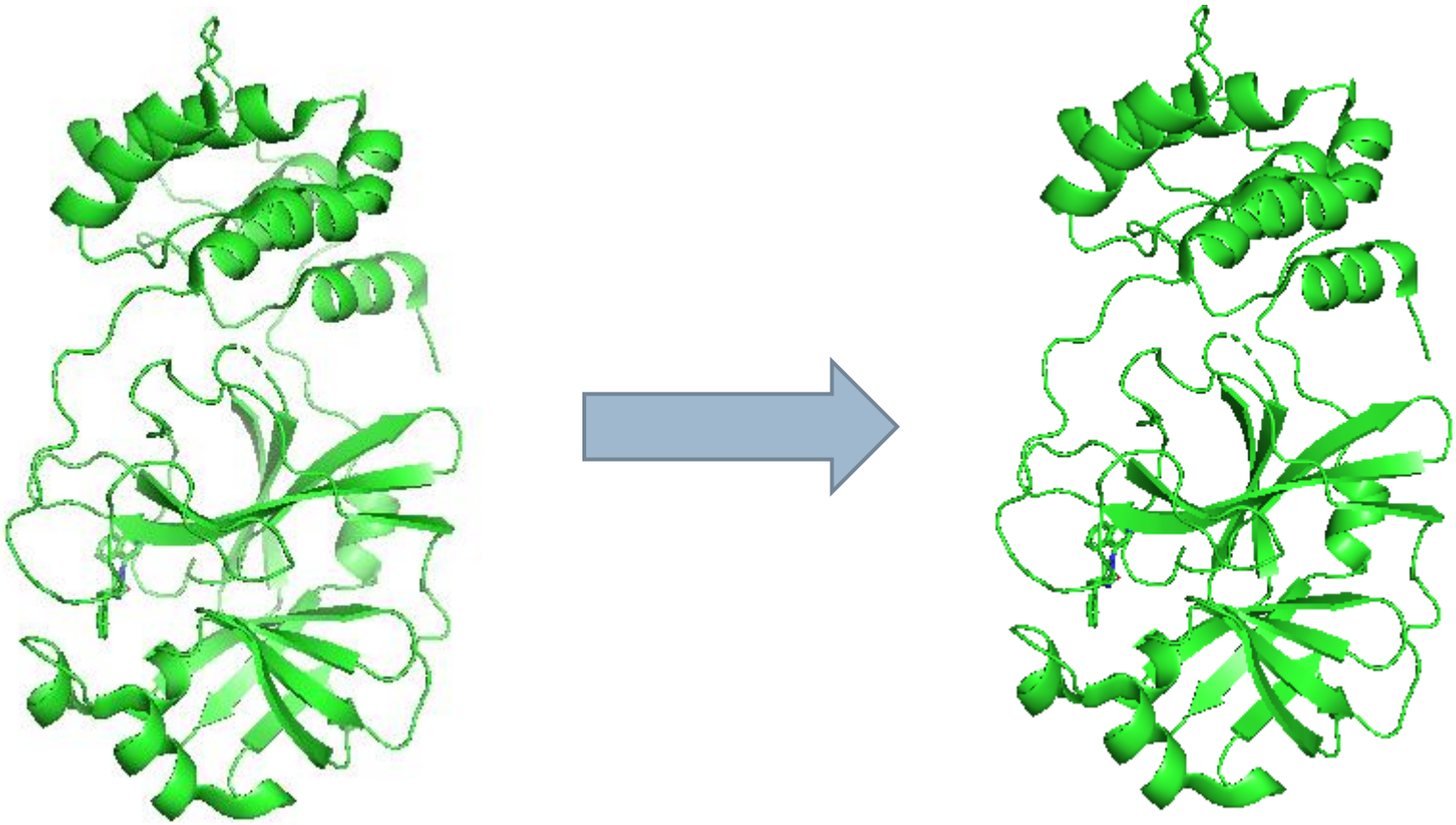


精 美 图 片 制 作



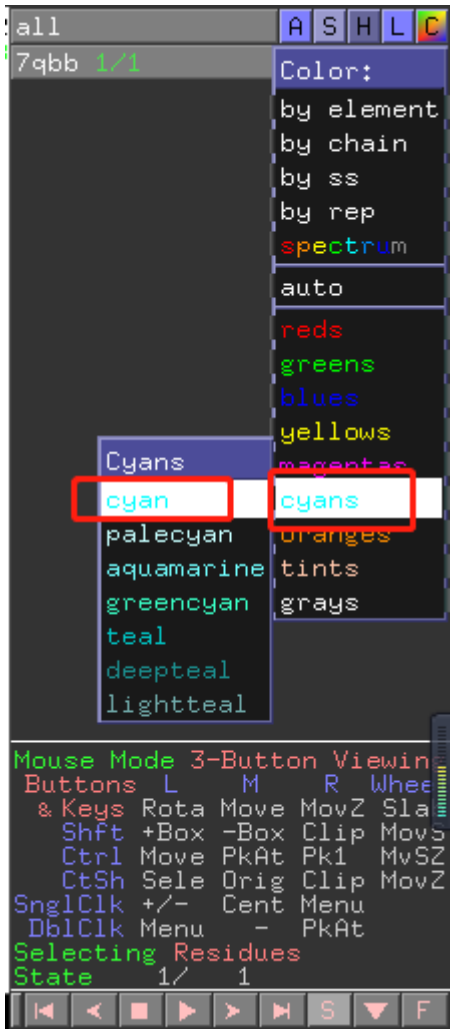
①用pymol打开7qbb文件，将背景调整白色，去除水分子和杂原子（DMS）

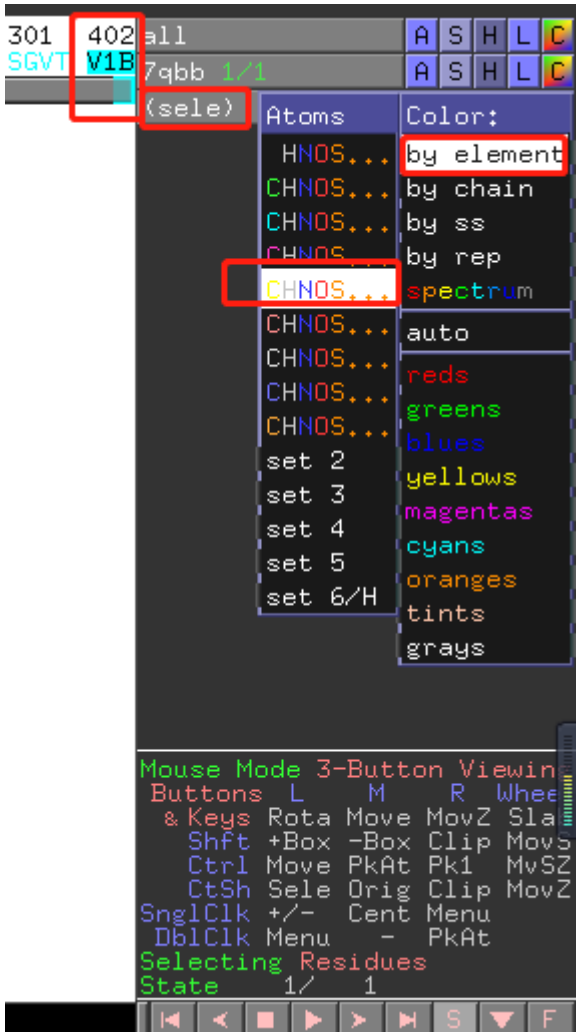
精 美 图 片 制 作



②去除景深效果，滚动鼠标滚轮，出现上图变化

精 美 图 片 制 作





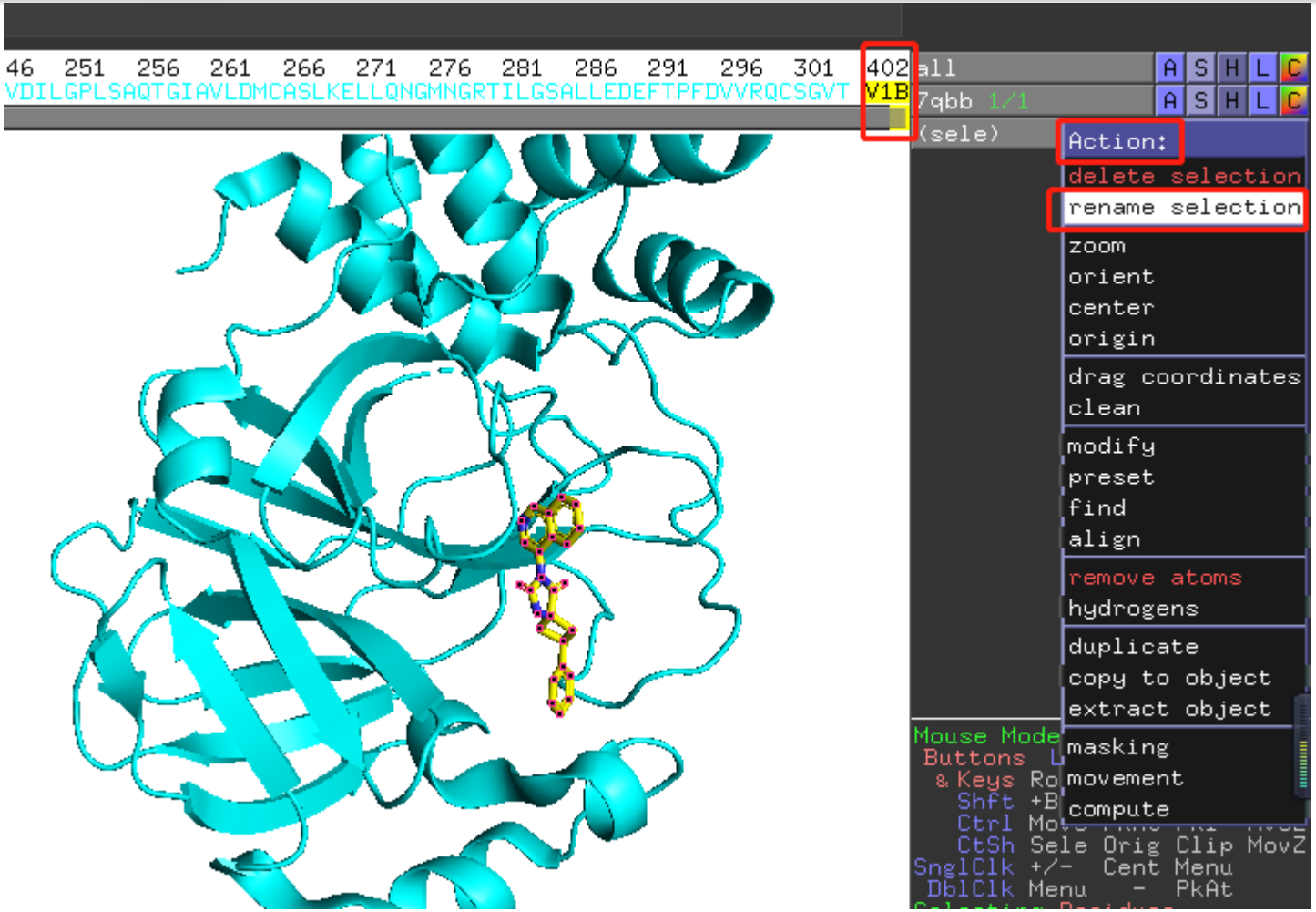
③调整颜色

蛋白颜色：

Color>cycans>cyan

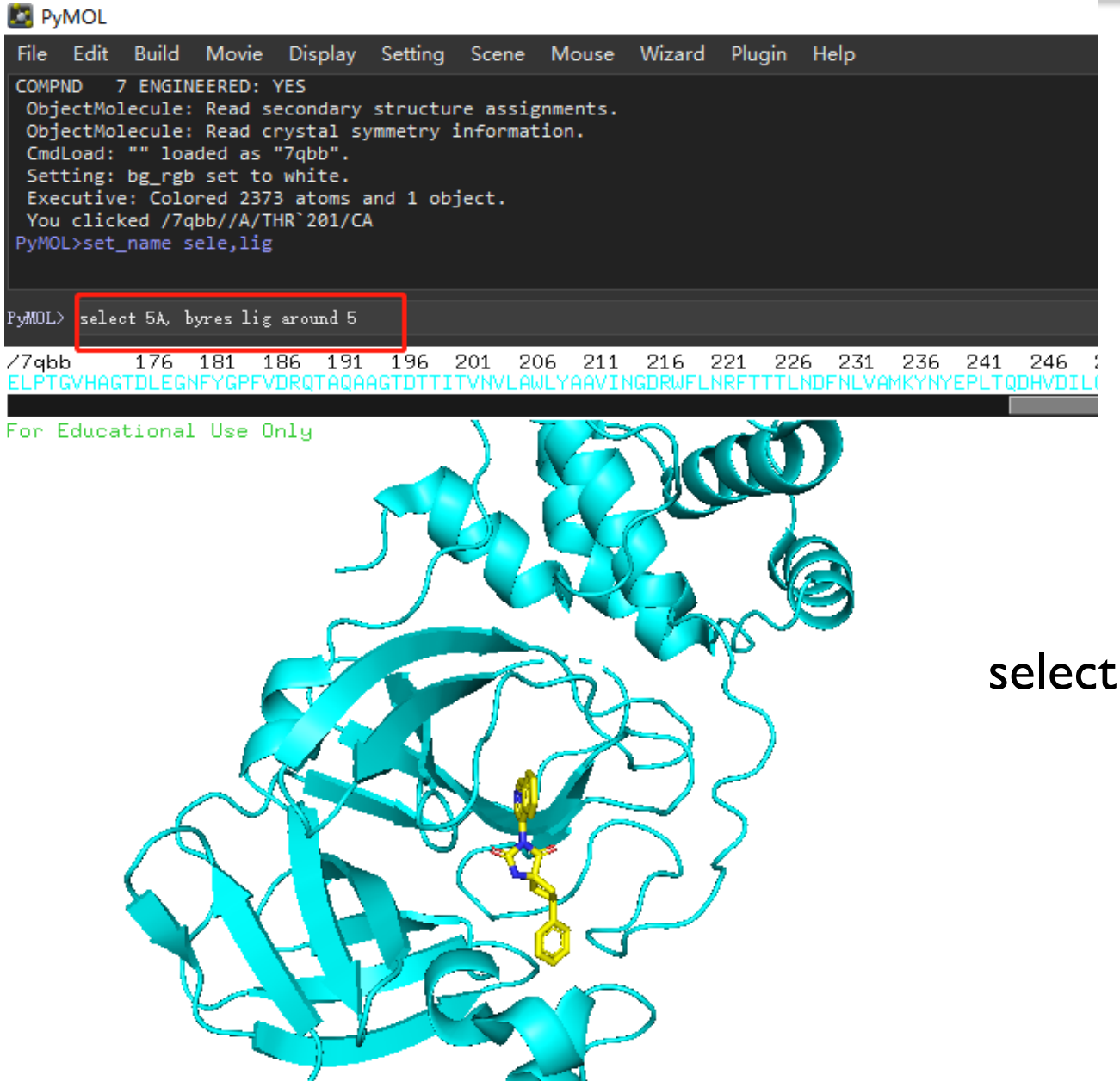
配体颜色：调出序列，选择配体V1B，（sele）>C(color)>by element>黄色

精 美 图 片 制 作



④选中配体后，（sele）>A(Action)>rename selection 将其命名为lig

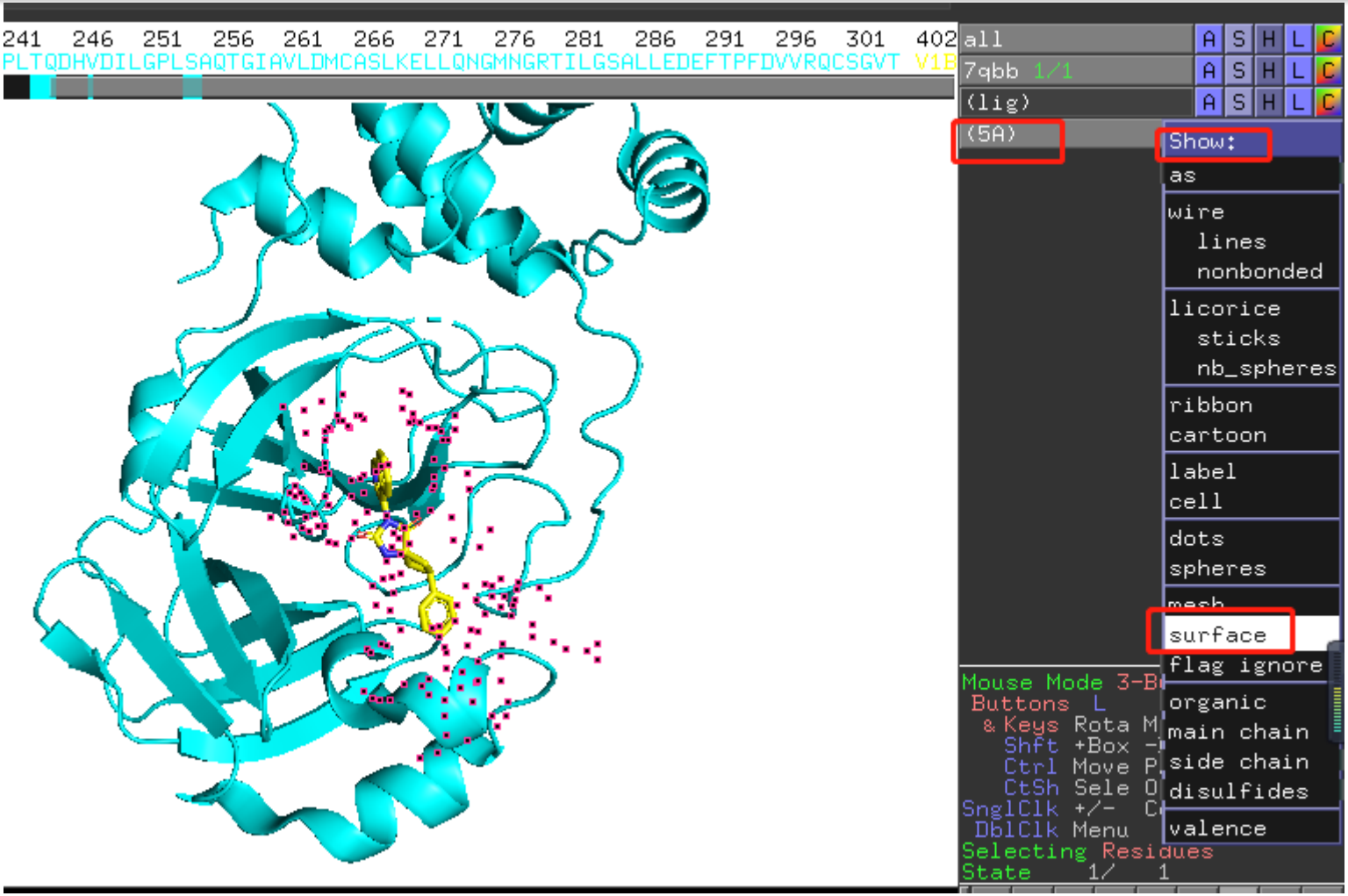
精 美 图 片 制 作



⑤输入命令选中距离配体5Å的残基，并命名为5A

select 5A, byres lig around 5

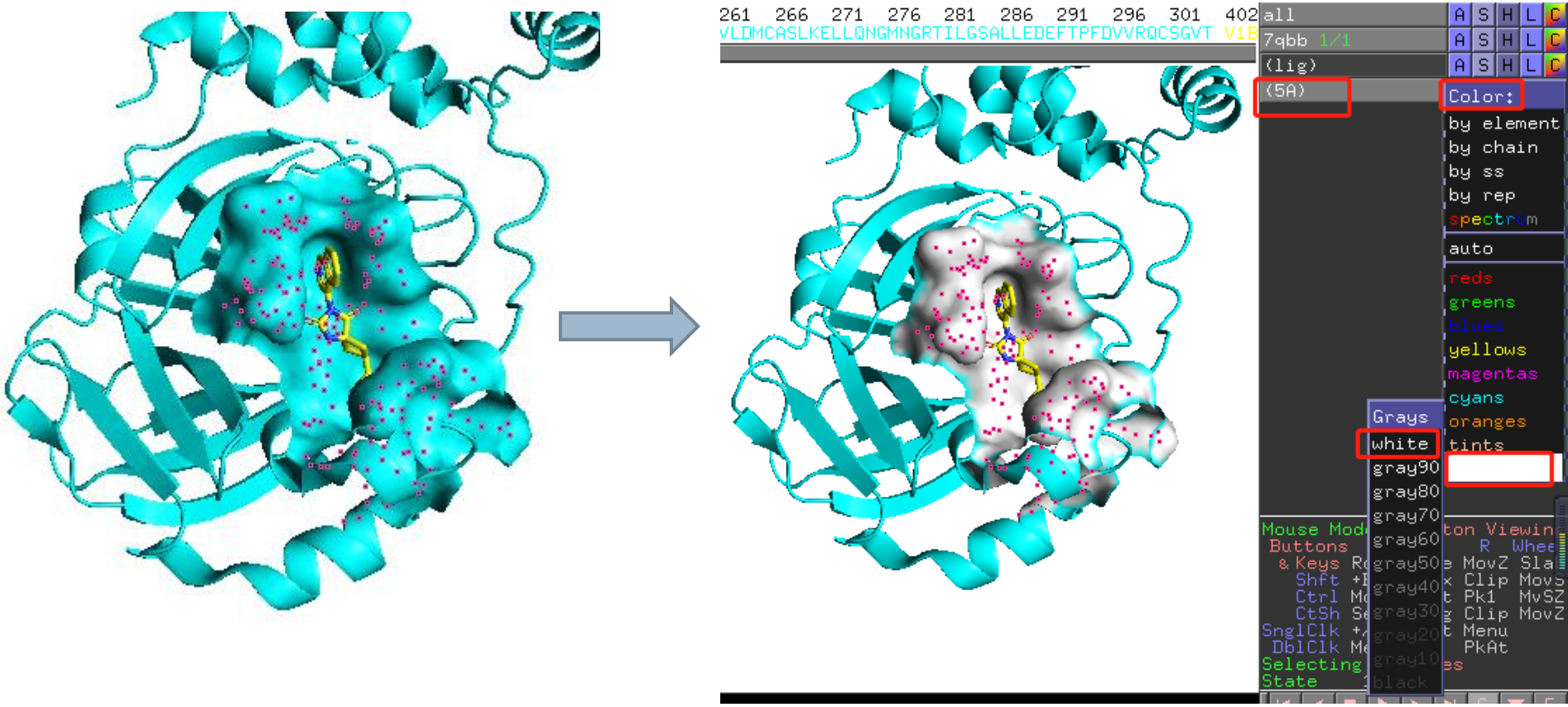
精 美 图 片 制 作



⑥将配体5Å范围内的残基，显示为surface

（5A）>S(show)>surface

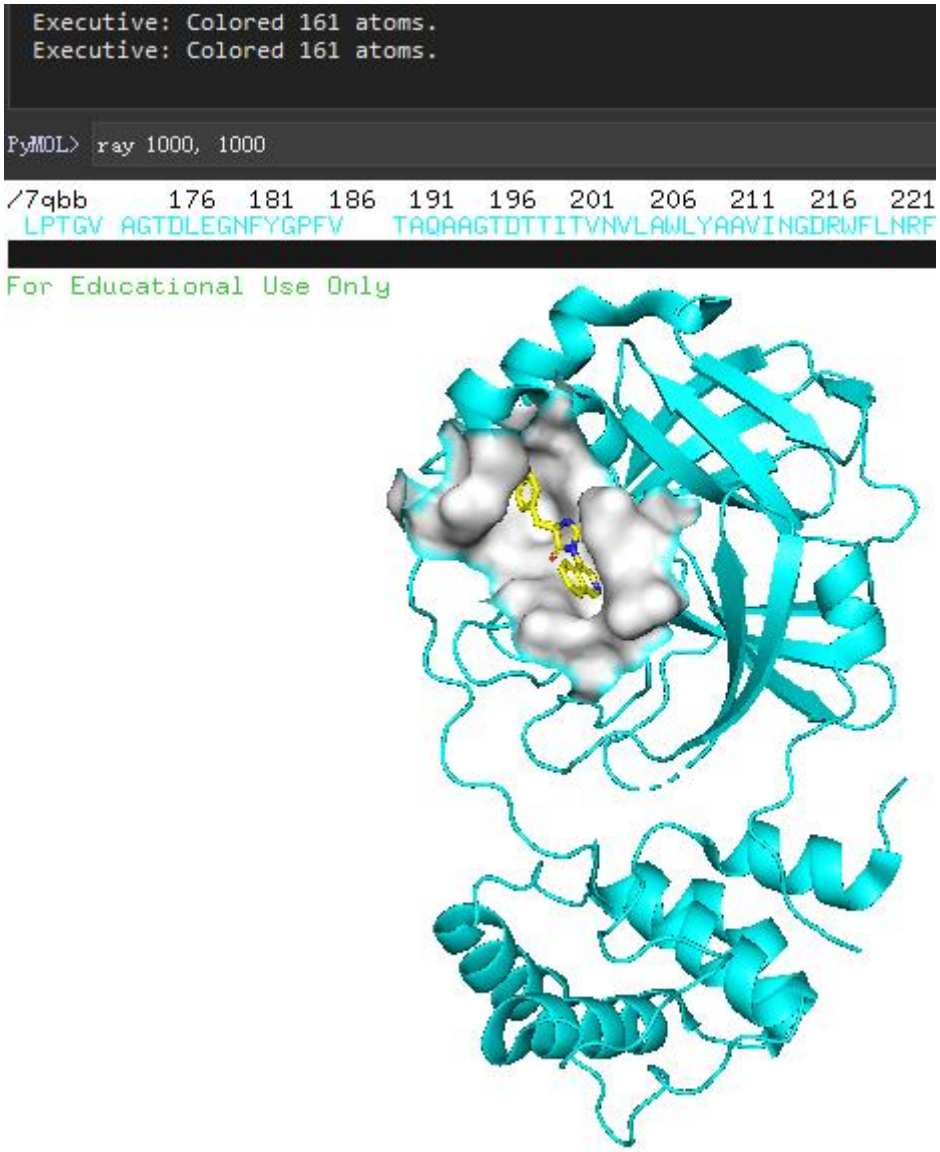
精 美 图 片 制 作



⑦变化表面的颜色为白色

（5A）>C(Color)>grays>white

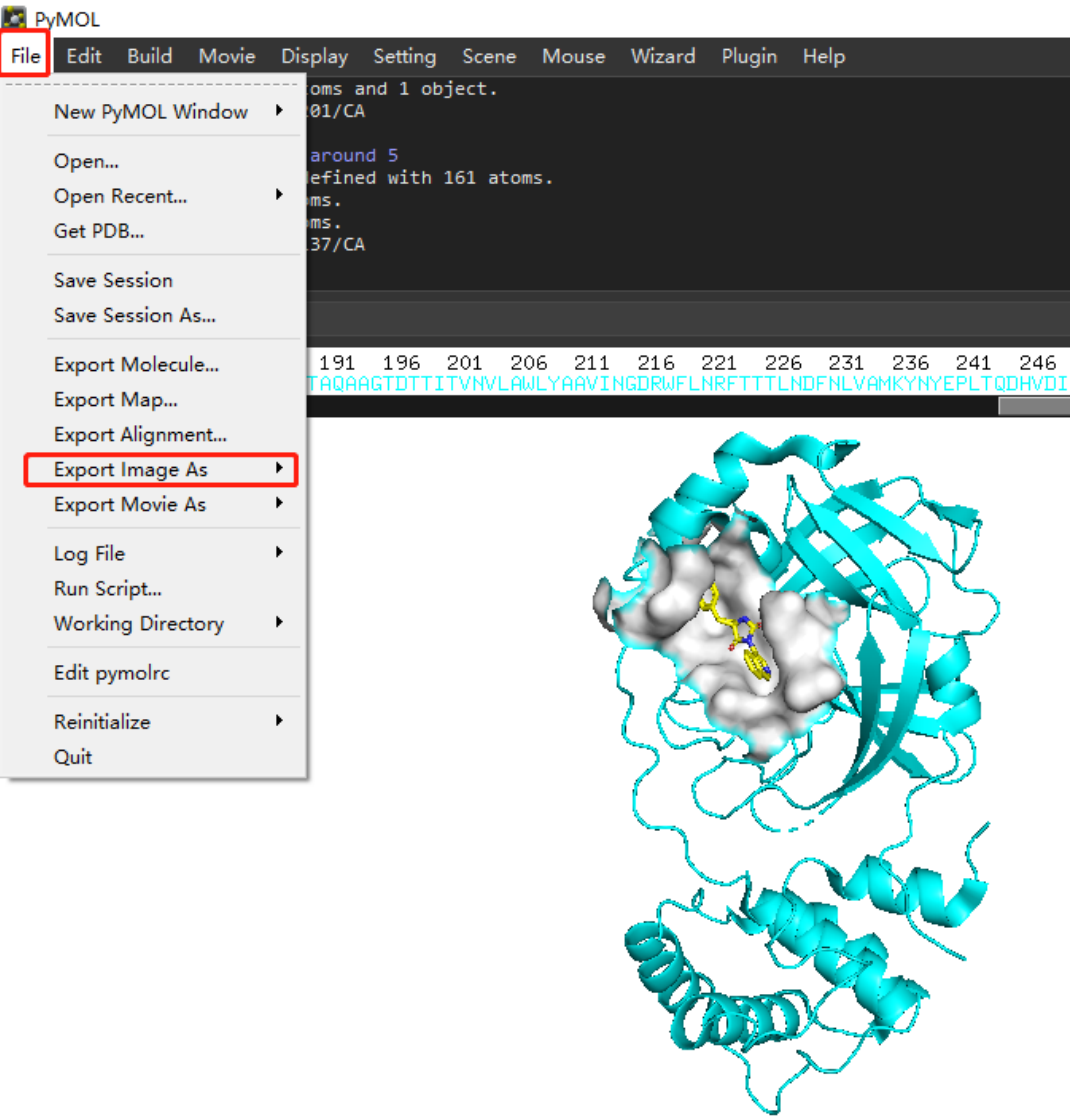
精 美 图 片 制 作



⑧调整合适角度，渲染图像，增加图片质量

在命令框输入ray 1000, 1000

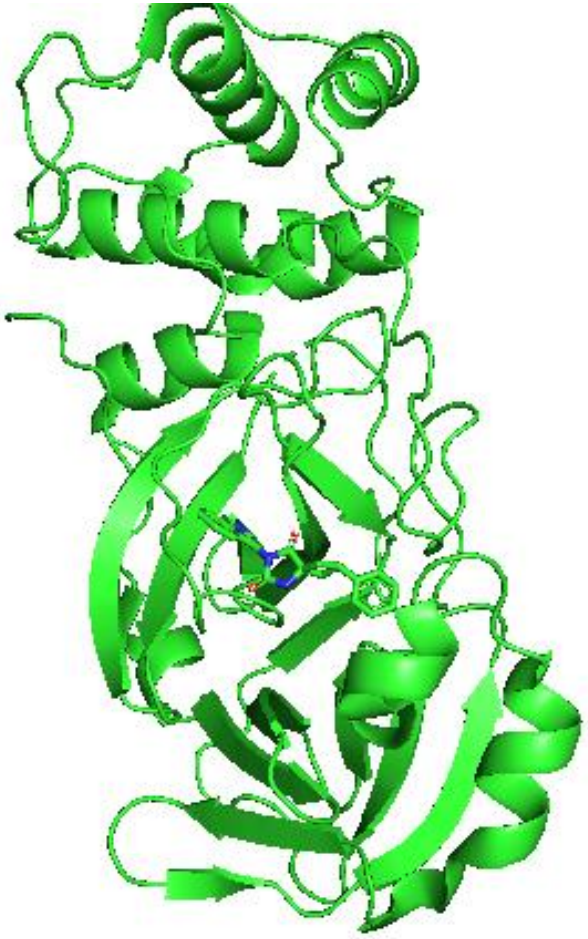
精 美 图 片 制 作



⑧保存图片

File>Export Image As>PNG

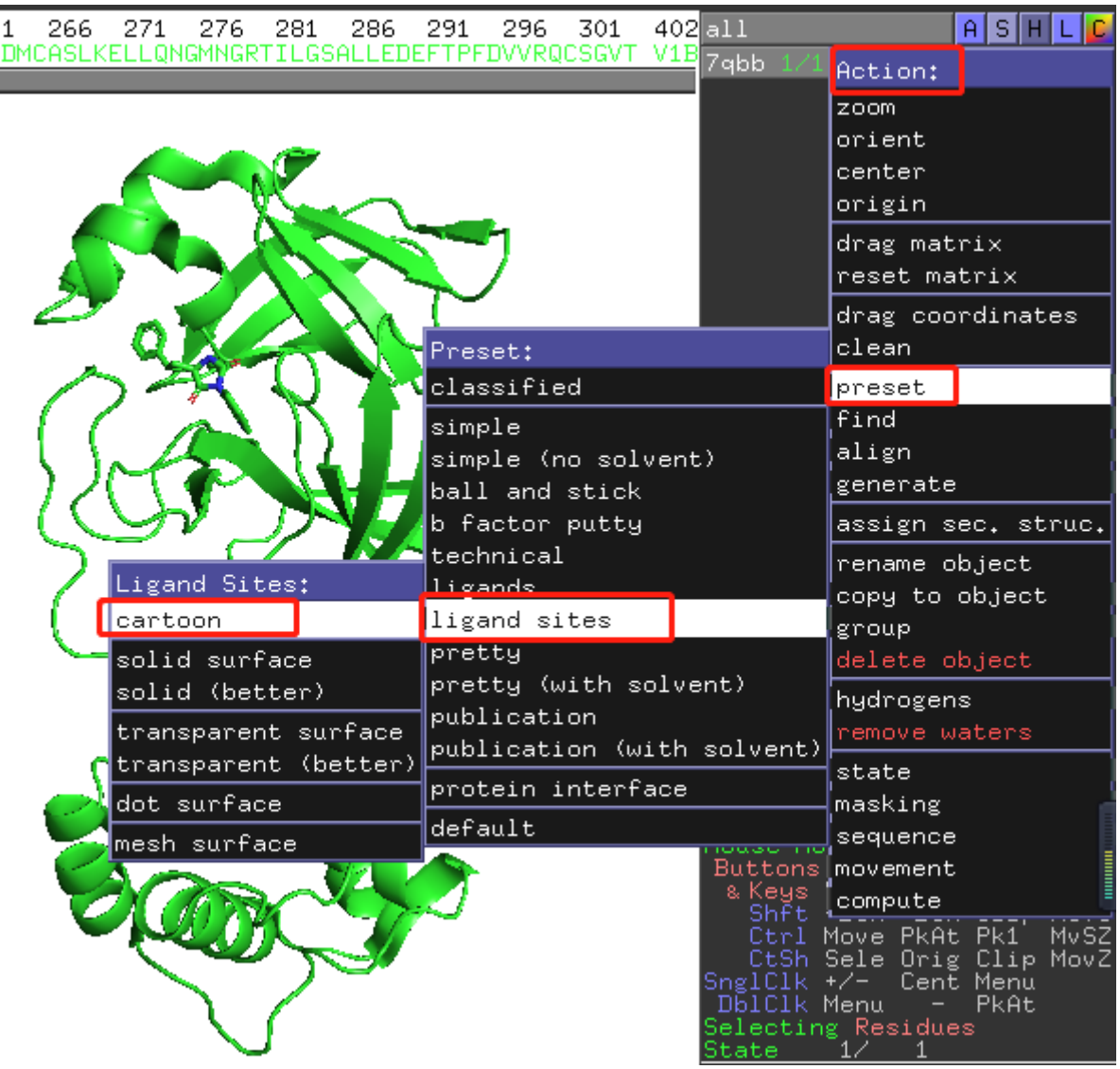
精 美 图 片 制 作



开始第二部分

⑨重新打开pdb文件，进行预处理：除去水分子和杂原子、背景调成白色、去除景深效果

精 美 图 片 制 作

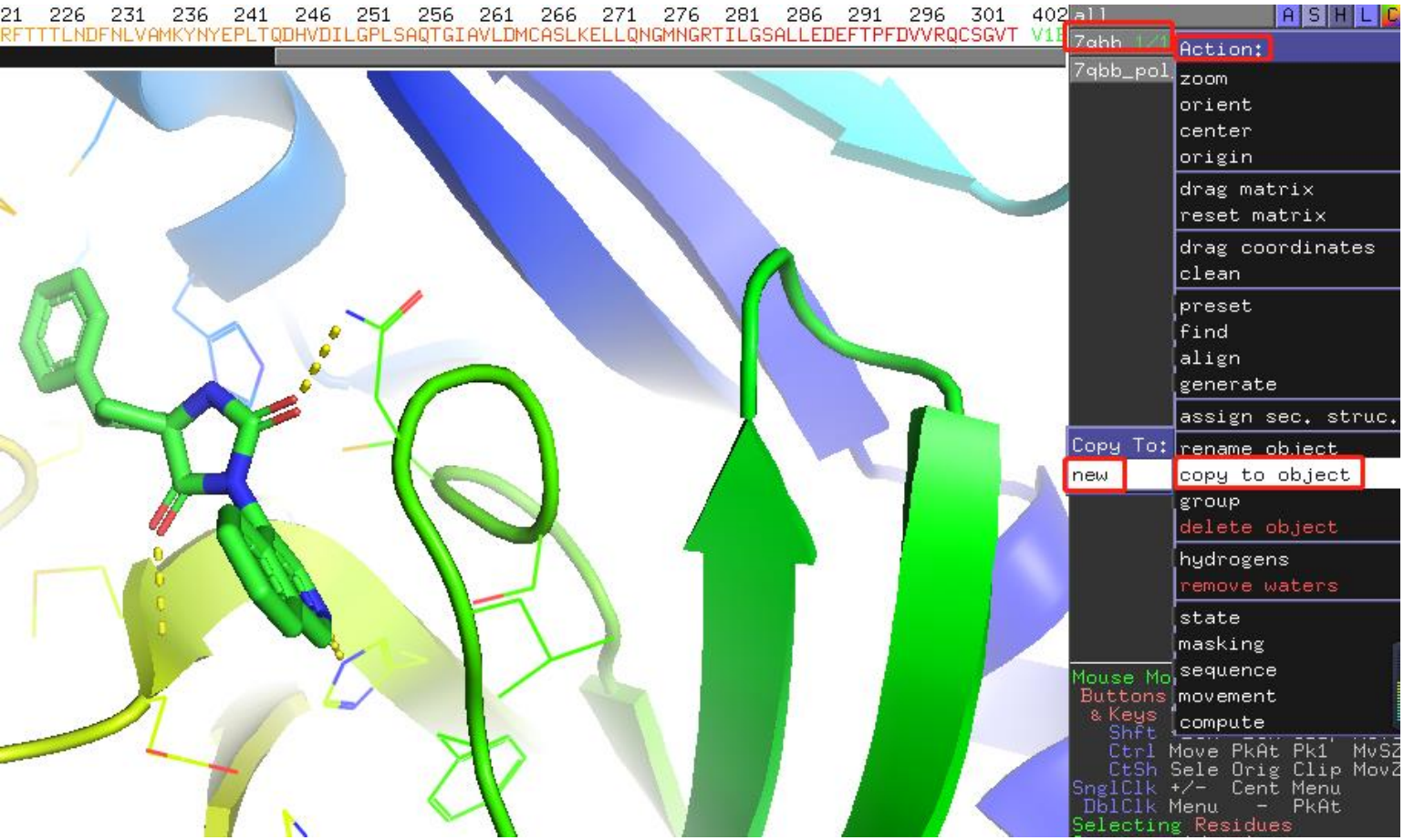


⑩调出活性位点

A（Action）>preset

>ligand site>cartoon

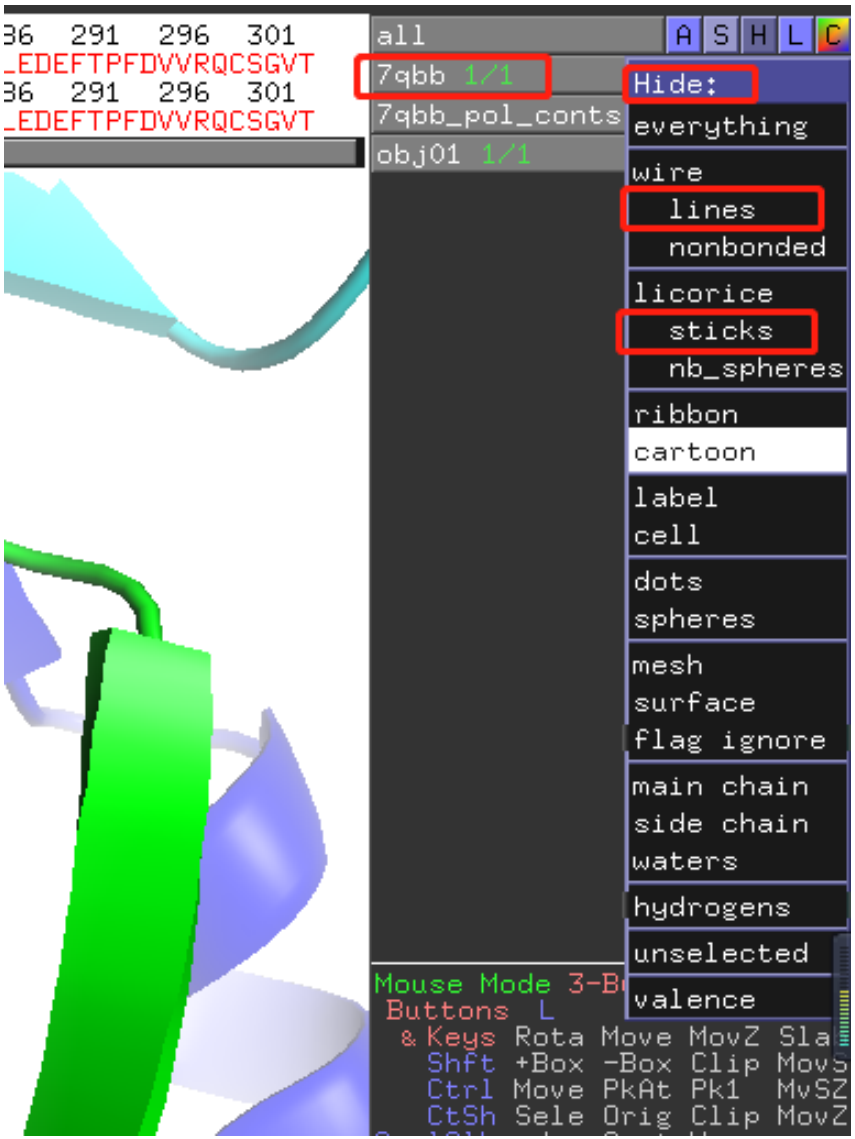
精 美 图 片 制 作



⑪复制7qbb项目(会把复制后的项目自动命名为obj01)

A（Action）>copy to object> new

精 美 图 片 制 作

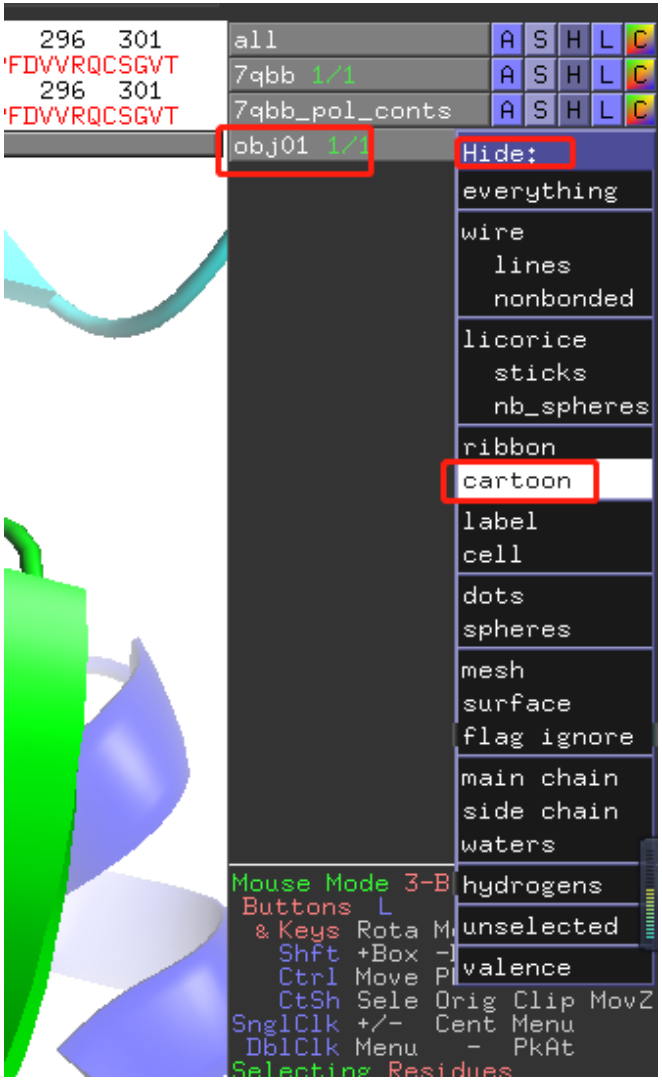


⑫隐藏7qbb的stick和line，

只显示cartoon

7qbb>Hide>lines(sticks)

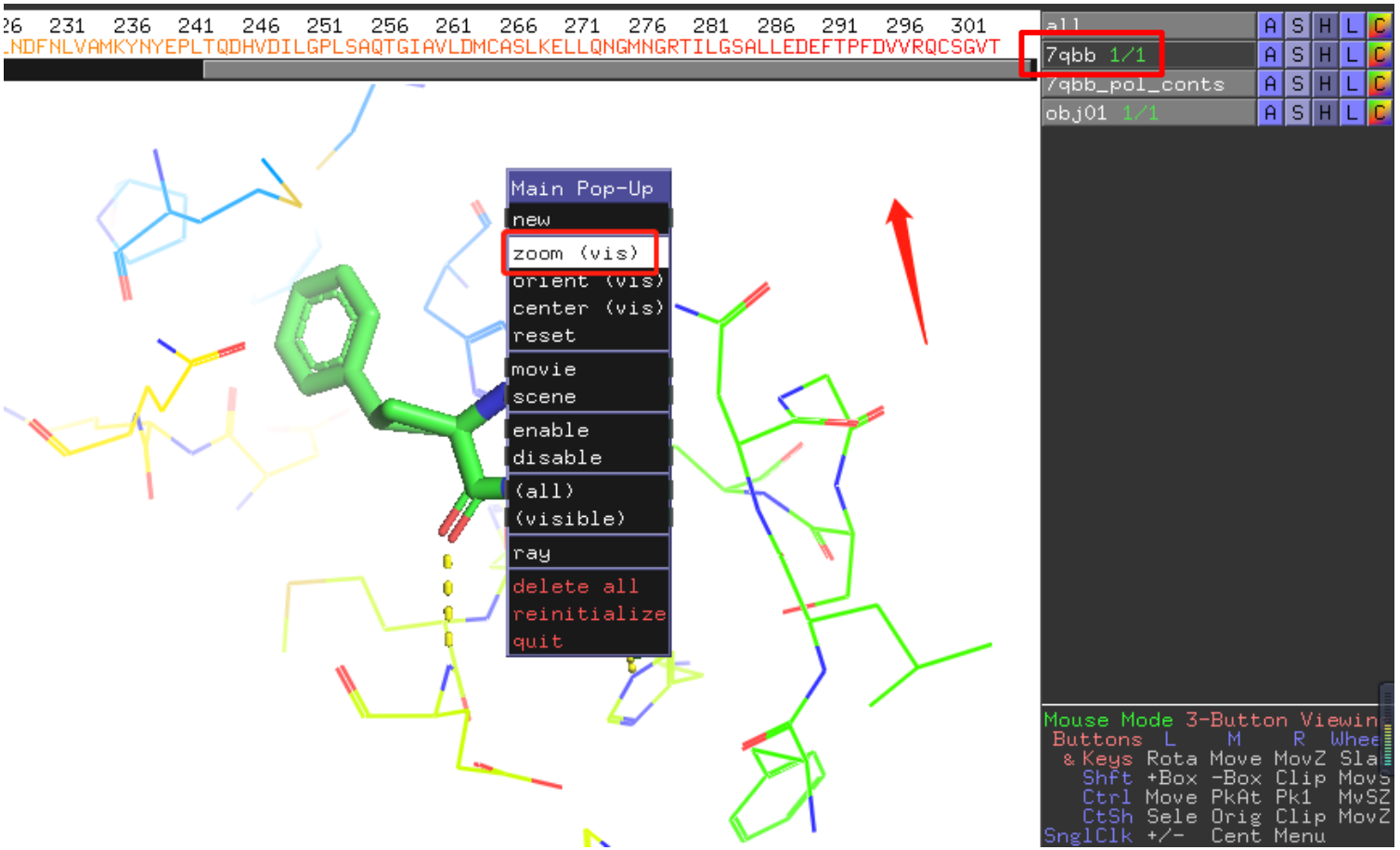
精 美 图 片 制 作



⑬隐藏obj01的cartoon，只显示lines

obj01>H(Hide)>cartoon

精 美 图 片 制 作



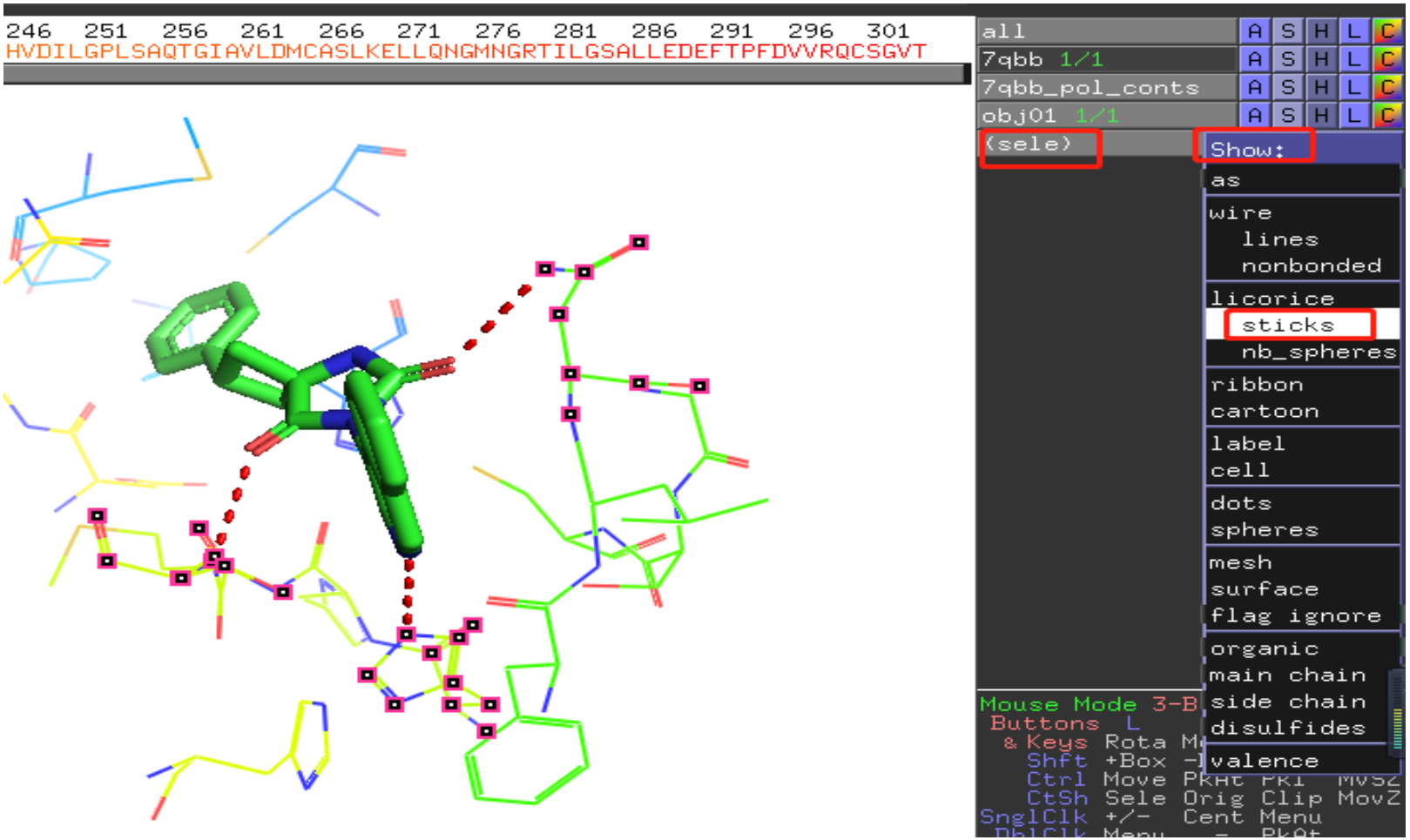
⑭点击一下7qbb，即可取消显示，然后右击屏幕空白处，再出现的选项中，选择zoom（vis）,让其居中

精 美 图 片 制 作

⑮改变氢键的颜色

7qbb_pol_conts>C(color)>reds>red

精 美 图 片 制 作

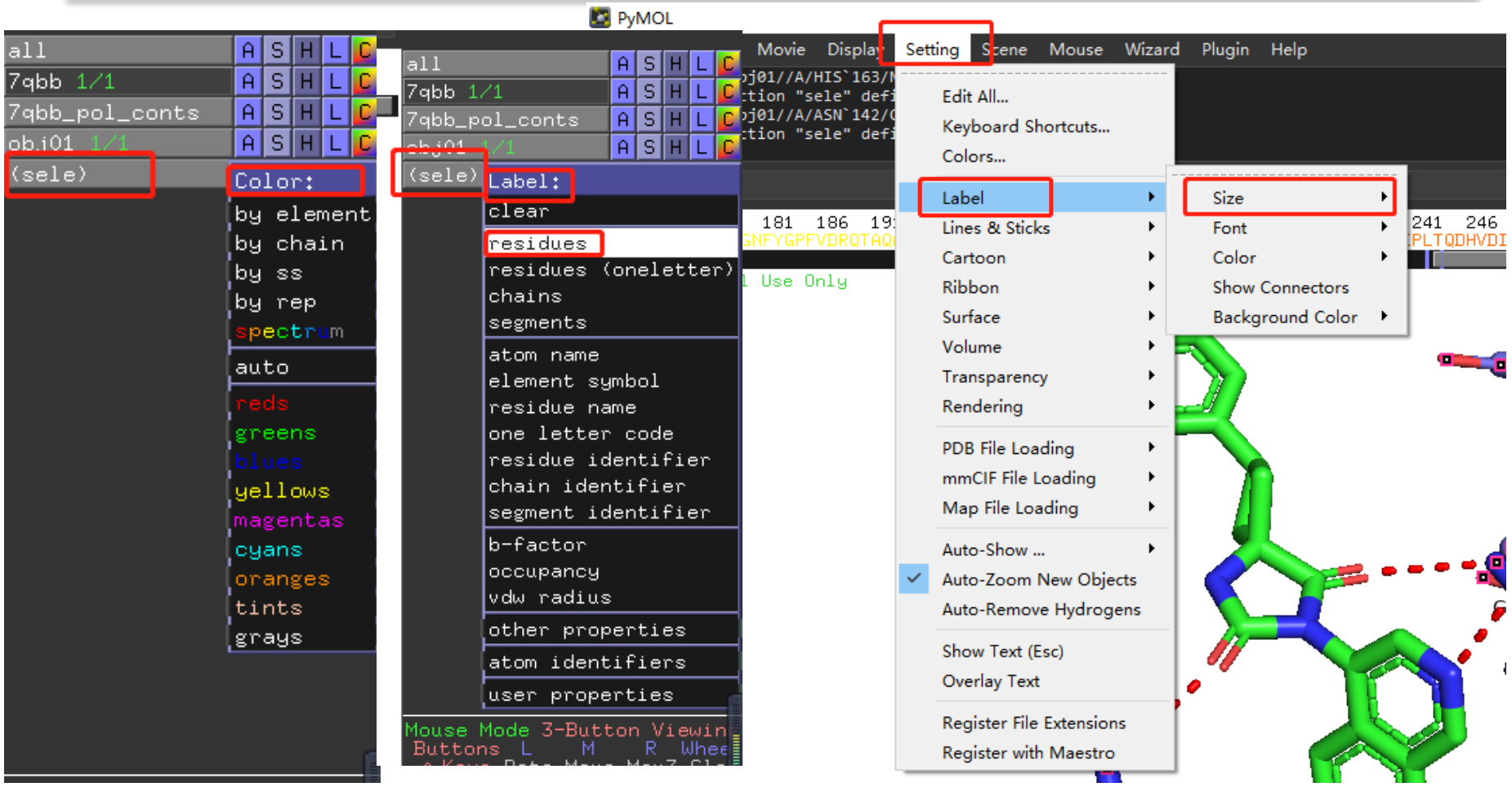


⑯在面板上选中参与氢键的残基，然后展示为stick

（sele）>S(show)>sticks

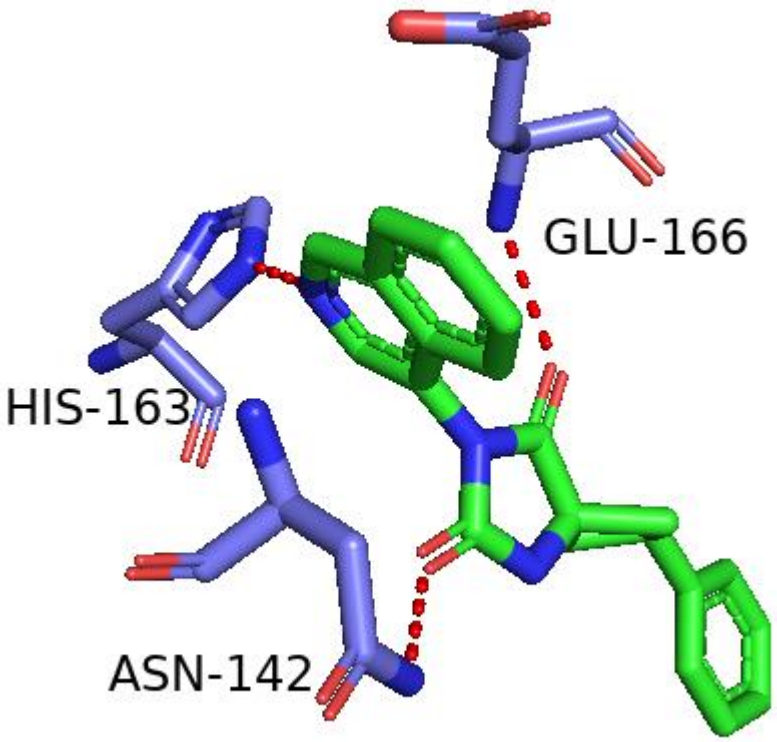
然后obj01>H(Hide)>lines

精 美 图 片 制 作



⑰调整关键残基的颜色，显示标记（label），并调整标记的大小（24 sizes）

精 美 图 片 制 作

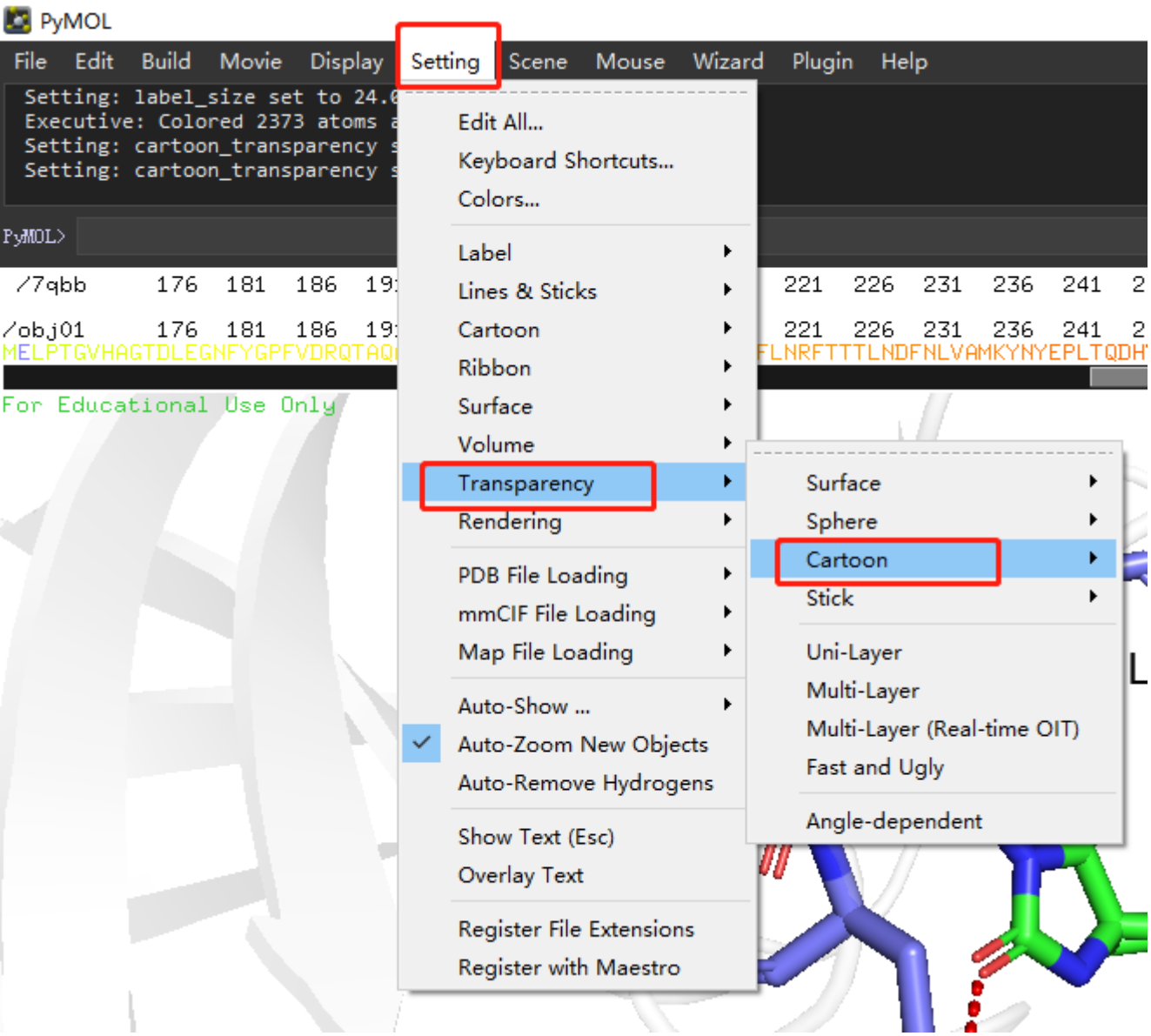


⑱调整合适位置，让标签和氢键以及残基都能很好的展示，并让其居中

精 美 图 片 制 作

⑲点击7qbb让其显示，并把颜色更改为白色

精 美 图 片 制 作



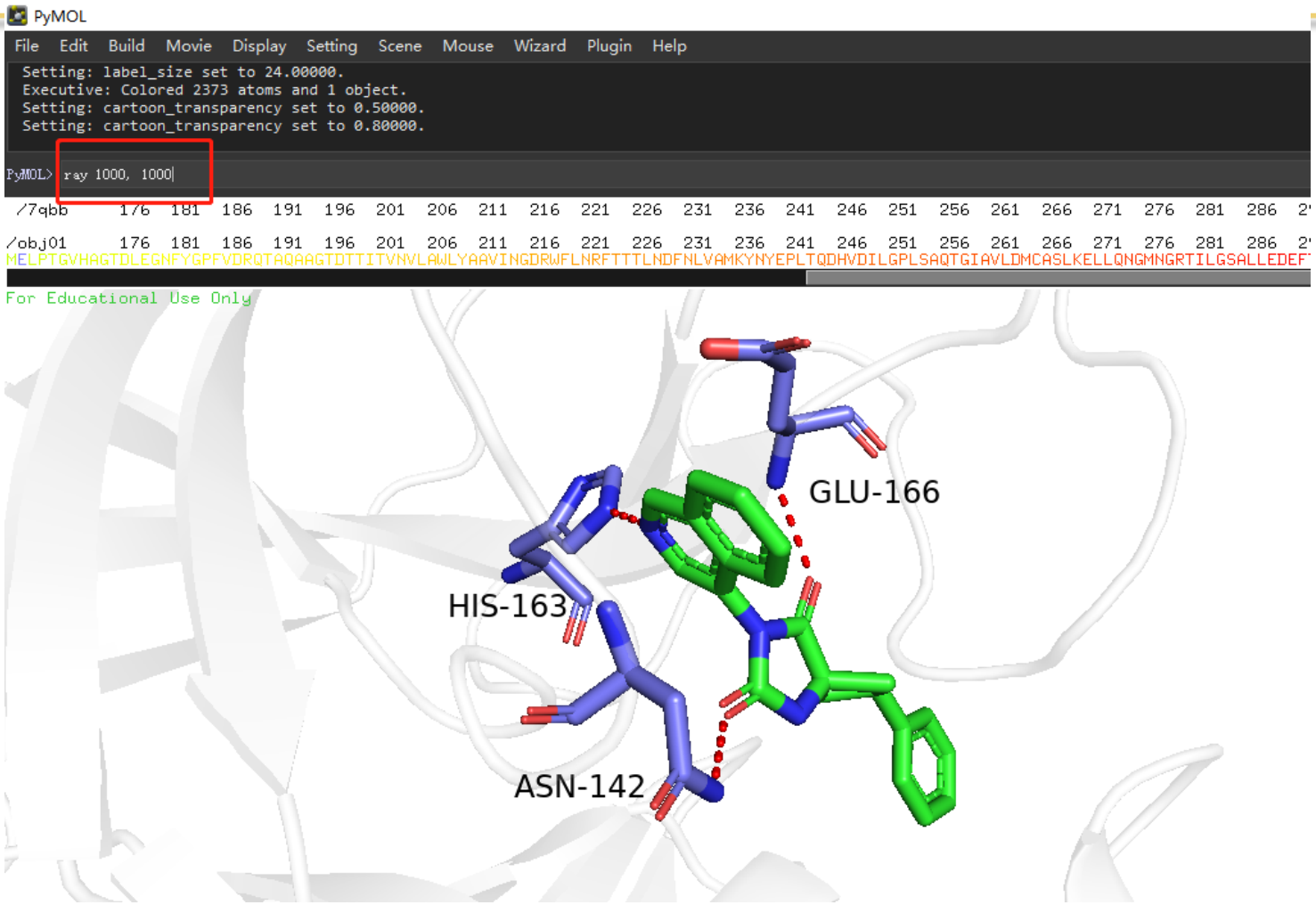
⑳设置cartoon的显示透明度为80%

Setting>

Transparency>

Cartoon>80%

精 美 图 片 制 作



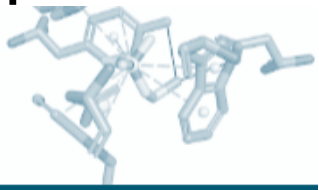
在命令框中输入ray 1000, 1000

渲染完毕后，保存图片即可

蛋白配体相互作用分析

https://plip-tool.biotec.tu-dresden.de/plip-web/plip/index

Protein-Ligand Interaction Profiler



Welcome to the PLIP web tool!

Easy and fast identification of non-covalent interactions between biological macromolecules and their ligands.

enter PDB ID (e.g. 1xdn)

Find PDB ID using our search tool

or

Drop PDB file here (max. 10 MB)

Choose file...

› Advanced Options

ANALYZE

PLIP (Protein-Ligand Interaction Profiler) 是一个蛋白配体非共价相互作用的分析工具；可以分析蛋白配体复合物在原子水平的非共价相互作用，包括氢键，水桥，盐桥，卤键，疏水相互作用，π-堆叠，π-离子相互作用和金属复合物；检测机制主要是基于原子间的空间位置和几何关系。

蛋 白 - 配 体 相 互 作 用 分 析

Binding Sites in 7VH8

SMALLMOLECULE
4WI
4WI-A-401

配体分子

DMS (Dimethyl Sulfoxide)
DMS-A-402

No Interactions
H2S (Hydrogen Sulfide)
H2S-A-403

Results in XML format

Results in RST format

Your results will be available for 30 days using the current URL.

7VH8 in the PDB

How to Cite Us

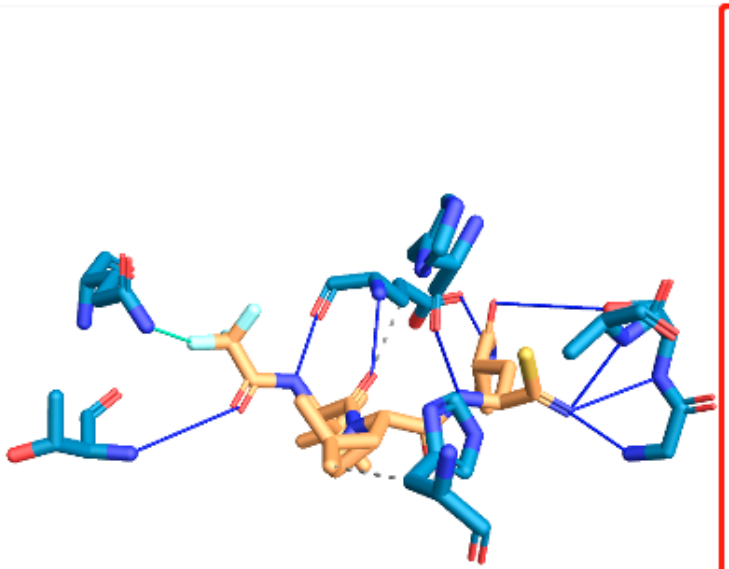
Run another analysis

SMALLMOLECULE

4WI

4WI-A-401

Interacting chains: A



3D开关

Click for 3D-View

可以分析的相互作用

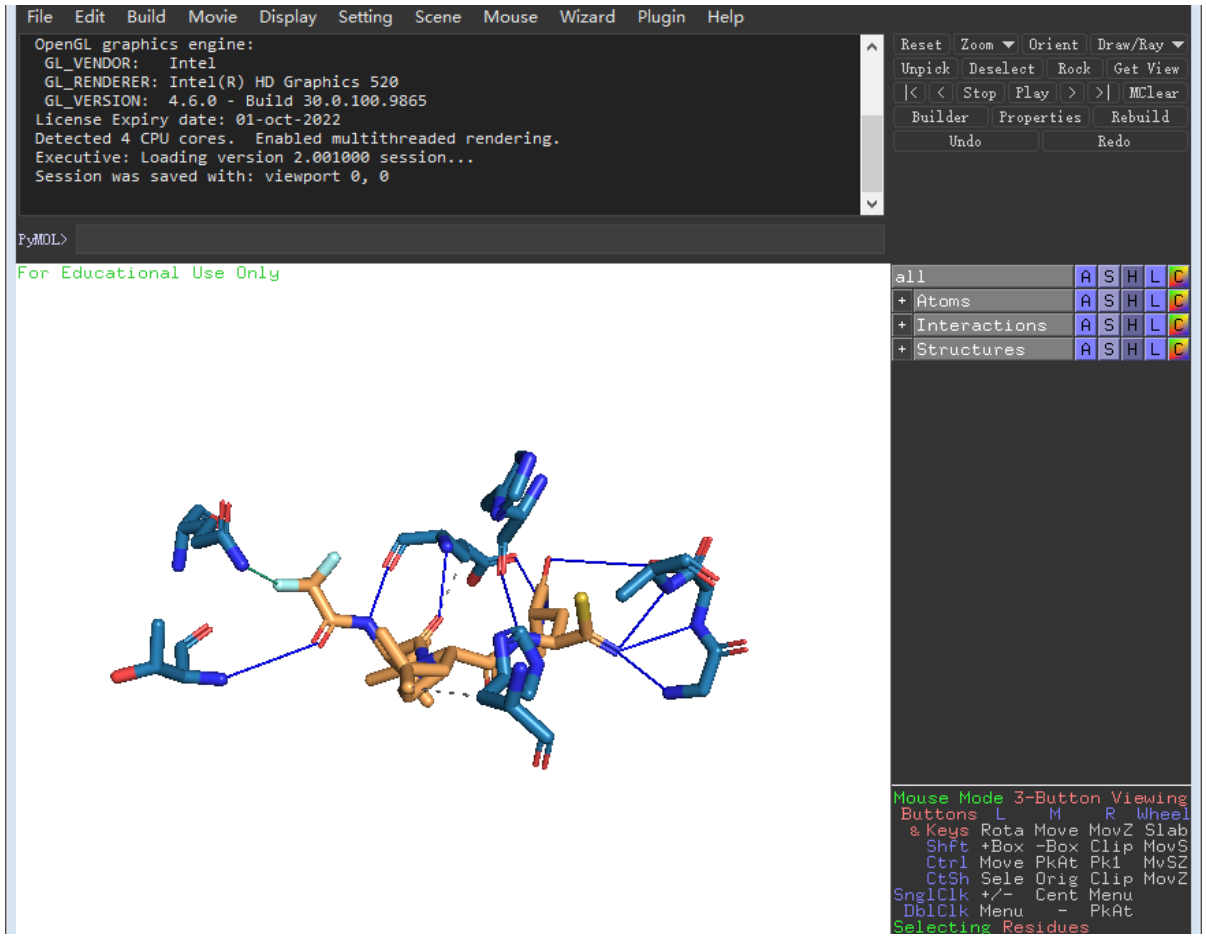
- Protein
- Ligand
- Water
- Charge Center
- Aromatic Ring Center
- Metal Ion
- Hydrophobic Interaction
- Hydrogen Bond
- Water Bridge
- π-Stacking (parallel)
- π-Stacking (perpendicular)
- π-Cation Interaction
- Halogen Bond
- Salt Bridge
- Metal Complexation

蛋 白 - 配 体 相 互 作 用 分 析

Download visualization in PyMol format (.pse)

pymol作图

Download visualization as image (.png)



蛋 白 - 配 体 相 互 作 用 分 析

Hydrophobic Interactions

Index	Residue	AA	Distance	Ligand Atom	Protein Atom
1	41A	HIS	3.61	2397	310
2	166A	GLU	3.69	2400	1284

Halogen Bonds

Index	Residue	AA	Distance	Donor Angle	Acceptor Angle	Donor Atom	Acceptor Atom
1	192A	GLN	3.15	142.55	96.82	2417 [F]	1485 [Nam]

蛋白-配体相互作用分析

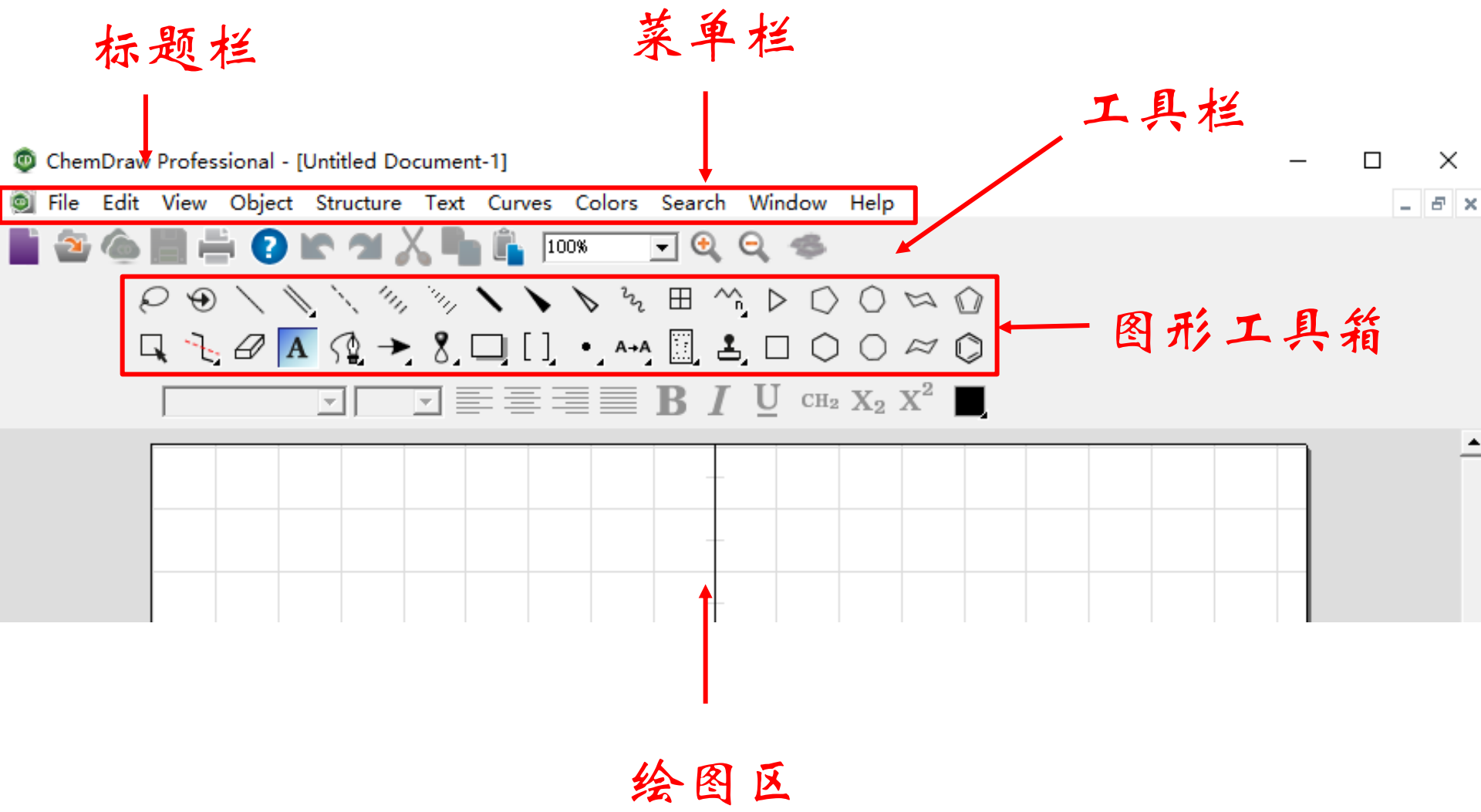
Hydrogen Bonds

Index	Residue	AA	Distance H-A	Distance D-A	Donor Angle	Protein donor?	Side chain	Donor Atom	Acceptor Atom
1	143A	GLY	2.38	3.15	134.16	✓	×	1111 [Nam]	2406 [N2]
2	144A	SER	3.12	3.44	100.59	✓	×	1115 [Nam]	2406 [N2]
3	144A	SER	3.66	4.07	108.36	✓	✓	1120 [O3]	2411 [O2]
4	145A	CYS	2.10	3.01	153.08	✓	×	1121 [Nam]	2406 [N2]
5	164A	HIS	2.05	3.02	167.36	×	×	2409 [Nam]	1265 [O2]
6	166A	GLU	1.79	2.77	170.61	×	×	2410 [Nam]	1283 [O2]
7	166A	GLU	1.88	2.85	166.18	✓	×	1280 [Nam]	2413 [O2]
8	166A	GLU	2.27	3.02	131.79	×	✓	2407 [Nam]	1287 [O2]
9	190A	THR	3.39	3.96	119.08	✓	×	1465 [Nam]	2414 [O2]

ChemDraw

ChemDraw 软件是目前国内外最流行、最受欢迎的化学绘图软件。它是美国CambridgeSoft 公司开发的 ChemOffice 系列软件中最重要的一员。Chemdraw 软件功能十分强大。可编辑、绘制与化学有关的一切图形，例如，建立和编辑各类分子式、方程式、结构式、立体图形、对称图形、轨道等，并能对图形进行编辑、翻转、旋转、缩放、存储、复制、粘贴等等多种操作。用它绘制的图形可以直接复制粘贴到word 软件中使用。最新版本的软件还可以生成分子模型、建立和管理化学信息库、增加了光谱化学工具等功能。

ChemDraw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菜单栏
工具栏
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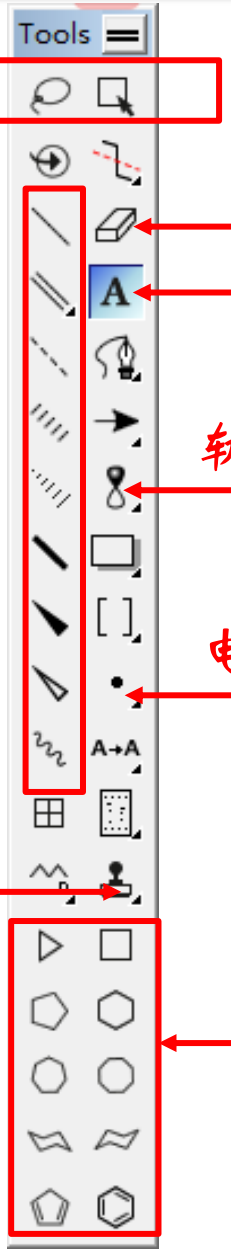
File Edit View Object Structure Text Curves Colors Search Window Help
100%
图形工具箱
绘图区

ChemDraw



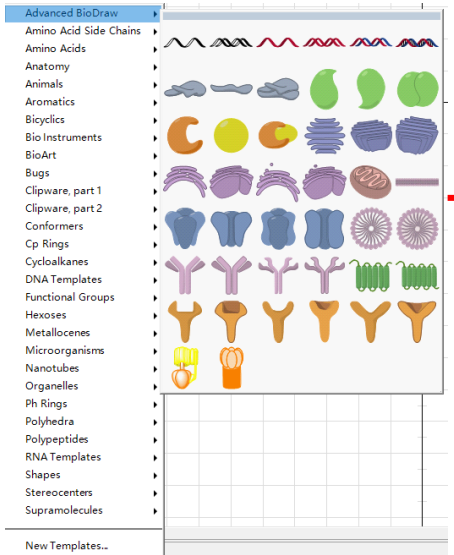
选择工具结构透视

橡皮擦

文本编辑

轨道

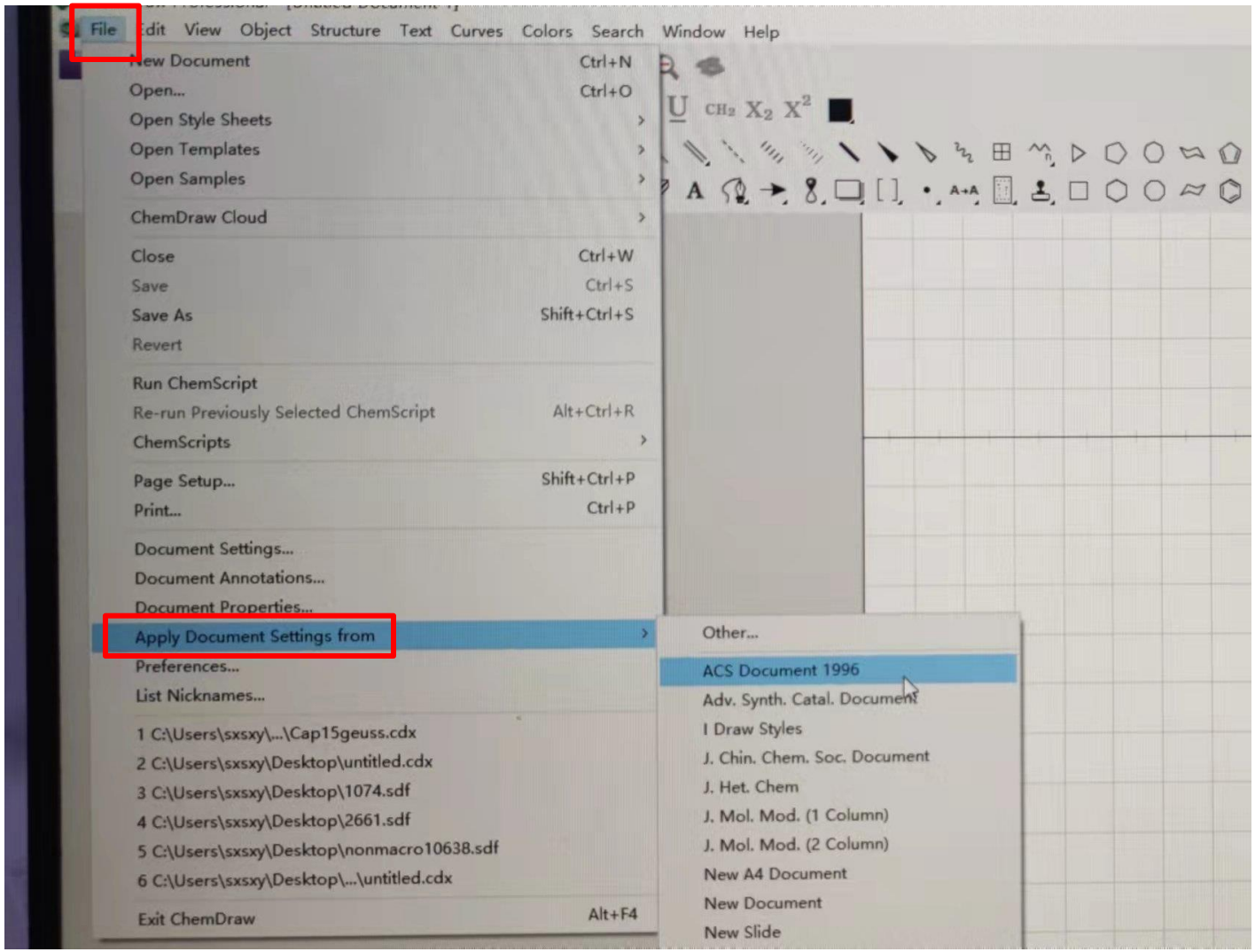
电子



模板

基本环系

ChemDraw


File
Edit
View
Object
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New Document Ctrl+N
Open... Ctrl+O
Open Style Sheets
Open Templates
Open Samples
ChemDraw Cloud
Close Ctrl+W
Save Ctrl+S
Save As Shift+Ctrl+S
Revert
Run ChemScript
Re-run Previously Selected ChemScript Alt+Ctrl+R
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Document Properties...
Apply Document Settings from
Preferences...
List Nicknames...
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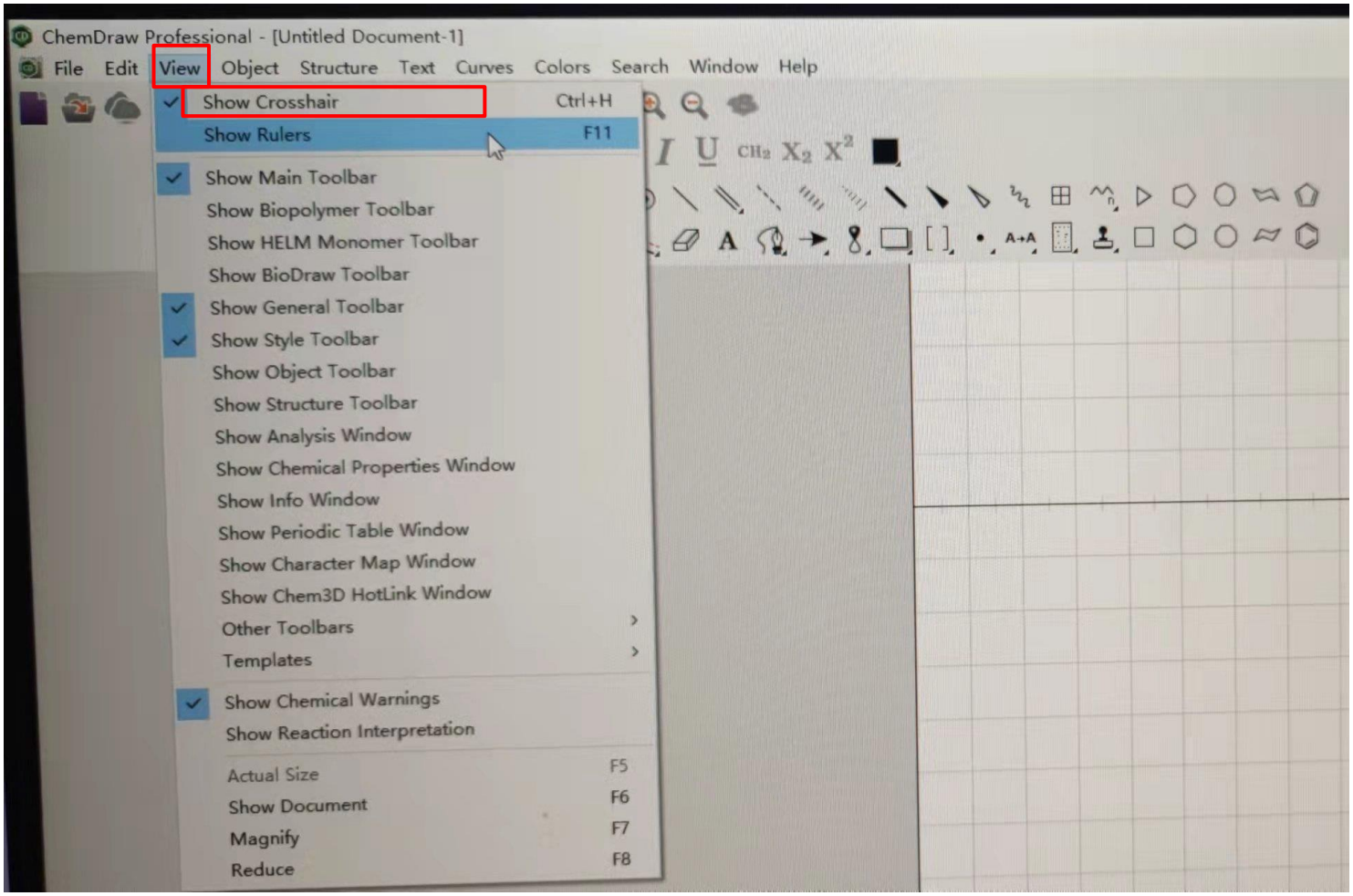
ACS Document 1996
Adv. Synth. Catal. Document
I Draw Styles
J. Chin. Chem. Soc. Document
J. Het. Chem
J. Mol. Mod. (1 Column)
J. Mol. Mod. (2 Column)
New A4 Document
New Document
New Slide

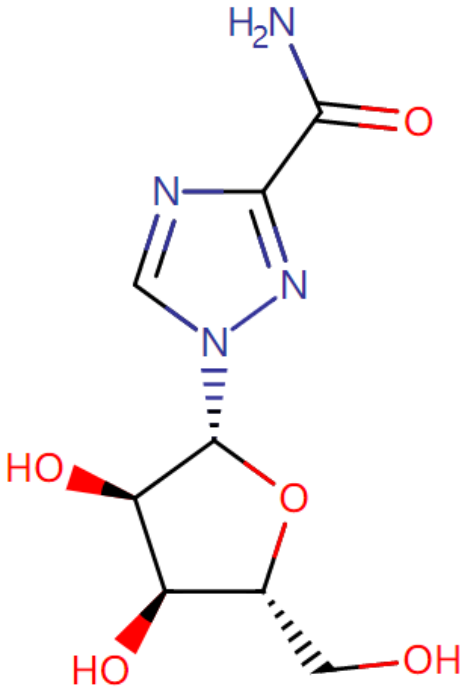
ChemDraw

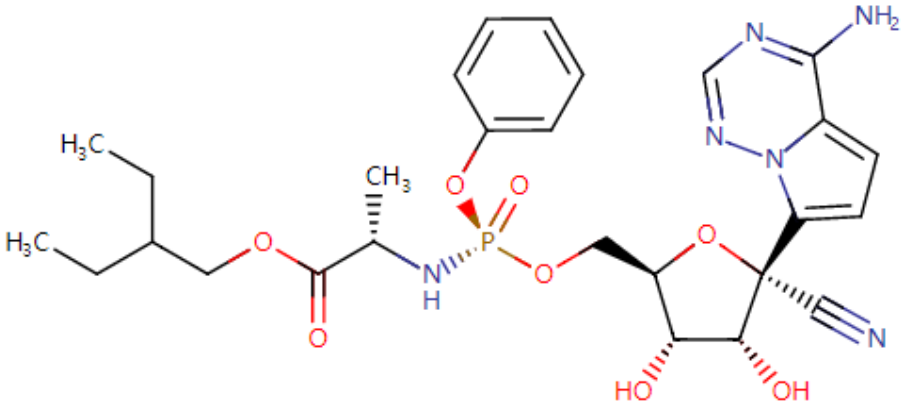
调出网格状



ChemDraw

小练习

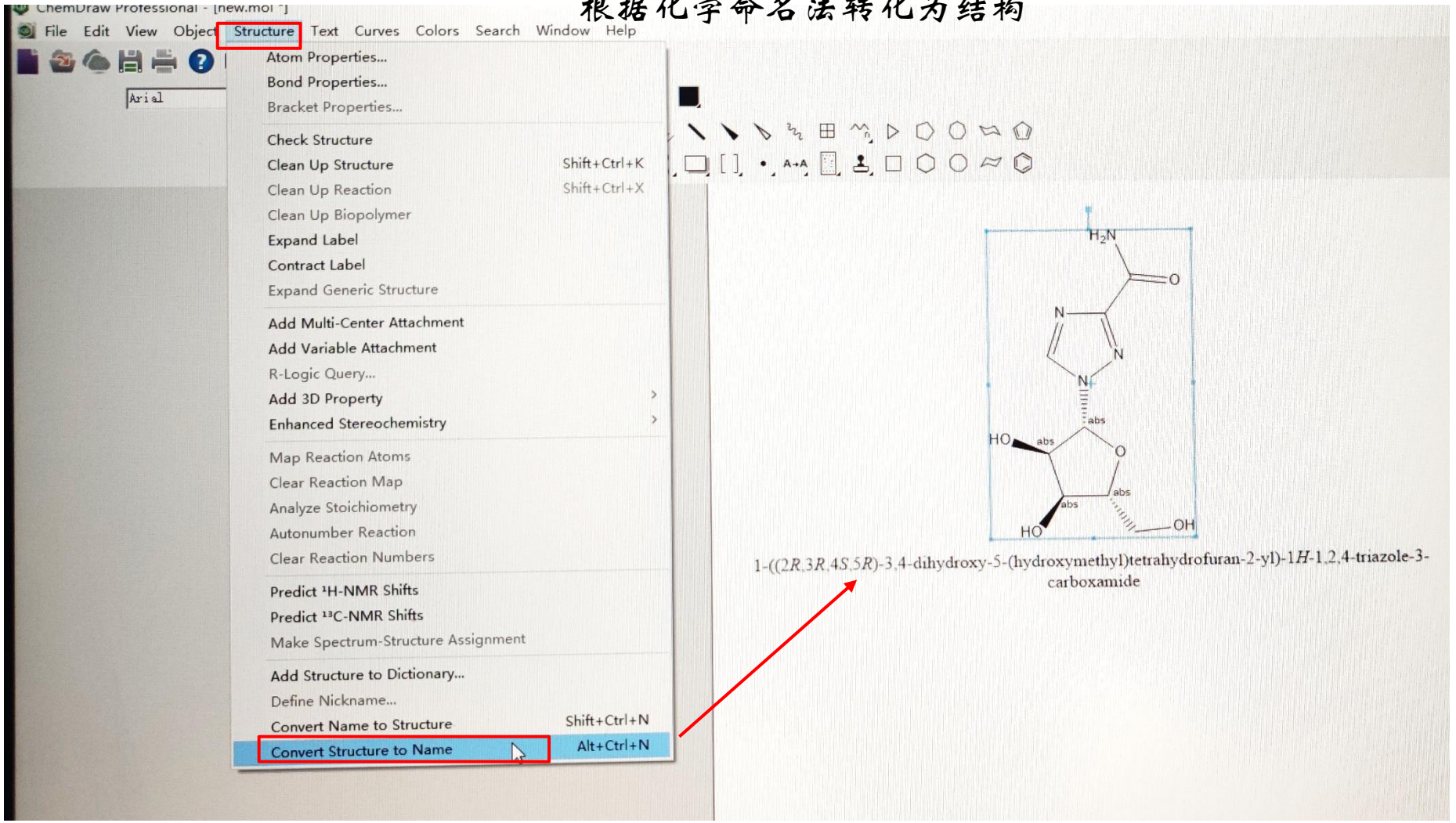




ChemDraw

根据结构转化为化学命名法

根据化学命名法转化为结构



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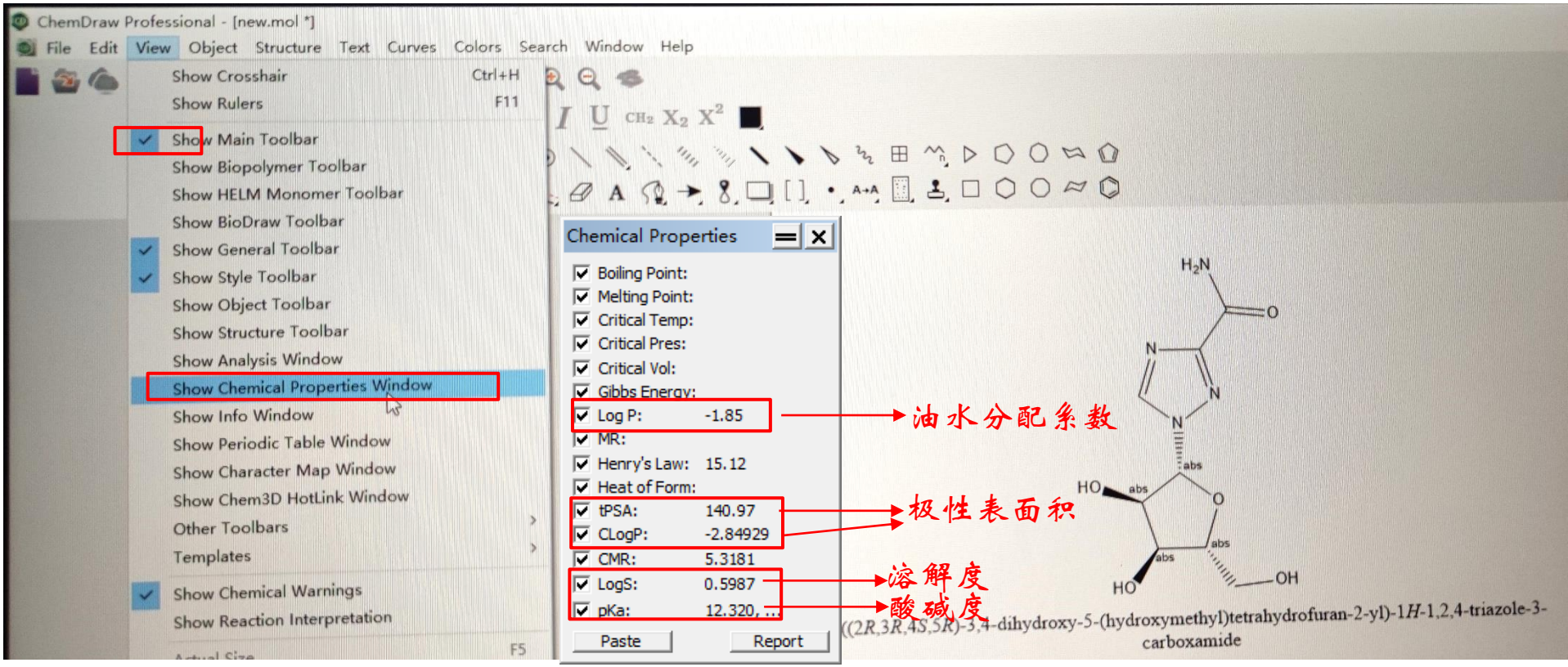


Rule of five

1.化合物的 分子量 不大于 500

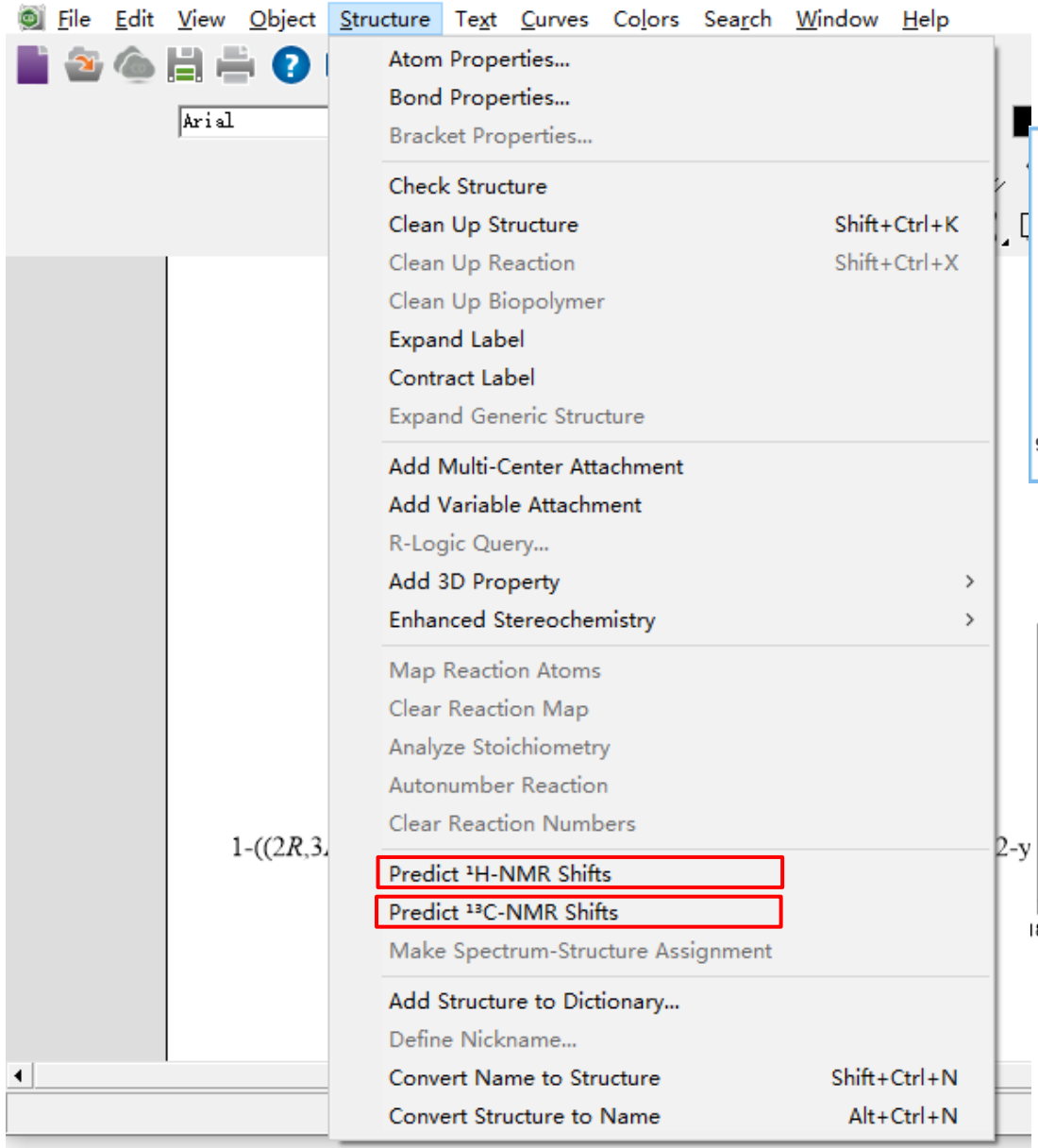
2.化合物结构中的 氢键 供体（包括羟基、氨基等）的数量不大于 5 个；

3.化合物中 氢键 受体 的数量不大于 10 个；

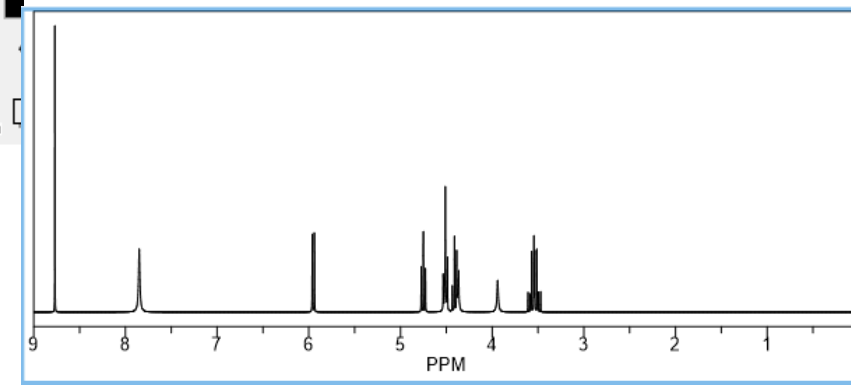
4.化合物的 脂水分配系数 的 对数 值 logP ）不大于 5

5.化合物中可旋转键的数量不大于 10 个。

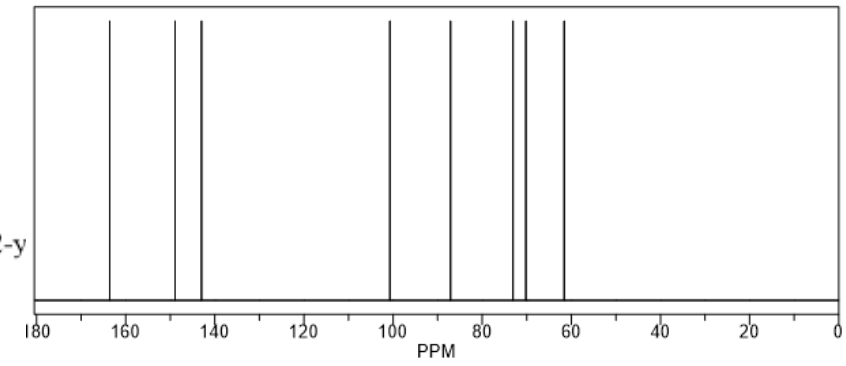
ChemDraw



H谱



C谱



Notepad++介绍和使用

Notepad++

主要功能：

Notepad++ 顾名思义就是 windows 下 notepad 的增强版，它采用 C++ 编写，属于轻量级的文本编辑类软件，可以快速对文本、数据、代码进行处理。

优势：

性能优秀，小巧（完整安装包仅 3.8MB），功能众多，插件丰富， 完全免费。启动更快，占用资源更少，但是从功能使用等方面来说，不亚于其他专业工具，而windows默认的notepad虽然更“轻量”，但是功能就太少。

Notepad++特色

1、自动保存

文本编辑过程中最怕的就是各种意外情况还没来得急保存，比如死机、进程僵死、奔溃等，如果你用了 Notepad++，完全不用担心，默认情况下它会实时的将正在编辑的内容保存一份副本到 %appdata% 下，每次打开未保存的文件都会自动从副本中恢复，完全不用担心任何编辑数据丢失！

2、列编辑

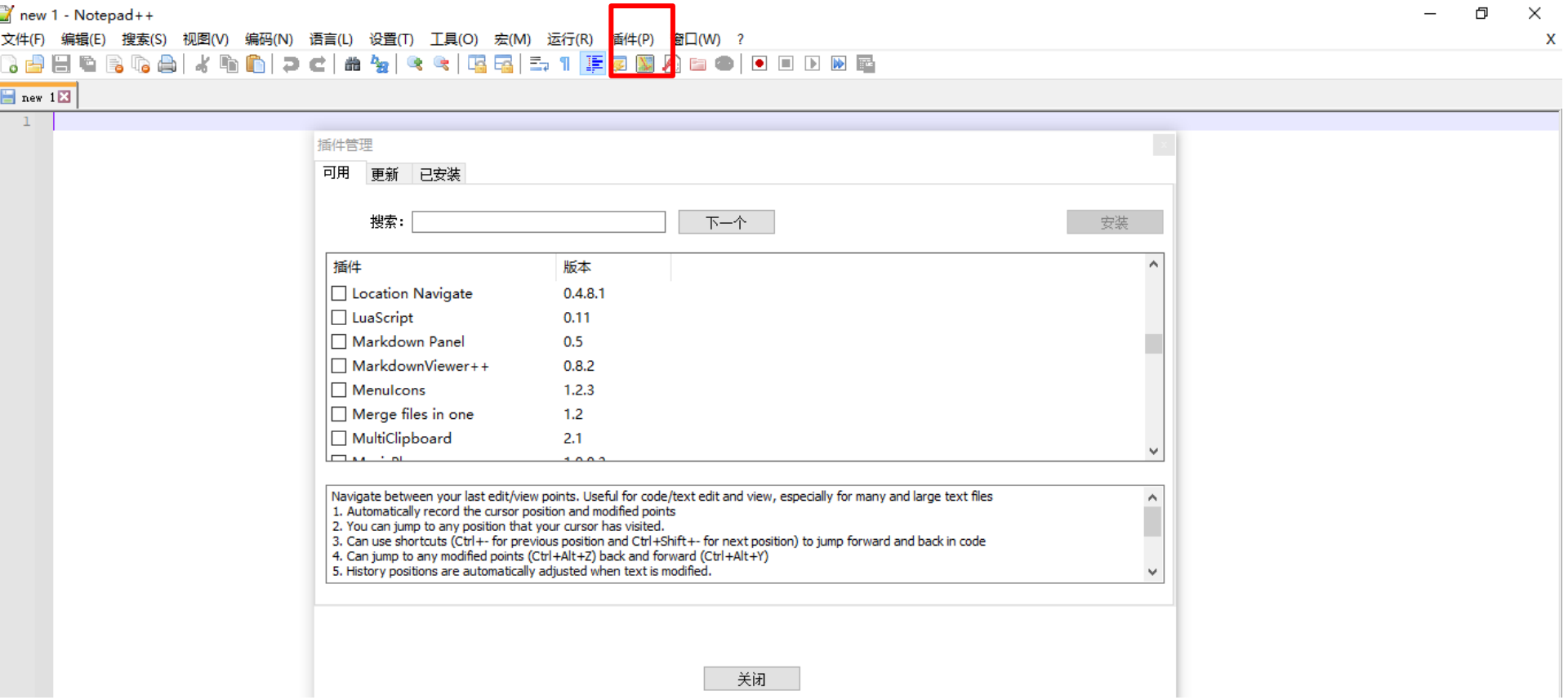
Notepad++里按下 alt 键即可进入列编辑模式，然后按下 tab 即可为选中的每一行执行相同的操作。那如果要给每行的开头加一个连续的数字做行号呢？Notepad++里按下 alt+c 组合键即可进入列编辑插入模式，设置相应的初始值、步长即可。

3、查找替换

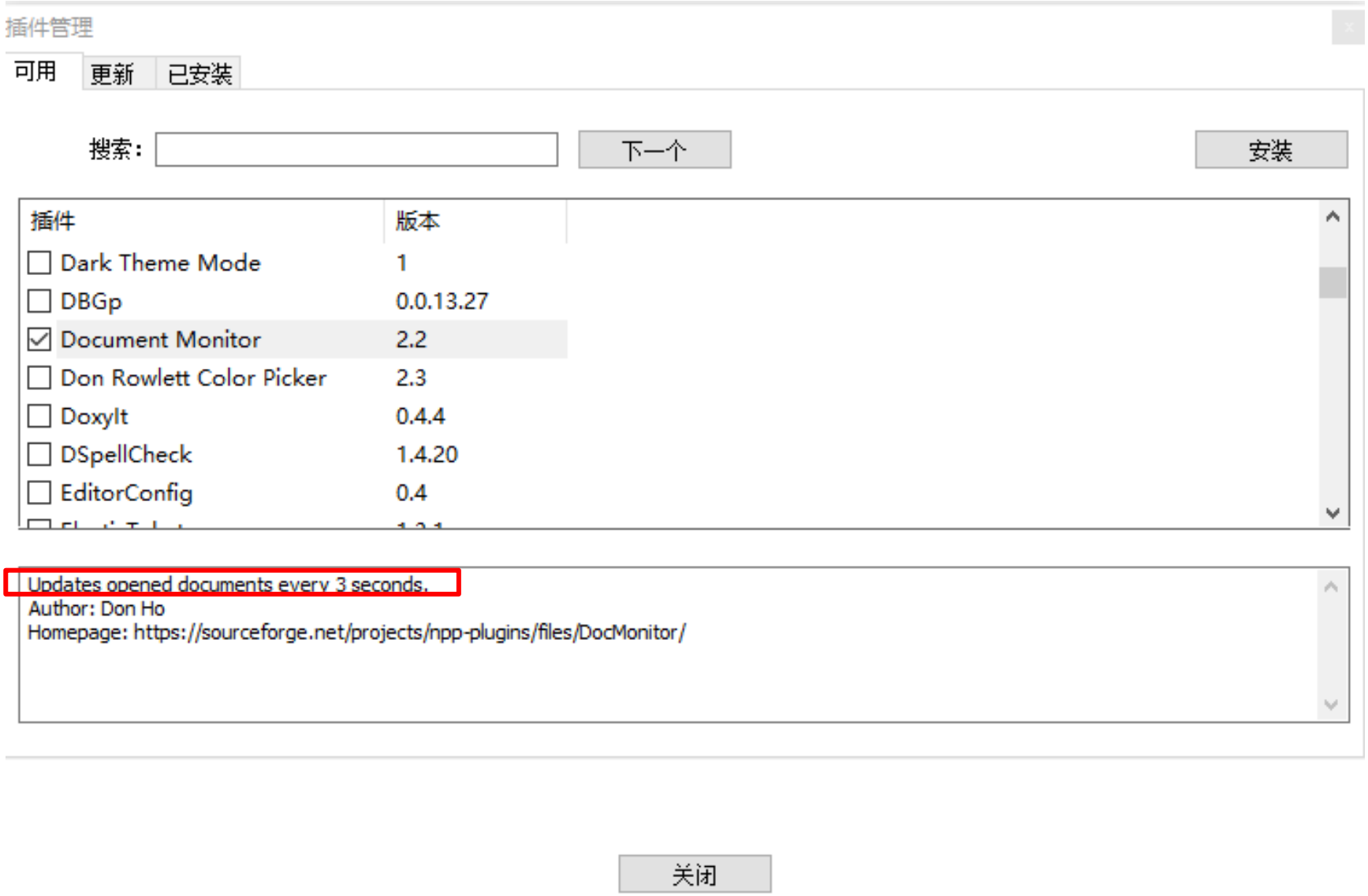
notepad++ 的查找替换非常强大，能在单独窗口输出匹配内容，或者更友好的方式标记出查找结果。

Notepad++插件

notepad++支持插件，添加对应不同的插件，以支持不同的功能。里面除了一些常见的插件之外，还有一些好玩的插件，比如将文字读出来的speech插件（插件》插件管理）



Notepad++插件


插件管理
可用
更新
已安装
搜索：
下一个
安装
插件
版本
Dark Theme Mode
1
DBGp
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Document Monitor
2.2
Don Rowlett Color Picker
2.3
DoxyIt
0.4.4
DSpellCheck
1.4.20
EditorConfig
0.4
Updates opened documents every 3 seconds.
Author: Don Ho
Homepage: https://sourceforge.net/projects/npp-plugins/files/DocMonitor/
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