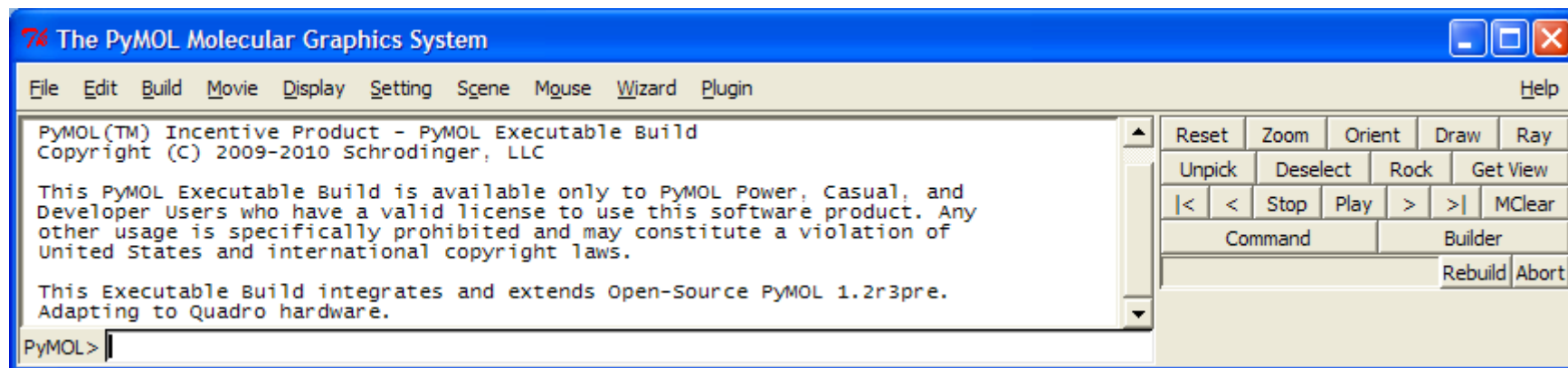
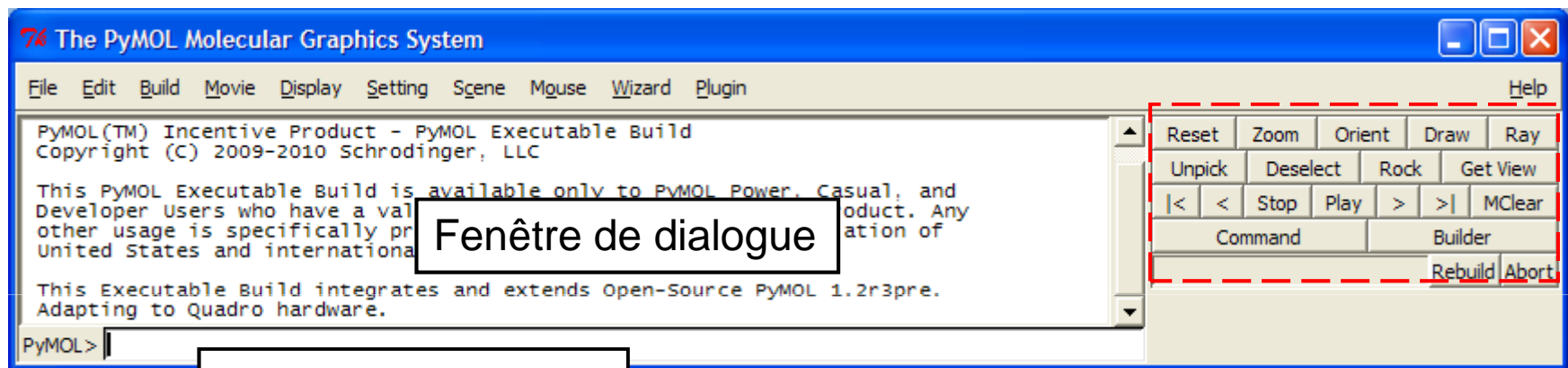




PyMol



La fenêtre de contrôle
Elle est indépendante

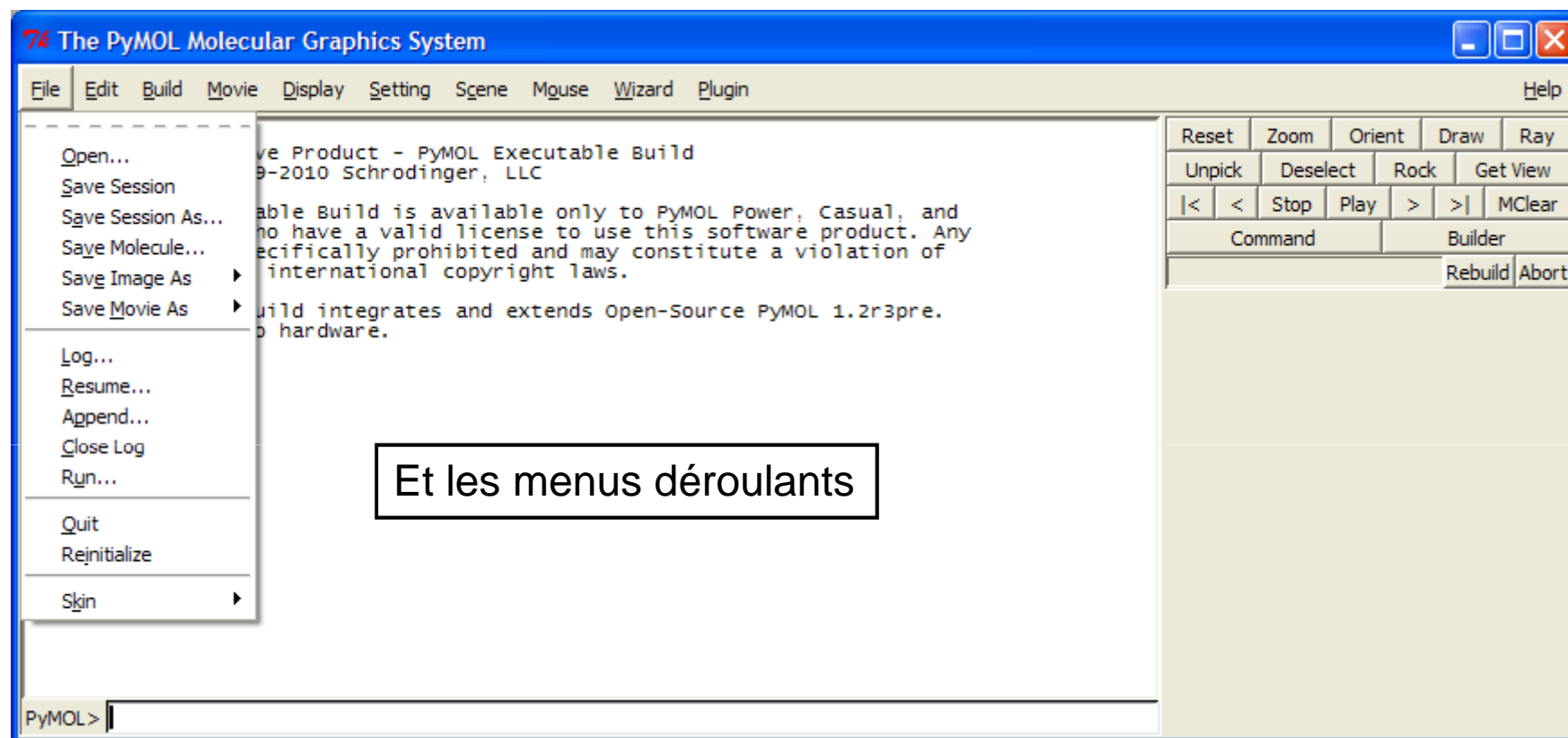


Fenêtre de dialogue

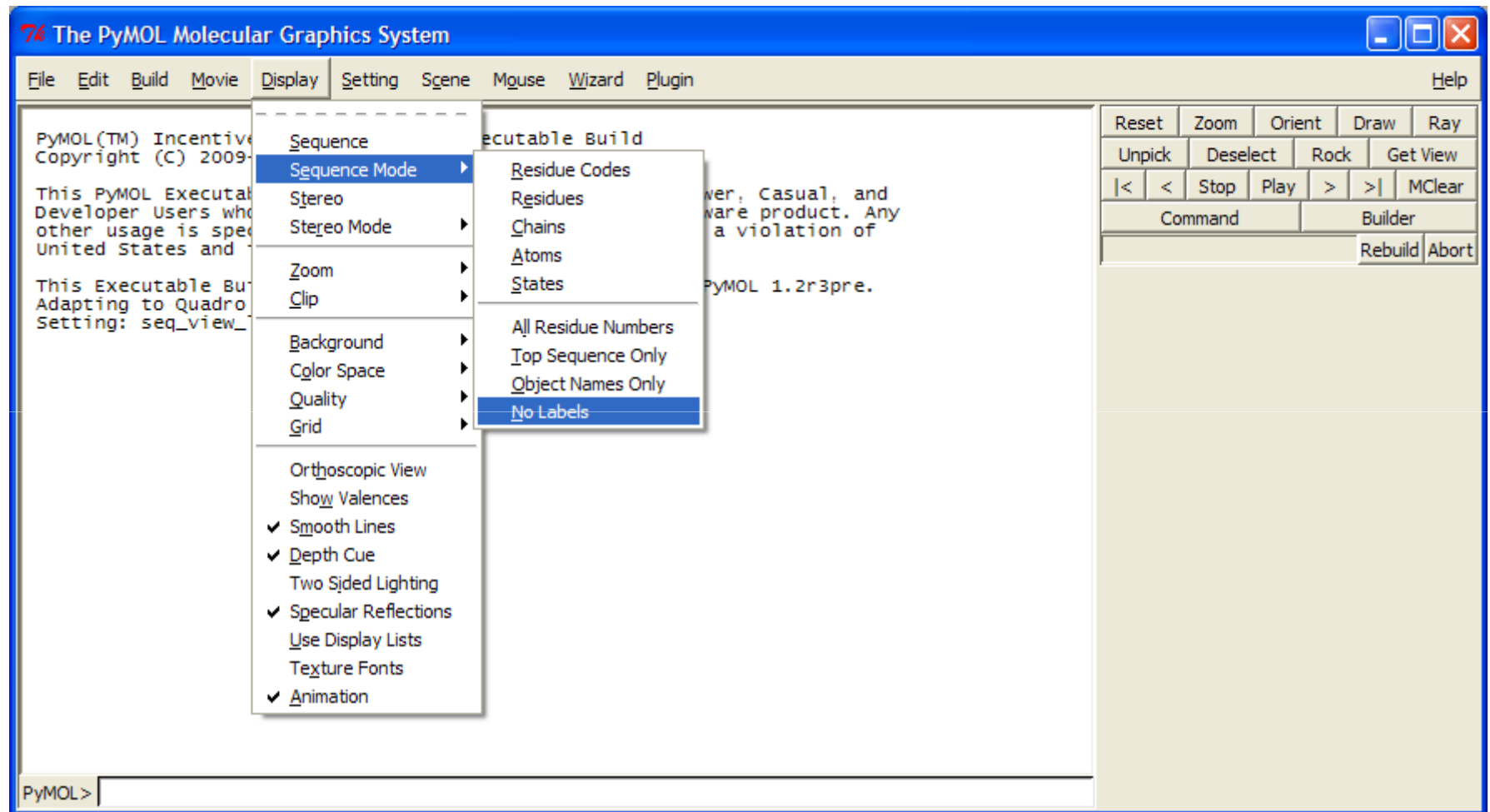
Ligne de commande

Raccourci de Visualisation

La fenêtre de contrôle



La fenêtre de contrôle



The PyMOL Molecular Graphics System

File Edit Build Movie Display Setting Scene Mouse Wizard Plugin Help

PyMOL(TM) Incentive Product - PyMOL Executable Build
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This Executable Build integrates and extends Open-Source PyMOL 1.2r3pre. Adapting to Quadro hardware.

PyMOL> |

Reset	Zoom	Orient	Draw	Ray		
Unpick	Deselect	Rock	Get View			
<	<	Stop	Play	>	>	MClear
Command			Builder			
			Rebuild Abort			

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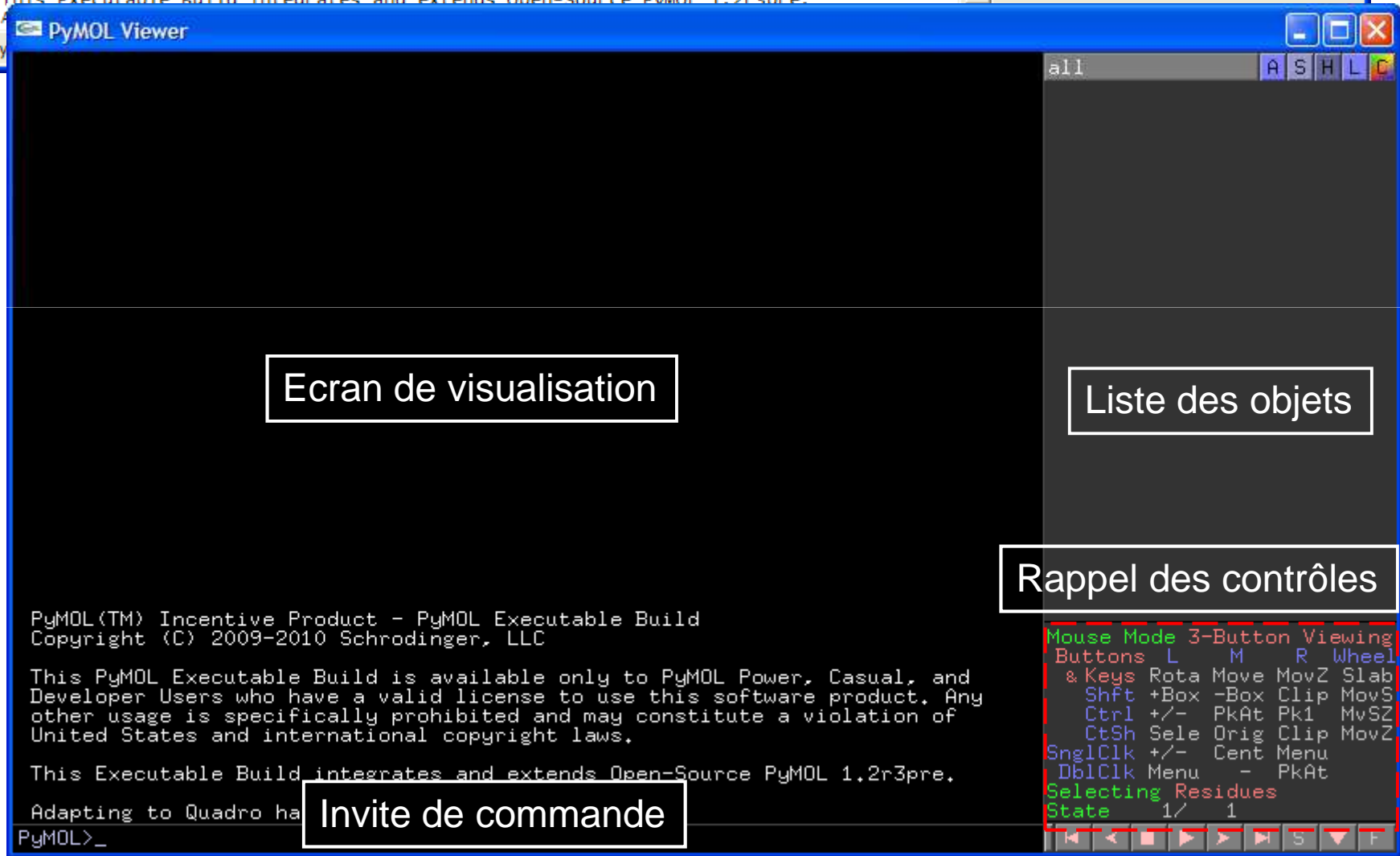
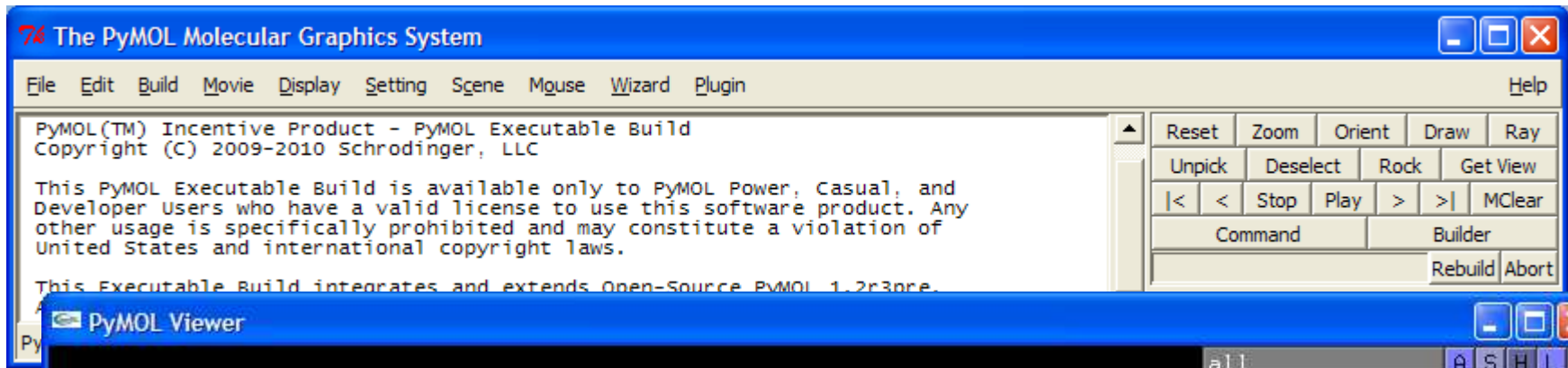
This Executable Build integrates and extends Open-Source PyMOL 1.2r3pre.

Adapting to Quadro hardware.

PyMOL>_

Mouse Mode 3-Button Viewing
Buttons L M R Wheel
& Keys Rota Move MovZ Slab
Shft +Box -Box Clip MovS
Ctrl +/- PkAt Pk1 MvSZ
CtSh Sele Orig Clip MovZ
SnglClk +/- Cent Menu
Db1Clk Menu - PkAt
Selecting Residues
State 1/ 1

⏪ ⏩ ⏴ ⏵ ⏶ ⏷ ⏸ ⏹ ⏺ ⏻ ⏼ ⏽ ⏾ ⏿



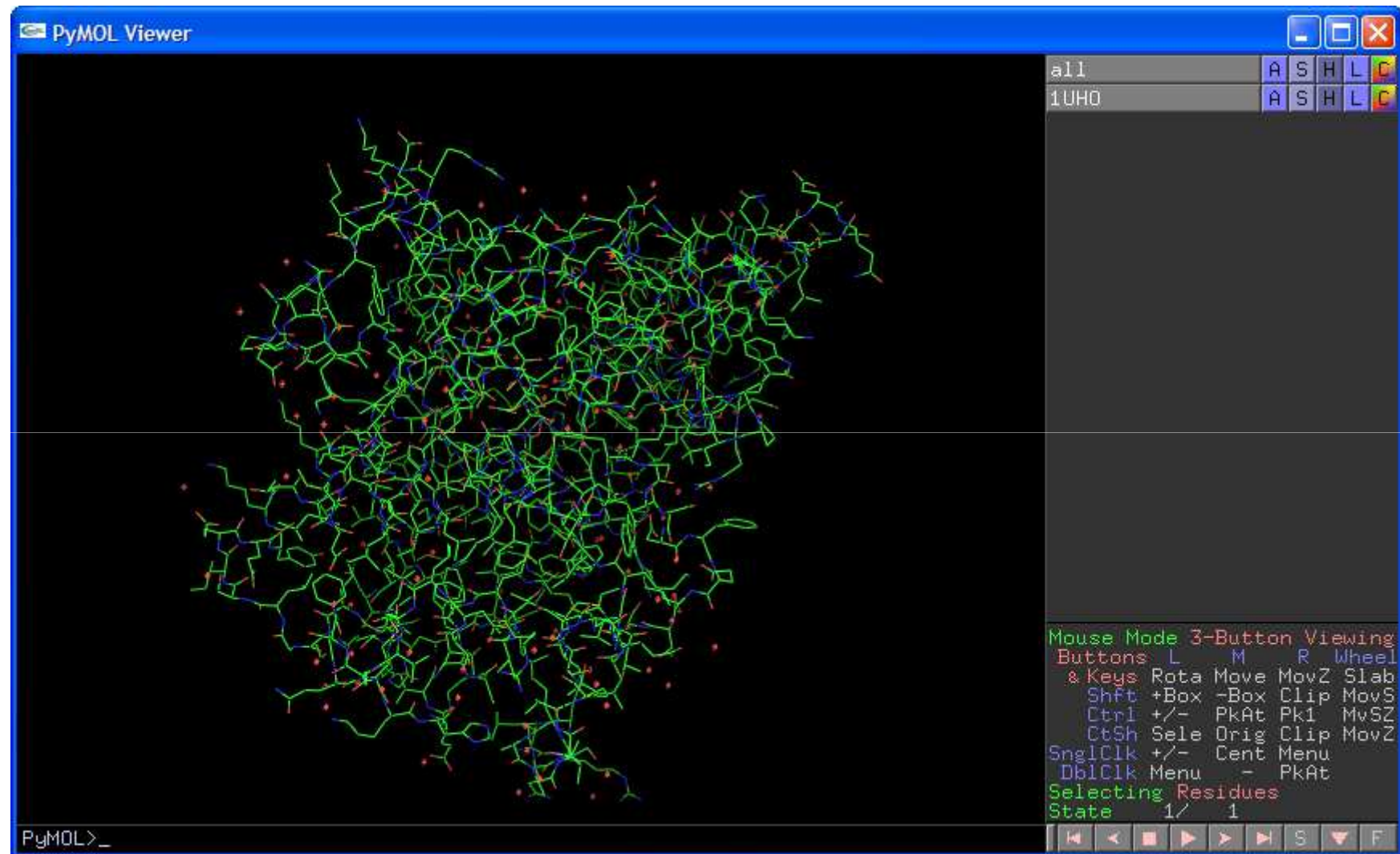
Ecran de visualisation

Liste des objets

Rappel des contrôles

Invite de commande

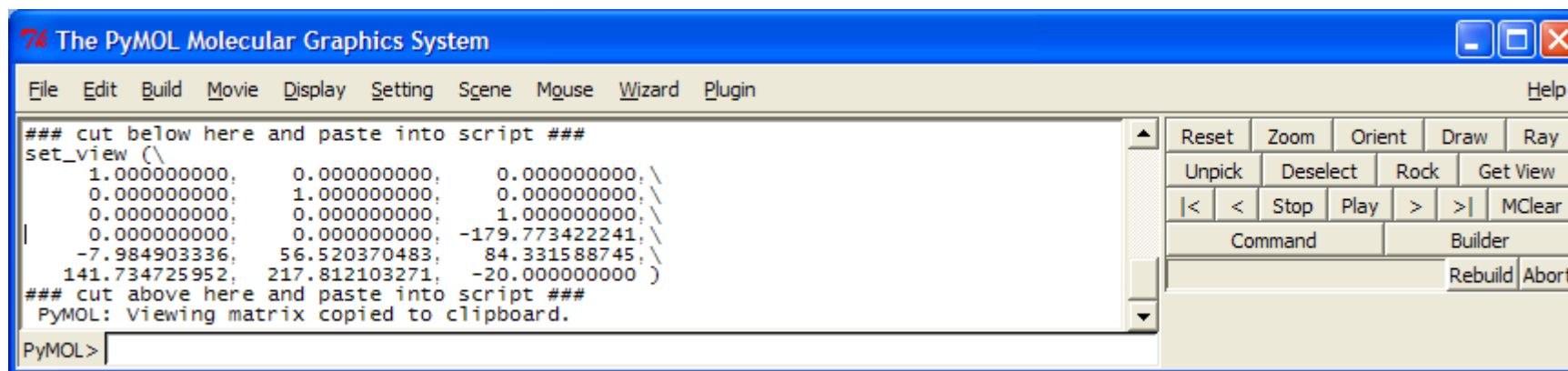
Load 1HUO ou fetch 1HUO

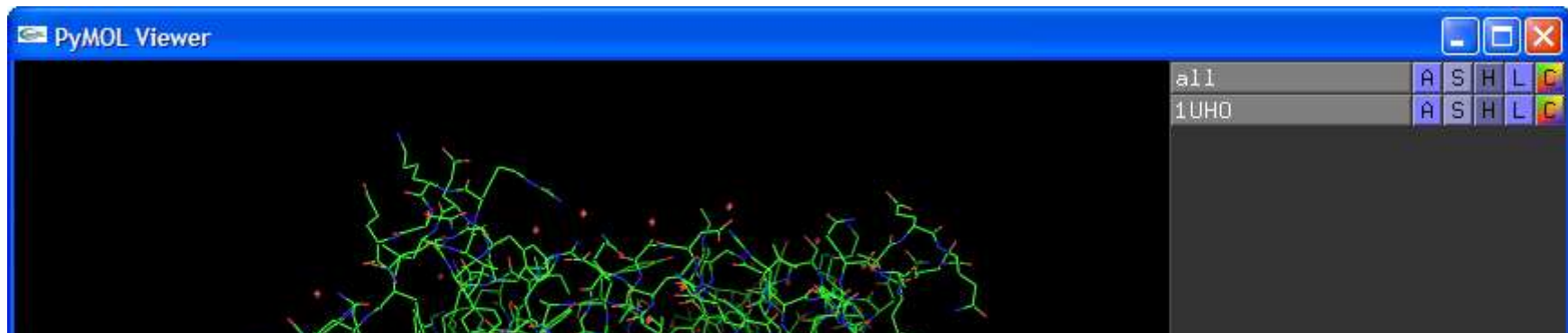


Familiarisation avec la souris

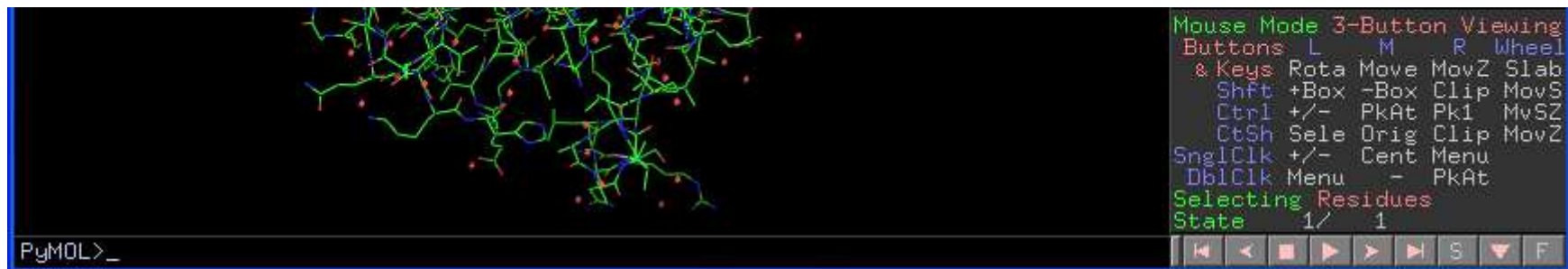
Tableau 2.1. Utilisation de la souris

Boutons et touches	boutons de la souris		
	Gauche	Milieu	Droite
Aucun	Rotation libre	Translation axes x,y	Translation axe z (zoom)
Shift	Agrandir une sélection	Supprimer une sélection	Déplacement du plan de coupe
Ctrl	Inverser la sélection	Sélection de type <i>PkAt</i>	Sélection de type <i>PkI</i>
Shift+Ctrl	Sélection d'un résidu	Centrer un atome	Menu de contrôle
double-clic	Menu de contrôle	Centrer un atome	Sélection de type <i>PkAt</i>

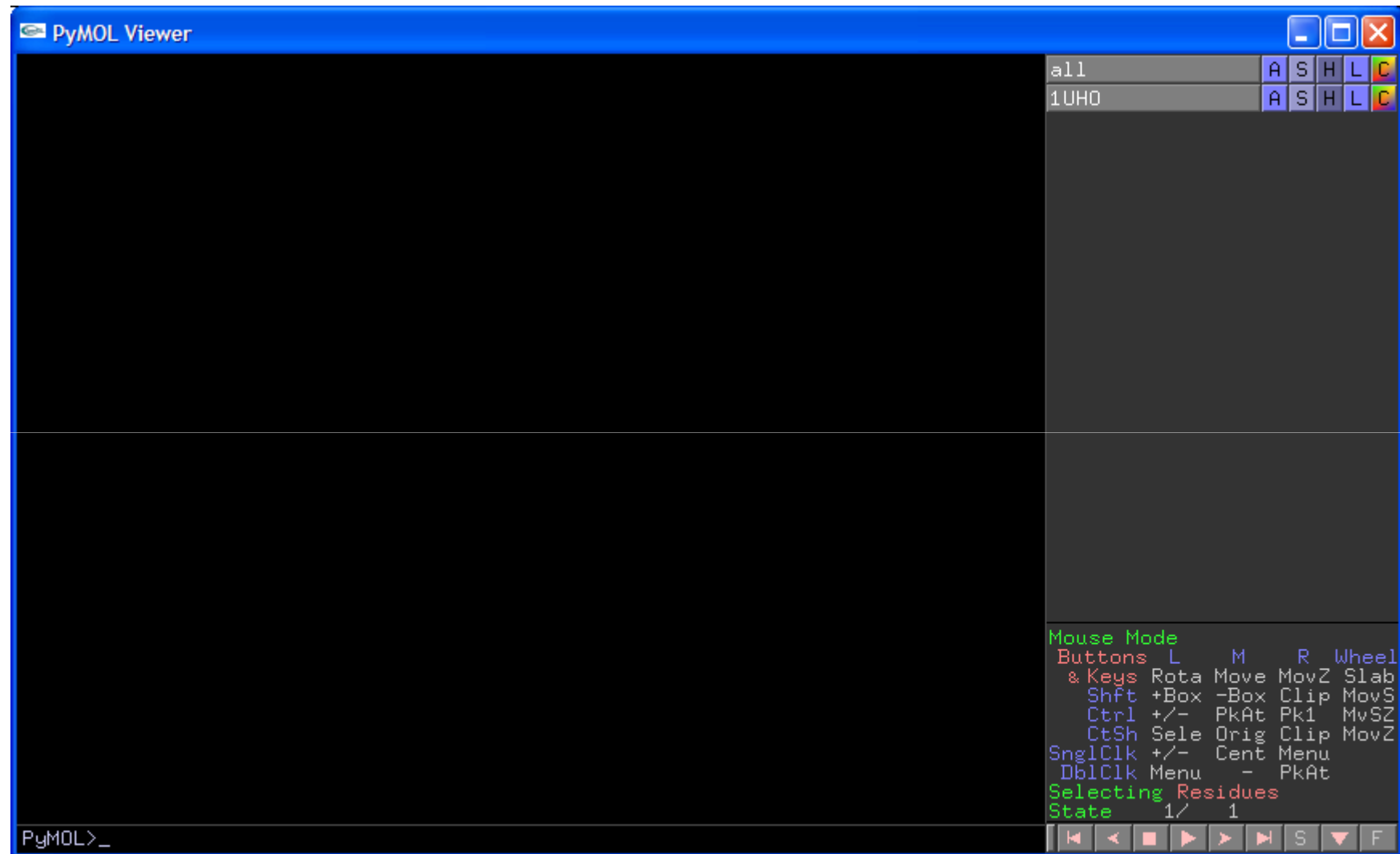




- A (Actions) : ce menu contient toutes les actions qui peuvent être réalisées sur les objets (zoom, alignement, duplication, suppression/ajout des atomes d'hydrogène, ...) ;
- S (Show) : ce menu permet de choisir un ou des styles de visualisation à appliquer à la molécule ;
- H (Hide) : ce menu permet de choisir un ou des styles de visualisation à ne plus appliquer à la molécule ;
- L (Labels) : ce menu permet d'ajouter certains labels sur l'objet, tels que le nom des atomes, des résidus, ... ;
- C (Color) : ce menu permet de changer le style de colorisation de l'objet.

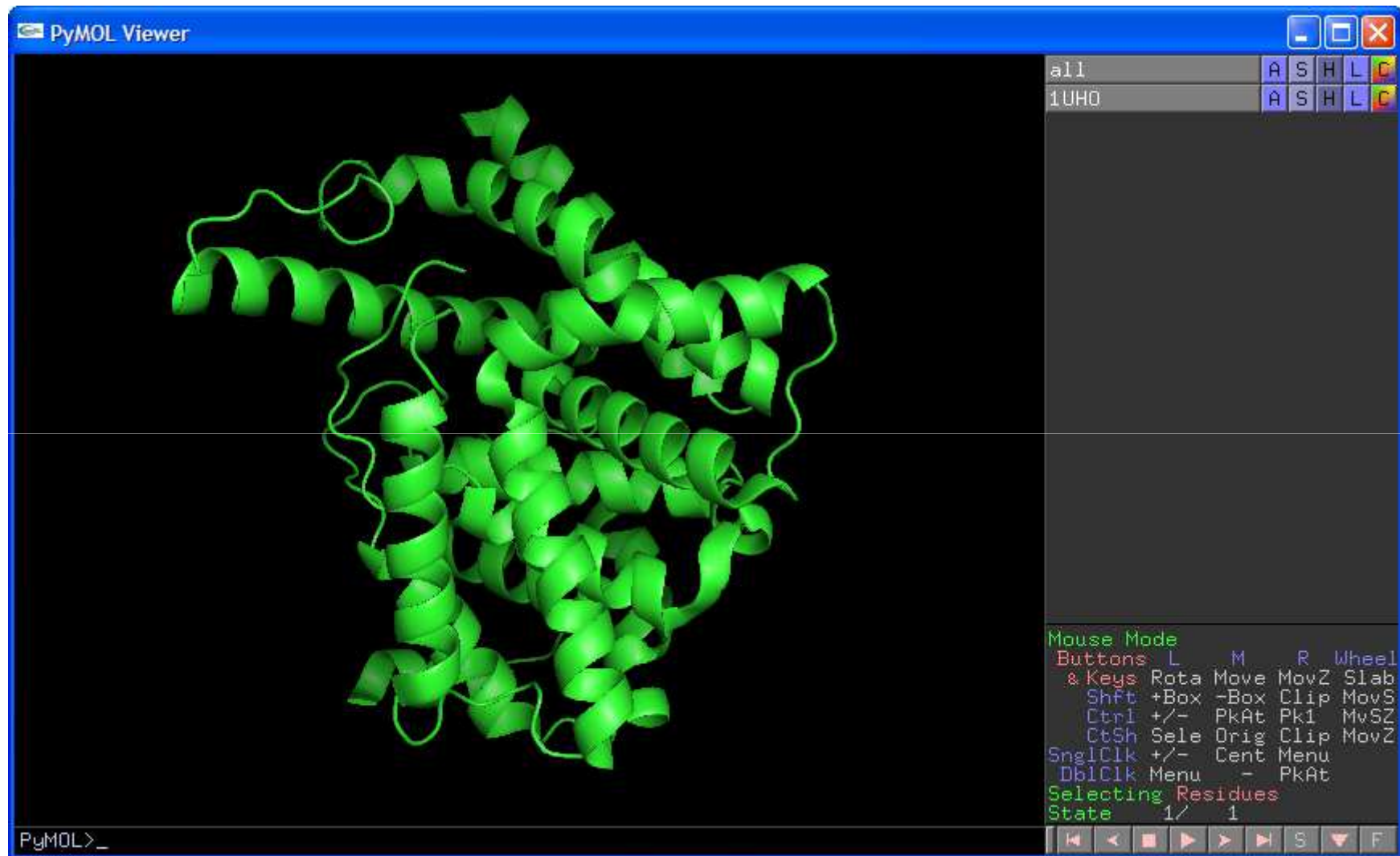


H everything



hide everything

S cartoon



show cartoon, 1huo

Show/hide [representation [, selection]]

representation =

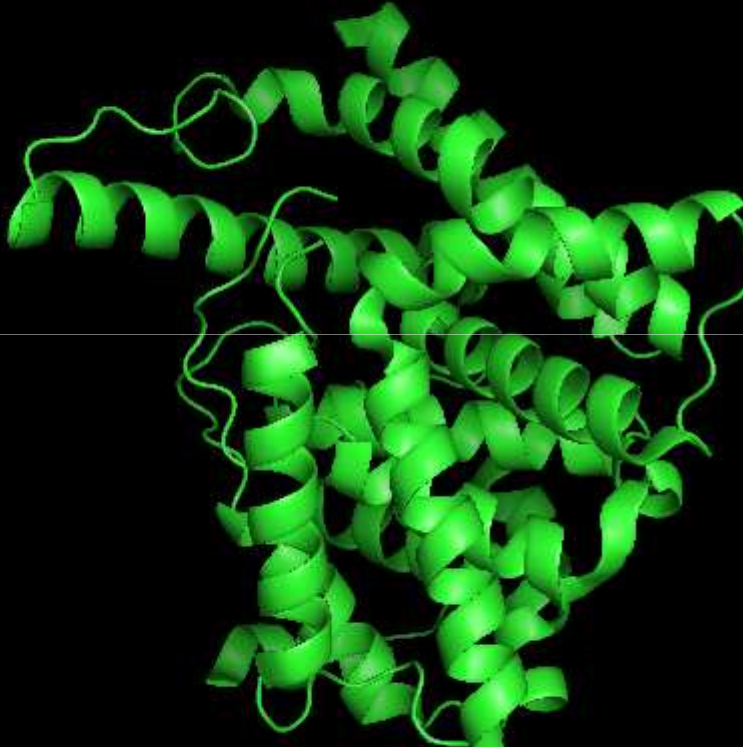
angles	cgo	ellipsoids	lines	<i>ribbon</i>	surface
callback	dashes	everything	mesh	slice	
<i>cartoon</i>	dihedrals	extent	nb_spheres	spheres	
cell	dots	labels	nonbonded	sticks	

Tableau 2.2. Les différents styles de visualisation

Style	Effet
lines	Affichage de l'objet avec des lignes fines
nonbonded	Affichage des éléments seuls d'un objet (comme l'oxygène de l'eau dans les fichiers PDB)
sticks	Affichage de l'objet avec des bâtons
ribbon	Affichage de la protéine sous la forme d'un fil
cartoon	Représentation de la protéine par un ruban plat pour les feuillets, un ruban en hélice pour les hélices et un fil pour les autres zones
labels	Affichage des labels
cell	Affichage de la cellule cristallographique
dots	Représentation de la surface de van der Waals de chaque atome par un nuage de point
spheres	Représentation de la surface de van der Waals de chaque atome en dure
nb_spheres	Représentation des éléments seuls (non liés) par des sphères
mesh	Représentation de la surface de l'objet par un réseau de fils
surface	Affichage de la surface de l'objet avec une texture pleine
main chain	Représentation de la chaîne principale de la protéine
side chain	Représentation des chaînes secondaires de la protéine

PyMOL Viewer

```
//1UHO//A/537 541 546 551 556 561 566 571 576 581 586 591 596 601  
TRELQSLAAAVPSAQTLLKITDFSFDFELSDLETALCTIRMFTDLNLVQNFQMKHEVLCRWILSVKKNY
```



all	A	S	H	L
1UHO	A	S	H	L

Mouse Mode
Buttons: L M R Wheel
& Keys: Rota Move MovZ Slab
Shft: +Box -Box Clip MovS
Ctrl: +/- PkAt Pk1 MvSZ
CtSh: Sele Orig Clip MovZ
SnglClk: +/- Cent Menu
DblClk: Menu - PkAt
Selecting Residues
State 1/ 1

PyMOL>_

Navigation icons: Home, Left, Right, Stop, Next, Previous, Refresh, F

Sélection des objets

Display sequence

Sequence mode

set seq_view_label_mode = 0,1,2,3

select object-name/segi_id/chain_id/resi_id/name_id/

select object-name and name C8 and resi 1 and resname ALA
and chain A and symbol C

resi 10-12

resi 10+12

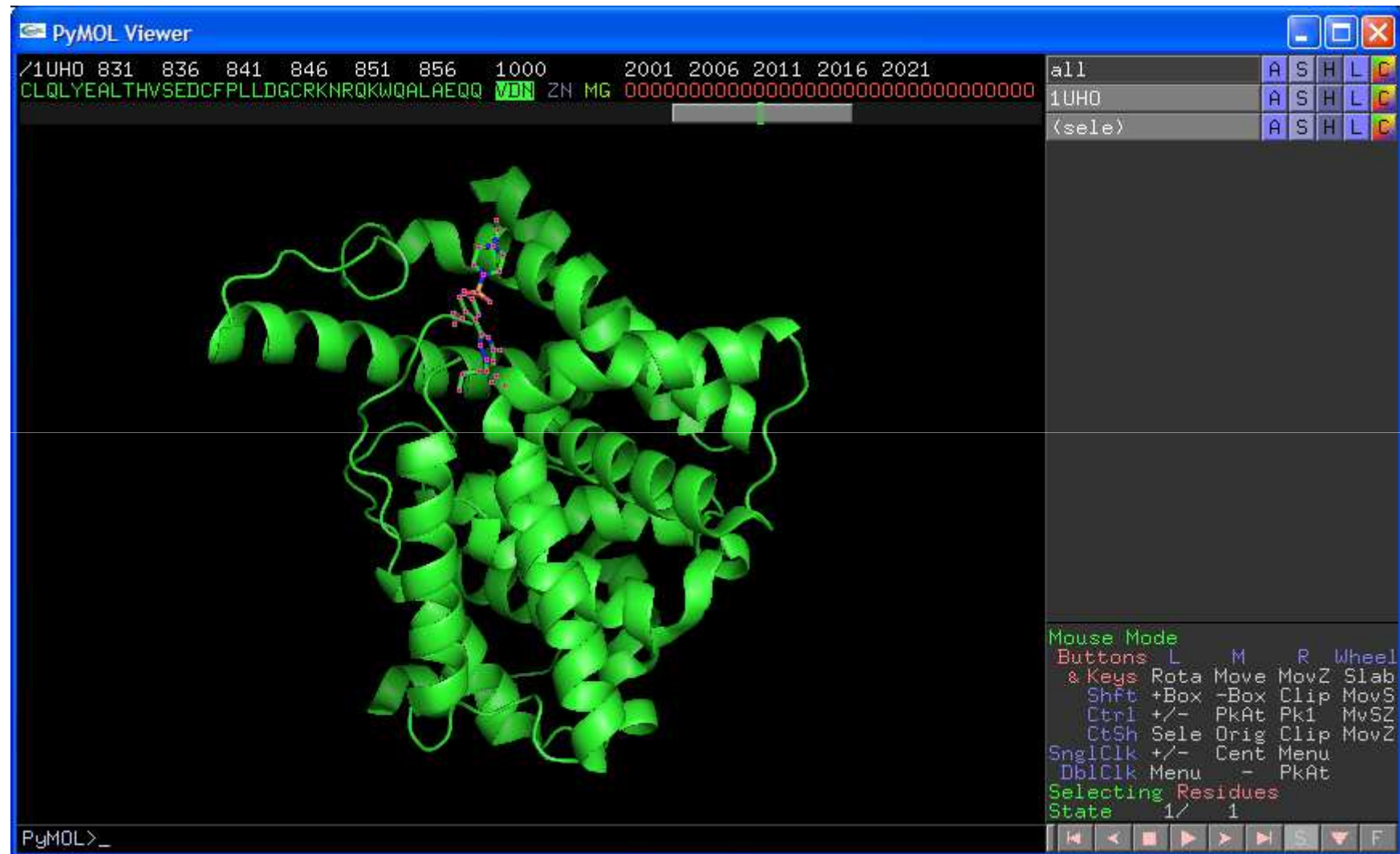
hide/show cartoon, !(c. A) = hide cartoon, not chain A

hide/show everything (type de représentations), selection

hide all (objets)

everything = line+sticks+ribbon+cartoon+spheres

Représentation stick du residue 1000 « VDN » (sele)



(sele) copy to object
rename vdn

obj01 est créé

The screenshot shows the PyMOL Viewer interface. The main window displays a protein structure in green ribbon representation. The command line at the top shows the following commands: `/1UHO 781 786 791 796 801 806 811 816 821 826 831 836 841 846`, `IQQRIAELVATEFFDQGDREKELNIEPTDLNREKKNKIPSMQVGFIDAICLQLYEALTHVSEDCFPLLDGCRKNRQK`, and `/obj01`. The object list on the right shows `all`, `<sele>`, `1UHO`, and `obj01`. The mouse mode control panel at the bottom right shows the following settings: `Buttons: L M R Wheel`, `& Keys: Rota Move MovZ Slab`, `Shft: +Box -Box Clip MovS`, `Ctrl: +/- PkAt Pk1 MvSZ`, `CtSh: Sele Orig Clip MovZ`, `SnglClk: +/- Cent Menu`, `DblClk: Menu - PkAt`, `Selecting Residues`, and `State 1/ 1`. The PyMOL prompt `PyMOL>_` is visible at the bottom left.

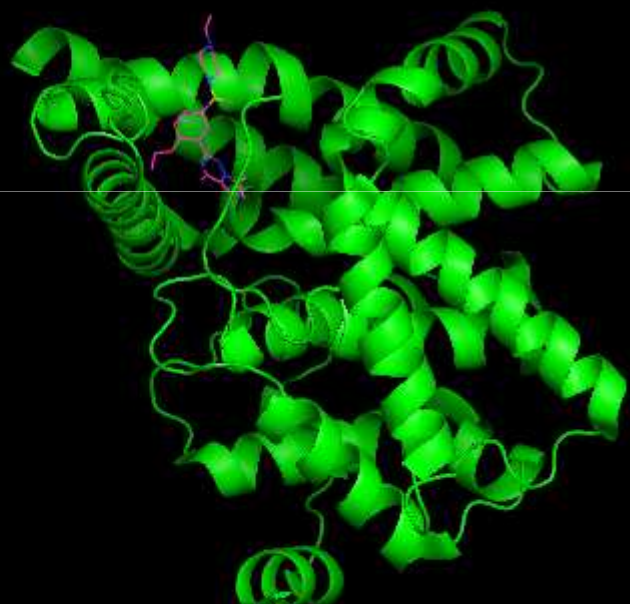
PyMOL Viewer

```

/1UHO 781 786 791 796 801 806 811 816 821 826 831 836 841 846
IQQRIAELVATEFFDQGDREKELNIEPTDLMNREKKNKIPSMQVGFIDAICLQLYEALTHVSEDCFPLLDGCRKNRQK
/obj01

```

Renaming obj01 to: vdn_



all	A	S	H	L	C
<sele>	A	S	H	L	C
1UHO	A	S	H	L	C
obj01	A	S	H	L	C

Renaming

Cancel

Mouse Mode

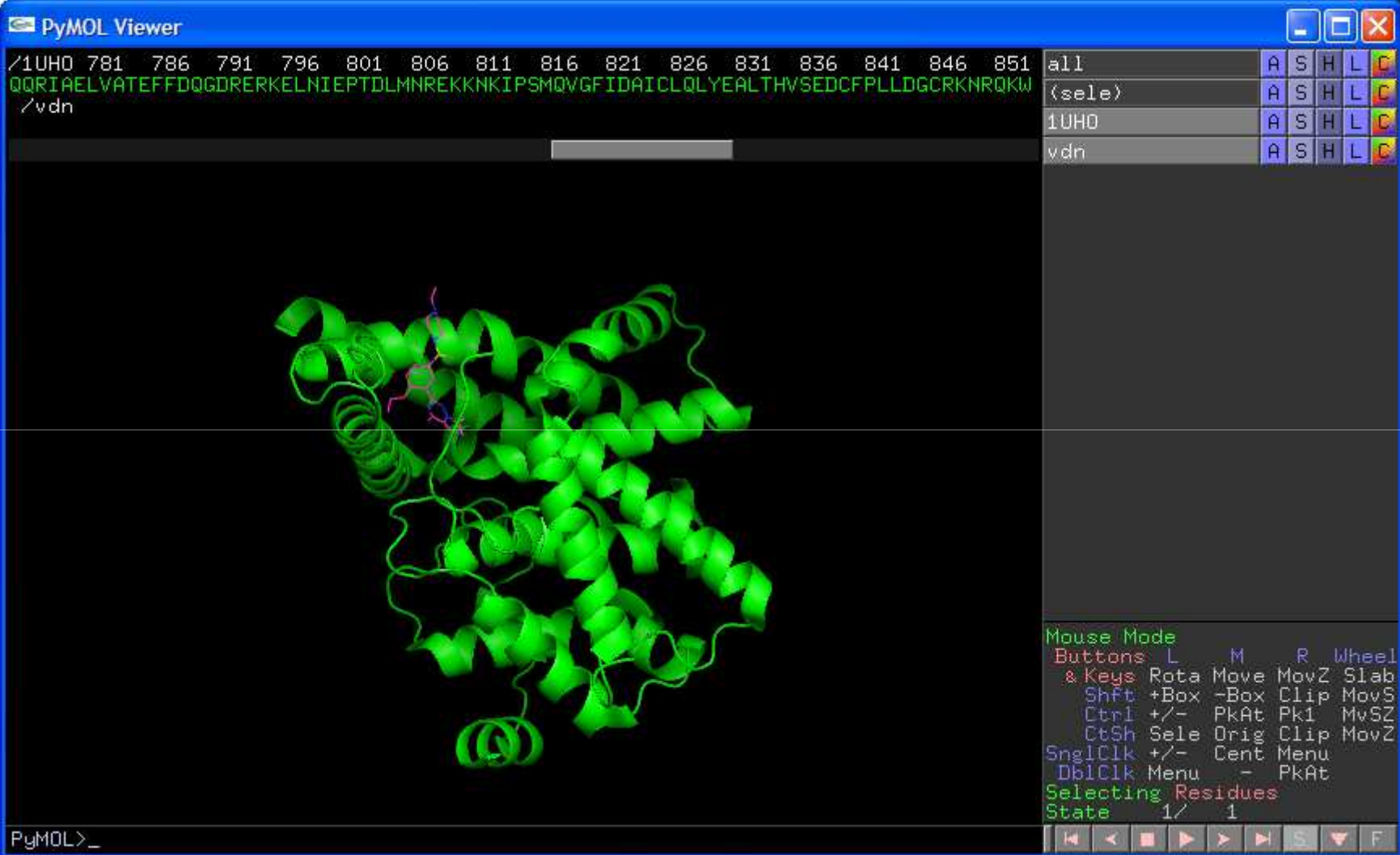
Buttons	L	M	R	Wheel
& Keys	Rota	Move	MovZ	Slab
Shft	+Box	-Box	Clip	MovS
Ctrl	+/-	PkAt	Pk1	MvSZ
CtSh	Sele	Orig	Clip	MovZ
SnglClk	+/-	Cent	Menu	
DblClk	Menu	-	PkAt	

Selecting Residues

State 1/ 1

PyMOL>_

Deux objets



The screenshot shows the PyMOL Viewer interface. The main window displays a protein structure in green ribbon representation. The command line at the top shows the following commands:

```
/1UHO 781 786 791 796 801 806 811 816 821 826 831 836 841 846 851  
QQRIAEVATEFFDQGDREKELNIEPTDLNREKKNKIPSMQVGFIDAICLQLYEALTHVSEDCFLLDGCRKNRQKW  
/vdn
```

The command list on the right side of the window is as follows:

Object	A	S	H	L	C
all					
<sele>					
1UHO					
vdn					

The Mouse Mode section at the bottom right of the command list shows the following settings:

```
Mouse Mode  
Buttons: L M R Wheel  
& Keys: Rota Move MovZ Slab  
Shft: +Box -Box Clip MovS  
Ctrl: +/- PkAt Pk1 MvSZ  
CtSh: Sele Orig Clip MovZ  
SnglClk: +/- Cent Menu  
DblClk: Menu - PkAt  
Selecting Residues  
State 1/ 1
```

The PyMOL prompt at the bottom left is `PyMOL>_`.

Nous voulons sauvegarder l'objet (la molécule) vdn

The PyMOL Molecular Graphics System

File Edit Build Movie Display Setting Scene Mouse Wizard Plugin Help

Open...
 Save Session
 Save Session As...
 Save Molecule...
 Save Image As
 Save Movie As
 Log...
 Resume...
 Append...
 Close Log
 Run...
 Quit
 Reinitialize
 Skin

```

E: RIBOSOMAL PROTEIN L30;
F:
50S RIBOSOMAL PROTEIN L30P, HMAL30, HL20, HL16;
23;
E: RIBOSOMAL PROTEIN L31E;
U:
50S RIBOSOMAL PROTEIN L31E, L34, HL30;
24;
E: RIBOSOMAL PROTEIN L32E;
V:
50S RIBOSOMAL PROTEIN L32E, HL5;
25;
E: RIBOSOMAL PROTEIN L37AE;
N:
26;
E: RIBOSOMAL
K:
50S RIBOS
27;
E: RIBOSOMA
Y:
50S RIBOS
28;
E: RIBOSOMA
Z:
50S RIBOS
COMPND 108 SYNONYM: 50S RIBOS
COMPND 109 MOL_ID: 29;
COMPND 110 MOLECULE: RIBOSOMA
COMPND 111 CHAIN: 1;
COMPND 112 SYNONYM: 50S RIBOS
ObjectMolecule: Read crystal
Symmetry: Found 8 symmetry o
CmdLoad: "C:/Documents and S
HEADER
HYDROLASE
TITLE
CRYSTAL STRUCTURE O
TITLE 2 WITH VARDENAFIL(L
COMPND
MOL_ID: 1;
COMPND 2 MOLECULE: CGMP-SPE
COMPND 3 CHAIN: A;
COMPND 4 FRAGMENT: CATALYTIC DOMAIN;
COMPND 5 SYNONYM: PDE5, PHOSPHODIESTERASE 5;
COMPND 6 EC: 3.1.4.17;
COMPND 7 ENGINEERED: YES
ObjectMolecule: Read secondary structure assignments.
ObjectMolecule: Read crystal symmetry information.
Symmetry: Found 8 symmetry operators.
CmdLoad: "C:/Documents and Settings/dautant/Bureau/PyMol/1UHO.pdb" loaded as "1UHO".
PyMOL>set_name obj01, vdn
PyMOL>set_name vdn, obj01
PyMOL>set_name obj01, vdn
PyMOL>
  
```

Reset Zoom Orient Draw Ray
 Unpick Deselect Rock Get View
 |< < Stop Play > >| MClear
 Command Builder
 Rebuild Abort

Save

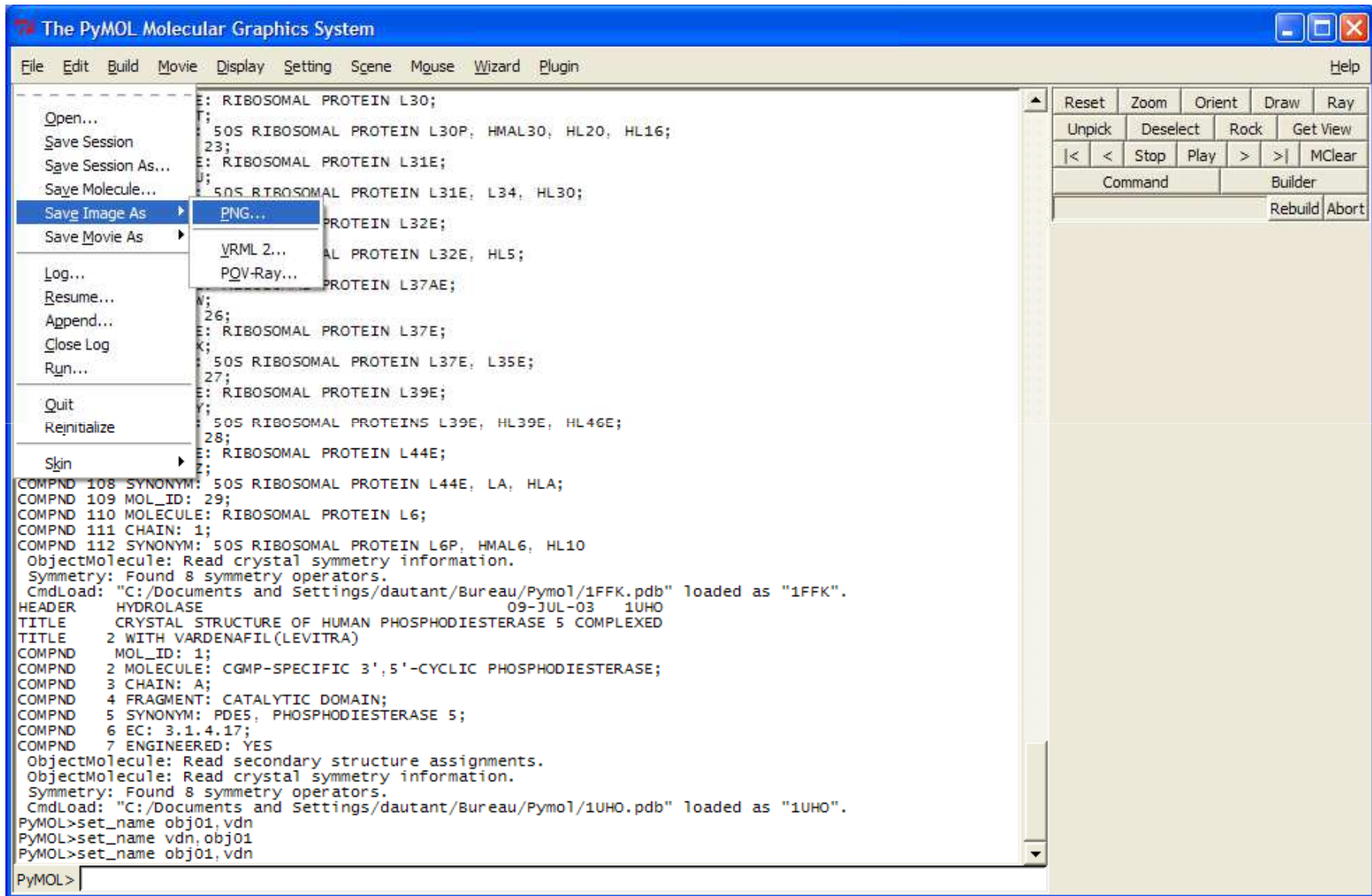
Which object or selection would you like to save?

sele
 1UHO
 vdn

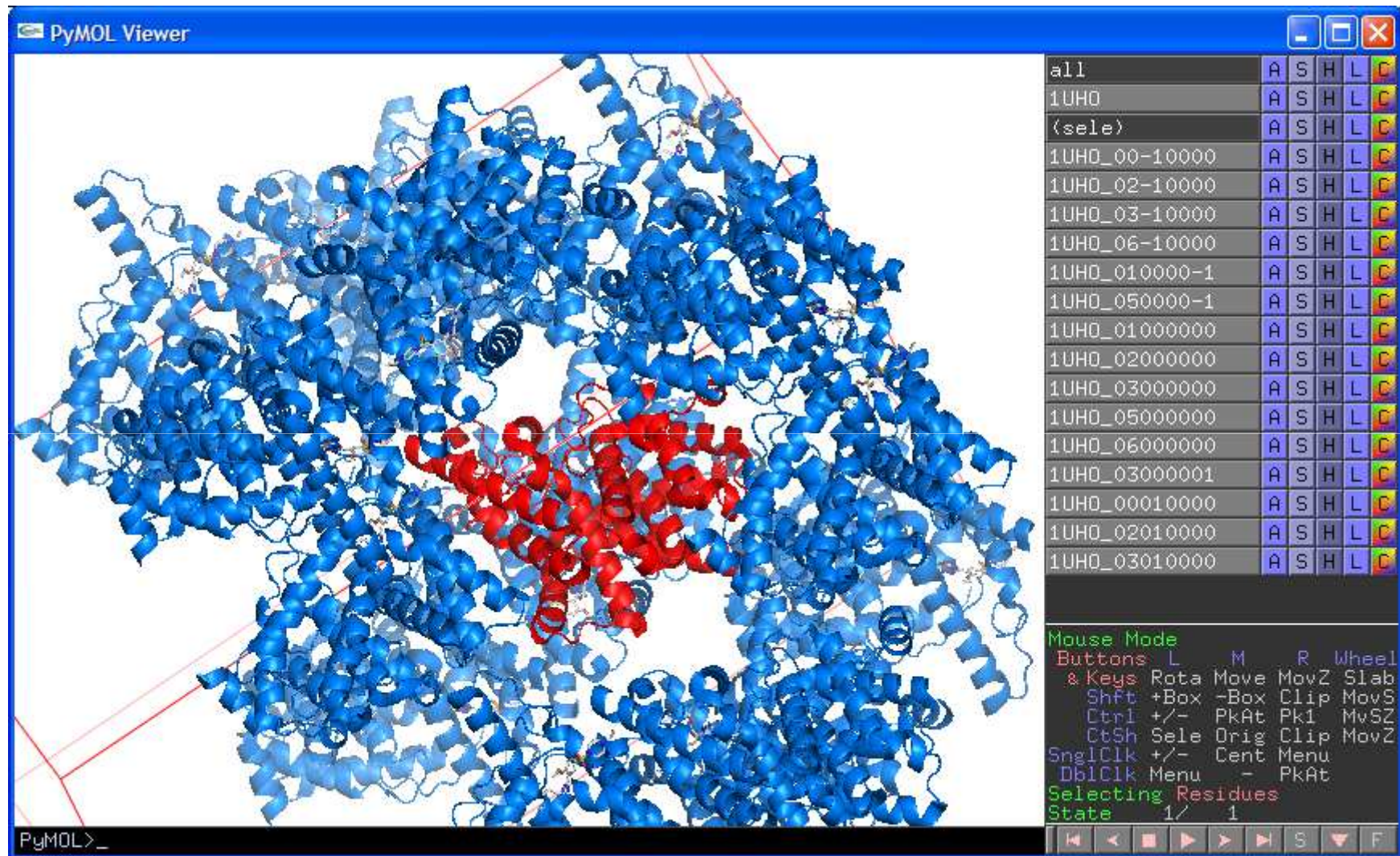
OK Cancel

ded as "1FFK".

Sauvegarde de l'image au format png



Action generate symmetry_mates within_20_A



delete 1uho_*

Faire du « Ball and stick »

```
h_add
```

```
show stick, vdn
```

```
show spheres, vdn
```

```
set sphere_scale = 0.15
```

```
set stick_radius, 0.10
```

```
set orthoscopic = 1
```

```
png ball-and-stick.png
```

```
ls
```

```
pwd
```

```
# labeling syntax
```

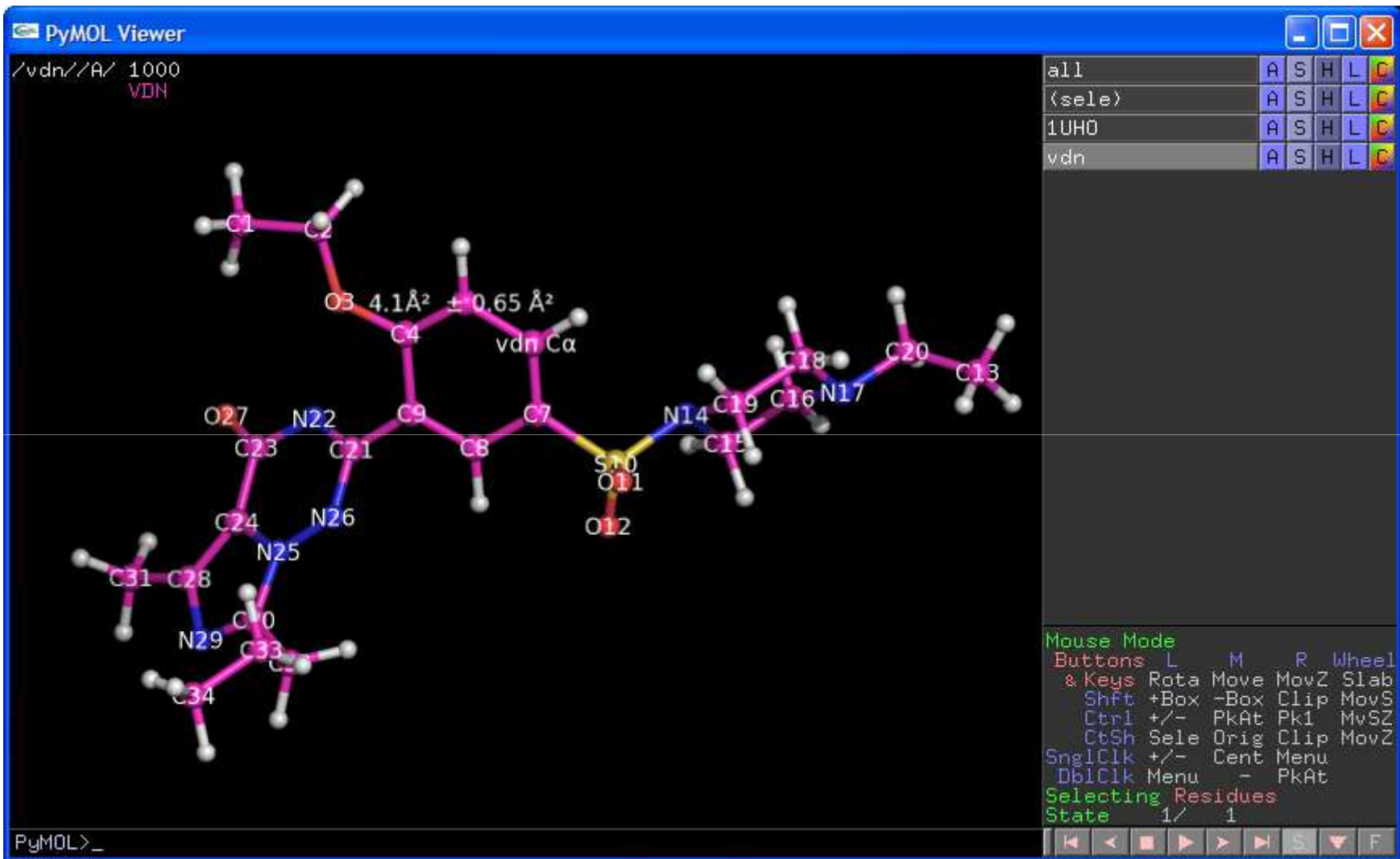
```
label [ selection[, expression]]
```

```
label vdn and name c6, " vdn " + u"C\u03b1"
```

```
set label_size, 40
```

```
set label_position,(2,0,0)
```

```
label vdn and name c5, "4.1" + u"\u00c5\u00b2 \u00b1 0.65 \u00c5\u00b2 "
```



Superposer des molécules (pairwise)

align lactame_L, lactame_D and n. O8+C3+N2+C4+C1

RMS = 0.054 (5 to 5 atoms)

Prendre des mesures et les tracer (Utiliser le Wizard)

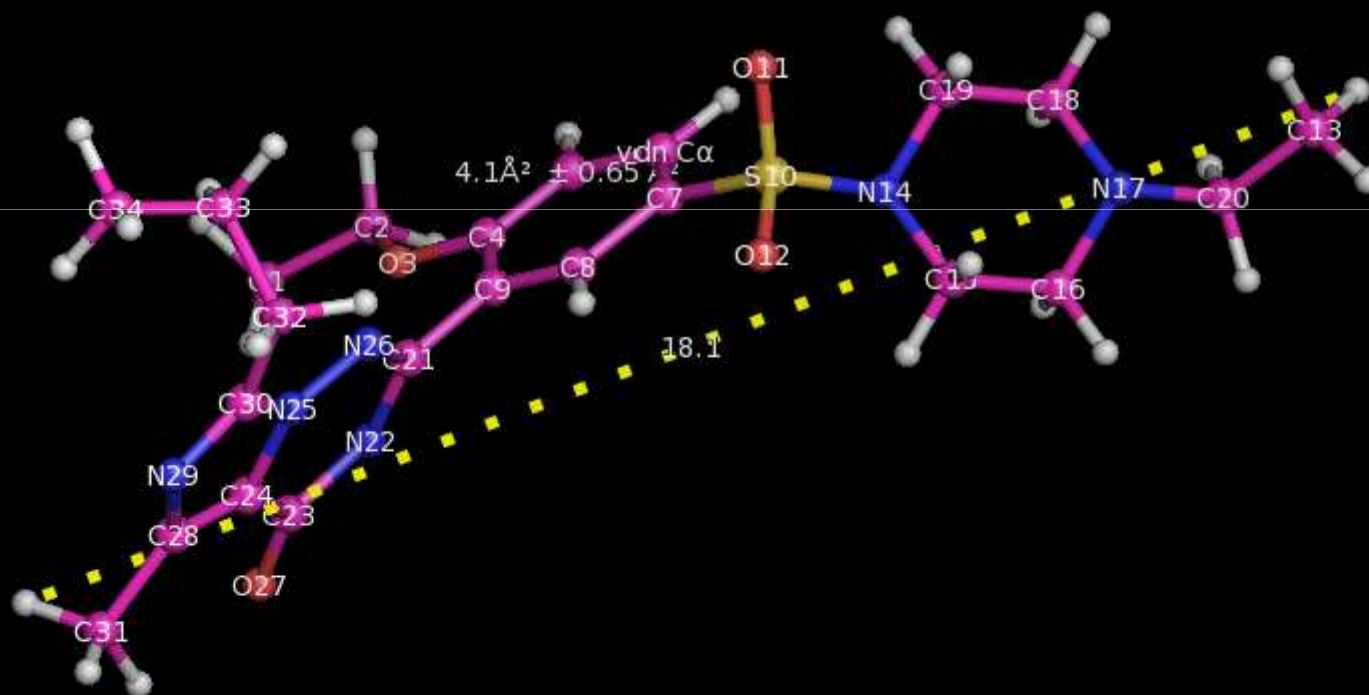
distance dist_1, atom1, atom2, cutoff = 2.5

angle angle_1, angle_1, sele1, sele2, sele3

dihedral dihe_1, atom1, atom2, atom3, atom4

000
DN

click on the first atom...



all
1UHO
vdn
measure01

Measurement

Distances

Create New Object

Delete Last Object

Delete All Measurements

Done

Mouse Mode

Buttons	L	M
& Keys	Rotate	Move
Shift	+Box	-Box
Ctrl	+/-	PkAt
CtSh	Sele	Orig
SnglClk	+/-	Cent
DblClk	Menu	-

Selecting Atoms

Les formats supportés

Entrée

Sortie

Ils sont très nombreux

pse
pml
pdb
png

Les scripts 1huo.pml

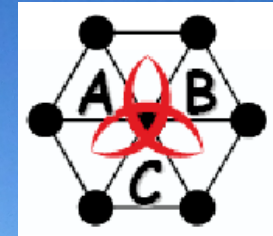
```
load 1UHO.pdb, 1UHO
hide everything, 1UHO
show cartoon, 1UHO
color grey, 1UHO
select vdn, (resn VDN)
show sticks, (vdn)
color wheat, (elem c & vdn)

color red, (elem o & vdn)
color blue, (elem n & vdn)
color orange, (elem s & vdn)
select voisins, (vdn around 6)
delete vdn
hide everything, (voisins)
show surface, (voisins)
color marine, (voisins)
rotate x, 140, (1UHO)
hide everything, (resi 663,664)
zoom (voisins)
delete voisins
ray
```

Rendez vous à Bordeaux

AFC 2013

2-5 juillet 2013



<http://www.afc.asso.fr/>



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afc2013@ibgc.cnrs.fr