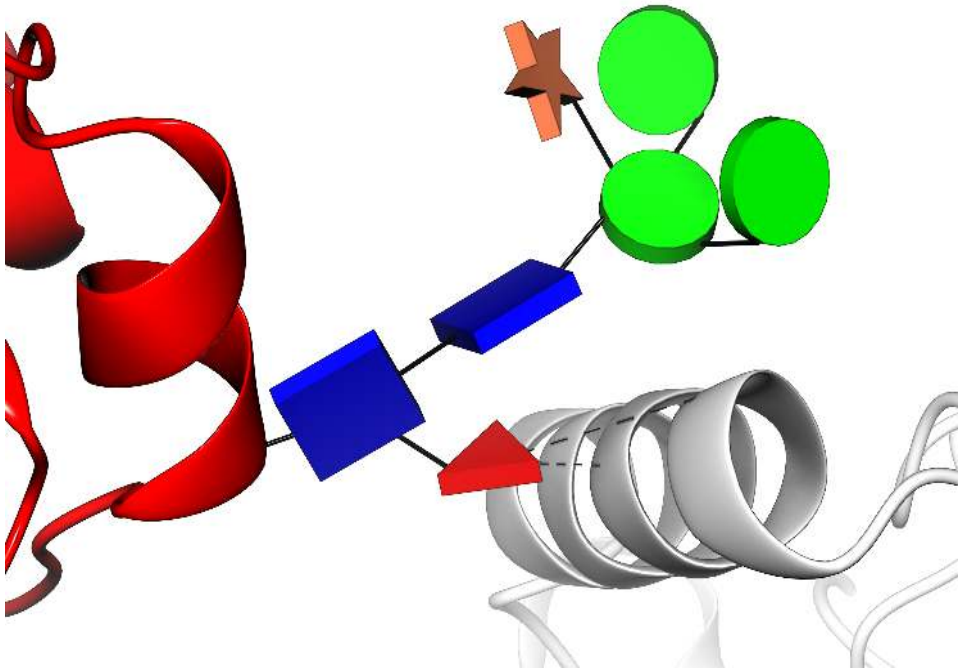
CCP4MG



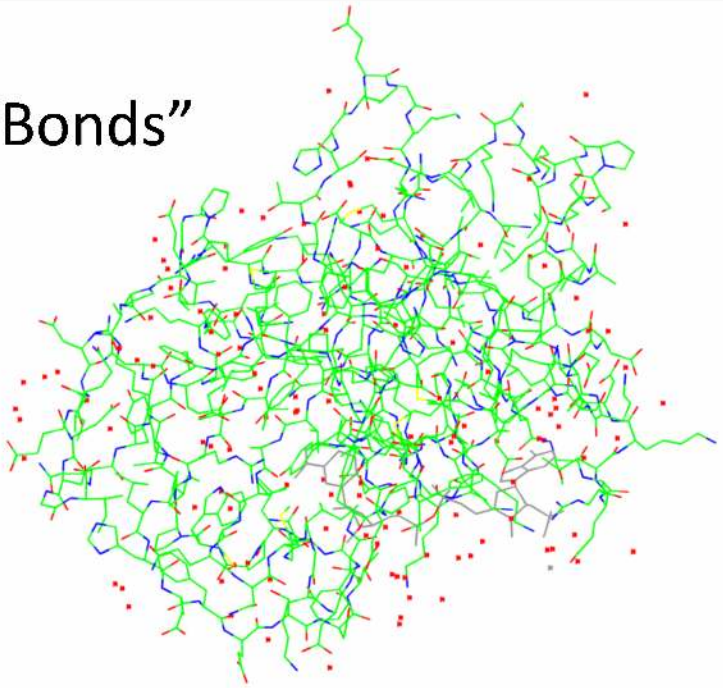
Stuart McNicholas, CCP4MG

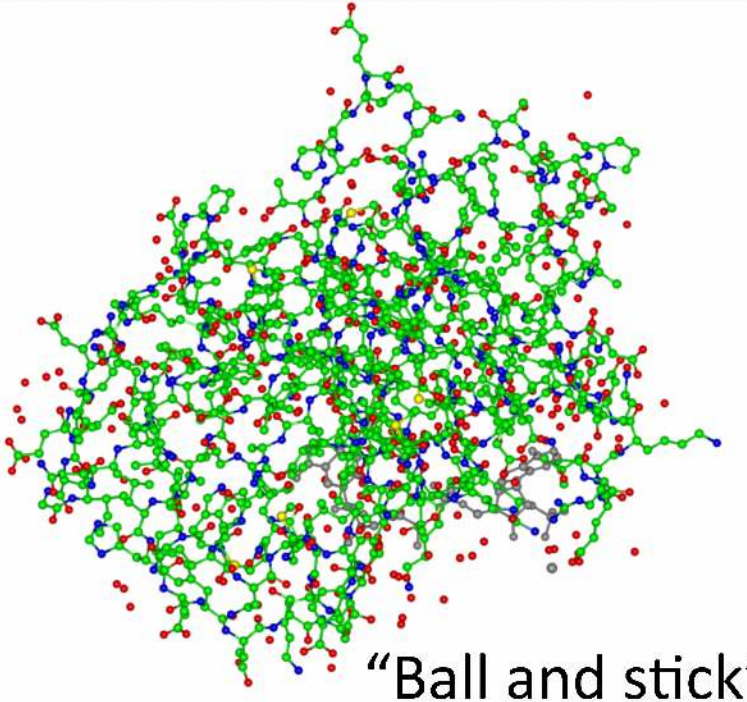
Diamond/CCP4 Workshop 2015

Introduction

- CCP4MG is a molecular graphics program funded by CCP4.
- Its primary focus is the visualization and analysis of macromolecular structure.
- It produces high quality rendered images and movies.
- http://www.ccp4.ac.uk/MG/
  - Binaries for Windows, Mac and Linux.
  - Source code freely available.

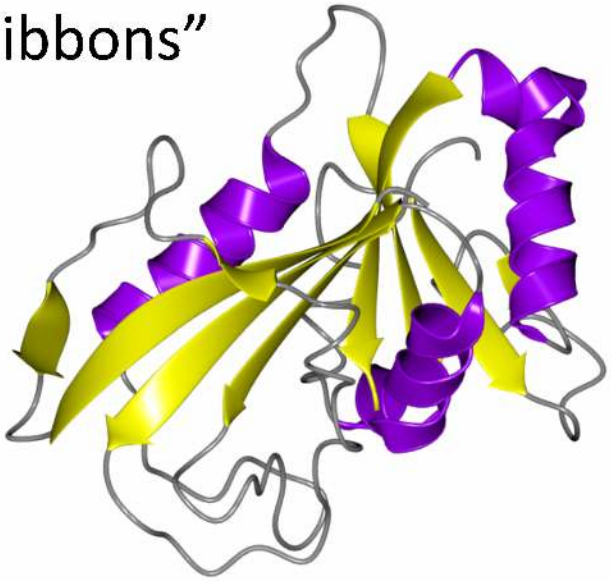
"Bonds"

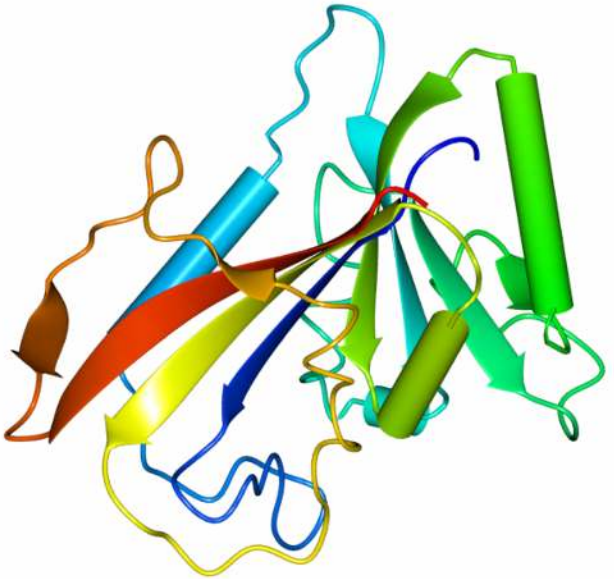




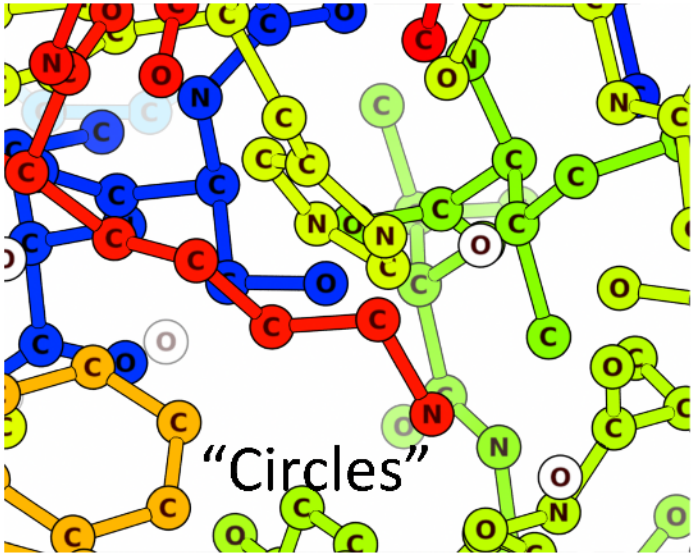
"Ball and stick"

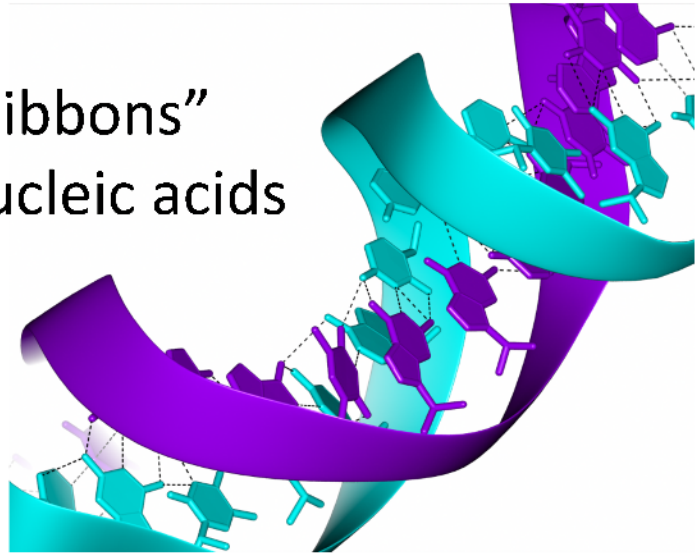
"Ribbons"

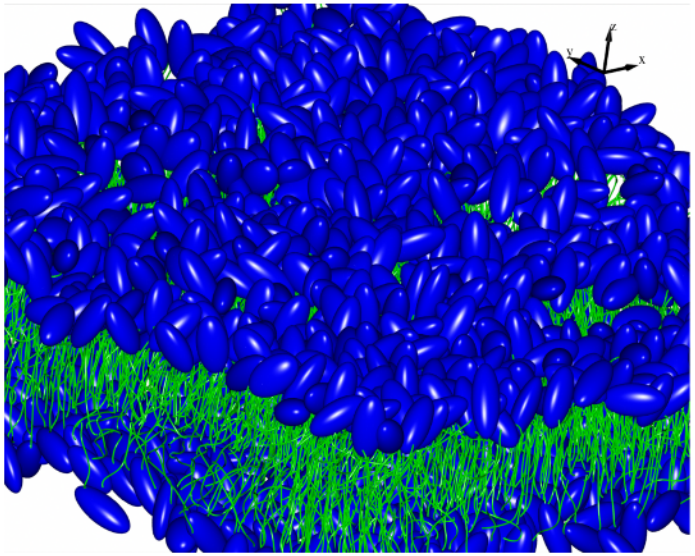




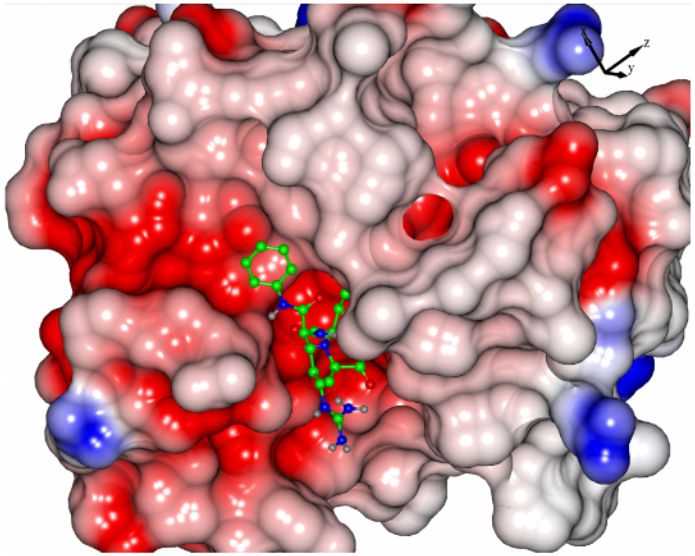
"Worms/tubes"



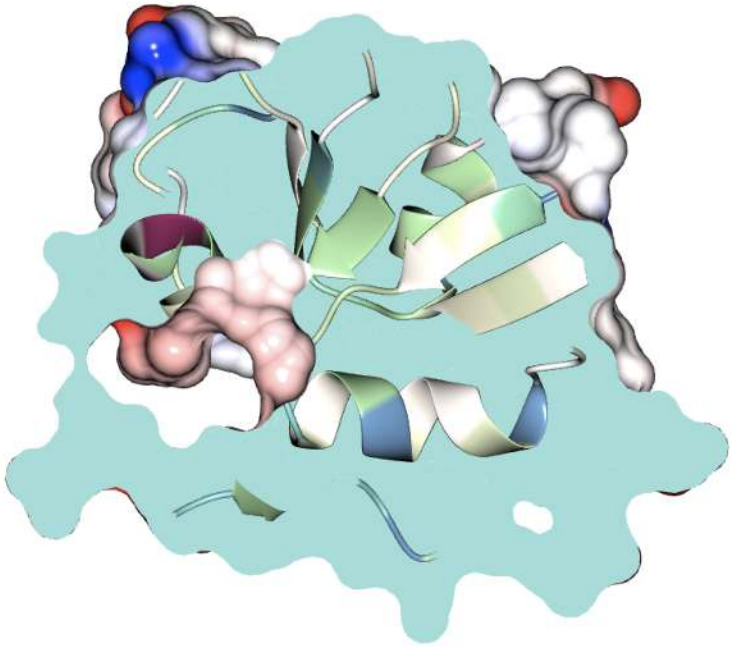


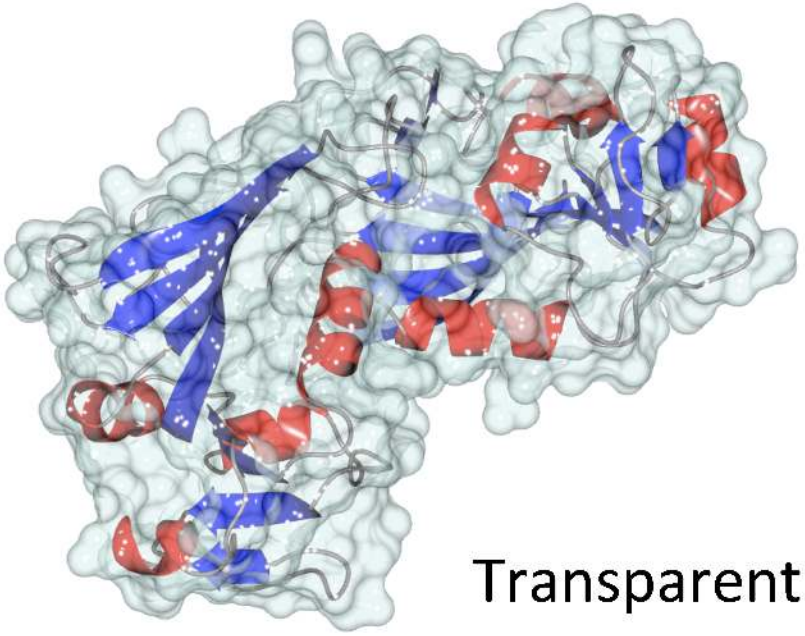


"Lipid Cartoon"



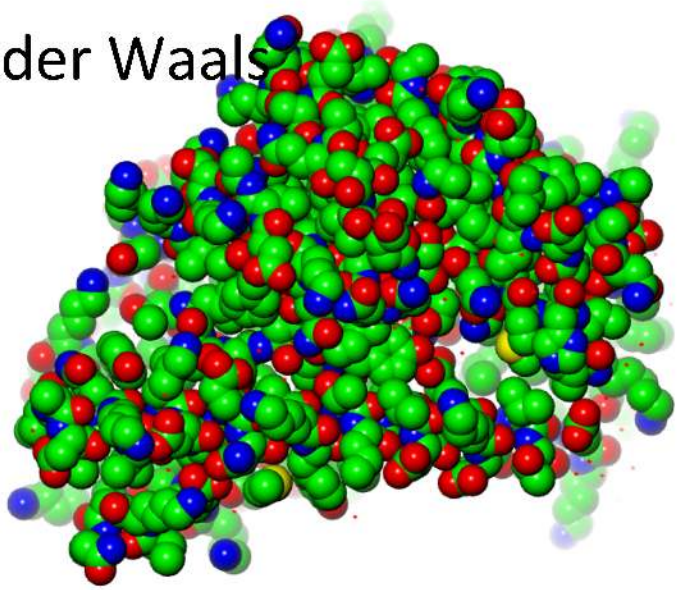
Electrostatic surface

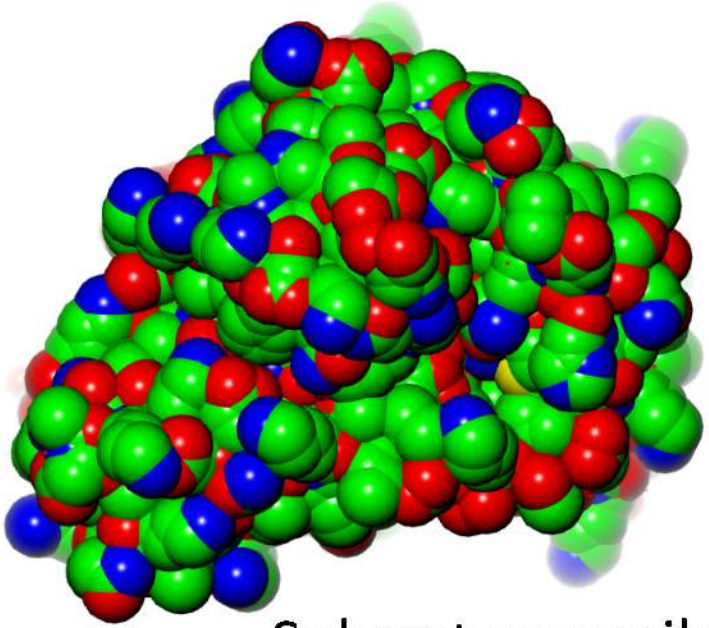




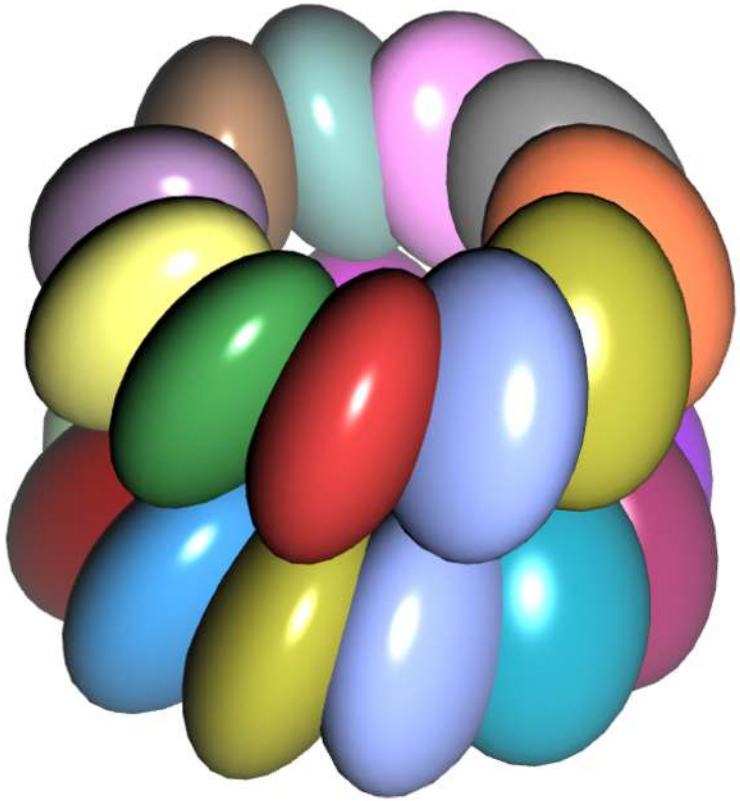
Transparent

Van der Waals

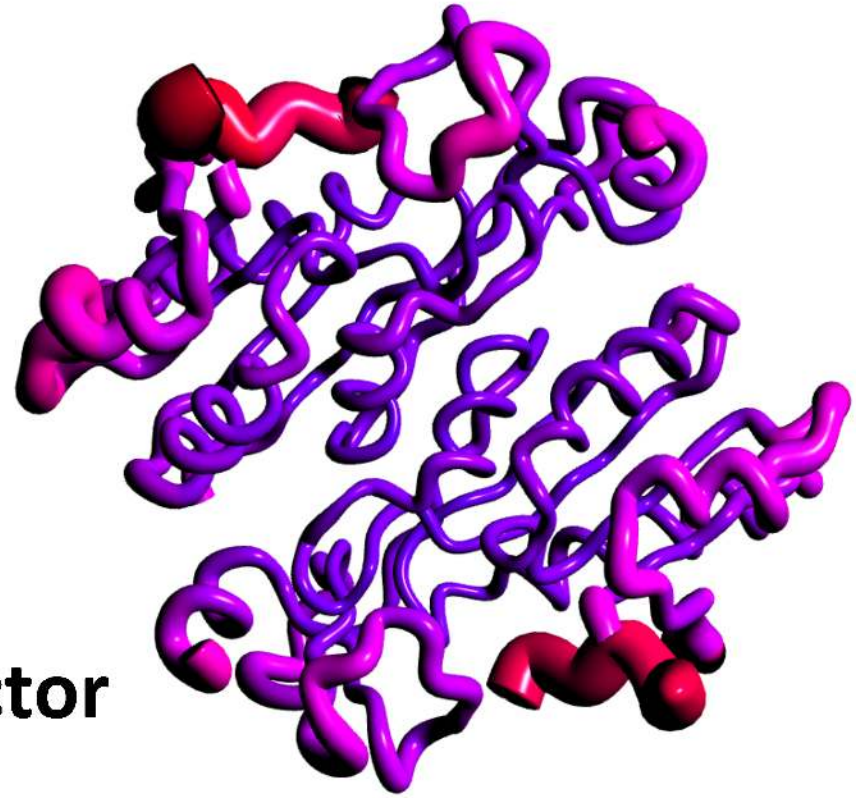




Solvent accessible

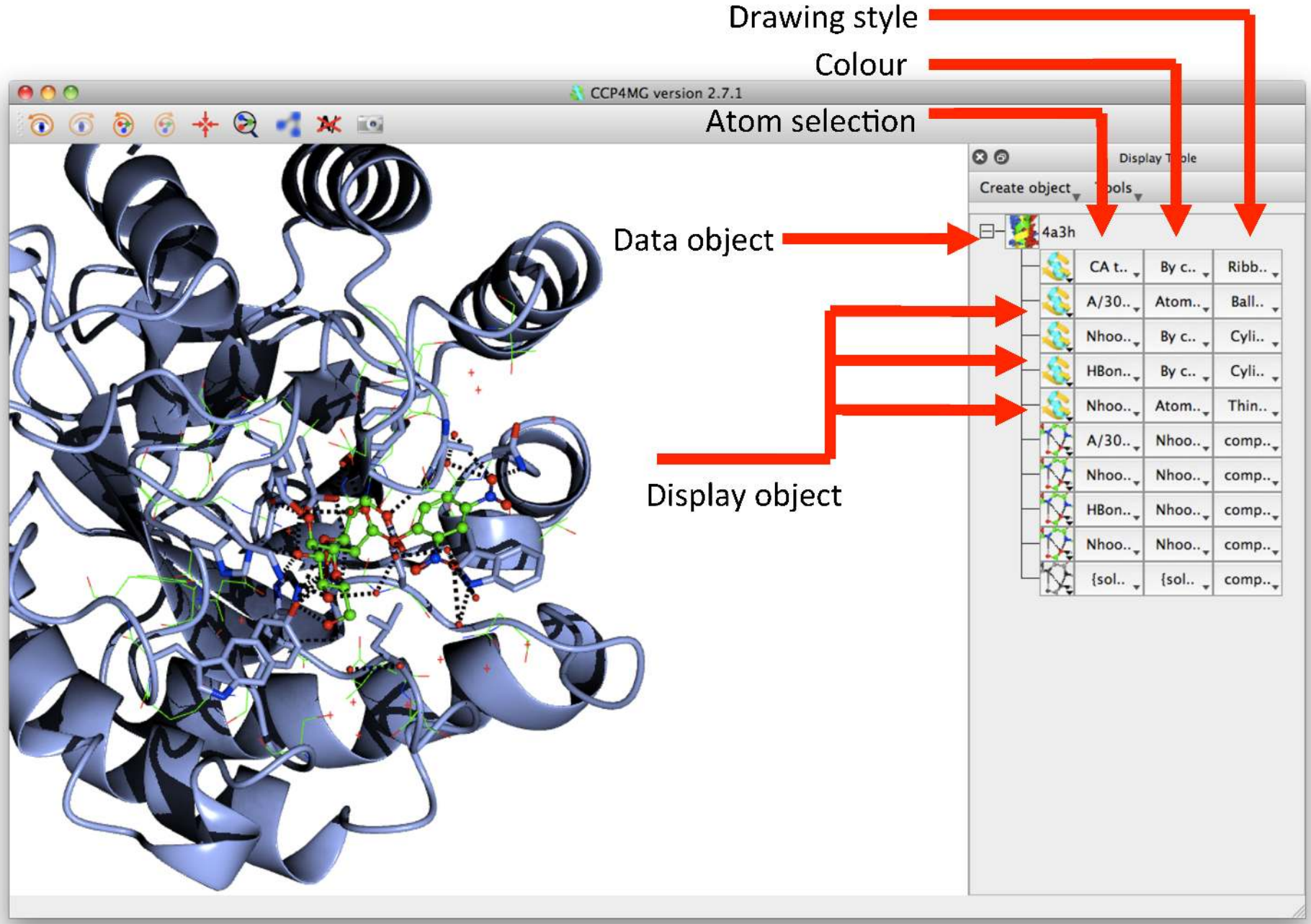


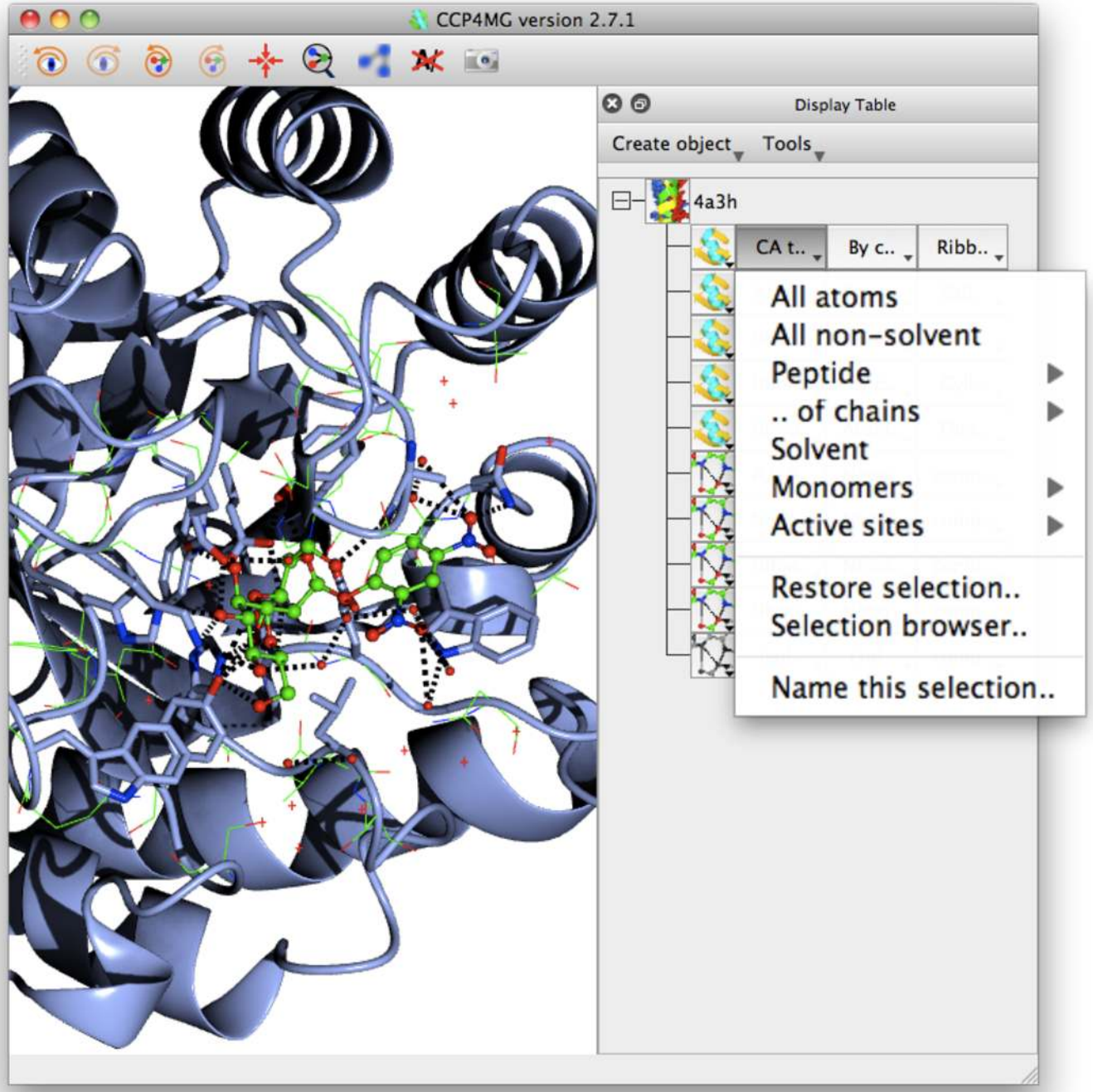
Bloboids



Worm scaled by Temperature factor

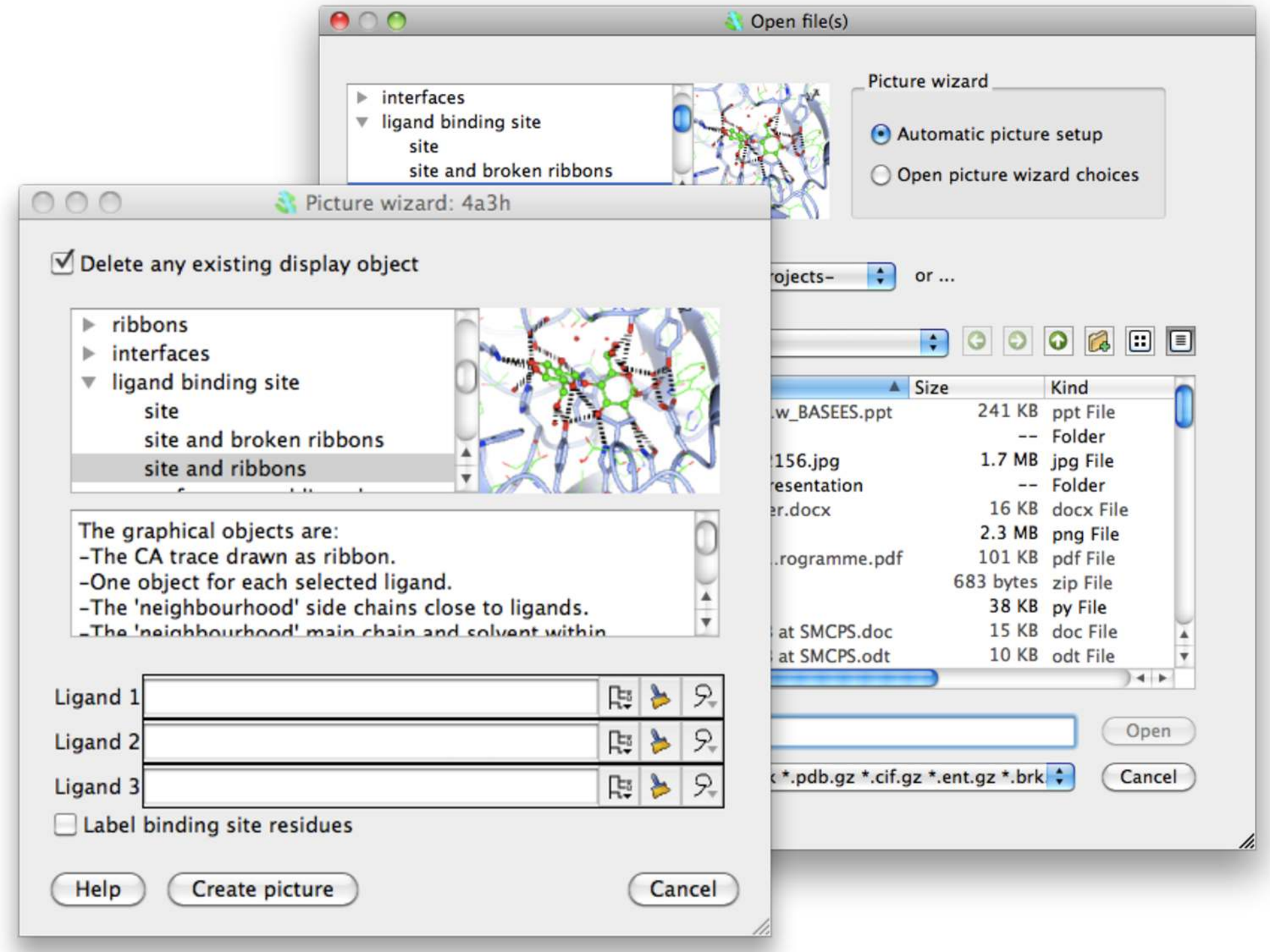
Basic user Interface

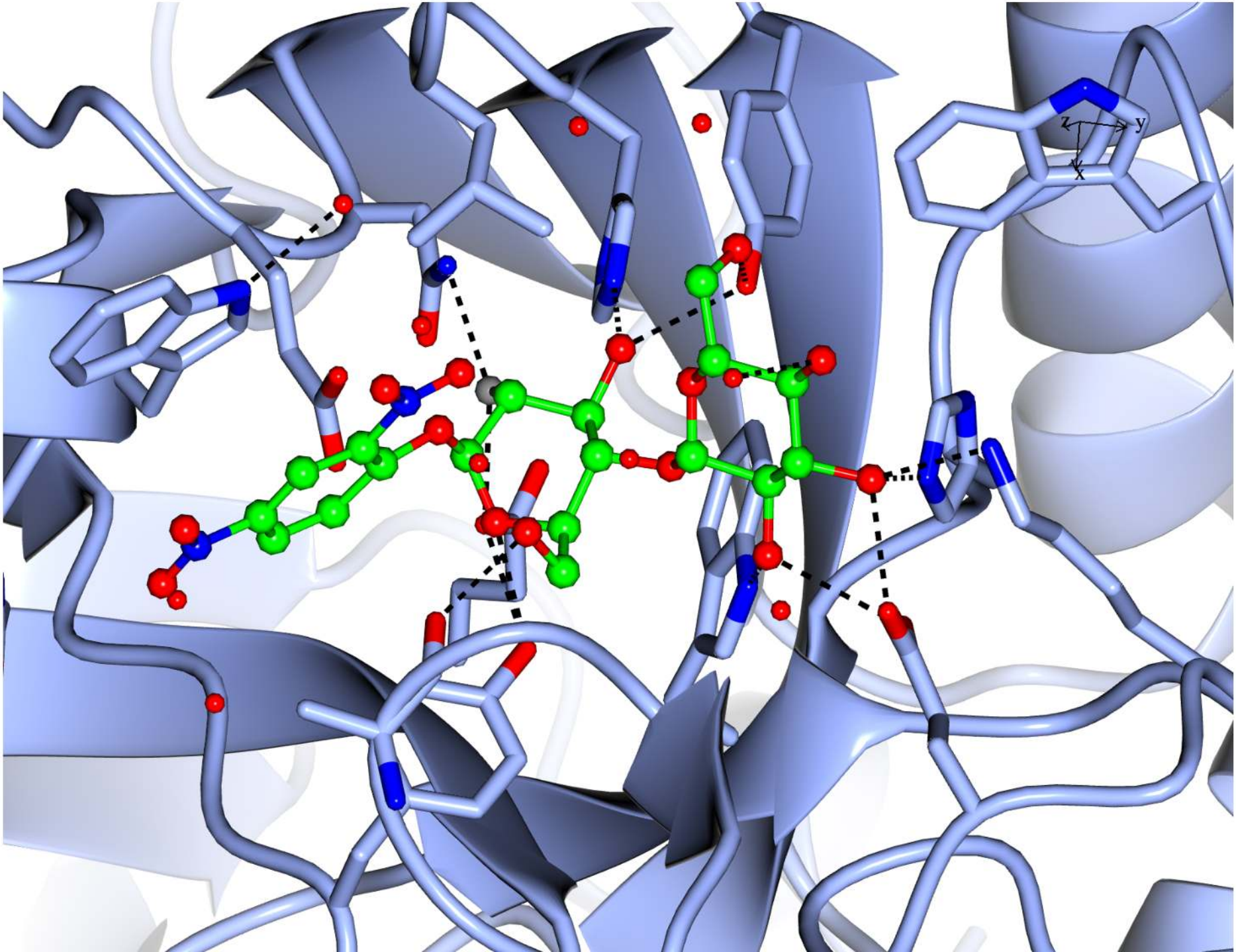

Drawing style
Colour
Atom selection
CCP4MG version 2.7.1
Data object
Display object
Create object
4a3h
CA t..
By c..
Ribb..
A/30..
Atom..
Ball..
Nhoo..
By c..
Cyli..
HBon..
By c..
Cyli..
Nhoo..
Atom..
Thin..
A/30..
Nhoo..
comp..
Nhoo..
Nhoo..
comp..
HBon..
Nhoo..
comp..
Nhoo..
Nhoo..
comp..
{sol..
{sol..
comp..

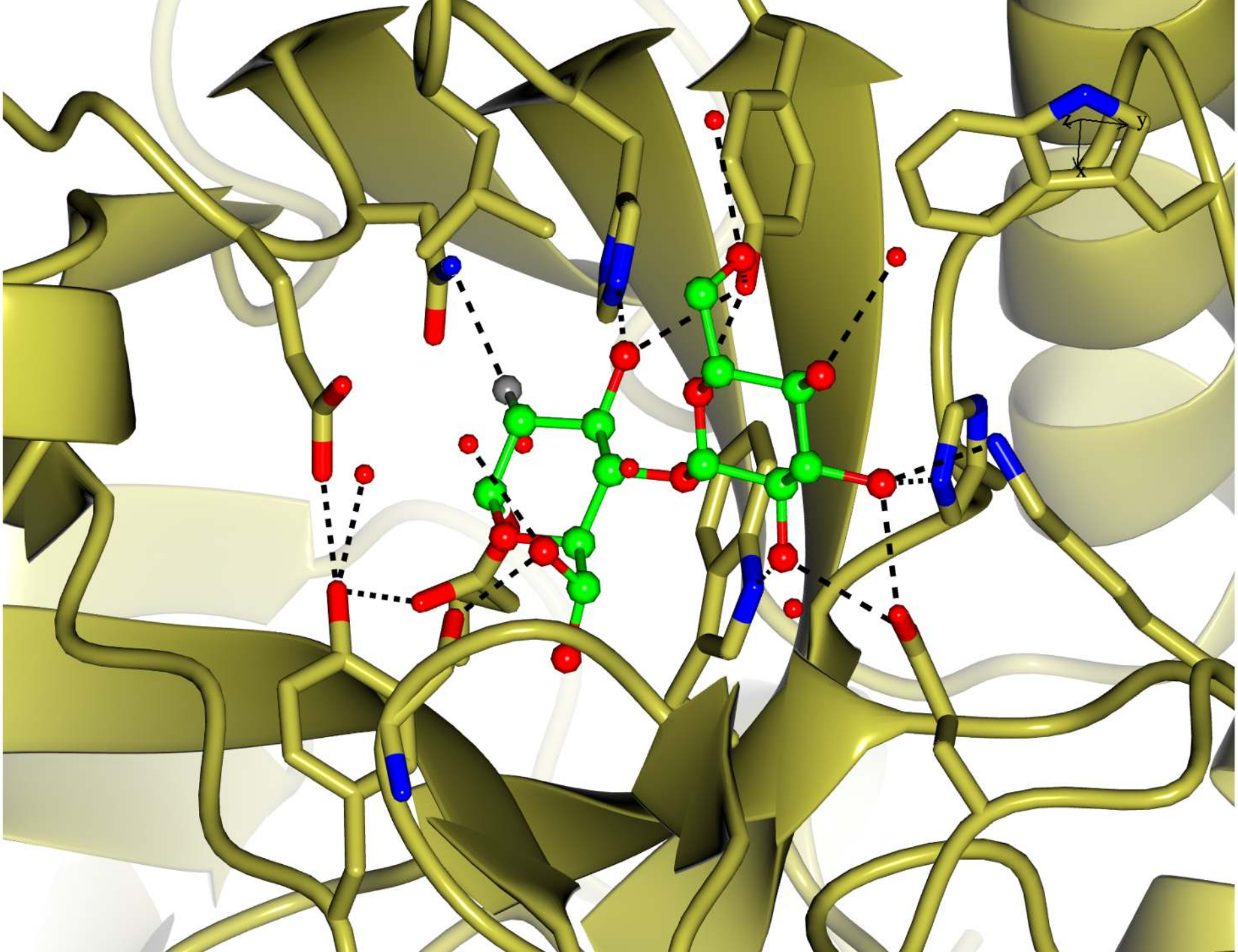

CCP4MG version 2.7.1
Display Table
Create object
Tools
4a3h
CA t..
By c..
Ribb..
All atoms
All non-solvent
Peptide
.. of chains
Solvent
Monomers
Active sites
Restore selection..
Selection browser..
Name this selection..

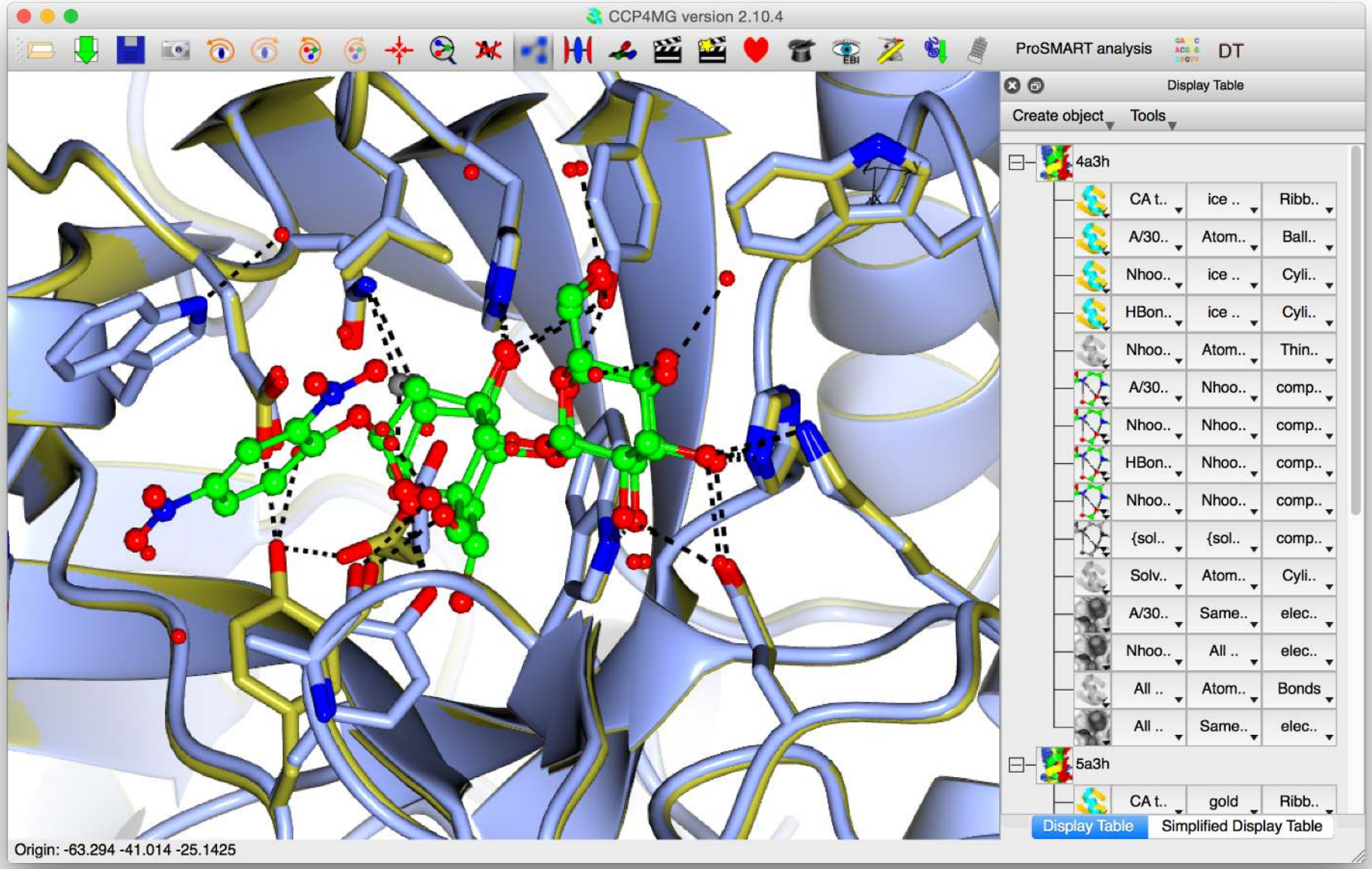
Picture Wizard

- The picture wizard is an automatic way of generating complex scenes with multiple selections, colouring, styles, etc.
- Representations are organised into various “styles”
- The picture wizard is shown at the top of the file browser window when a coordinate file is loaded, or can be accessed from the display table.

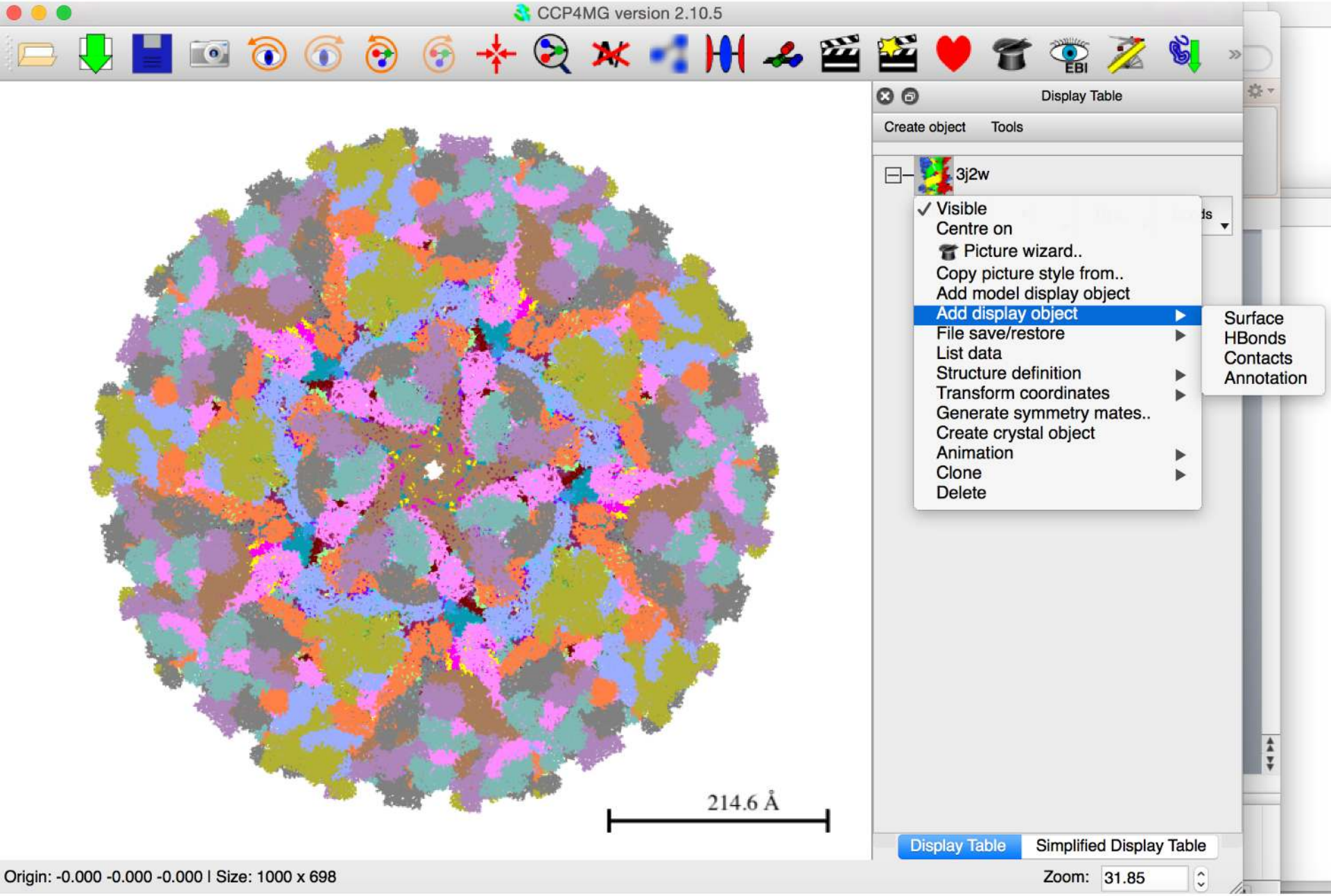

Open file(s)
interfaces
ligand binding site
site
site and broken ribbons
Picture wizard
Automatic picture setup
Open picture wizard choices
or ...
Size
Kind
w_BASEES.ppt 241 KB ppt File
-- Folder
156.jpg 1.7 MB jpg File
esentation -- Folder
r.docx 16 KB docx File
2.3 MB png File
rogramme.pdf 101 KB pdf File
683 bytes zip File
38 KB py File
at SMCPS.doc 15 KB doc File
at SMCPS.odt 10 KB odt File
Open
*.pdb.gz *.cif.gz *.ent.gz *.brk
Cancel
Picture wizard: 4a3h
Delete any existing display object
ribbons
interfaces
ligand binding site
site
site and broken ribbons
site and ribbons
The graphical objects are:
-The CA trace drawn as ribbon.
-One object for each selected ligand.
-The 'neighbourhood' side chains close to ligands.
Ligand 1
Ligand 2
Ligand 3
Label binding site residues
Help
Create picture
Cancel

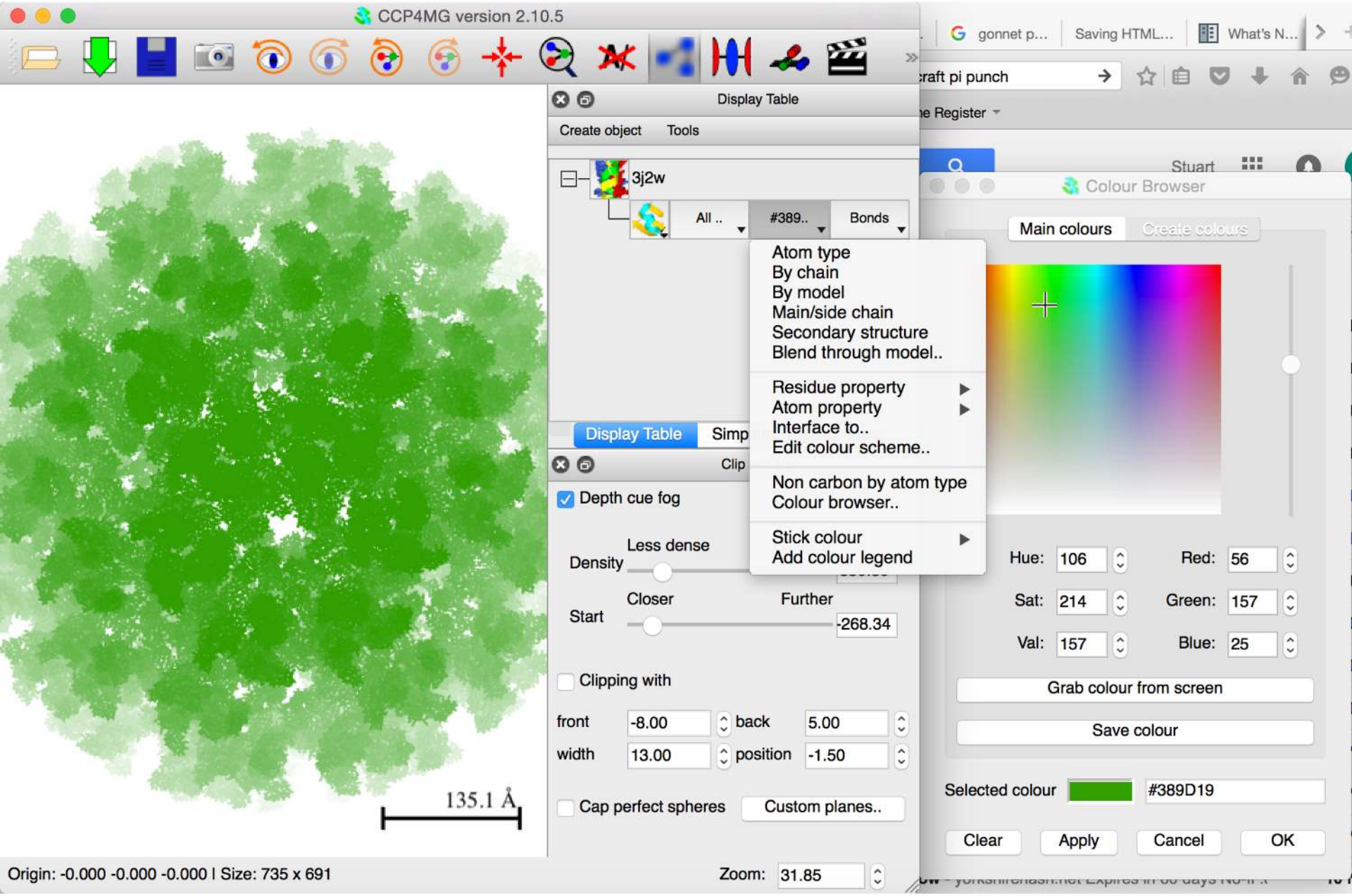

z
y
x

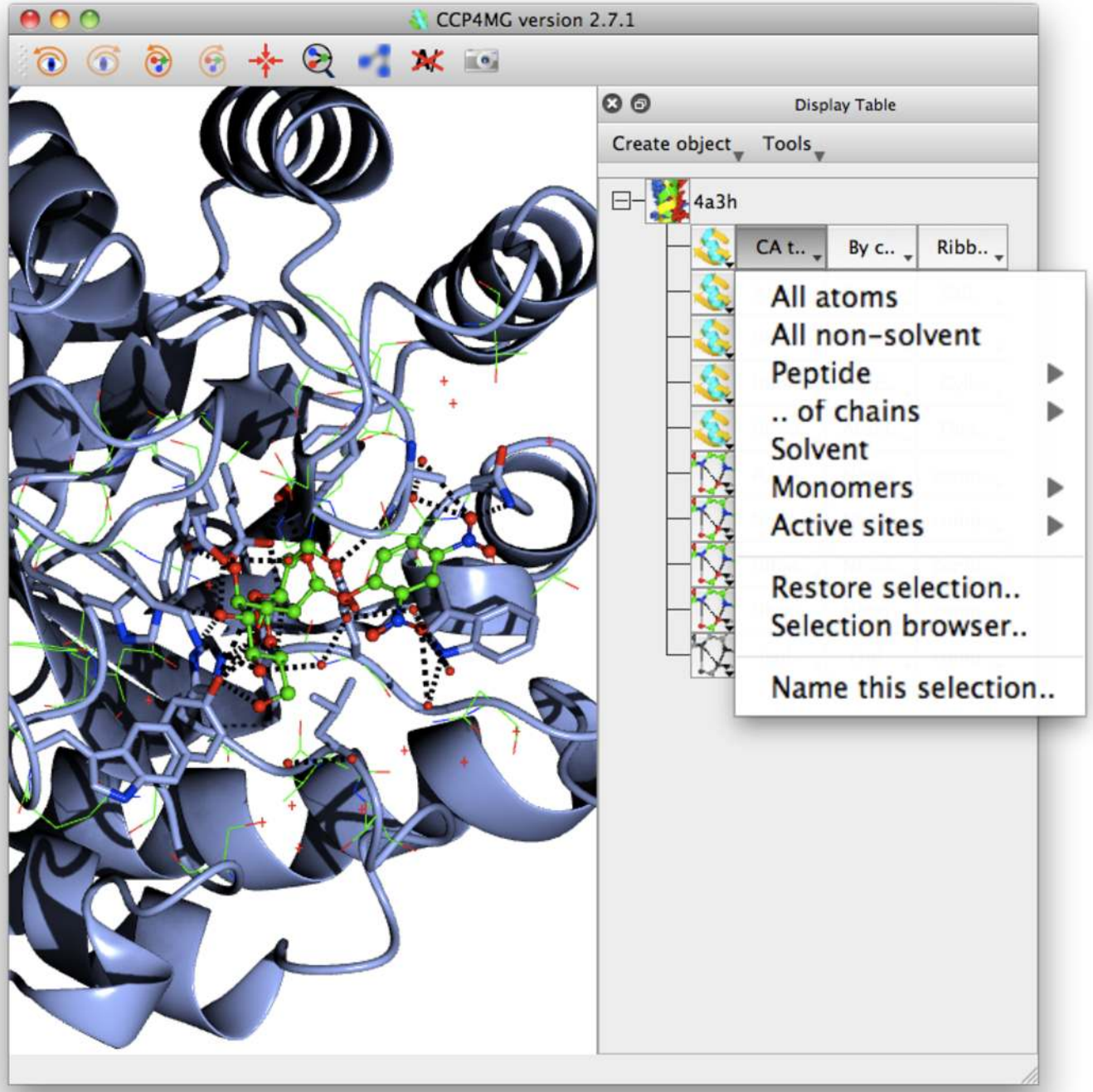

z
y
x

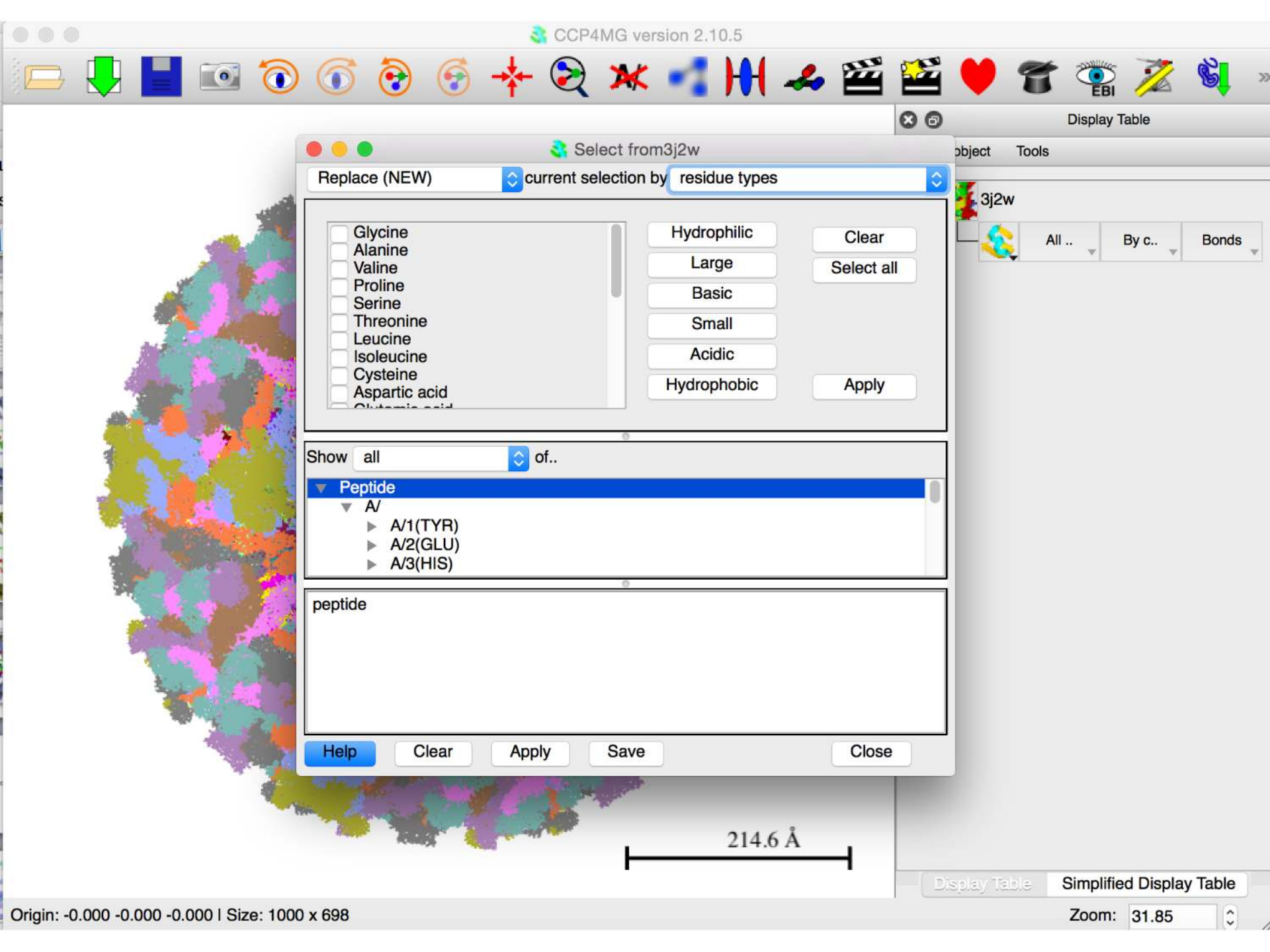

CCP4MG version 2.10.4
ProSMART analysis
DT
Display Table
Create object
Tools
4a3h
CA t.. ice .. Ribb..
A/30.. Atom.. Ball..
Nhoo.. ice .. Cyli..
HBon.. ice .. Cyli..
Nhoo.. Atom.. Thin..
A/30.. Nhoo.. comp..
Nhoo.. Nhoo.. comp..
HBon.. Nhoo.. comp..
Nhoo.. Nhoo.. comp..
{sol.. {sol.. comp..
Solv.. Atom.. Cyli..
A/30.. Same.. elec..
Nhoo.. All .. elec..
All .. Atom.. Bonds
All .. Same.. elec..
5a3h
CA t.. gold Ribb..
Display Table
Simplified Display Table
Origin: -63.294 -41.014 -25.1425

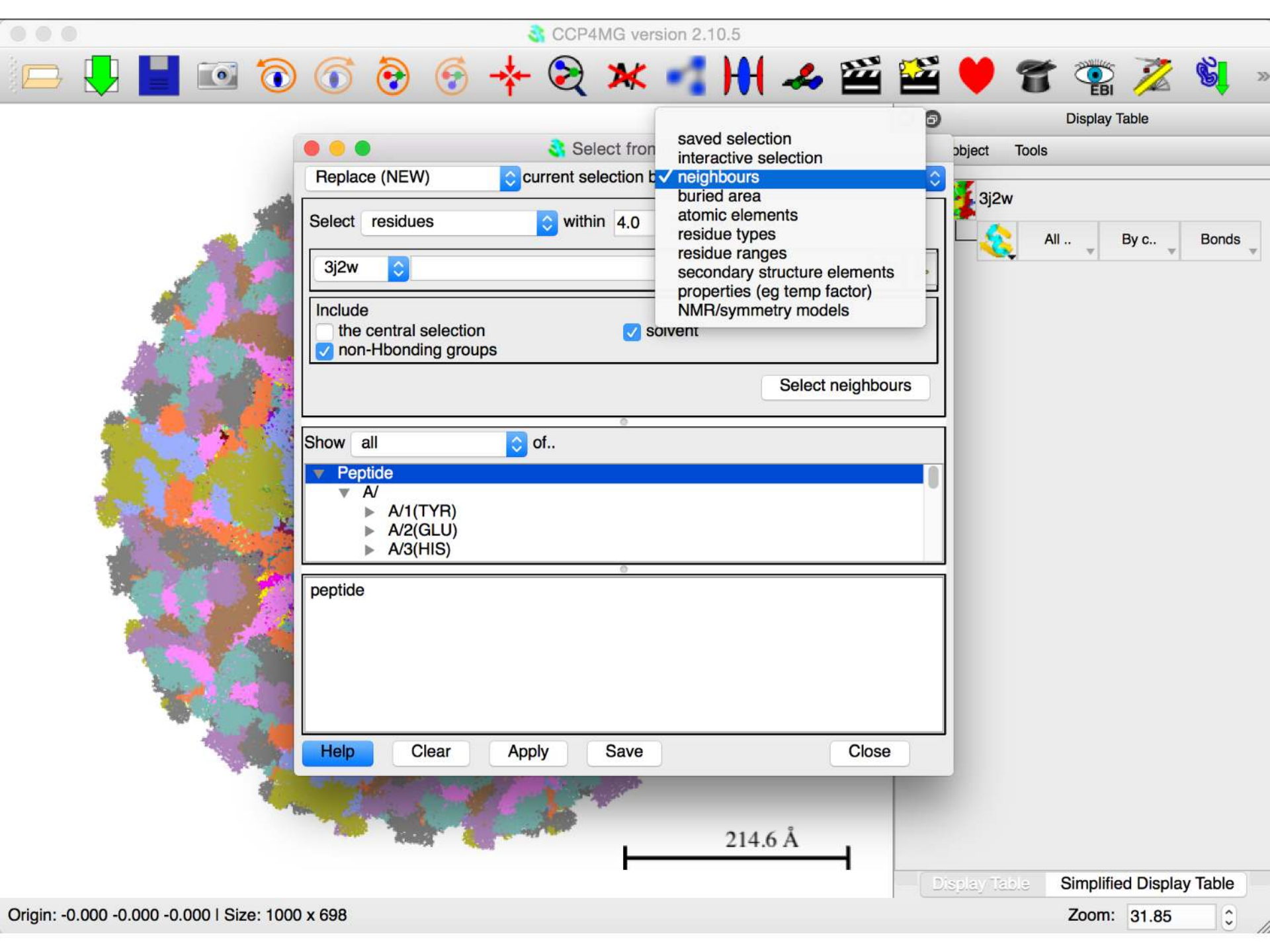
Doing it all Manually

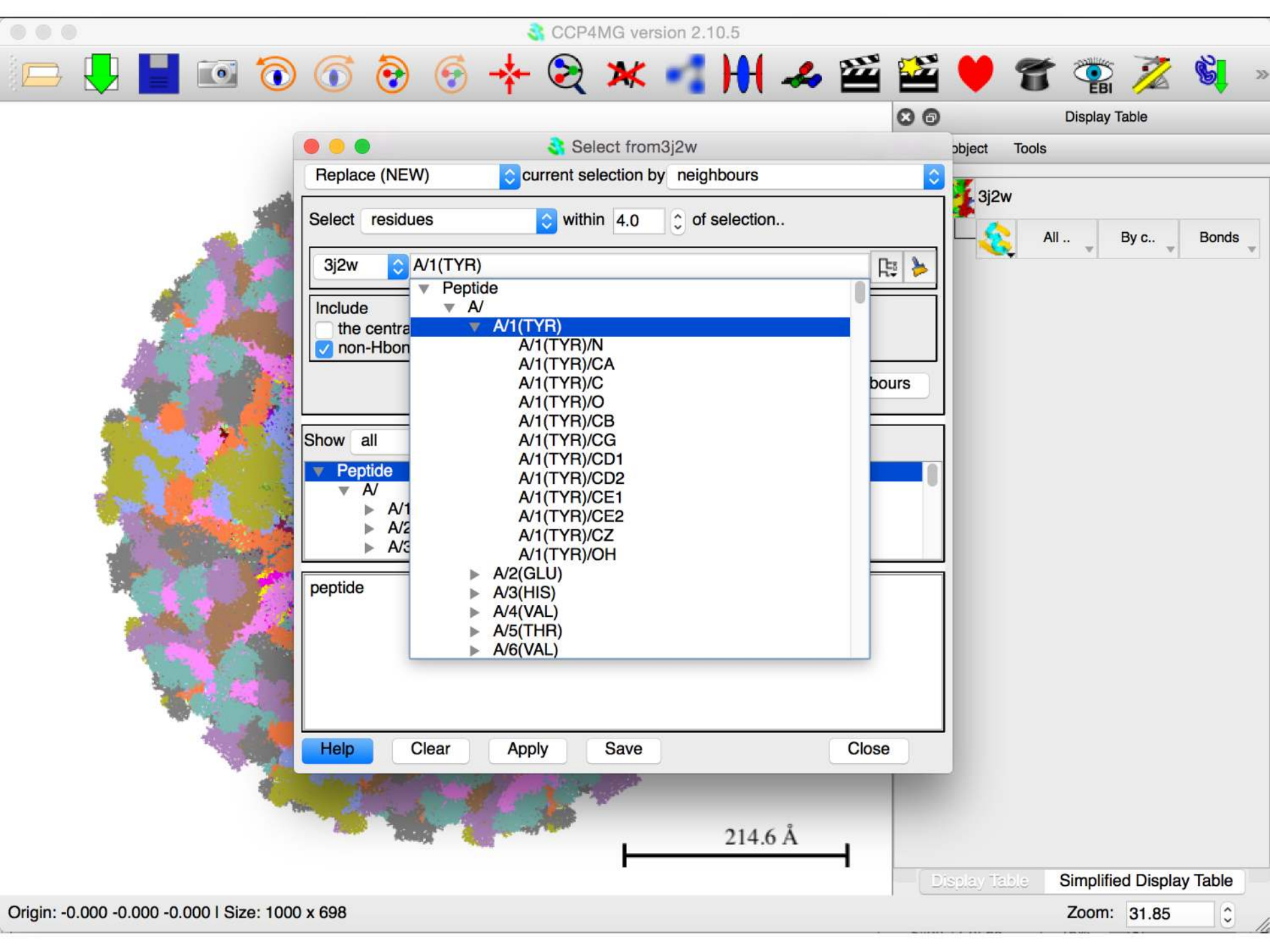

CCP4MG version 2.10.5
Display Table
Create object
Tools
3j2w
Visible
Centre on
Picture wizard..
Copy picture style from..
Add model display object
Add display object
File save/restore
List data
Structure definition
Transform coordinates
Generate symmetry mates..
Create crystal object
Animation
Clone
Delete
Surface
HBonds
Contacts
Annotation
214.6 Å
Display Table
Simplified Display Table
Origin: -0.000 -0.000 -0.000 | Size: 1000 x 698
Zoom: 31.85


CCP4MG version 2.10.5
Display Table
Create object
Tools
3j2w
All ..
#389..
Bonds
Atom type
By chain
By model
Main/side chain
Secondary structure
Blend through model..
Residue property
Atom property
Interface to..
Edit colour scheme..
Non carbon by atom type
Colour browser..
Stick colour
Add colour legend
Display Table
Simp
Clip
Depth cue fog
Density
Less dense
Start
Closer
Further
-268.34
Clipping with
front
-8.00
back
5.00
width
13.00
position
-1.50
Cap perfect spheres
Custom planes..
135.1 Å
Origin: -0.000 -0.000 -0.000 I Size: 735 x 691
Zoom:
31.85
Colour Browser
Main colours
Create colours
Hue:
106
Sat:
214
Val:
157
Red:
56
Green:
157
Blue:
25
Grab colour from screen
Save colour
Selected colour
#389D19
Clear
Apply
Cancel
OK

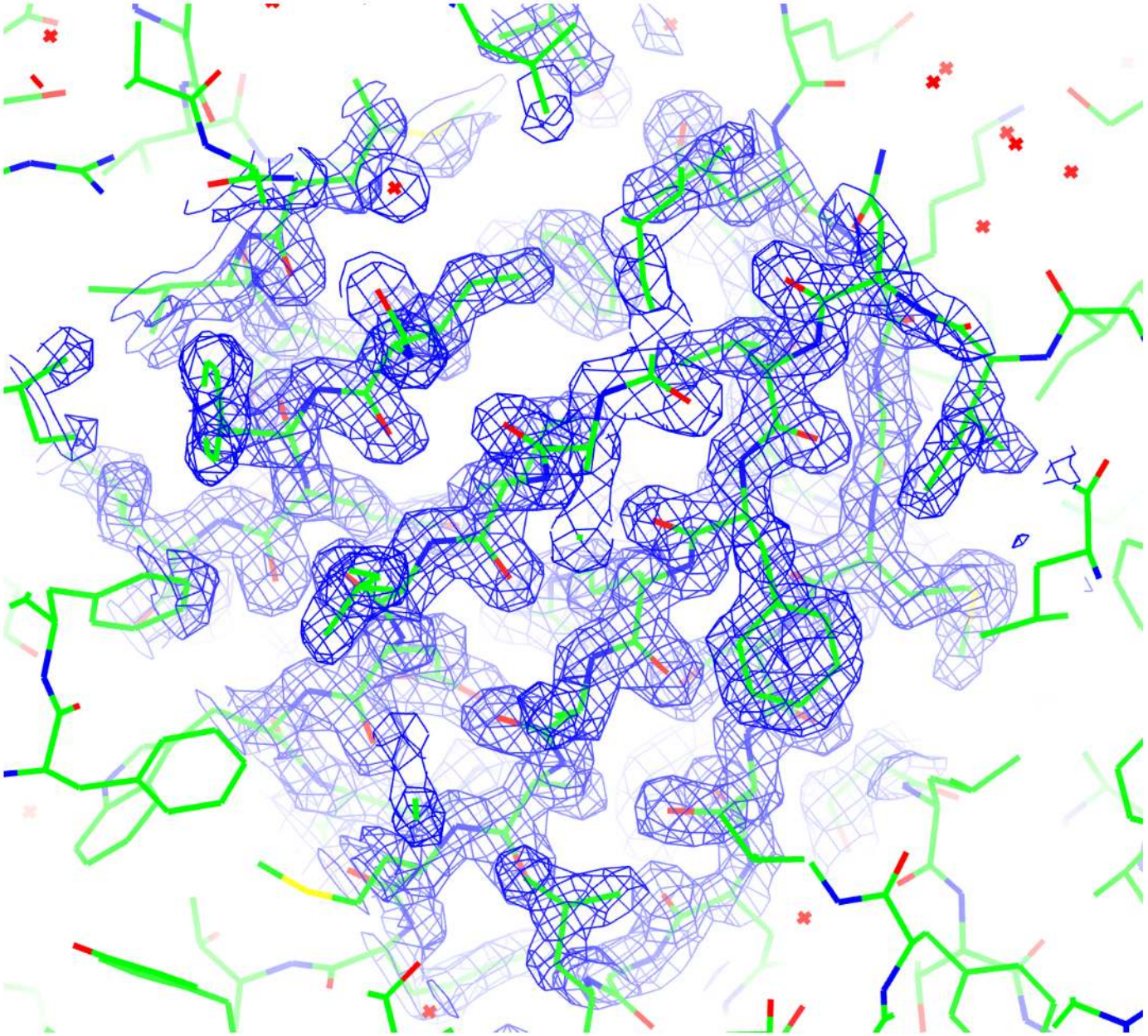

CCP4MG version 2.7.1
Display Table
Create object
Tools
4a3h
CA t..
By c..
Ribb..
All atoms
All non-solvent
Peptide
.. of chains
Solvent
Monomers
Active sites
Restore selection..
Selection browser..
Name this selection..

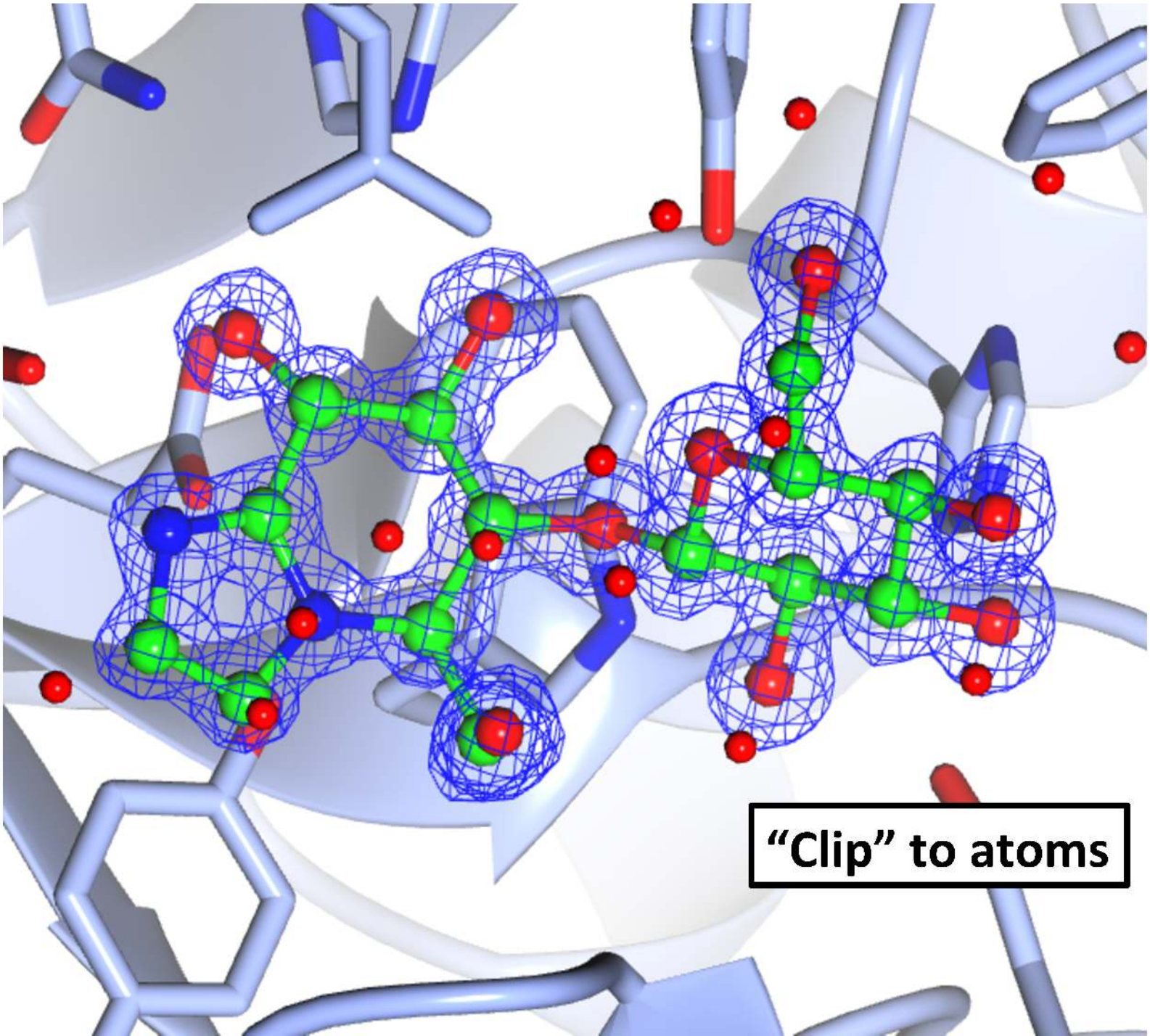

CCP4MG version 2.10.5
Display Table
Select from3j2w
Replace (NEW)
current selection by
residue types
Glycine
Alanine
Valine
Proline
Serine
Threonine
Leucine
Isoleucine
Cysteine
Aspartic acid
Hydrophilic
Large
Basic
Small
Acidic
Hydrophobic
Clear
Select all
Apply
Show
all
of..
Peptide
A/
A/1(TYR)
A/2(GLU)
A/3(HIS)
peptide
Help
Clear
Apply
Save
Close
3j2w
All ..
By c..
Bonds
214.6 Å
Display Table
Simplified Display Table
Origin: -0.000 -0.000 -0.000 I Size: 1000 x 698
Zoom:
31.85

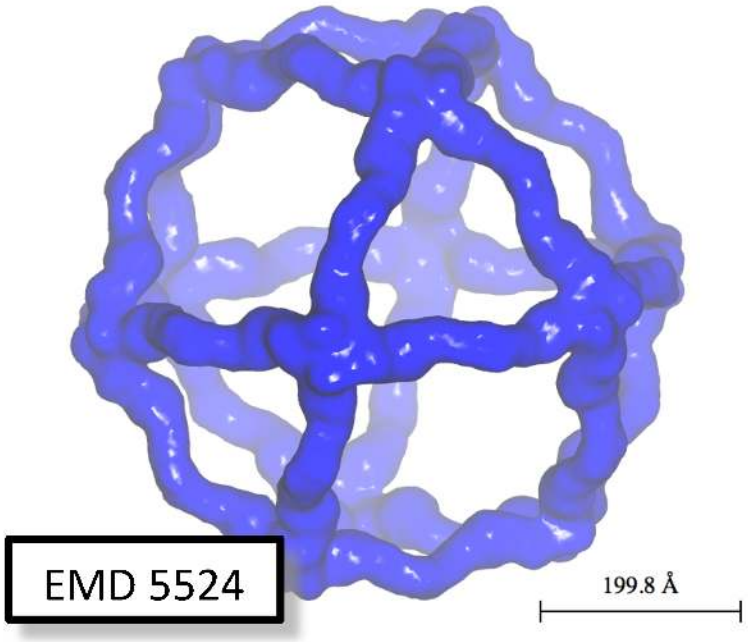

CCP4MG version 2.10.5
Display Table
saved selection
interactive selection
neighbours
buried area
atomic elements
residue types
residue ranges
secondary structure elements
properties (eg temp factor)
NMR/symmetry models
Replace (NEW)
current selection b
Select
residues
within
4.0
3j2w
Include
the central selection
non-Hbonding groups
solvent
Select neighbours
Show
all
of..
Peptide
A/
A/1(TYR)
A/2(GLU)
A/3(HIS)
peptide
Help
Clear
Apply
Save
Close
3j2w
All ..
By c..
Bonds
214.6 Å
Display Table
Simplified Display Table
Origin: -0.000 -0.000 -0.000 | Size: 1000 x 698
Zoom:
31.85

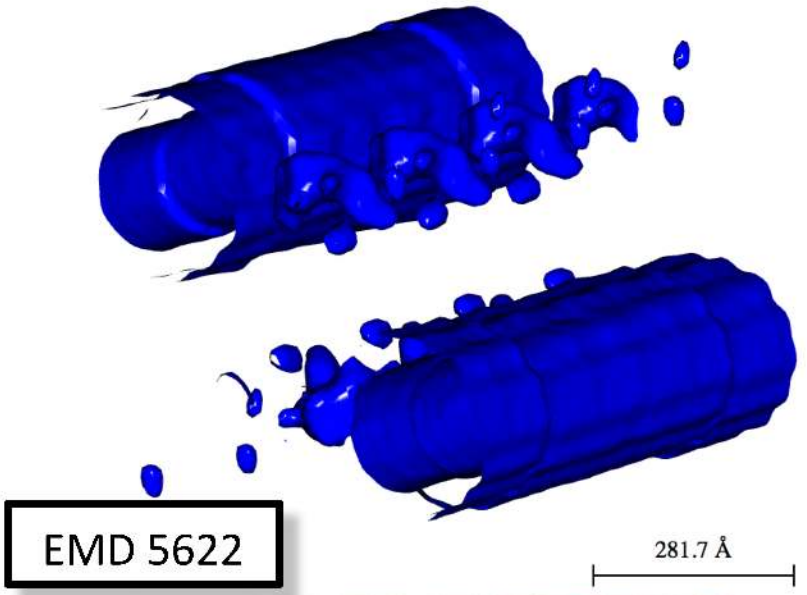

CCP4MG version 2.10.5
Display Table
Select from3j2w
Replace (NEW)
current selection by
neighbours
Select
residues
within
4.0
of selection..
3j2w
A/1(TYR)
Peptide
A/
A/1(TYR)
A/1(TYR)/N
A/1(TYR)/CA
A/1(TYR)/C
A/1(TYR)/O
A/1(TYR)/CB
A/1(TYR)/CG
A/1(TYR)/CD1
A/1(TYR)/CD2
A/1(TYR)/CE1
A/1(TYR)/CE2
A/1(TYR)/CZ
A/1(TYR)/OH
A/2(GLU)
A/3(HIS)
A/4(VAL)
A/5(THR)
A/6(VAL)
Include
the centra
non-Hbon
Show
all
peptide
Help
Clear
Apply
Save
Close
Object
Tools
All ..
By c..
Bonds
214.6 Å
Display Table
Simplified Display Table
Origin: -0.000 -0.000 -0.000 | Size: 1000 x 698
Zoom:
31.85

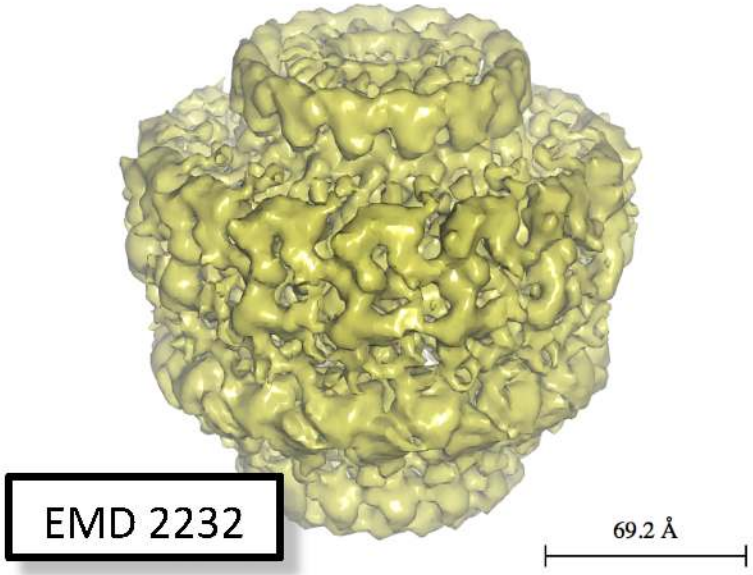
Electron Density

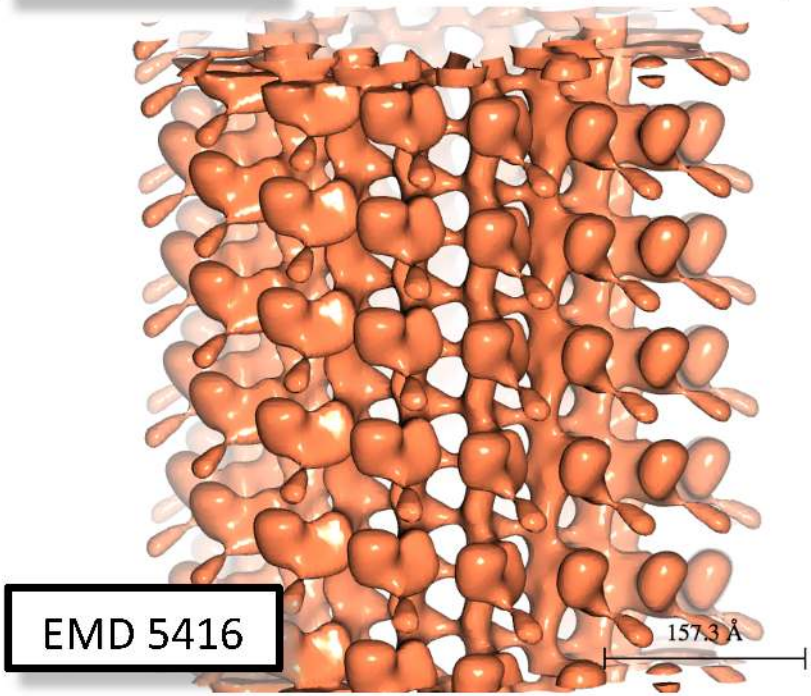


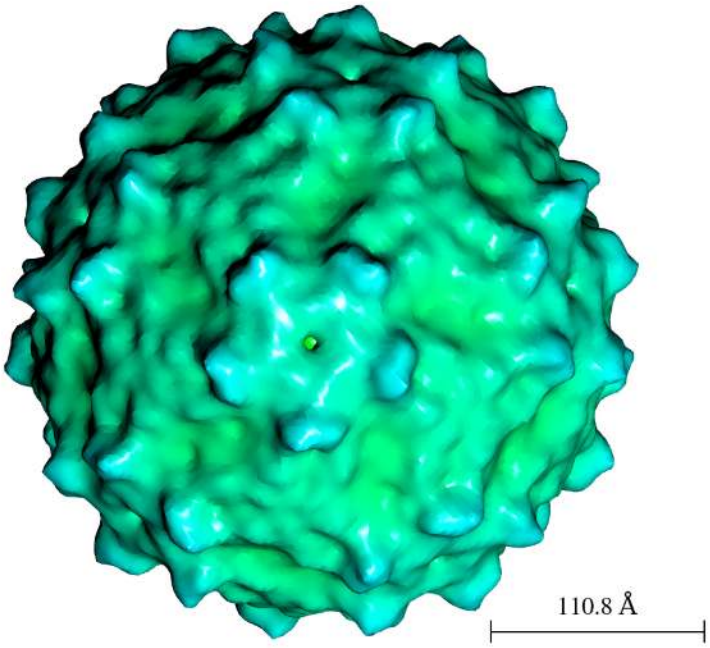

“Clip” to atoms

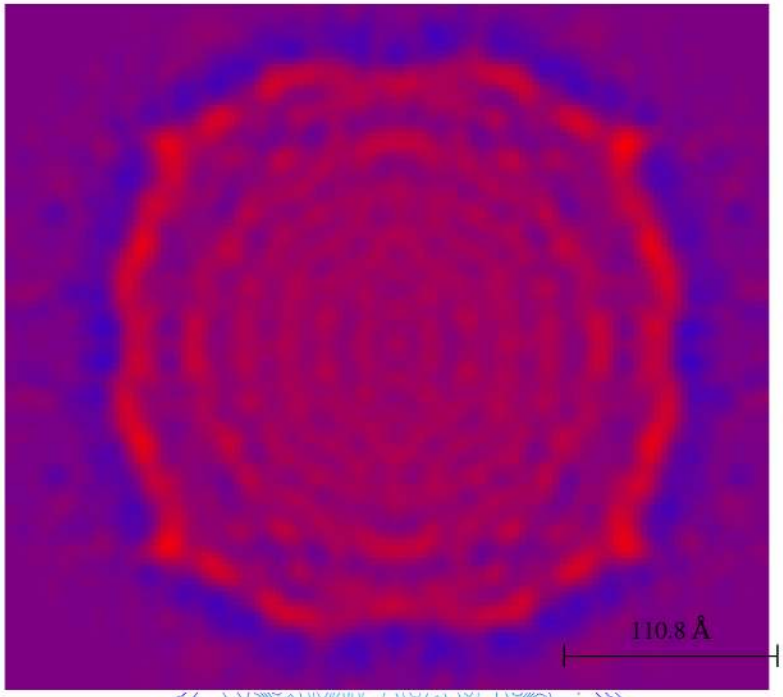

EMD 5524
199.8 Å

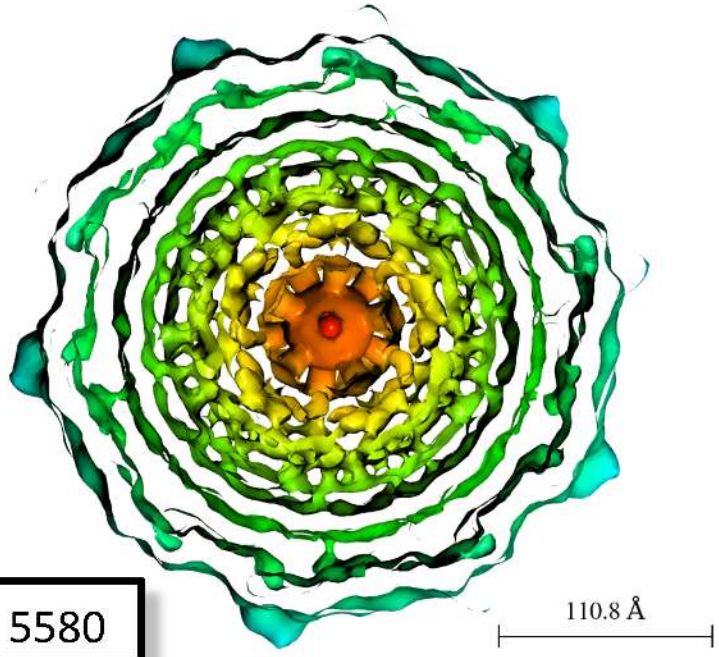

EMD 5622
281.7 Å

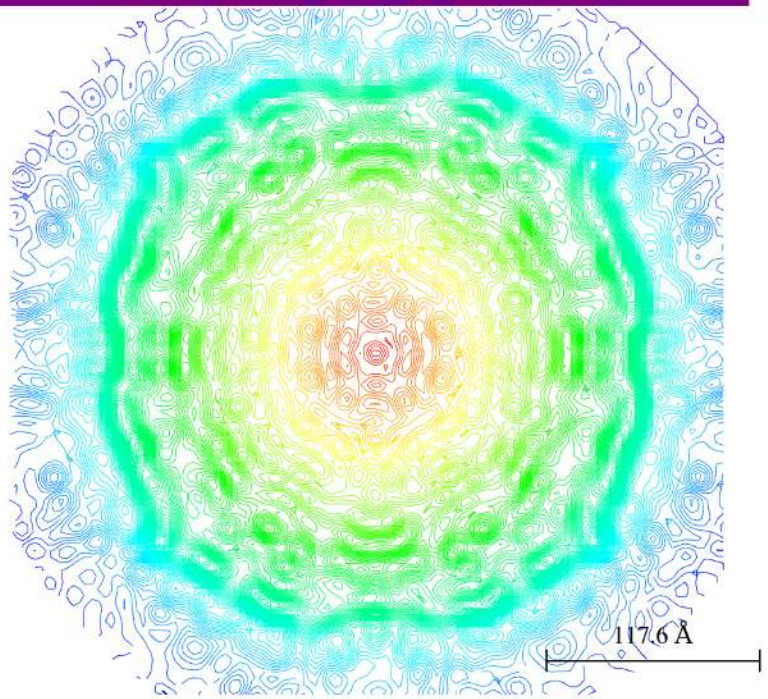

EMD 2232
69.2 Å


EMD 5416
157.3 Å

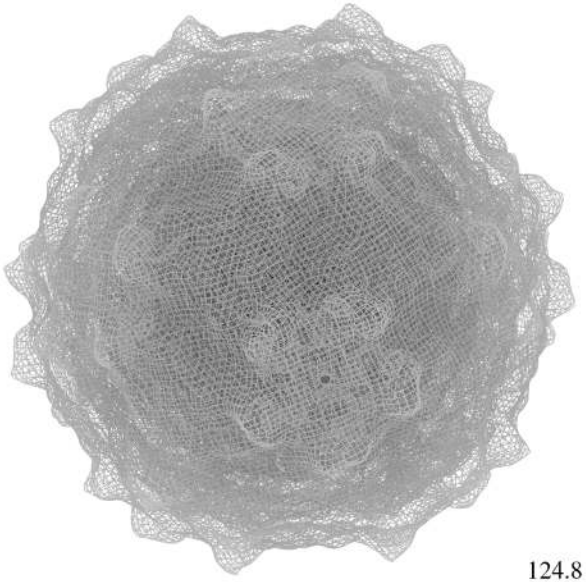




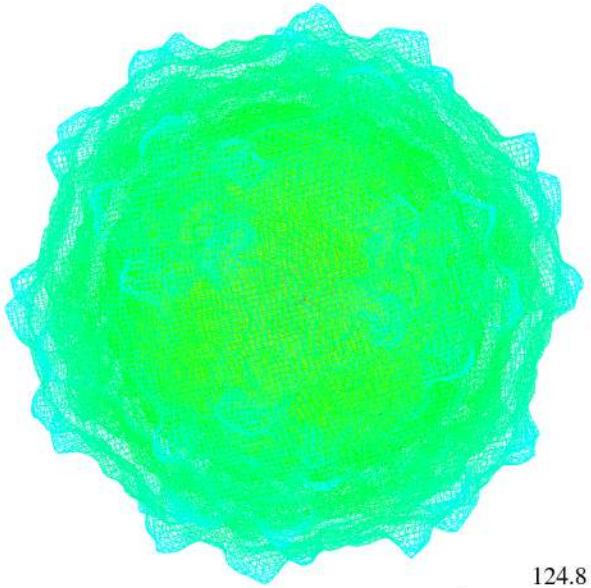




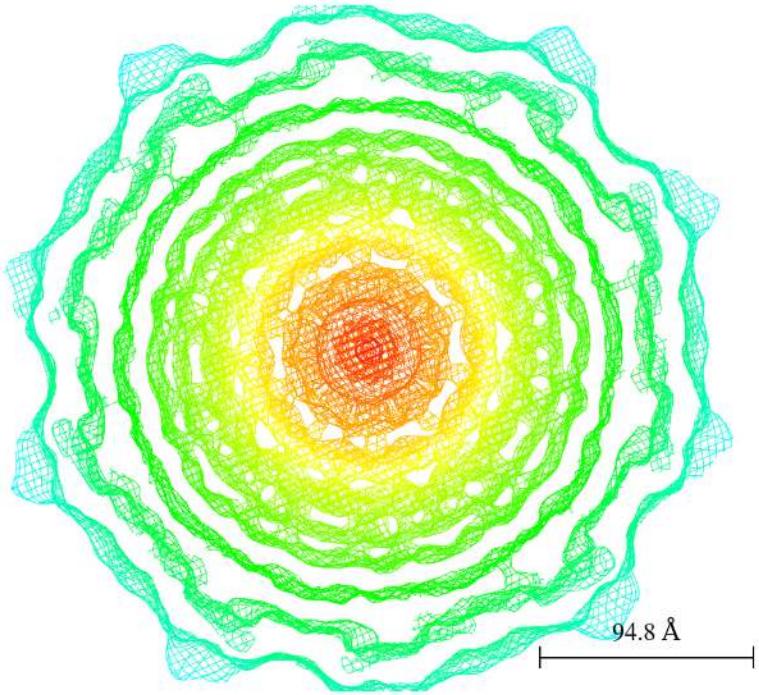
EMD 5580



124.8 Å



124.8 Å

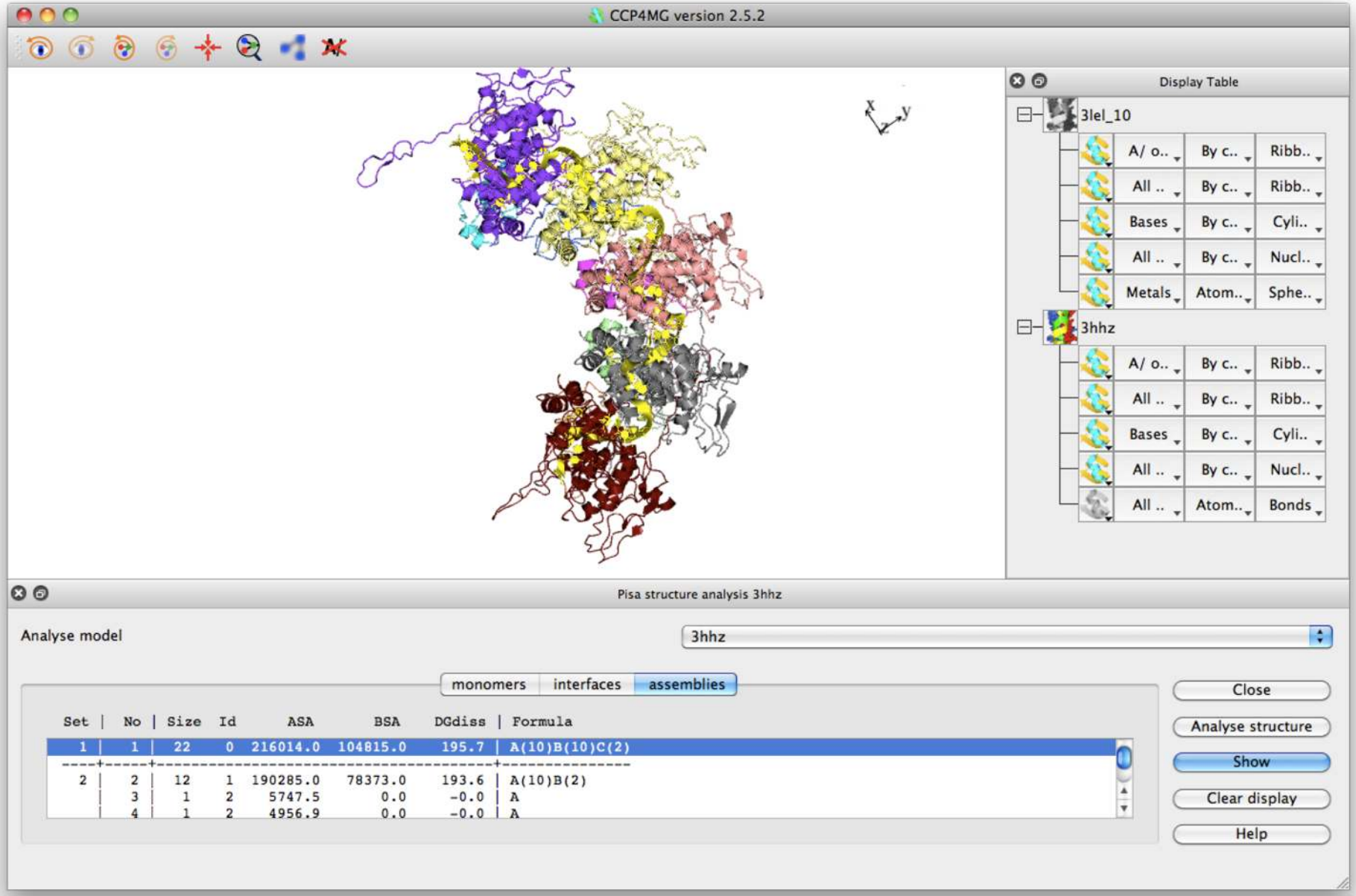


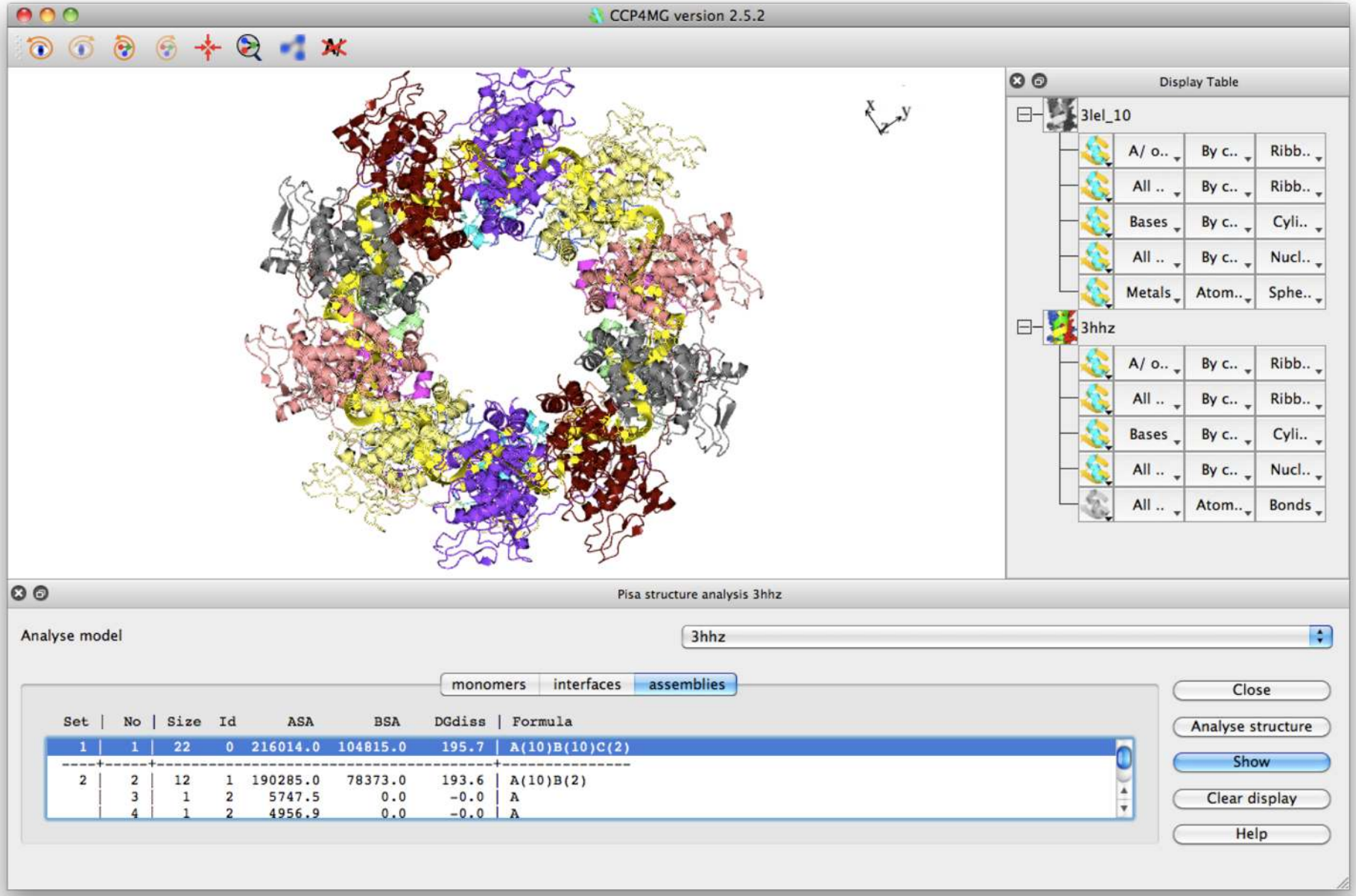
94.8 Å

EMD 5580

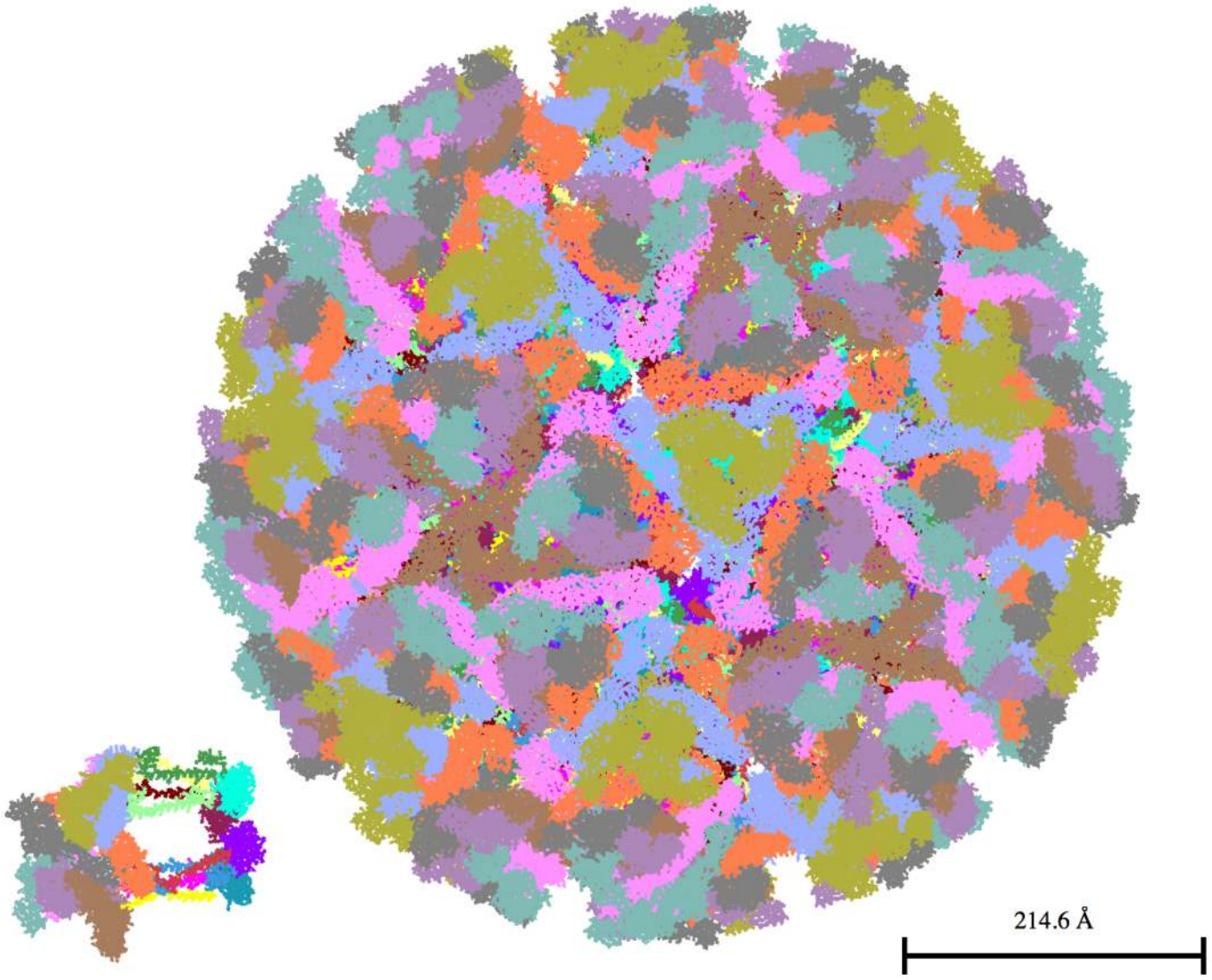
Other stuff

- PISA
- Structure superposition
- Sequence viewer/aligment/blast searches + more (see later).
- Biological assembly generation.
- Distance/angle measurement.
- Fancy lighting effects (shadows/occlusion).
- Normal modes calculation/visualization.
- Text/image overlays.


CCP4MG version 2.5.2
Display Table
3lel_10
A/ o..
By c..
Ribb..
All ..
By c..
Ribb..
Bases
By c..
Cyli..
All ..
By c..
Nucl..
Metals
Atom..
Sphe..
3hhz
A/ o..
By c..
Ribb..
All ..
By c..
Ribb..
Bases
By c..
Cyli..
All ..
By c..
Nucl..
All ..
Atom..
Bonds
Pisa structure analysis 3hhz
Analyse model
3hhz
monomers
interfaces
assemblies
Set | No | Size Id ASA BSA DGdiss | Formula
1 | 1 | 22 0 216014.0 104815.0 195.7 | A(10)B(10)C(2)
2 | 2 | 12 1 190285.0 78373.0 193.6 | A(10)B(2)
3 | 1 2 5747.5 0.0 -0.0 | A
4 | 1 2 4956.9 0.0 -0.0 | A
Close
Analyse structure
Show
Clear display
Help

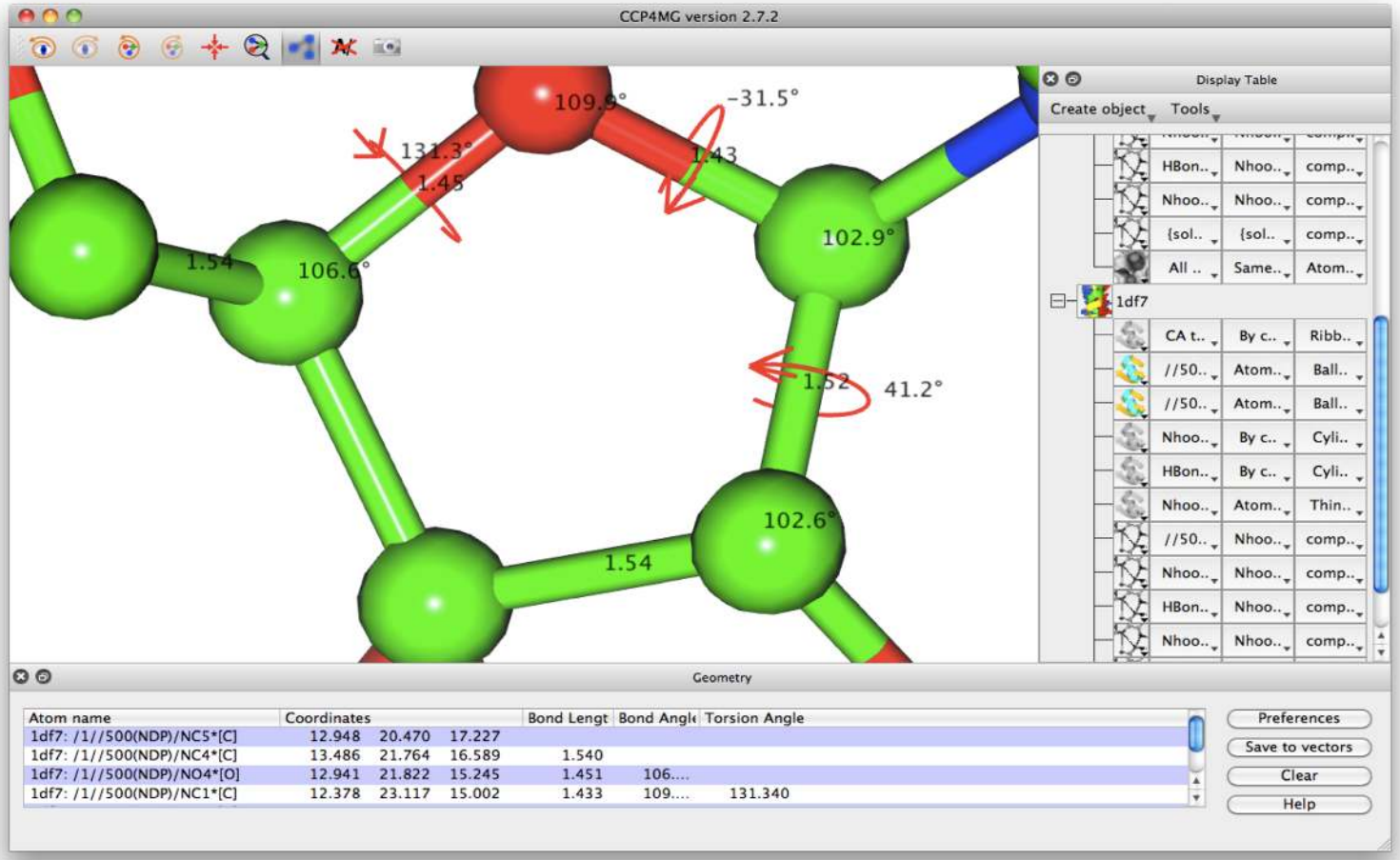

CCP4MG version 2.5.2
Display Table
3lel_10
A/ o..
By c..
Ribb..
All ..
By c..
Ribb..
Bases
By c..
Cyli..
All ..
By c..
Nucl..
Metals
Atom..
Sphe..
3hhz
A/ o..
By c..
Ribb..
All ..
By c..
Ribb..
Bases
By c..
Cyli..
All ..
By c..
Nucl..
All ..
Atom..
Bonds
Pisa structure analysis 3hhz
Analyse model
3hhz
monomers
interfaces
assemblies
Set | No | Size Id ASA BSA DGdiss | Formula
1 | 1 | 22 0 216014.0 104815.0 195.7 | A(10)B(10)C(2)
2 | 2 | 12 1 190285.0 78373.0 193.6 | A(10)B(2)
3 | 1 2 5747.5 0.0 -0.0 | A
4 | 1 2 4956.9 0.0 -0.0 | A
Close
Analyse structure
Show
Clear display
Help

Biological assemblies (3j2w)

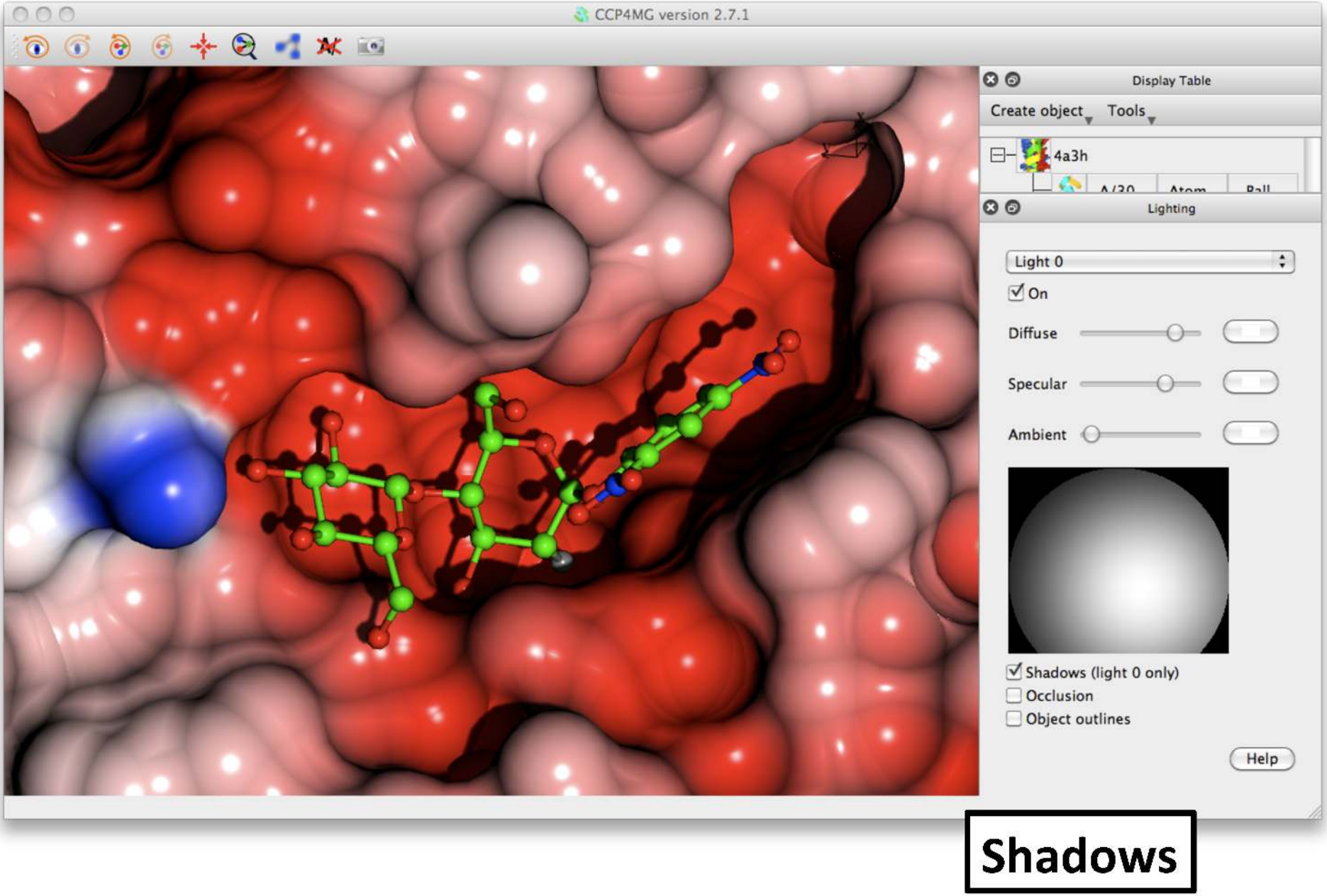


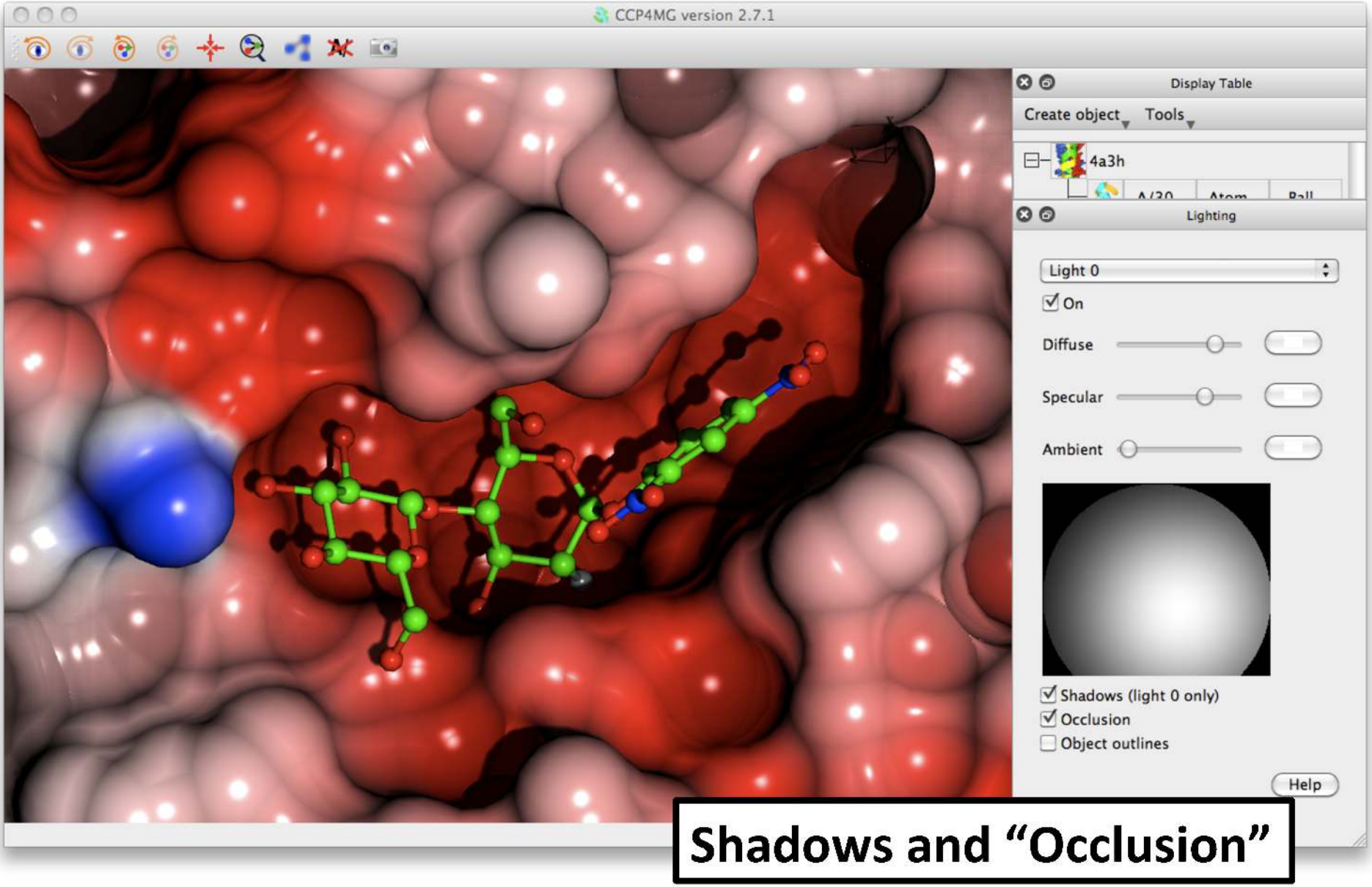
Distances and angles

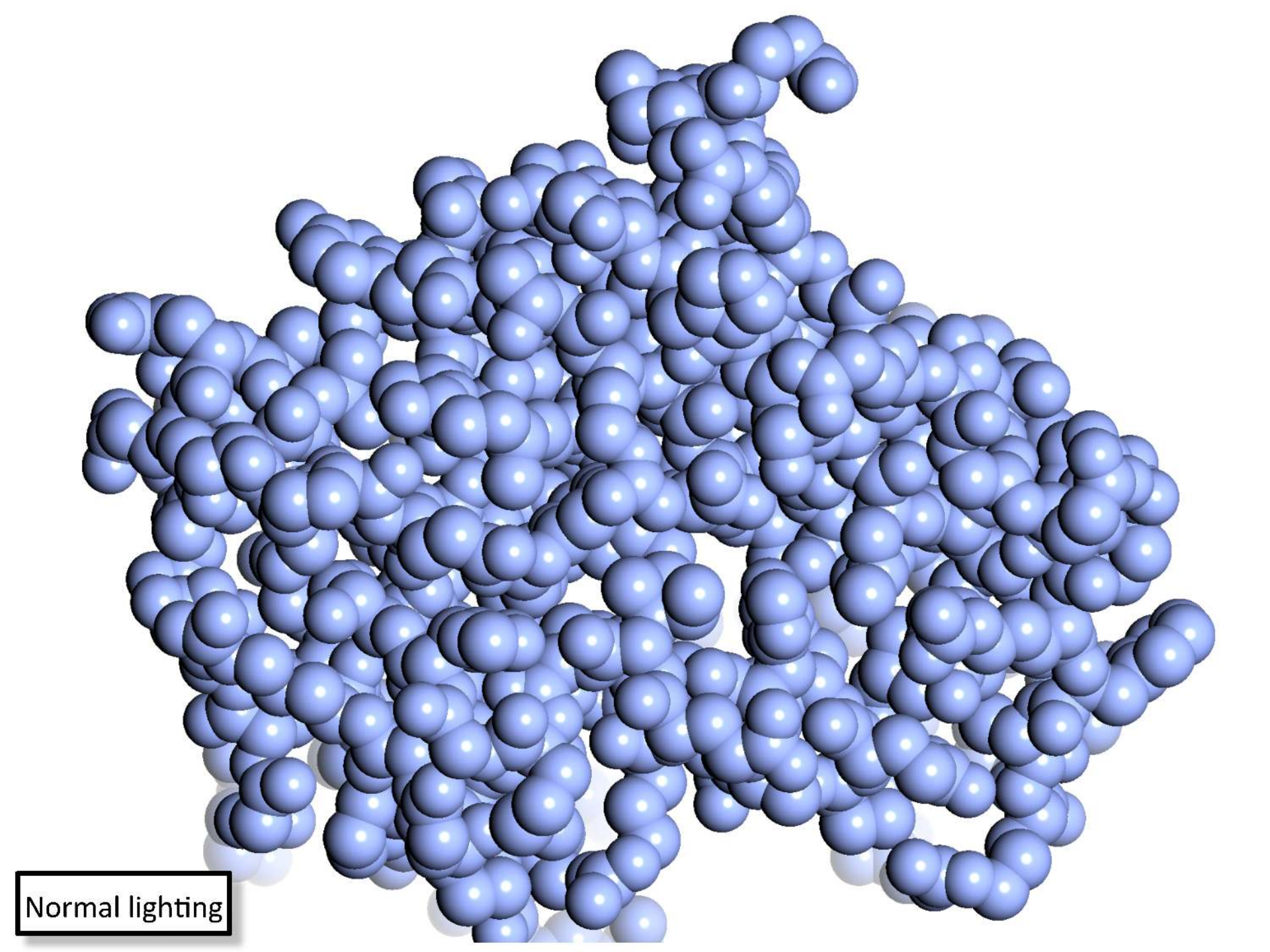
- Open “Geometry window” : Applications -> Geometry
- Double-click on one atom then another to measure bonds.
- Shift-double click on other atoms will measure angles.
- Results appear in table below and in graphics window.

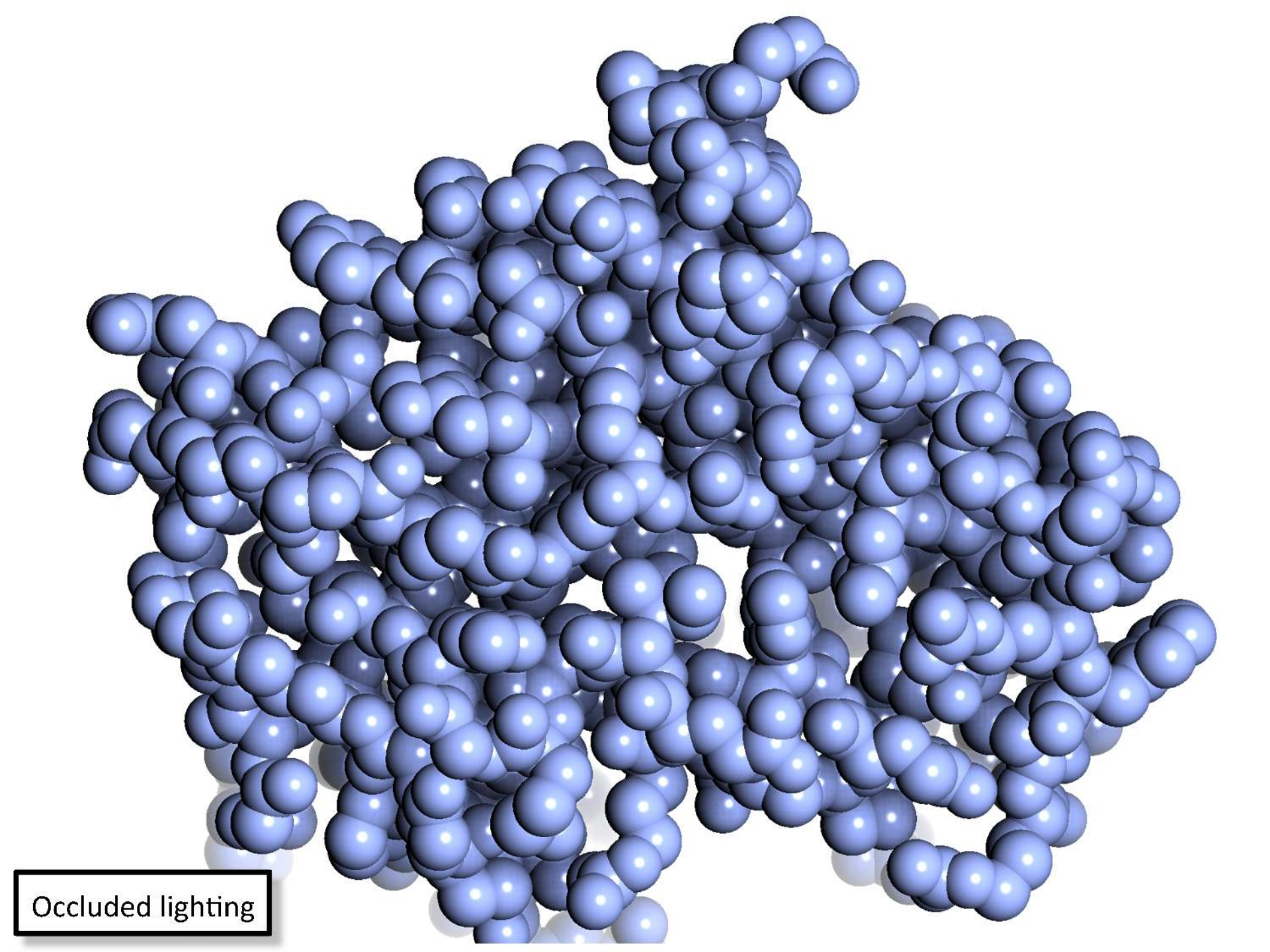


Lighting and Shadows

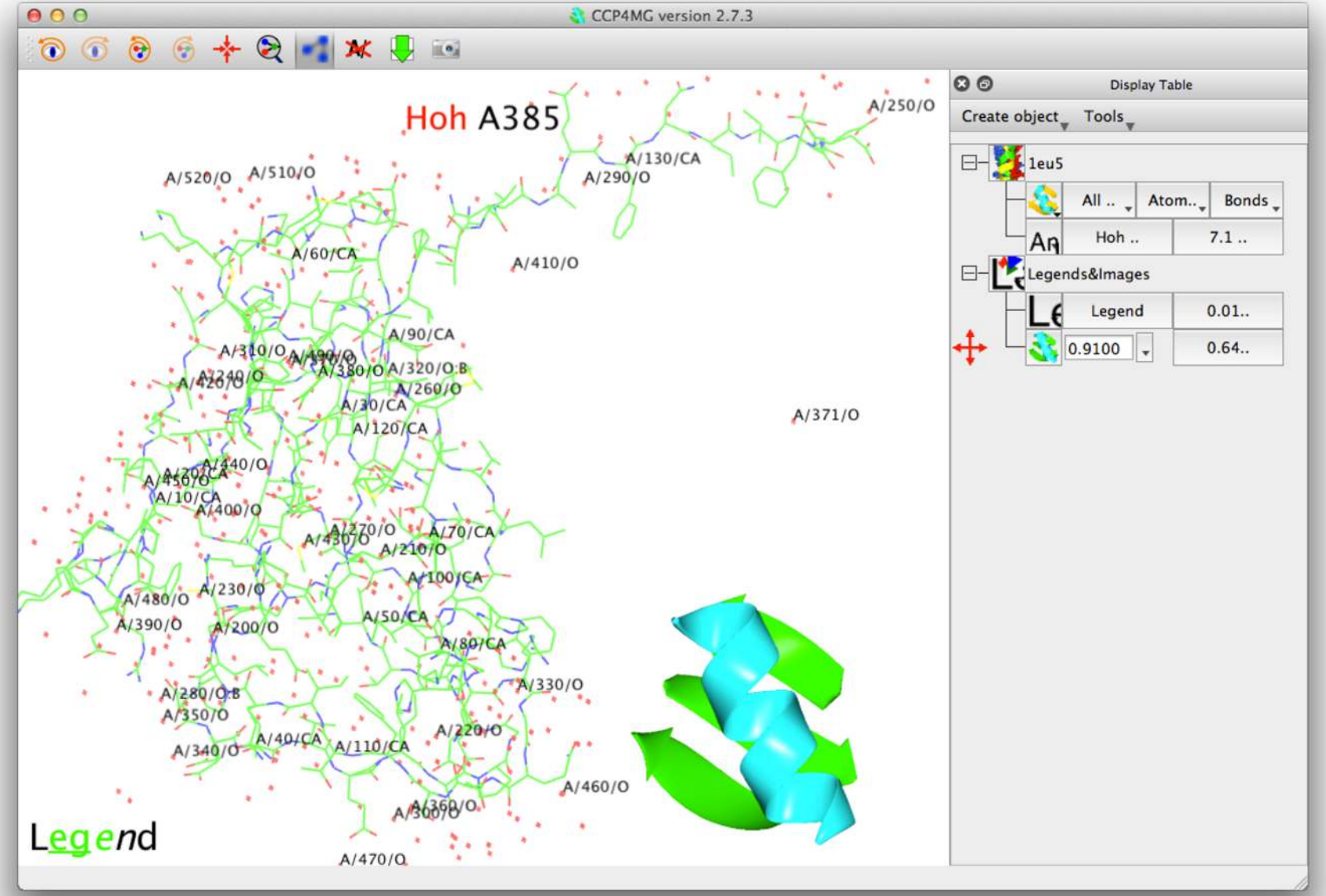

CCP4MG version 2.7.1
Display Table
Create object
Tools
4a3h
Lighting
Light 0
On
Diffuse
Specular
Ambient
Shadows (light 0 only)
Occlusion
Object outlines
Help
Shadows


CCP4MG version 2.7.1
Display Table
Create object
Tools
4a3h
Lighting
Light 0
On
Diffuse
Specular
Ambient
Shadows (light 0 only)
Occlusion
Object outlines
Help
Shadows and “Occlusion”

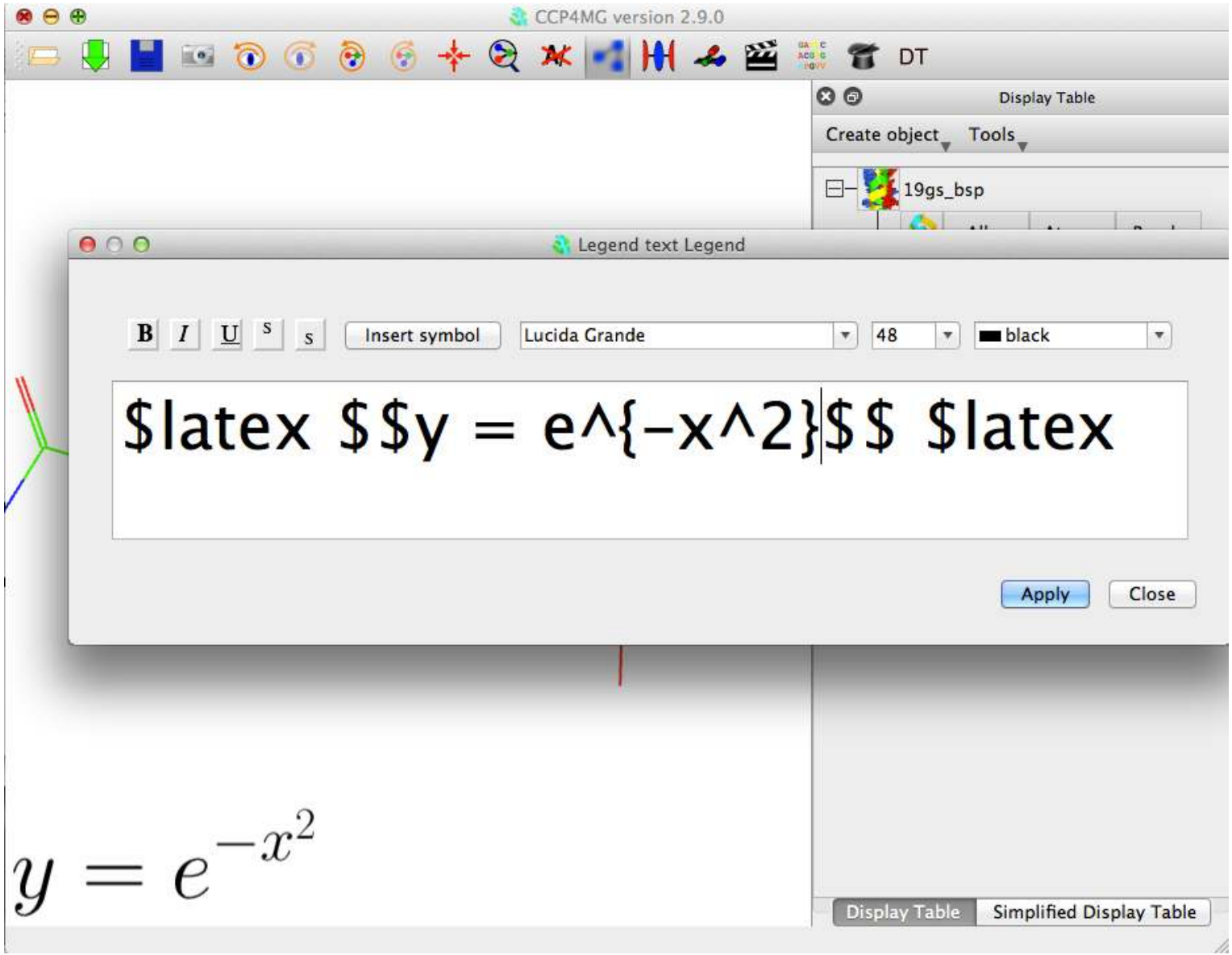

Normal lighting


Occluded lighting

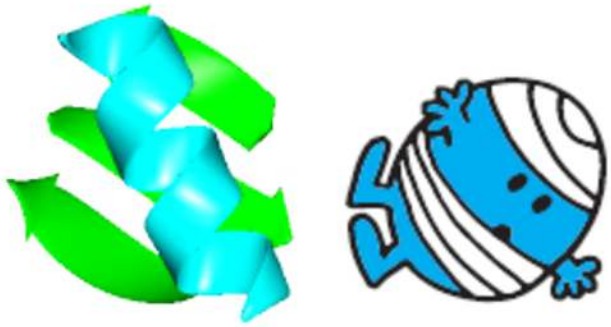
On screen text and images



On screen text and images



MrBump



Mr Bump

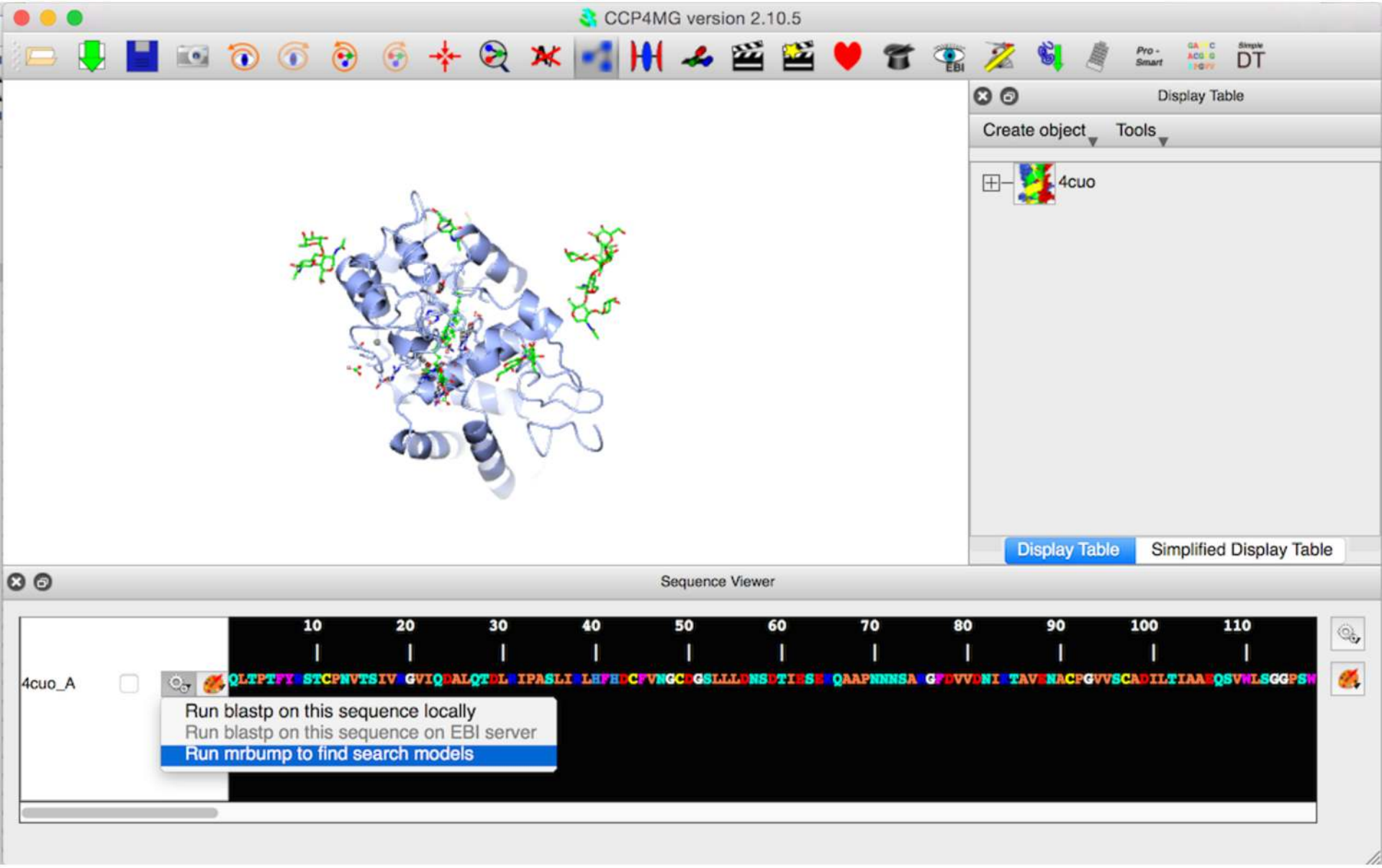
- Mr Bump is an automated scheme for Molecular Replacement. Given a target sequence and experimental structure factors, it will search for homologous structures, create a set of suitable search models from the template structures, do molecular replacement, and test the solutions with some rounds of restrained refinement.
- A component of the CCP4 suite of programs.

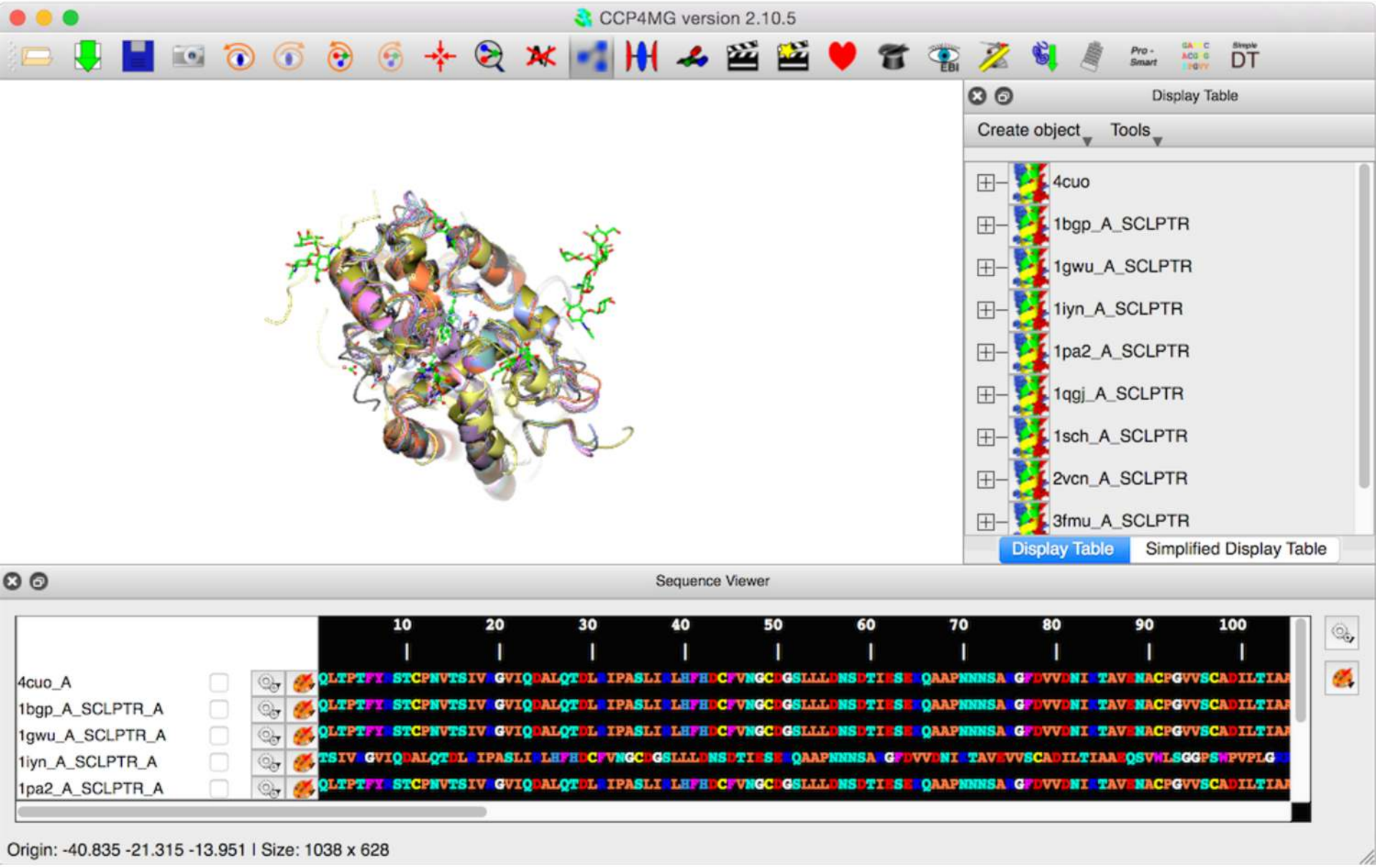
CCP4MG and Mr Bump

- CCP4MG uses initial steps of the Mr Bump to interactively edit molecular replacement models.
- Scheme:
  - Mr Bump is sent a sequence from CCP4MG
  - uses the hmmer tool to search for 70% homologous structures,
  - selects just the relevant chains from the structures,
  - prunes side chains,
  - structurally aligns the pruned structures (gesamt).
  - CCP4MG loads the structures.

CCP4MG and Mr Bump

- Then CCP4MG can be used to select subsets of atoms from the newly loaded structures:
  - Completely hide some structures.
  - Select e.g. just alpha-helices
  - Prune terminating loops.
  - Whatever …
- And then everything visible can be saved into one ensemble coordinate file for use in a molecular replacement calculation.


CCP4MG version 2.10.5
Display Table
Create object
Tools
4cuo
Display Table
Simplified Display Table
Sequence Viewer
10
20
30
40
50
60
70
80
90
100
110
4cuo_A
Run blastp on this sequence locally
Run blastp on this sequence on EBI server
Run mrbump to find search models


CCP4MG version 2.10.5
Display Table
Create object
Tools
4cuo
1bgp_A_SCLPTR
1gwu_A_SCLPTR
1iyn_A_SCLPTR
1pa2_A_SCLPTR
1qgj_A_SCLPTR
1sch_A_SCLPTR
2vcn_A_SCLPTR
3fmu_A_SCLPTR
Display Table
Simplified Display Table
Sequence Viewer
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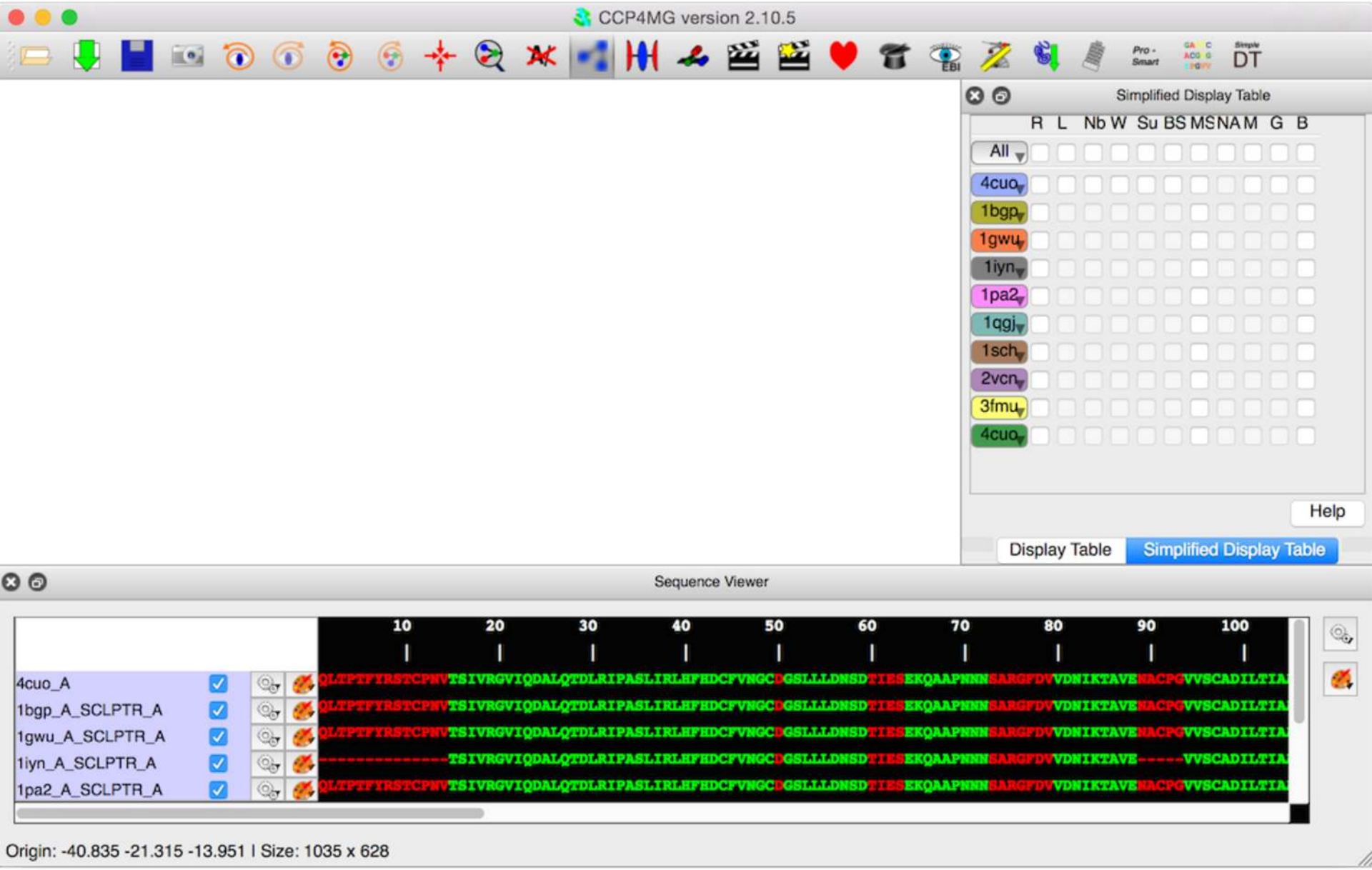
1iyn_A_SCLPTR_A
1pa2_A_SCLPTR_A
Origin: -40.835 -21.315 -13.951 I Size: 1038 x 628


CCP4MG version 2.10.5
Simplified Display Table
R L Nb W Su BS MS NA M G B
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4cuo
1bgp
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1iyn
1pa2
1qgj
1sch
2vcn
3fmu
4cuo
Help
Display Table
Simplified Display Table
Sequence Viewer
10 20 30 40 50 60 70 80 90 100
4cuo_A
1bgp_A_SCLPTR_A
1gwu_A_SCLPTR_A
1iyn_A_SCLPTR_A
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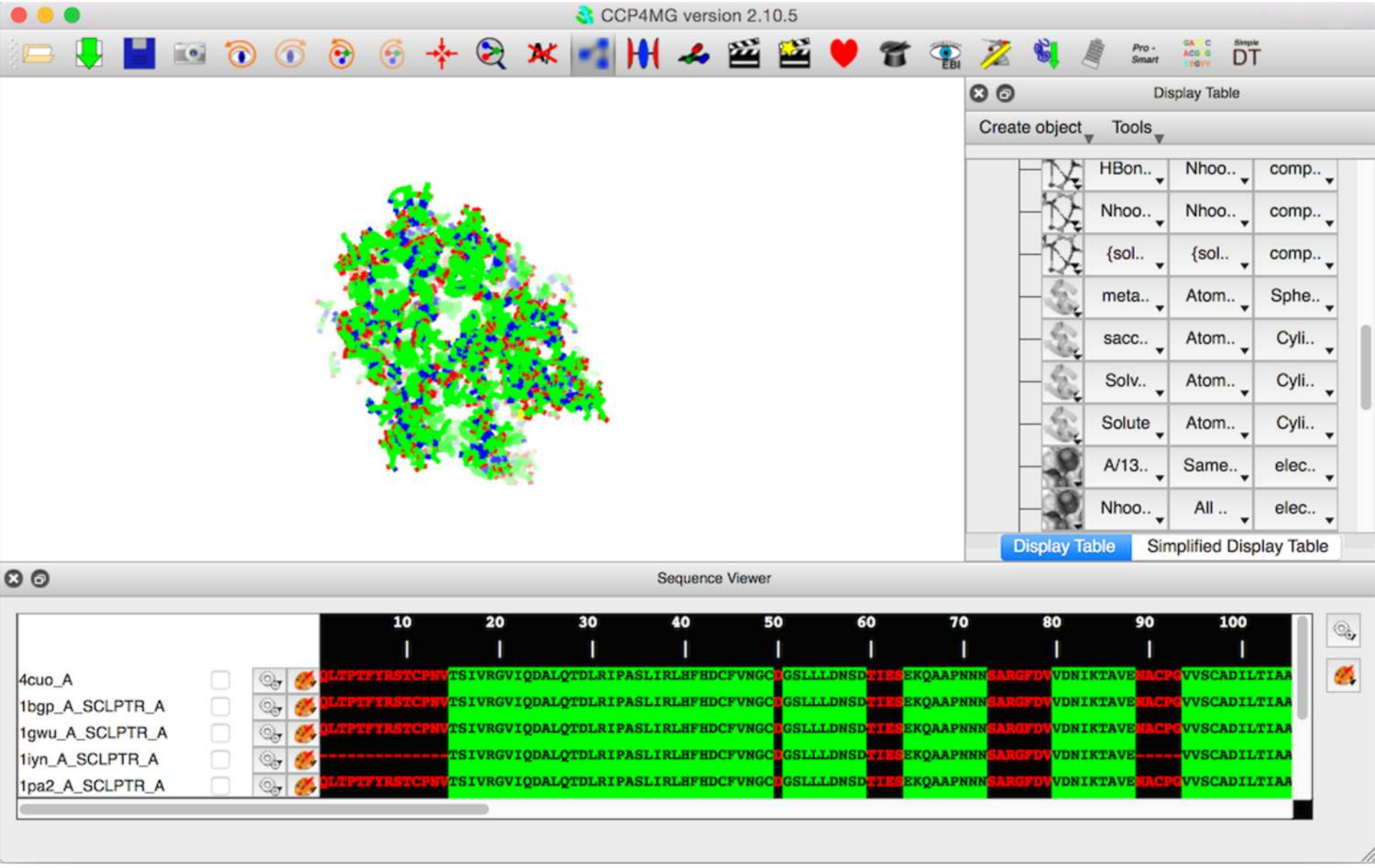
CCP4MG version 2.10.5
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Nhoo..
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Simplified Display Table
Sequence Viewer
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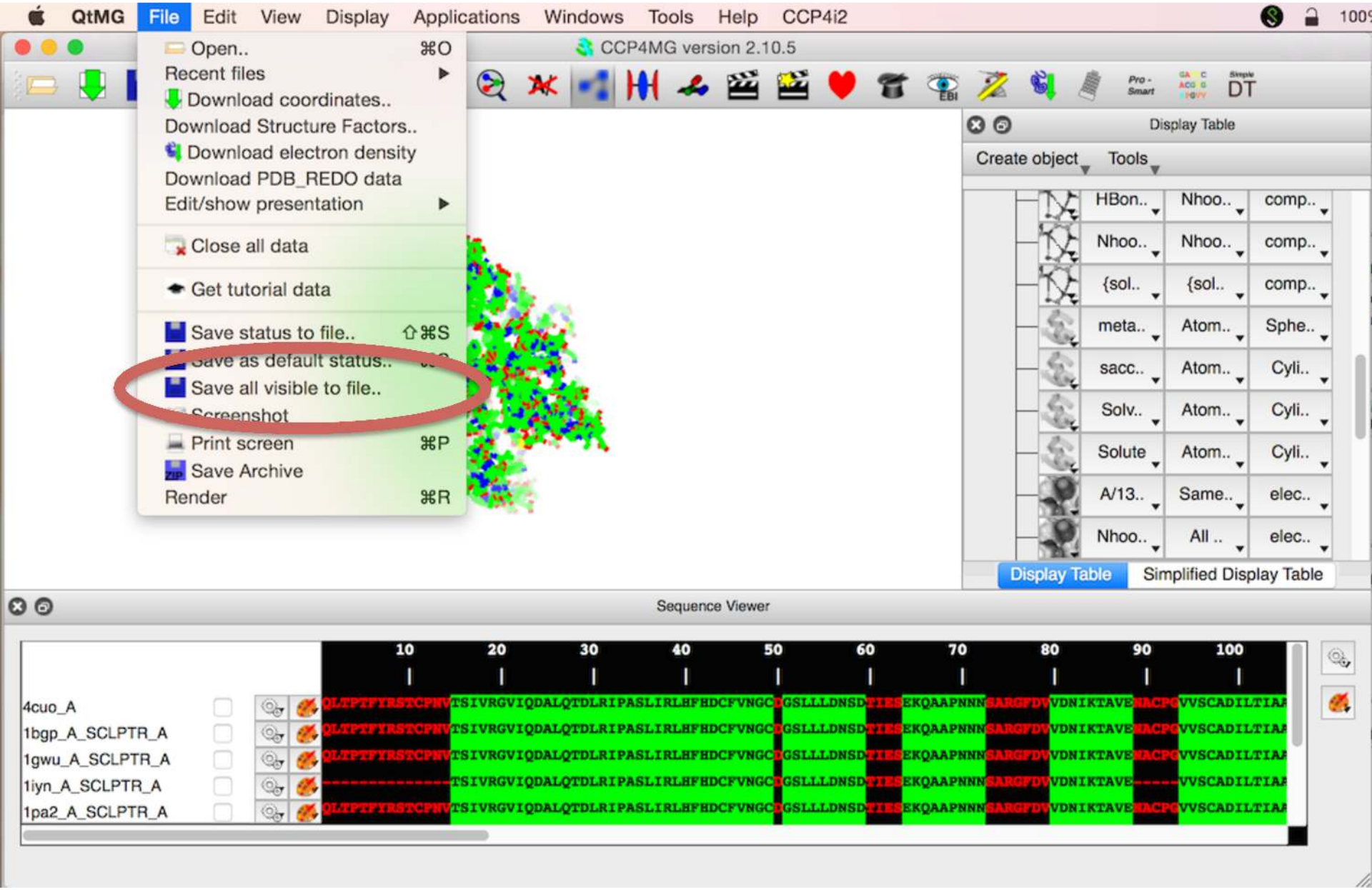
1pa2_A_SCLPTR_A


QtMG
File
Edit
View
Display
Applications
Windows
Tools
Help
CCP4i2
CCP4MG version 2.10.5
Open..
⌘O
Recent files
Download coordinates..
Download Structure Factors..
Download electron density
Download PDB_REDO data
Edit/show presentation
Close all data
Get tutorial data
Save status to file..
⇧⌘S
Save as default status..
Save all visible to file..
Screenshot
Print screen
⌘P
Save Archive
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Display Table
Simplified Display Table
Sequence Viewer
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4cuo_A
1bgp_A_SCLPTR_A
1gwu_A_SCLPTR_A
1iyn_A_SCLPTR_A
1pa2_A_SCLPTR_A

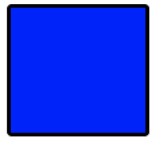
Glycoblocks

Glycosylation depiction in 3D

- Electrostatic interactions provided by N- and O-linked glycans are essential for correct folding of glycoproteins.
- Depicting these protein-glycan contacts can be challenging; glycans can have many branched sugars.
- With eukaryotic expression systems ramping up the production of glycoproteins and thus the deposition rate of their three-dimensional structures, the need for a clear way of depicting these interactions is more pressing than ever.
- CCP4MG brings the familiar two-dimensional identification convention used by the glycobiology community into three dimensions.
- All Jon's genius, insight, encouragement, etc.

McNicholas and Agirre – manuscript in preparation

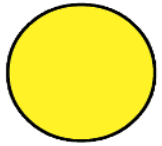
Saccharide display in 2D



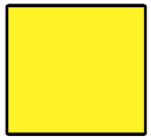
N-Acetyl-glucosamine
(NAG)

Mannose
(BMA, MAN)

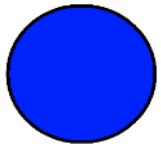
Fucose
(FCA, FCB, FUC)



Galactose
(GAL)



N-Acetyl-galactosamine
(NGA)



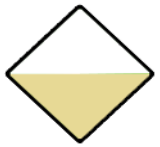
Glucose
(GLC, BGC)

2-keto-3-deoxynononic acid
(KDN)

Galacturonic acid
(ADA, GTR)

Glucosamine
(GCS)

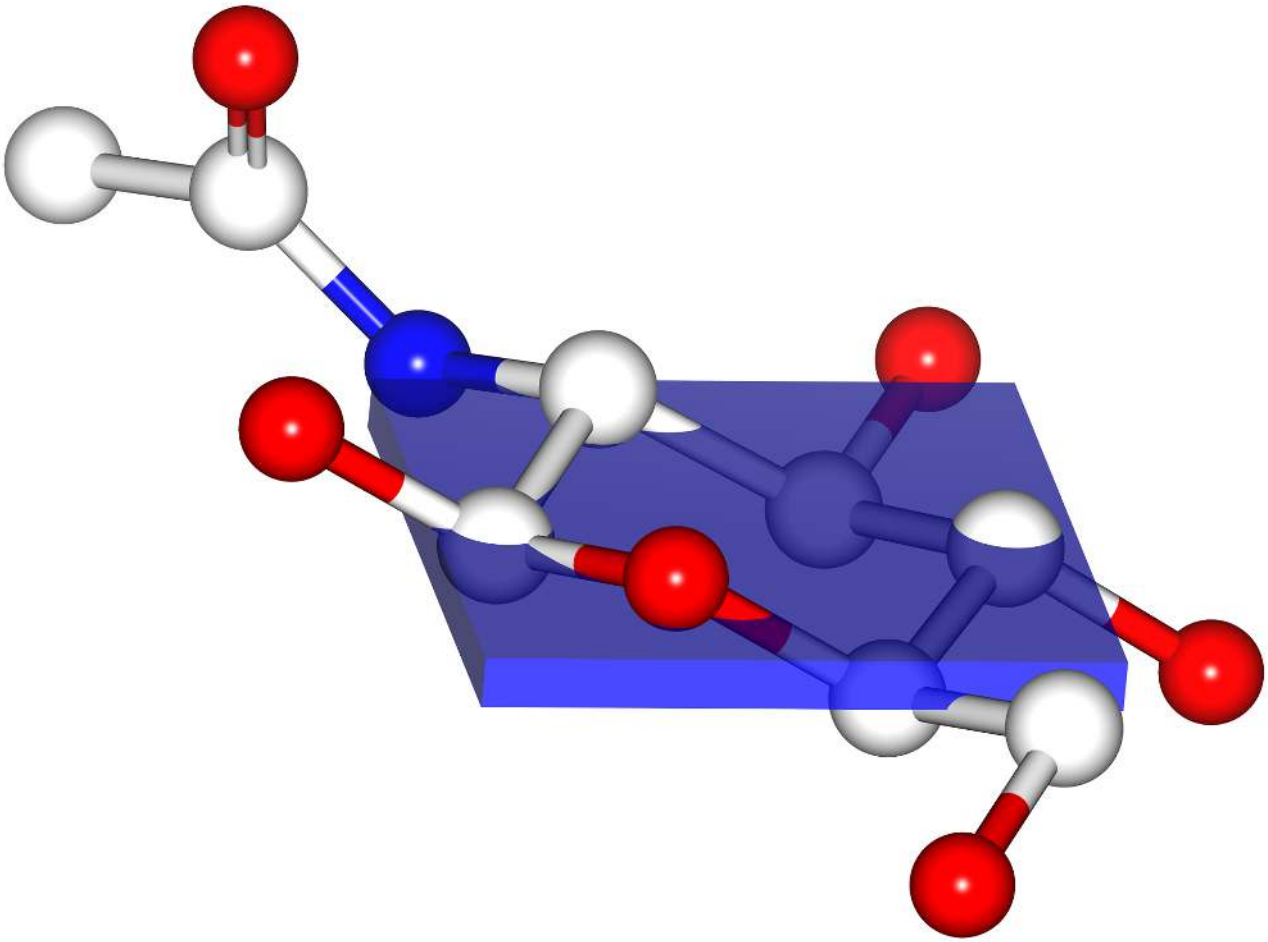
Xylose
(XYS, XYP)



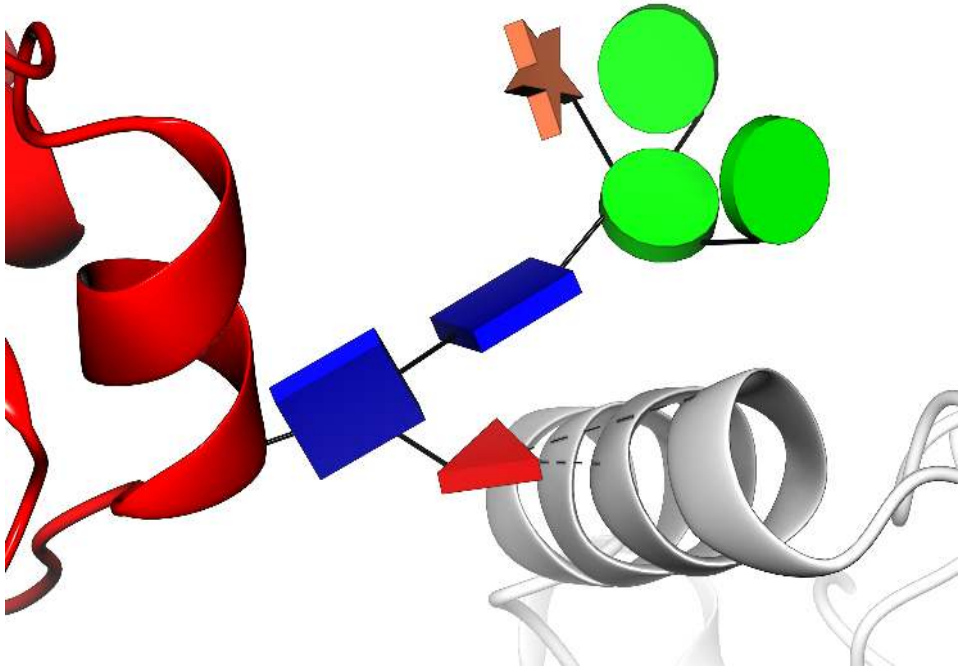
Iduronic acid
(IDR)

Mannuronic acid
(BEM)

Saccharide display in 3D

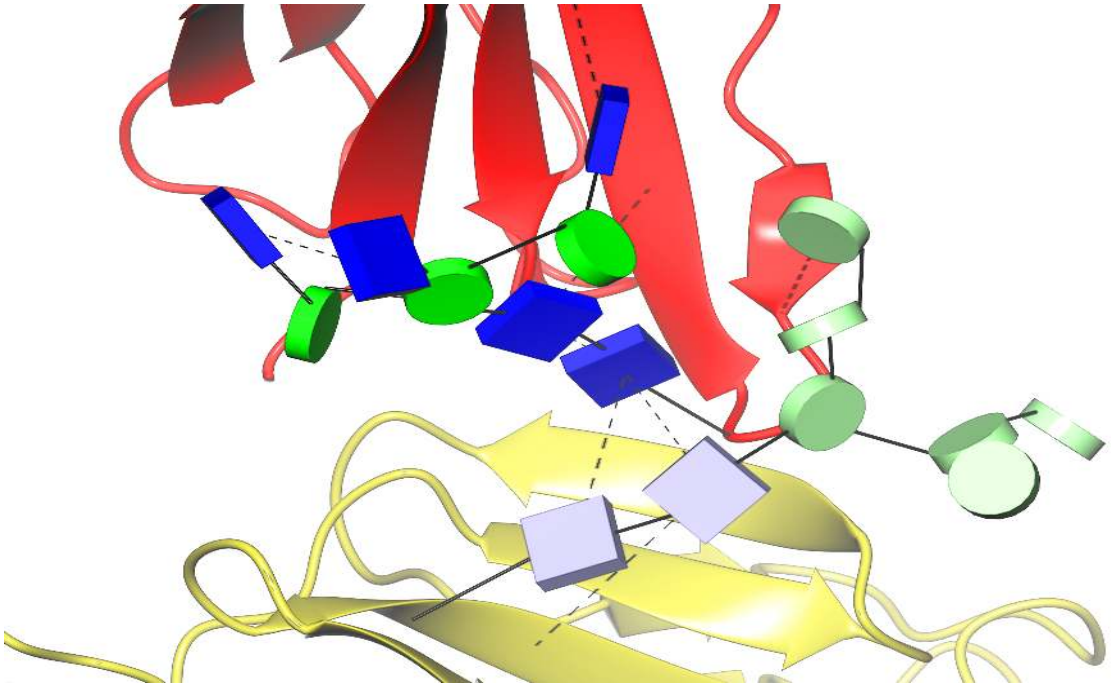


Saccharide display in 3D



Glycoblocks representation of a plant N-glycan and its interactions (PDB 4CUO). In this structure, the Fucose sugar attached to the first N-acetyl-β-D-glucosamine residue establishes two hydrogen bonds to a neighbouring chain (depicted in white) that is related by crystallographic symmetry to the one the tree is covalently bound to (in red). L-sugars (Fucose, red triangle, and Xylose, orange star) are only present in plant glycans and make for less than 1% of all the N-glycan forming pyranosides deposited in the wwPDB.

Saccharide display in 3D



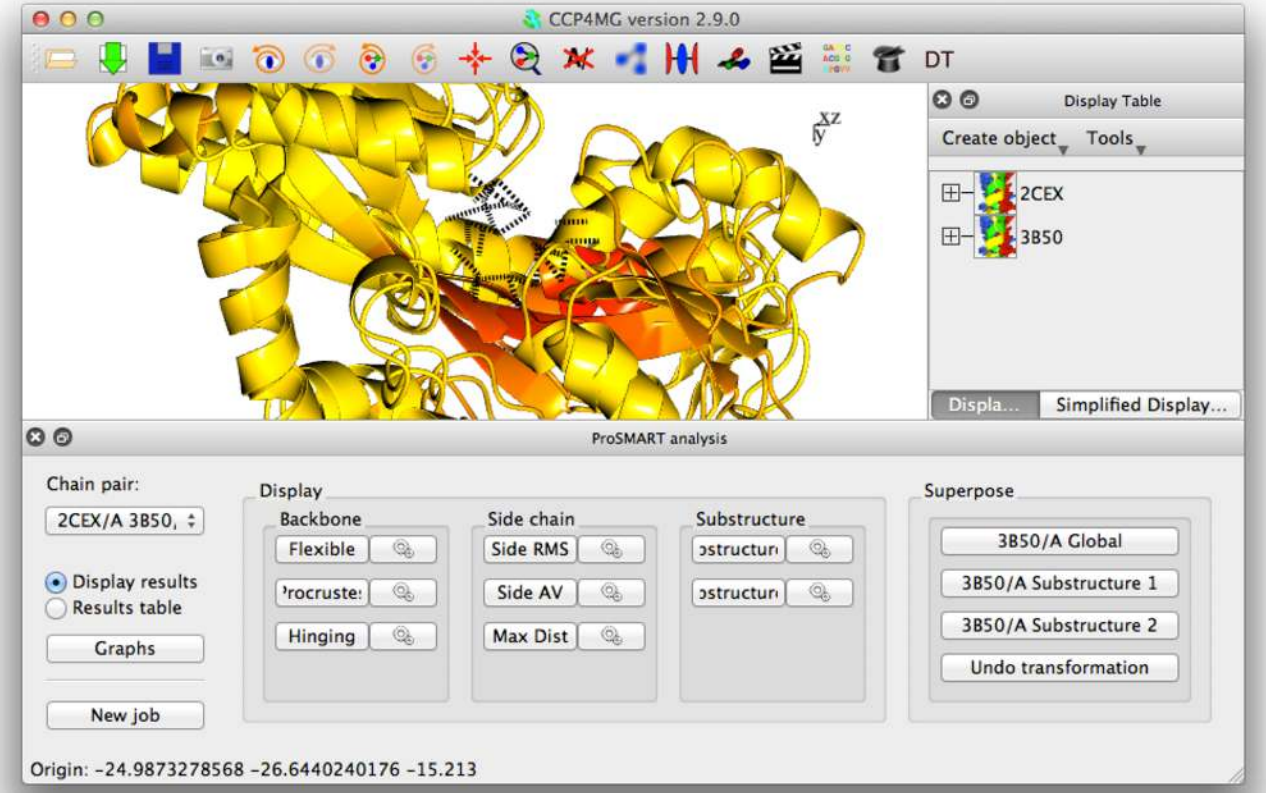
Glycoblocks view of carbohydrate-carbohydrate interactions (PDB 3SGK). Two N-glycans attached to two separate Fc fragments (depicted in red and gold) establish hydrogen bonds with each other and the protein part. These interactions, along with others that are described in Ferrara et al. (2011), make a key contribution to the increased binding between these two antibody fragments. The representation shows a clean view of an otherwise very complex network of H-bonds.

ProSMART

- http://www2.mrc-lmb.cam.ac.uk/groups/murshudov/content/prosmart/documentation.html#summary
- http://www2.mrc-lmb.cam.ac.uk/groups/murshudov/content/prosmart/docs/rob_nicholls_thesis.pdf
- ProSMART (Procrustes Structural Matching Alignment and Restraint Tool) is a software tool designed for the conformation-independent structural comparison of protein chains. At current, ProSMART has two components:
  - **ProSMART ALIGN - for the alignment, superposition, and scoring of protein chains;**
  - ProSMART RESTRAIN - for the generation of external restraints for use in the crystallographic refinement of protein structures.

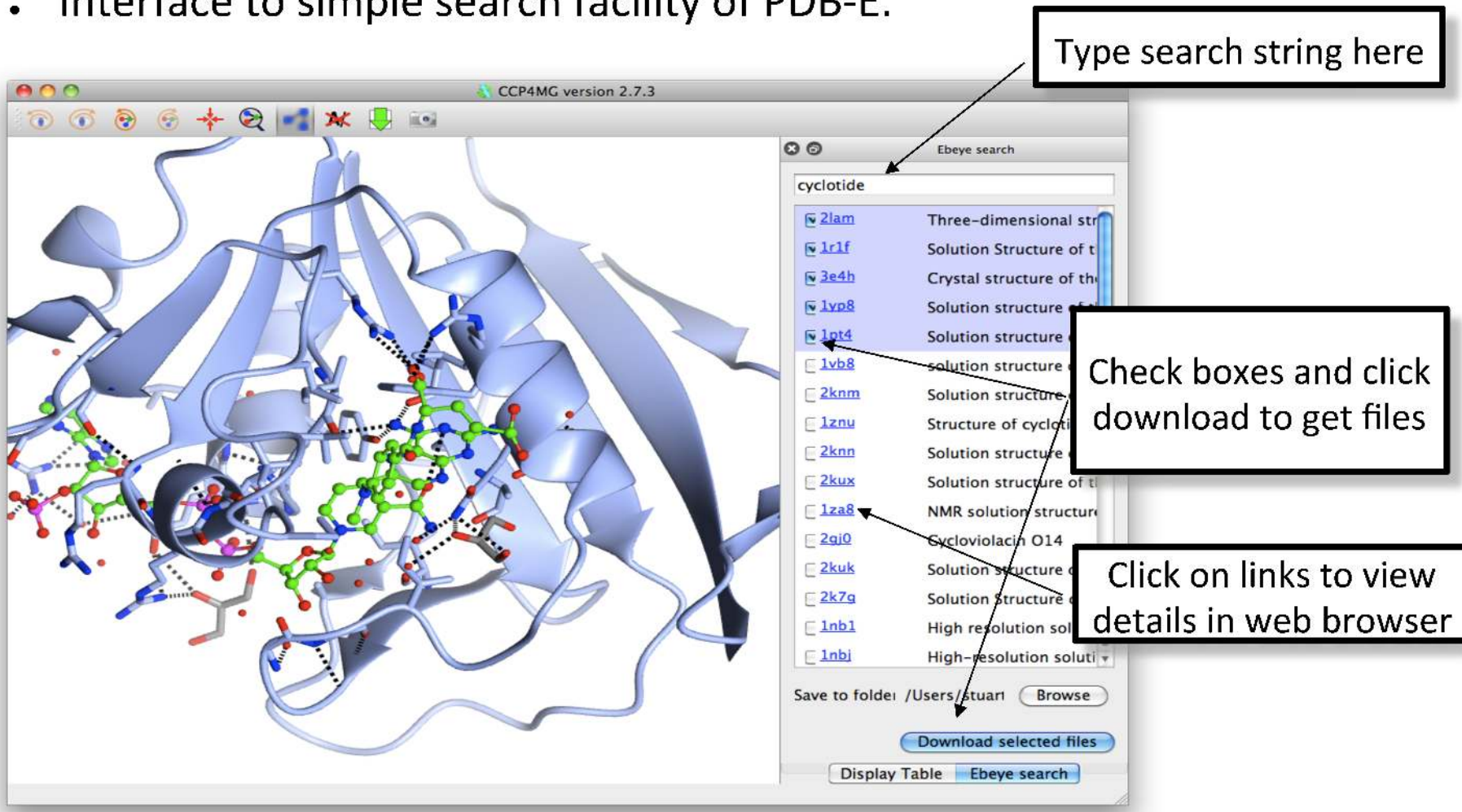
ProSMART interface

- ProSMART interface is a simple “push button to see stuff”.



Ebeye - search

- Interface to simple search facility of PDB-E.



“Batch” rendering

- Images may be rendered from command line or from scripts without starting up the main program.
- `ccp4mg -norestore -picture mypic.mgpic.py -R test.png -RO '{"size":"1600x1600","smoothribbons":"1", "raytrace":"1"}' -quit`
- The file mypic.mpic.py is a file containing a scene description: lists of data files, representations, view, etc.

CCP4MG on the Web

Web GL

- WebGL is a JavaScript technology for displaying 3D (and 2D) graphics in a web browser.
- WebGL is very similar to OpenGL ES, a technology which is very similar to OpenGL which is what CCP4MG uses for its graphics.
- Should be reasonably straightforward to write a WebGL application which uses existing CCP4MG code/expertise to do molecular graphics.

WebGL

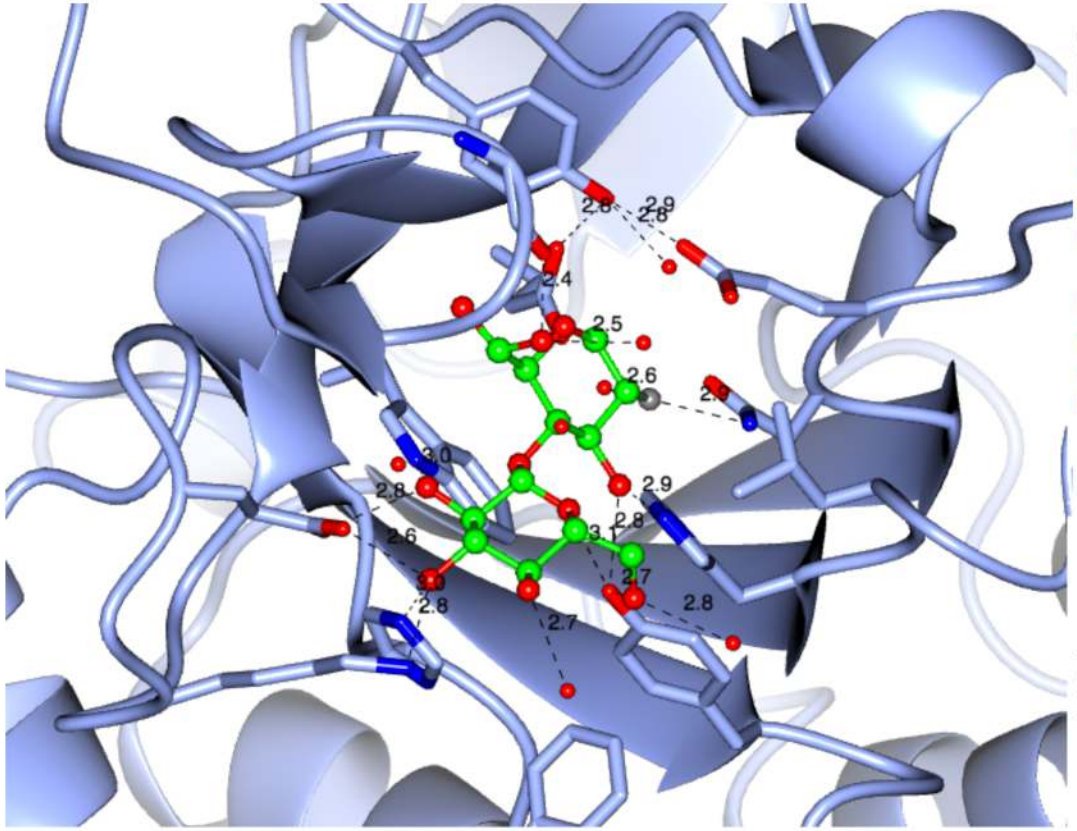
- Most of the hard work in CCP4MG is done in a mixture of Python and C++ programming languages. This is not *trivially* portable to JavaScript.
- However if the hard work (converting macromolecular coordinates to picture elements – lines, triangles) was done on a server, the WebGL application (browser) could just draw the triangles which are computed.

Stuart's client server WebG ×

StuartAndSarah

localhost:8000/server_client-onebig.html

Stuart's client server WebGL



Fog

Clip

5A3H +

-63.602 -40.116 -24.590
0.4228
-0.007 -0.192 -0.916 0.352
700 540

Choose File ascene.scene.xml Load file

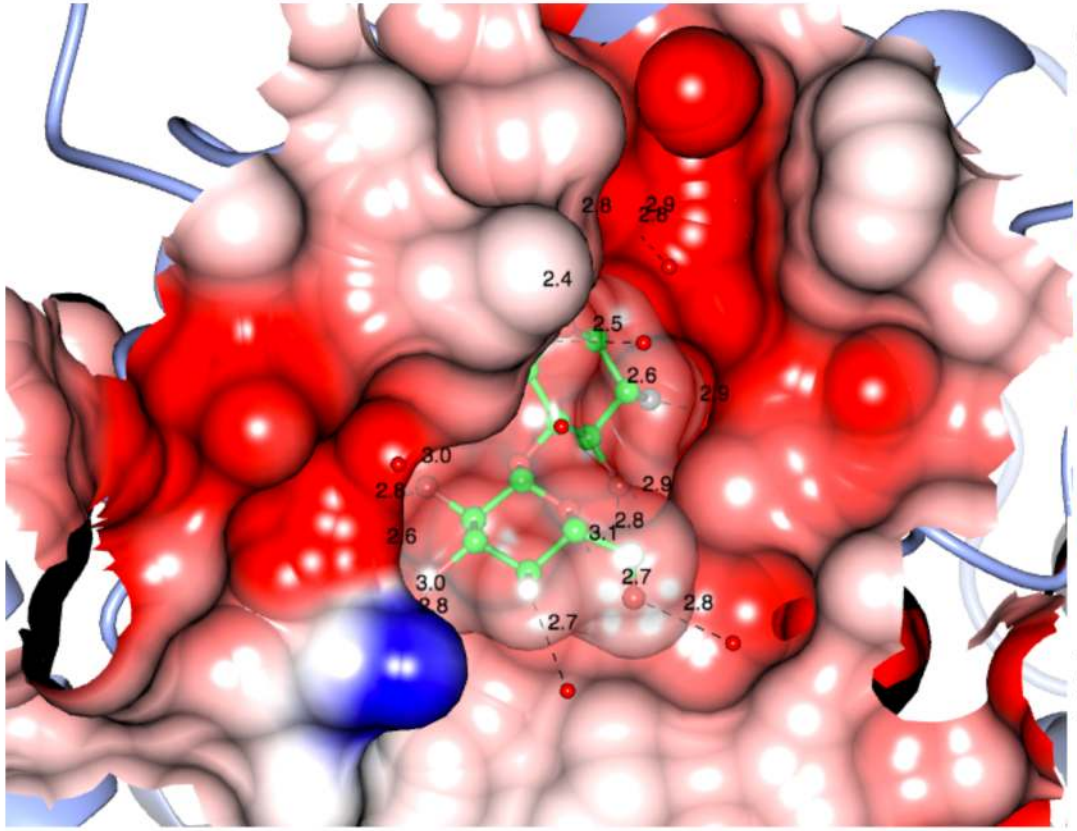
Load PDB code

Stuart's client server WebG ×

StuartAndSarah

localhost:8000/server_client-onebig.html

Stuart's client server WebGL



Fog

Clip

5A3H +

-63.602 -40.116 -24.590
0.4228
-0.007 -0.192 -0.916 0.352
700 540

Choose File ascene.scene.xml Load file

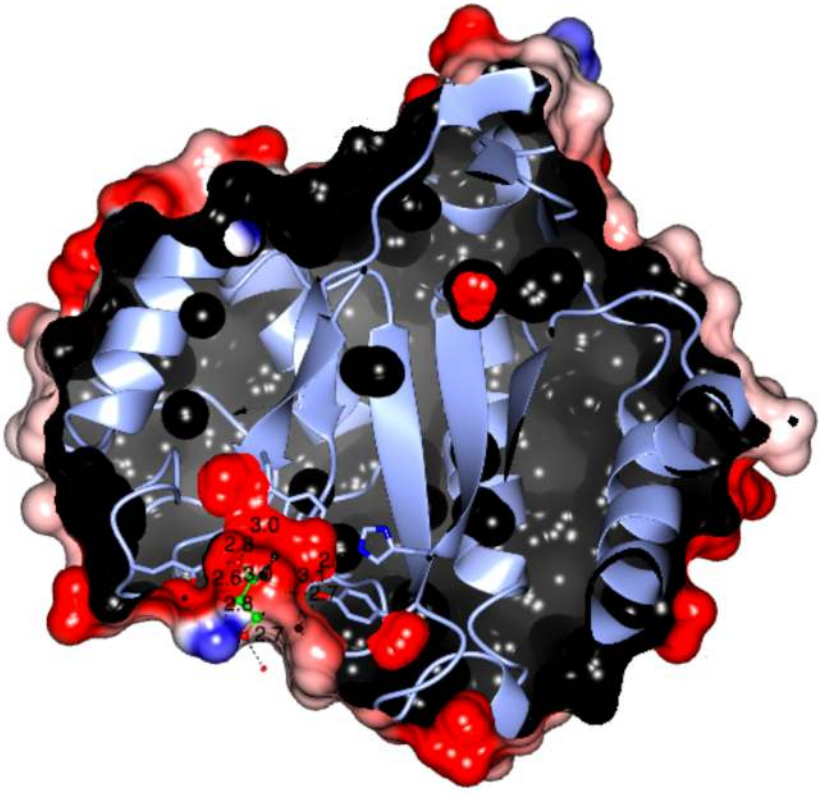
Load PDB code

Stuart's client server WebC ×

StuartAndSarah

localhost:8000/server_client-onebig.html

Stuart's client server WebGL



Fog

Clip

5A3H +

-63.602 -40.116 -24.590
1.0924
0.181 0.377 -0.821 0.389
700 540

Choose File ascene.scene.xml Load file

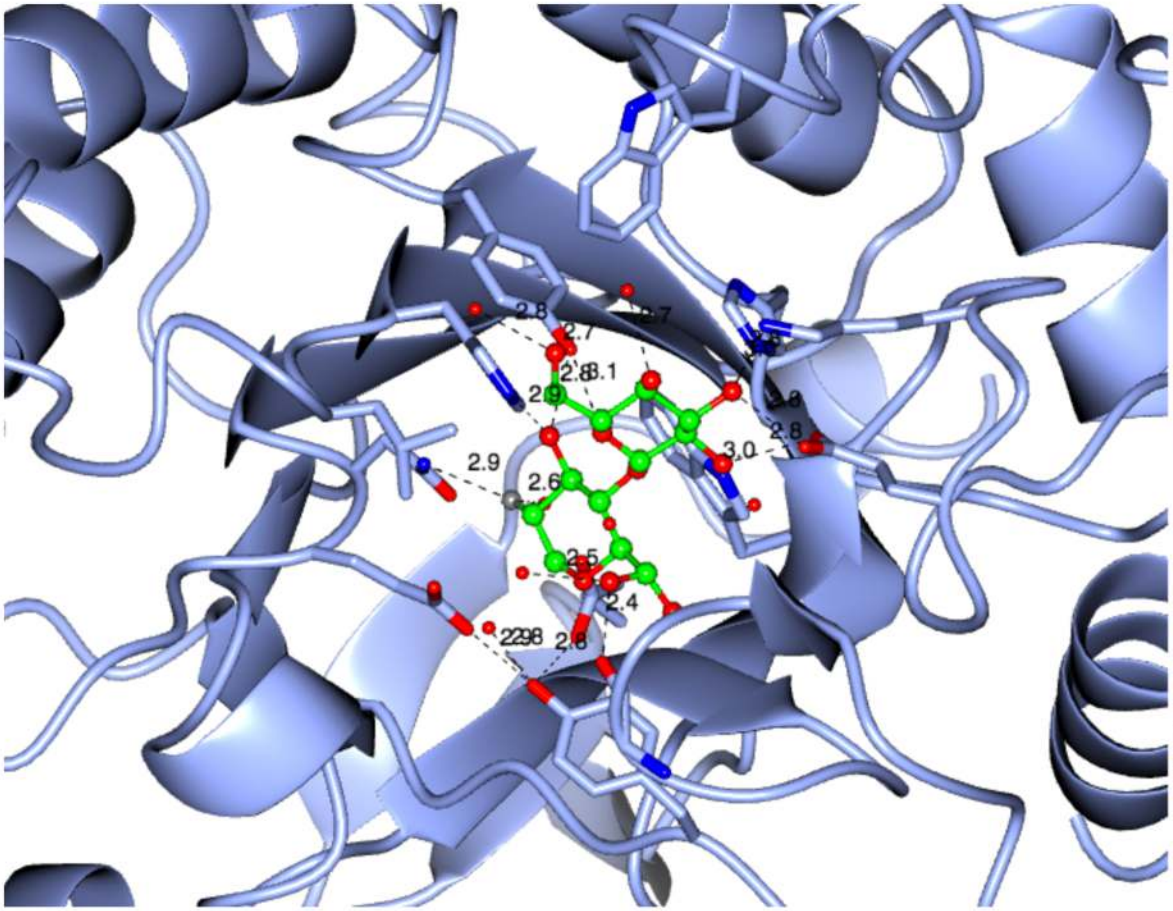
Load PDB code

Stuart's client server WebG ×

StuartAndSarah

localhost:8000/server_client-onebig.html

Stuart's client server WebGL



Fog

Clip

5A3H +

- Atom type
- By chain
- By model
- Main/side chain
- Secondary structure
- Blend through model
- Residue property
- Residue type
- Residue solvent access
- Atom property
- Temperature factor
- Occupancy
- Alternate location
- Charge
- Atom solvent access
- Colour browser
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-63.602 -40.116 -24.590
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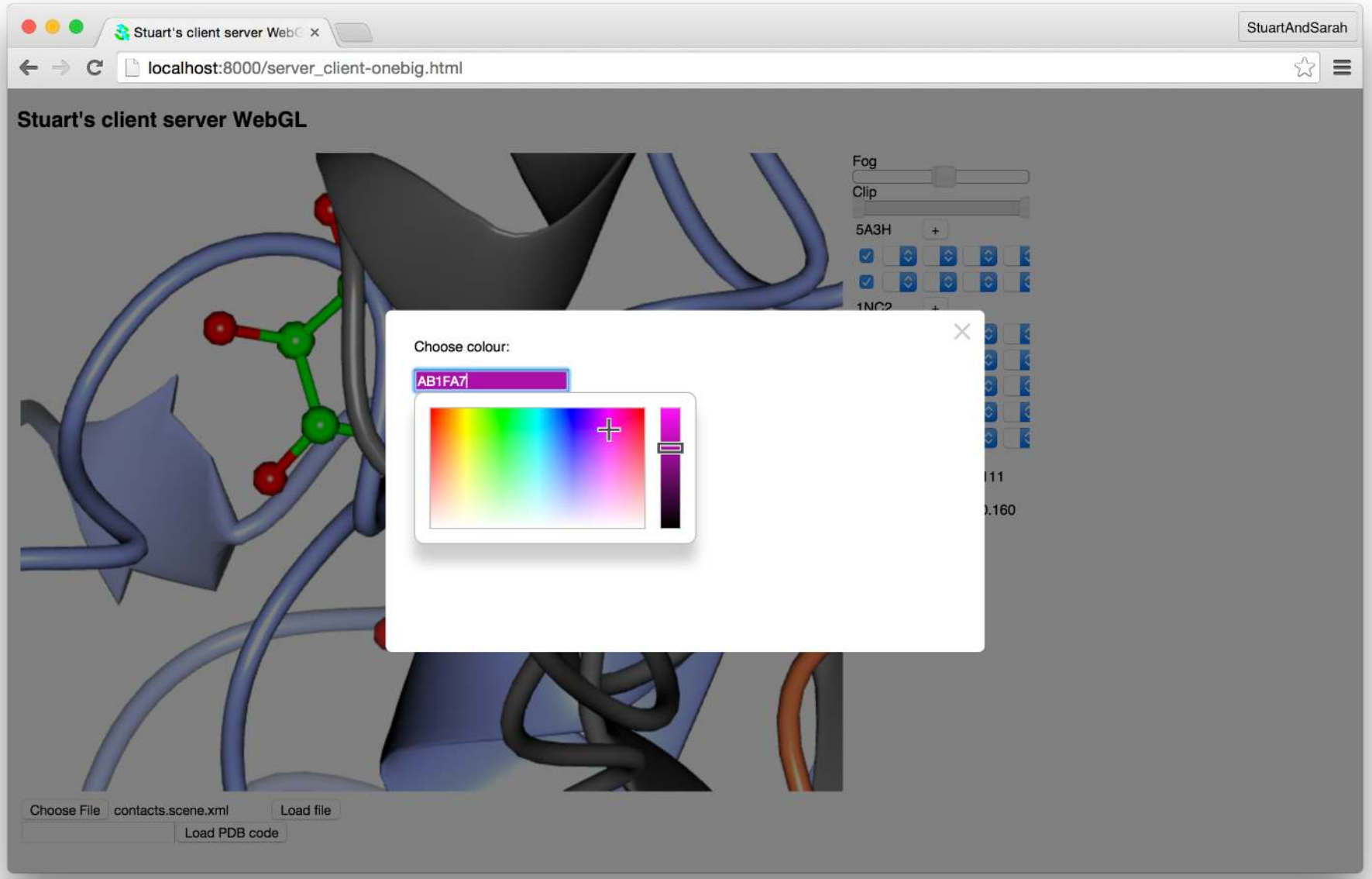
Choose File | ascene.scene.xml | Load file

Load PDB code

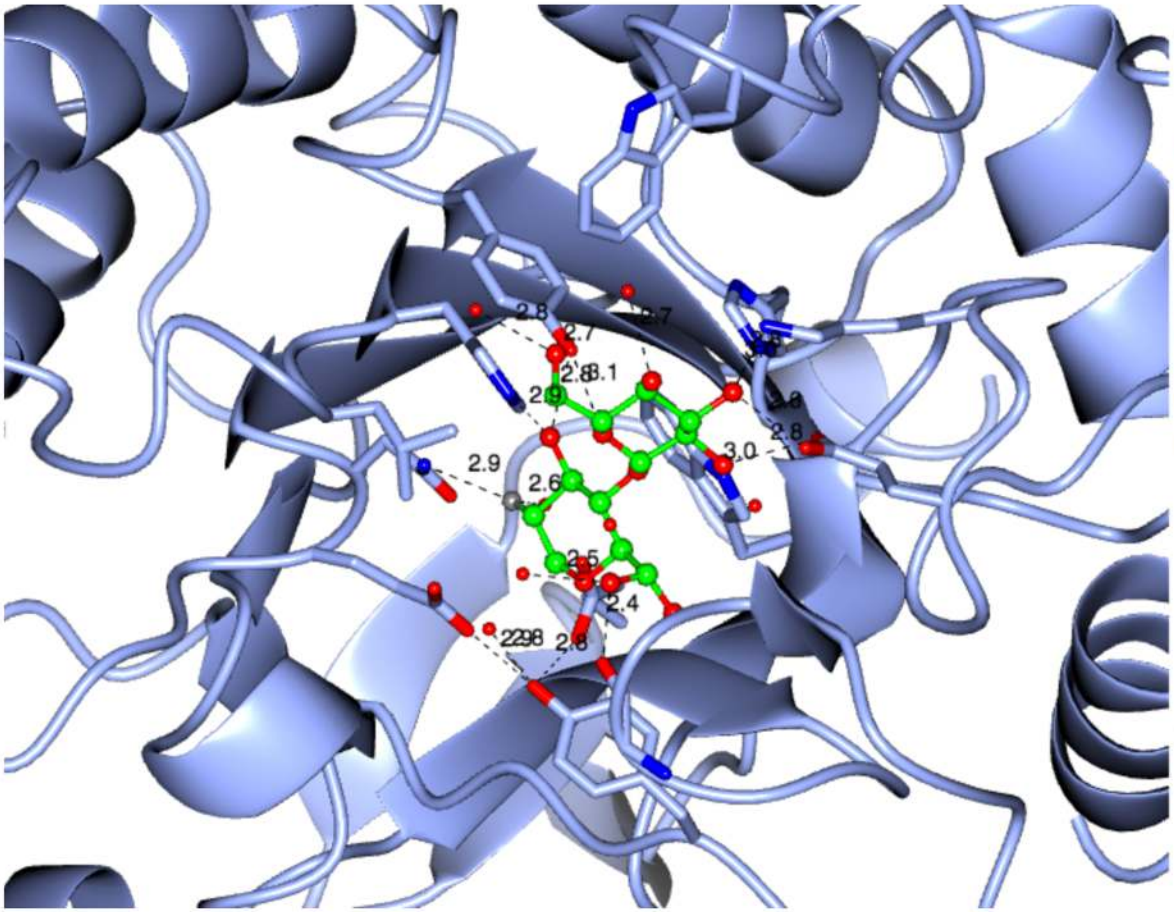

Stuart's client server Web
StuartAndSarah
localhost:8000/server_client-onebig.html
Stuart's client server WebGL
Fog
Clip
5A3H
Choose colour:
AB1FA7
Choose File
contacts.scene.xml
Load file
Load PDB code

Stuart's client server WebG ×

StuartAndSarah

localhost:8000/server_client-onebig.html

Stuart's client server WebGL



Fog

Clip

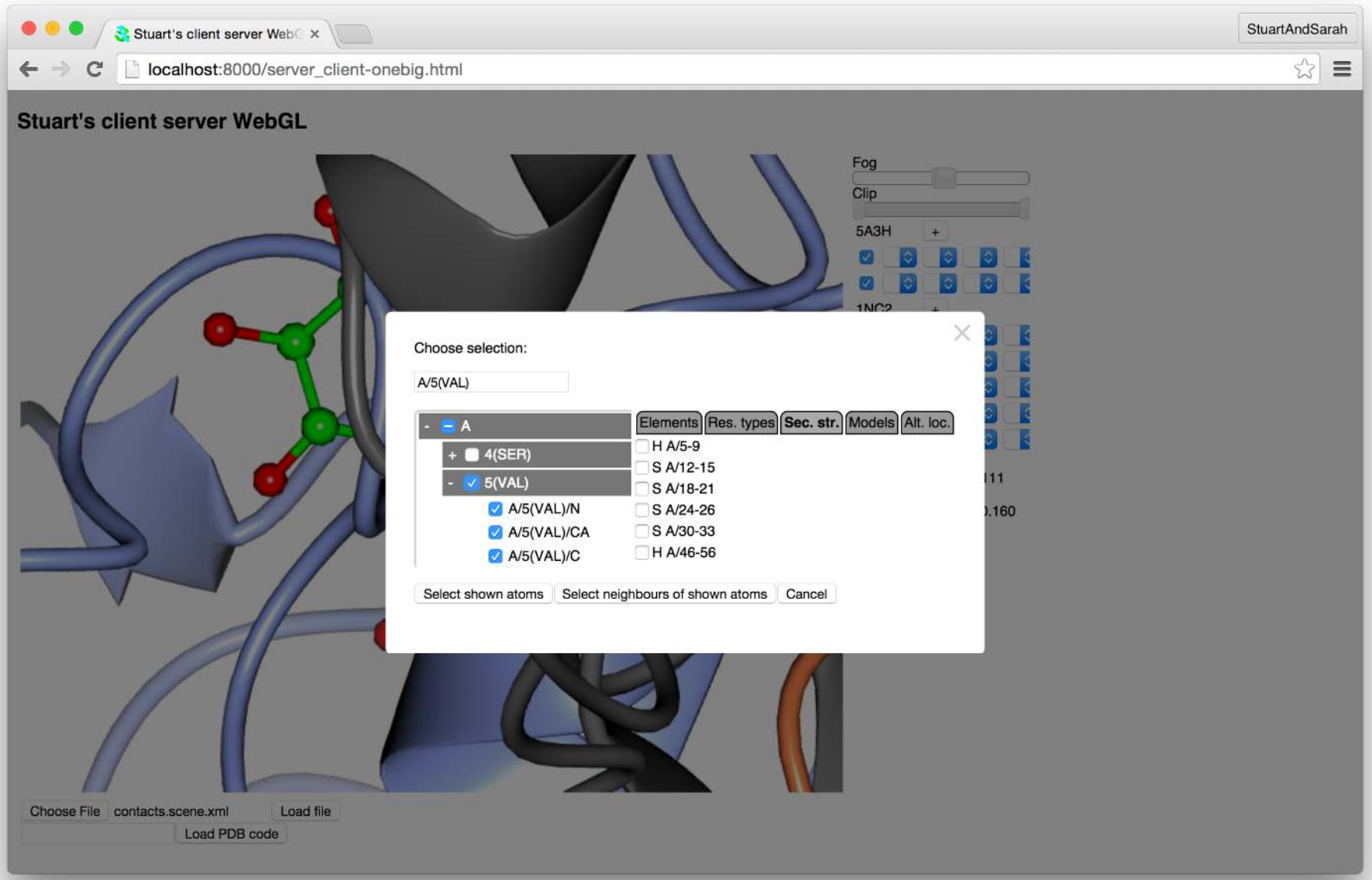
5A3H +

- All atoms
- All non-solvent
- Peptide
- All peptide
- CA trace
- Main chain
- Side chains
- SS bridges
- .. of chains
- A
- Solvent
- Saccharides
- Active sites
- ACI
- NUC
- AC1
- Neighbourhood of Saccharides
- Selection browser
- browser selection:

-63.602 -40.116 -24.590
0.5299
-0.235 -0.035 0.406 0.882
700 540

Choose File | ascene.scene.xml | Load file

Load PDB code

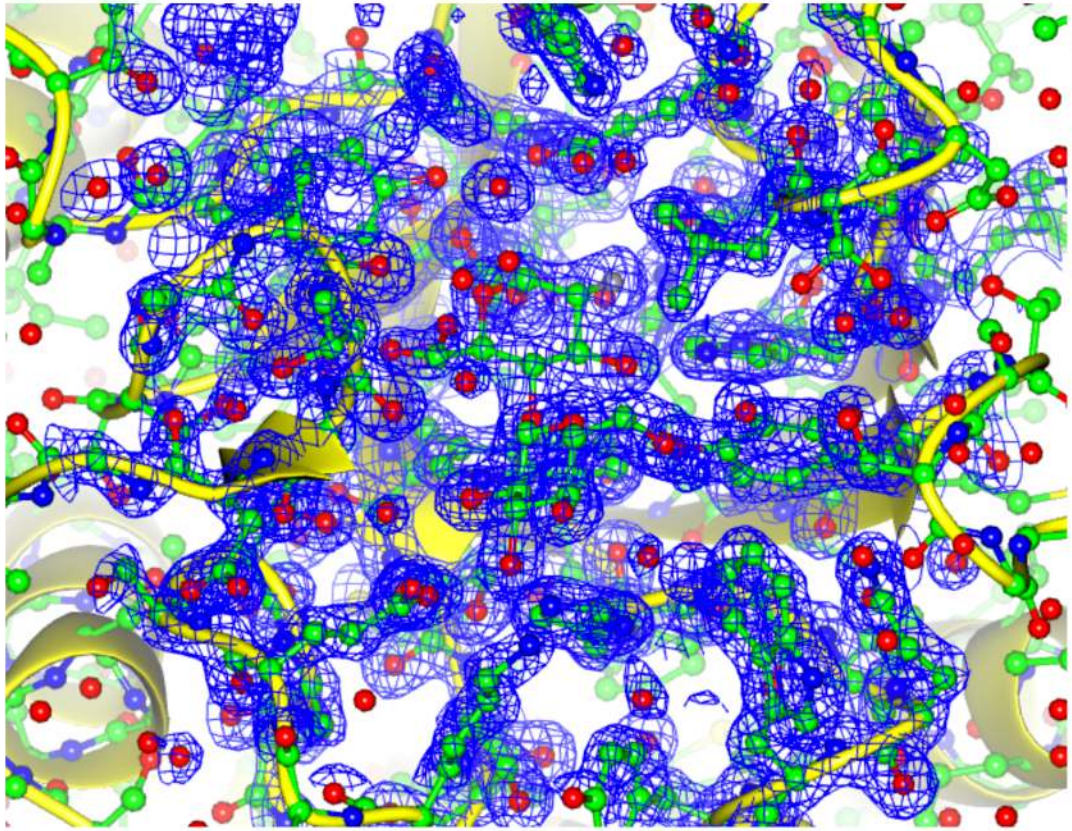

Stuart's client server Web
StuartAndSarah
localhost:8000/server_client-onebig.html
Stuart's client server WebGL
Fog
Clip
5A3H
Choose selection:
A/5(VAL)
A
4(SER)
5(VAL)
A/5(VAL)/N
A/5(VAL)/CA
A/5(VAL)/C
Elements
Res. types
Sec. str.
Models
Alt. loc.
H A/5-9
S A/12-15
S A/18-21
S A/24-26
S A/30-33
H A/46-56
Select shown atoms
Select neighbours of shown atoms
Cancel
Choose File
contacts.scene.xml
Load file
Load PDB code

Stuart's client server WebG ×

StuartAndSarah

localhost:8000/server_client-onebig.html

Stuart's client server WebGL



Fog

Clip

5A3H +

-61.172 -45.721 -36.111
0.4466
0.221 -0.146 -0.964 0.015
700 540

Choose File ascene2.scene.xml Load file

Load PDB code

WebGL and CCP4MG

- “Client” is a web page on which user can load a CCP4MG status file. e.g. saved status from CCP4MG, but *not* currently .pkl), or a hand crafted one (from a template hopefully).
- The client sends the status file to a server. The server runs a “headless” version of CCP4MG which interprets status file, generates CCP4MG “data and display objects” and transforms the display objects into collections of triangles/lines.
- The server sends back the triangles and lines (plus other information) to the client which draws them.

WebGL and CCP4MG

- Advantages:
  - Absolutely rock solid (sort of); server can currently be confused by dodgy uploaded files; but client is fairly indestructible – JavaScript is hard to crash browser with or to cause other unwelcome behaviour with.
  - User interface is currently quite simple (it will get more complicated), requires very little to no interaction with internal complexities of CCP4MG and is thus very fast.
  - Extremely similar programming language (OpenGL ES) as required for Android/iOS 3D graphics. So Android port of this should be easy. iOS client which just draws without connecting to server already exists.

WebGL and CCP4MG

- Disadvantages:
  - Client/server communication is by plain text (json). Although the packing of triangle data is pretty efficient, the server side packing is slower than ideal.
  - Requires server to be running, so not as simple to install as most applications. However a centralized server at institution would make this a non-issue. *Care would be required to avoid accidental transmission of sensitive data.*

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