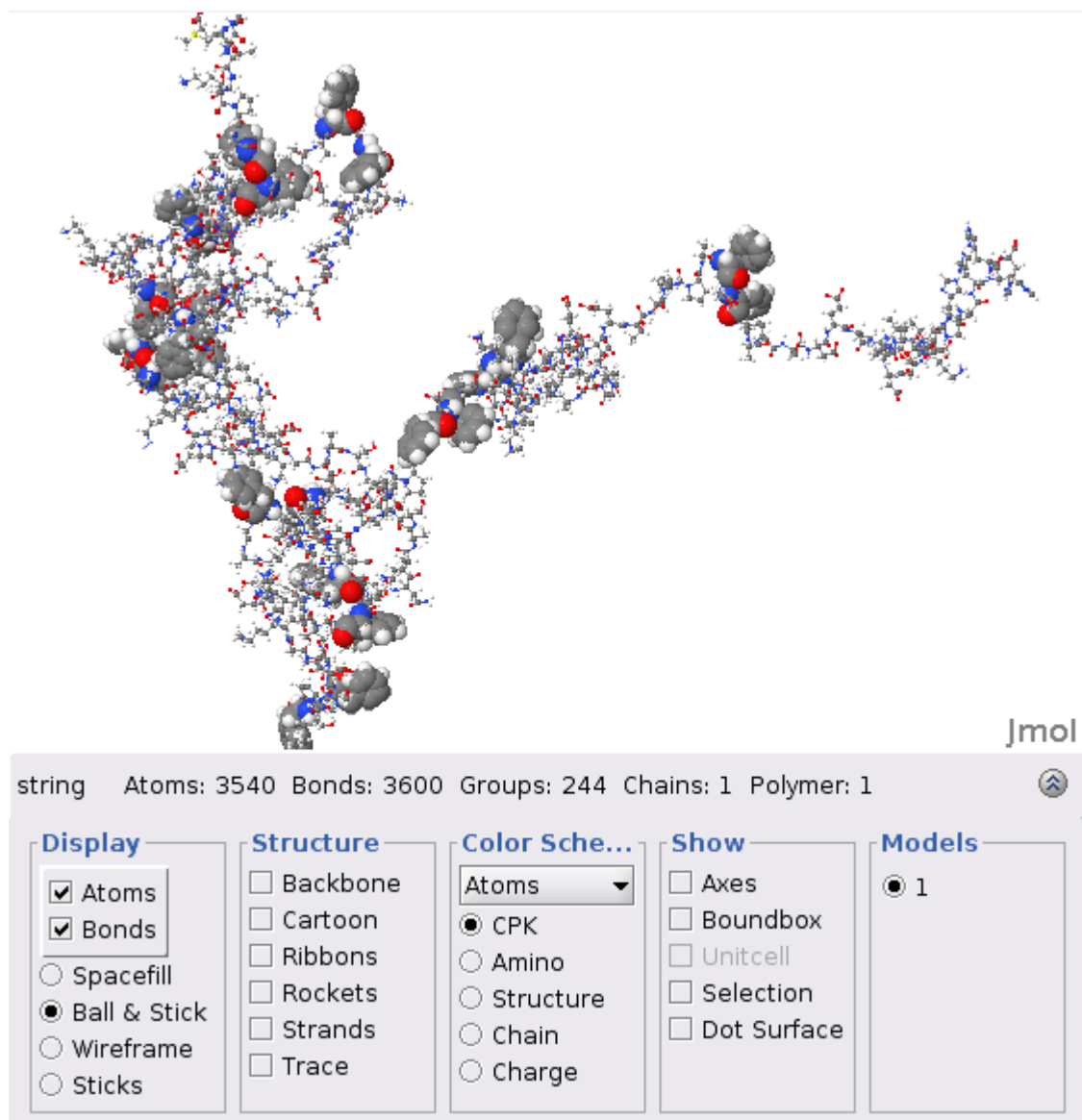


test phe phe differences

```
ips=[1 100 1000 10000 100000 1000000]; close all;
addpath(' ../lib1');
for ii=ips
    [out, file]=gettmppdb(ii);
    Atom=out.Model.Atom;
    disp(file);
    drawnow;

    for jj=1:numel(Atom)
        maskp(jj)=isequal(Atom(jj).resName, 'PHE');
        maksh(jj) = contains(Atom(jj).AtomName, 'H');
        co(jj,1:3)=[Atom(jj).X Atom(jj).Y Atom(jj).Z];
    end
    mask=maskp & maksh;
    co=co(mask,:);
    dr=zeros(size(co,1));
    dr=hypot23u(co);
    f(ii)=figure;
    tmp=sqrt(dr(dr>0));
    %tmp=tmp./sum(tmp);
    mtmp=max(tmp);
    q(ii)=histogram(tmp,50, 'Normalization','probability');
    xlabel('D'); ylabel('Pop'); title ([ 'Phe H distances ' file ]);
    axis([0 150 0 0.07]);
    drawnow;
end
```

Warning: MOLVIEWER will be removed in a future release.

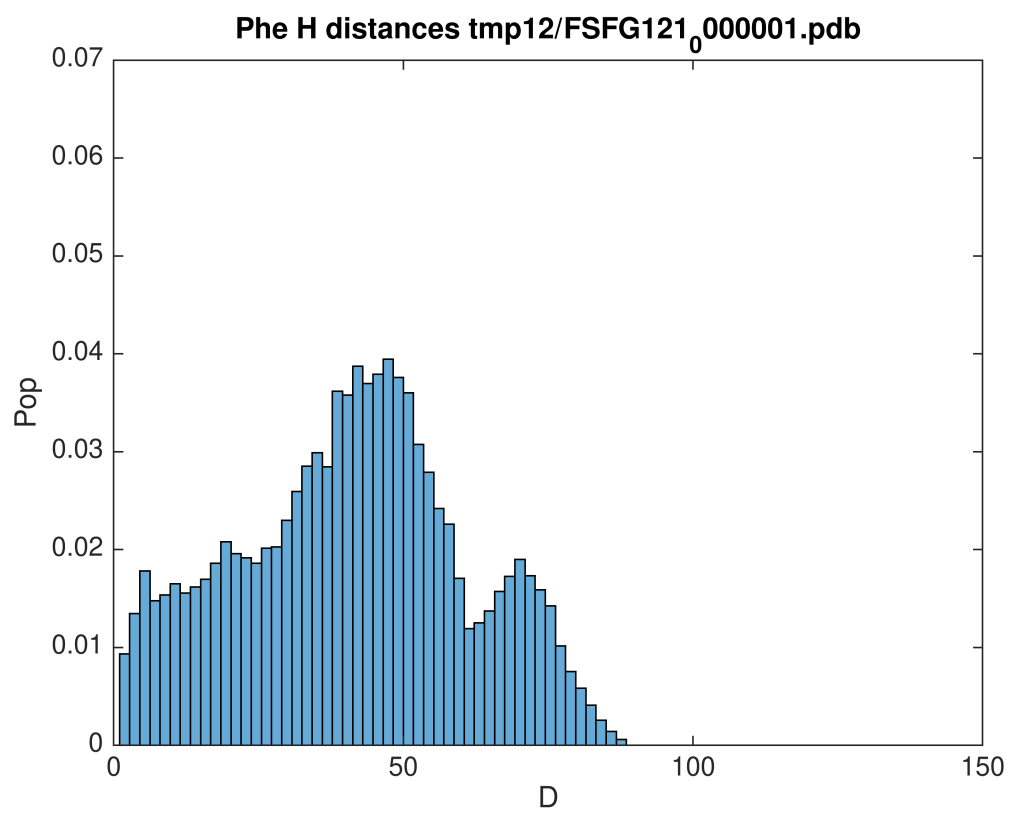


Warning: All the mandatory fields are missing from the input PDB structure.

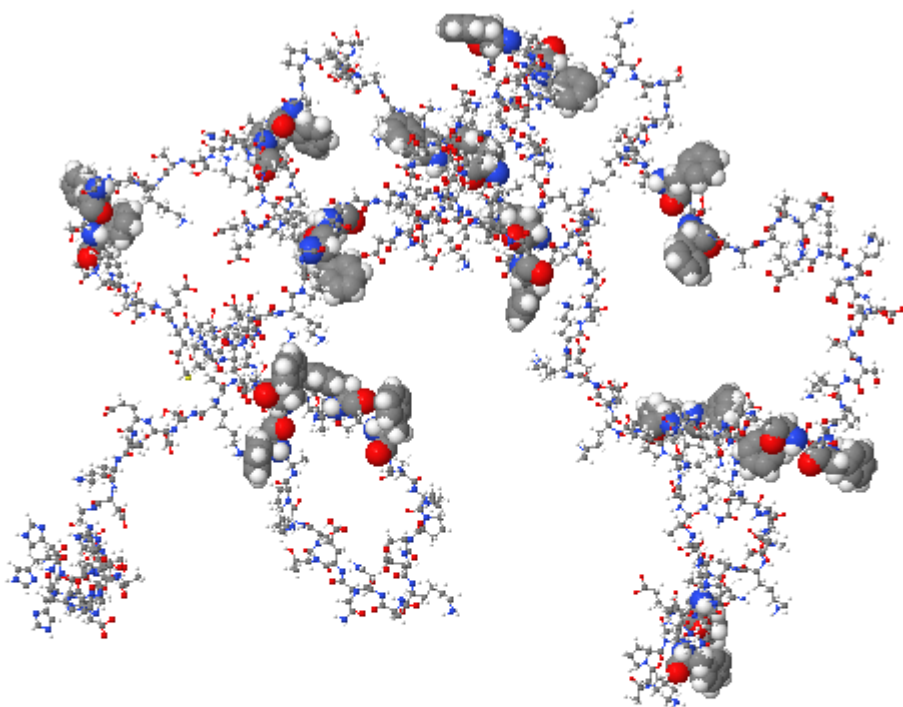
Warning: EVALRASMOLSCRIPT will be removed in a future release.

tmp12/FSFG121_0000001.pdb

Warning: MATLAB has disabled some advanced graphics rendering features by switching to software OpenGL. For more information, [click here](#).



Warning: MOLVIEWER will be removed in a future release.



Jmol

string Atoms: 3540 Bonds: 3609 Groups: 244 Chains: 1 Polymer: 1



Display

- ☒ Atoms
- ☒ Bonds
- ☐ Spacefill
- ☒ Ball & Stick
- ☐ Wireframe
- ☐ Sticks

Structure

- ☐ Backbone
- ☐ Cartoon
- ☐ Ribbons
- ☐ Rockets
- ☐ Strands
- ☐ Trace

Color Scheme

- Atoms ▼
- ☒ CPK
 - ☐ Amino
 - ☐ Structure
 - ☐ Chain
 - ☐ Charge

Show

- ☐ Axes
- ☐ Boundbox
- ☐ Unitcell
- ☐ Selection
- ☐ Dot Surface

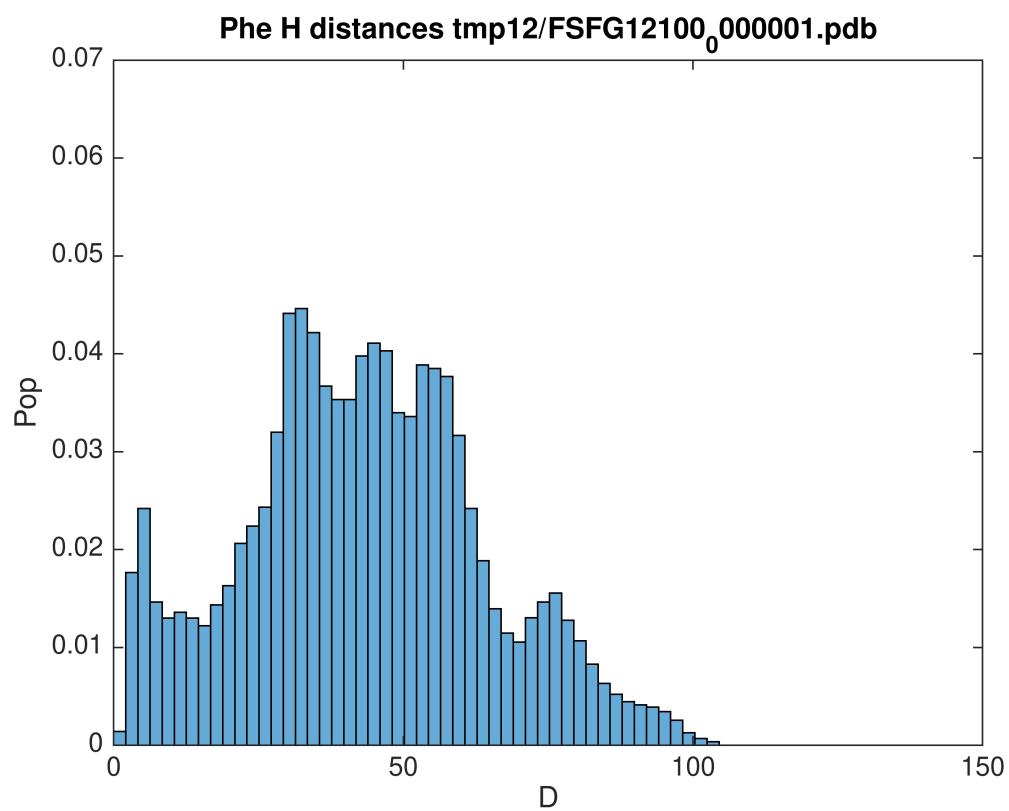
Models

- ☒ 1

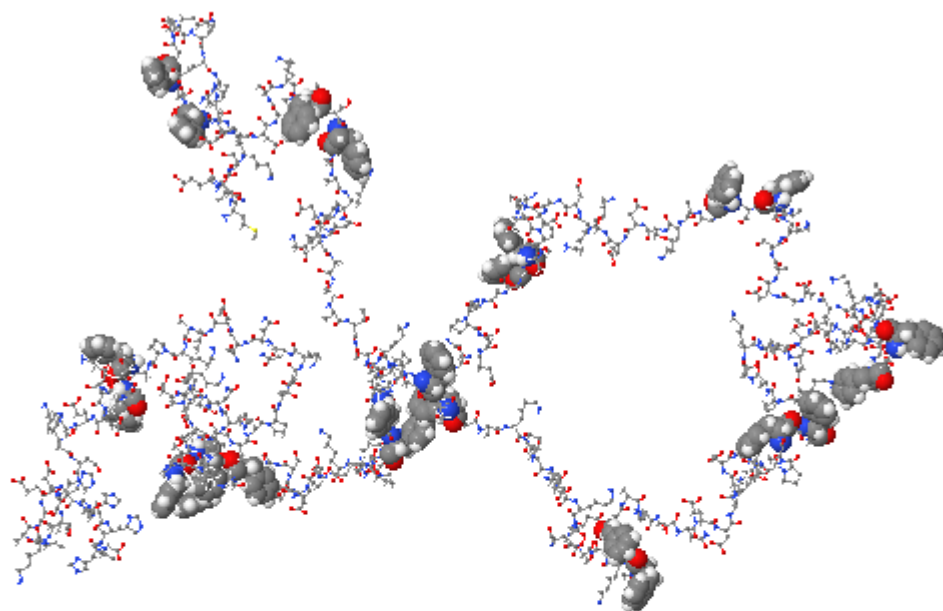
Warning: All the mandatory fields are missing from the input PDB structure.

Warning: EVALRASMOLSCRIPT will be removed in a future release.

tmp12/FSFG12100_0000001.pdb



Warning: MOLVIEWER will be removed in a future release.



Jmol

string Atoms: 3540 Bonds: 3600 Groups: 244 Chains: 1 Polymer: 1

Display

- ☒ Atoms
- ☒ Bonds
- ☐ Spacefill
- ☒ Ball & Stick
- ☐ Wireframe
- ☐ Sticks

Structure

- ☐ Backbone
- ☐ Cartoon
- ☐ Ribbons
- ☐ Rockets
- ☐ Strands
- ☐ Trace

Color Sche...

- Atoms ▼
- ☒ CPK
- ☐ Amino
- ☐ Structure
- ☐ Chain
- ☐ Charge

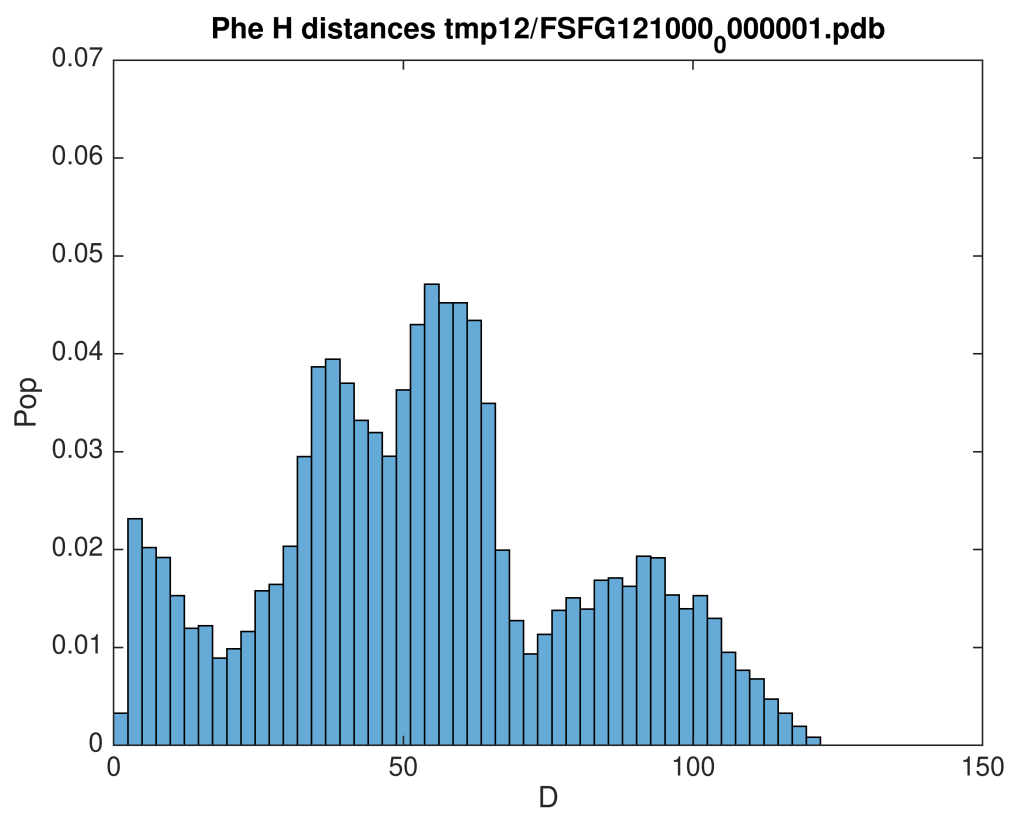
Show

- ☐ Axes
- ☐ BoundingBox
- ☐ Unitcell
- ☐ Selection
- ☐ Dot Surface

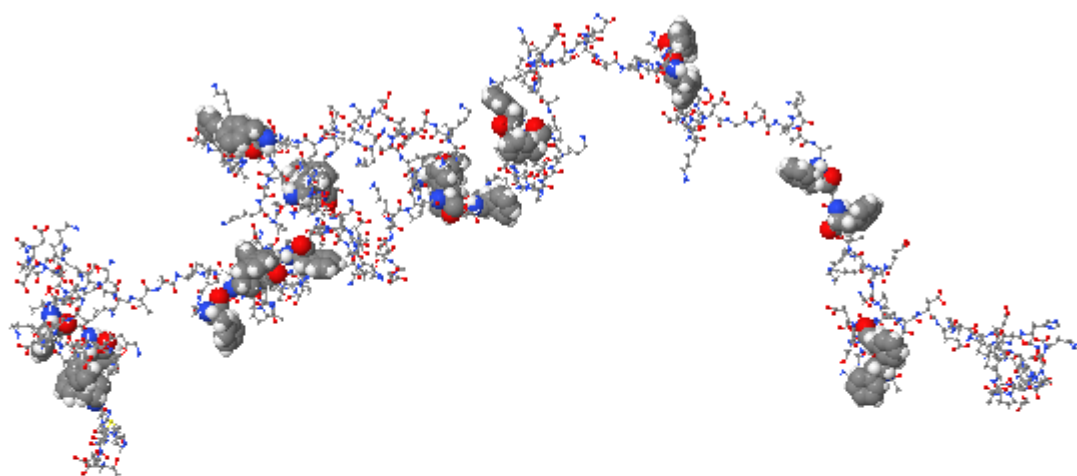
Models

- ☒ 1

Warning: All the mandatory fields are missing from the input PDB structure.
 Warning: EVALRASMOLSCRIPT will be removed in a future release.
 tmp12/FSFG121000_0000001.pdb



Warning: MOLVIEWER will be removed in a future release.



Jmol

string Atoms: 3540 Bonds: 3599 Groups: 244 Chains: 1 Polymer: 1



Display

- ☒ Atoms
- ☒ Bonds
- ☐ Spacefill
- ☒ Ball & Stick
- ☐ Wireframe
- ☐ Sticks

Structure

- ☐ Backbone
- ☐ Cartoon
- ☐ Ribbons
- ☐ Rockets
- ☐ Strands
- ☐ Trace

Color Sche...

- Atoms ▼
- ☒ CPK
 - ☐ Amino
 - ☐ Structure
 - ☐ Chain
 - ☐ Charge

Show

- ☐ Axes
- ☐ Boundbox
- ☐ Unitcell
- ☐ Selection
- ☐ Dot Surface

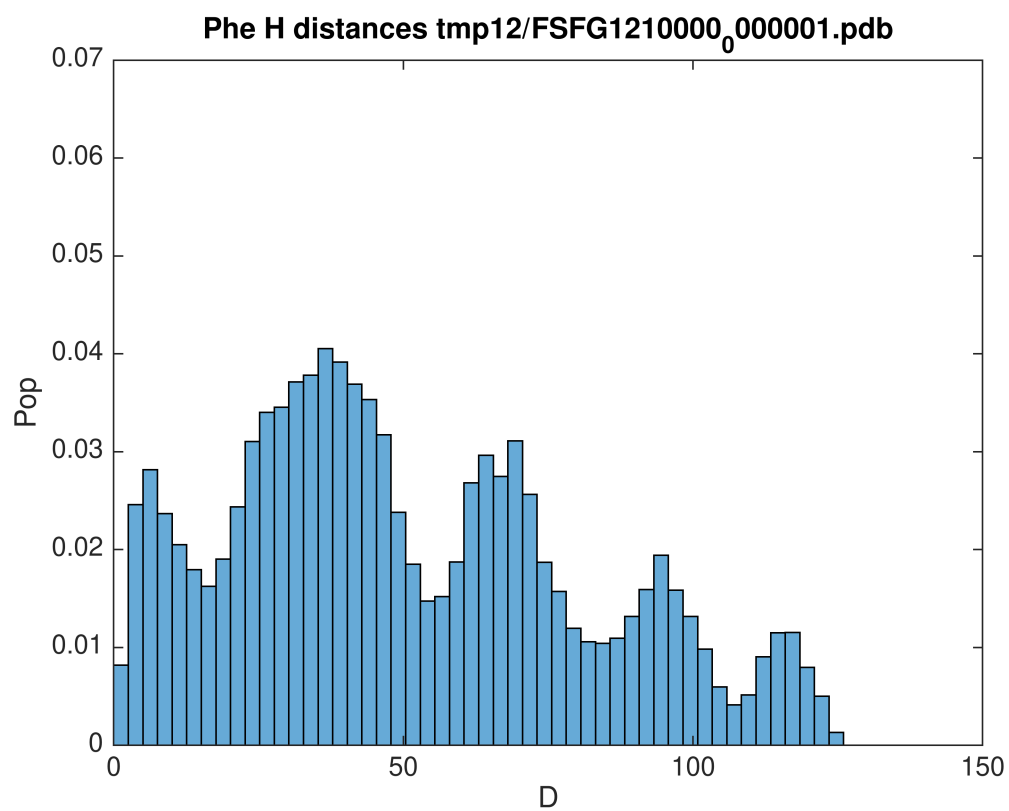
Models

- ☒ 1

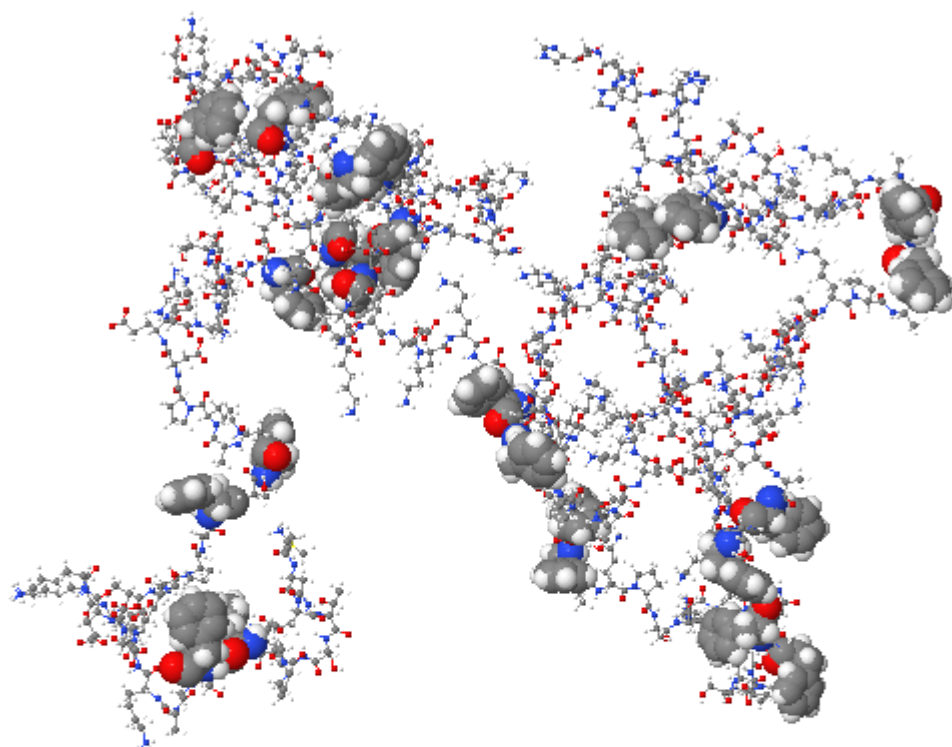
Warning: All the mandatory fields are missing from the input PDB structure.

Warning: EVALRASMOLSCRIPT will be removed in a future release.

tmp12/FSFG1210000_0000001.pdb



Warning: MOLVIEWER will be removed in a future release.



Jmol

string Atoms: 3540 Bonds: 3612 Groups: 244 Chains: 1 Polymer: 1

Display

- ☒ Atoms
- ☒ Bonds
- ☐ Spacefill
- ☒ Ball & Stick
- ☐ Wireframe
- ☐ Sticks

Structure

- ☐ Backbone
- ☐ Cartoon
- ☐ Ribbons
- ☐ Rockets
- ☐ Strands
- ☐ Trace

Color Sche...

- Atoms ▼
- ☒ CPK
- ☐ Amino
- ☐ Structure
- ☐ Chain
- ☐ Charge

Show

- ☐ Axes
- ☐ BoundingBox
- ☐ Unitcell
- ☐ Selection
- ☐ Dot Surface

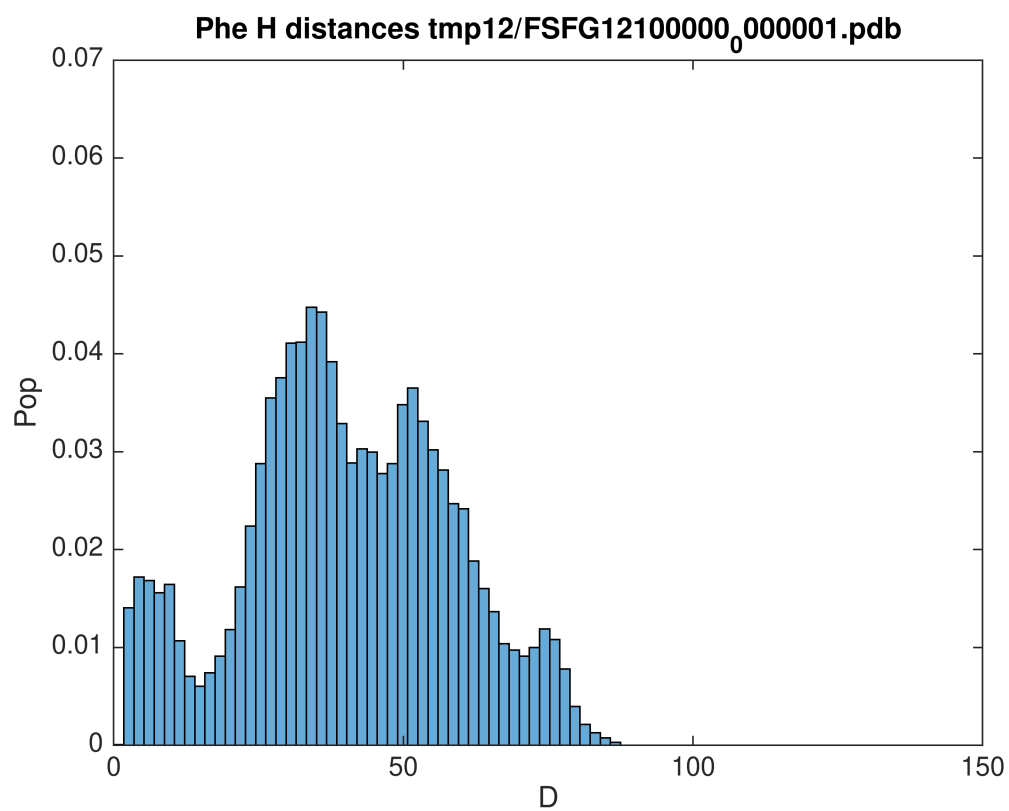
Models

- ☒ 1

Warning: All the mandatory fields are missing from the input PDB structure.

Warning: EVALRASMOLSCRIPT will be removed in a future release.

tmp12/FSFG12100000_0000001.pdb



Warning: MOLVIEWER will be removed in a future release.

