

calc sans fort variable D2O fraction (not %)

dc 11/19, 12/22, 7/23 8/23 modify for existing out's

```
datetime
```

```
ans = datetime  
      06-Sep-2023 11:15:15
```

```
clearvars  
close all  
cd ( '/gs/gsfss0/shared-lab/cowburnlab' ); % working areas  
Lbase=pwd;  
addpath(genpath('./lib1')) % DC library  
addpath( './TraDES-2' )    % local  
cd ( 'ATSAS' );  
P=pwd;  
addpath(P);  
  
pwd
```

```
ans =  
      '/gs/gsfss0/shared-lab/cowburnlab/ATSAS'
```

```
delete(gcp('nocreate'));
```

Parallel pool using the 'Threads' profile is shutting down.

```
parpool('processes');
```

Starting parallel pool (parpool) using the 'processes' profile ...
Connected to parallel pool with 32 workers.

```
datetime
```

```
ans = datetime  
      06-Sep-2023 11:17:27
```

```
narginX=0;  
switch narginX % Use defaults, all changeable  
case 0 % just for test cases, Relic of function call  
    N0=1; % case A , 0 was 9000001  
    N=2e6;  
    fD2O=0.43;  
    fDeut=1;  
    ROOT='FSFG12';  
    new=0;  
case 1 % make a lot more with default values  
    fD2O=0.42; fDeut=1; ROOT='FSFG12'; new=0;  
case 2
```

```

        fDeut=1;      ROOT='FSFG12';      new=0;
    case 3
        ROOT='FSFG12'; new=0;
    case 4
        new=0;
    otherwise    % exit
end
% make strings of values
fD20=iif(ischar(fD20),fD20,strip(num2str(fD20)));
fDeut=iif(ischar(fDeut),fDeut,strip(num2str(fDeut)));

```

```

% set up TRADES scripts
BIN='/public/apps/xplor/xplor-nih-3.5/bin/calcSAXS';

BIN_T=([Lbase filesep 'TraDES-2']);
TRADES=[BIN_T filesep 'trades -p T -a F ']; % executable command
TEMP='./tmp12';                             % working tmp dir, must survive
to analysis
TAG='_0000001';                             % relic of trades
P=pwd;          %push current
cd (BIN_T);
xStatus=0;
if new || ~exist ([ROOT '.trj'],'file')      % do the default setup for Trades
    % adapted from SaSp DaCo 11/19, uses default values
    system ([BIN_T filesep 'benchtraj']);
    [xStatus, cmdout]=system([BIN_T filesep 'seq2trj -f ' ROOT '.faa -o '
ROOT ' -cT -v ' ]]);
    if xStatus, error(cmdout); end
    cd (P);

end          % pop current
if xStatus , error(cmdout); end
checkPDB=1000;      % check files of reasonable size
checkPHE=100;
outM=struct([]);

```

from the past

```

try
    %load Aug2
    N0= 1;
catch
    % R=readmatrix('out1400000R.txt');
    %Q=readmatrix('out1400000Q.txt');
    %R=single(R);    Q=single(Q);
    %N0=numel(R)+1;
    %save Aug2
end

```

```
istep=10000;  
N=2000006
```

```
N = 2000006
```

```
quick=false
```

```
quick = logical  
0
```

```
for iout=N0:istep:N  
    nz=min(iout+istep-1, N);  
    parfor jj=iout:nz  
  
        cmdout=''; Status=1;  
        s_N=strip(num2str(jj));           % simple number as char  
        tmpS=[TEMP filesep ROOT s_N ]    % root for current file  
if ~quick  
    if ~exist ([tmpS TAG '.phe'],'file')  
  
        if exist ([tmpS TAG '.pdb.gz'],'file') && ~exist([tmpS TAG  
'pdb'],'file')  
            gunzip([tmpS TAG '.pdb.gz']);  
        end % probably may need to run in for loop once  
        if exist([tmpS '.pdb'],'file')  
            movefile([tmpS '.pdb'],[tmpS TAG '.pdb'])  
        end  
        if ~exist([tmpS TAG '.pdb'],'file') % execute Trades case  
            cmd=[TRADES ' -f ' ROOT ' -o ' tmpS ' -b 1 '];  
            [Status, cmdout]= system (cmd); %#ok<*ASGLU>  
        end  
        if Status, error(cmdout); end  
  
        ff=fileread([tmpS TAG '.pdb']);  
  
        if numel(ff) < checkPDB  
            warning(' PDB short, deleted');  
            delete ([tmpS TAG '.pdb']);  
            continue;  
        end  
  
        infi=[tmpS TAG '.phe'];  
        cmd = ['grep '^ATOM.*PHE' ' ' tmpS TAG '.pdb > ' infi '];  
        [a,b]=system(cmd);  
        if a, error(b); end  
        ff=fileread([tmpS TAG '.phe']);  
        if numel(ff) < checkPHE  
            warning(' PHE short, deleted');  
            delete ([tmpS TAG '.phe']);  
        end  
    end  
end
```

```

        continue;
    end
end
end % quick
outf=[tmpS TAG s_N '.out']; % file for SANS profile
tmpQ=[BIN ' -sans -fractionD20 ' fD20 ...
    ' -fractionDeuterated ' fDeut ' ' tmpS TAG '.phe > ' outf ...
    ' ; sync ' ] ; % set up command

if new || ~exist(outf,'file') % look for file
    if new || ~exist([outf '.gz'],'file')

        [Status, cmdout]=system(tmpQ);
        if Status, error(cmdout); end
    else
        gunzip([outf '.gz']);
    end
end

Status=-10;
while Status
    try
        out(jj)=getoutf(outf);
        Status=0;
    catch
        disp([ 'error outf, retry ' tmpS] );
        system('sync');
        [Status2, cmdout]=system(tmpQ); % retry
        if Status2 , warning (cmdout); end
        Status=Status+1; % seems not needed, but was at one time,
possibly because of file sync issues
        if ~Status, warning(['file not processed ' tmpS]); end
    end
end

if ~rem(jj,1000), disp(jj); system('sync'); end % system monitor

% end
end
%save Aug2
end

```

3000

4000

5000

1000

```

1989000
1990000
1995000
1991000
1992000
1994000
1993000
1997000
1996000
1998000
1999000
2000000

```

```

close all;

save("out.mat","-v7.3");           % -v needed for size

```

do preliminary plots for survey

```
datetime
```

```

ans = datetime
    06-Sep-2023 14:04:41

```

```

% fix R I2
%
%I2=Q(:,2:2:end);
%for ii=numel(R)+1:numel(out)
parfor ii=1:numel(out)
    R(ii)=out(ii).R;
    I2(:,ii)=out(ii).Q(:,2);
end

rq=out(end).Q(:,1); % range of q

```

```

set(groot,'defaultAxesColorOrder',[1 0 0;0 1 0;0 0 1], ...
    'defaultAxesLineStyleOrder','-|--|:|-.');           % plot formatF

```

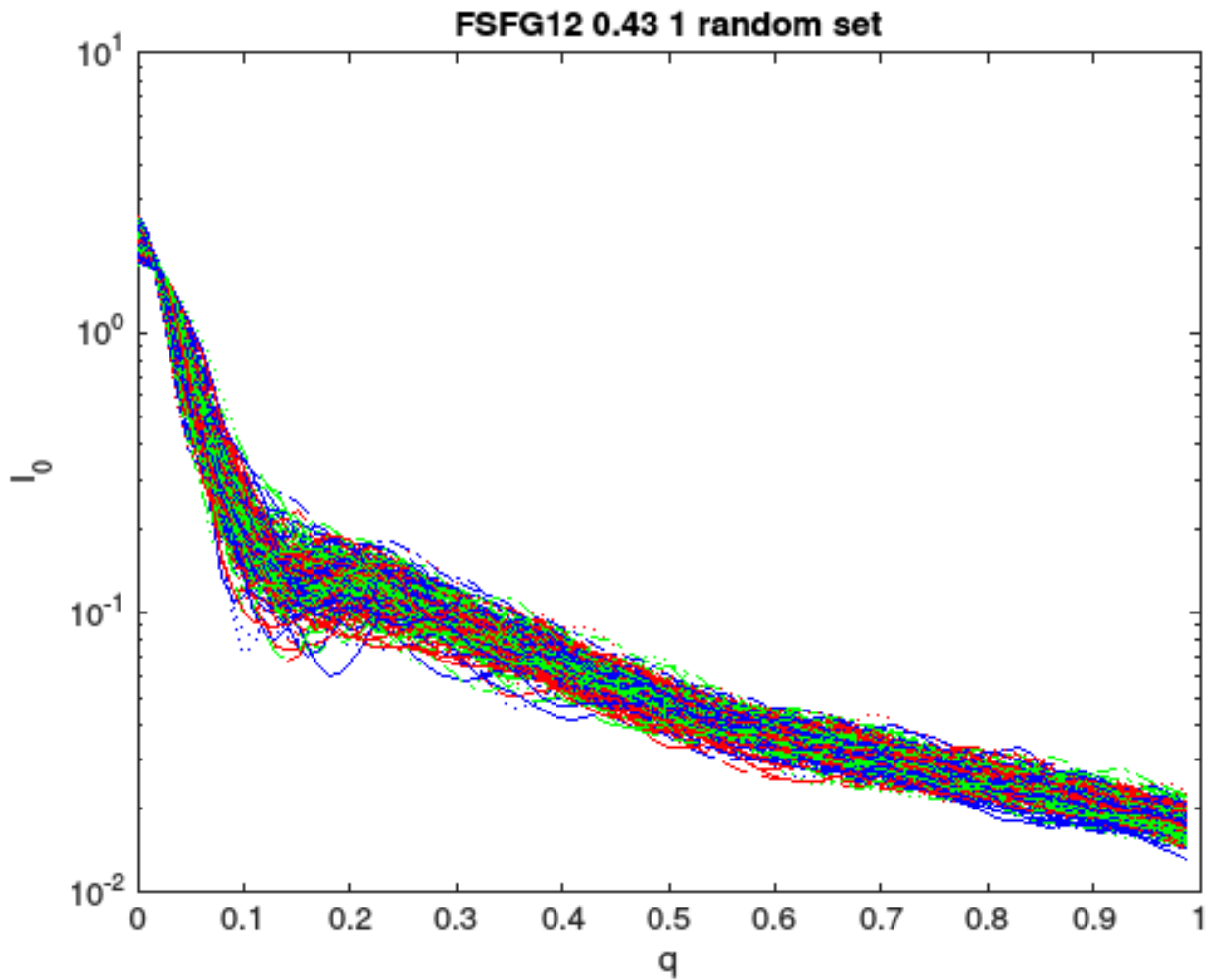
```

h0=figure;

iran=300;
dN=randperm(numel(out),iran);
dN=max(dN,1);

for jji=1:iran
    jj=dN(jji);
    semilogy(rq,I2(:,jj));
    if jji==1, hold on; end % slow, but not easily done otherwise
end
xlabel('q'); ylabel('I_0'); title([ROOT ' ' fD20 ' ' fDeut ' random set']);
axis([0 1 0.01 10]);

```



```

savefig(h0,'fig0', 'compact');

```

plot extreme cases

```

qset=rq; % assumes q's same in all
iset=zeros(numel(qset),N,'single');
iset=I2;

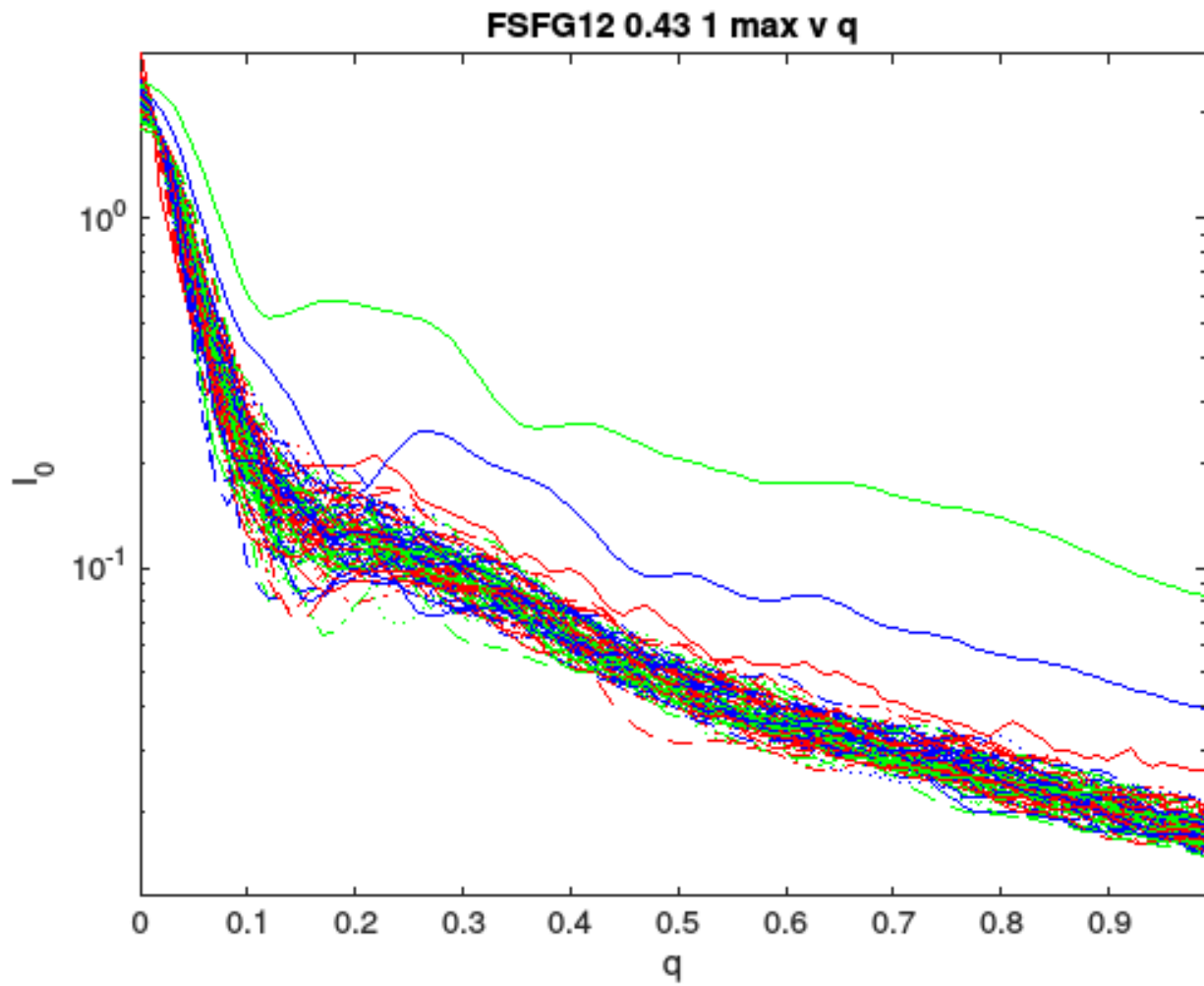
```

```
%for ii=1:N
%   iset(:,ii)=out(ii).Q(:,2);      %matrix of I values
%end
mxis=max(iset(:));
mnis=min(iset(:));
```

datetime

```
ans = datetime
      06-Sep-2023 14:06:09
```

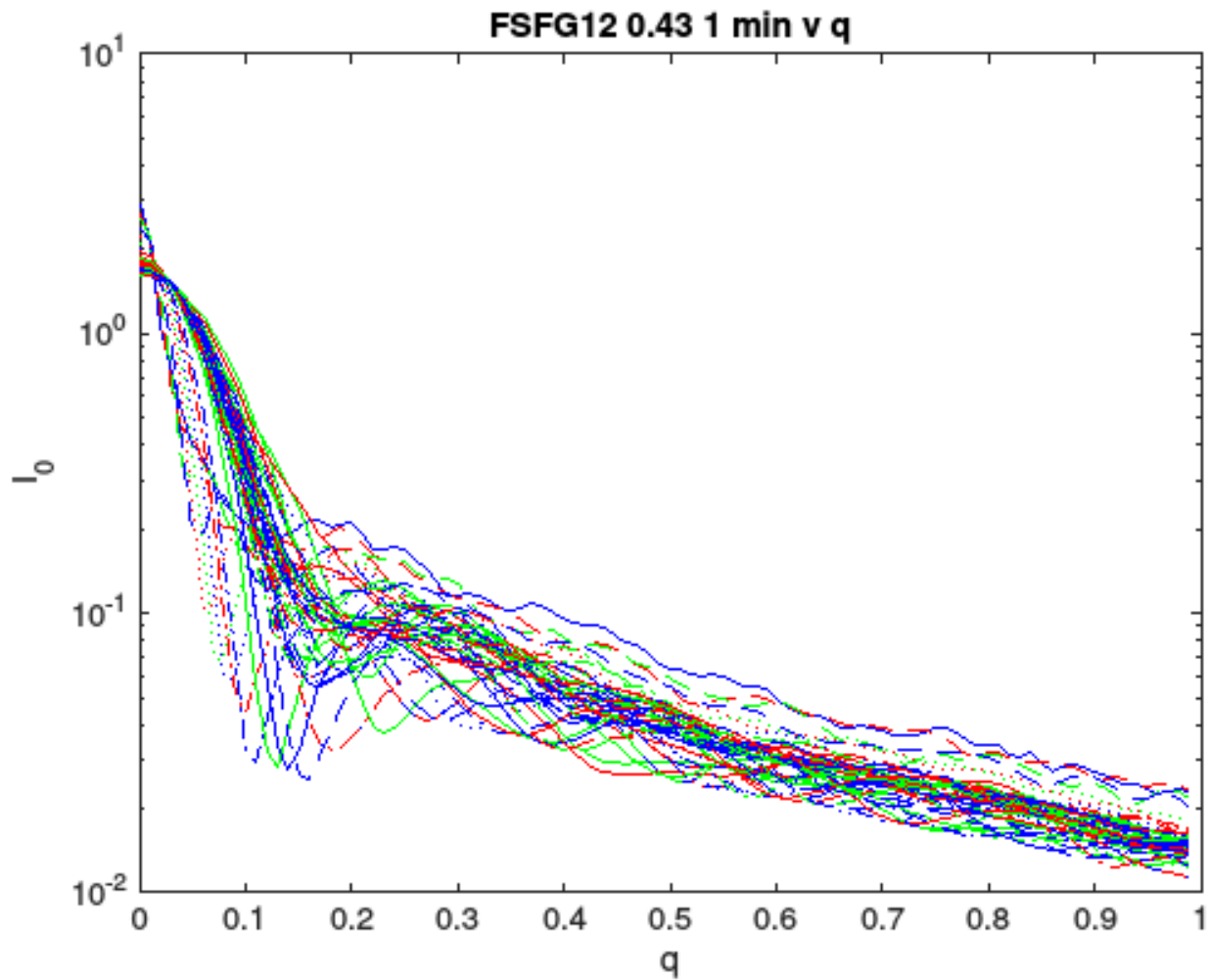
```
h1=figure;
mask=true(size(I2,2),1);
for jj=1:numel(qset)
    [imax,ind]=max(I2(jj,mask));
    semilogy(qset,I2(:,ind));
    Pind(1)=ind;
    mask(ind)=false;
    if jj==1, hold on; end
end
xlabel('q'); ylabel('I_0'); title([ROOT ' ' fD2O ' ' fDeut ' max v q']);
axis([0 qset(end) mnis mxis]);
```



```

savefig(h1,'fig1','compact');
h2=figure;
for jj=1:numel(qset)
    [imax,ind]=min(I2(jj,:));
    semilogy(qset,I2(:,ind));
    Pind(2)=ind;
    if jj==1, hold on; end
end
%axis([0 qset(end) mnis mxis]);
xlabel('q'); ylabel('I_0'); title([ROOT ' ' fD20 ' ' fDeut ' min v q' ]);

```

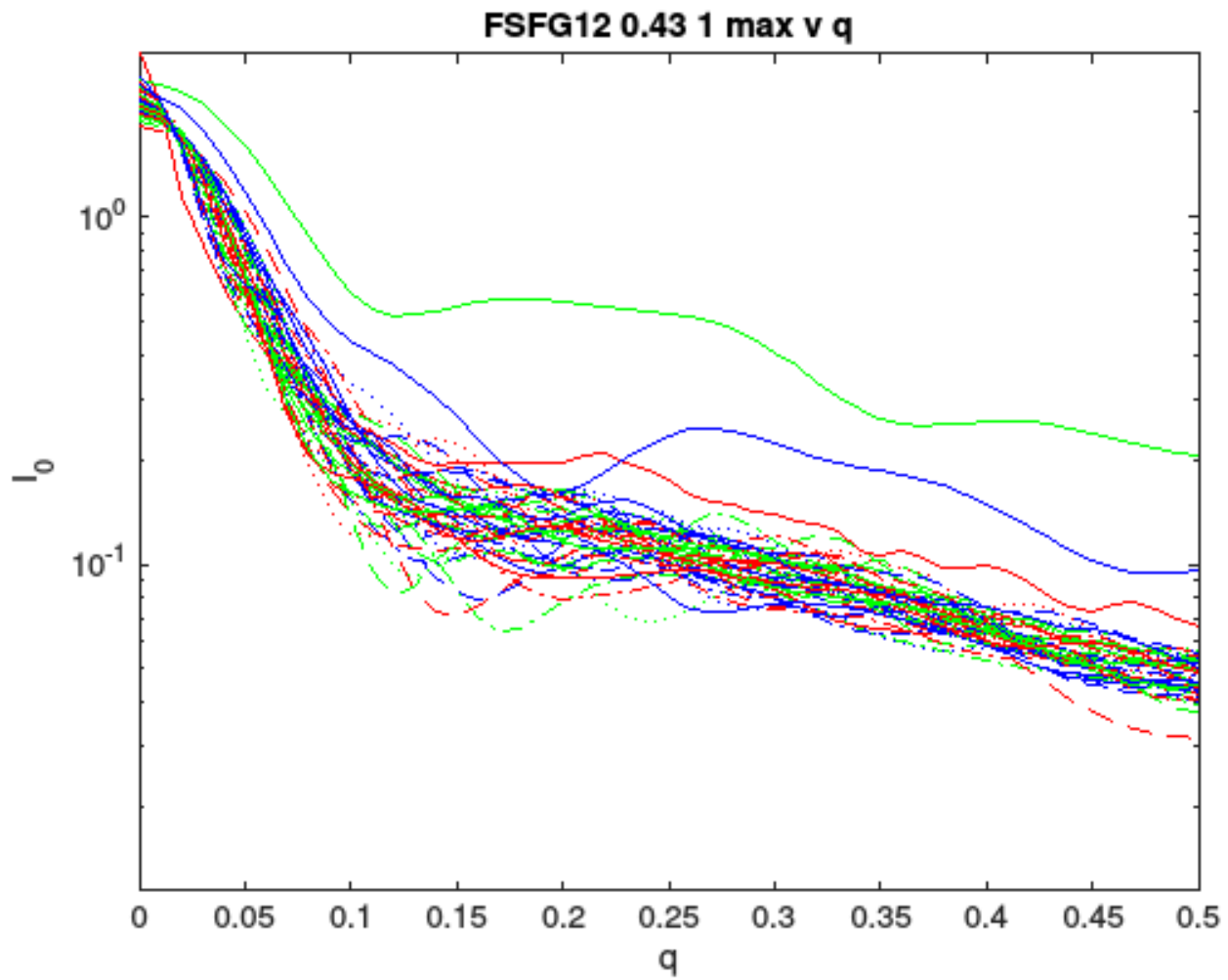
reduced range

```

savefig(h2,'fig2','compact');
qset2=qset(qset <= 0.5);
n2= numel(qset2);

h3=figure;
mask=true(size(iset,2),1) ;
for jj=1:numel(qset2)
    [imax,ind]=max(I2(jj,mask));
    semilogy(qset2,I2(1:n2,ind));
    Pind(jj,1)=ind;
    mask(ind)=false;
    if jj==1, hold on; end
end
xlabel('q'); ylabel('I_0'); title([ROOT ' ' fD20 ' ' fDeut ' max v q']);
axis([0 qset2(end) mnis mxis]);

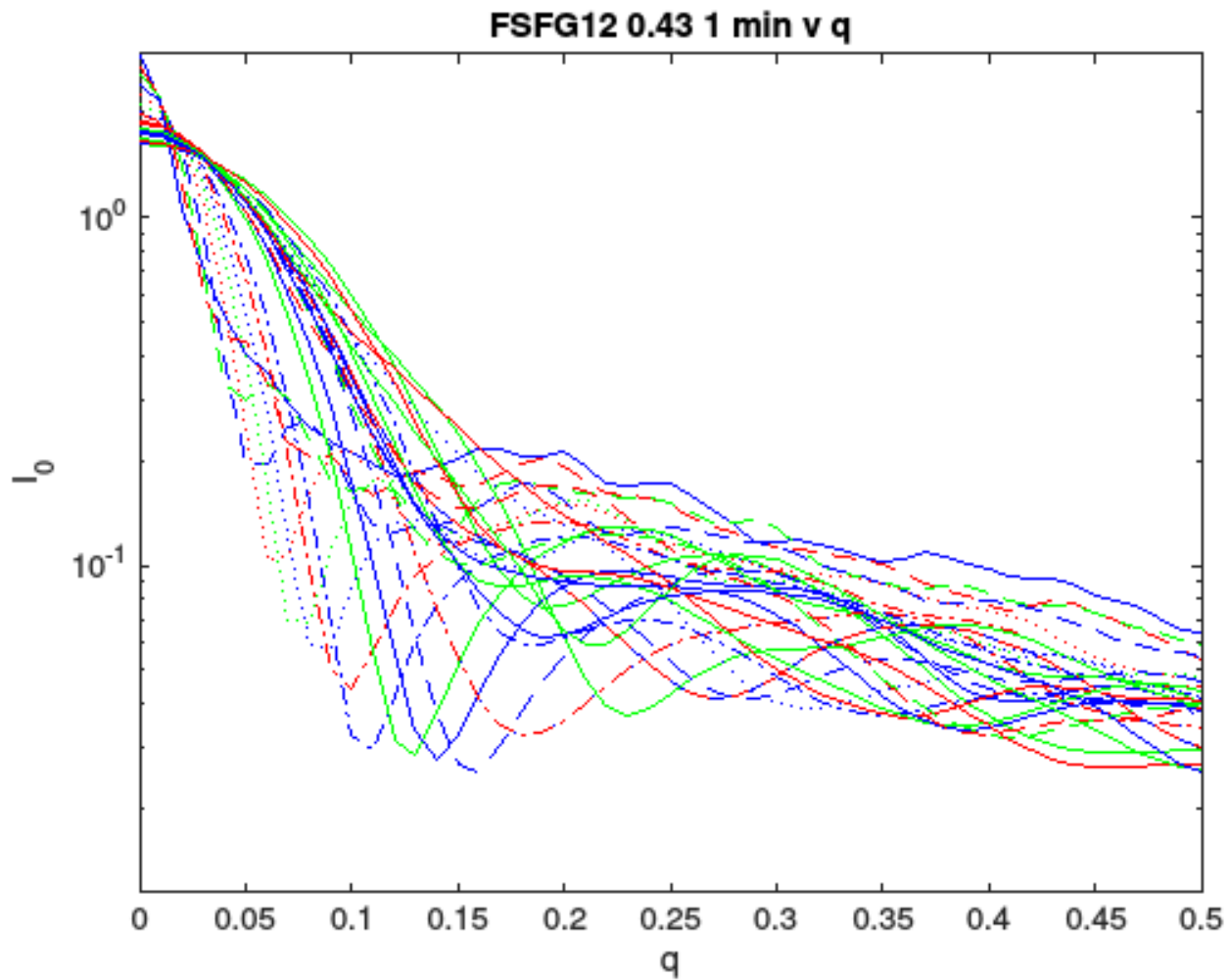
```



```

savefig(h3,'fig3','compact');
h4=figure;
for jj=1:numel(qset2)
    [imax,ind]=min(I2(jj,:));
    semilogy(qset2,I2(1:n2,ind));
    Pind(jj,2)=ind; %#ok<*SAGROW>
    if jj==1, hold on; end
end
axis([0 qset2(end) mnis mxis]);
xlabel('q'); ylabel('I_0'); title([ROOT ' ' fD20 ' ' fDeut ' min v q' ]);

```



```
savefig(h4,'fig4','compact');
```

```
%save out
```

get structures

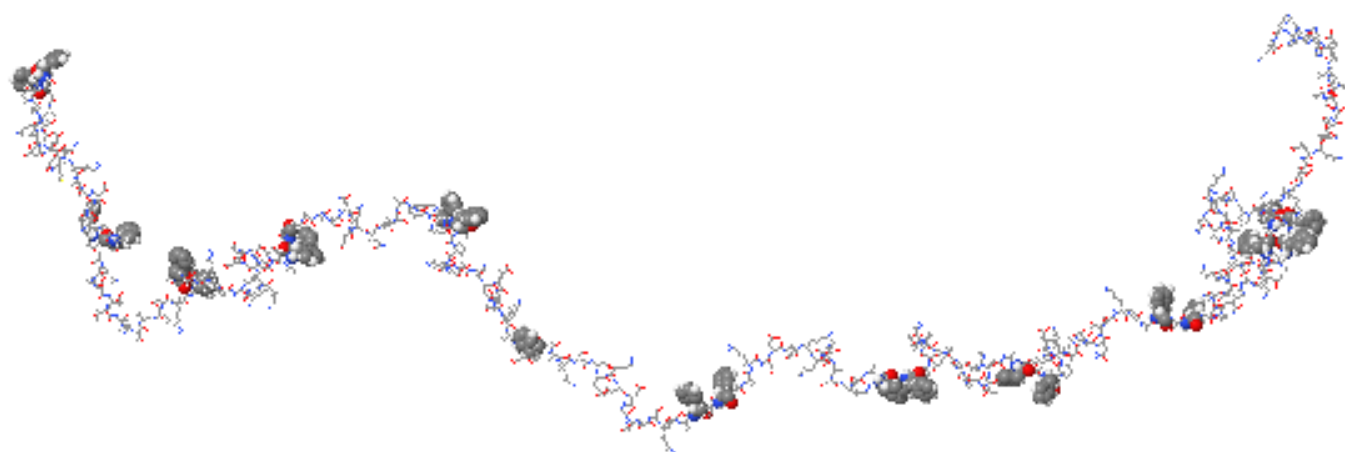
```
datetime
```

```
ans = datetime
      06-Sep-2023 14:06:21
```

```
fS=@(x) strip(num2str(x));
for ii=1:5
    inds=Pind(ii,:);
    sii=fS(ii);
    u=gettmppdb(inds(1));
    disp(num2str([inds(1) R(inds(1))]));
    movefile ('tmpget.pdb', ['tmp' sii 'X.pdb']);
    u=gettmppdb(inds(2 ));
    disp(num2str([inds(2) R(inds(2) )]));
```

```
movefile('tmpget.pdb',['tmp' sii 'm.pdb']);  
end
```

Warning: MOLVIEWER will be removed in a future release.



Jmol

string Atoms: 3540 Bonds: 3602 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

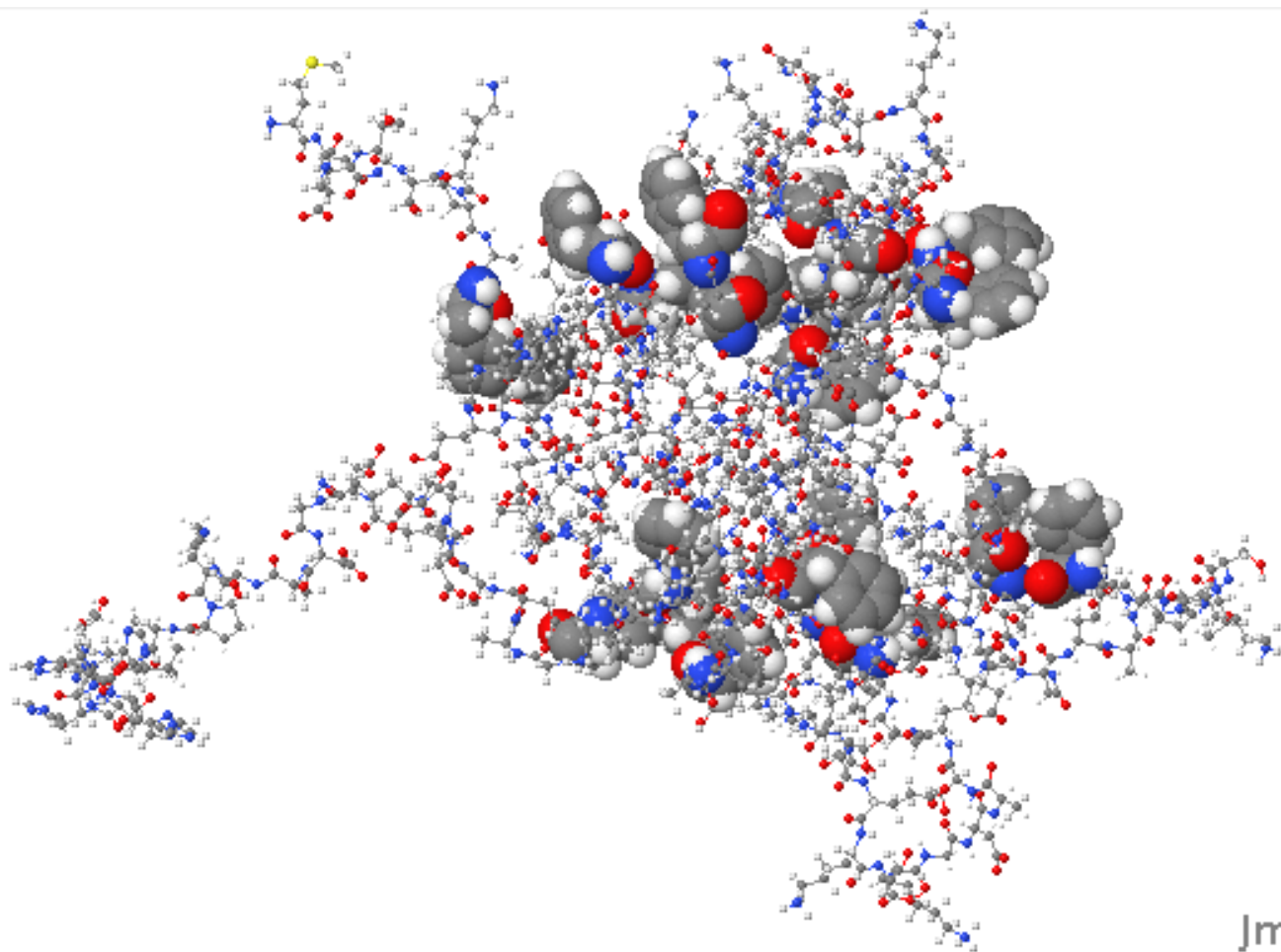
- ☒ 1

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

Warning: EVALRASMOLSCRIPT will be removed in a future release.

1669209 99.369239807

Warning: MOLVIEWER will be removed in a future release.



Jmol

string Atoms: 3540 Bonds: 3629 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

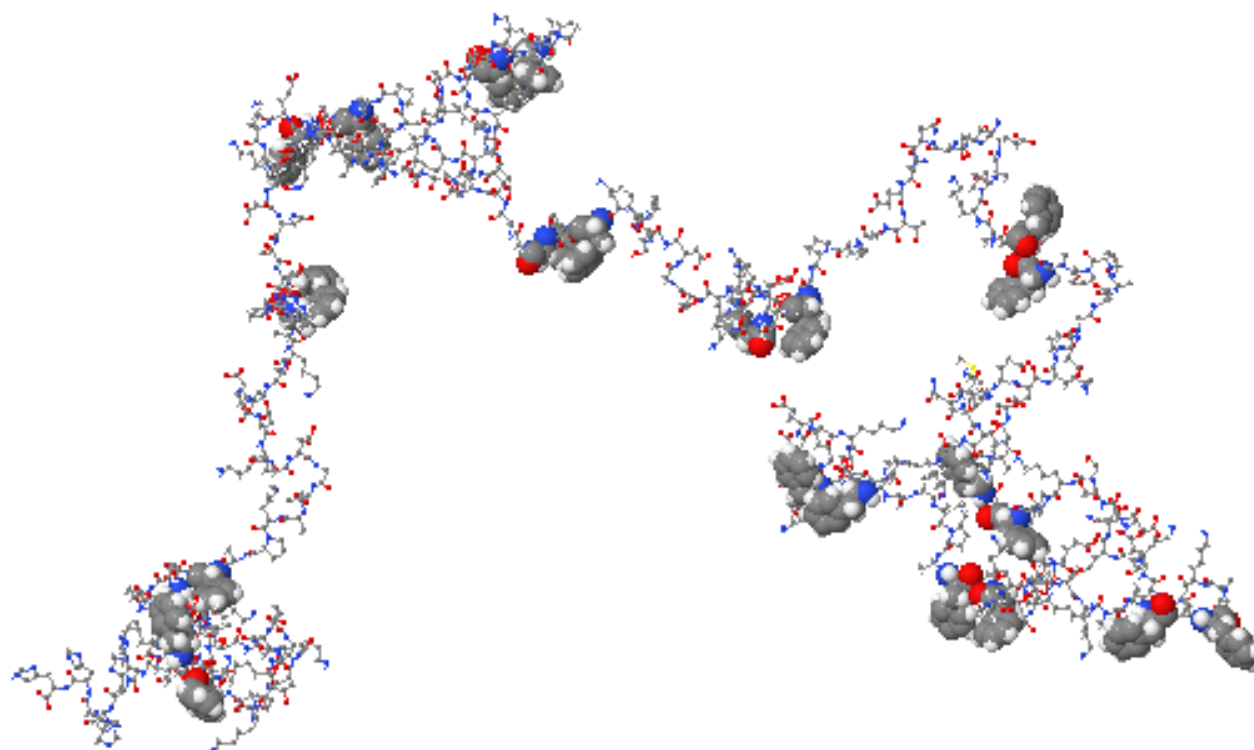
- ☒ 1

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

Warning: EVALRASMOLSCRIPT will be removed in a future release.

1142651 16.972011566

Warning: MOLVIEWER will be removed in a future release.



Jmol

string Atoms: 3540 Bonds: 3608 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

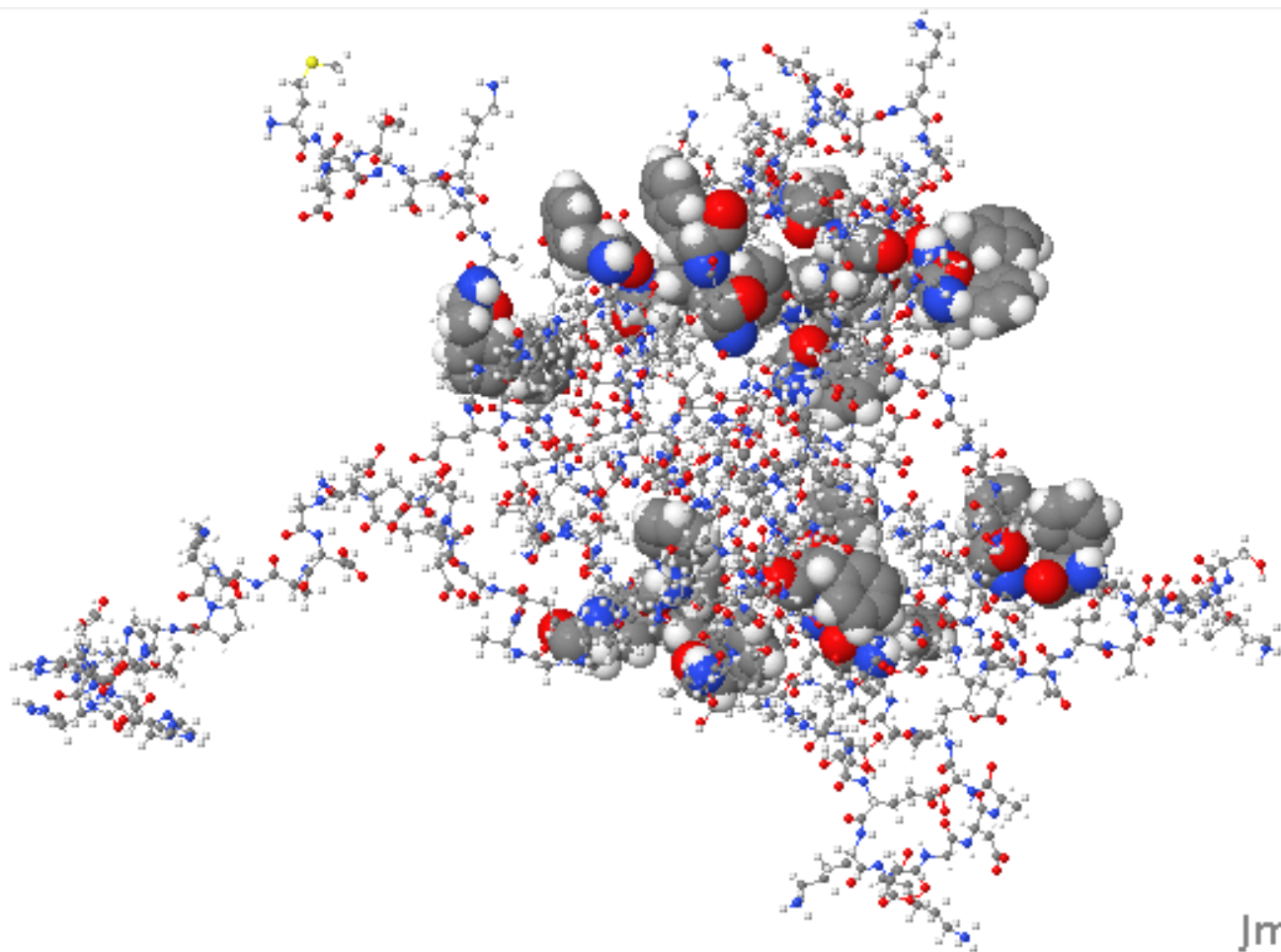
- ☒ 1

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

Warning: EVALRASMOLSCRIPT will be removed in a future release.

44685 23.1513748

Warning: MOLVIEWER will be removed in a future release.



string Atoms: 3540 Bonds: 3629 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

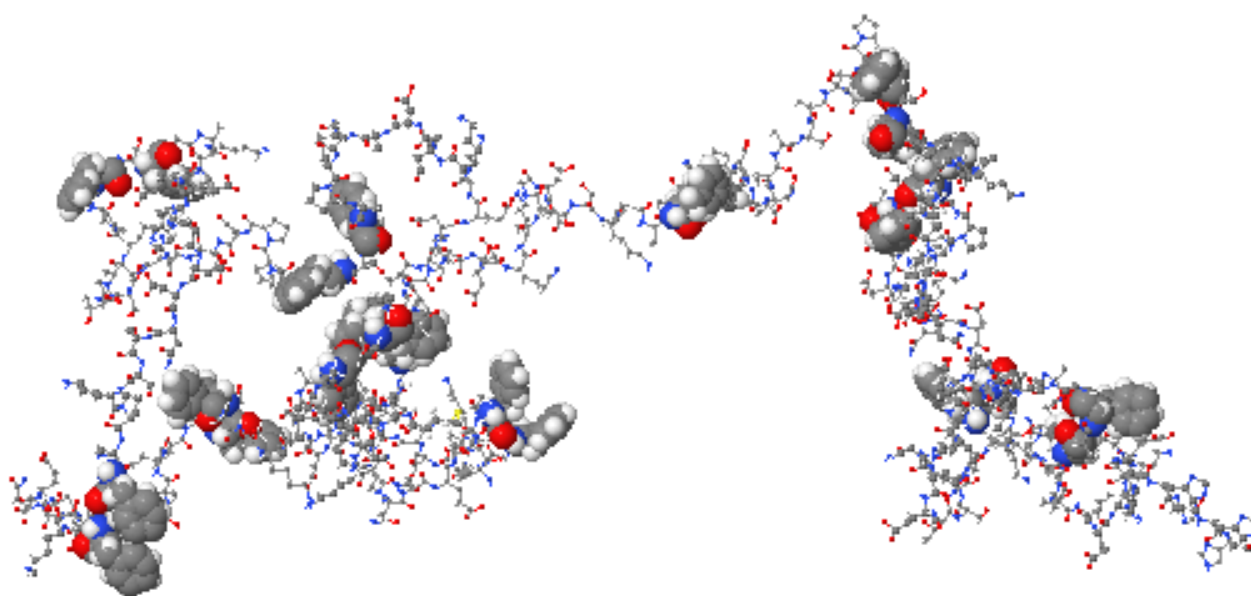
- ☒ 1

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

Warning: EVALRASMOLSCRIPT will be removed in a future release.

1142651 16.972011566

Warning: MOLVIEWER will be removed in a future release.



Jmol

string Atoms: 3540 Bonds: 3602 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
- ☐ BoundingBox
- ☐ Unitcell
- ☐ Selection
- ☐ Dot Surface

Models

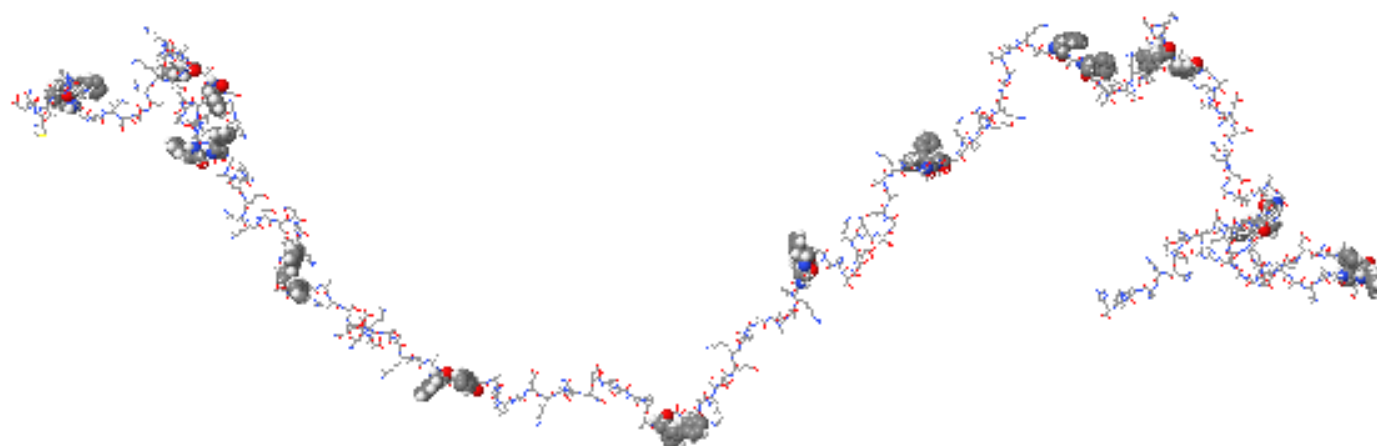
- ☒ 1

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

Warning: EVALRASMOLSCRIPT will be removed in a future release.

50 28.8684

Warning: MOLVIEWER will be removed in a future release.



Jmol

string Atoms: 3540 Bonds: 3597 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

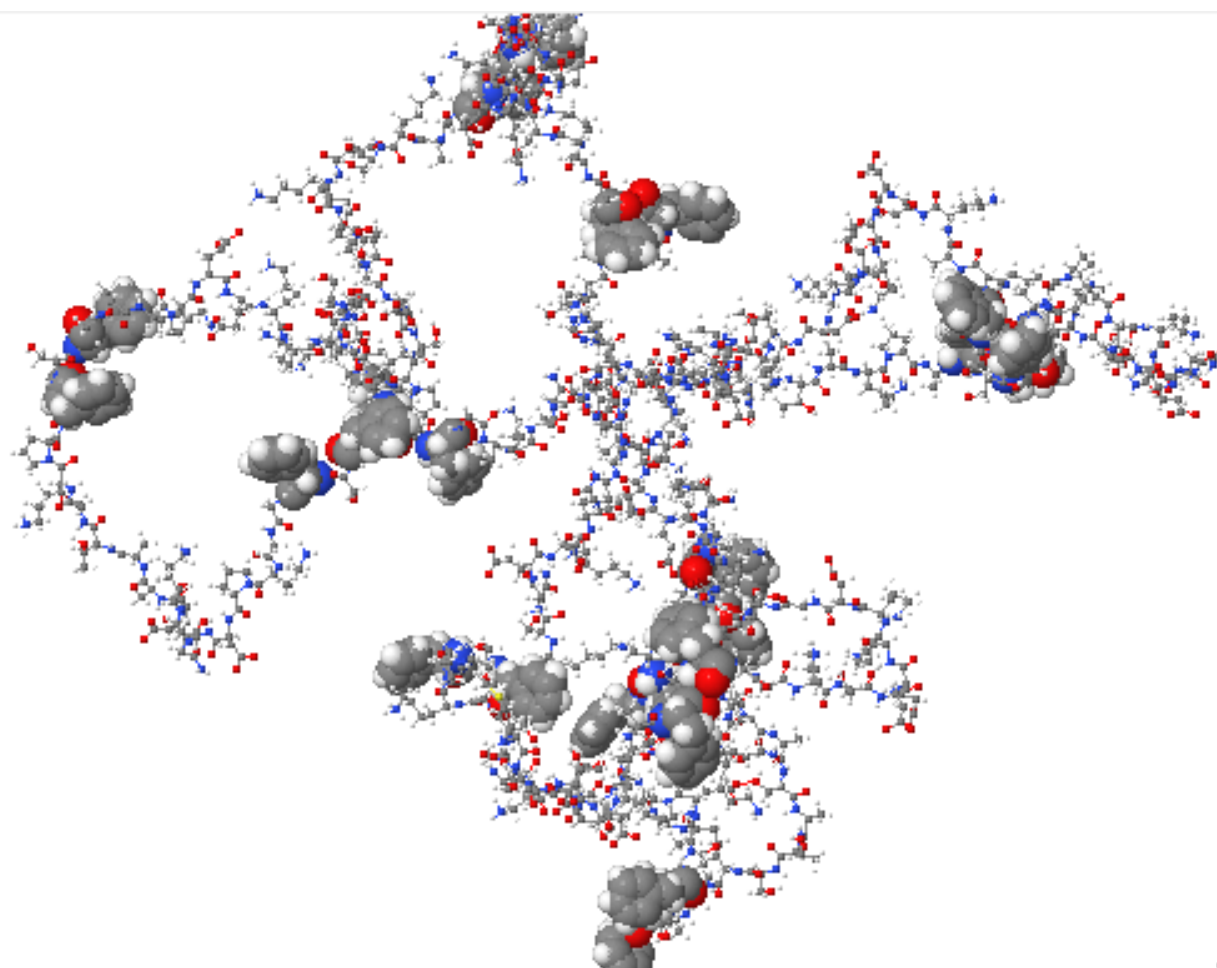
- ☒ 1

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

Warning: EVALRASMOLSCRIPT will be removed in a future release.

1239893 99.42199707

Warning: MOLVIEWER will be removed in a future release.



Jmol

string Atoms: 3540 Bonds: 3602 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

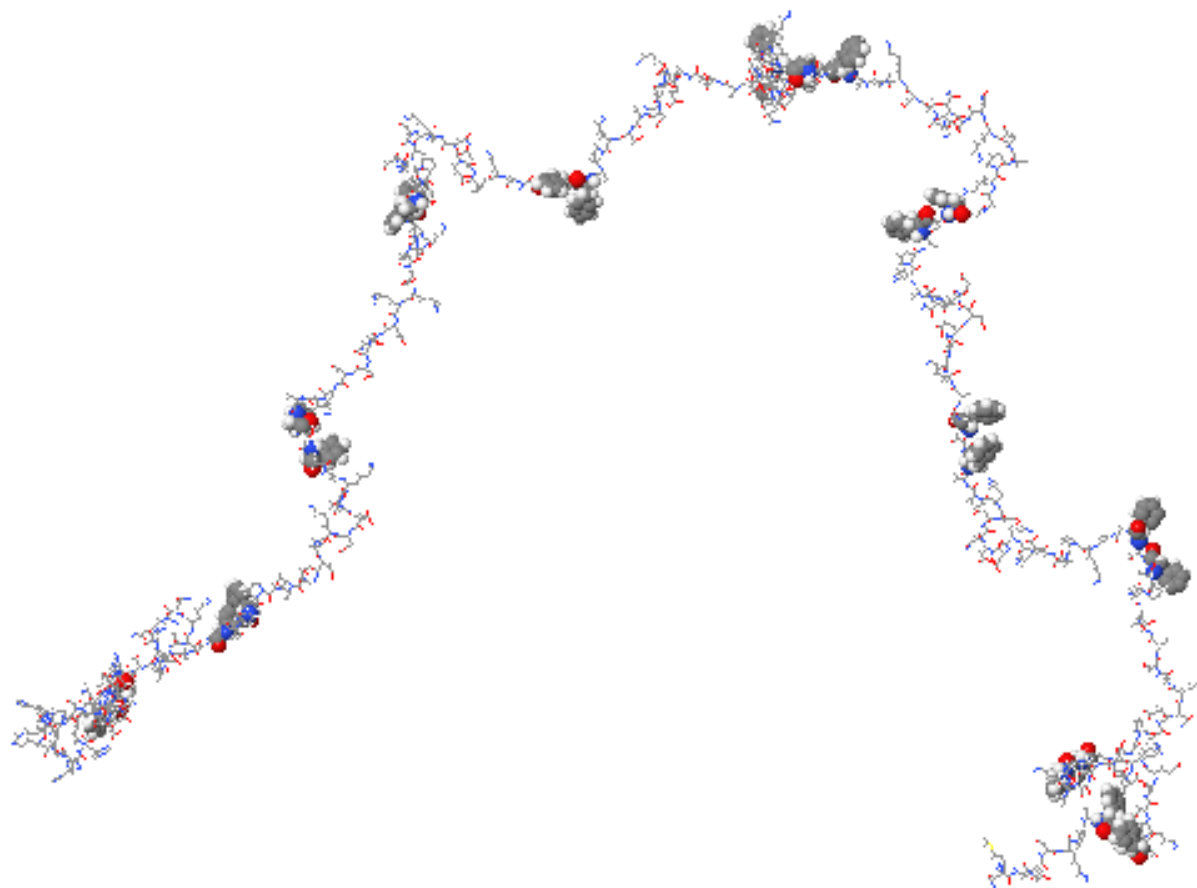
- ☒ 1

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

Warning: EVALRASMOLSCRIPT will be removed in a future release.

1009867 31.733154297

Warning: MOLVIEWER will be removed in a future release.



Jmol

string Atoms: 3540 Bonds: 3596 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

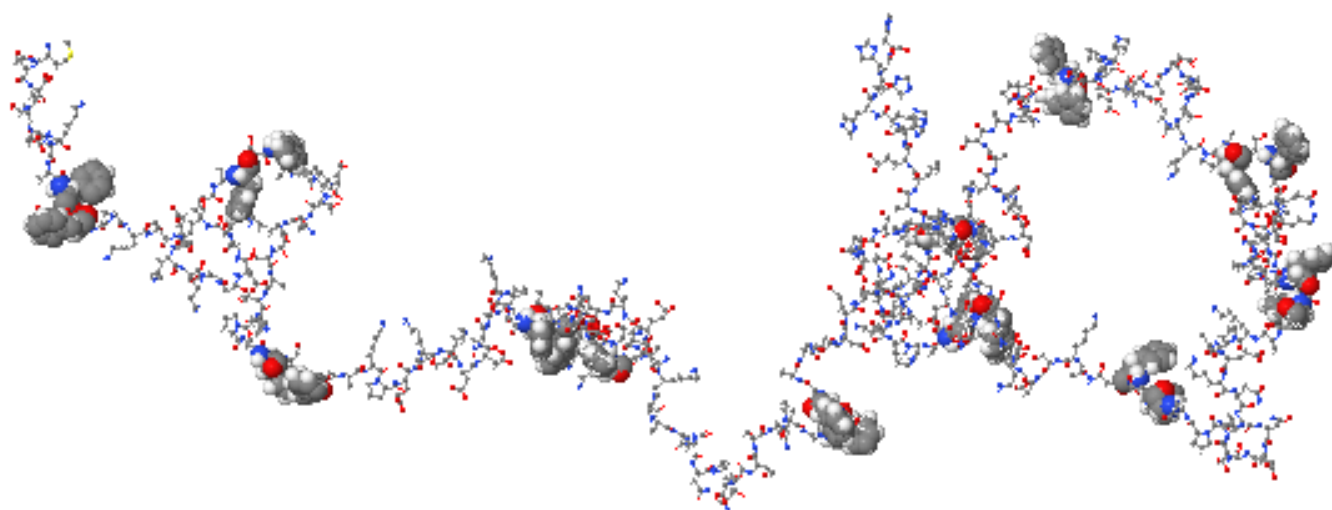
- ☒ 1

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

Warning: EVALRASMOLSCRIPT will be removed in a future release.

477494 77.09577942

Warning: MOLVIEWER will be removed in a future release.



Jmol

string Atoms: 3540 Bonds: 3596 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

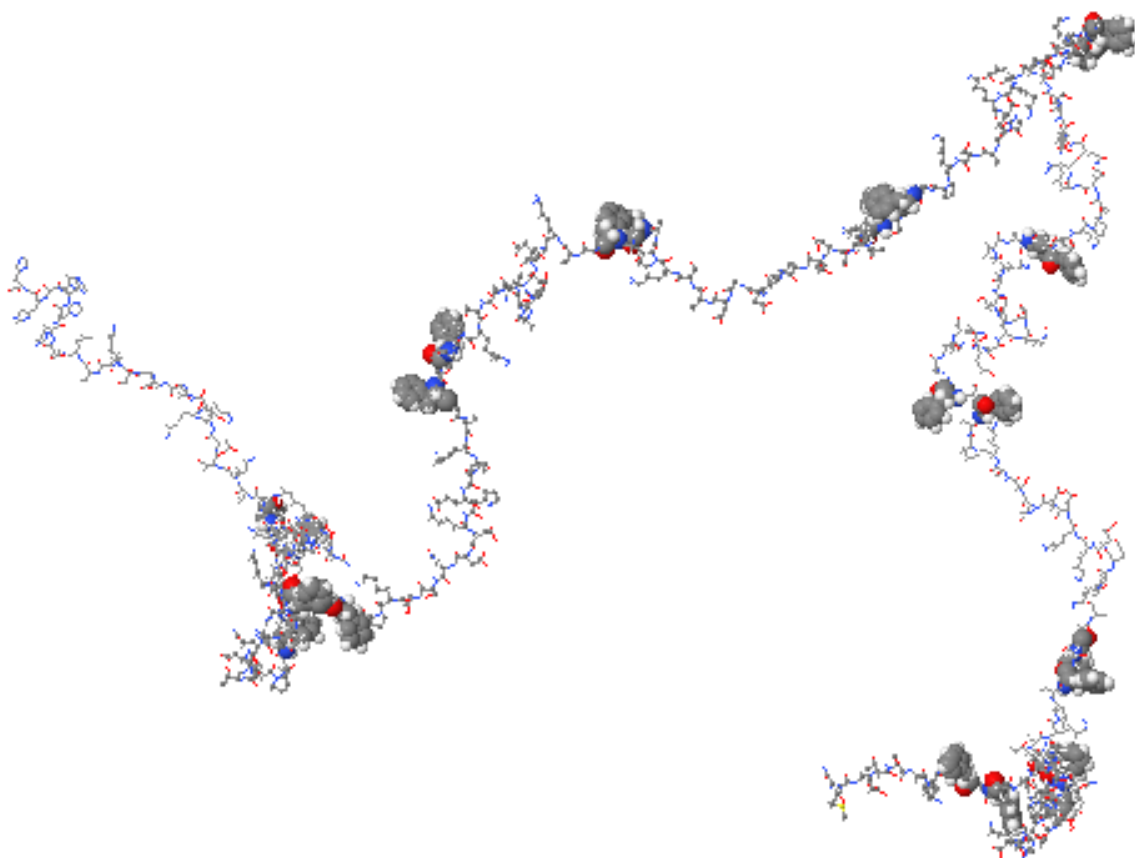
- ☒ 1

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

Warning: EVALRASMOLSCRIPT will be removed in a future release.

1370820 57.321182251

Warning: MOLVIEWER will be removed in a future release.



Jmol

string Atoms: 3540 Bonds: 3610 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.

1214997 66.142753601

new members

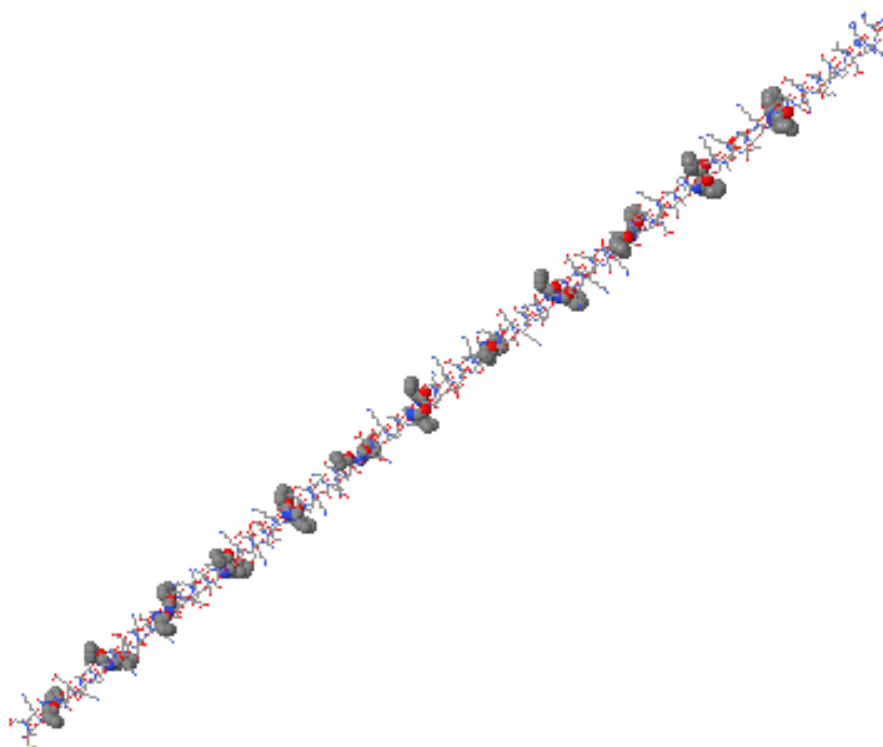
```
fS=@(x) strip(num2str(x));
for ii=2e6+1:2e6+6
```

```

sii=fS(ii);
u=gettmppdb(ii);
disp(num2str([ii R(ii)]));
% movefile ('tmpget.pdb', ['tmp' sii 'X.pdb']);
% u=gettmppdb(inds(2 ));
% disp(num2str([inds(2) R(inds(2 ))]));
% movefile('tmpget.pdb',['tmp' sii 'm.pdb']);
end

```

Warning: MOLVIEWER will be removed in a future release.



Jmol

string Atoms: 1825 Bonds: 1892 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

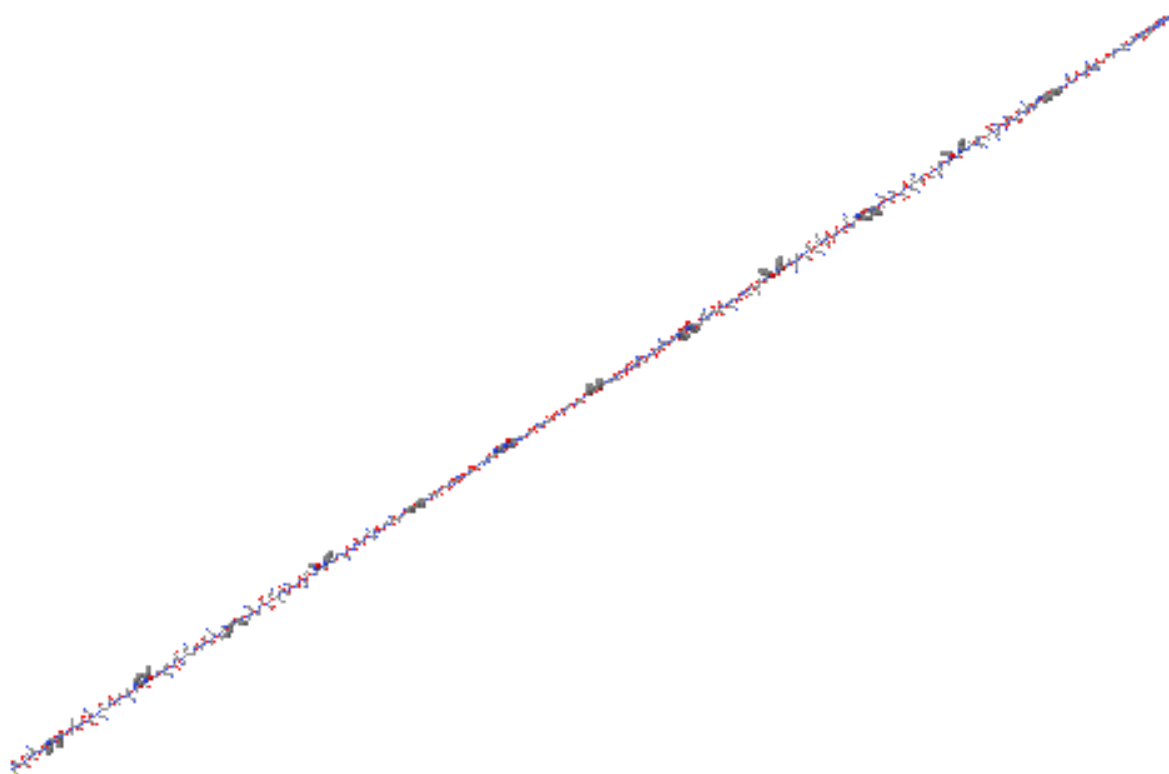
- ☒ 1

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

Warning: EVALRASMOLSCRIPT will be removed in a future release.

2000001 51.19789505

Warning: MOLVIEWER will be removed in a future release.



Jmol

string Atoms: 1825 Bonds: 1873 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

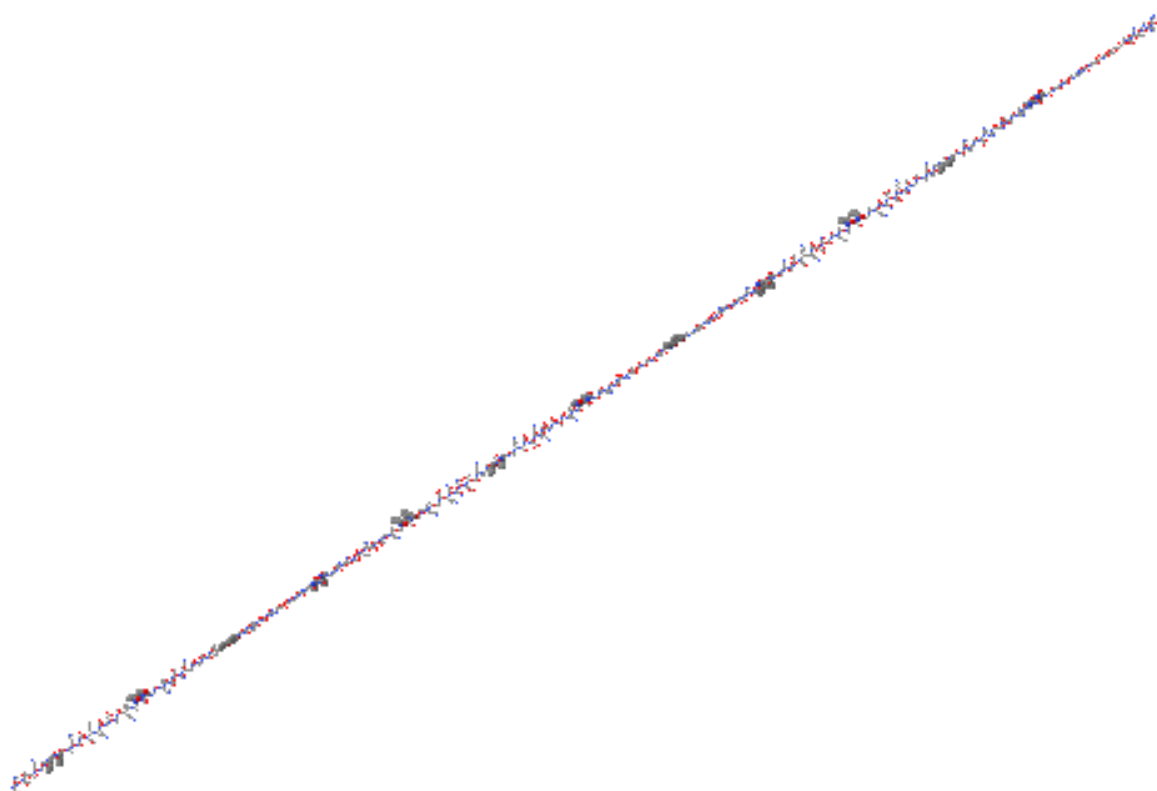
- ☒ 1

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

Warning: EVALRASMOLSCRIPT will be removed in a future release.

2000002 36.006622314

Warning: MOLVIEWER will be removed in a future release.



Jmol

string Atoms: 1825 Bonds: 1873 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

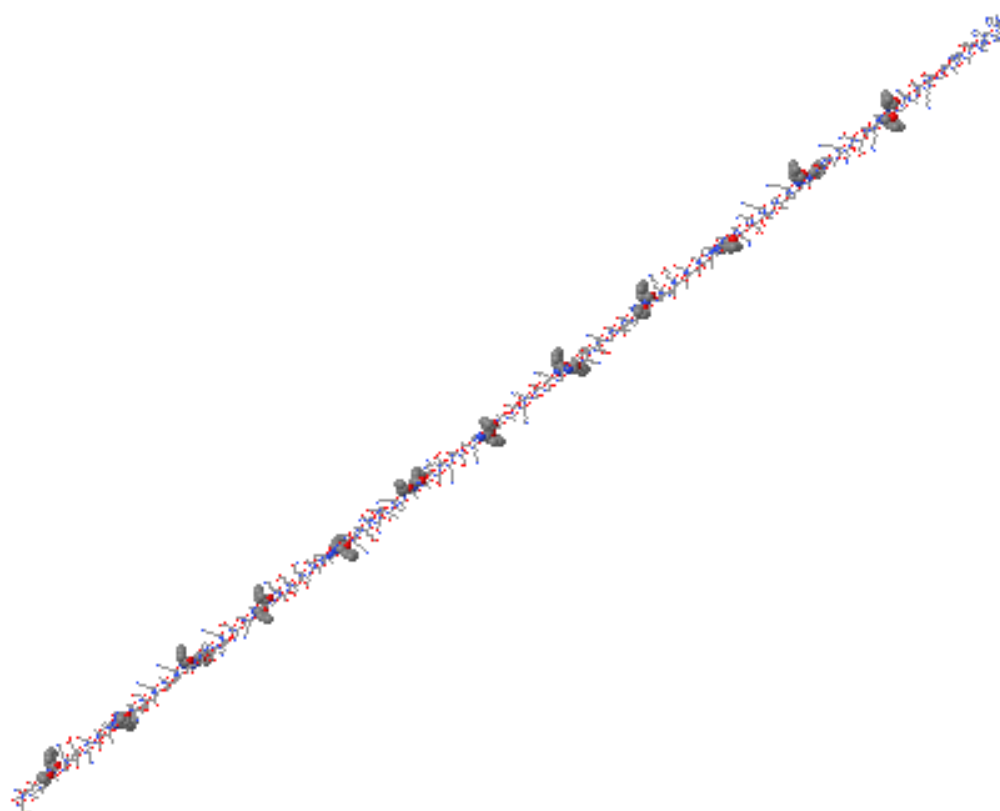
- ☒ 1

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

Warning: EVALRASMOLSCRIPT will be removed in a future release.

2000003 39.223724365

Warning: MOLVIEWER will be removed in a future release.



Jmol

string Atoms: 1825 Bonds: 1892 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

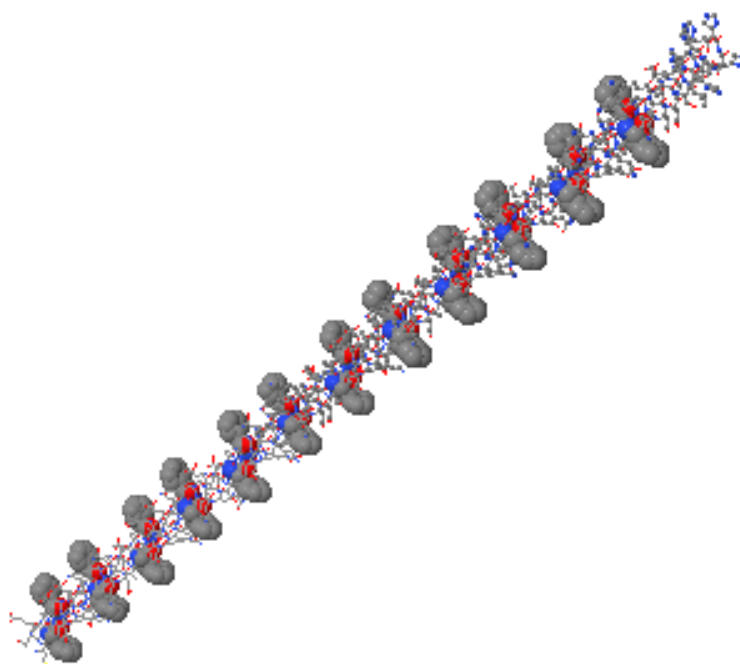
- ☒ 1

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

Warning: EVALRASMOLSCRIPT will be removed in a future release.

2000004 37.658313751

Warning: MOLVIEWER will be removed in a future release.



Jmol

string Atoms: 1825 Bonds: 1892 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

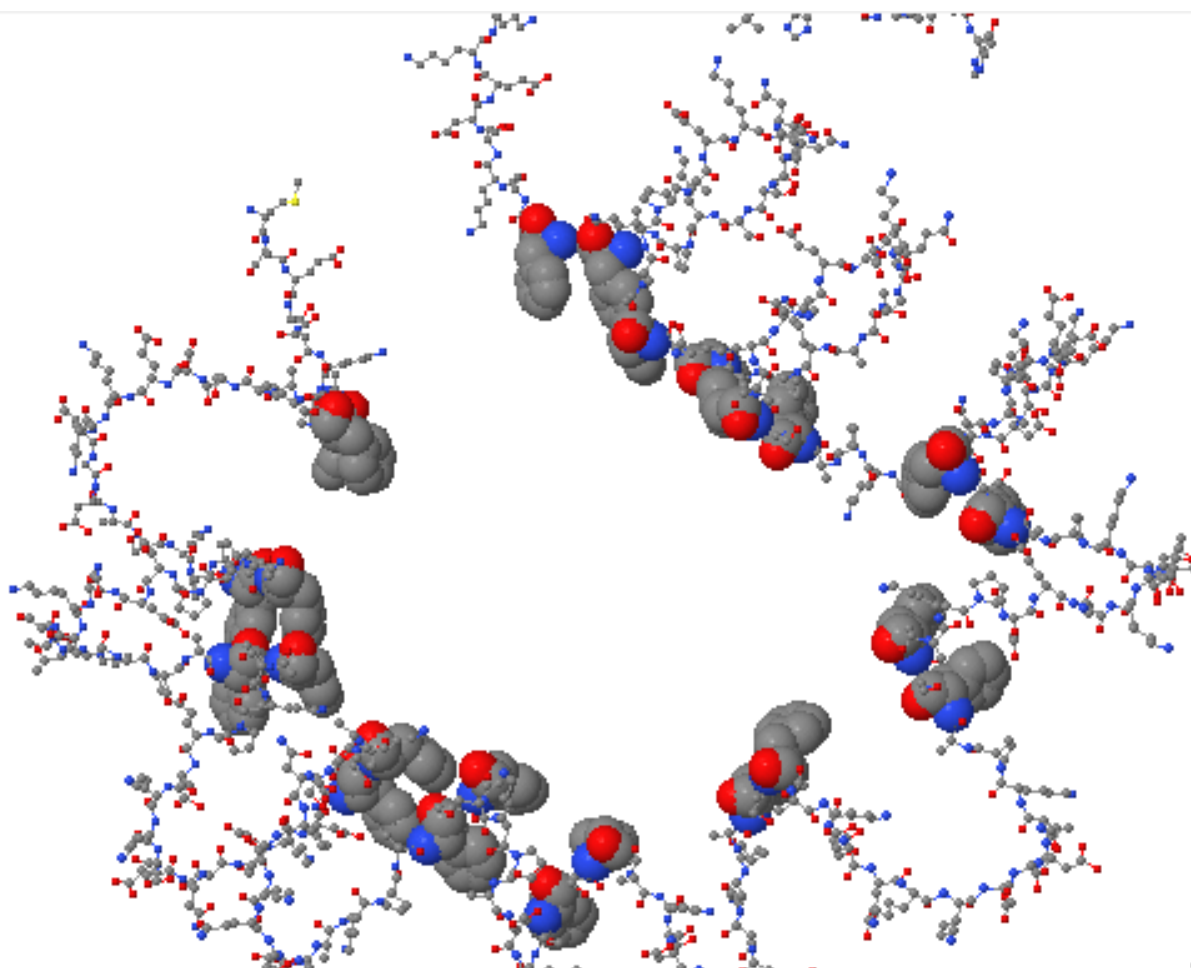
- ☒ 1

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

Warning: EVALRASMOLSCRIPT will be removed in a future release.

2000005 37.945552826

Warning: MOLVIEWER will be removed in a future release.



string Atoms: 1824 Bonds: 1873 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

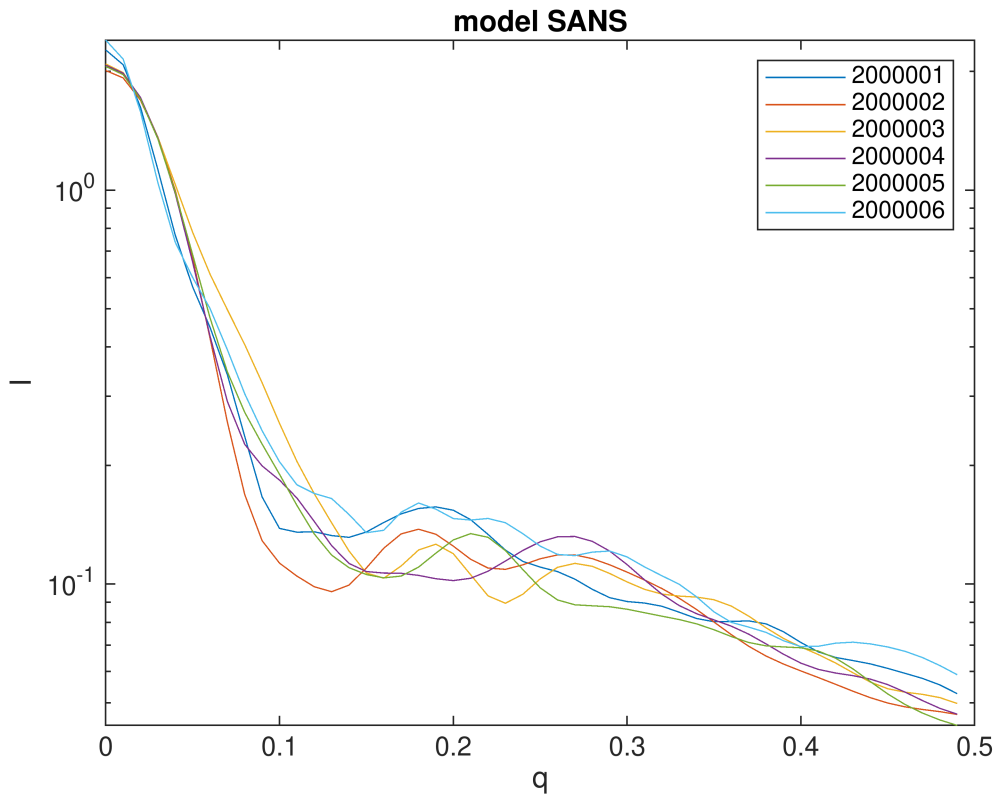
Warning: All the mandatory fields are missing from the input PDB structure.
 Warning: EVALRASMOLSCRIPT will be removed in a future release.
 2000006 57.939476013

```
figure; legs=[];
ran=1:50;
for ii=1:6
    jj=ii+2e6;
    qq=out(jj).Q;
    semilogy(qq(ran,1),qq(ran,2));
```

```

    legs{ii}=num2str(jj);
    hold on;
end
xlabel('q'); ylabel('I'); title ('model SANS'); legend(legs);

```

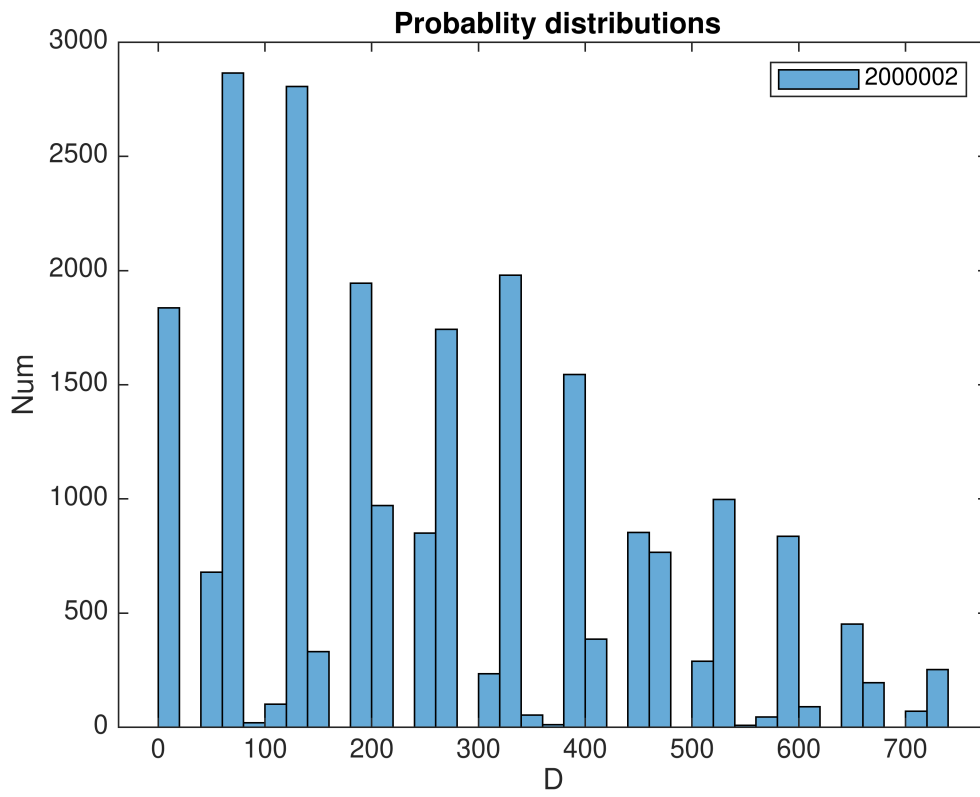
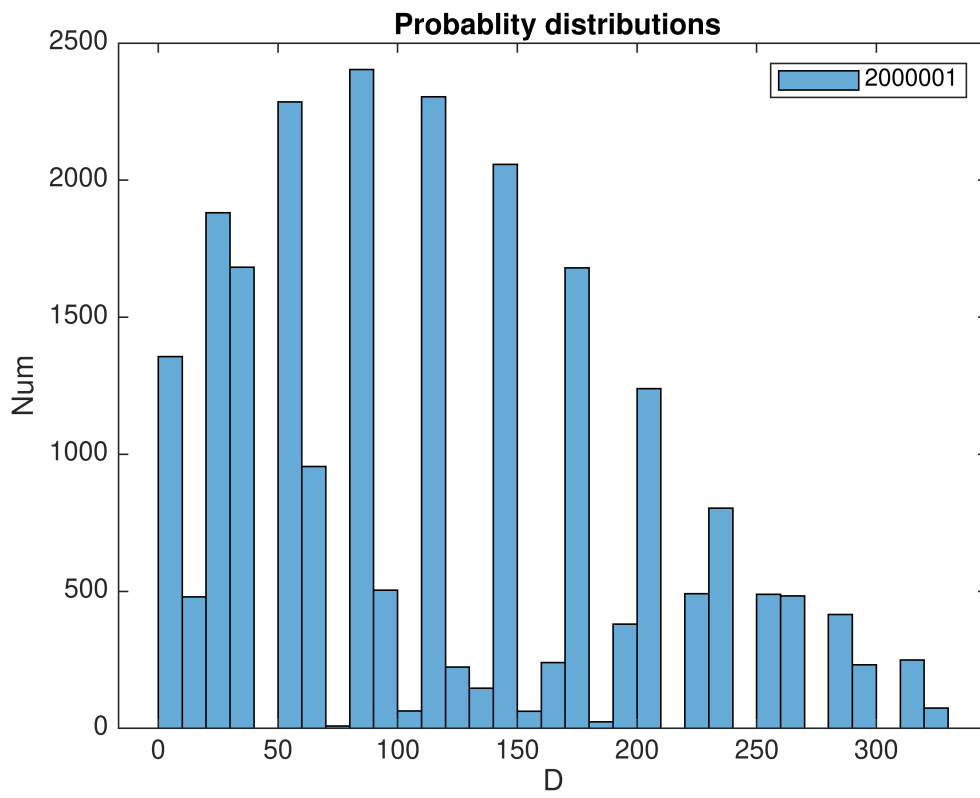


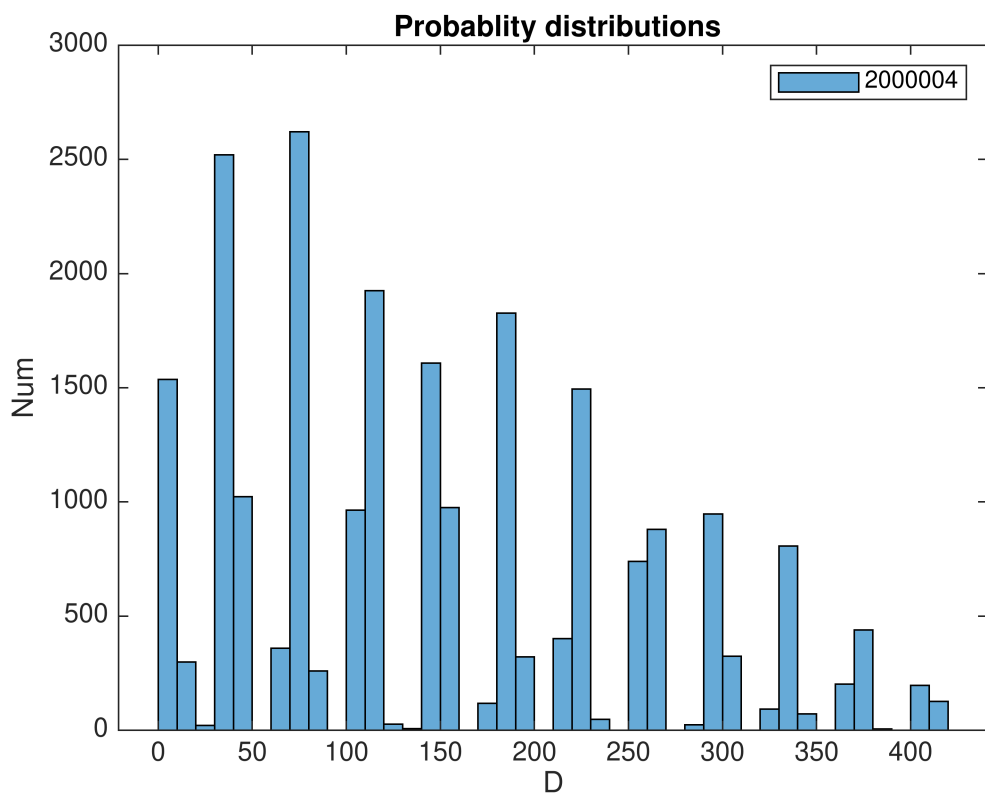
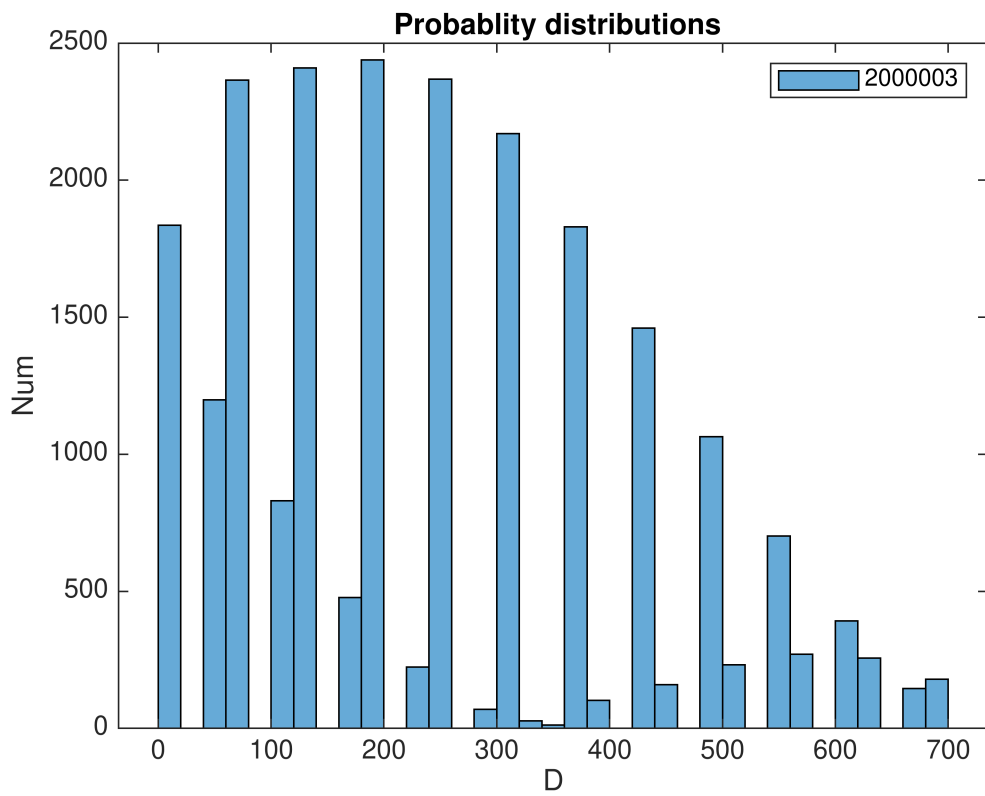
```

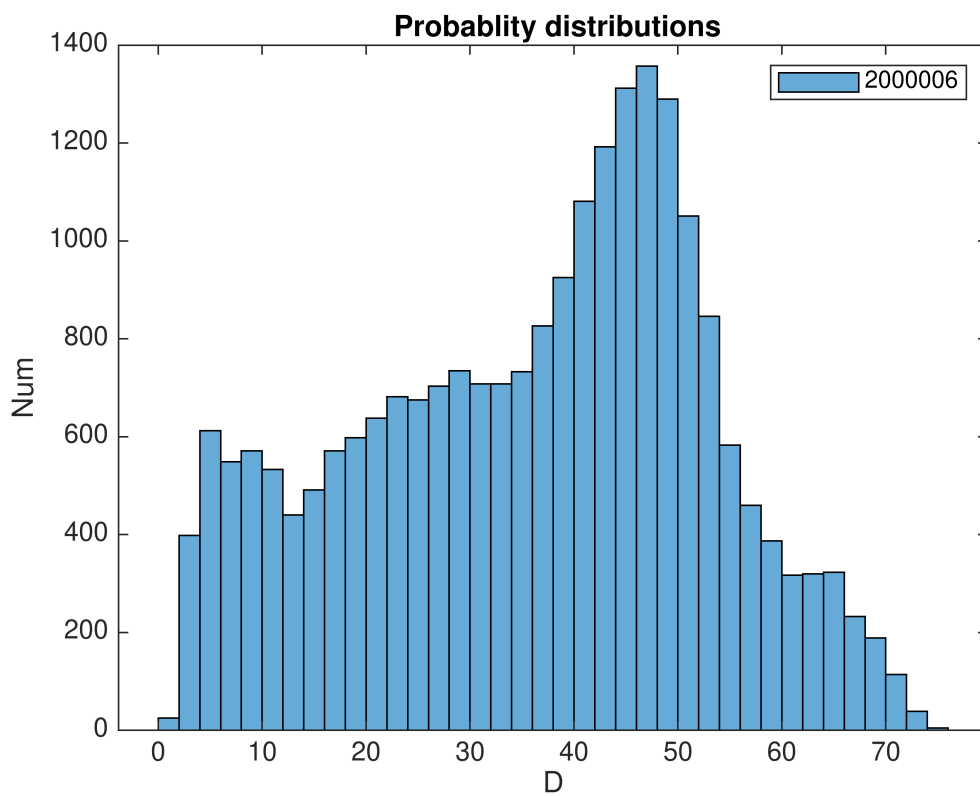
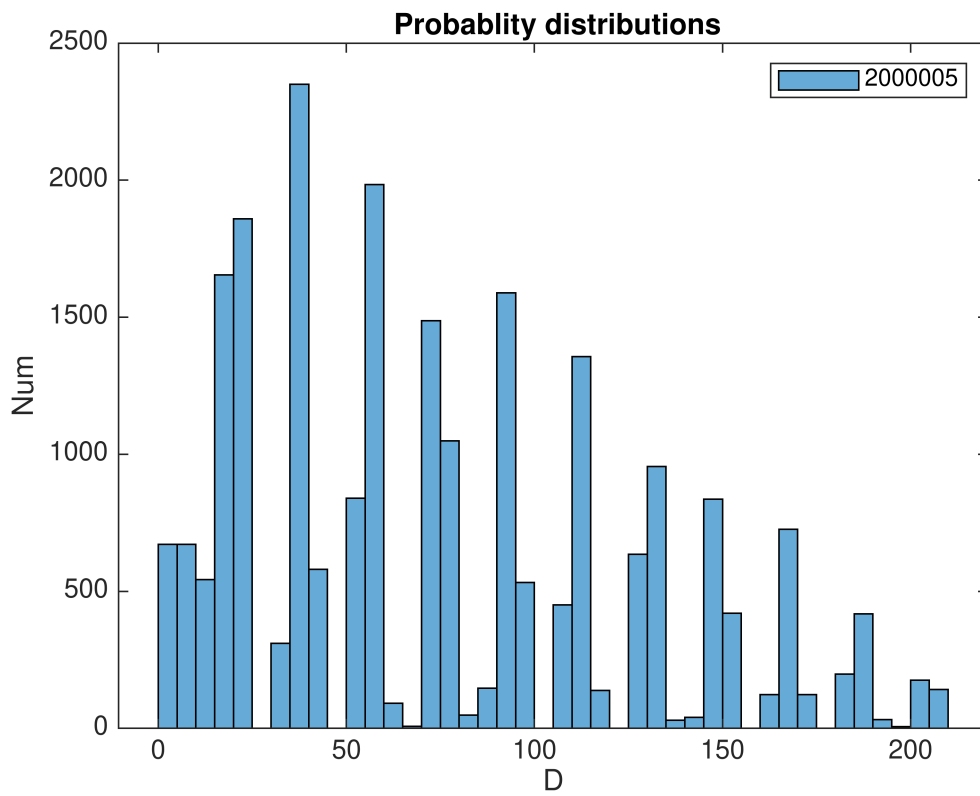
bdis=FFdis(2000001:2000006);

for ii=2000001:2000006
    tmp=bdis{ii};
    mx=max([mx ; tmp(:)]);
end
for ii=2000001:2000006
    tmp=bdis{ii}; figure; legs=[]; mx=0; ilegs=1;
    tmp=tmp(tmp(:)>0);
    histogram(tmp);% hold on;
    legs{ilegs}=int2str(ii);
    ilegs=ilegs+1;
    xlabel('D'); ylabel('Num'); title ( ' Probablity distributions');
    legend(legs);
end

```







```
return
```