





• Simplicity: Complex code fits neither into processor caches nor into programmer minds. It is thus prone to be slow, faulty and not widely implemented.

J. Huwald, et al., J. Comp. Chem. (2016) 37, 1897-1906

## MMTF JS Decoder ~6kb (~2kb gzipped)

r decodeStructure=function(){"use strict"; function t(){function r(t){for(var r={}),e=0;t=e;e+}){var n=0();r[n]=0()}return r}function e(r){var e=t. subarray(i,i+r);return i=r,e}function n(r){var e=t.subarray(i,i+r),restring.fromCharCode apply(null,e);return i=r,e}function a(t){for(var r=new Array(t),e=0;t=e;e+i)r[e]=0();return r}function o(){var o,s,c,f=t[i];if(e=t1286f))return i++,f:if(128e=t2466f))return s=156f,i++,r(s);if(144e=t2406f))return s=156f,i++,r(s);if(160e=t2246f))return s=156f,i++,r(s);if(160e=t246f))return s=156f,i++,r(s);if(161e=t246f))return s=156f,i++,r(s);if(160e=t246f))return s=156f,i++,r(s);if(160e=t246f))return s=156f,i++,r(s);if(160e=t246f))return s=156f,i++,r(s);if(160e=t246f))return s=156f,i++,r(s);if(161e=t246f))return s=156f,i++,r(s);if(161e=t246f))return s=156f,i++,r(s);if(161e=t246f))return s=156f,i++,r(s);if(161e=t246f))return s=156f,i++,r(s);if(161e=t246f))return s=156f,i++,r(s);if(161e=t246f))return s=156f,i++,r(s);if(161e=t246f))return s=156f,i++,r(s);if(161e=t246f))return s=156f,i++,r(s);if(161e=t246f))return var decodeStructure=function(){"use strict"; function t(t){function r(t){for(var r={},e=0;t>e;e++){var n=0(); r[n]=0()}return r}function e(r){var e=t. msgpack decoder mmtf  $buffer), u=\emptyset, s=\emptyset, c=o/4; c>s; ++s)e=i.getInt32(a+4*s,r), u+=t.groupMap[e]. bondOrders. length; return u] function f(e) {e instance} f(e$ Uint8Array(e));var a=t(e);console.log(a);var u,f,\_,g,y=c(a),b=a.numAtoms,d=a.resOrder.length/4,w=a.chainList.length/4,U=a.chainsPerModel.length,v=a.groupMap,h=new Uint32Array(y+d),A=new Uint32Array(y+d),m=new Uint8Array(y+d),p=new Uint32Array(b),I=new Float32Array(b),C=new Float32Array(b),S=new Int32Array(b),F=new Uint8Array(b),L=new Uint32Array(d),D=new Uint32Array(d),M=new Uint32Array(d),M=new Uint32Array(d),D=new Uint32Arr decoder Uint16Array(d), V=new Uint16Array(d), z=new Int32Array(d), P=new Uint8Array(d), G=new Uint16Array(w), k=new Uint32Array(w), q=new Uint32Array(w), d=new Uint32Array(w), d=new Uint32Array(w), z=new Ui cartn\_z\_big,a.cartn\_z\_small,1e3,0),a.b\_factor\_bigss(a.b\_factor\_big,a.b\_factor\_small,100,x),a.\_atom\_site\_idssi(o(n(a.\_atom\_site\_id),S)),a. \_atom\_site\_label\_alt\_id){for(u=0,f=a.\_atom\_site\_label\_alt\_id.length;f>u;u+=2){var j=a.\_atom\_site\_label\_alt\_id[u];"?"===j?a. \_atom\_site\_label\_alt\_id[u]=0:a.\_atom\_site\_label\_alt\_id[u]=a.\_atom\_site\_label\_alt\_id[u]-charCodeAt(0),a.\_atom\_site\_label\_alt\_id[u+1]=parseInt(a. \_atom\_site\_label\_alt\_id[u+1])}o(a.\_atom\_site\_label\_alt\_id,F)}r(a.chainList,B);var\_H,J=a.chainsPerModel,K=0;for(u=0;U=u;+u){for(H=J[u],E[u]=K,T[u]=H,\_=0;H=\_;++\_]o[\_+K]=u;K+=H}var\_N,Q=a.groupsPerChain,R=0;for(u=0;w=u;++=u){for(N=Q[u],k[u]=R,q[u]=N,\_=0;N=\_;++\_]L[\_+R]=u;R+=N}i(o(n(a.\_atom\_site\_auth\_seq\_id),z));var\_W=n(a.resOrder,V),X=r(a.secStruct),Y=0,Z=0;for(u=0;d=u;++u){var\_s=v[W[u]],tt=\$.atomInfo,rt=tt.length/2,et=\$. bondIndices, nt=\$.bondOrders; for (\_=0,g=nt.length;g>\_;++\_)h[Z]=Y+et[2\*\_],A[Z]=Y+et[2\*\_+1],m[Z]=nt[\_],Z+=1; for (P[u]=(l[X[u]]||"l").charCodeAt(),D[u ]=Y,M[u]=rt,\_=0;rt>\_;++\_)p[Y]=u,Y+=1}return{bondStore:{atomIndex1:h,atomIndex2:A,bondOrder:m},atomStore:{groupIndex:p,x:I,y:C,z:0,bfactor:x, API serial:S,altloc:F},groupStore:{chainIndex:L,atomOffset:D,atomCount:M,groupTypeId:V,resno:z,sstruc:P},chainStore:{modelIndex:G,groupOffset:k, groupCount:q,chainname:B},modelStore:{chainOffset:E,chainCount:T},groupMap:v,unitCell:a.unitCell,spaceGroup:a.spaceGroup,bioAssembly:a. bioAssembly,pdbCode:a.pdbCode,title:a.title,bondCount:y,atomCount:b,groupCount:d,chainCount:w,modelCount:U}\var l=\{0:"i",1:"s",2:"h",3:"e",4:"g' ,5:"b",6:"t",7:"l","-1":""}; return f}();





## Fetching

MMTF.fetch and MMTF.fetchReduced are helper functions to quickly load and decode PDB IDs in MMTF format.

```
// Fetch PDB ID 3PQR in MMTF format and print the decoded MMTF data (or an loading/decoding error)

MMTF.fetch(
"3PQR",

// onLoad callback
function( mmtfData ) { console.log( mmtfData ) },

// onError callback
function( error ) { console.error( error ) }

);
```



### Traversal

MMTF.traverse is a helper function to loop over the structural data in the decoded MMTF data object.

```
- raw
    // `bin` is an Uint8Array containing the MMTF MessagePack
    var mmtfData = MMTF.decode( bin );
 3
 4
    // create event callback functions
    var eventCallbacks = {
        onModel: function( modelData ) { console.log( modelData ) },
        onChain: function( chainData ) { console.log( chainData ) },
        onGroup: function(groupData) { console.log(groupData) },
        onAtom: function(atomData) { console.log(atomData) },
 9
        onBond: function(bondData) { console.log(bondData) }
11
    };
12
13
    // traverse the structure and listen to the events
14
    MMTF.traverse( mmtfData, eventCallbacks );
```

## Decoding

The decoder is exposed as MMTF.decode which accepts an <code>Uint8Array</code> containing the MMTF MessagePack and returns the decoded MMTF data as an object. Note, when using MMTF.fetch or MMTF.fetchReduced, decoding is not necessary.

```
- raw 5

// bin is Uint8Array containing the mmtf msgpack
var mmtfData = MMTF.decode( bin );
console.log( mmtfData.numAtoms );
```



# MMTF JavaScript API - Resources

### Github repository

https://github.com/rcsb/mmtf-javascript

#### API docs

https://rcsb.github.io/mmtf-javascript/docs/api/v1.0.0/

### Examples

- JSON <a href="https://codepen.io/arose/pen/LLzVXg">https://codepen.io/arose/pen/LLzVXg</a>
- Traversal <a href="https://codepen.io/arose/pen/QgqbRG">https://codepen.io/arose/pen/QgqbRG</a>
- Loader <a href="https://codepen.io/arose/pen/qjPdzQ">https://codepen.io/arose/pen/qjPdzQ</a>

#### CDN

https://cdn.rawgit.com/rcsb/mmtf-javascript/v1.0.0/dist/mmtf.js

## **Example**

The following code creates a viewer and loads the structure of PDB entry *1CRN* from the RCSB PDB. The result is seen on the right. For more information on how to control the viewer see the API reference, starting with the Stage class.

```
<!DOCTYPE html>
<html lang="en">
<head>
    <meta charset="utf-8">
</head>
<body>
    <script src="path/to/ngl.js"></script>
    <script>
        document.addEventListener( "DOMContentLoaded", function() {
            var stage = new NGL.Stage( "viewport" );
            stage.loadFile( "rcsb://lcrn", { defaultRepresentation: true } );
        } );
    </script>
    <div id="viewport" style="width:400px; height:300px;"></div>
</body>
</html>
```

# **NGL** - Objects and Concepts

Stage -> Component -> Representation

```
// create a `stage` object
var stage = new NGL.Stage("viewport");
// load a PDB structure and consume the returned `Promise`
stage.loadFile("rcsb://1CRN").then(function (component) {
   // add a "cartoon" representation to the structure component
   component.addRepresentation("cartoon");
   // provide a "good" view of the structure
   component.autoView();
});
```

http://arose.github.io/ngl/api/manual/usage/embedding.html http://arose.github.io/ngl/api/class/src/stage/stage.js~Stage.html



## **NGL** - File Formats

#### Structure

 mmCIF, PDB/PQR, GRO, SDF, MOL2, MMTF, PSF, DCD

#### Volume

 MRC/MAP/CCP4, DSN6/BRIX, CUBE, DX/DXBIN, XPLOR/CNS

#### Surface

- OBJ, PLY
- General
  - JSON, CSV, TXT, XML



Or add your own...

https://arose.github.io/ngl/api/manual/usage/file-formats.html

# **NGL** - Representations

#### Structure data

 cartoon, ball+stick, spacefill, backbone, surface, ...

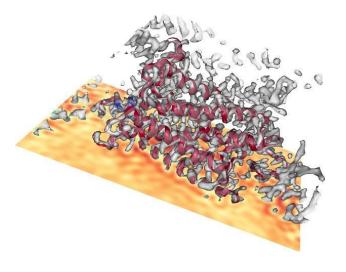


surface, slice, dot

### User shapes

 sphere, cylinder, ellipsoid, cone, arrow, label, mesh





https://arose.github.io/ngl/api/manual/usage/molecular-representations.html https://arose.github.io/ngl/build/docs/manual/usage/volume-representations.html https://arose.github.io/ngl/api/manual/usage/custom-geometries.html

# **NGL** - Coloring

#### Predefined

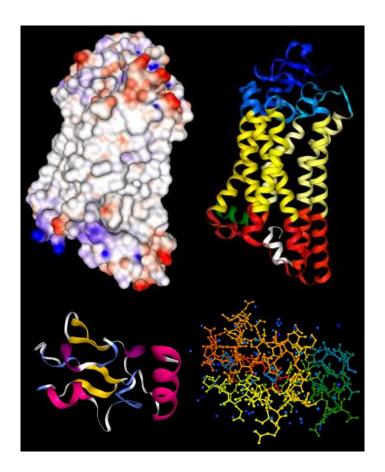
 residue index, electrostatic, secondary structure, element, volume, B factor, ...

#### Custom

 Function that receives an Atom object and returns a color

#### Parameters

- scale, e.g. red-white-blue, also any from "ColorBrewer"
- domain, e.g. [ 0, 1 ]
- value: e.g. lightgreen



https://arose.github.io/ngl/api/manual/usage/coloring.html

## **NGL** - User Interaction

- stage.mouseControls
  - Bind actions to mouse and key combinations
- stage.animationControls
  - Orient the whole scene or individual components

Animate structure to align with principal axes:

```
stage.loadFile("rcsb://3pqr").then(function (o) {
  o.addRepresentation("cartoon");
  var pa = o.structure.getPrincipalAxes();
  stage.animationControls.rotate(pa.getRotationQuaternion(), 1500);
});
```

https://arose.github.io/ngl/api/manual/usage/interaction-controls.html



# **NGL - Working with Molecules**

#### Structure data

 Iterate over the hierarchy model/chain/residue/atom

### Selection language

 Concisely specify a set of atoms to work with

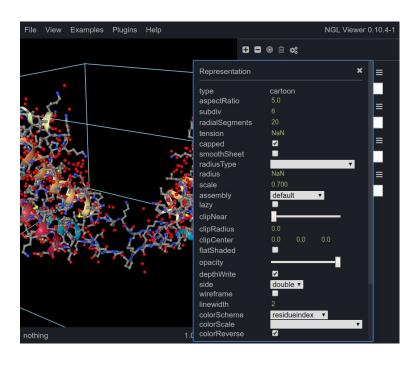
```
// Calculate B-factor statistics
stage.loadFile("rcsb://lcrn").then(function(component) {
  var bfactorSum = 0
  var bfactorMin = +Infinity
  var bfactorMax = -Infinity
  component.structure.eachAtom(function(atom) {
    bfactorSum += atom.bfactor;
    if (bfactorMin > atom.bfactor) bfactorMin = atom.bfactor
    if (bfactorMax < atom.bfactor) bfactorMax = atom.bfactor
  });
  var bfactorAvg = bfactorSum / component.structure.atomCount
  console.log(bfactorSum, bfactorMin, bfactorMax, bfactorAvg)
});</pre>
```

http://arose.github.io/ngl/api/manual/usage/selection-language.html http://arose.github.io/ngl/api/manual/usage/structure-data.html

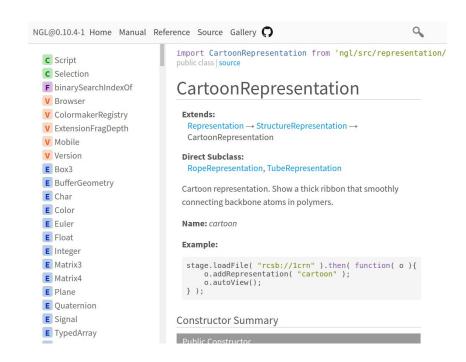




### **NGL - Discover Parameters**



Webapp: <a href="http://arose.github.io/ngl/">http://arose.github.io/ngl/</a>



Docs: <a href="http://arose.github.io/ngl/api/">http://arose.github.io/ngl/api/</a>





# **NGL Viewer/Library - Resources**

- Github repository
  - https://github.com/arose/ngl
- API docs & manual
  - http://arose.github.io/ngl/api/
- Examples Gallery
  - https://arose.github.io/ngl/gallery/
- CDN
  - <a href="https://unpkg.com/ngl">https://unpkg.com/ngl</a> (latest release)
  - https://unpkg.com/ngl@0.10.3

## **Hands-on exercises**

### MMTF JavaScript API

- Play around with examples on CodePen
- Change examples to use MMTF.fetch()
- Write your own callback functions for MMTF.traverse()

### NGL Library/Viewer

- Play around with examples from gallery on CodePen
- Load your favorite structure and add your favorite representations
- Iterate over the atoms in a structure and print a label
- Calculate B-factor statistics for backbone atoms only
- Print the distance between two clicked-on atoms

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