

# RDF, Jena, Bioclipse, Eclipse, Zest #2: icons and an extension point

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## Keywords

Rdf, Bioclipse, Jena

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## chem-bla-ics

Jonathan worked this week on new features for the [Bioclipse](#) RDF editor (see [these two](#) earlier items). This version still does not edit, but only display using [Zest](#). Jonathan created for me an extension point so that anyone can make the editor aware of domain objects, by simply registering the extension implementation along with the *rdf:Class* URI of the *rdf:type* of an object. This fixes the problem of having to hardcode dependencies of the RDF editor on all the domain code, as was the case [earlier](#) .

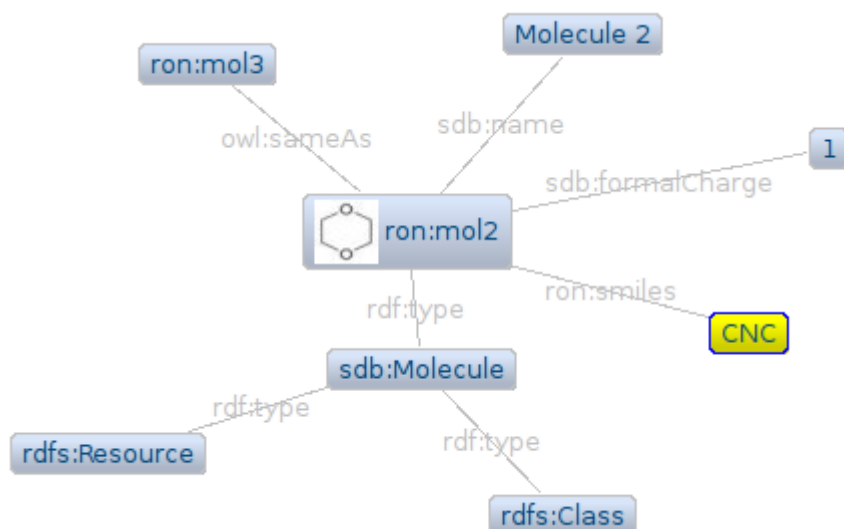
For example, the cheminformatics [IMolecule](#) object is now linked to the *rdf:type* `<http://www.bioclipse.net/structuredb/#Molecule>`:

```
<extension point="net.bioclipse.rdf.rdf2bioobjectfactory">
  <Factory
    instance="net.bioclipse.rdf.ui.RDFToCDKMoleculeFactory"
    uri="http://www.bioclipse.net/structuredb/#Molecule" >
  </Factory>
</extension>
```

The API for this factory looks like:

```
public IBioObject rdfToBioObject( Model model, Resource res );
public ImageDescriptor getImageDescriptor();
```

This is very much tied into the Jena data model, so not entirely clean, but has to do for now. The first method converts RDF content into a Bioclipse *IBioObject*, such as an *IMolecule* (see this [list of currently supported objects](#)). The second method returns an icon, which makes the editor more visually pleasing, and provides a nice way to see when you can double click the RDF node to have it open in an domain specific editor:



For example, double clicking the *ron:mol2* node, would open up a JChemPaint editor.