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Subject: Molecule style & color

Posted by [Paul](#) on Wed, 08 Jul 2020 18:39:16 GMT

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Hello,

In version 5.02.01, the molecule style and color defaults for conformers have changed. How do I change the defaults back to ball and stick and color by atomic number?

Thanks,

Paul

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Subject: Re: Molecule style & color

Posted by [thomas](#) on Wed, 08 Jul 2020 20:09:47 GMT

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Hallo Paul,

with version 5.0.0 DataWarrior switched from Jmol as 3D-molecule-viewer to FXMolViewer. This involved many changes, e.g. instead of having a grid view of 3x3 conformers, all conformers are now superpositioned in one view. A slider allows to separate the conformers. The new viewer is much more flexible, has lots of features, which DataWarrior will use in future updates and is based on the same cheminformatics library that DataWarrior itself uses, this was an overdue and obvious change. However, you are right that the default molecule mode changed from ball&sticks to sticks only, which seemed more appropriate for superpositioned conformers. To better distinguish superposed conformers they have different colors.

Nevertheless,

hetero atoms are shown in their native color (N=blue, O=red, etc).

Currently, DataWarrior does not use Settings of any kind. Would it help in your opinion, if you could

change all molecules to ball&sticks with a new popup menu item?

Thomas

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Subject: Re: Molecule style & color

Posted by [nbehrnd](#) on Wed, 08 Jul 2020 22:42:28 GMT

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Hello Paul,

if the window including the 3D representation is large enough, you may mark a bond or an atom of the molecule displayed (left mouse click, turning the selected red) then

followed by a right click. This action opens a new menu with adjustable entries about molecule style (including «Ball And Sticks») and molecule colour (with «By atomic No»).

This works equally well for the representation of single molecules (as shown in the series of 01.png till 03.png, attached below), as well as for the simultaneous display of conformers (04.png and 05.png). This menu may be closed by «Esc».

Norwid

### File Attachments

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- 1) [01.png](#), downloaded 290 times
  - 2) [02.png](#), downloaded 607 times
  - 3) [03.png](#), downloaded 314 times
  - 4) [04.png](#), downloaded 299 times
  - 5) [05.png](#), downloaded 295 times
- 

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Subject: Re: Molecule style & color  
Posted by [Paul](#) on Thu, 09 Jul 2020 00:59:32 GMT  
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Thanks for the information (and the program in general).

Carbon and hydrogen atoms are displayed in the same color - 7ffd4. Nitrogen and oxygen atoms are their usual colors (blue and red).

It would be somewhat of an improvement if carbon were grey, dark grey or black. Or different from hydrogen.

I am able to use the right click menu to change molecule style and colors, on a per molecule basis.

When working with files of thousands of different molecules, the right click option is impractical.

Sticks versus balls and sticks is purely cosmetic, so I can live with just sticks, and might actually appreciate the benefits of superimposition of conformers.

I need to be able to differentiate carbon from hydrogen atoms, though.

Again, thanks!

Paul

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Subject: Re: Molecule style & color  
Posted by [nbehrnd](#) on Thu, 09 Jul 2020 07:57:52 GMT  
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Hello Paul,

a quick work-around could employ the platform independent Jmol.(1) It is possible to save all of the conformers generated in one .sdf file in common -- just take care that the export retains the 3D coordinates (which is not the default).

In Jmol running, the entry File -> Console opens the programs' own little terminal. Then indicate Jmol the .sdf to read; it will recognize that the .sdf contains multiple models, but by default will display only the first one. This is the chance to disable the display of double / aromatic / triple bonds with more than one line (by the second command), to adjust the diameter of the sticks and balls (third command) and eventually display all models (here: all superimposed conformers) at once by the instruction of model 0.

The scene may be exported like below.

The interaction with Jmol may be scripted (e.g., 2,3,4) thus you may reuse instructions more than once. If the color of an atom type does not fit your needs, for example, you could alter the representation by

```
select hydrogen  
color gray
```

for all models load at once. You may return to the default color scheme by

```
select all  
color cpk
```

Norwid

- 1) [http://wiki.jmol.org/index.php/Main\\_Page](http://wiki.jmol.org/index.php/Main_Page)
- 2) <https://chemapps.stolaf.edu/jmol/docs/>
- 3) [https://earth.callutheran.edu/Academic\\_Programs/Departments/BioDev/omm/jmol/scripting/molmast.htm#V](https://earth.callutheran.edu/Academic_Programs/Departments/BioDev/omm/jmol/scripting/molmast.htm#V)
- 4) Hanson, J.Appl.Cryst.(2010).43, 12501260, doi: 10.1107/S0021889810030256

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## File Attachments

- 1) [console.png](#), downloaded 663 times
- 2) [example.png](#), downloaded 674 times

- 3) [liquid\\_crystal.dwar](#), downloaded 414 times
  - 4) [DW\\_conformer\\_generation.png](#), downloaded 291 times
  - 5) [conformers.sdf](#), downloaded 370 times
- 

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Subject: Re: Molecule style & color  
Posted by [Paul](#) on Thu, 09 Jul 2020 16:52:57 GMT  
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Nice!

Thanks for the help.

I will need to explore these options.

Best Regards,

Paul

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Subject: Re: Molecule style & color  
Posted by [thomas](#) on Fri, 10 Jul 2020 10:58:04 GMT  
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Dear Paul,

I updated the behaviour. Hydrogen atoms of molecules, which are shown in a custom color, are now painted in an intermediate color:

Thomas

#### File Attachments

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- 1) [t.png](#), downloaded 659 times
- 

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Subject: Re: Molecule style & color  
Posted by [Paul](#) on Mon, 13 Jul 2020 13:14:37 GMT  
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That works good, Thomas.

Now I can benefit from conformer superposition and recognize methyl branches.

Thanks,

Paul

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