

Getting Jmol's 'cartoon on' to work in Bioclipse

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Bioclipse, Jmol, Protein

Abstract

Bioclipse 1.0 is to be released in May, and the cartoon on script command is still not working in the Jmol viewer. For those who do not know yet, Bioclipse is a cool Eclipse RCP based Java chemo- and bioinformatics workbench. To have a better idea what goes on inside Bioclipse, I wrote a new BioPolymer tree to show me the strands in the protein.

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chem-bla-ics

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The contents of the ChemTree view in the middle and the Properties view below that look fine:

The screenshot displays the Bioclipse application window with several panels:

- BioResource Navigator:** A tree view on the left showing a project structure with files like 'PPARG_HUMAN.seq', 'sequence2.fasta', 'spectra', and various molecular files.
- PDB Files:** Three tabs at the top show 'pdb_1crn.pdb', 'pdb_1jr8.pdb', and 'pdb_1d66.pdb'.
- Jmol View:** A 3D visualization of a protein-DNA complex. The protein is shown as a grey ribbon, and the DNA is shown as an orange double helix.
- ChemTree:** A tree view in the center showing a 'Polymer' with a 'Strand A' containing monomers CA1 through CA6.
- Sequence View:** A sequence alignment view showing the amino acid sequence: CCGGAGGACAGTCTCCGGCCGGAGGACTGTCTCCGGMKL... I CRLKLLKCS KEKPKCAKCLKNNWECRYS PKTKR SPLTRAH... R L E F M K L L S S I E Q A C D I C R L K L K C S K E K P K C A K C L K N N W E... S P L T R A H L T E V E S R L E R L E F... The sequence is displayed in a grid format with column indices.
- Console:** A text area at the bottom right showing Jmol command logs: 'Jmol cmd: wireframe off', 'Script completed', 'Jmol cmd: spacefill 0', 'Script completed', 'Jmol cmd: cartoon on', 'Script completed', 'Jmol cmd: select all; color CPK; select 4; color 1762 atoms selected', '22 atoms selected', 'Script completed'.
- Properties:** A panel at the bottom left showing 'Bioclipse Web Service - WSDbfet' and a link to 'Result of pdb_1jr8'.

So I'll have to dig a bit further.