


# VMD

**Purpose:** Molecular Dynamics  
**Latest version:** 1.9.4  
**Licence:**  Free of use  
GNU GPL  
**Website:** [https://www.ks.uiuc.edu/\\_ext-link](https://www.ks.uiuc.edu/_ext-link)

**Visual Molecular Dynamics (VMD)** is a visualisation program to visualise, model and analyse bio-molecular systems. Can generate PSF (Protein Structure File) files, perform live simulations using NAMD and modelling and analyse systems through its plugins. Is also fully compatible with the most part of Molecular file formats (PDB, PSF, CHARM, AMBER...).

The GPU compatibility makes VMD able to manage large atom number bio-molecules in various representations.

## How to launch VMD on a VNC Session

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1. Follow the instructions( <https://confluence.csuc.cat/x/VIEIAw> ) to start a vnc session.
  2. Open a terminal at the VNC desktop and load the module
    - a. module load vmd/1.9.4
  3. Type 'vglrun vmd' to start VMD using GPUs.
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