Requirements ChromatinMC - update

* ~~Python 2.7~~ Python 3.6
* HelixMC (<https://github.com/fcchou/HelixMC>)
  + def coord**s**(self) -> def coord(self) in line 470 of helixmc/pose.p
  + Babette, might this be a problem?
* ~~For the graphical interface: Wx python (~~[~~https://www.wxpython.org/~~](https://www.wxpython.org/)~~)~~
* ~~For rendering 3d pictures: Vapory (~~[~~https://github.com/Zulko/vapory~~](https://github.com/Zulko/vapory)~~)~~
* For rendering 3D DNA pictures: POVRAY 2.7
* For installing HelixMC: Visual Studio Buildtools
  + Install VC++ 2015.3 (contains **v14.0** toolset for desktop x86,x64)
  + Install windows 10 SDK (10.0.16299.0 works for me)
* Python packages
  + pip install opencv-python
  + pip install pandas
  + pip install openpyxl==1.8.6 (for reading excel files)
* Adjust file references