Ambertools(https://ambermd.org/AmberTools.php):
For linux/windows-subsystem linux, install the requirements as follows:

```
mkdir amber
cp AmberTools24.tar.bz2 amber/
sudo apt-get install tcsh make
sudo apt-get install gcc gfortran
sudo apt-get install flex bison patch bc wget
sudo apt-get update --fix-mixing
apt-get install xorg-dev libz-dev libbz2-dev
```

Then start installing amber

```
cd amber/
ls
tar xvfj AmberTools24.tar.bz2
cd amber24_src/
ls
cd build/
ls
vi run_cmake
./run_cmake
make install
sudo apt-get install bison
./run_cmake
make install
ls
ll
cd AmberTools/
ls
cd ..
ls
cd build/
ls
cd ../../
ls
cd amber24
ls
source amber.sh
vi ~/.bashrc #give path of amber/bin
bash ~/.bashrc
ls
make test.serial
```

NAB is not included in ambertool recent versions. NAB is important to create any shape of rna dna molecules for md simulation. To install it, download the zip file from the github (https://github.com/dacase/nabc) and then do the following.

```
unzip nabc-main.zip
cd nabc-main/
ls
./configure # configure
make clean && make install #clean and install
ls
make nab #To compile nap
nab
ls
cd test/
ls
cd nab/
ls
make test #to see if tests passed or failed
cd ../shifts/
make shifts
make test # to see if shift is installed
cd ..
ls
source nabc.sh #first source the nabc.sh file; then only use it
nab bin/dna.nab The input is in bin and named as dna. nab
./a.out #to execute nab
ls
vi dna.pdb
vmd dna.pdb #To visualize the output “dna.pdb” file
```