

# ■ Docking Pipeline Installation & Setup Guide

## 1■■■ Install Python 3

Check version:

```
python3 --version
```

If older than 3.9:

```
sudo apt update
```

```
sudo apt install -y python3 python3-pip python3-venv
```

## 2■■■ Install Miniconda

```
cd ~/Downloads
```

```
wget https://repo.anaconda.com/miniconda/Miniconda3-latest-Linux-x86_64.sh
```

```
bash Miniconda3-latest-Linux-x86_64.sh
```

Then restart shell or run: `source ~/.bashrc`

## 3■■■ Create and Activate Conda Environment

```
conda create -n docking_env python=3.12 -y
```

```
conda activate docking_env
```

## 4■■■ Install Open Babel

```
conda install -c conda-forge openbabel -y
```

Confirm: `obabel -V`

## 5■■■ Install AutoDock Vina

```
conda install -c conda-forge autodock-vina -y
```

Confirm: `vina --version`

## 6■■■ Enable Bioconda (Optional)

```
conda config --add channels defaults
```

```
conda config --add channels bioconda
```

```
conda config --add channels conda-forge
```

## 7■■■ Install RDKit (Optional)

```
conda install -c conda-forge rdkit -y
```

## 8■■■ Install UCSF ChimeraX (Optional)

Download from: <https://www.cgl.ucsf.edu/chimerax/download.html>

Or:

wget [https://www.cgl.ucsf.edu/chimerax/downloads/ChimeraX-1.8-linux\\_x86\\_64.bin](https://www.cgl.ucsf.edu/chimerax/downloads/ChimeraX-1.8-linux_x86_64.bin)

bash ChimeraX-1.8-linux\_x86\_64.bin

Launch: chimerax

## 9■■■ Verify Installation

python3 --version

conda list | grep vina

obabel -V

vina --version

## ■ Export Environment (Optional)

Create shareable YAML:

conda env export --name docking\_env > environment.yml

Recreate later:

conda env create -f environment.yml

## ■ You are now ready to run the docking pipeline!

Proceed with editing your `docking_config.yml` and running:

**`python3 run_pipeline.py docking_config.yml`**