



*Python-based Hierarchical ENvironment for Integrated Xtallography*

## Install Cryo\_fit2

### Contents

- [1. Install Phenix](#)
- [2. Link cryo\\_fit2 to phenix](#)
- [3. Troubleshooting](#)
- [4. Test run](#)

## 1. Install Phenix

See the [installation notes for Phenix](#)

## 2. Link cryo\_fit2 to phenix

At <user phenix>/modules

```
git clone git@github.com:cryoFIT/cryo_fit2.git
```

At any folder,

```
libtbx.configure cryo_fit2
```

## 3. Troubleshooting

If user's OS doesn't have git

-> [install git](#)

If a user sees the error during git clone, "Permission denied (publickey).fatal: Could not read from remote repository. Please make sure you have the correct access rights and the repository exists.",

-> user's computer needs to be registered to his/her github account. Therefore, make github account (free), [Generate a new SSH key](#) and [Add a new SSH key to your GitHub account](#)

If user's macOS shows, "xcode-select: note: no developer tools were found at '/Applications/Xcode.app', requesting install. Choose an option in the dialog to download the command line developer tools."

```
download commandline as instructed (this may take ~7 minutes)
```

"-bash: libtbx.configure: command not found"

```
Run export PATH="/Users/.../phenix-xxxx/build/bin":$PATH
source /Users/.../phenix-xxxx/phenix_env.sh
in commandline, and try "libtbx.configure cryo_fit2" again
```

## 4. Test run

See the [cryo\\_fit2 tutorial](#)