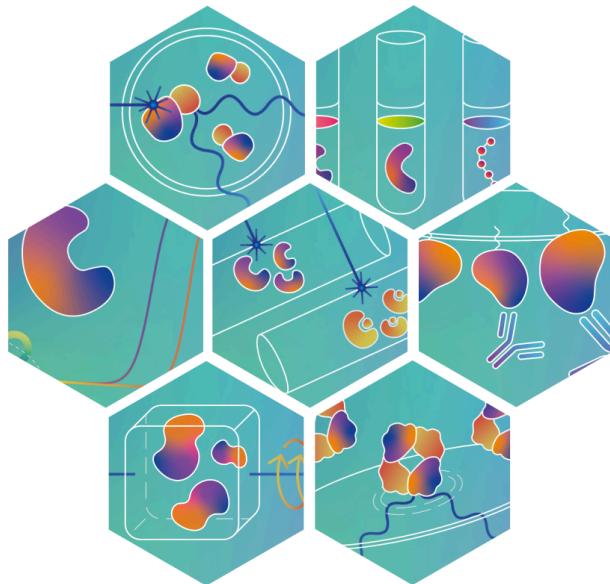


Running the eSPC tools on Windows

February 2026



1. Install WSL2

- a. Open **PowerShell as Administrator** and run:
`$ wsl --install`
- b. Verify the installation and restart the PC if required:
`$ wsl --status`

2. Install a Linux distribution

- a. Open **PowerShell as Administrator** and run:
`$ wsl --install -d Ubuntu`

3. Install Docker

- a. Go to the official Docker website and follow the instructions to install the Docker engine:

<https://docs.docker.com/engine/install/ubuntu/>

4. Pull the docker image and run it

- a. In the Ubuntu **Terminal** run:

- i. For **ThermoAffinity**:

```
$ docker pull emblspc/thermoaffinity_espc:1.0  
$ docker run -p 3838:3838 emblspc/thermoaffinity_espc:1.0
```

- ii. For **MoltenProt**:

```
$ docker pull emblspc/moltenprot_espc:1.1  
$ docker run -p 3838:3838 emblspc/moltenprot_espc:1.1
```

- iii. For **FoldAffinity**:

```
$ docker pull emblspc/foldaffinity_espc:1.0  
$ docker run -p 3838:3838 emblspc/foldaffinity_espc:1.0
```

- iv. For **ChiraKit**:

```
$ docker pull emblspc/chirakit_espc:1.0  
$ docker run -p 3838:3838 emblspc/chirakit_espc:1.0
```

- v. For **PhotoMol**:

```
$ docker pull emblspc/photomol_espc:2.0  
$ docker run -p 3838:3838 emblspc/photomol_espc:2.0
```

- vi. For **KinGenie**:

```
$ docker pull emblspc/kingenie_esp:1.0
$ docker run -p 3838:3838 emblspc/kingenie_esp:1.0
```

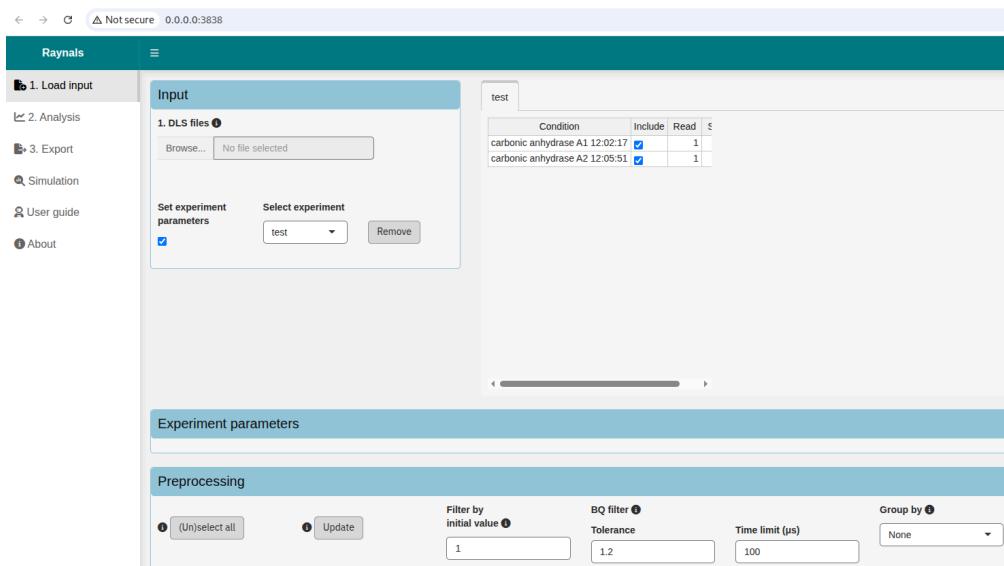
vii. For **Raynals**:

```
$ docker pull emblspc/raynals_esp:1.0
$ docker run -p 3838:3838 emblspc/raynals_esp:1.0
```

5. Open the tool

- Open any Browser and go to <http://0.0.0.0:3838/>

Congratulations! The tool should be open and ready for use.



The screenshot shows the Raynals web application interface. On the left, a sidebar menu includes 'Raynals' (selected), '1. Load input', '2. Analysis', '3. Export', 'Simulation', 'User guide', and 'About'. The main area has two tabs: 'Input' (selected) and 'Analysis'. In the 'Input' tab, there's a 'DLS files' section with a 'Browse...' button and a 'No file selected' message. Below it are 'Set experiment parameters' (checkbox checked) and 'Select experiment' dropdown (set to 'test'). To the right, a table lists experimental conditions: 'carbonic anhydrase A1 12:02:17' and 'carbonic anhydrase A2 12:05:51', both marked as 'Include' and 'Read'. In the 'Experiment parameters' tab, there are sections for 'Preprocessing' (with 'Filter by initial value' set to '1'), 'BQ filter' (Tolerance 1.2, Time limit 100), and 'Group by' (None). A large central panel is currently empty.