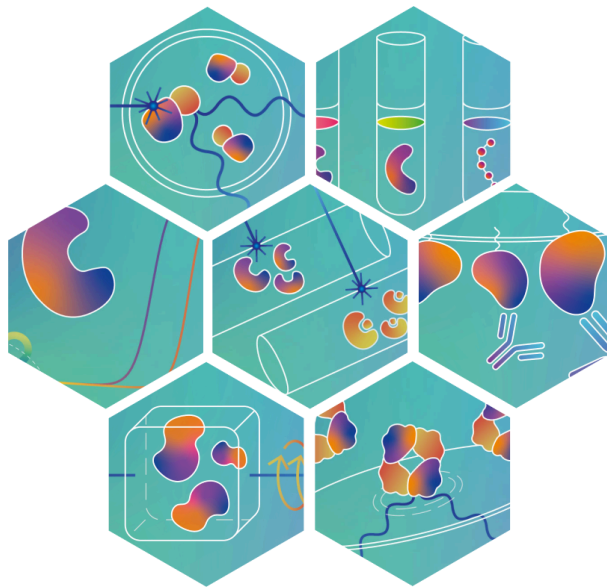


---

# Running the eSPC tools on macOS

February 2026



To run the eSPC tools on macOS there are two alternatives:

- a) To use Docker Desktop
- b) To use Colima and the Docker Engine

The best option depends on the required license. As of Feb. 2026, Docker Desktop is free for: Small businesses (fewer than 250 employees AND less than \$10 million in annual revenue); Personal use; Education; Non-commercial open source projects. On the other hand, the Docker Engine is open-source software licensed under the Apache License, Version 2.0, making it free to use, modify, and distribute for any purpose, including commercial use.

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## Option A

### 1. Download Docker Desktop

- a. Go to the official Docker website:  
<https://www.docker.com/products/docker-desktop/>
- b. Click **Download for Mac**
- c. Choose the correct version:
  - i. Mac with Apple chip (M1/M2/M3)
  - ii. Mac with Intel chipThe **.dmg** file will download to your computer.

### 2. Install Docker Desktop

- a. Open the downloaded **.dmg** file
- b. Drag the **Docker** icon into the **Applications** folder
- c. Open **Applications** → Double-click **Docker**
- d. Click **Open** if macOS asks for confirmation
- e. Enter your Mac password if prompted (Docker needs privileged access)
- f. Docker will start and the whale icon 🐋 will appear in the menu bar.

### 3. Pull the docker image and run it

- a. Open **Terminal** and 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**:

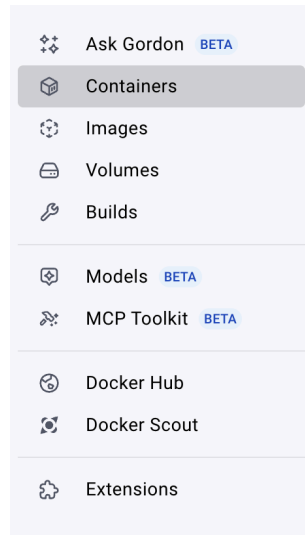
```
$ docker pull emblspc/kingenie_espc:1.0  
$ docker run -p 3838:3838 emblspc/kingenie_espc:1.0
```

vii. For **Raynals**:

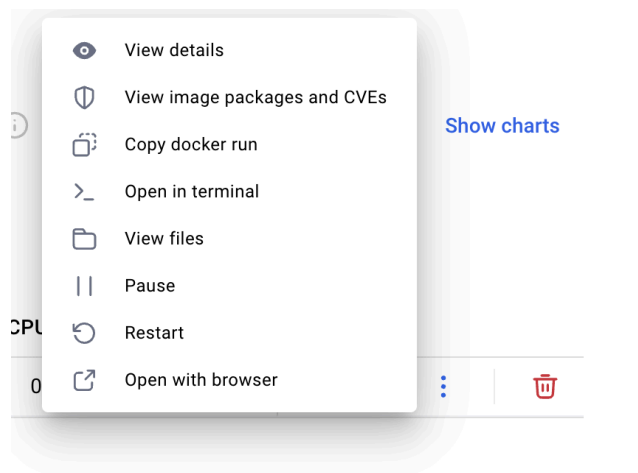
```
$ docker pull emblspc/raynals_espc:1.0  
$ docker run -p 3838:3838 emblspc/raynals_espc:1.0
```

## 4. Open the tool

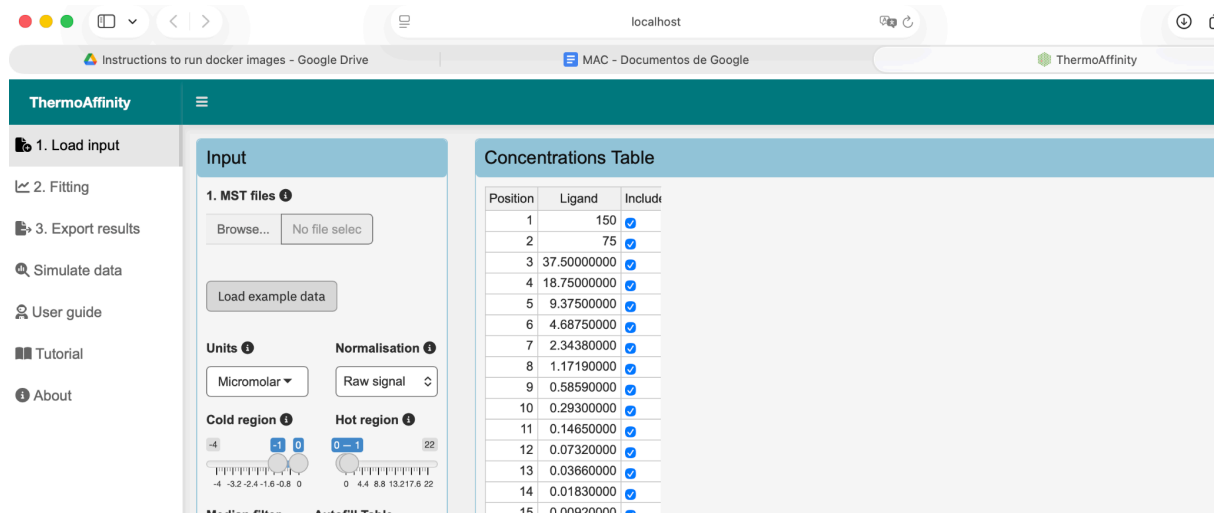
- a. Open Docker Desktop and navigate to the *Containers* tab



- b. Press on the three dots, right to the square and click on *Open with browser*



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



## Option B

### 1. Install Docker CLI and Colima

- a. Open **Terminal** and run:
 

```
$ brew install docker
```

```
$ brew install colima
```

### 2. Pull the docker image and run it

- a. Open **Terminal** and run:

```
$ colima start
```

For **ThermoAffinity**:

```
$ docker pull emblspc/thermoaffinity_espc:1.0
```

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

For **MoltenProt**:

---

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

For **FoldAffinity**:

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

For **ChiraKit**:

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

For **PhotoMol**:

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

For **KinGenie**:

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

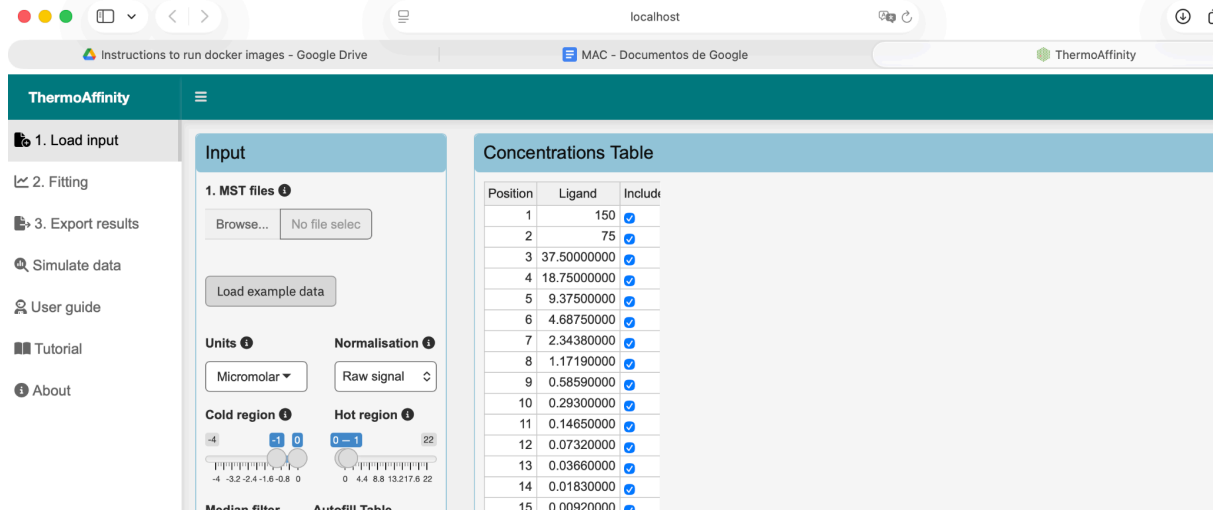
For **Raynals**:

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

### 3. Open the tool

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

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



**ThermoAffinity**

**1. Load input**

2. Fitting

3. Export results

Simulate data

User guide

Tutorial

About

**Input**

1. MST files

Browse... No file select

Load example data

**Units**

Micromolar

**Normalisation**

Raw signal

**Cold region**

-4 -3.2 -2.4 -1.6 -0.8 0

**Hot region**

0 4.4 8.8 13.2 17.6 22

**Concentrations Table**

Position	Ligand	Include
1	150	<input checked="" type="checkbox"/>
2	75	<input checked="" type="checkbox"/>
3	37.5000000	<input checked="" type="checkbox"/>
4	18.7500000	<input checked="" type="checkbox"/>
5	9.3750000	<input checked="" type="checkbox"/>
6	4.6875000	<input checked="" type="checkbox"/>
7	2.3438000	<input checked="" type="checkbox"/>
8	1.1719000	<input checked="" type="checkbox"/>
9	0.5859000	<input checked="" type="checkbox"/>
10	0.2930000	<input checked="" type="checkbox"/>
11	0.1465000	<input checked="" type="checkbox"/>
12	0.0732000	<input checked="" type="checkbox"/>
13	0.0366000	<input checked="" type="checkbox"/>
14	0.0183000	<input checked="" type="checkbox"/>
15	0.0092000	<input checked="" type="checkbox"/>