
Collaborative OPen Omics (COPO) Project Documentation

Release 1.0

The Collaborative OPen Omics (COPO) project team

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Welcome to the guidelines for submission, updates and retrieval for the Collaborative OPen Omics project. Please use the links to find instructions specific to your needs.

GETTING STARTED

Collaborative OPEN Omics (COPO) is a website portal where scientists describe their research objects (raw or processed data, reads, samples, images etc.) using community-sanctioned metadata sets and vocabularies¹.

As a metadata broker, COPO encourages data generators to adhere to FAIR (Findable, Accessible, Interoperable and Reusable)² principles when submitting research objects, using semantic terms to add meaning to them and specify relationships between them.

COPO uses public or institutional repositories like [European Nucleotide Archive \(ENA\)](#) and [National Center for Biotechnology Information \(NCBI\)](#) to share the research objects to the wider scientific community.

COPO is developed by a team of Research Software Engineers at the [Earlham Institute](#). Contributions are welcomed in the [GitHub repository](#). All contributors must abide by the code of conduct described in the [Contributor Covenant Code of Conduct](#) section.

Visit the [COPO website](#) to make manifest submissions. An ORCID ID is required to access the application.

The website requires cookies, fonts and the limited processing of your personal data in order to function well. By using the portal you are consenting to this. To find out more about how COPO uses cookies and your personal data, please see our [Privacy Notice](#) and [Terms of Use](#).

Hint: You can register for an ORCID ID on the [ORCID website](#) for free.

1.1 Accessing COPO Website

There are two ways to access the COPO website: **Demo** mode and **Production** mode.

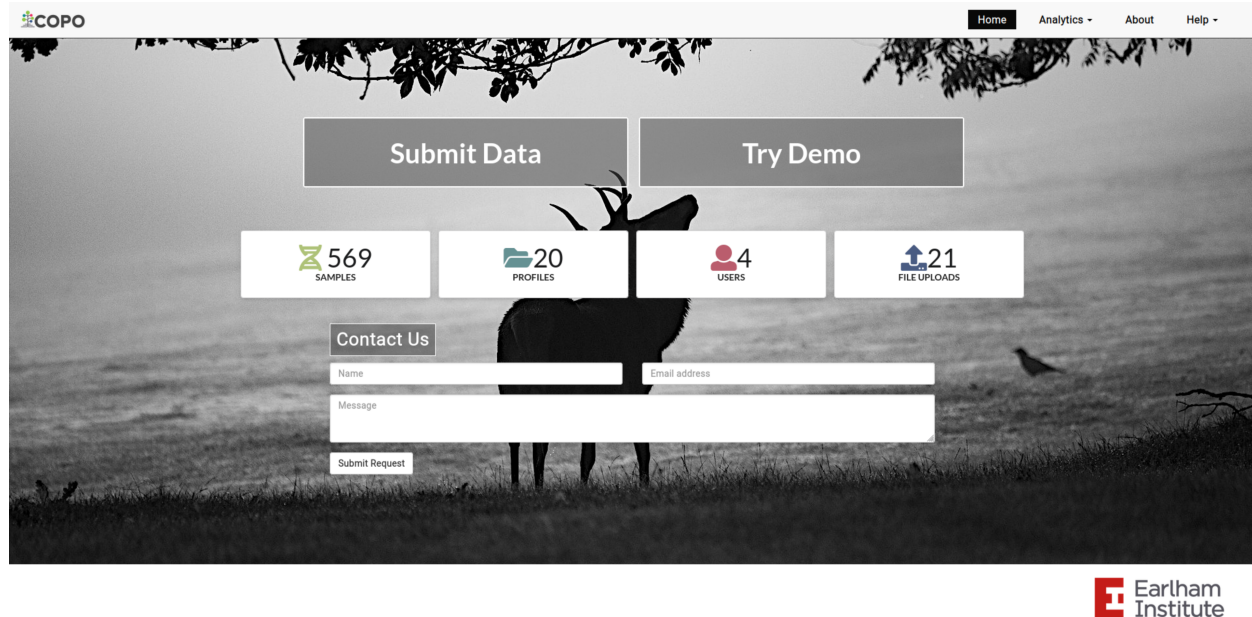
Navigate to [COPO live website](#) to access the production mode **or** navigate to the [COPO demo website](#) to access the demonstration mode.

Note:

- **Production mode** is the live version of the COPO application. It is recommended to submit real data to the production mode because the submissions are made to the final repository.
 - **Demo mode** is a testing environment for the COPO application. It is not recommended to submit real data to the demo mode because any submissions done are considered test submissions and there will be no submissions to the final repository.
-

¹ SOPs (Standard Operating Procedures) guide the metadata sets and vocabularies for manifests. See: [SOP guidelines](#).

² See: [COPO FAIR data principles](#).



COPO homepage: Click **Submit Data** button to proceed to the **ORCID sign-in form** (as shown below)


Alternatively, click **Try Demo** button to access the demo mode.



COPO homepage: Click **Sign in with Orcid.org** button to proceed to the **ORCID sign-in form** (as shown below)

Orcid sign-in form: Enter your **Orcid login credentials** or click **Register now** to sign-up for an **ORCID** account.

If the login is successful, a redirection is made to the COPO application.



Sign in to ORCID

Email or 16-digit ORCID iD

example@email.com or 0000-0001-2345-6789


Password


SIGN IN


[Forgot your password or ORCID ID?](#)

Don't have an ORCID iD yet? [Register now](#)

OR

 Access through your institution

 Sign in with Google

 Sign in with Facebook

PROJECTS BROKERED THROUGH COPO

Hint:

- Primary projects are also known as umbrella projects or main projects and are the main focus of the project. In COPO, primary projects are regarded as **Profile type** or ToL (Tree of Life)¹ project.
 - Secondary projects are also known as subprojects or child projects and are part of the main project. In COPO, secondary projects are regarded as **Associated profile type** or associated ToL project.
-

2.1 Primary Projects

- Aquatic Symbiosis Genomics (ASG)²
- Darwin Tree of Life Samples (DToL)³
- Darwin Tree of Life Environmental Samples
- (DToL_ENV)
- European Reference Genome Atlas (ERGA)⁴
- Stand-alone

2.2 Secondary Projects

Note: In addition to the secondary projects outlined below, all projects listed under **Primary Projects** except Stand-alone, can be added as a subproject of a larger project.

- Biodiversity Genomics Europe (BGE)
- European Reference Genome Atlas - Pilot (ERGA_PILOT)
- European Reference Genome Atlas - Satellites (ERGA_SATELLITES)
- Population Genomics (POP_GENOMICS)

See also:

- *Standard Operating Procedure (SOP)* for the various projects
- *Manifest template* for the various projects
- *Using manifest wizard to prefill manifests*
- *Sequencing Centres that utilise COPO* FAQ (Frequently Asked Question)

¹ See term: *Tree of Life (ToL)*

² See term: *ASG*.

³ See term: *DToL*.

⁴ See term: *ERGA*.

NEW USER

3.1 First time login

If signing in for the first time, a prompt requesting for an email address is displayed.

Enter an email address to proceed. A valid email address and agreement lead to the main web page that comprises all the **work profiles** associated with a user.

The email address supplied will be associated with the user's COPO account and will be used in COPO for tasks such as depositing data to remote repositories involving the user.

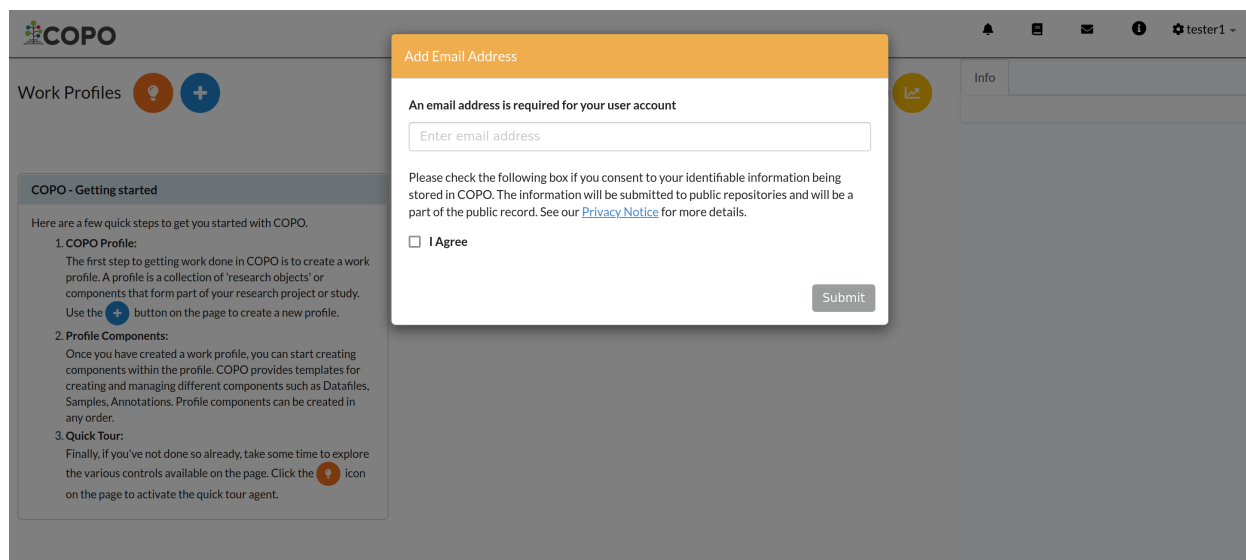


Fig. 1: First time user: Email address prompt shown when a user logs into COPO for the first time

SAMPLE MANAGERS

This section gives an overview of the COPO features that are delegated to Biodiversity Genomics Europe (BGE) checker or sample managers¹ who are responsible for accepting or rejecting samples produced by sample submitters².

Note:


- Make a request to the indicating the type of profile manifest group that you would like to be assigned to as a sample manager BGE (Biodiversity Genomics Europe).

The permission will be granted after the request has been approved.

See also:


- *View images produced by sample submitters*
- *Download permits produced by sample submitters*
- *Sample Managers' Frequently Asked Questions*

4.1 Accessing the Accept or Reject Samples web page

Note: The  button will only appear on the web page if you are granted permission to be a sample manager. Once the button is clicked, the **accept/reject samples** web page will be displayed.

If you have been granted permission as a sample manager, you will receive an email notifying you that sample(s) has been submitted after a user uploads a manifest.

Similarly, you will receive an email when samples have been rejected.

Click the  button to accept or reject samples.

Alternatively, navigate to [Accept/Reject Samples' web page](#).

¹ See term: *Sample manager*

² See term: *Sample submitter*. Sample submitter may also be referred to as a manifest provider or manifest submitter.

4.2 Guidelines for Sample Managers Assigned to More than one Manifest Group

Note: The manifest dropdown menu will only be displayed on the **Accept or Reject samples** web page if you as a sample manager, belongs to more than one sample manager manifest group.

Hint: If the **dtol** sample manager group dropdown menu option is selected, both Aquatic Symbiosis Genomics (ASG)³ profiles and Darwin Tree of Life (DTOL)⁴ profiles will be displayed in the **All profiles** tab (if any exists).

If you have been granted permission to be a sample manager for more than one manifest group, you can accept or reject samples for more than one manifest group by following the steps below:

1. Click the dropdown menu displayed beside the **Choose to Accept or Reject** web page title on the left side of the **Accept or Reject Samples** web page as shown below:

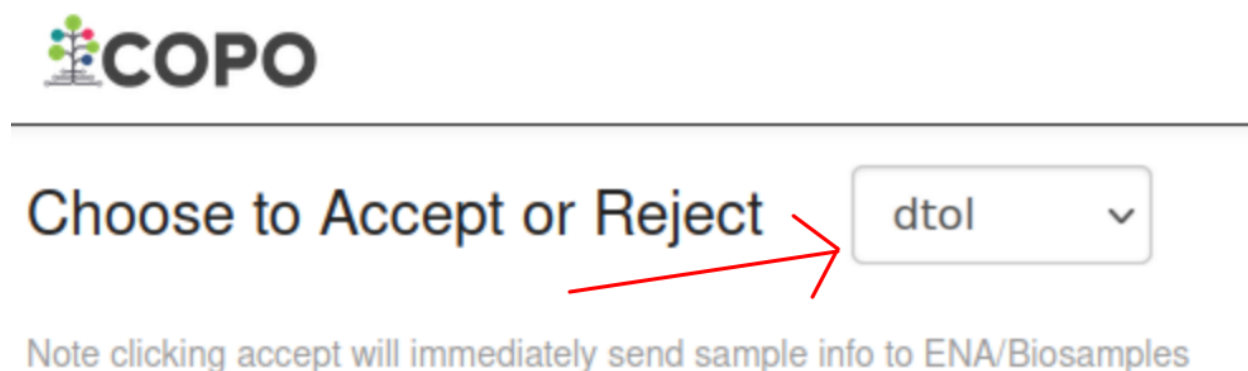


Fig. 1: **Accept or Reject Samples web page: Manifest dropdown menu beside ‘Choose to Accept or Reject’ web page title**

2. A list of all the manifest groups that you have been assigned to is then displayed.
Choose the desired manifest group from the dropdown menu as shown below:
3. To **accept** samples, see the *Accepting samples* section

OR

To **reject** samples, see the *Rejecting samples* section

³ See term: *ASG*.

⁴ See term: *DTOL*. *DTOL* may sometimes be referred to as *DTOL*.



Choose to Accept or Reject

Note clicking accept will immediately send sample in

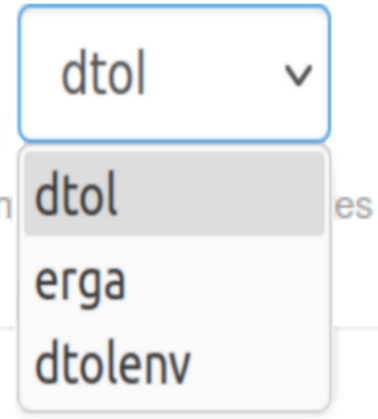


Fig. 2: Accept or Reject Samples web page: Manifest dropdown menu with options displayed

4.3 Accepting or Rejecting Samples

Note: A **Samples** table record will only be displayed if the desired profile that is clicked/highlighted on the left of the web page has submitted samples.

Hint:

- See *Accept or Reject Samples for more than one manifest group* section for guidance if you are assigned to more than one manifest group and would like to accept or reject samples.

4.3.1 Accepting samples

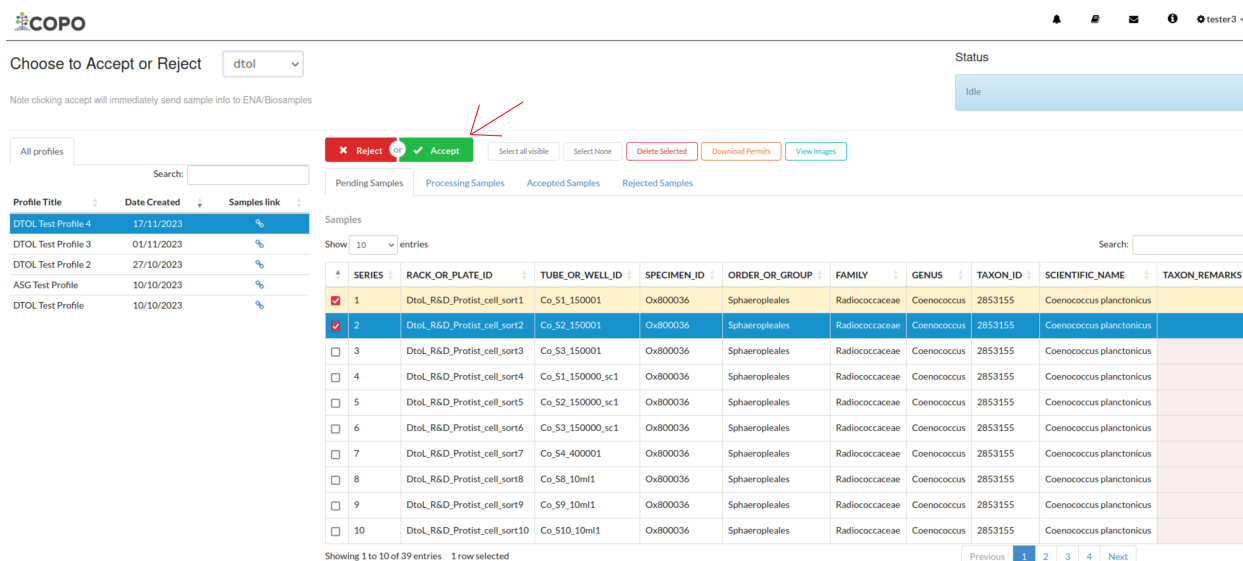
The following sections describe how to accept samples depending on the type of manifest group that you have been assigned as a sample manager to:

- *Accepting ASG or DTOL samples*
- *Accepting ERGA samples as a BGE checker*
- *Accepting ERGA samples as a Sample Manager*

4.3.2 Accepting ASG or DTOL samples

1. Choose desired profile on the left of the **Accept or Reject Samples** web page
 - From the **All Profiles** tab if desired profile is an ASG (Aquatic Symbiosis Genomics)^{Page 12, 3} or DTOL (Darwin Tree of Life)^{Page 12, 4} profile
2. In the **Pending Samples** tab, select desired sample record(s) by clicking the checkbox(es) associated with the sample record(s).

Then, click the  button as shown below.



COPO

Choose to Accept or Reject: dtol

Status: Idle

Note: clicking accept will immediately send sample info to ENA/Biosamples

Buttons: **Reject** **Accept** Select all visible Select None Delete Selected Download Permits View Images

Tabs: Pending Samples Processing Samples Accepted Samples Rejected Samples

Search: [Search bar]

Profile Title	Date Created	Samples link
DTOL Test Profile 4	17/11/2023	[link]
DTOL Test Profile 3	01/11/2023	[link]
DTOL Test Profile 2	27/10/2023	[link]
ASG Test Profile	10/10/2023	[link]
DTOL Test Profile	10/10/2023	[link]

Showing 1 to 10 of 39 entries 1 row selected

SERIES	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY	GENUS	TAXON_ID	SCIENTIFIC_NAME	TAXON_REMARKS
<input checked="" type="checkbox"/>	1	Dtol_R&D_Protist_cell_sort1	Co_S1_150001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus
<input checked="" type="checkbox"/>	2	Dtol_R&D_Protist_cell_sort2	Co_S2_150001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus
<input type="checkbox"/>	3	Dtol_R&D_Protist_cell_sort3	Co_S3_150001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus
<input type="checkbox"/>	4	Dtol_R&D_Protist_cell_sort4	Co_S1_150000_sc1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus
<input type="checkbox"/>	5	Dtol_R&D_Protist_cell_sort5	Co_S2_150000_sc1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus
<input type="checkbox"/>	6	Dtol_R&D_Protist_cell_sort6	Co_S3_150000_sc1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus
<input type="checkbox"/>	7	Dtol_R&D_Protist_cell_sort7	Co_S4_400001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus
<input type="checkbox"/>	8	Dtol_R&D_Protist_cell_sort8	Co_S8_10ml1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus
<input type="checkbox"/>	9	Dtol_R&D_Protist_cell_sort9	Co_S9_10ml1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus
<input type="checkbox"/>	10	Dtol_R&D_Protist_cell_sort10	Co_S10_10ml1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus

Showing 1 to 10 of 39 entries 1 row selected

Navigation: Previous 1 2 3 4 Next

Fig. 3: Accept or Reject Samples web page: Accepting samples within ASG or DTOL profiles

4.3.3 Accepting ERGA samples as a BGE checker

Note:

- In the **Samples** table, sample record(s) will only be displayed in the **Pending BGE Checker Samples** tab, if you are assigned as a **Biodiversity Genomics Europe (BGE) checker** for the desired profile.
- All COPO ERGA (European Reference Genome Atlas)⁵ profiles are displayed in the **All Profiles** tab but submitted samples within them cannot be accepted or rejected.

1. Choose desired profile on the left of the **Accept or Reject Samples** web page
 - From the **Profiles for My Sequencing Centre** tab
2. In the **Pending BGE Checker Samples** tab, select desired sample record(s) by clicking the checkbox(es) associated with the sample record(s).

Then, click the  button as shown below.

⁵ See term: *ERGA*.

Choose to Accept or Reject erga

Note clicking accept will immediately send sample info to ENA/Biosamples

Profiles for My Sequencing Centre All profiles

Search:

☒ Reject
 ☒ Accept

[Pending BGE Checker Samples](#)
[Pending Samples](#)
[Processing Samples](#)
[Accepted Samples](#)
[Rejected Samples](#)

Profile Title | Date Created | Samples link
 ERGA Test Profile 2 | 26/11/2023 | [%](#)
 ERGA Test Profile 11 | 27/11/2023 | [%](#)

Samples

Show 10 entries

	SERIES	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY	GENUS	TAXON_ID	SCIENTIFIC_NAME	TAXON_REMARKS	INFRASPECIES
<input checked="" type="checkbox"/>			FF06763893	ERGA_FOS_4557_001	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
<input checked="" type="checkbox"/>			FF06763894	ERGA_FOS_4557_002	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
<input type="checkbox"/>			FF06763895	ERGA_FOS_4557_003	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
<input type="checkbox"/>			FF06763896	ERGA_FOS_4557_004	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
<input type="checkbox"/>			FF06763897	ERGA_FOS_4557_005	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
<input type="checkbox"/>			FF06763898	ERGA_FOS_4557_006	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
<input type="checkbox"/>			FF06763899	ERGA_FOS_4557_007	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
<input type="checkbox"/>			FF06763900	ERGA_FOS_4557_008	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
<input type="checkbox"/>			FF06763901	ERGA_FOS_4557_009	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		

Showing 1 to 9 of 9 entries 1 row selected

Previous 1 Next

Fig. 4: Accept or Reject Samples web page: Accepting samples within ERGA profiles as a Biodiversity Genomics Europe (BGE) checker

- In the **Pending BGE Checker Samples** tab, select desired sample record(s) by clicking the checkbox(es) associated with the sample record(s).

Then, click the  button as shown below.

Choose to Accept or Reject erga

Note clicking accept will immediately send sample info to ENA/Biosamples

Profiles for My Sequencing Centre All profiles

Search:

☒ Reject
 ☒ Accept

[Pending BGE Checker Samples](#)
[Pending Samples](#)
[Processing Samples](#)
[Accepted Samples](#)
[Rejected Samples](#)

Profile Title | Date Created | Samples link
 ERGA Test Profile 2 | 26/11/2023 | [%](#)
 ERGA Test Profile 11 | 27/11/2023 | [%](#)

Samples

Show 10 entries

	SERIES	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY	GENUS	TAXON_ID	SCIENTIFIC_NAME	TAXON_REMARKS	INFRASPECIES
<input type="checkbox"/>			FF06763893	ERGA_FOS_4557_001	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
<input type="checkbox"/>			FF06763894	ERGA_FOS_4557_002	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		

Showing 1 to 2 of 2 entries

Previous 1 Next

Fig. 5: Accept or Reject Samples web page: Samples accepted by Biodiversity Genomics Europe (BGE) checker are displayed in 'Pending Samples' tab

4.3.4 Accepting ERGA samples as a Sample Manager

Note:

- In the **Samples** table, sample record(s) will only be displayed in the **Pending Samples** tab for the desired profile **after** they have been accepted by a Biodiversity Genomics Europe (BGE) checker.
- All COPO ERGA⁵ profiles are displayed in the **All Profiles** tab but submitted samples within them cannot be accepted or rejected.

Hint: Rejected samples are displayed in the **Rejected Samples** tab.

1. Choose desired profile on the left of the **Accept or Reject Samples** web page
 - From the **Profiles for My Sequencing Centre** tab
2. In the **Pending Samples** tab, select desired sample record(s) by clicking the checkbox(es) associated with the sample record(s).

Then, click the  button as shown below.

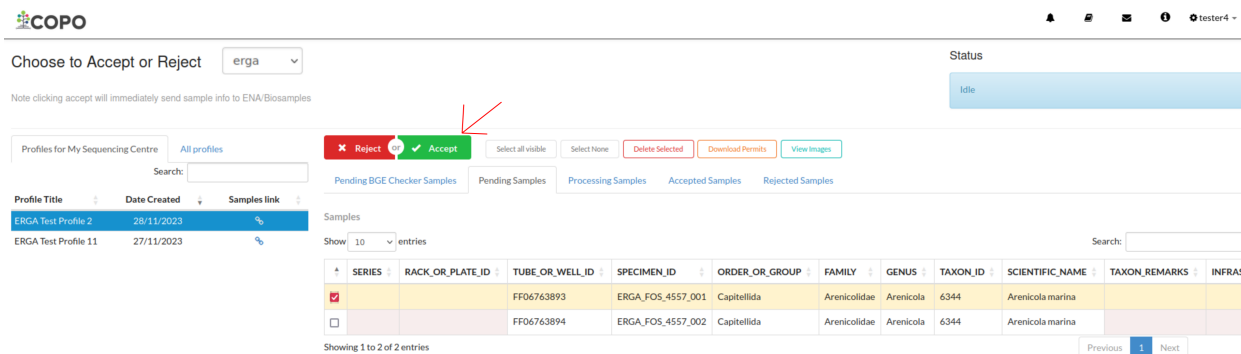


Fig. 6: **Accept or Reject Samples** web page: Accepting samples within ERGA profiles

A confirmation popup dialogue will be displayed as shown below.

Click the **Ok** button to accept the selected sample record(s) or click the **Cancel** button to cancel the action.

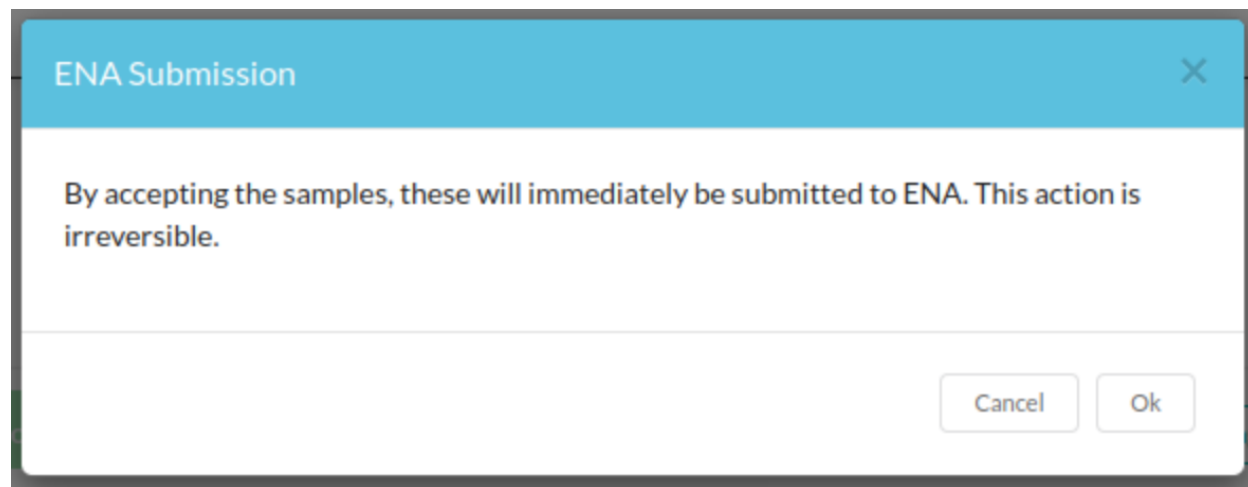


Fig. 7: **Accept or Reject Samples** web page: Accept samples confirmation dialogue

3. If the **Ok** button is clicked, the accepted samples will proceed to the processing stage and will be displayed in the **Processing Samples** tab as shown below:

OR

4. After the samples have been processed, the samples will proceed to the accepted stage and will be displayed in the **Accepted Samples** tab as shown below:

COPO

Choose to Accept or Reject dtol

Note clicking accept will immediately send sample info to ENA/Biosamples

Status: Adding to Sample 65578db801a736763afde3c8 Batch: Ox800036

Profiles: All profiles Search:

Buttons: ✖ Reject or ✔ Accept Select all visible Select None Delete Selected Download Permits View Images

Tabs: Pending Samples Processing Samples Accepted Samples Rejected Samples

Profile Title | Date Created | Samples link

Profile Title	Date Created	Samples link
DTOL Test Profile 4	17/11/2023	🔗
DTOL Test Profile 3	01/11/2023	🔗
DTOL Test Profile 2	27/10/2023	🔗
ASG Test Profile	10/10/2023	🔗
DTOL Test Profile	10/10/2023	🔗

Samples

Show 10 entries

Search:

SERIES	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY	GENUS	TAXON_ID	SCIENTIFIC_NAME	TAXON_REMARKS
1	Dtol_R&D_Protist_cell_sort1	Co_51_150001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
2	Dtol_R&D_Protist_cell_sort2	Co_52_150001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	

Showing 1 to 2 of 2 entries

Previous 1 Next

Fig. 8: Accept or Reject Samples web page: Accepted ASG or DTOL samples at the processing stage

COPO

Choose to Accept or Reject erga

Note clicking accept will immediately send sample info to ENA/Biosamples

Status: Nothing more to submit

Profiles for My Sequencing Centre: All profiles Search:

Buttons: ✖ Reject or ✔ Accept Select all visible Select None Delete Selected Download Permits View Images

Tabs: Pending BGE Checker Samples Pending Samples Processing Samples Accepted Samples Rejected Samples

Profile Title | Date Created | Samples link

Profile Title	Date Created	Samples link
ERGA Test Profile 2	28/11/2023	🔗
ERGA Test Profile 11	27/11/2023	🔗

Samples

Show 10 entries

Search:

SERIES	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY	GENUS	TAXON_ID	SCIENTIFIC_NAME	TAXON_REMARKS	INFRASPECIFIC
		FF06763893	ERGA_F05_4557_001	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		

Showing 1 to 1 of 1 entries

Previous 1 Next

Fig. 9: Accept or Reject Samples web page: Accepted ERGA samples at the processing stage

COPO

Choose to Accept or Reject dtol

Note clicking accept will immediately send sample info to ENA/Biosamples

Status: Biosample not submitted

Profiles: All profiles Search:

Buttons: ✖ Reject or ✔ Accept Select all visible Select None Delete Selected Download Permits View Images

Tabs: Pending Samples Processing Samples Accepted Samples Rejected Samples

Profile Title | Date Created | Samples link

Profile Title	Date Created	Samples link
DTOL Test Profile 4	17/11/2023	🔗
DTOL Test Profile 3	01/11/2023	🔗
DTOL Test Profile 2	27/10/2023	🔗
ASG Test Profile	10/10/2023	🔗
DTOL Test Profile	10/10/2023	🔗

Samples

Show 10 entries

Search:

SERIES	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY	GENUS	TAXON_ID	SCIENTIFIC_NAME	TAXON_REMARKS
1	Dtol_R&D_Protist_cell_sort1	Co_51_150001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
2	Dtol_R&D_Protist_cell_sort2	Co_52_150001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	

Showing 1 to 2 of 2 entries

Previous 1 Next

Fig. 10: Accept or Reject Samples web page: Accepted ASG or DTOL samples at the accepted stage

OR

The screenshot shows the COPO interface for managing samples. At the top, there's a 'Choose to Accept or Reject' dropdown set to 'erga'. Below it, a note states: 'Note clicking accept will immediately send sample info to ENA/Biosamples'. The main area has tabs for 'Profiles for My Sequencing Centre' and 'All profiles'. Under 'Profiles for My Sequencing Centre', there's a search bar and a list of profiles: 'ERGA Test Profile 2' (28/11/2023) and 'ERGA Test Profile 11' (27/11/2023). To the right, there are buttons for 'Reject', 'Accept', 'Select all visible', 'Select None', 'Delete Selected', 'Download Permits', and 'View Images'. Below these are tabs for 'Pending BGE Checker Samples', 'Pending Samples', 'Processing Samples', 'Accepted Samples', and 'Rejected Samples'. The 'Accepted Samples' tab is active, showing a table of samples. The table has columns: SERIES, RACK_OR_PLATE_ID, TUBE_OR_WELL_ID, SPECIMEN_ID, ORDER_OR_GROUP, FAMILY, GENUS, TAXON_ID, SCIENTIFIC_NAME, TAXON_REMARKS, and INFRASPECIES. One sample is listed: SERIES FF06763893, RACK_OR_PLATE_ID ERGA_FOS_4557_001, ORDER_OR_GROUP Capitellida, FAMILY Arenicolidae, GENUS Arenicola, TAXON_ID 6344, SCIENTIFIC_NAME Arenicola marina. At the bottom, it says 'Showing 1 to 1 of 1 entries'.

Fig. 11: Accept or Reject Samples web page: Accepted ERGA samples at the accepted stage

4.3.5 Rejecting samples

1. Choose desired profile on the left of the **Accept or Reject Samples** web page

- From the **Profiles for My Sequencing Centre** tab - if desired profile is an ERGA^{Page 14, 5} profile

OR

- From the **All Profiles** tab if desired profile is not an ERGA^{Page 14, 5} profile

2. In the **Pending Samples** tab, select desired sample record(s) by clicking the checkbox(es) associated with the sample record(s).

Similarly, if you are a Biodiversity Genomics Europe (BGE) checker, select desired sample record(s) from the **Pending BGE Checker Samples** tab.

Then, click the **Reject** button as shown below:

The screenshot shows the COPO interface for managing samples. At the top, there's a 'Choose to Accept or Reject' dropdown set to 'dtol'. Below it, a note states: 'Note clicking accept will immediately send sample info to ENA/Biosamples'. The main area has tabs for 'All profiles' and 'All profiles'. Under 'All profiles', there's a search bar and a list of profiles: 'DTOL Test Profile 4' (17/11/2023), 'DTOL Test Profile 3' (01/11/2023), 'DTOL Test Profile 2' (27/10/2023), 'ASG Test Profile' (10/10/2023), and 'DTOL Test Profile' (10/10/2023). To the right, there are buttons for 'Reject', 'Accept', 'Select all visible', 'Select None', 'Delete Selected', 'Download Permits', and 'View Images'. Below these are tabs for 'Pending Samples', 'Processing Samples', 'Accepted Samples', and 'Rejected Samples'. The 'Pending Samples' tab is active, showing a table of samples. The table has columns: SERIES, RACK_OR_PLATE_ID, TUBE_OR_WELL_ID, SPECIMEN_ID, ORDER_OR_GROUP, FAMILY, GENUS, TAXON_ID, SCIENTIFIC_NAME, TAXON_REMARKS, and INFRASPECIES. 12 samples are listed, with the first 5 selected (checkboxes checked). At the bottom, it says 'Showing 1 to 10 of 37 entries 1 row selected'.

Fig. 12: Accept or Reject Samples web page: Rejecting samples

- The samples will proceed to the rejected stage and will be displayed in the **Rejected Samples** tab as shown below:

COPO

tester3

Choose to Accept or Reject: dtol

Note clicking accept will immediately send sample info to ENA/Biosamples

Status: Idle

Search:

Reject Accept Select all visible Select None Delete Selected Download Permits View Images

Pending Samples Processing Samples Accepted Samples Rejected Samples

Profile Title Date Created Samples link

Profile Title	Date Created	Samples link
DTOL Test Profile 4	17/11/2023	
DTOL Test Profile 3	01/11/2023	
DTOL Test Profile 2	27/10/2023	
ASG Test Profile	10/10/2023	
DTOL Test Profile	10/10/2023	

Samples

Show 10 entries

Search:

SERIES	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY	GENUS	TAXON_ID	SCIENTIFIC_NAME	TAXON_REMARKS
6	Dtol_R&D_Protist_cell_sort6	Co_S3_150000_sc1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
7	Dtol_R&D_Protist_cell_sort7	Co_S4_400001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	

Showing 1 to 2 of 2 entries

Previous 1 Next

Fig. 13: Accept or Reject Samples web page: Rejected samples at the rejected stage

4.4 Download Submitted Sample Manifests

As a **sample manager**, you can download submitted (filled) manifests by following the steps below:

- Navigate to the **Accept or Reject Samples** web page.

See [How to access Accept or Reject Samples web page](#) section for guidance.

- On the left of the **Accept or Reject Samples** web page, click the icon in the **Samples link** table column of the table row for the profile that you would like upload a manifest for or update a submitted manifest for as shown below:

If the desired profile is an ASG profile or DTOL profile, navigate to the **Samples** web page by clicking the icon in the **Samples link** table column of the table row for the desired profile in the **All Profiles** tab as shown below:

Similarly, if the desired profile is an ASG profile, the same action occurs.

OR

If the desired profile is an ERGA profile, navigate to the **Samples** web page by clicking the icon in the **Samples link** table column of the table row for the desired profile in the **Profiles for My Sequencing Centre** tab as shown below:

- The **Samples** web page will be displayed as shown below:

Similarly, if the desired profile is an ASG profile, the **Samples** web page will be displayed.

OR

- Download the submitted manifest by following the guidelines described in the [How to Download Submitted Sample Manifest](#) section

COPO

Choose to Accept or Reject: dtol

Note clicking accept will immediately send sample info to ENA/Biosamples

Status: Idle

Profiles for My Sequencing Centre: All profiles

Search:

Profile Title	Date Created	Samples link
DTOL Test Profile 4	17/11/2023	Link
DTOL Test Profile 3	01/11/2023	Link
DTOL Test Profile 2	27/10/2023	Link
ASG Test Profile	10/10/2023	Link
DTOL Test Profile	10/10/2023	Link

Samples

Show: 10 entries

SERIES	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY	GENUS	TAXON_ID	SCIENTIFIC_NAME	TAXON_REMARKS
3	DtOL_R&D_Protist_cell_sort3	Co_53_150001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
4	DtOL_R&D_Protist_cell_sort4	Co_51_150000_sc1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
5	DtOL_R&D_Protist_cell_sort5	Co_52_150000_sc1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
8	DtOL_R&D_Protist_cell_sort8	Co_58_10ml1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
9	DtOL_R&D_Protist_cell_sort9	Co_59_10ml1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
10	DtOL_R&D_Protist_cell_sort10	Co_510_10ml1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
11	DtOL_R&D_Protist_cell_sort11	Pt_51_150001	Ox800057	Chlamydomonadales	Phacotaceae	Pteromonas	77548	Pteromonas angulosa	
12	DtOL_R&D_Protist_cell_sort12	Pt_52_150001	Ox800057	Chlamydomonadales	Phacotaceae	Pteromonas	77548	Pteromonas angulosa	
13	DtOL_R&D_Protist_cell_sort13	Pt_53_150001	Ox800057	Chlamydomonadales	Phacotaceae	Pteromonas	77548	Pteromonas angulosa	
14	DtOL_R&D_Protist_cell_sort14	Pt_51_100000_sc1	Ox800057	Chlamydomonadales	Phacotaceae	Pteromonas	77548	Pteromonas angulosa	

Showing 1 to 10 of 35 entries

Previous 1 2 3 4 Next

Fig. 14: Accept or Reject Samples web page: Navigate to ‘Samples’ web page by clicking the link associated with a DTOL profile

COPO

Choose to Accept or Reject: erga

Note clicking accept will immediately send sample info to ENA/Biosamples

Status: Idle

Profiles for My Sequencing Centre: All profiles

Search:

Profile Title	Date Created	Samples link
ERGA Test Profile 2	28/11/2023	Link
ERGA Test Profile 11	27/11/2023	Link

Samples

Show: 10 entries

SERIES	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY	GENUS	TAXON_ID	SCIENTIFIC_NAME	TAXON_REMARKS	INFRASPECIES
		FF06763893	ERGA_FOS_4557_001	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
		FF06763894	ERGA_FOS_4557_002	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
		FF06763895	ERGA_FOS_4557_003	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
		FF06763896	ERGA_FOS_4557_004	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
		FF06763897	ERGA_FOS_4557_005	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
		FF06763898	ERGA_FOS_4557_006	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
		FF06763899	ERGA_FOS_4557_007	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
		FF06763900	ERGA_FOS_4557_008	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
		FF06763901	ERGA_FOS_4557_009	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		

Showing 1 to 9 of 9 entries

Previous 1 Next

Fig. 15: Accept or Reject Samples web page: Navigate to ‘Samples’ web page by clicking the link associated with an ERGA profile

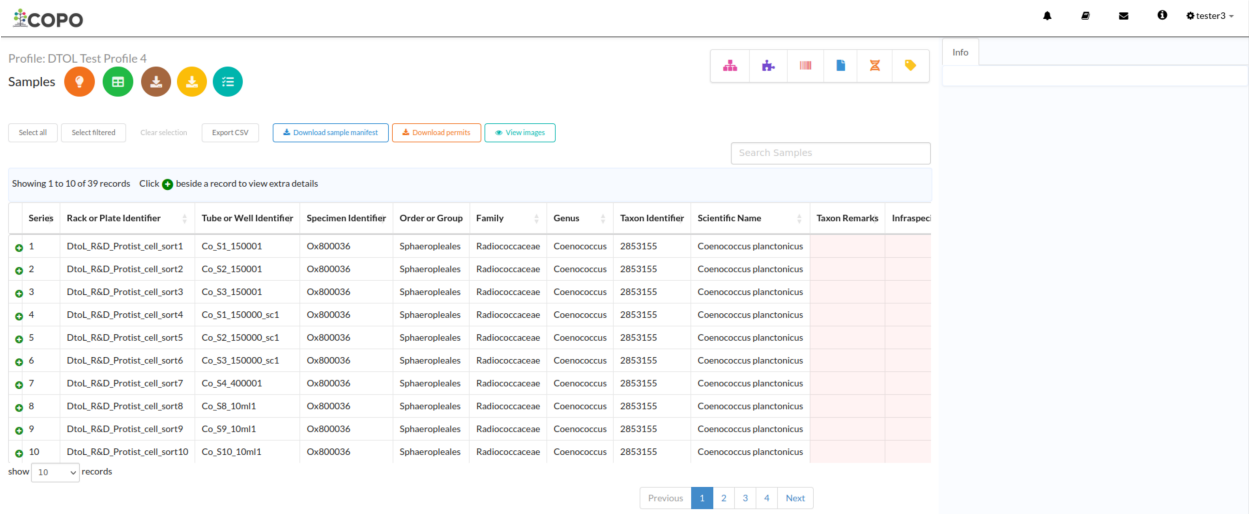


Fig. 16: Samples web page for a DTOL profile

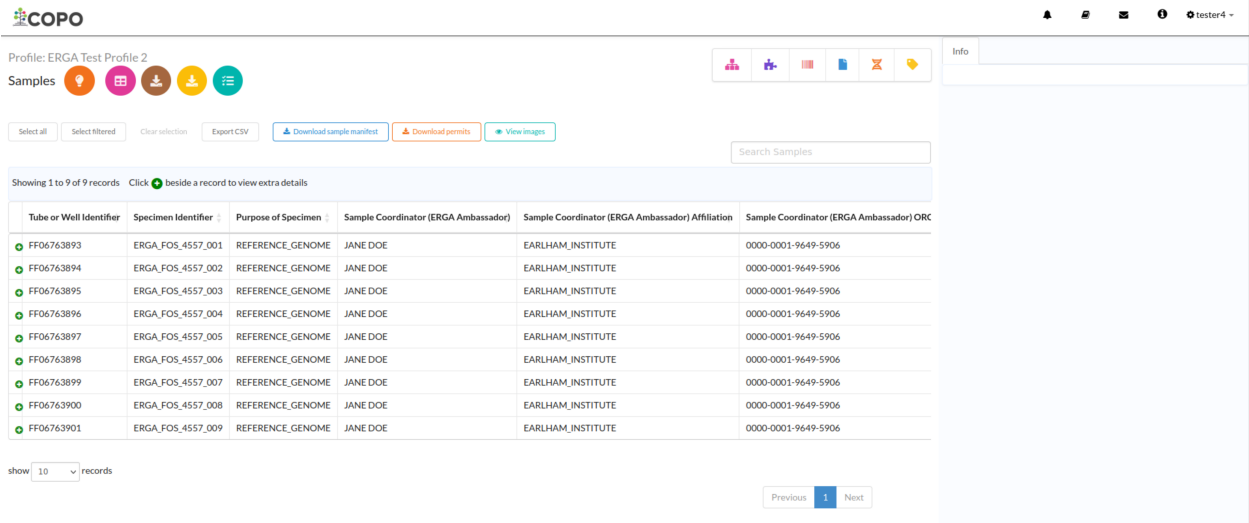



Fig. 17: Samples web page for an ERGA profile

4.5 Download Submitted Permits

If you have been assigned as a **sample manager**, you can view the permits submitted for submitted sample(s) on the [Accept/Reject Samples' web page](#) by following the steps below:

Note:


- Permits can only be downloaded for submitted samples that are **pending** action by a sample manager or have been **accepted** by a sample manager.
 - Permits exist for ERGA ^{Page 14, 5} profiles only.
-

Hint: To download submitted permits for samples within the **Accepted Samples** tab, CTRL + Click the desired sample record(s) then, click the  button to download permit(s) submitted for the selected record(s).

1. Navigate to the **Accept or Reject Samples** web page.

See [How to access Accept or Reject Samples web page](#) section for guidance on how to access the **Accept or Reject Samples** web page.

2. Select the sample record(s) that you would like to download the permits for.

Then, click the  button to download permit(s) submitted for the selected sample record(s).


3. If any permit submission(s) exist for the selected sample record(s), the permits will be automatically downloaded for the selected sample record(s) as shown below:

Hint: Permits are downloaded as a .zip file

If no permits were submitted for the selected sample record(s), a message is displayed in the popup dialogue indicating such as shown below:

4.6 View Submitted Images

If you have been assigned as a **sample manager**, you can view the images submitted for submitted sample(s) on the [Accept/Reject Samples' web page](#) by following the steps below:

Hint: To view submitted images for samples within the **Accepted Samples** tab, CTRL + Click the desired sample record(s) then, click the  button to view image(s) submitted for the selected record(s).

1. Navigate to the **Accept or Reject Samples** web page.

See [How to access Accept or Reject Samples web page](#) section for guidance on how to access the **Accept or Reject Samples** web page.

2. Select the sample record(s) that you would like to view the images for.

Then, click the  button to view image(s) submitted for the selected sample record(s).

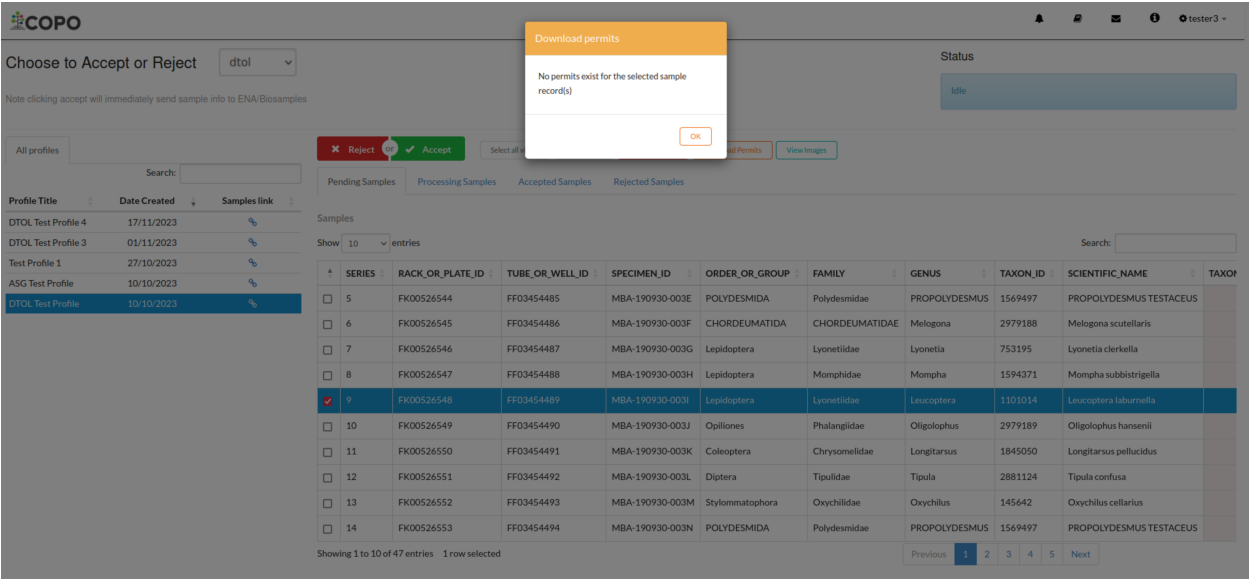


Fig. 18: Accept or Reject Samples web page: Popup dialogue displaying message, ‘No permits exist for selected sample record(s)’

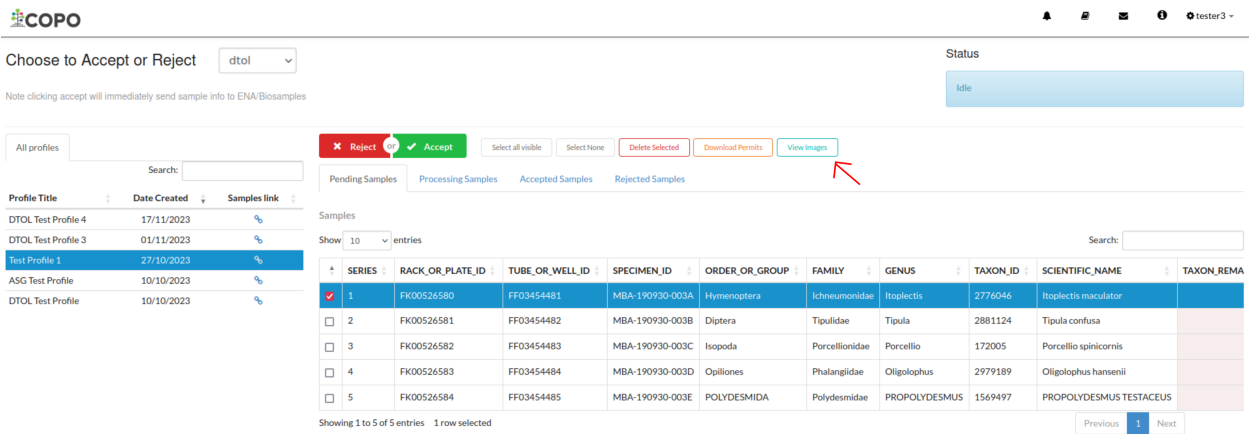


Fig. 19: Accept or Reject Samples web page: Pointer to ‘View images’ button

- If any image submission(s) exist for the selected sample record(s), a popup dialogue will be displayed with the image(s) submitted for the selected sample record(s) as shown below:

Hint: Click the image to view a larger version.

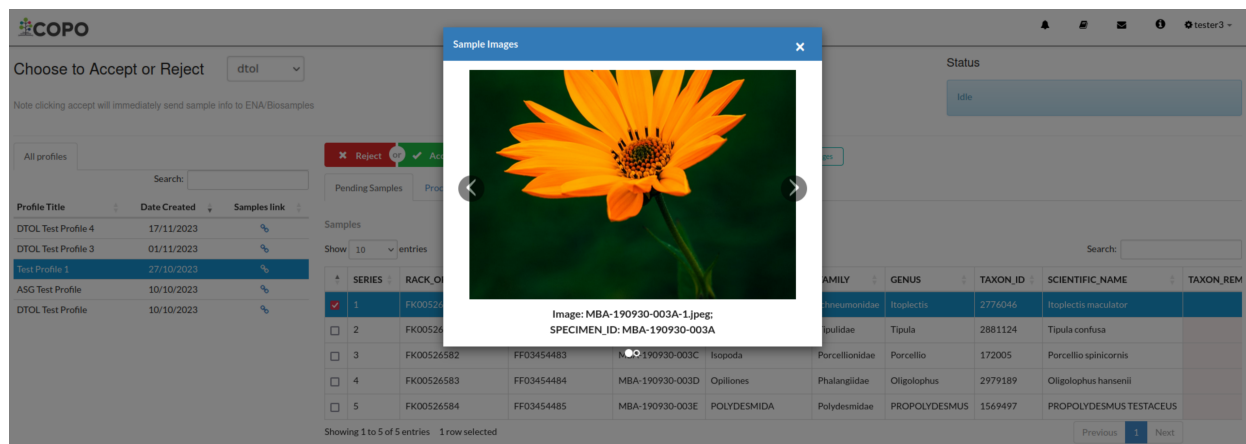


Fig. 20: Accept or Reject Samples web page: Popup dialogue displaying submitted image(s) for selected sample record(s)

OR

If no images were submitted for the selected sample record(s), a message is displayed in the popup dialogue indicating such as shown below:

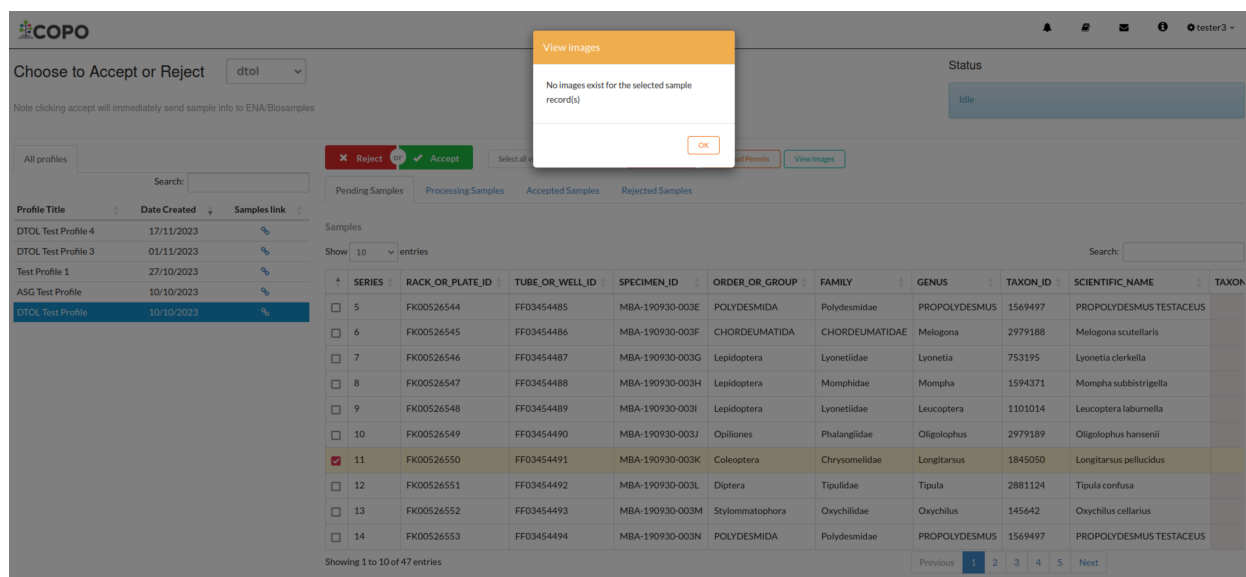


Fig. 21: Accept or Reject Samples web page: Popup dialogue displaying message, 'No images exist for selected sample record(s)'

4.7 Upload Manifest or Update Submitted Manifest on behalf of Manifest Submitters

Note:

- The manifest dropdown menu will only be displayed on the **Accept or Reject samples** web page if you as a sample manager, belongs to more than one sample manager manifest group.
 - If the **dtol** sample manager group dropdown menu option is selected, both Aquatic Symbiosis Genomics (ASG) profiles and Darwin Tree of Life (DTOL) profiles will be displayed in the **All profiles** tab (if any exists).
 - The **Samples** table will only be displayed if the selected/highlighted profile has submitted samples.
-


Hint:


- **All** sample field values can be updated by sample managers.
 - **Some** sample field values can be updated by sample providers. See the [Updating Samples](#) section for information about which field values can be updated by sample providers.
 - Samples can be updated by resubmitting the manifest with the updated metadata.
-

The following steps can be followed to upload a manifest or update a submitted manifest on behalf of a manifest submitter^{Page 11, 2}:

1. Navigate to the **Accept or Reject Samples** web page.


See [How to access Accept or Reject Samples web page](#) section for guidance.

2. On the left of the **Accept or Reject Samples web page**, click the  icon in the **Samples link** table column of the table row for the profile that you would like upload a manifest for or update a submitted manifest for as shown below:

If the desired profile is an ASG profile or DTOL profile, navigate to the **Samples** web page by clicking the  icon in the **Samples link** table column of the table row for the desired profile in the **All Profiles** tab as shown below:

Similarly, if the desired profile is an ASG profile, the same action occurs.

OR

If the desired profile is an ERGA profile, navigate to the **Samples** web page by clicking the  icon in the **Samples link** table column of the table row for the desired profile in the **Profiles for My Sequencing Centre** tab as shown below:

3. The **Samples** web page will be displayed as shown below:

Similarly, if the desired profile is an ASG profile, the **Samples** web page will be displayed.

OR

4. If you do not have the submitted manifest for the profile, see the [How to Download Submitted Sample Manifest](#) section for guidance on how to download the submitted sample manifest. Then, refer to the [Updating Samples](#) section for guidance on how to submit the modified manifest.

OR

If you have the submitted manifest for the profile, see the [Updating Samples](#) section for guidance on how to update the submitted manifest.

COPO

Choose to Accept or Reject: dtol

Note clicking accept will immediately send sample info to ENA/Biosamples

Profiles: All profiles

Search:

Profile Title	Date Created	Samples link
DTOL Test Profile 4	17/11/2023	Link
DTOL Test Profile 3	01/11/2023	Link
DTOL Test Profile 2	27/10/2023	Link
ASG Test Profile	10/10/2023	Link
DTOL Test Profile	10/10/2023	Link

Buttons: Reject, Accept, Select all visible, Select None, Delete Selected, Download Permits, View Images

Tabs: Pending BGE Checker Samples, Pending Samples, Processing Samples, Accepted Samples, Rejected Samples

Samples

Show: 10 entries

SERIES	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY	GENUS	TAXON_ID	SCIENTIFIC_NAME	TAXON_REMARKS
3	Dtol_R&D_Protist_cell_sort3	Co_53_150001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
4	Dtol_R&D_Protist_cell_sort4	Co_51_150000_sc1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
5	Dtol_R&D_Protist_cell_sort5	Co_52_150000_sc1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
8	Dtol_R&D_Protist_cell_sort8	Co_58_10ml1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
9	Dtol_R&D_Protist_cell_sort9	Co_59_10ml1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
10	Dtol_R&D_Protist_cell_sort10	Co_510_10ml1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
11	Dtol_R&D_Protist_cell_sort11	Pt_51_150001	Ox800057	Chlamydomonadales	Phacotaceae	Pteromonas	77548	Pteromonas angulosa	
12	Dtol_R&D_Protist_cell_sort12	Pt_52_150001	Ox800057	Chlamydomonadales	Phacotaceae	Pteromonas	77548	Pteromonas angulosa	
13	Dtol_R&D_Protist_cell_sort13	Pt_53_150001	Ox800057	Chlamydomonadales	Phacotaceae	Pteromonas	77548	Pteromonas angulosa	
14	Dtol_R&D_Protist_cell_sort14	Pt_51_100000_sc1	Ox800057	Chlamydomonadales	Phacotaceae	Pteromonas	77548	Pteromonas angulosa	

Showing 1 to 10 of 35 entries

Navigation: Previous, 1, 2, 3, 4, Next

Fig. 22: Accept or Reject Samples web page: Navigate to ‘Samples’ web page by clicking the link associated with a DTOL profile

COPO

Choose to Accept or Reject: erga

Note clicking accept will immediately send sample info to ENA/Biosamples

Profiles for My Sequencing Centre: All profiles

Search:

Profile Title	Date Created	Samples link
ERGA Test Profile 2	28/11/2023	Link
ERGA Test Profile 11	27/11/2023	Link

Buttons: Reject, Accept, Select all visible, Select None, Delete Selected, Download Permits, View Images

Tabs: Pending BGE Checker Samples, Pending Samples, Processing Samples, Accepted Samples, Rejected Samples

Samples

Show: 10 entries

SERIES	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY	GENUS	TAXON_ID	SCIENTIFIC_NAME	TAXON_REMARKS	INFRASPECIES
		FF06763893	ERGA_FOS_4557_001	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
		FF06763894	ERGA_FOS_4557_002	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
		FF06763895	ERGA_FOS_4557_003	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
		FF06763896	ERGA_FOS_4557_004	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
		FF06763897	ERGA_FOS_4557_005	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
		FF06763898	ERGA_FOS_4557_006	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
		FF06763899	ERGA_FOS_4557_007	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
		FF06763900	ERGA_FOS_4557_008	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
		FF06763901	ERGA_FOS_4557_009	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		

Showing 1 to 9 of 9 entries

Navigation: Previous, 1, Next

Fig. 23: Accept or Reject Samples web page: Navigate to ‘Samples’ web page by clicking the link associated with an ERGA profile

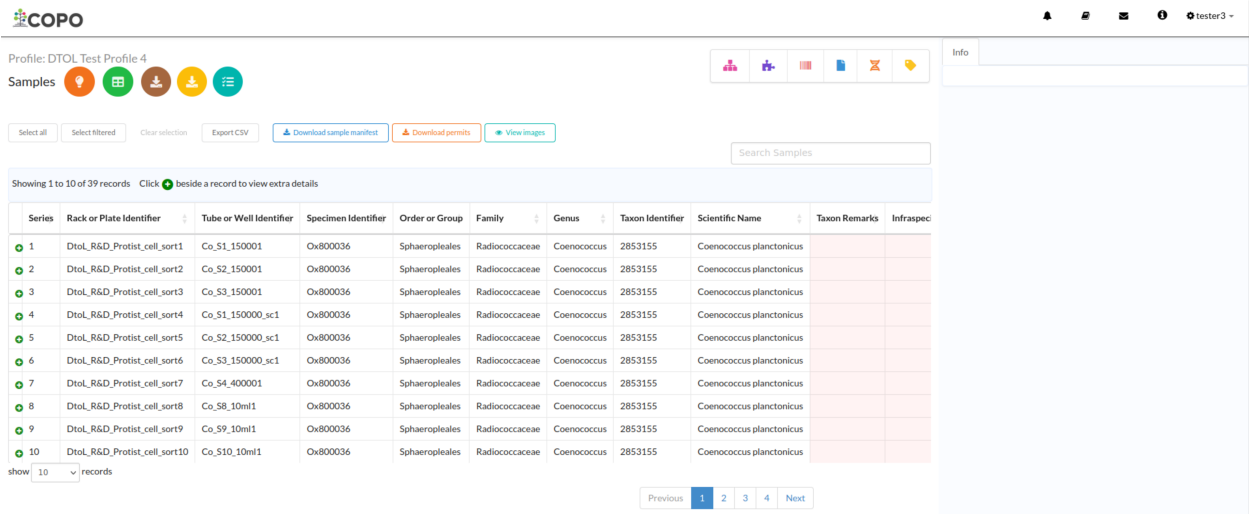


Fig. 24: Samples web page for a DTOL profile

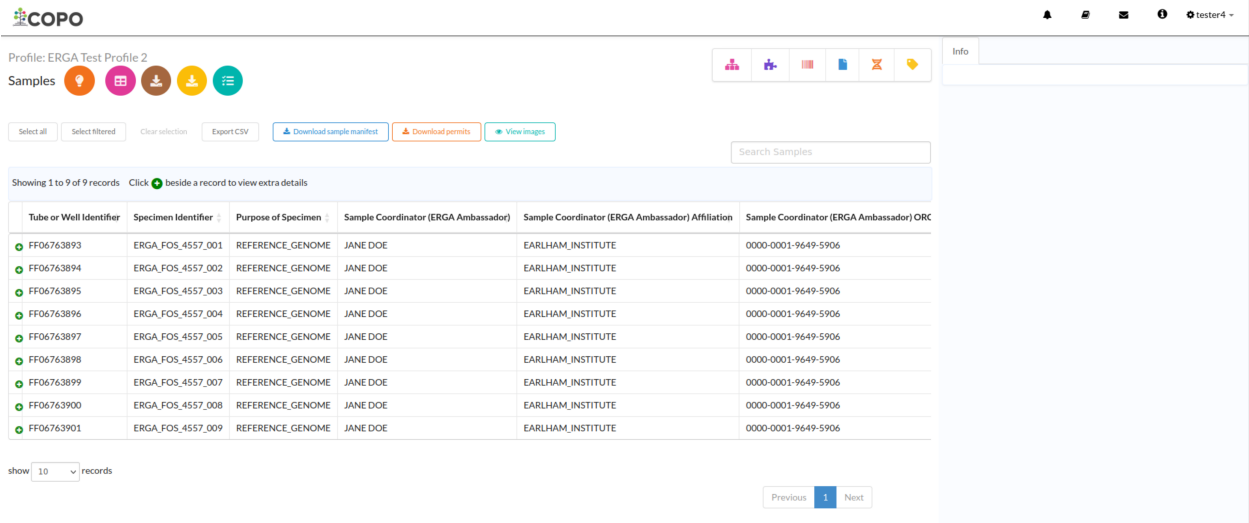


Fig. 25: Samples web page for an ERGA profile

OR

If you would like to upload a newer version of a manifest that has already been submitted on behalf of the manifest provider, please follow the steps below:

1. Download the submitted manifest by following the guidelines described in the [How to Download Submitted Sample Manifest](#) section if you do not have the newer version of the manifest with the sample metadata information.
2. Transfer the sample metadata from the submitted manifest into the newer version of the manifest.
3. Send an email to the COPO team at , indicating the profile type as well as the profile title and requesting that the samples be **removed** from the profile.

The samples has to be removed from the profile so that the sample metadata in the newer version of the manifest can be registered in the profile.

Important: Please request that the samples be removed from the profile **only** if you are certain and have the newer version of the manifest with the sample metadata information.

The samples **cannot** be restored after they have been removed from the profile.

4. Upload the newer version of the manifest by referring to the guidelines described in the desired link below to learn more about each type of manifest submission:
 - Aquatic Symbiosis Genomics (ASG) manifest submission
 - Darwin Tree of Life (DToL) manifest submission
 - Darwin Tree of Life Environmental (DToL_ENV) manifest submission
 - European Reference Genome Atlas (ERGA) manifest submission

Hint: See [Downloading Manifest Templates](#) section for information about downloading manifest templates.

The COPO development team documentation was done to help users understand the COPO system and how to use it. The documentation is a living document and will be updated as the COPO system evolves.

Future members of the COPO team can use the documentation as a guide to understand the COPO system and how to use it. This limits the need for extensive training and allows new members to get up to speed quickly. Additionally, the documentation can be used as a reference guide for the COPO team members. Advantages include the ability to quickly look up information and to have a consistent reference guide for all team members. to continue the development of the COPO system.

The documentation is also useful for the COPO users. It provides a guide on how to use the COPO system and how to navigate the system.

The COPO documentation is a living document and will be updated as the COPO system evolves. The documentation will be updated to reflect the changes in the COPO system.

Notable impacts of the COPO project team documentation include:

- Limiting the need for extensive training and allows new project team members to get up to speed quickly and efficiently
- Provides a consistent reference guide for all project team members
- Allows for quick look up of information
- **Provides a guide on how to use the COPO system, solve notable bugs/user requests and how to navigate the system for the COPO users**

- The documentation is a living document and will be updated as the COPO system evolves
- The documentation reflects up-to-date procedures, methods and guidelines to navigate the COPO system from a project developer's perspective

STAND-ALONE PROFILE


In COPO, a Stand-alone work profile¹ is required to submit research objects² such as files, reads, assemblies and sequence annotations.

Hint: COPO work profiles are regarded as *project* research objects. The projects are created in ENA (European Nucleotide Archive)³ after *reads have been submitted*. Thus, any modifications that you would like to be done to a project in ENA must be done to the desired profile in COPO.

See also:

- See *Steps to create Tree of Life (ToL) profile* if you would like to make ToL manifest submissions
- *How to Update Profiles*
- *How to Delete Profiles*
- *How to Make Profiles (also known as Projects) Public*
- *Sharing Profiles*
- *Sorting Profiles*
- *Profile Types Legend*

5.1 Steps to Create a Stand-alone Profile

1. Click the  **Add new record** icon to view the **Add Profile** form
2. **Contact COPO via email** dialogue is displayed indicating that the user is not a member of any manifest group and that the user must make a request to be added to a manifest group to make ToL manifest submissions if the user would like to do so.

Click **Okay** to close the dialogue.

3. Provide details for the new profile then, click **Save**

¹ Also known as COPO profile. See: *COPO profile or work profile*.

² Also known as profile component. See term: *Profile component*.

Research objects refer to files, reads, assemblies, files and sequence annotations.

A Stand-alone profile is considered as a *project* research object.

³ See term: *ENA*.

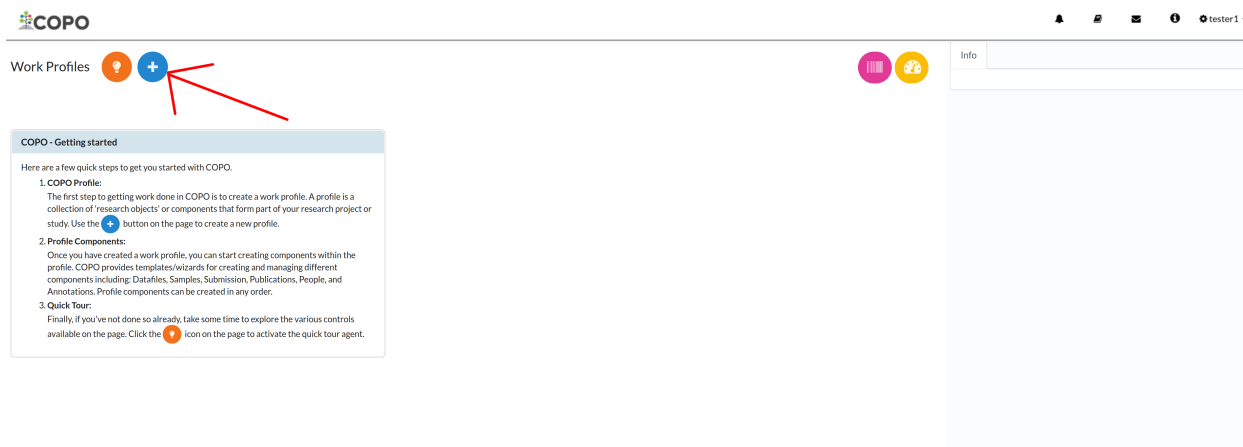


Fig. 1: Stand-alone Profile: Add new profile record icon

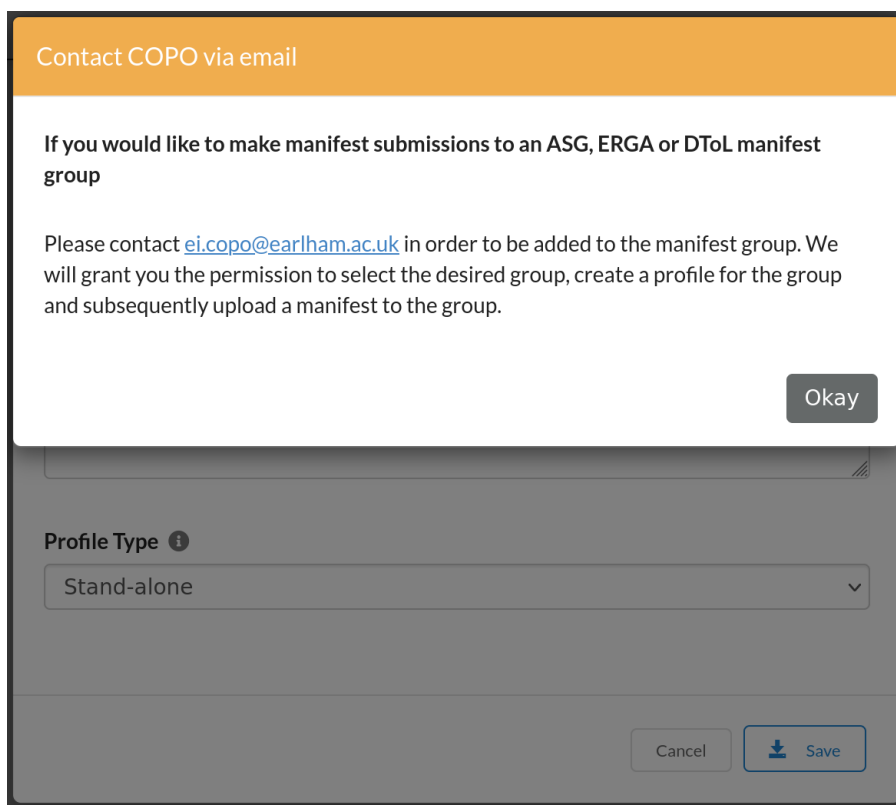
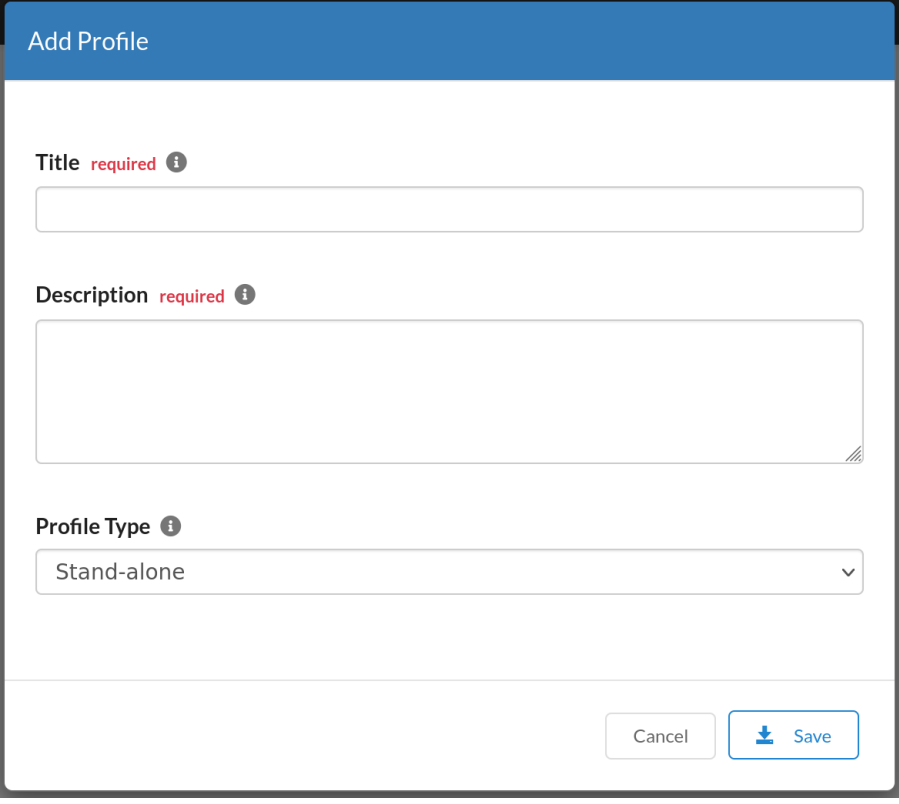


Fig. 2: Stand-alone Profile: Contact COPO dialogue is displayed regarding getting access to make Tree of Life (ToL) manifest submissions



The image shows a web-based form titled "Add Profile" with a blue header bar. The form contains three main input sections: a "Title" field with a "required" label and an information icon, a "Description" field with a "required" label and an information icon, and a "Profile Type" dropdown menu with an information icon. The dropdown menu currently shows "Stand-alone" with a downward arrow. At the bottom right of the form are two buttons: "Cancel" and "Save" (which includes a download icon).

Add Profile

Title required ⓘ

Description required ⓘ

Profile Type ⓘ

Stand-alone ▼

Cancel Save

Fig. 3: Stand-alone Profile: Add profile form dialogue

Hint: Both profile **Title** and profile **Description** are mandatory form fields.

Meaningful field values are recommended in the form boxes because the information will appear in submissions of the research objects associated with the profile, in public remote repositories.

4. The new profile will be displayed in the **Profile** list

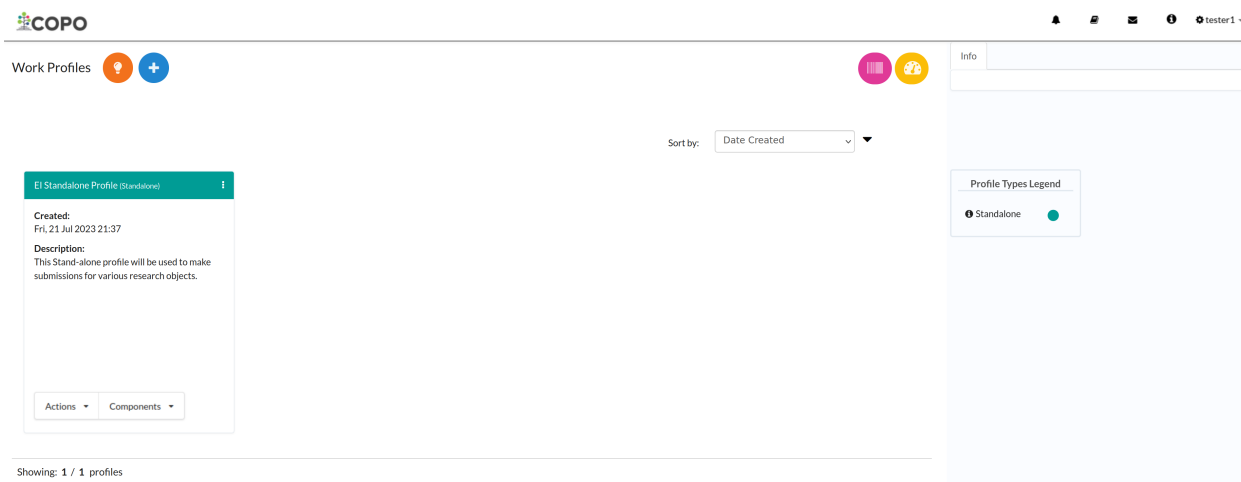


Fig. 4: Stand-alone Profile: Work profiles' web page displaying the created profile

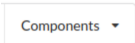
Hint: The **Work Profiles'** list can be sorted by date created, profile title or profile type.

Choose the desired sort type from the **Sort by** dropdown menu (at the top-right of the profile record).

5.2 Stand-alone Profile Components

A COPO profile defines a set of component types from which instances of research objects^{Page 31, 2} can be created.

The following component types are currently defined:

1. Accessions
 2. *Assembly*
 3. *Files*
 4. *Reads*
 5. *Sequence Annotations*
- Component instances defined within a profile will only be visible within that profile^{Page 31, 1}.
 - To access a component within a profile, click the component button displayed within the popup after the  button was clicked (see the screenshot above).

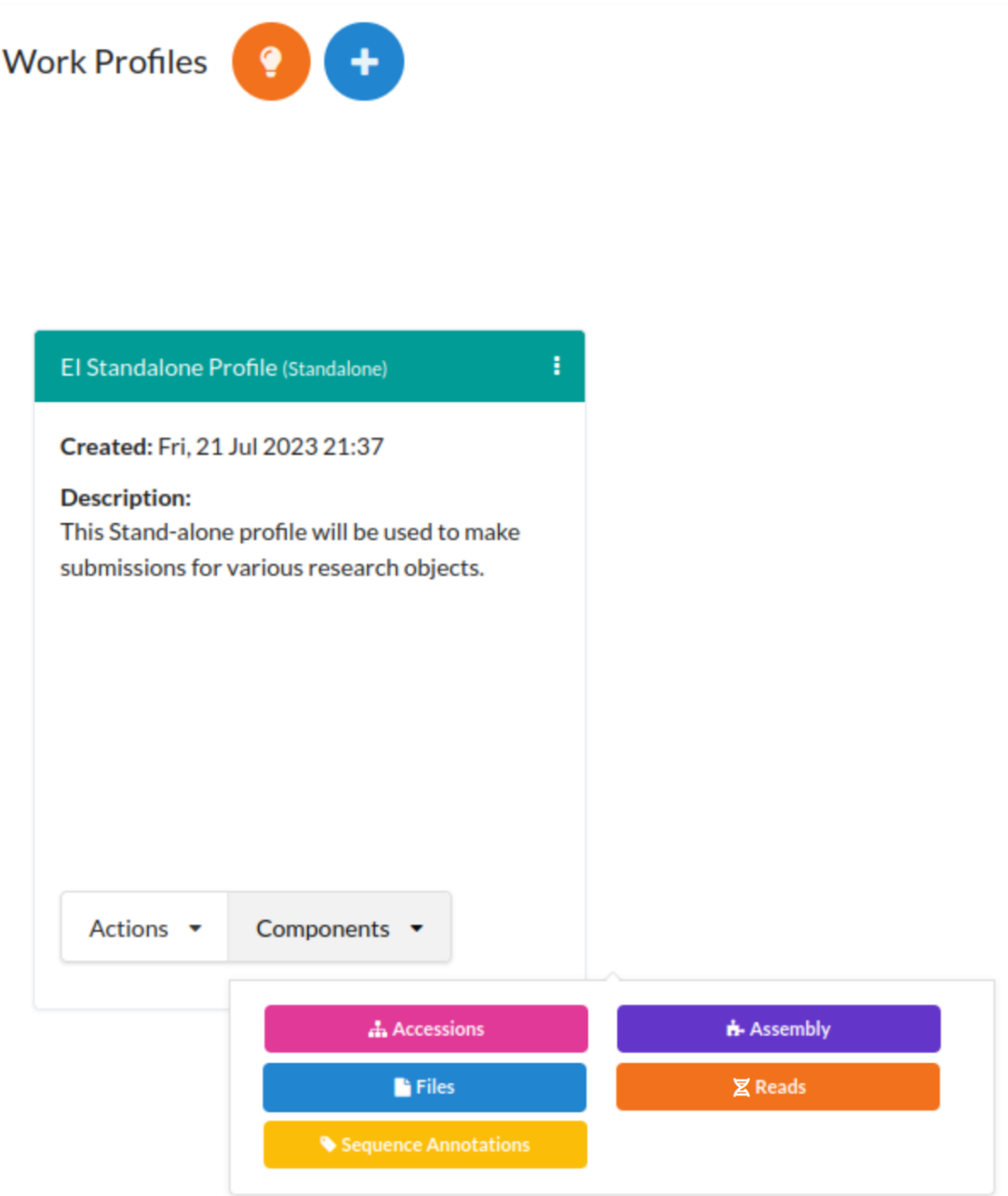
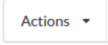


Fig. 5: Stand-alone Profile Components

- Profile actions⁴ can be accessed via the  button. The actions describe the process of each component within a profile.

5.3 Submitting Virtual Samples

Please follow the steps below to submit virtual samples⁵:

1. Create a Stand-alone profile or select an existing one. See *Steps to create a Stand-alone profile*.
2. Submit reads to the Stand-alone profile. See *Submitting Reads* section.

Important:

- Files **must** be uploaded before reads submission can be made.
 - Reads submission is required before making a virtual sample submission.
-

3. All virtual sample submissions require a description.

Provide the virtual sample description to the as well as the (completed) reads manifest file. COPO will add the sample description in ENA^{Page 31, 3}.

Hint: Accessions are available a few minutes after reads have been submitted.

⁴ See term: *Profile action*.

⁵ See term: *Virtual sample*.

TREE OF LIFE PROFILE

In COPO, a Tree of Life (ToL)¹ work profile² is required to submit research objects³ such as samples, barcoding manifests, sequence annotations, reads, assemblies and files.


A ToL profile can be used to create one of the following biodiversity projects:

- Aquatic Symbiosis Genomics (ASG)
- European Reference Genome Atlas (ERGA)
- Darwin Tree of Life Environmental (DTOL_ENV)
- Darwin Tree of Life (DTOL)

See also:

- *[How to Update Profiles](#)*
- *[How to Delete Profiles](#)*
- *[How to Make Profiles \(also known as Projects\) Public](#)*
- *[Sharing Profiles](#)*
- *[Releasing Profiles \(Studies\)](#)*
- *[Sorting Profiles](#)*
- *[Profile Types Legend](#)*

6.1 Steps to Create a Tree of Life Profile

1. Click the  **Add new record** icon to view the **Add Profile** form
2. **Contact COPO via email** dialogue is displayed indicating that the user is not a member of any manifest group and that the user must make a request to be added to a manifest group to make ToL manifest submissions if the user would like to do so.

Click **Okay** to close the dialogue.

¹ See term: *Tree of Life (ToL)*.

² Also known as COPO profile. See term: *COPO profile*.

³ Also known as profile component. See term: *Profile component*.

Research objects refer to files, reads, assemblies, files samples, barcodes (also known as targeted sequences in European Nucleotide Archive (ENA)) and sequence annotations.

A Tree of Life (ToL) profile is considered as a *project* research object.

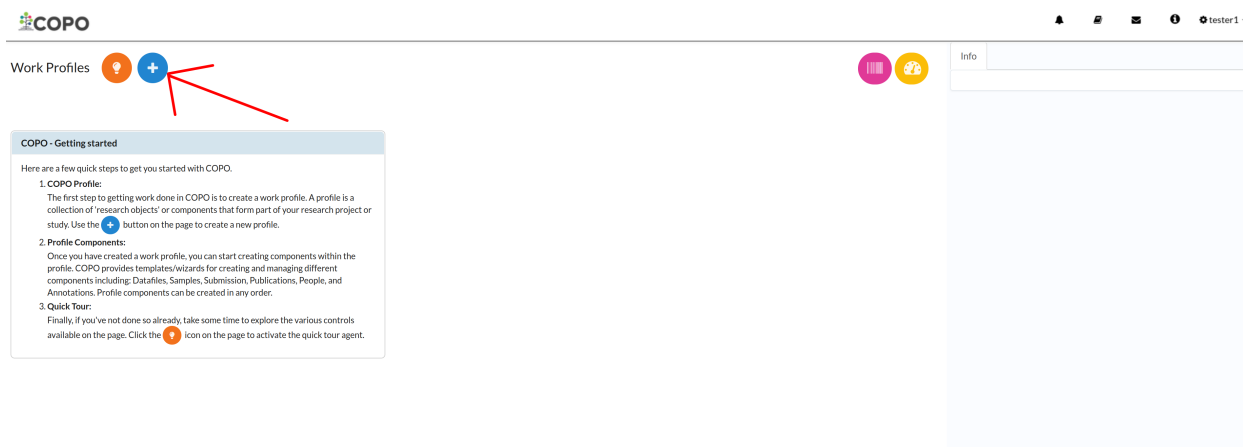


Fig. 1: ToL Profile: Add new profile record icon

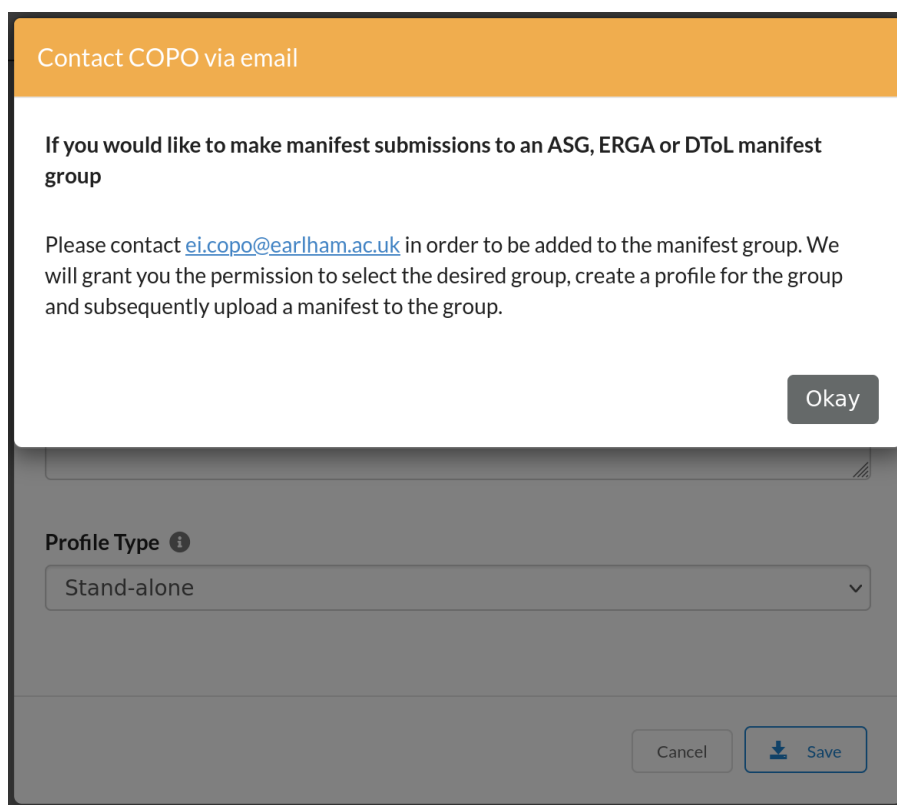


Fig. 2: ToL Profile: Contact COPO dialogue is displayed regarding getting access to make ToL manifest submissions

6.1.1 Provide Profile Title & Description

3. In the **Add Profile** form dialogue, provide details for the new profile then, click **Save**

Note: The **Profile Type** dropdown menu by default will only display the **Stand-alone** option.

If your desired profile type is not displayed in the **Profile Type** dropdown menu, indicating the type of profile group that you would like to be granted access to. Thereafter, the desired profile type option will be displayed in the dropdown menu.

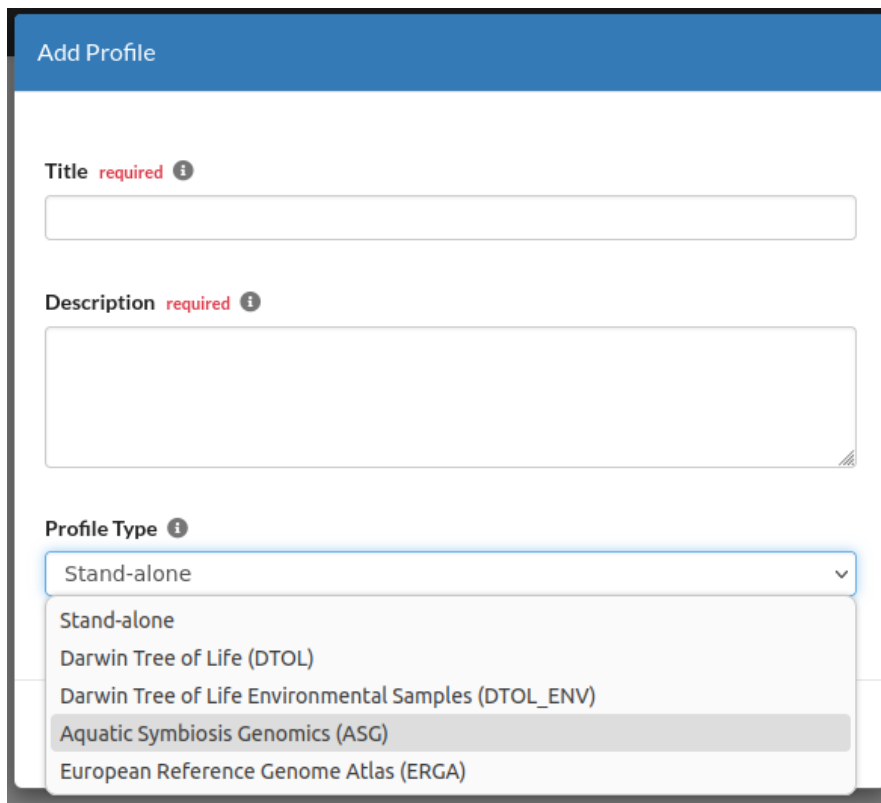


Fig. 3: ToL Profile: Add profile form dialogue

Hint: Both profile **Title** and profile **Description** are mandatory form fields.

Meaningful field values are recommended in the form boxes because the information will appear in submissions of the research objects associated with the profile, in public remote repositories.

6.1.2 Choose Profile Type

Fig. 4: ToL Profile form: Choose profile type

If you request to be added to any of the profile types displayed (excluding the default **Stand-alone** profile type), only that profile type will be listed in the **Profile type** dropdown menu.

6.1.3 Choose Associated Profile Type(s) (if required)

Note: The **Associated Profile Type** dropdown menu will only display if the **European Reference Genome Atlas (ERGA)** profile type is selected.

- More than one associated type also known as subproject or child project can be chosen.

OR

OR

⁴ See term: *ASG*.

⁵ See term: *DTOL*.

⁶ See term: *ERGA*.

Add Profile

Title required ⓘ

Description required ⓘ

Profile Type ⓘ

Aquatic Symbiosis Genomics (ASG) ▾

Associated Profile Type ⓘ

Select associated type(s)

Darwin Tree of Life (DTOL)

Darwin Tree of Life Environmental Samples (DTOL_ENV)

European Reference Genome Atlas (ERGA)

Fig. 5: ASG Profile Type: Choose associated profile type or a subproject^{Page 40, 4}

Add Profile

Title required ⓘ

Description required ⓘ

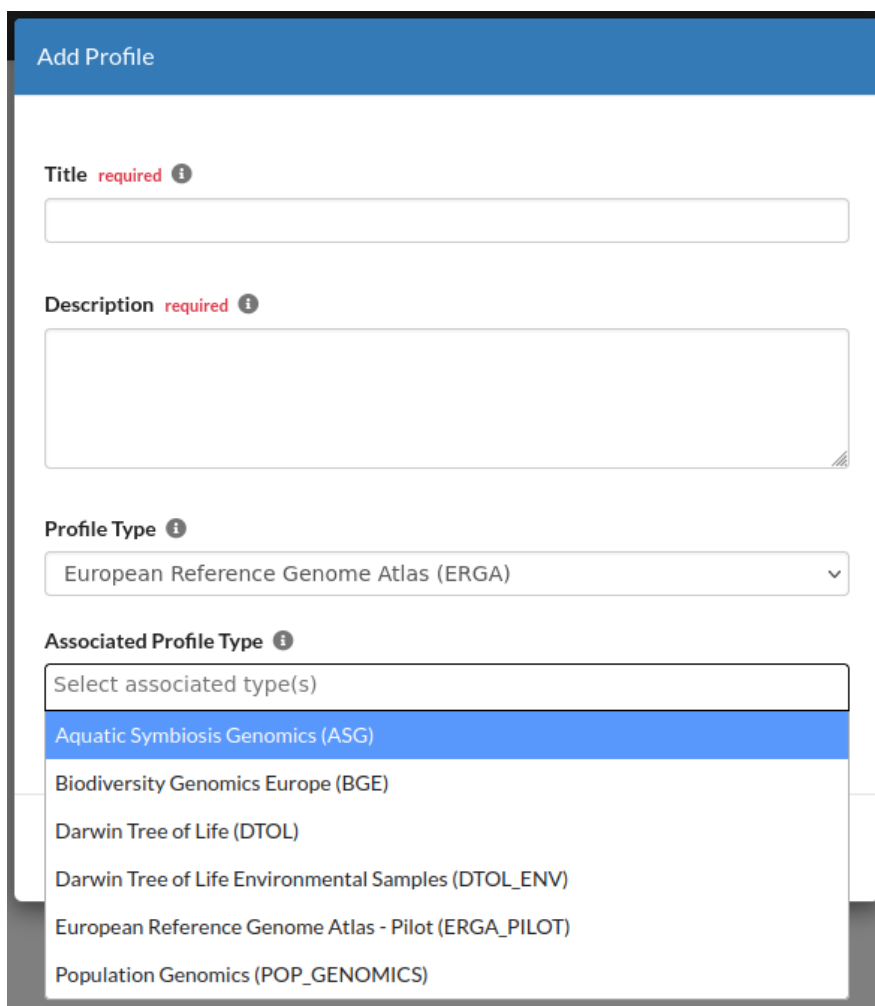
Profile Type ⓘ

Darwin Tree of Life (DTOL)

Associated Profile Type ⓘ

Select associated type(s)
Aquatic Symbiosis Genomics (ASG)
Darwin Tree of Life Environmental Samples (DTOL_ENV)
European Reference Genome Atlas (ERGA)

Fig. 6: DTOL Profile Type: Choose associated profile type or a subproject^{Page 40, 5}



The screenshot shows a web form titled "Add Profile". It contains several input fields and a dropdown menu. The "Title" field is required and has an information icon. The "Description" field is also required and has an information icon. The "Profile Type" dropdown is currently set to "European Reference Genome Atlas (ERGA)". The "Associated Profile Type" dropdown is open, showing a list of options: "Select associated type(s)", "Aquatic Symbiosis Genomics (ASG)", "Biodiversity Genomics Europe (BGE)", "Darwin Tree of Life (DTOL)", "Darwin Tree of Life Environmental Samples (DTOL_ENV)", "European Reference Genome Atlas - Pilot (ERGA_PILOT)", and "Population Genomics (POP_GENOMICS)".

Add Profile

Title required ⓘ

Description required ⓘ

Profile Type ⓘ

European Reference Genome Atlas (ERGA) ▼

Associated Profile Type ⓘ

Select associated type(s)

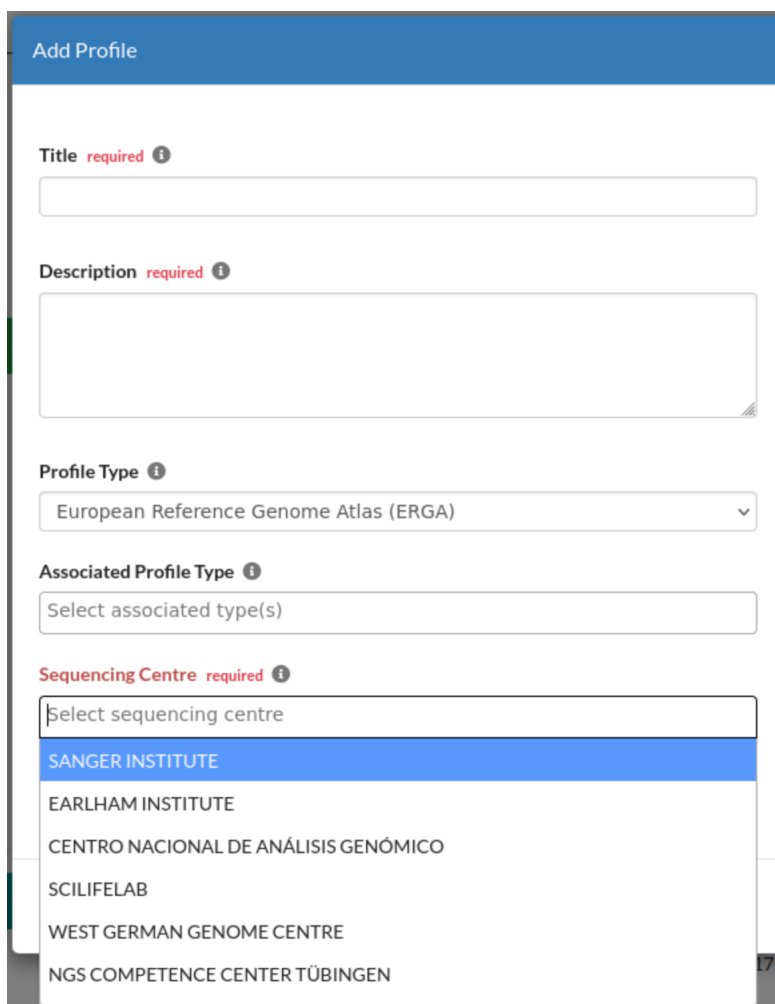
- Aquatic Symbiosis Genomics (ASG)
- Biodiversity Genomics Europe (BGE)
- Darwin Tree of Life (DTOL)
- Darwin Tree of Life Environmental Samples (DTOL_ENV)
- European Reference Genome Atlas - Pilot (ERGA_PILOT)
- Population Genomics (POP_GENOMICS)

Fig. 7: ERGA Profile Type: Choose associated profile type or a subproject^{Page 40, 6}

6.1.4 Choose Sequencing Centre (if required)

Note: The **Sequencing Centre** dropdown menu will only display if the **European Reference Genome Atlas (ERGA)** profile type is selected.

See the *Sequencing Centres that utilise COPO* FAQ for additional information.



The screenshot shows a web form titled "Add Profile". It contains several fields: "Title" (required), "Description" (required), "Profile Type" (a dropdown menu currently showing "European Reference Genome Atlas (ERGA)"), "Associated Profile Type" (a text input field with the placeholder "Select associated type(s)"), and "Sequencing Centre" (required). The "Sequencing Centre" dropdown menu is open, displaying a list of institutions: SANGER INSTITUTE (highlighted in blue), EARLHAM INSTITUTE, CENTRO NACIONAL DE ANÁLISIS GENÓMICO, SCILIFELAB, WEST GERMAN GENOME CENTRE, and NGS COMPETENCE CENTER TÜBINGEN.

Fig. 8: ERGA Profile Type: Choose sequencing centre

6.1.5 Profile created

4. The new profile will be displayed in the **Profile** list

Hint: The list of profiles or profile records on the **Work Profiles** web page can be sorted by date created, profile title or profile type.

Choose the desired sort type from the **Sort by** dropdown menu (at the top-right of the profile record).

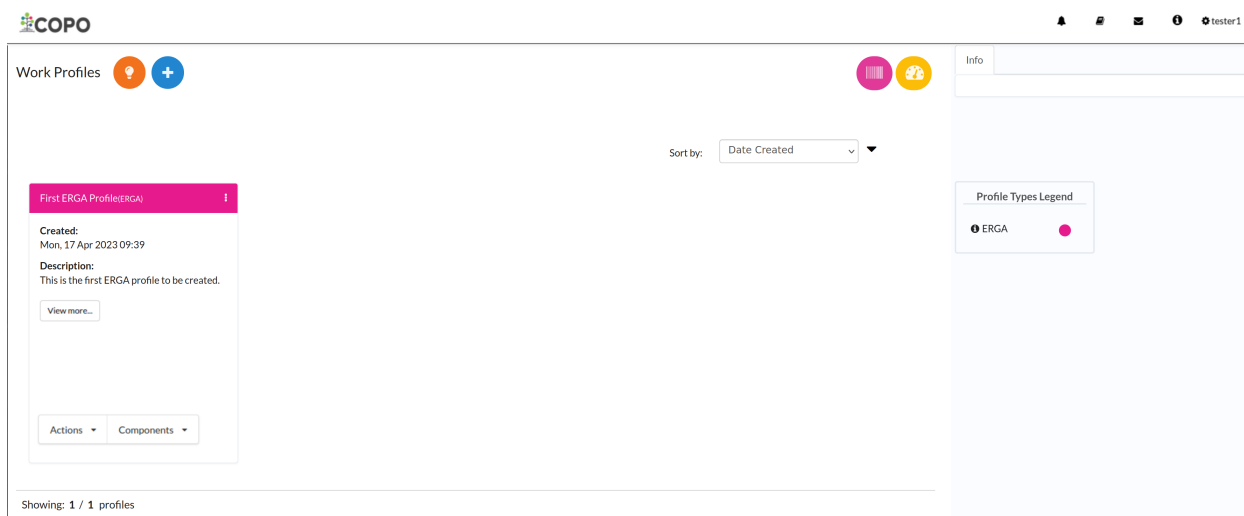


Fig. 9: ToL Profile: ‘Work Profiles’ web page displaying the created profile

See more information in the [Sorting Profiles](#) section.

See also:

- See [Steps to create Stand-alone profile](#) if you would like to make other submissions

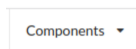
6.2 Tree of Life Profile Components

A COPO profile^{Page 37, 2} defines a set of component types from which instances of research objects can be created.

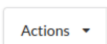
The following component types are currently defined:

1. Accessions
2. *Assembly*
3. Barcoding manifests
4. *Files*
5. *Reads*
6. Samples
7. *Sequence Annotations*

- Component instances defined within a profile will only be visible within that profile.
- To access a component within a profile, click the component button displayed within the popup after the



button was clicked (see the screenshot above).

- Profile actions can be accessed via the  button. The actions describe the process of each component within a profile.

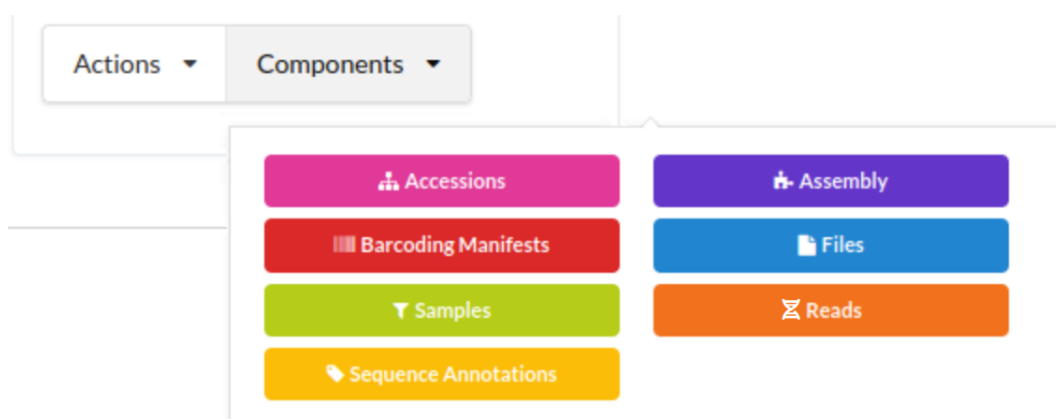


Fig. 10: Tree of Life Profile Components

SHARING PROFILES

Sharing profiles or creating a group enable other COPO users to upload or submit research objects such as samples, experiment, runs, reads, assemblies and sequence annotations etc. to a profile owned or created by another COPO user.

Hint:

- **Profile owner** or **Sharer** refers to the person who created the profile.
 - **Shared user** or **Sharee** refers to the person who has been granted permission by the profile owner to upload or submit research objects to the profile created by the profile owner.
-

In general, the **sharer** shall create a profile, create a group, add the profile to be shared to the created group then, add the COPO user(s) to the created group.

Thereafter, the shared profile shall appear on the **Work Profiles** web page of the **sharee**.

The following describes how to share a profile or create a group on COPO:

7.1 Sharer

1. Click your name in the top right hand corner of the web page (after you have logged in) to access settings
2. Click the **View Groups** option from the settings dropdown menu as shown below to navigate to the **Groups** web page

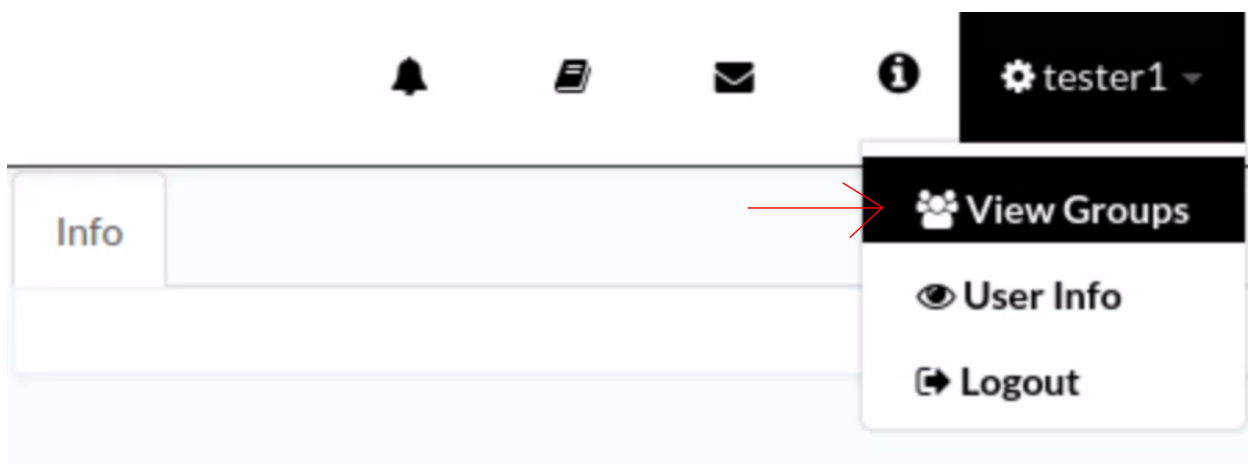



Fig. 1: Groups: Navigating to Groups web page via the ‘View Groups’ settings dropdown menu option

3. Click the  button to create a new group

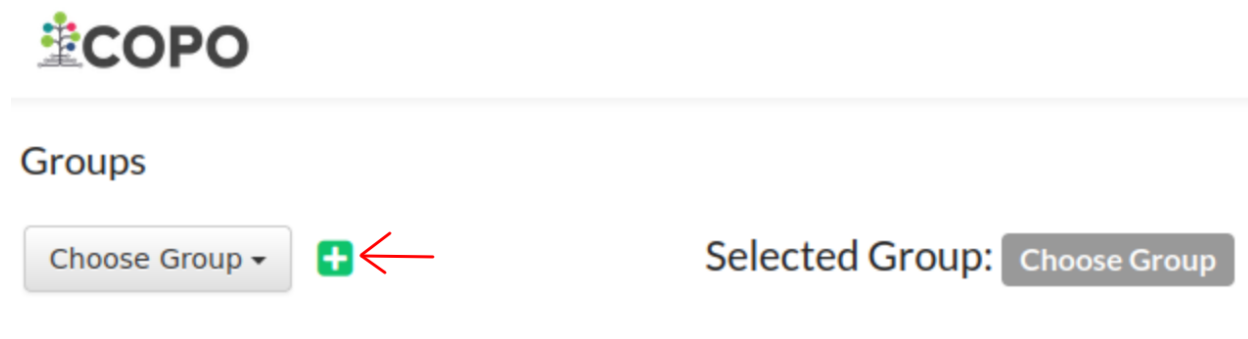


Fig. 2: Groups: Groups web page

4. Provide details for the new group as shown below then, click **Submit**

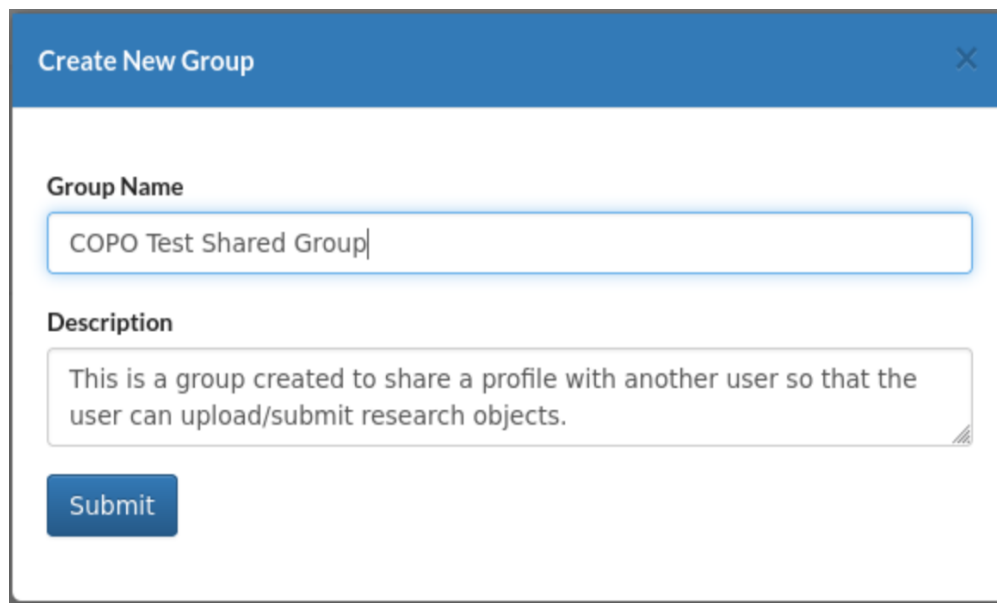


Fig. 3: Groups: Add new group form dialogue

Hint: Both group **Name** and profile **Description** are required form fields.

Meaningful field values are recommended in the form boxes.

5. In the **Your Profiles** section under the **Profiles in Group** header, choose a profile from the list of profiles that you would like to share with another user (so that the user can upload/submit research objects to) by **double-clicking** the profile title.

The profile is then, transferred to the **Added to Group** section after the profile title was double-clicked as shown below.

6. Search for the user who you would like to share the profile with in the **Users in Group** section located at the right of the web page. Then, click the name of the user to add the user to the group.

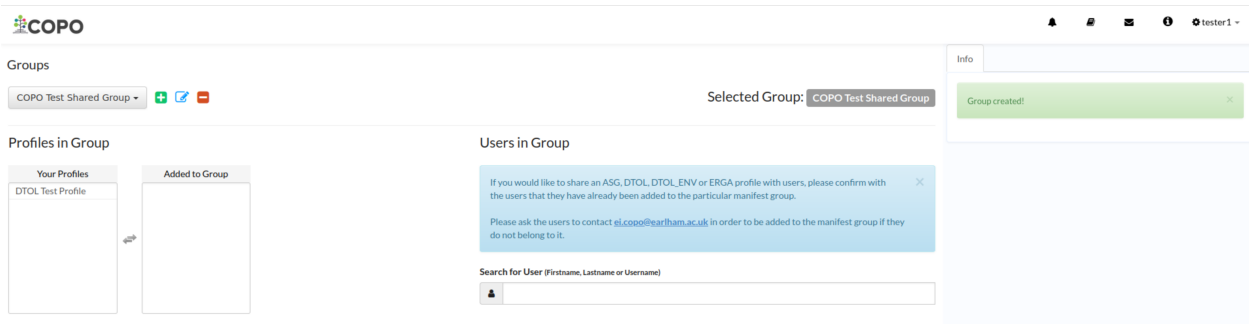


Fig. 4: Groups: Group created successfully

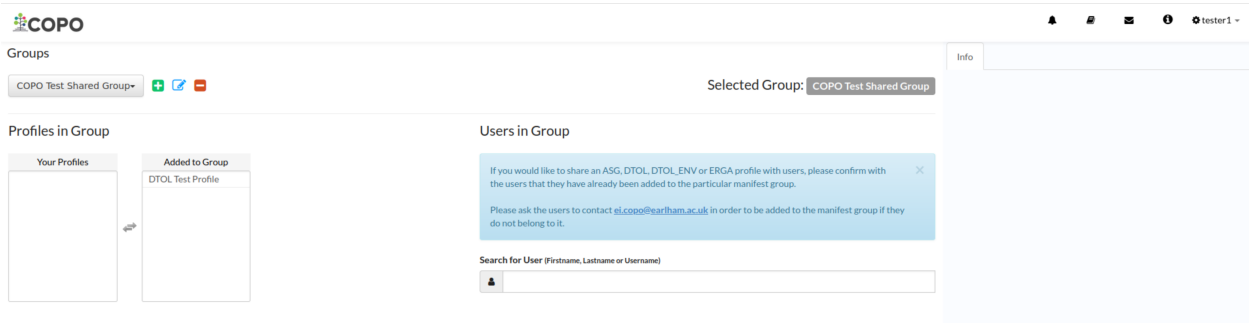


Fig. 5: Groups: Profile appears in ‘Added to Group’ section after having been double-clicked in the ‘Your Profiles’ section

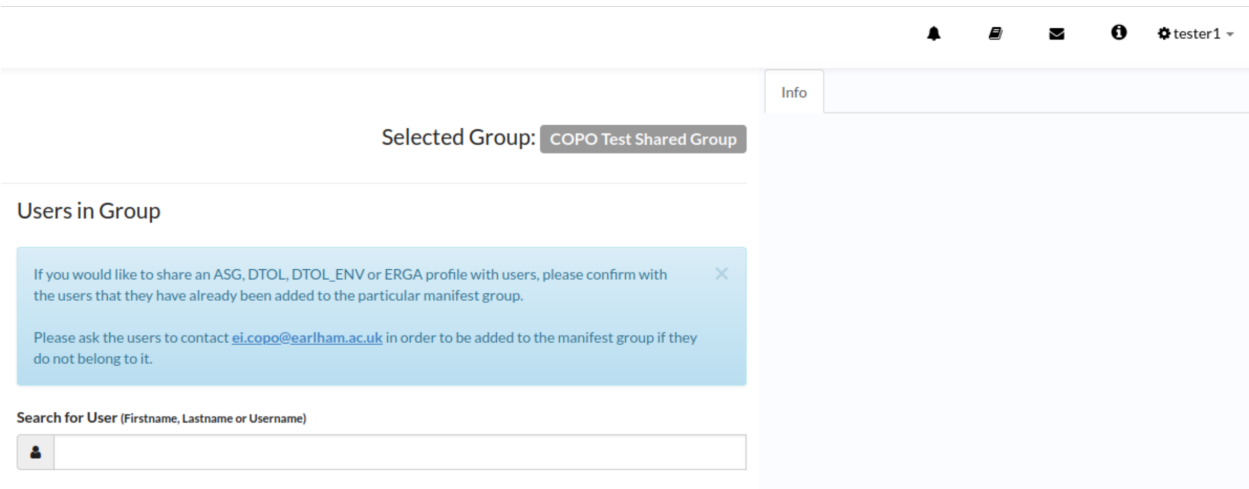


Fig. 6: Groups: Use search box to search for users to add to the created group

7.2 Sharee

1. Login to COPO.
2. Request to be added to a profile group associated with that the profile type that you would like to be added if you would like to submit or upload research objects to a Tree of Life (ToL) project.

If you have not been added to the profile group, make a request to the indicating the type of profile group that you would like to be assigned to.

See the *Projects Brokered through COPO* section for information about types of ToL projects.

3. After the sharer has added you to the group, you will see the shared profile on the **Work Profiles** web page as shown below:

Note:

- If the profile owner has shared the profile with you and you do not see the shared profile on the **Work Profiles** then, please perform step 2.
- Shared profiles are indicated by an orange label as shown below.

See *Profile Types Legend* section for more information about profile types' colour labels.

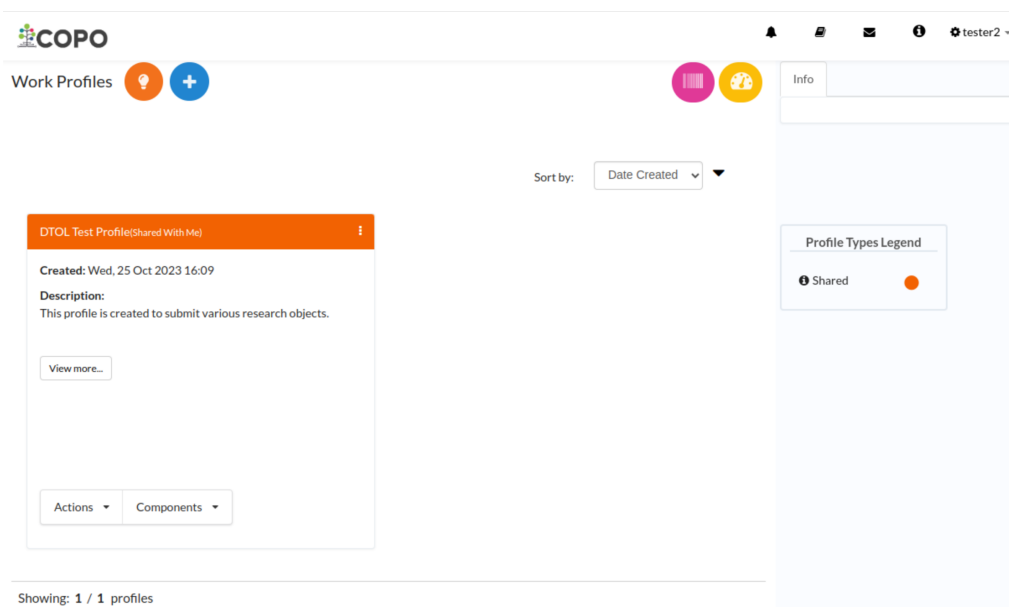


Fig. 7: Groups: Shared profile appears on the sharee's 'Work Profiles' web page

RELEASING PROFILES (STUDIES)

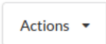
Hint: Profiles¹ (in COPO) are referred to as projects or studies (in ENA²).

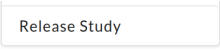
Note: The ability to make a profile public is **only** available after reads have been submitted.

Thus, the **Release Study** profile action, , is only displayed after reads have been submitted.

By default, all profiles^{Page 51, 1} created in COPO are private. This means that the profile is only visible to the user who created it on COPO and as such, it cannot be accessed on public repositories such as ENA².

To make a profile public, please follow the steps below:

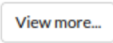
1. Click the  button associated with the desired profile. A list of actions will be displayed in a popup menu.

Then, click the  profile action to make the profile public as shown below depending on the profile type.

The profile i.e. project will be automatically be made public and can be viewed publicly in ENA.

OR

OR

2. If you would like to view the release status and release date of the profile (also known as study or project). Click the  button associated with the desired profile.

See the [View more COPO profile information](#) FAQ for more details.

See also:

- [How to Submit Reads](#)

¹ Also known as COPO profile. See: [COPO profile or work profile](#).

² See term: [ENA](#).

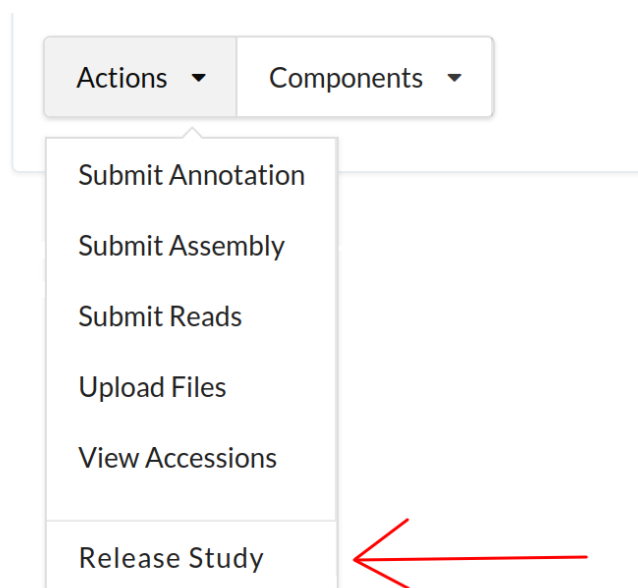


Fig. 1: **Stand-alone Profile Actions: Release study**

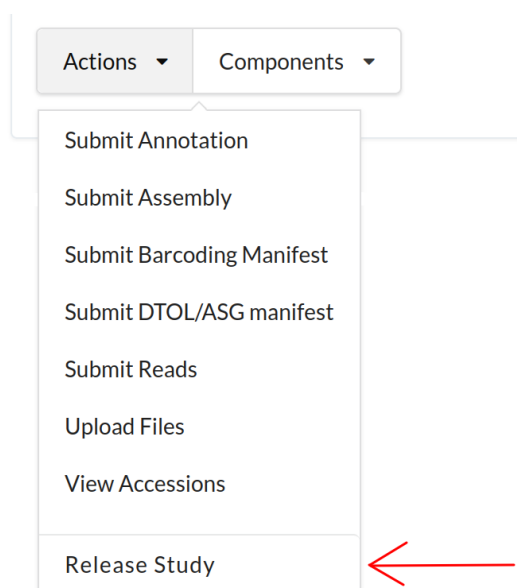


Fig. 2: **Tree of Life (ToL) Release Study Profile Action for Aquatic Genome Symbiosis (ASG) or Darwin Tree of Life Samples (DTOL) Profiles**

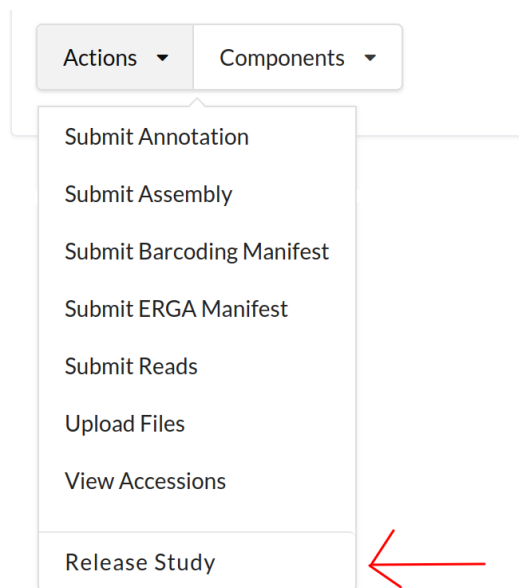


Fig. 3: Tree of Life (ToL) Release Study Profile Action for European Reference Genome Atlas (ERGA) Profiles

SORTING PROFILES

On the **Work Profiles** web page, profiles¹ can be sorted by **date created**, **profile title** or **profile type**.

Choose the desired sort option from the **Sort by** dropdown menu, Sort by: ▼, (at the top-right of the profile record section) as shown below.

Then, click the ▼ arrow to sort in descending order or the ▲ arrow to sort in ascending according to the chosen sort option.

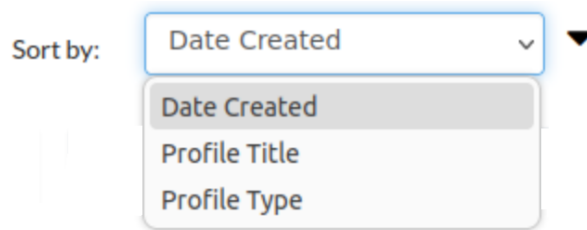



Fig. 1: **Profile Sort Menu: Sort options displayed**

¹ Also known as COPO profile. See term: *COPO profile*.

PROFILE TYPES LEGEND

The **Profile Types legend**¹ is displayed at the right of the **Work Profiles** web page.

It displays the acronym as well as the corresponding profile type colour for each profile that has been created.

Hint: Hover over the  icon located beside the profile type acronym in the **Profile Types Legend**, the backronym for the profile type will be displayed.

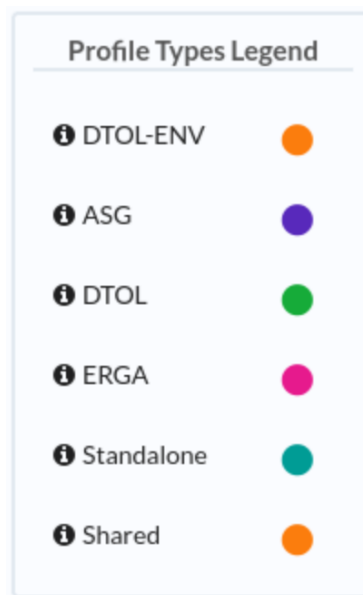







Fig. 1: **Profile Types Legend:** Various profiles types that can be created in COPO and their corresponding label colours

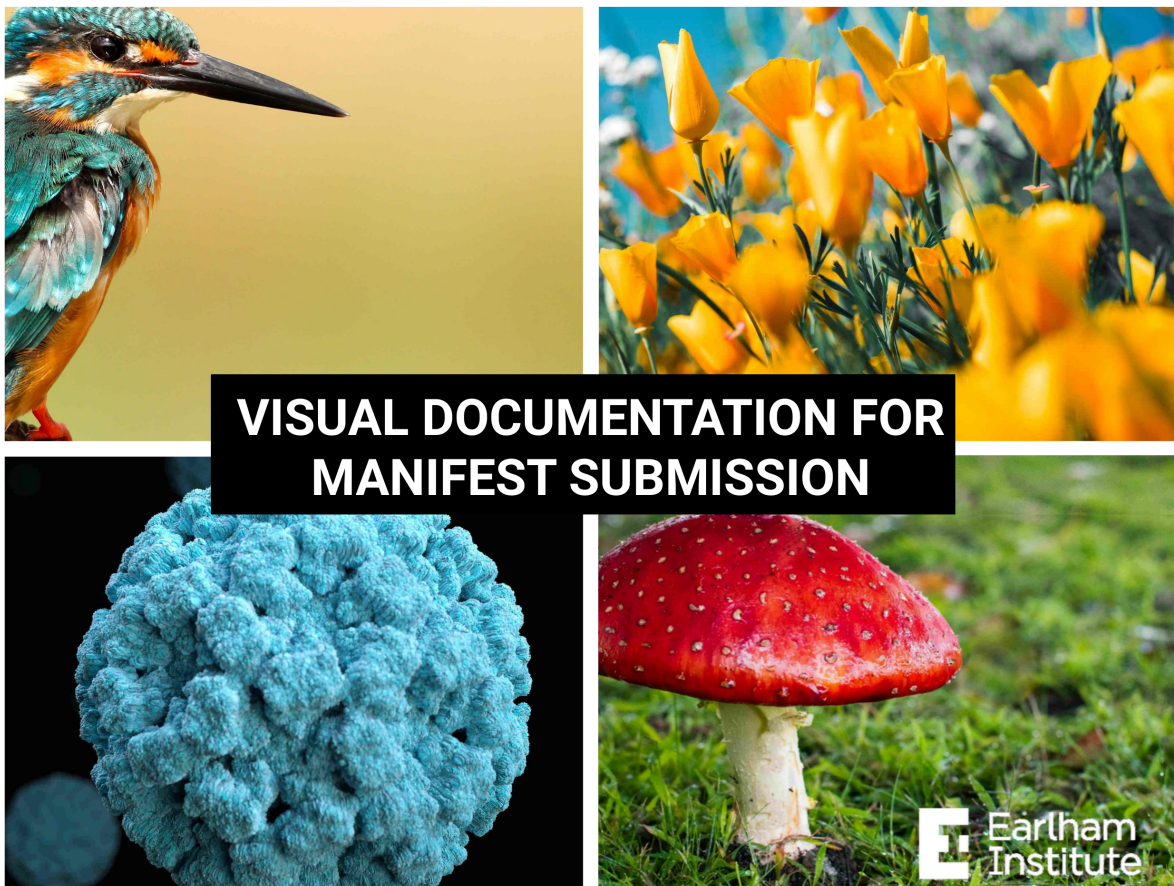
¹ See term: *Profile Types legend*.

Table 1: Explanation of Profile Types Legend

Colour		Acronym	Backronym
Orange		DTOL-ENV or Shared	Darwin Tree of Life Environmental or Shared
Purple		ASG	Aquatic Symbiosis Genomics
Green		DTOL	Darwin Tree of Life
Pink		ERGA	European Reference Genome Atlas
Teal		Standalone	Stand-alone

GENERAL TREE OF LIFE VISUAL SUBMISSION DOCUMENTATION

Download visual documentation



FILES SUBMISSION

12.1 How to Submit Files

Hint:

- See ENA [assembly submission file types documentation](#) for the types of files that can be submitted in COPO for assembly submissions.
 - See ENA [read submission file types documentation](#) for the types of files that can be submitted in COPO for read submissions.
-

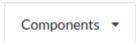
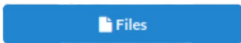
See also:

- *How to Delete Files*
- *How to check if data files associated with a metadata submission have been uploaded to ENA*
- *How to Submit Reads*
- *How to Submit Assemblies*

12.1.1 Accessing the Files' Web Page

The Files' web page can be accessed from the **Components** button or **Actions** button associated with a profile¹.

Use Components' Button to Navigate to Files' Web Page

Click the  button associated with a profile. Then, click the  from the popup menu displayed as shown below:

¹ Also known as COPO profile. See: *COPO profile or work profile*.

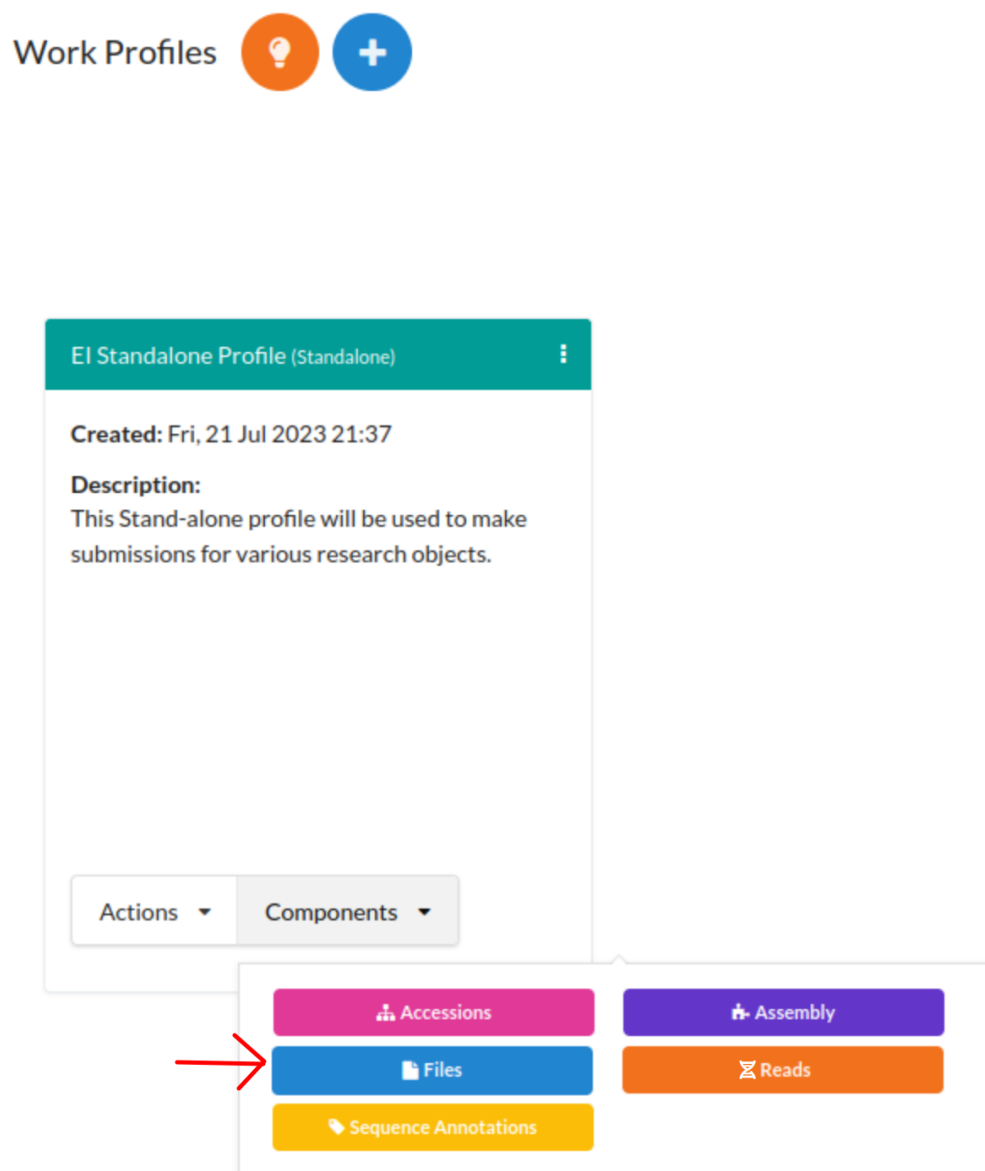
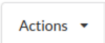


Fig. 1: Stand-alone Profile Components: Files component button

Use Actions' Button to Navigate to Files' Web Page

Click the  button associated with a profile. Then, click the action, **Upload Files** action from the popup menu displayed as shown below:

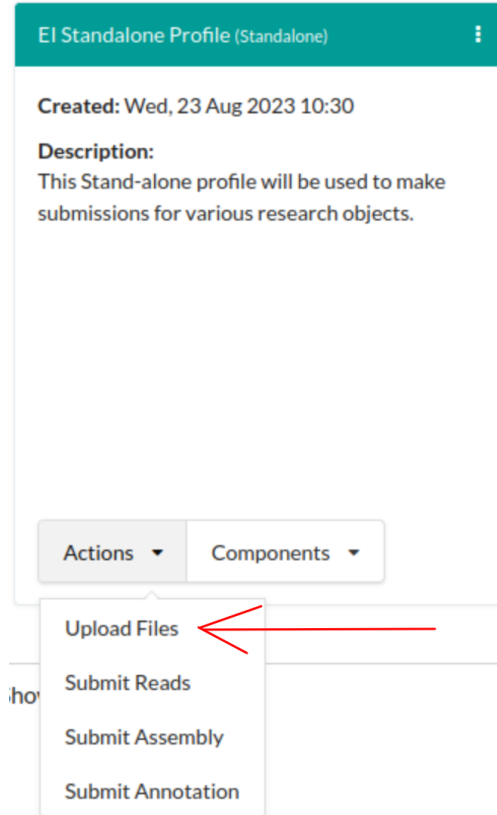



Fig. 2: Stand-alone Profile Actions: 'Upload Files' action

12.1.2 Submit Files from your Local (Computer) System

Note: The total **maximum** file size that can be uploaded from your local (computer) system is around **2 GB**. If you have a file larger than 2 GB or have multiple files whose combined total size exceeds 2 GB, please *submit the file(s) via the terminal*.

1. Click the  button on the Files web page to add a new file by browsing your local file system
2. An **Upload File** dialogue is displayed. Click the **Upload** button to choose a file from your local system.
3. The new file(s) will be displayed on the **Files** web page after a successful submission.

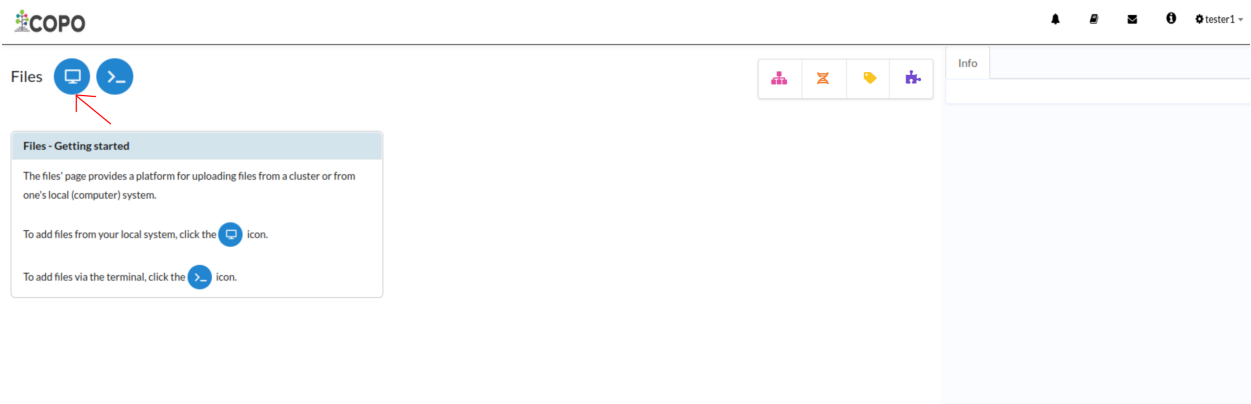


Fig. 3: Files web page: ‘Add new file by browsing local file system’ button

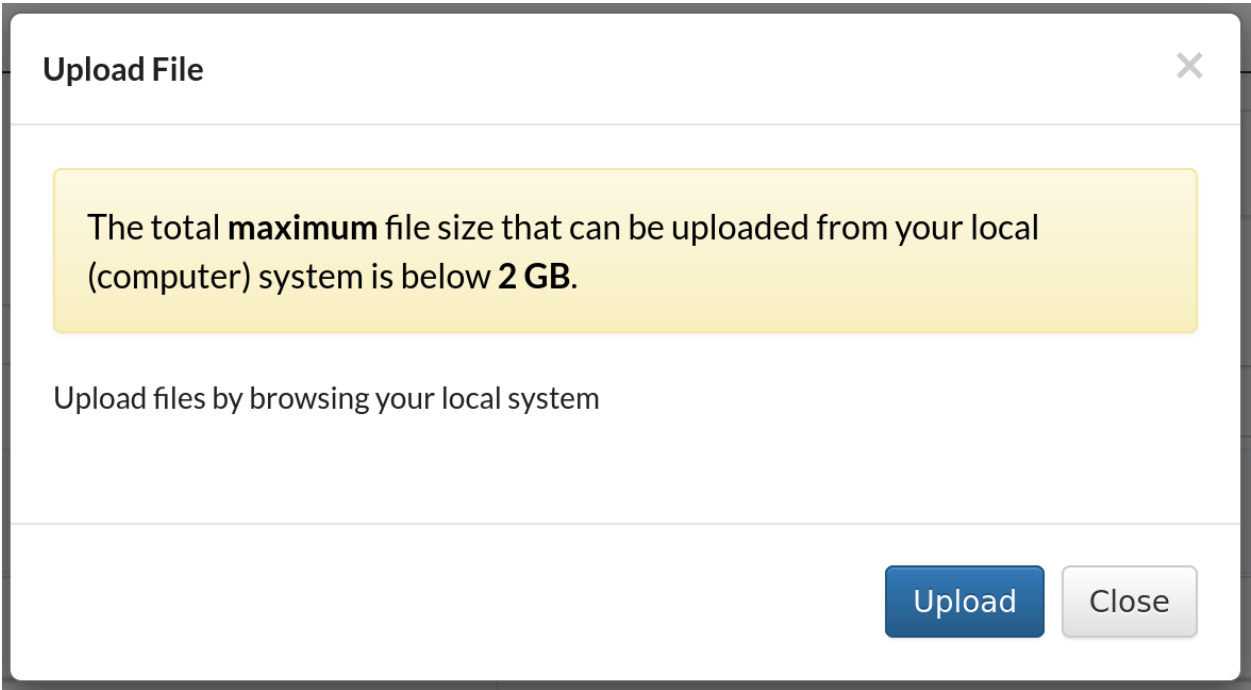


Fig. 4: Files submission: Upload File dialogue

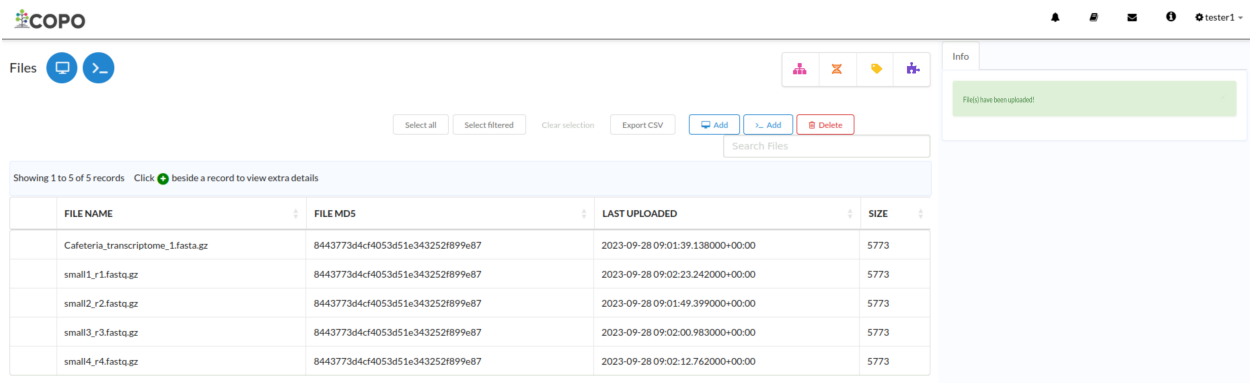





Fig. 5: Files submission: Files’ web page displaying the uploaded file(s)

Hint: To add more files from your local system, click the  button (once files have been submitted to the profile) as an alternative to clicking the  button.

12.1.3 Submit Files via the Terminal

1. Click the  button on the Files web page to add a new file from a cluster via the terminal.

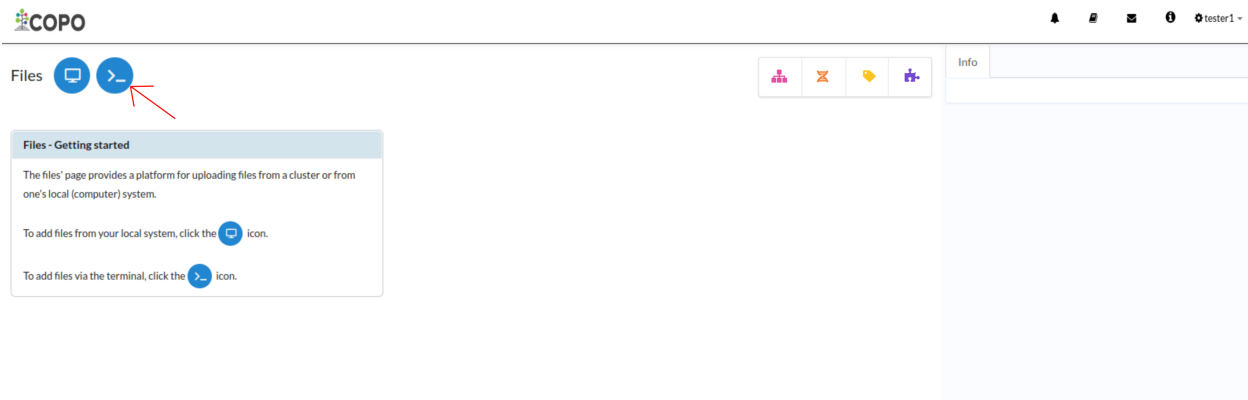




Fig. 6: Files web page: 'Add new file via terminal' button

2. A **Move Data** dialogue is displayed. Follow the instructions displayed then, click the **Process** button to submit the file(s) to the profile.
3. The new file(s) will be displayed on the **Files** web page after a successful file submission via the terminal i.e. after the command has been executed successfully in the terminal.

Hint: To add more files via the terminal, click the  button (once files have been submitted to the profile) as an alternative to clicking the  button.

12.2 How to Delete Files

Click the desired file from the list of files displayed on the Files' web page. Then, click the **Delete** button (located in the top-right corner of the table) as shown below:

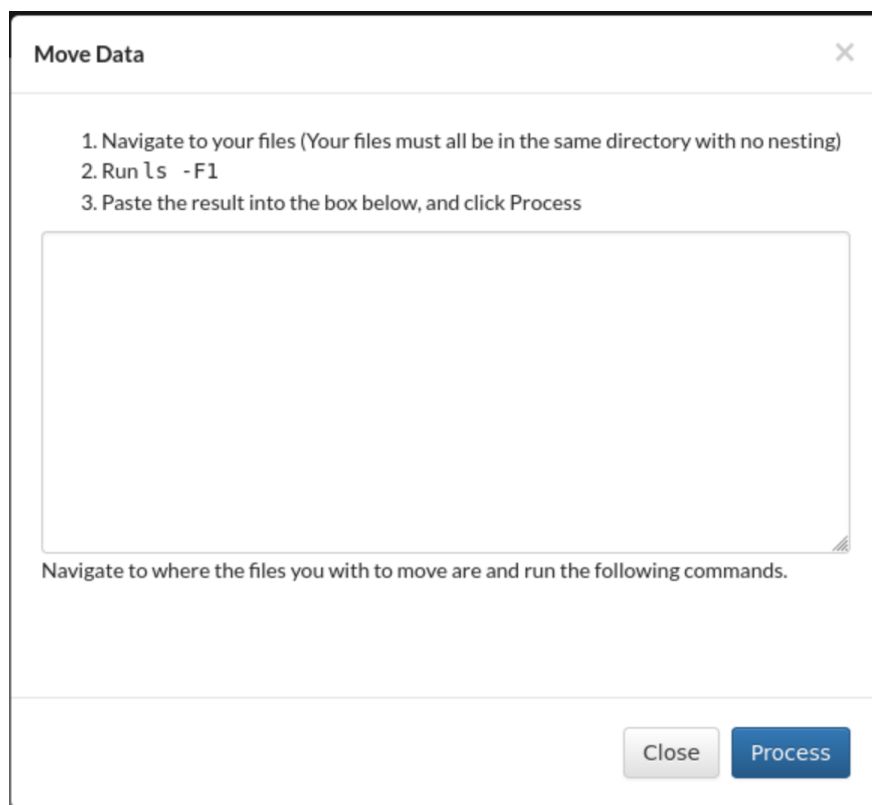
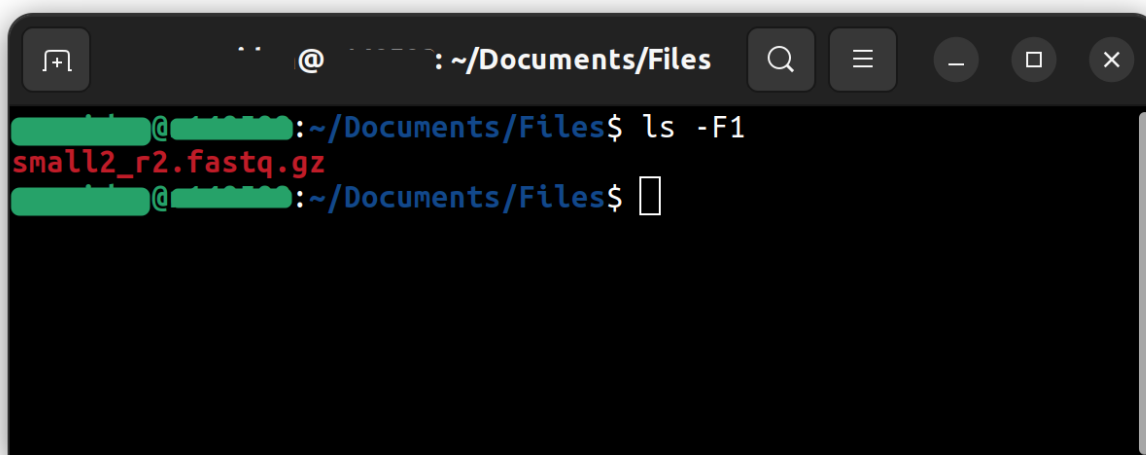


Fig. 7: Files submission: Move Data dialogue

Fig. 8: Input `$ ls - F1` command in the terminal

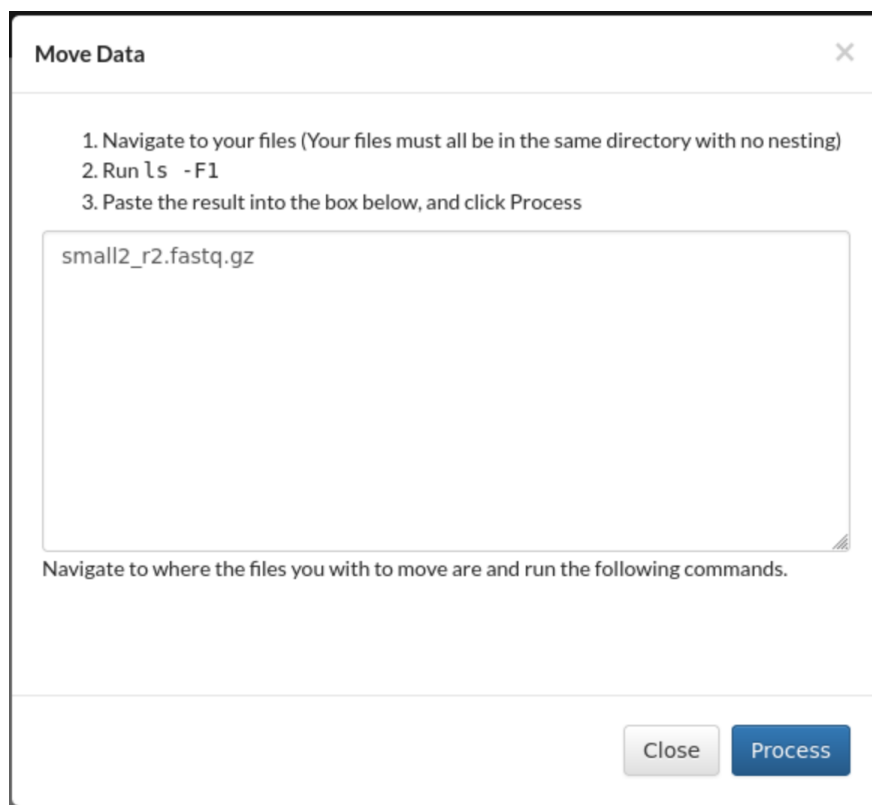


Fig. 9: Move Data dialogue: Input the filename(s) returned after having ran the `$ ls -F1` command in the terminal. Then, click the Process button.

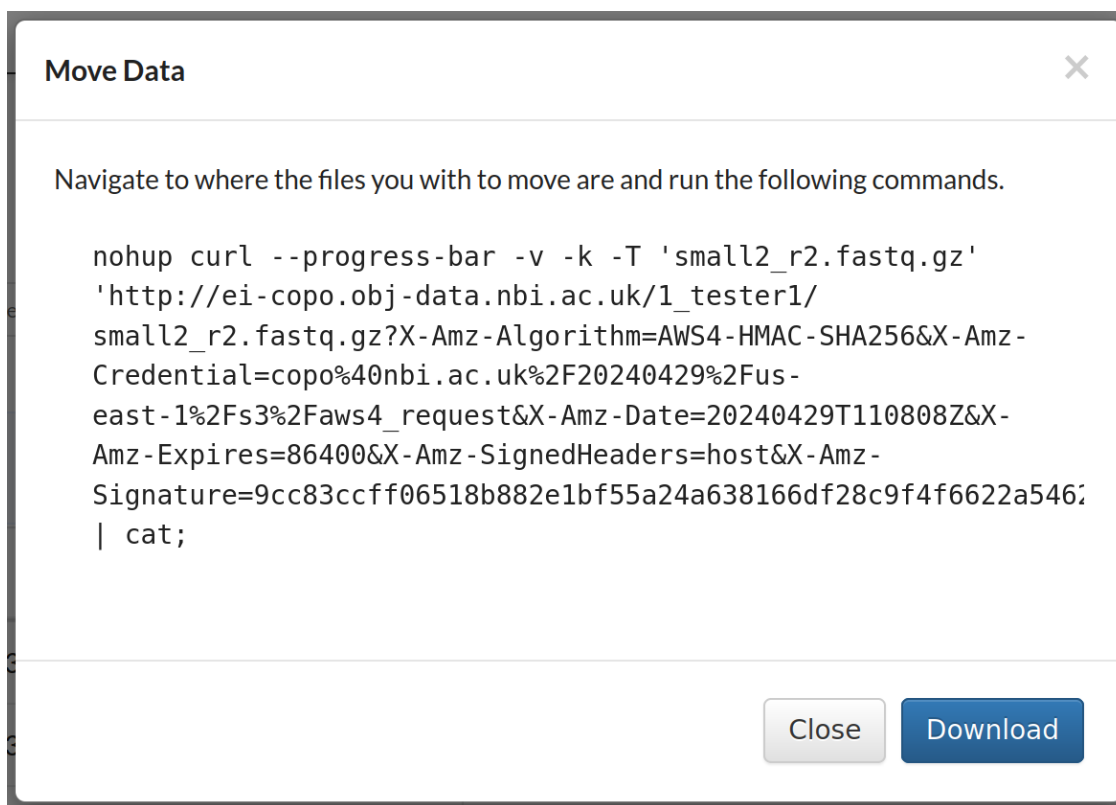


Fig. 10: **Move Data** dialogue: Command outputted after having clicked command in the Process button. Download the command displayed.

The downloaded file will have *unknown* or *download* as the file name depending on the browser you are using.

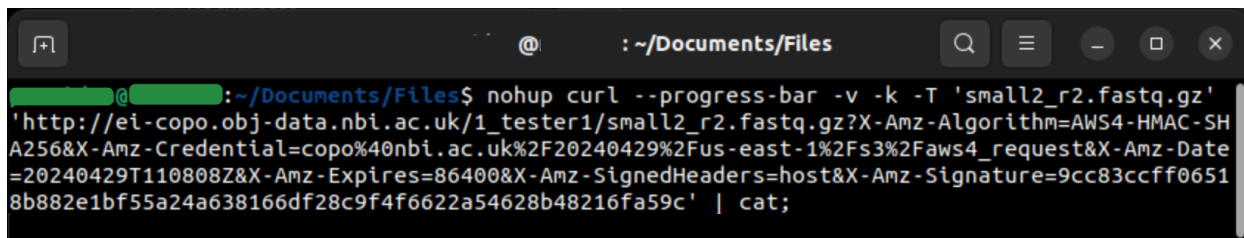


Fig. 11: **Paste the copied command in the terminal**

Alternatively, you can make the downloaded file executable then, run the file in the directory where the files are located:

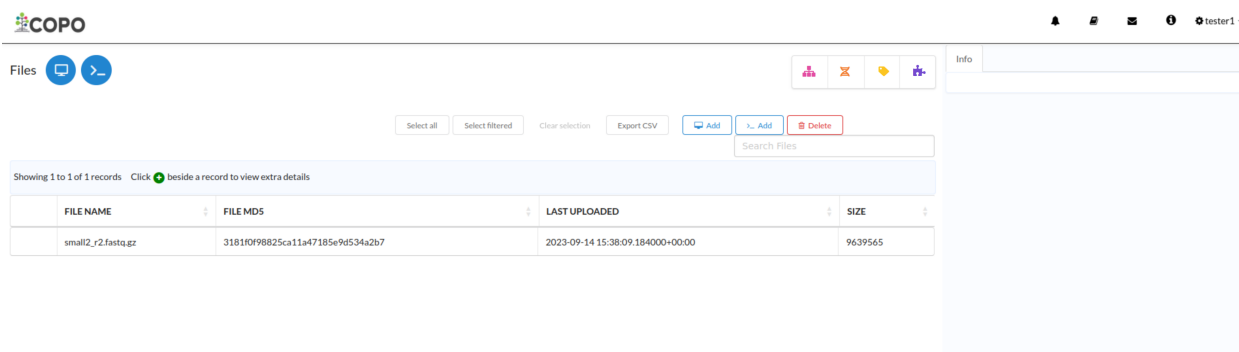


Fig. 12: **Files submission: Files' web page displaying the uploaded file(s)**

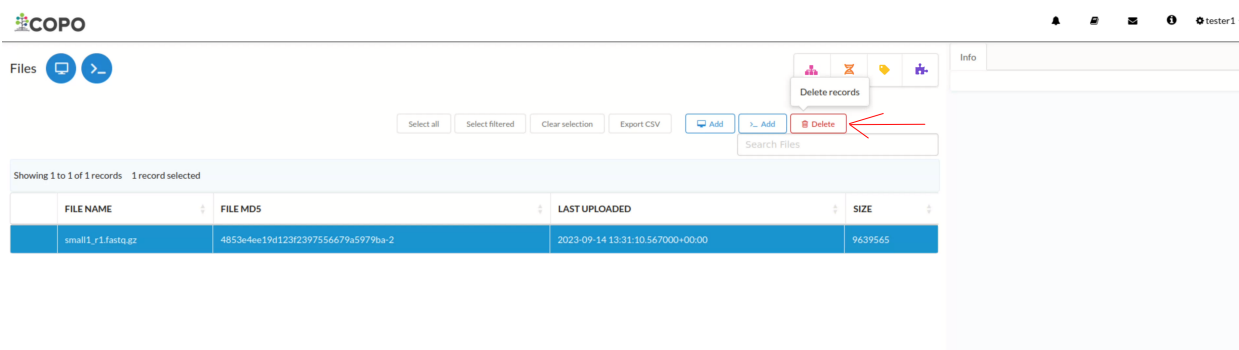


Fig. 13: File deletion: Click the “Delete” button to remove the highlighted file from the profile

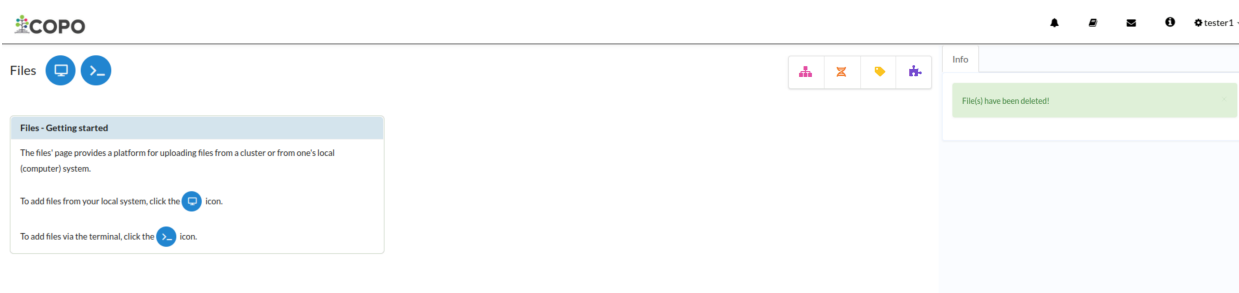


Fig. 14: File deletion: File has been deleted

12.3 Checking ENA File Upload Status

Note: A reads, annotations or assembly submission must be completed before the file(s) can be uploaded to ENA (European Nucleotide Archive).

After having completed a reads, annotations or assembly submission and associated a file(s) to it during the submission process in COPO, the file(s) are submitted to ENA (European Nucleotide Archive).

The status of the file(s) uploaded to the ENA can be checked in the column, **ENA File Processing Status**, on the reads, annotations or assembly web page.

The **ENA File Processing Status** column is highlighted with a red rectangle border in the image below:

Hint:

- Rows with a status of **“File archived: PUBLIC”** or in a green colour indicate that the file(s) have been successfully submitted to ENA.
- Rows with a status of **“Invalid file integrity: PRIVATE”** or in a red colour indicate that the file(s) failed to be submitted to ENA.

Profile: El Standalone Profile

Sequence Annotations

Select all

Select filtered

Clear selection

Export CSV

+ Add

Edit

Delete

Submit

Search Sequence Annotations

Showing 2 to 2 of 2 records

Click beside a record to view extra details

EXPERIMENT	TITLE	DESCRIPTION	FILES	ACCESSION	SUBMISSION ERROR	ENA FILE PROCESSING STATUS
	Test Annotation1	Evidence based annotation of the test assembly	testv1.0.gff.gz	ERZ21822619		testv1.0.gff.gz : Invalid file integrity : PRIVATE
	Test Annotation	Transcripts generated for test annotation	Cafeteria_transcriptome.fastq.gz	ERZ21822618		Cafeteria_transcriptome.fastq.gz : File archived : PUBLIC

show 10 records

Previous

1

Next

Info

Fig. 15: ENA File Processing Status: The status of the file(s) uploaded to ENA (European Nucleotide Archive)

ASSEMBLY SUBMISSION

Note:

- Once **assemblies** have been submitted, they cannot be updated.
 - Files must be uploaded before **assemblies** can be submitted. See: *How to Submit Files*.
-

See also:

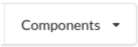

- *How to Delete Assemblies*
- *How to Submit Files*
- *Types of Files for Assembly Submissions*
- *How to check if data files associated with assembly submissions have been uploaded to ENA*
- *Assigning your own Locus Tag Prefix to Assemblies*

13.1 How to Submit Assemblies

13.1.1 Accessing the Assembly Web Page

The **Assembly**³ web page can be accessed from the **Components** button or **Actions** button associated with a profile⁴.

Use Components' Button to Navigate to Assembly Web Page

Click the  button associated with a profile. Then, click the  from the popup menu displayed as shown below:

³ See: *Assembly*.

⁴ Also known as COPO profile. See: *COPO profile or work profile*.

Work Profiles



El Standalone Profile (Standalone) ⋮

Created: Fri, 21 Jul 2023 21:37

Description:
This Stand-alone profile will be used to make submissions for various research objects.

Actions ▾ Components ▾

Accessions

Files

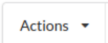
Sequence Annotations

Assembly

Reads

Fig. 1: Stand-alone Profile Components: Assembly component button

Use Actions' Button to Navigate to Assembly Web Page

Click the  button associated with a profile. Then, click the action, **Submit Assembly** action from the popup menu displayed as shown below:

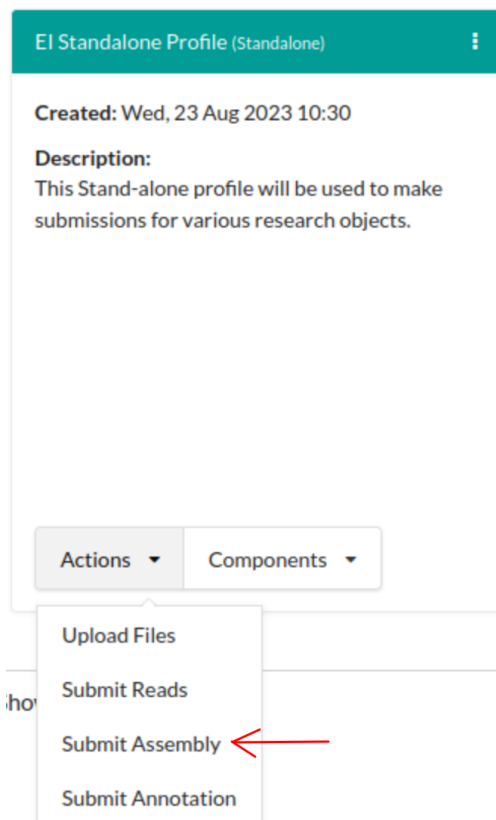



Fig. 2: Stand-alone Profile Actions: 'Submit Assembly' action

13.1.2 Submit Assembly

1. Click  button to add an **assembly** as shown below:
2. An **Add Assembly** dialogue is displayed. Provide the details then, click the **Submit Assembly** button.
3. The new assembly will be displayed on the **Assembly** web page after a successful submission.

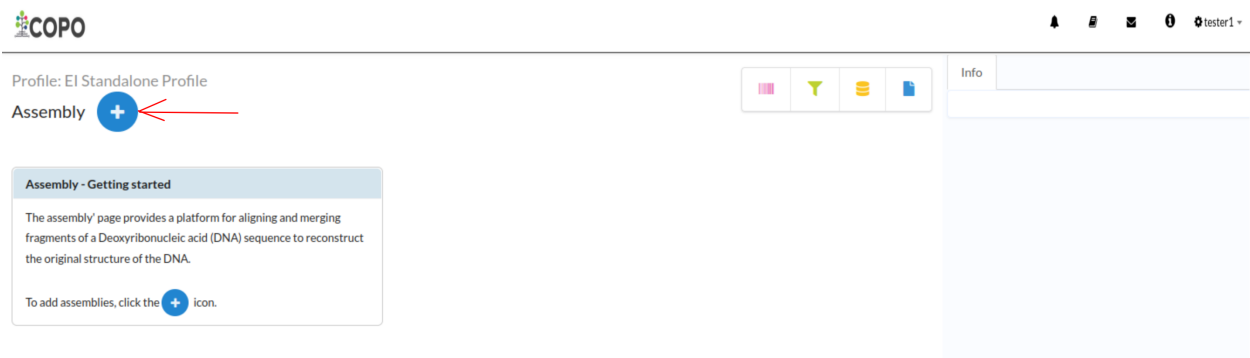


Fig. 3: Assembly submission: Click ‘Add record’ button

Add Assembly

Submit Assembly

Upload assembly files and fill in metadata, you must have already created a study in ENA and have uploaded samples and reads. You will be requested the relative accessions.

STUDY*

PRJEB66432

SAMPLE*

ERS16431676

ASSEMBLYNAME*

Unique assembly name, user provided

ASSEMBLY_TYPE*

clone

COVERAGE*

The estimated depth of sequencing coverage

PROGRAM*

The assembly program

PLATFORM*

The sequencing platform, or comma-separated list of platforms

MINGAPLENGTH

Minimum length of consecutive Ns to be considered a gap

MOLECULETYPE

genomic DNA

DESCRIPTION

Free text description of the genome assembly

RUN_REF

Comma separated list of run accessions

FASTA

None

FLATFILE

None

AGP

None

CHROMOSOME_LIST

None

UNLOCALISED_LIST

None

Submit Assembly

Close

Fig. 4: Assembly submission: ‘Add Assembly’ dialogue

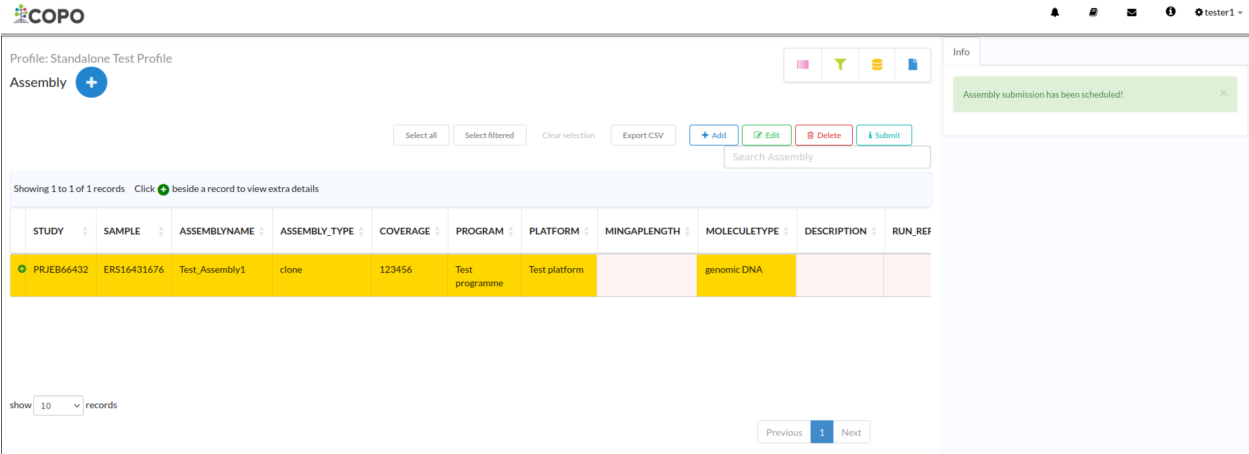


Fig. 5: Assembly submission: Assembly web page displaying the uploaded assemblies

13.2 How to Delete Assemblies

Click the desired assembly from the list of assemblies displayed on the **Assembly** web page. Then, click the **Delete** button (located in the top-right corner of the table) as shown below:

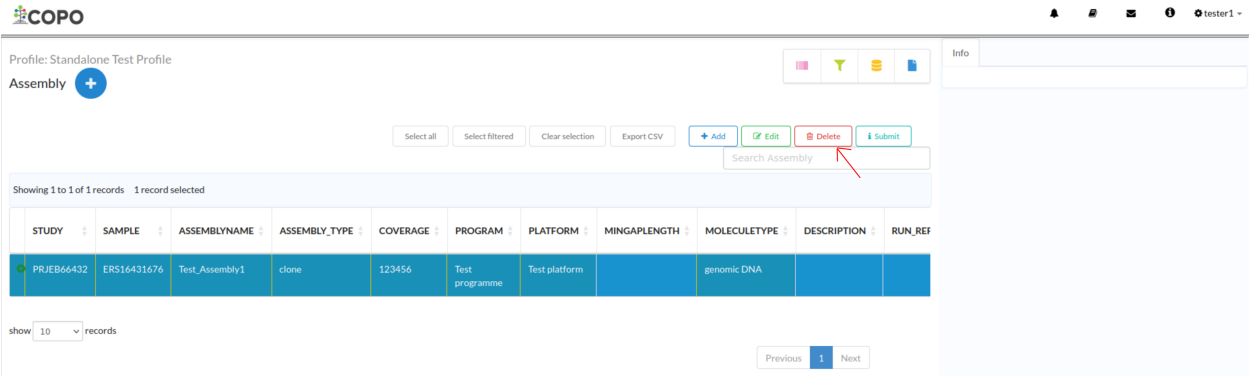


Fig. 6: Assembly deletion: Click the “Delete” button to remove the highlighted assembly from the profile

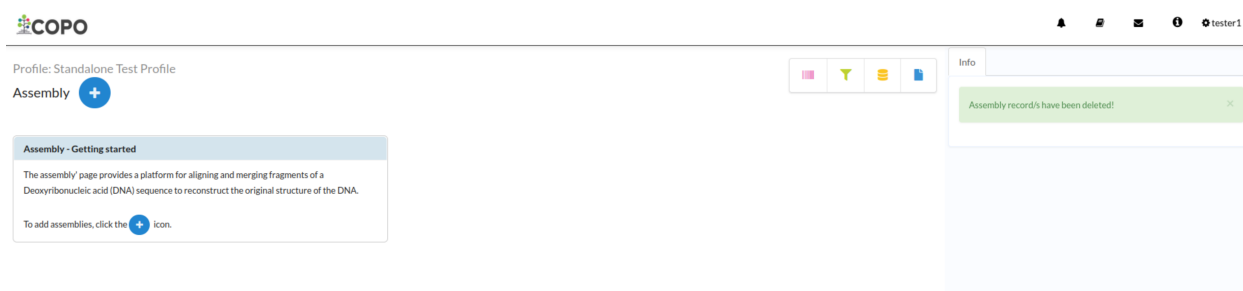


Fig. 7: Assembly deletion: Assembly record has been deleted

BARCODING MANIFEST SUBMISSION

Note:

- **Barcoding manifest** submission can only be done via a ToL¹ profile². Please see: *Steps to Create a Tree of Life Profile* for guidance.
 - Samples must be submitted before barcoding manifests can be submitted. Once the samples have been approved their biosample accessions, specimen ID (identification) and taxon ID are needed to fill in the barcoding manifest prior submission.
-

See also:

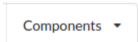
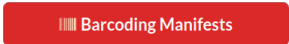
- *How to Delete Barcoding Manifests*
- How to Submit Aquatic Symbiosis Genomics (ASG) samples
- How to Submit Darwin Tree of Life (DToL) samples
- How to Submit Darwin Tree of Life Environmental (DToL_ENV) samples
- How to Submit European Reference Genome Atlas (ERGA) samples

14.1 How to Submit Barcoding Manifests

14.1.1 Accessing the Barcoding Manifest Web Page

The **Barcoding Manifest** web page can be accessed from the **Components** button or **Actions** button associated with a profile.

Use Components' Button to Navigate to Barcoding Manifest Web Page

Click the  button associated with a profile. Then, click the  from the popup menu displayed as shown below:

¹ See term: *Tree of Life (ToL)*.

² Also known as COPO profile. See: *COPO profile or work profile*.

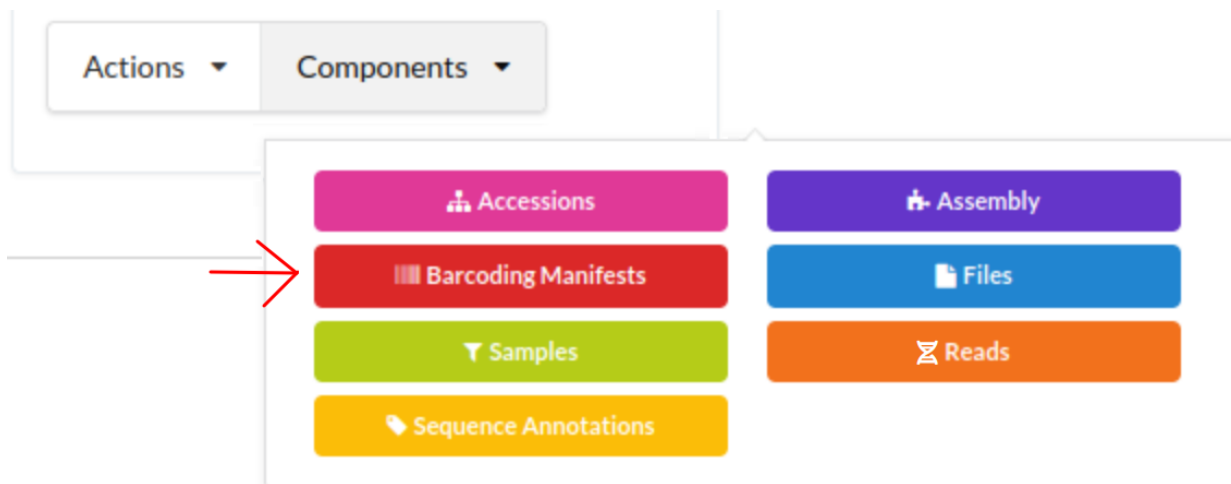
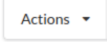


Fig. 1: Tree of Life Profile Components: Barcoding Manifest component button


Use Actions' Button to Navigate to Barcoding Manifest Web Page




Click the  button associated with a profile. Then, click the action, **Submit Barcoding Manifest** action from the popup menu displayed as shown below:

Note: The action will be available for all of the **Tree of Life** profile types.

14.1.2 Upload Barcoding Manifest

Hint:

- To download a blank **Barcoding Manifest** template, click the  button.
- In the **Barcoding Manifest**, the field, **Organism**, refers to the biosample accession of the sample.

1. On the **Barcoding Manifests'** web page, click the checklist dropdown to view a list of available checklists that support **Barcoding Manifests'** submission as shown below:
2. Click  button to add **Barcoding manifest** for the chosen tagged sequence checklist as shown below:
3. An **Upload Barcoding Manifest** dialogue is displayed. Click the  button to choose a file from your local system.
4. The uploaded manifest is shown in a table in the **Upload Barcoding Manifest** dialogue as shown below. Click the  button to submit the barcoding manifest.

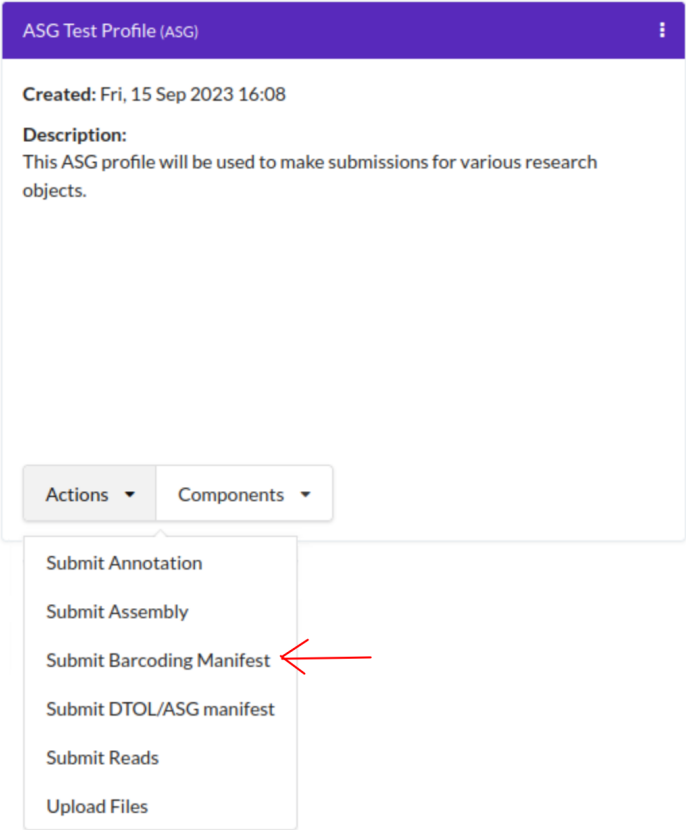


Fig. 2: Tree of Life Profile Actions: ‘Submit Barcoding Manifest action

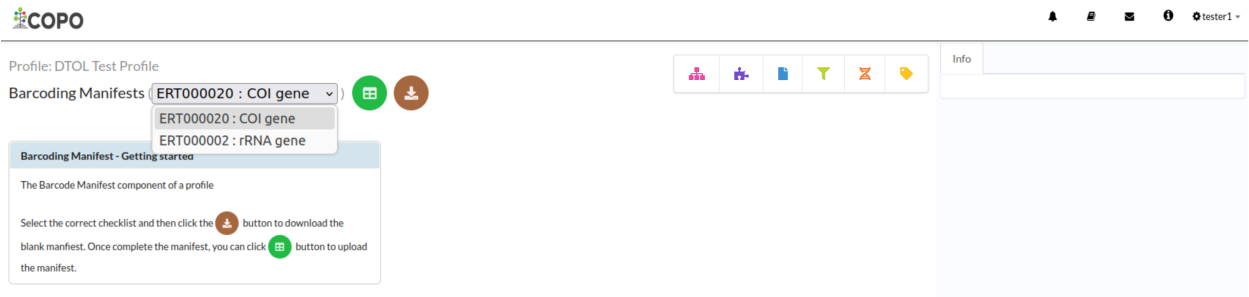


Fig. 3: Barcoding Manifests’ web page: Checklist dropdown menu with checklist options displayed

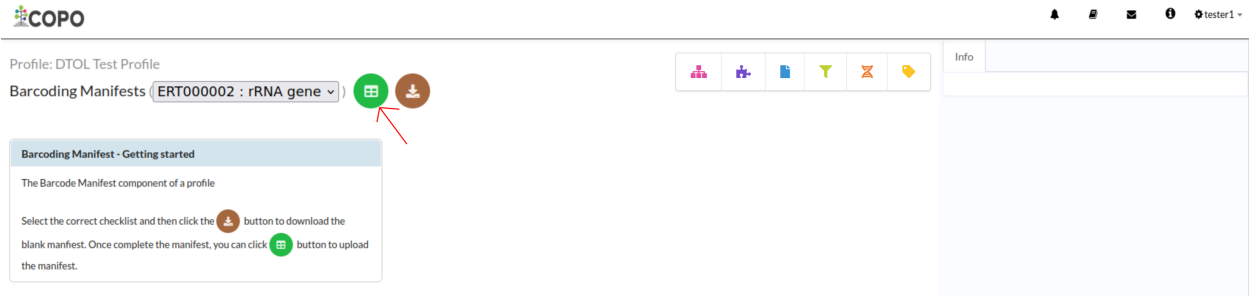


Fig. 4: Barcoding Manifest upload: Click ‘Add Tagged Sequence (s) from Tagged Sequence Spreadsheet’ from Spreadsheet’ button

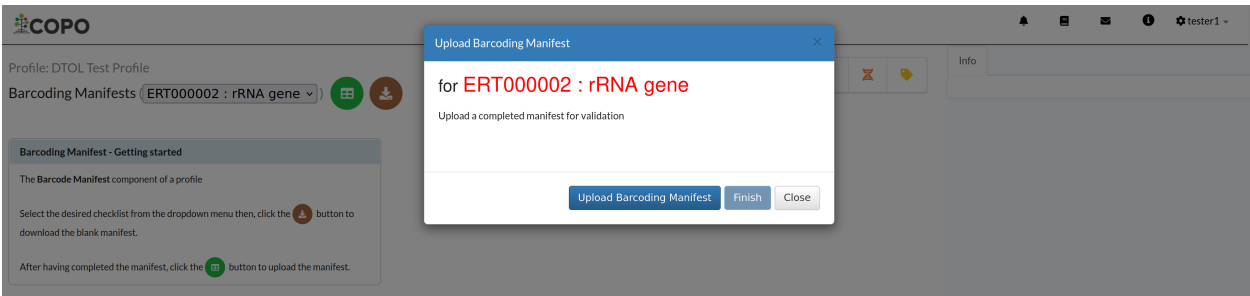


Fig. 5: Barcoding Manifest upload: ‘Upload Barcoding Manifest’ dialogue

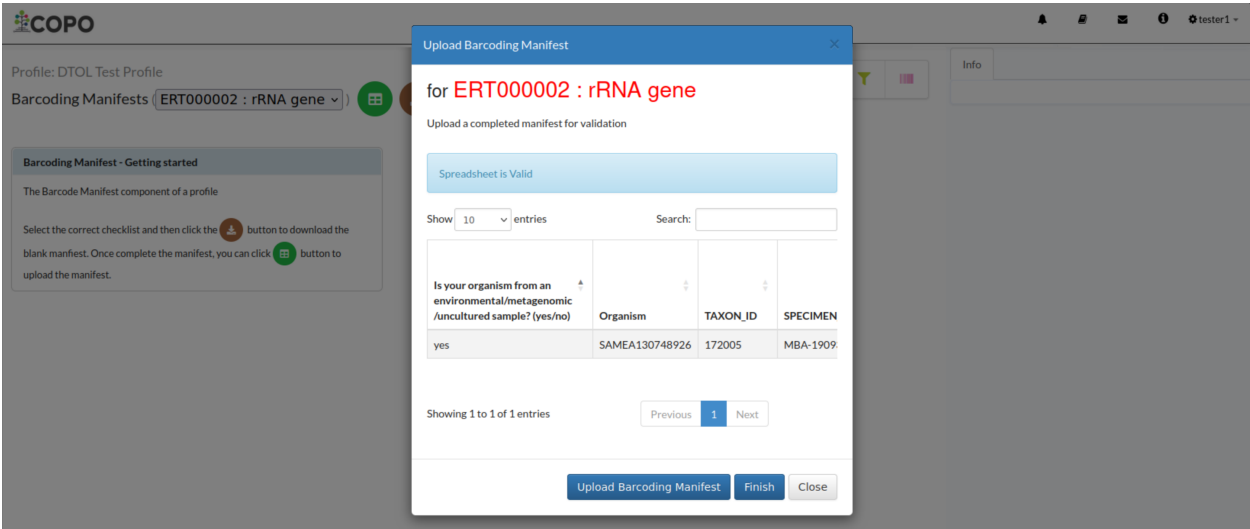


Fig. 6: Barcoding Manifest upload: ‘Upload Barcoding Manifest’ dialogue with uploaded manifest

- The new barcoding manifest(s) will be displayed on the **Barcoding Manifests** web page after a successful submission.

Hint: Barcoding manifest records that are highlighted **yellow** indicate that the records are pending submission. The records will be highlighted **green** after a successful submission.

The screenshot shows the COPO web interface. At the top, the profile is 'DTOL Test Profile' and the barcoding manifests are for 'ERT000002 : rRNA gene'. A green notification box on the right says 'Barcoding manifest submission has been scheduled!'. Below the table, there are buttons for 'Select all', 'Select filtered', 'Clear selection', 'Export CSV', 'Delete', and 'Submit'. The table has columns: Organism, Is your organism from an environmental/metagenomic /uncultured sample? (yes/no), Organelle, Sedimentation coefficient, Clone identifier, Isolate name, Isolation source, Cultivar, Variety (varietas), Ecotype, and Breed. The first record, SAMEA130748926, is highlighted in yellow and has 'yes' in the second column and '5.85' in the fourth column. The 'Submit' button is highlighted in blue.

Organism	Is your organism from an environmental/metagenomic /uncultured sample? (yes/no)	Organelle	Sedimentation coefficient	Clone identifier	Isolate name	Isolation source	Cultivar	Variety (varietas)	Ecotype	Breed
SAMEA130748926	yes		5.85							

Fig. 7: Barcoding manifest upload: Barcoding Manifests' web page displaying the uploaded barcoding manifests(s)

14.1.3 Submit Barcoding Manifests

Hint: The submitted barcoding manifest record will be highlighted **green**.

Click the desired barcoding manifests records from the list of barcoding manifests displayed on the **Barcoding manifests** web page. Then, click the **Submit** button (located in the top-right corner of the table) as shown below:

The screenshot shows the COPO web interface. At the top, the profile is 'DTOL Test Profile' and the barcoding manifests are for 'ERT000002 : rRNA gene'. A green notification box on the right says 'Barcoding manifest submission has been scheduled!'. Below the table, there are buttons for 'Select all', 'Select filtered', 'Clear selection', 'Export CSV', 'Delete', and 'Submit'. The table has columns: Organism, Is your organism from an environmental/metagenomic /uncultured sample? (yes/no), Organelle, Sedimentation coefficient, Clone identifier, Isolate name, Isolation source, Cultivar, Variety (varietas), Ecotype, and Breed. The first record, SAMEA130748926, is highlighted in green and has 'yes' in the second column and '5.85' in the fourth column. The 'Submit' button is highlighted in blue.

Organism	Is your organism from an environmental/metagenomic /uncultured sample? (yes/no)	Organelle	Sedimentation coefficient	Clone identifier	Isolate name	Isolation source	Cultivar	Variety (varietas)	Ecotype	Breed
SAMEA130748926	yes		5.85							

Fig. 8: Barcoding manifest submission: Click the “Submit” button to submit the highlighted barcoding manifest from the profile

Profile: DTOL Test Profile

Barcoding Manifests (ERT000002 : rRNA gene)

Select all Select filtered Clear selection Export CSV Delete Submit

Showing 1 to 1 of 1 records Click + beside a record to view extra details

Organism	Is your organism from an environmental/metagenomic /uncultured sample? (yes/no)	Organelle	Sedimentation coefficient	Clone identifier	Isolate name	Isolation source	Cultivar	Variety (varietas)	Ecotype	Breed
SAMEA130748926	yes		5.85							

show 10 records

Previous 1 Next

Barcoding sequence has been submitted with accession ERZ21826949

Biocoding manifest submission has been scheduled!

Fig. 9: Barcoding manifest submission: The barcoding manifest has been submitted

14.2 How to Delete Barcoding Manifests

Note: Barcoding manifests can only be deleted **before** they have been submitted.

Click the desired barcoding manifest from the list of barcoding manifests displayed on the **Barcoding Manifests** web page. Then, click the **Delete** button (located in the top-right corner of the table) as shown below:

Profile: DTOL Test Profile

Barcoding Manifests (ERT000002 : rRNA gene)

Select all Select filtered Clear selection Export CSV Delete Submit

Showing 1 to 1 of 1 records 1 record selected

Organism	Is your organism from an environmental/metagenomic /uncultured sample? (yes/no)	Organelle	Sedimentation coefficient	Clone identifier	Isolate name	Isolation source	Cultivar	Variety (varietas)	Ecotype	Breed
SAMEA130748926	yes		5.85							

Barcoding sequence has been submitted with accession ERZ21826949

Biocoding manifest submission has been scheduled!

Fig. 10: Barcoding manifest deletion: Click the “Delete” button to remove the highlighted barcoding manifest from the profile

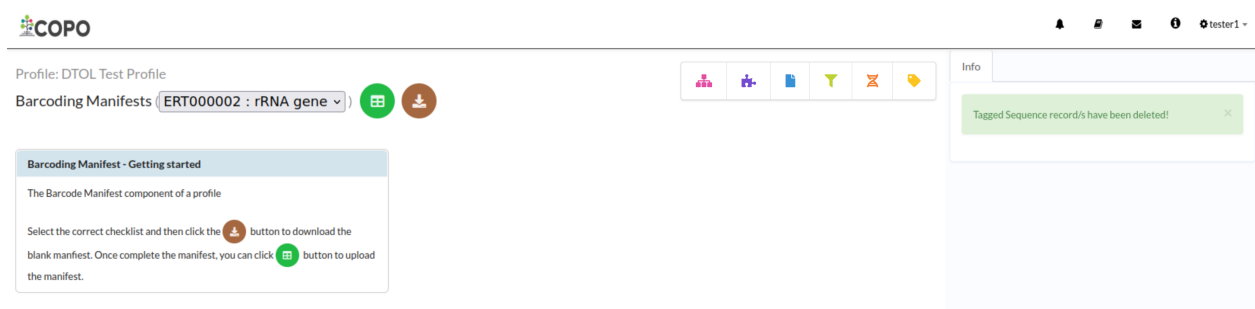


Fig. 11: Barcoding manifest deletion: Barcoding manifest record has been deleted

IMAGES SUBMISSION

15.1 How to Submit Images

Note:

- Images can only be submitted after samples have been uploaded in the **Upload Spreadsheet** dialogue.
 - Images can only be submitted via a ToL¹ profile. Please see: *Steps to Create a Tree of Life Profile* for guidance.
 - The filename of sample images must be named as {Specimen_ID}-{n}.[jpg|png] where {n} is the image number, {Specimen_ID} is the specimen ID of the sample in the manifest and jpg or png is the extension of the file.
-

See also:

- *Viewing Submitted Images*
- *Permits Submission*
- How to Submit ASG Manifests
- How to Submit DTOL Manifests
- How to Submit ERGA Manifests
- *How to Submit Barcoding Manifests*

1. The images table is empty under the **Sample Images** tab in the **Upload Spreadsheet** dialogue.

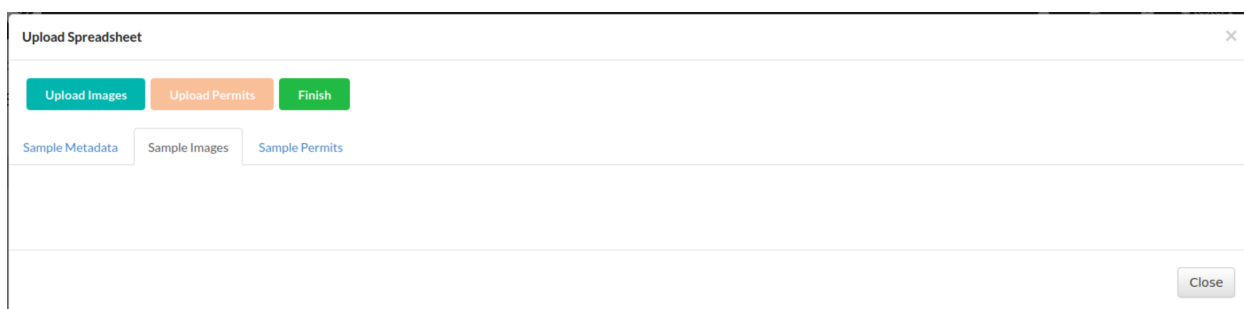


Fig. 1: Manifest submission: ‘Upload Spreadsheet’ dialogue with no images uploaded

¹ See term: *Tree of Life (ToL)*.

- The images table is populated with the images uploaded under the **Sample Images** tab in the **Upload Spreadsheet** dialogue.


Fig. 2: Manifest submission: ‘Upload Spreadsheet’ dialogue with image(s) uploaded

- Click the **Finish** button to submit the images and samples.

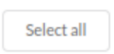
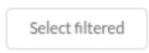
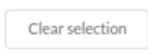
A **Submit Samples** confirmation dialogue is displayed. If you decide to confirm the samples submission, click the **Confirm** button.

15.2 View Submitted Images

Note:

- Images can only be viewed **after** they have been submitted.
- Images **cannot** be deleted or modified after they have been submitted.
- The  button will only appear on the web page if you are assigned as a sample manager.

Hint:

- To **select multiple** sample records, hold down the **Ctrl** key on your keyboard and click on the sample records that you would like to select.
- To **select a range** of sample records, hold down the **Shift** key on your keyboard and click on the first and last sample records that you would like to select.
- To **select all** sample records, click 
- To **select filtered** sample records, click 
- To **clear selection** of sample records, click 

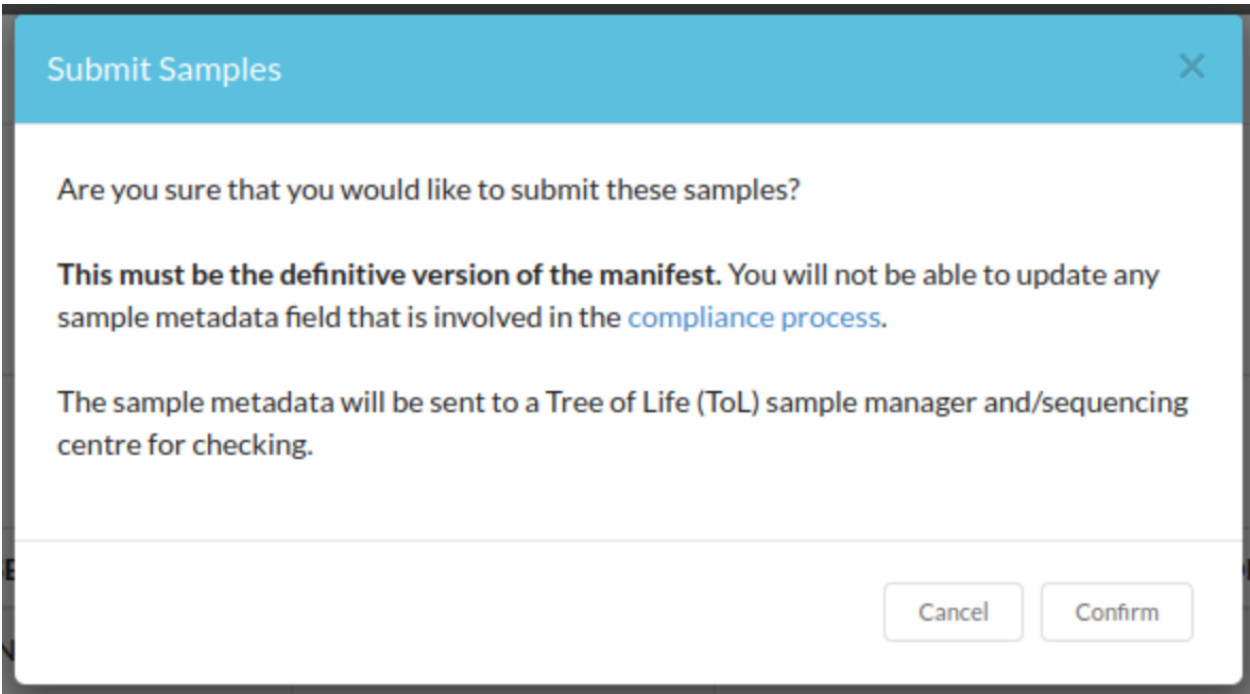


Fig. 3: Manifest submission: ‘Submit Samples’ confirmation dialogue

15.2.1 On Samples web page

1. Navigate to the **Samples** web page.
See How to access Samples web page section for guidance.
2. Select the sample record(s) that you would like to view images for.

Then, click the  button to view image(s) submitted for the selected sample record(s).

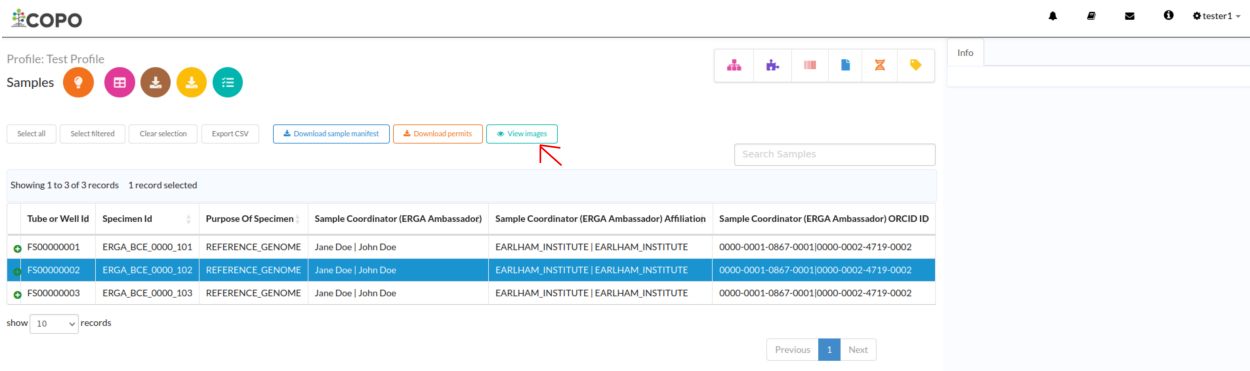


Fig. 4: Samples web page: Pointer to ‘View images’ button

3. If any image submission(s) exist for the selected sample record(s), a popup dialogue will be displayed with the image(s) submitted for the selected sample record(s) as shown below:

Hint: Click the image to view a larger version.

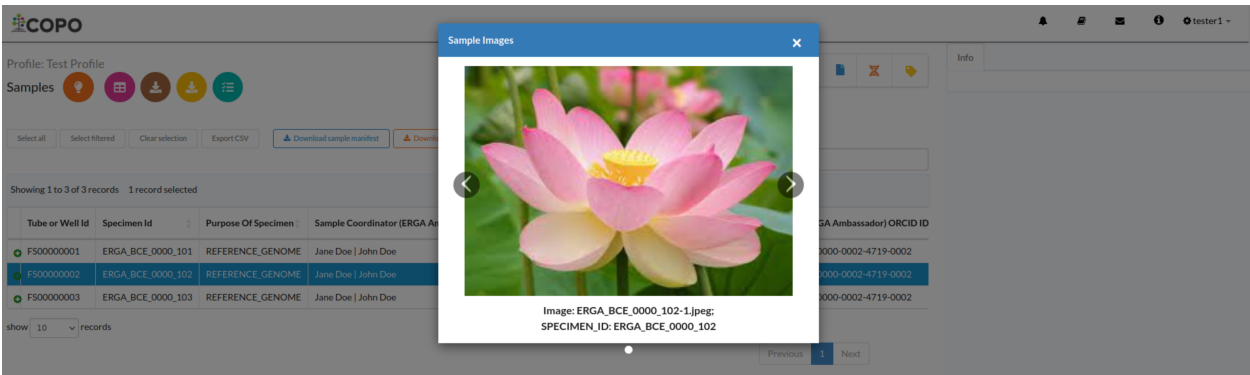


Fig. 5: Samples web page: Popup dialogue displaying submitted image(s) for selected sample record(s)

OR

If no images were submitted for the selected sample record(s), a message is displayed in the popup dialogue indicating such as shown below:

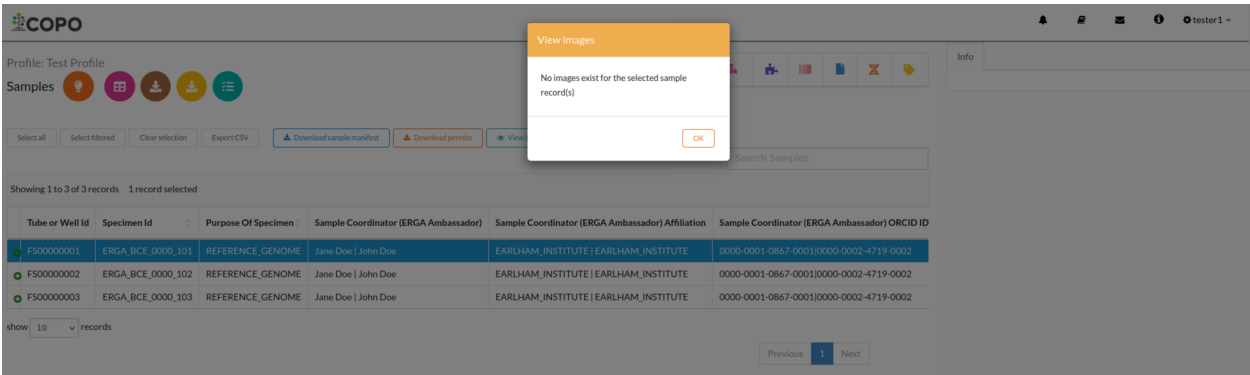


Fig. 6: Samples web page: Popup dialogue displaying message, ‘No images exist for selected sample record(s)’

15.2.2 On Accept or Reject Samples web page

If you have been assigned as a **sample manager**, see *View submitted images section for sample managers <images-submission-view-images-sample-managers>* for more information.


PERMITS SUBMISSION

16.1 How to Submit Permits

Note:


- Permits can only be submitted after ERGA¹ samples have been uploaded in the **Upload Spreadsheet** dialogue.
 - Permits can only be submitted via a ToL² profile³. Please see: *Steps to Create a Tree of Life Profile* for guidance.
-

Warning:

- If you have more than one permit file to upload, they **must** be uploaded at the same time i.e. after you have clicked the  button, navigate to the directory where the permits are stored and CTRL + click all of the permits so that all the permits are highlighted and uploaded at the same time.

See also:

- *Downloading Submitted Permits*
- *Images Submission*
- How to Submit ERGA Manifests
- *How to Submit Barcoding Manifests*

1. The uploaded samples are shown in a table in the **Upload Spreadsheet** dialogue as shown below. Click the  button to browse your local (computer) system for .pdf permits for the samples.
2. The permits table is empty under the **Sample Permits** tab in the **Upload Spreadsheet** dialogue.
3. The permits table is populated with the permits uploaded under the **Sample Permits** tab in the **Upload Spreadsheet** dialogue

¹ See term: *ERGA*.

² See term: *Tree of Life (ToL)*.

³ Also known as COPO profile. See: *COPO profile or work profile*.

Upload Spreadsheet

Upload Images

Upload Permits

Sample Metadata

Sample Images

Sample Permits

Show 10 entries

Search:

TUBE_OR_WELL_ID	SPECIMEN_ID	PURPOSE_OF_SPECIMEN	SAMPLE_COORDINATOR	SAMPLE_COORDINATOR_AFFILIATION	SAMPLE_COORDINATOR_ORCID_ID	OR
FS42596104	ERGA_BCE_9858_104	REFERENCE_GENOME	Tester1 Tester2	INSTITUTE_OF_EVOLUTIONARY_BIOLOGY INSTITUTE_OF_EVOLUTIONARY_BIOLOGY	0000-0000-0000-0001 0000-0000-0000-0002	Mo
FS42596105	ERGA_BCE_9858_105	REFERENCE_GENOME	Tester1 Tester2	INSTITUTE_OF_EVOLUTIONARY_BIOLOGY INSTITUTE_OF_EVOLUTIONARY_BIOLOGY	0000-0000-0000-0001 0000-0000-0000-0002	Mo
FS42596106	ERGA_BCE_9858_106	REFERENCE_GENOME	Tester1 Tester2	INSTITUTE_OF_EVOLUTIONARY_BIOLOGY INSTITUTE_OF_EVOLUTIONARY_BIOLOGY	0000-0000-0000-0001 0000-0000-0000-0002	Mo

Showing 1 to 3 of 3 entries

Previous

1

Next

Close

Fig. 1: ERGA manifest submission: ‘Upload Spreadsheet’ dialogue with uploaded samples

Upload Spreadsheet

Upload Images

Upload Permits

Sample Metadata

Sample Images

Sample Permits

Showing 1 to 3 of 3 entries

Previous

1

Next

Close

Fig. 2: ERGA manifest submission: ‘Upload Spreadsheet’ dialogue with no permits uploaded

90

Chapter 16. Permits Submission

Upload Spreadsheet

Upload Images

Upload Permits

Finish

Sample Metadata

Sample Images

Sample Permits

Show 10 entries

Search:

Specimen ID	Permit Type	Permit Files	Notes
ERGA_BCE_9858_104	Ethics Permit	SAMPLING_PERMITS.pdf	
ERGA_BCE_9858_104	Sampling Permit	SAMPLING_PERMITS.pdf	
ERGA_BCE_9858_104	Nagoya Permit	SAMPLING_PERMITS.pdf	
ERGA_BCE_9858_105	Ethics Permit	SAMPLING_PERMITS.pdf	
ERGA_BCE_9858_105	Sampling Permit	SAMPLING_PERMITS.pdf	
ERGA_BCE_9858_105	Nagoya Permit	SAMPLING_PERMITS.pdf	
ERGA_BCE_9858_106	Ethics Permit	SAMPLING_PERMITS.pdf	
ERGA_BCE_9858_106	Sampling Permit	SAMPLING_PERMITS.pdf	
ERGA_BCE_9858_106	Nagoya Permit	SAMPLING_PERMITS.pdf	

Showing 1 to 9 of 9 entries

Previous

1

Next

Close

Fig. 3: ERGA manifest submission: ‘Upload Spreadsheet’ dialogue with permits uploaded

4. Click the


Finish

 button to submit the permits and samples.

A **Submit Samples** confirmation dialogue is displayed. If you decide to confirm the samples submission, click the **Confirm** button.

16.2 Download Submitted Permits

Note:

- Permits can only be downloaded **after** they have been submitted.
- Permits **cannot** be deleted or modified after they have been submitted.
- The  button will only appear on the web page if you are assigned as a sample manager.

Hint:

- To **select multiple** sample records, hold down the **Ctrl** key on your keyboard and click on the sample records that you would like to select.
- To **select a range** of sample records, hold down the **Shift** key on your keyboard and click on the first and last sample records that you would like to select.
- To **select all** sample records, click

Select all

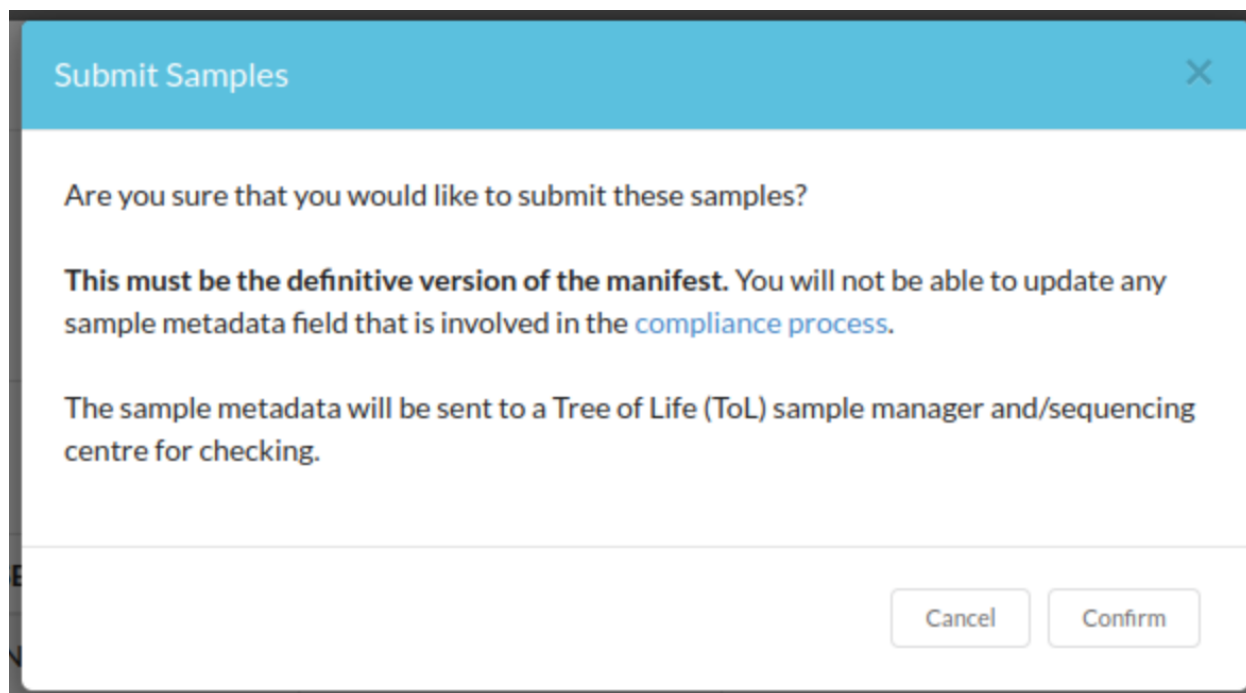
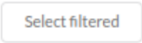
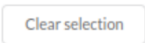



Fig. 4: ERGA manifest submission: ‘Submit Samples’ confirmation dialogue

- To **select filtered** sample records, click 
- To **clear selection** of sample records, click 

16.2.1 On Samples web page

1. Navigate to the **Samples** web page.
See How to access Samples web page section for guidance.
2. Select the sample record(s) that you would like to download permits for.

Then, click the  button to download permit(s) submitted for the selected sample record(s).

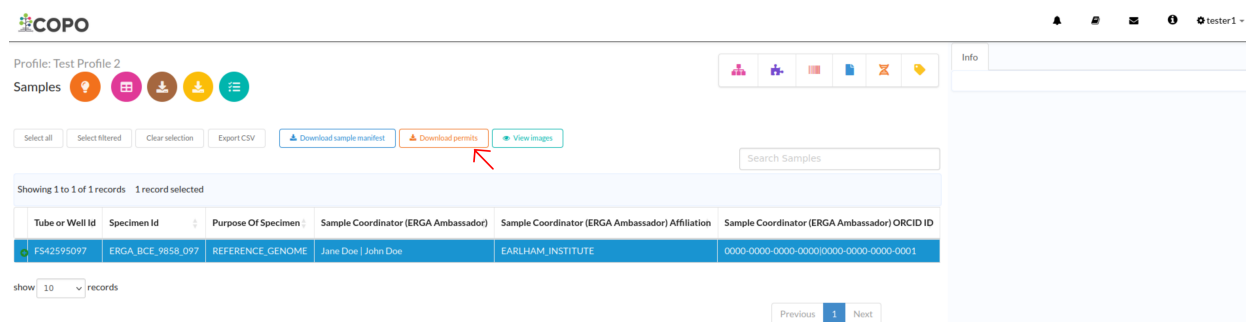


Fig. 5: Samples web page: Pointer to ‘Download permits’ button

3. If any permit submission(s) exist for the selected sample record(s), the permits will be automatically downloaded for the selected sample record(s) as shown below:

Hint: Permits will be downloaded as a .zip file

If no permits were submitted for the selected sample record(s), a message is displayed in the popup dialogue indicating such as shown below:

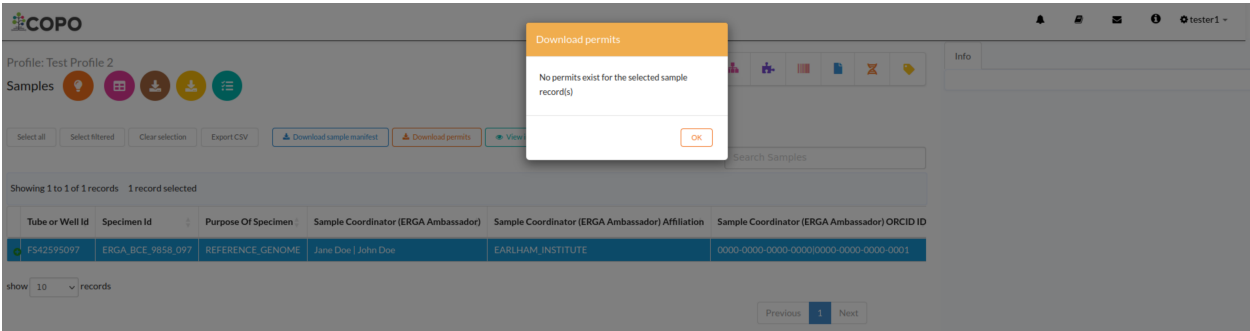


Fig. 6: Samples web page: Popup dialogue displaying message, ‘No permits exist for selected sample record(s)’

16.2.2 On Accept or Reject Samples web page

If you have been assigned as a **sample manager**, see *Download submitted permits section for sample managers* <permits-submission-download-permits-sample-managers> for more information.

READS SUBMISSION

17.1 How to Submit Reads

Note:

- Once **reads** have been submitted, they cannot be deleted.
 - Files must be uploaded before a **reads** manifest can be submitted. See: *How to Submit Files*.
-

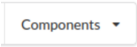

See also:

- *How to Update Reads*
- *Explore Various Types of Reads Checklist*
- *How to Submit Files*
- *How to check if data files associated with reads submissions have uploaded to ENA*
- *Types of Files for Read Submissions*

17.1.1 Accessing the Reads' Web Page

The **Reads**'¹ web page can be accessed from the **Components** button or **Actions** button associated with a profile².

Use Components' Button to Navigate to Reads' Web Page

Click the  button associated with a profile. Then, click the  from the popup menu displayed as shown below:

¹ See: *Reads*.

² Also known as COPO profile. See: *COPO profile or work profile*.

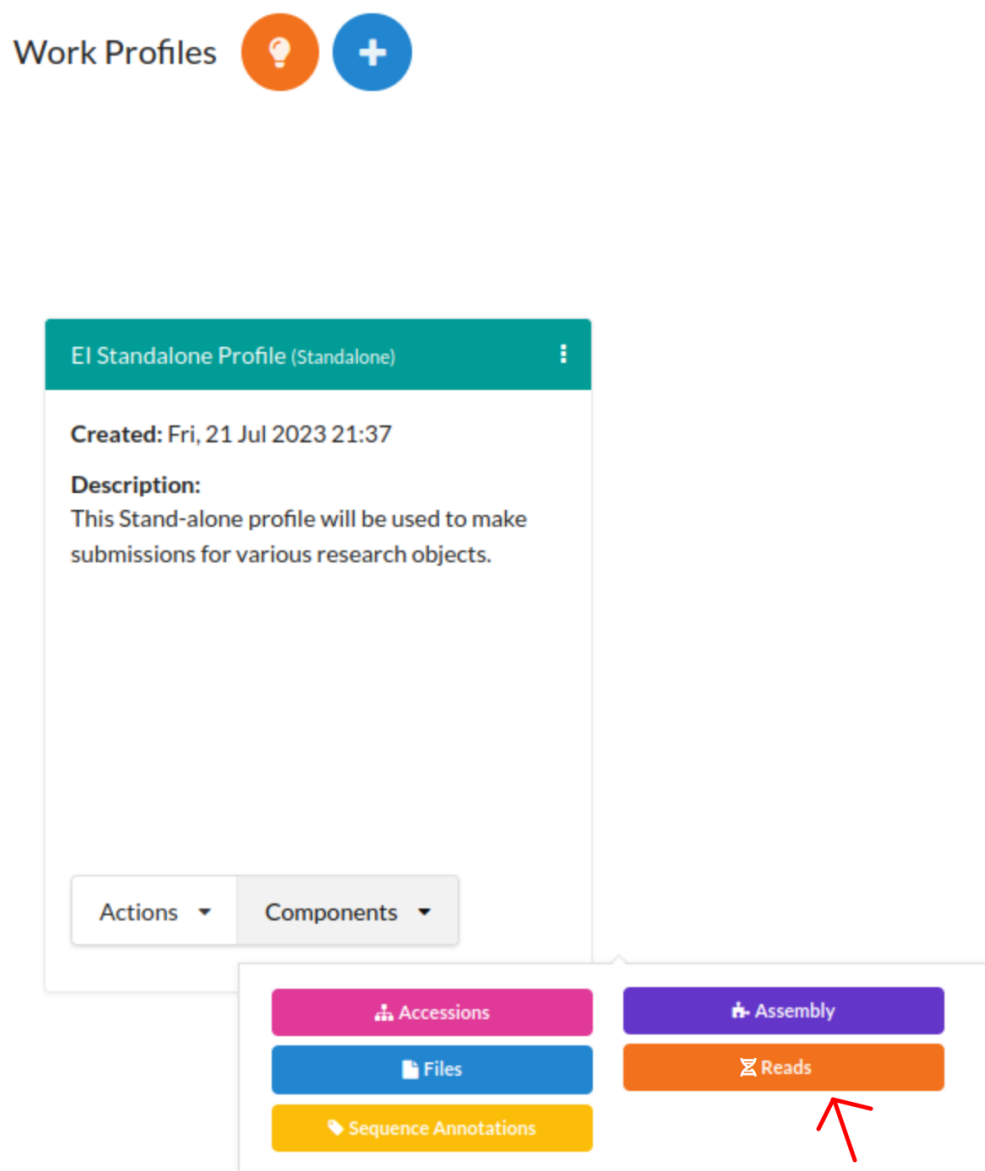
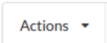


Fig. 1: Stand-alone Profile Components: Reads component button

Use Actions' Button to Navigate to Reads' Web Page

Click the  button associated with a profile. Then, click the action, **Submit Reads** action from the popup menu displayed as shown below:

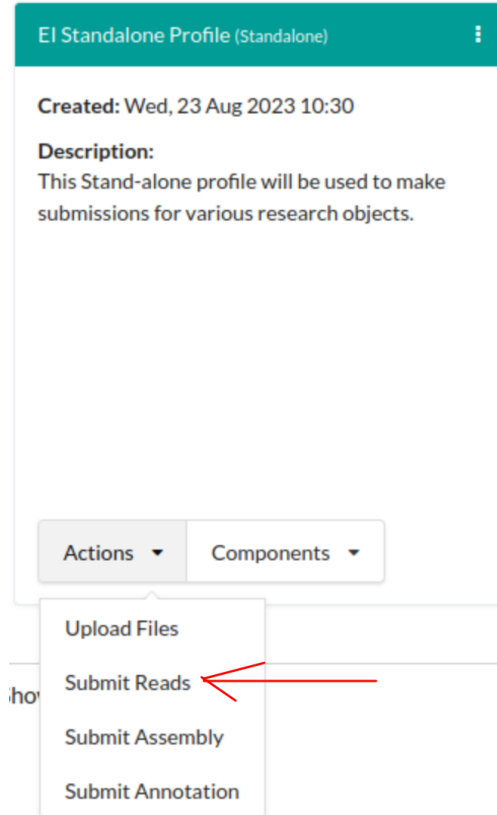




Fig. 2: Stand-alone Profile Actions: 'Submit Reads' action


17.1.2 Upload Reads

Hint:

- To download a blank **Reads'** manifest template, click the  button.
- For guidance on how to fill in the **Reads** manifest to submit *paired* reads, please see the [Reads manifest for paired reads](#) FAQ.

Important: The **reads** checklist dropdown menu is only available for **Stand-alone** profiles.

If you are submitting **reads** for a profile other than a Stand-alone profile, please proceed to upload the reads from your local file system after you have clicked the  button.

Note: The colour of the  button is based on the type of profile that you are submitting a Reads for. See the [Profile Types Legend](#) section regarding the colour code for the various types of project profiles on COPO.

1. On the **Reads'** web page, click the checklist dropdown to view a list of available checklists that support **Reads'** submission as shown below:

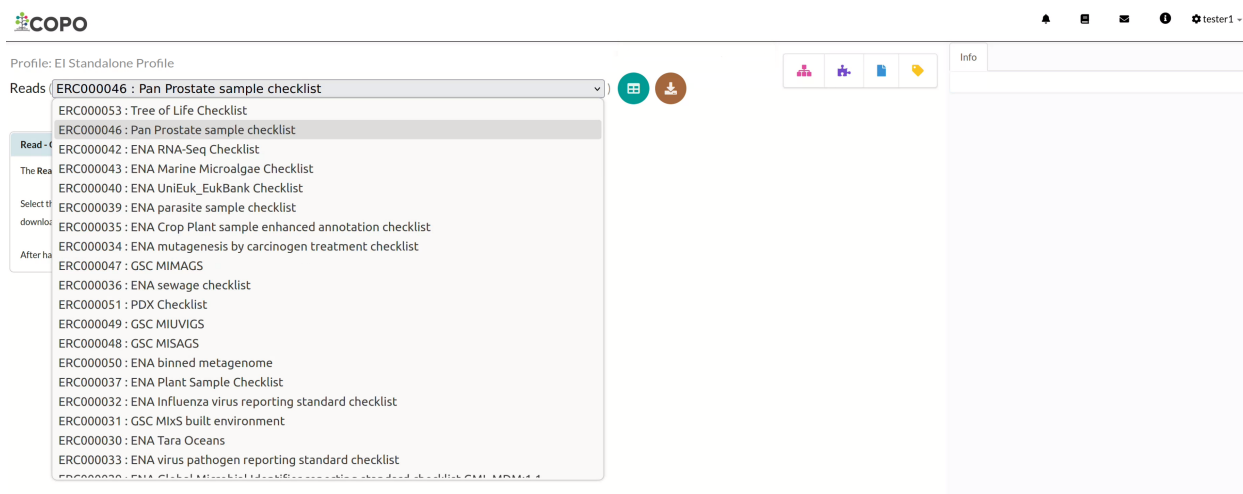



Fig. 3: Reads' web page: Checklist dropdown menu with checklist options displayed

An overview of each **Reads** checklist option is explained in the [Reads' checklist section](#).

2. Click  button to add **Reads'** from a spreadsheet for the chosen checklist as shown below:

Note: The colour of the  button is based on the type of profile that you are submitting a Reads for. See the [Profile Types Legend](#) section regarding the colour code for the various types of project profiles on COPO.

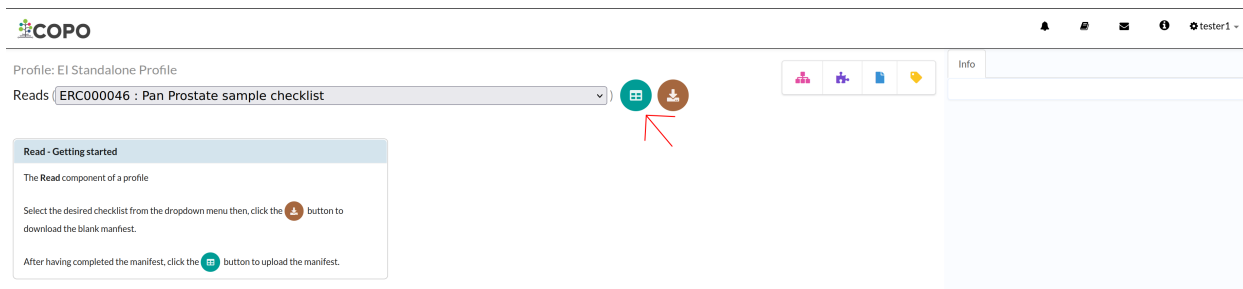


Fig. 4: Reads' upload: Click 'Add Reads' from Spreadsheet' button

3. An **Upload Read Manifest** dialogue is displayed. Click the  button to choose a file from your local system.

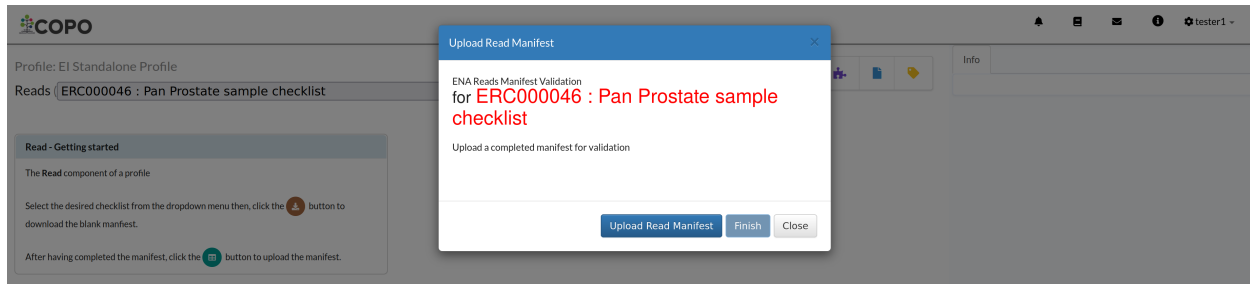



Fig. 5: Reads' upload: 'Upload Read Manifest' dialogue

4. The uploaded manifest is shown in a table in the **Upload Read Manifest** dialogue as shown below. Click the  button to submit the reads manifest.
5. The new read(s) will be displayed on the **Reads** web page after a successful submission.

Hint: Reads records that are highlighted **yellow** indicate that the records are pending submission. The records will be highlighted **green** after a successful submission.

17.1.3 Submit Reads

Hint: The submitted read record will be highlighted **green**.

Click the desired reads records from the list of reads displayed on the **Reads'** web page. Then, click the **Submit** button (located in the top-right corner of the table) as shown below:

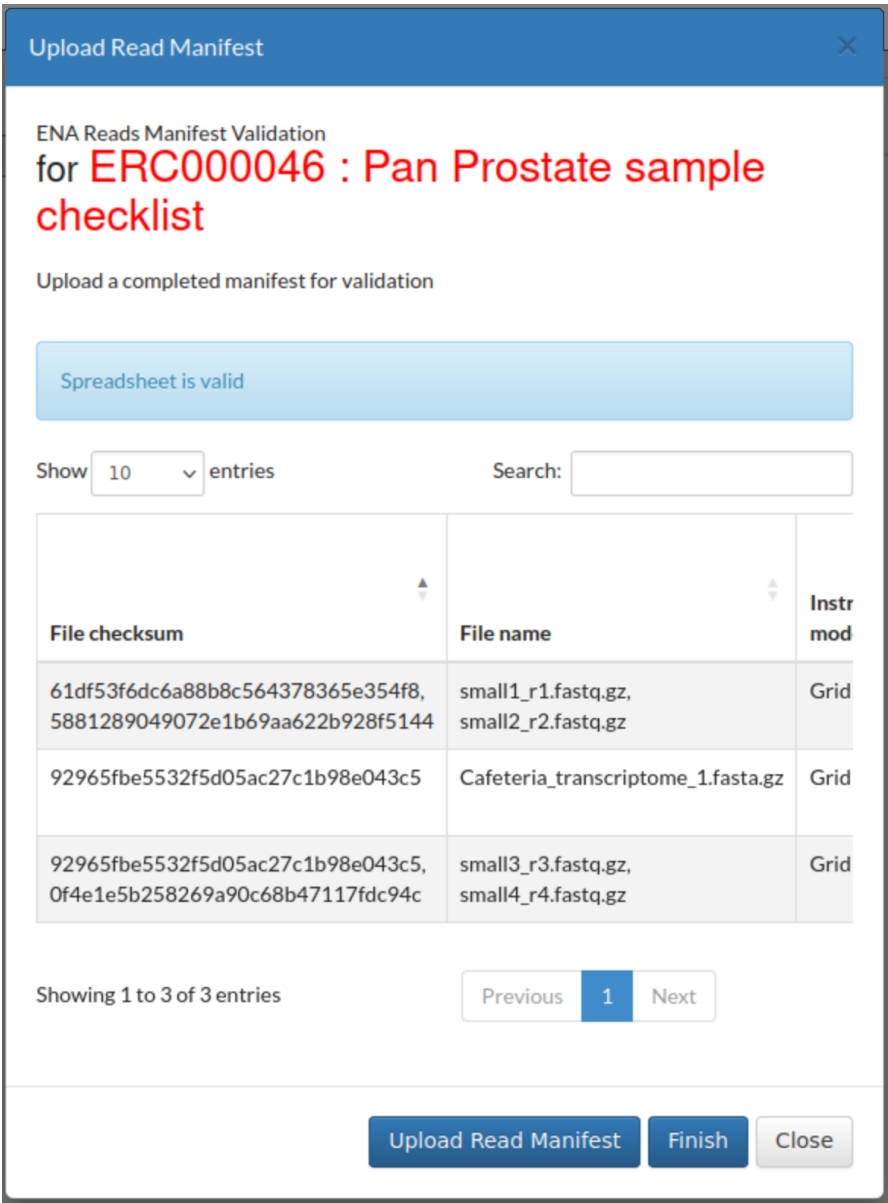


Fig. 6: Reads' upload: 'Upload Read Manifest' dialogue with uploaded manifest

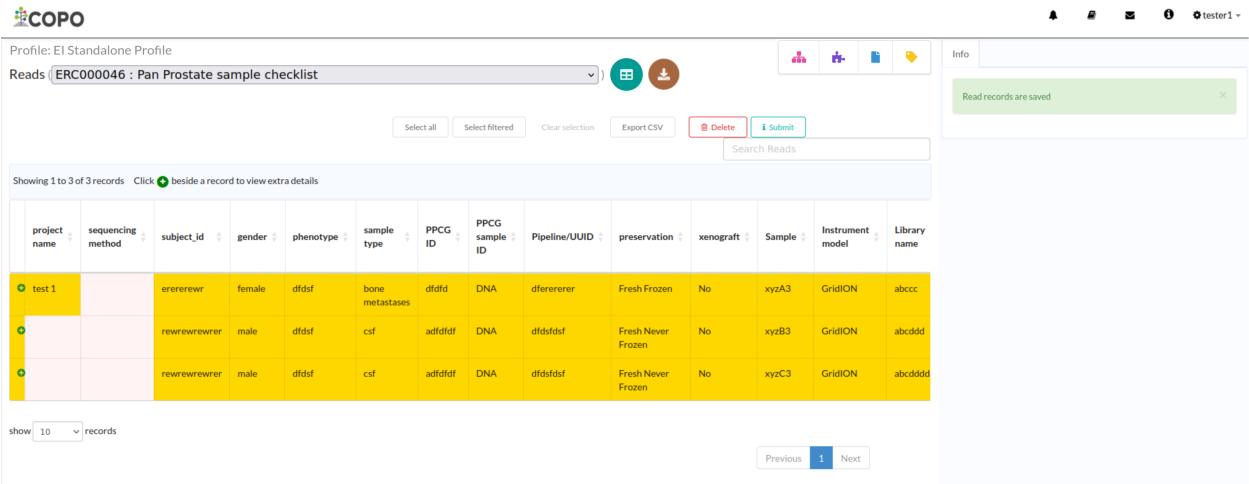


Fig. 7: Reads' upload: Reads' web page displaying the uploaded read(s)

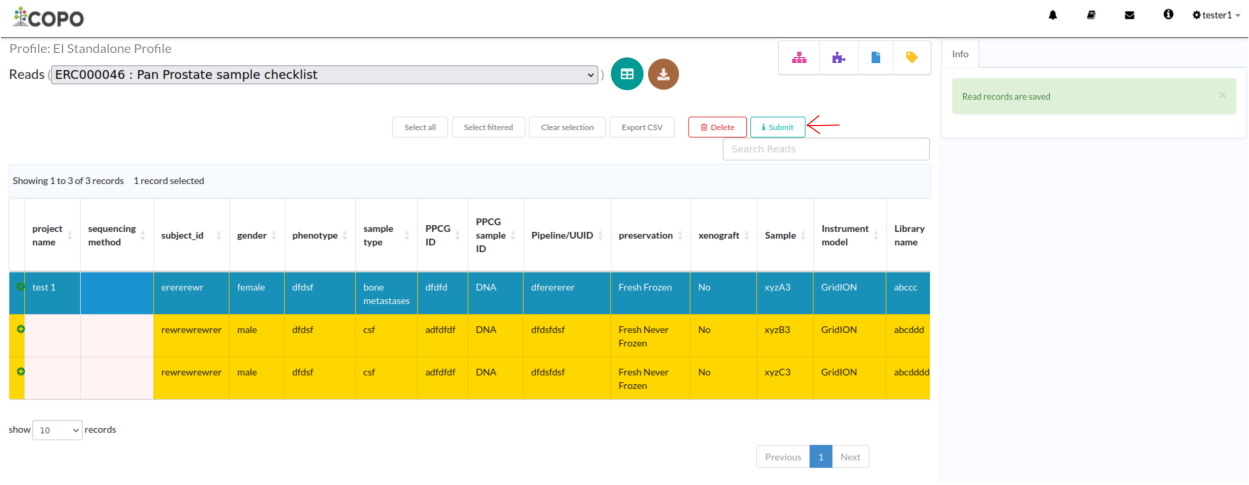


Fig. 8: Reads submission: Click the “Submit” button to submit the highlighted read from the profile

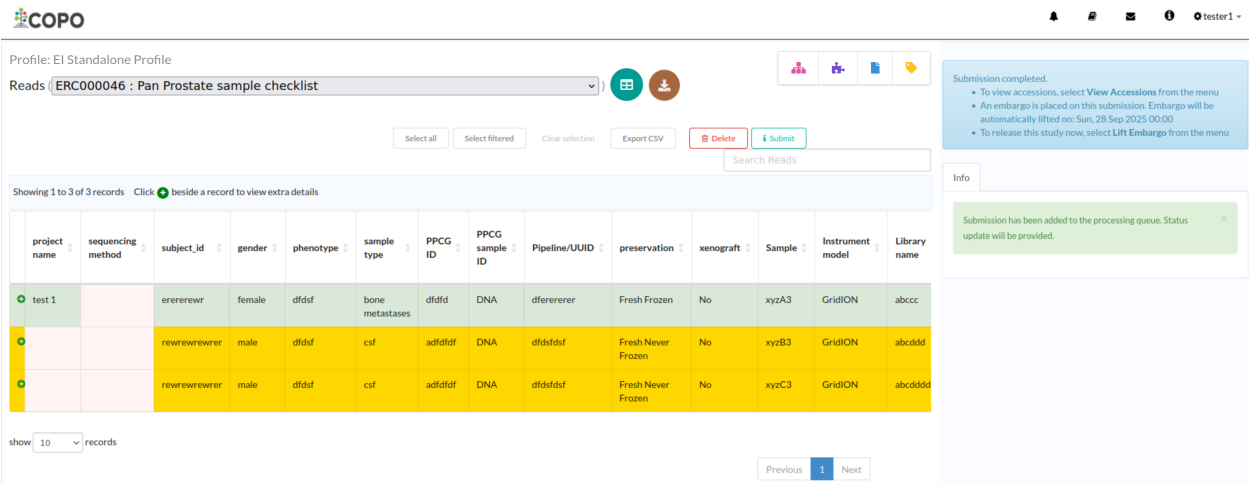


Fig. 9: Reads submission: The Read has been submitted

SAMPLES SUBMISSION

The following are the types of sample manifests that can be submitted.

Click the links below to learn more about each type of manifest submission:

- [Aquatic Symbiosis Genomics \(ASG\) manifests](#)
- [Darwin Tree of Life \(DToL\) manifests](#)
- [Darwin Tree of Life Environmental \(DToL_ENV\) manifests](#)
- [European Reference Genome Atlas \(ERGA\) manifests](#)

Samples submission and validation process in COPO

See also:


- [How to access Samples web page](#)
- [How to submit Assemblies](#)
- [Barcoding manifest submissions](#)
- [How to upload Files](#)
- [How to submit Reads](#)
- [How to submit Sequence Annotations](#)

18.1 How to Download Submitted Sample Manifest

Hint: This is useful if you would like to update sample metadata for a manifest or retrieve the actual manifest that was submitted.

Samples can be updated by resubmitting the manifest with the updated metadata. See [Updating Samples](#) section for more information about which fields can be updated.

Note:

- At least one sample record (in a manifest) must be submitted before a manifest can be downloaded.
- The colour of the  button is based on the type of profile that you are making a submission to.

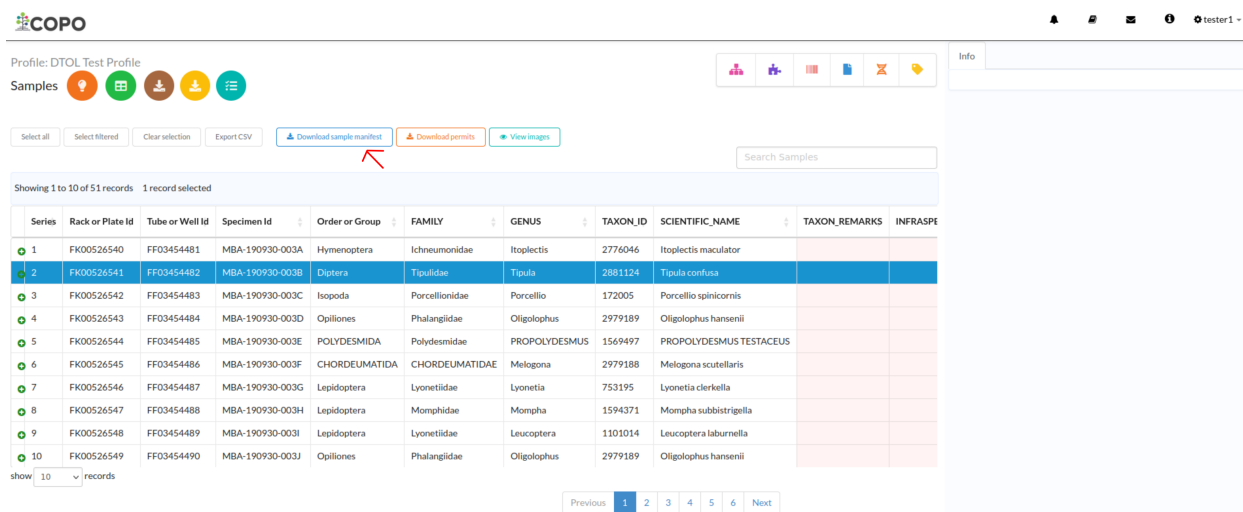
See the [Profile Types Legend](#) section regarding the colour code for the various types of project profiles on COPO.

The following steps describe how to download a submitted sample manifest:

1. Navigate to the **Samples** web page.
See How to access Samples web page section for guidance.
2. On the **Samples** web page, select **only one** sample record from the sample record table displayed.

Then, click the  button to download the manifest.

Hint: The manifest will be automatically downloaded as a .xlsx file



COPO

Profile: DTOL Test Profile

Samples

Select all Select filtered Clear selection Export CSV Download sample manifest Download permits View images

Showing 1 to 10 of 51 records 1 record selected

Series	Rack or Plate Id	Tube or Well Id	Specimen Id	Order or Group	FAMILY	GENUS	TAXON_ID	SCIENTIFIC_NAME	TAXON_REMARKS	INFRASPE
1	FK00526540	FF03454481	MBA-190930-003A	Hymenoptera	Ichneumonidae	Itopectis	2776046	Itopectis maculator		
2	FK00526541	FF03454482	MBA-190930-003B	Diptera	Tipulidae	Tipula	2881124	Tipula confusa		
3	FK00526542	FF03454483	MBA-190930-003C	Isopoda	Porcellionidae	Porcellio	172005	Porcellio spinicornis		
4	FK00526543	FF03454484	MBA-190930-003D	Opiliones	Phalangidae	Oligolophus	2979189	Oligolophus hansenii		
5	FK00526544	FF03454485	MBA-190930-003E	POLYDESMIDA	Polydesmidae	PROPOLYDESMUS	1569497	PROPOLYDESMUS TESTACEUS		
6	FK00526545	FF03454486	MBA-190930-003F	CHORDEUMATIDA	CHORDEUMATIDAE	Melogona	2979188	Melogona scutellaris		
7	FK00526546	FF03454487	MBA-190930-003G	Lepidoptera	Lyonetidae	Lyonetia	753195	Lyonetia clerkella		
8	FK00526547	FF03454488	MBA-190930-003H	Lepidoptera	Momphidae	Mompha	1594371	Mompha subbistrigella		
9	FK00526548	FF03454489	MBA-190930-003I	Lepidoptera	Lyonetidae	Leucoptera	1101014	Leucoptera laburnella		
10	FK00526549	FF03454490	MBA-190930-003J	Opiliones	Phalangidae	Oligolophus	2979189	Oligolophus hansenii		

show 10 records

Previous 1 2 3 4 5 6 Next

Fig. 1: Samples web page: Pointer to ‘Download sample manifest’ button

SEQUENCE ANNOTATIONS SUBMISSION

Note:

- Reads must be uploaded before a **Sequence Annotation** can be submitted.
-

See also:

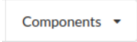

- *How to Update Sequence Annotations*
- *How to Delete Sequence Annotations*
- *How to check if data files associated with sequence annotation submissions have been uploaded to ENA*
- *How to Submit Reads*

19.1 How to Submit Sequence Annotations

19.1.1 Accessing the Sequence Annotations' Web Page

The **Sequence Annotations**¹ web page can be accessed from the **Components** button or **Actions** button associated with a profile².

Use Components' Button to Navigate to Sequence Annotations' Web Page

Click the  button associated with a profile. Then, click the  from the popup menu displayed as shown below:

¹ See: *Sequence Annotation*.

² Also known as COPO profile. See: *COPO profile or work profile*.

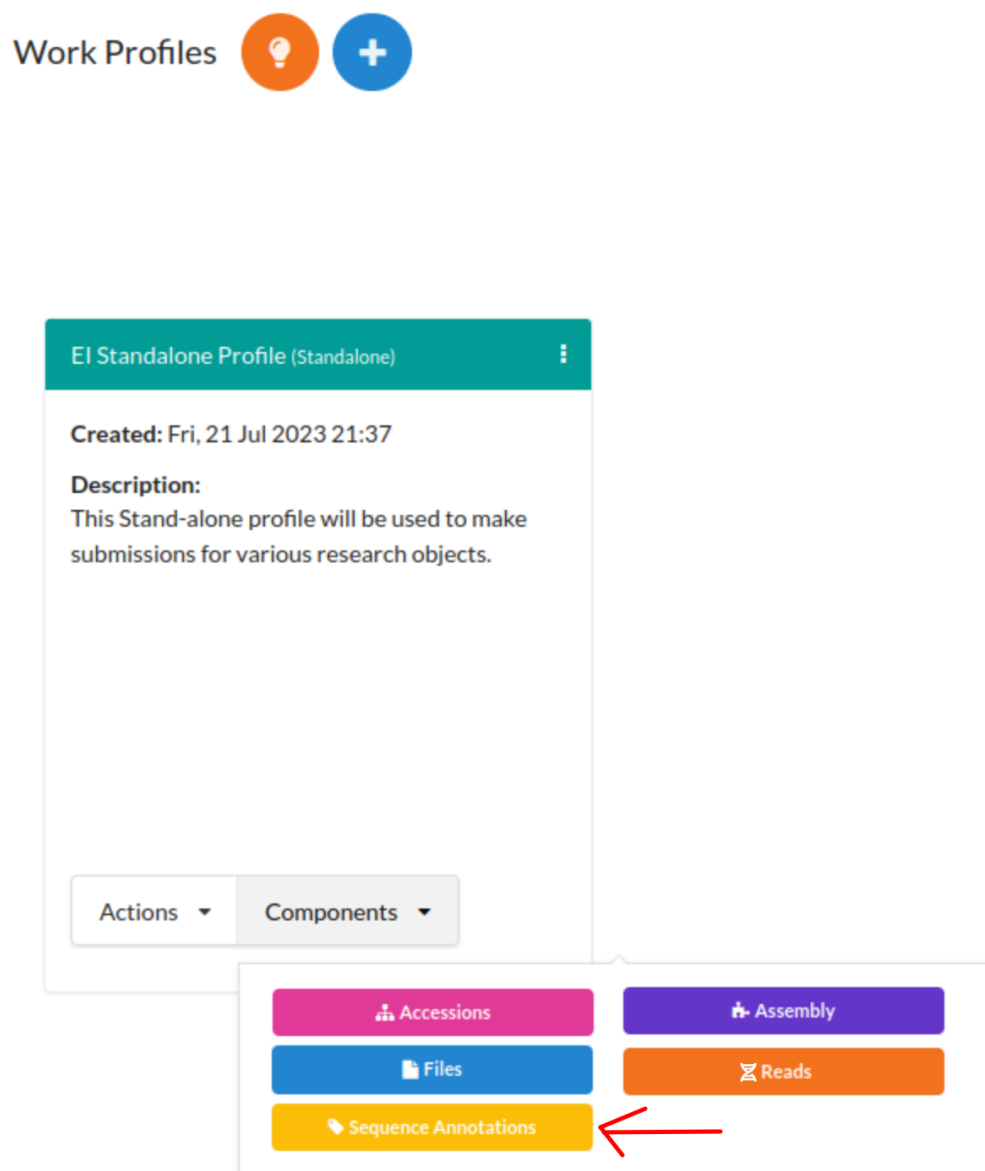
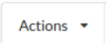


Fig. 1: Stand-alone Profile Components: Sequence Annotations' component button

Use Actions' Button to Navigate to Sequence Annotations' Web Page

Click the  button associated with a profile. Then, click the action, **Submit Annotation** action from the popup menu displayed as shown below:

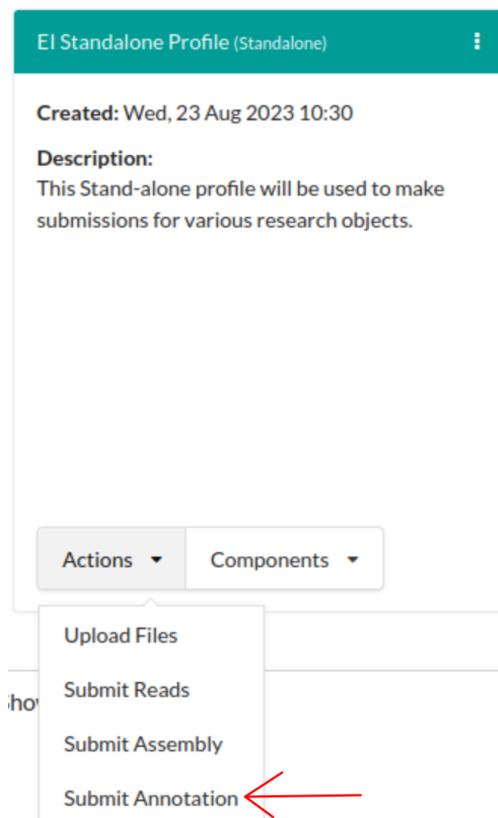



Fig. 2: Stand-alone Profile Actions: 'Submit Annotation' action

19.1.2 Submit Sequence Annotations

1. Click  button to add **Sequence Annotations'** as shown below:
2. An **Add Sequence Annotation** dialogue is displayed. Provide the details then, click the **Submit Annotation** button.
Select a sample accession from the **SAMPLE** dropdown field menu. The dropdown menu will display the reads that were previously uploaded.
3. The new sequence annotation(s) will be displayed on the **Sequence Annotations** web page after a successful submission.

Hint: Sequence annotation records that are highlighted **yellow** indicate that the records are pending

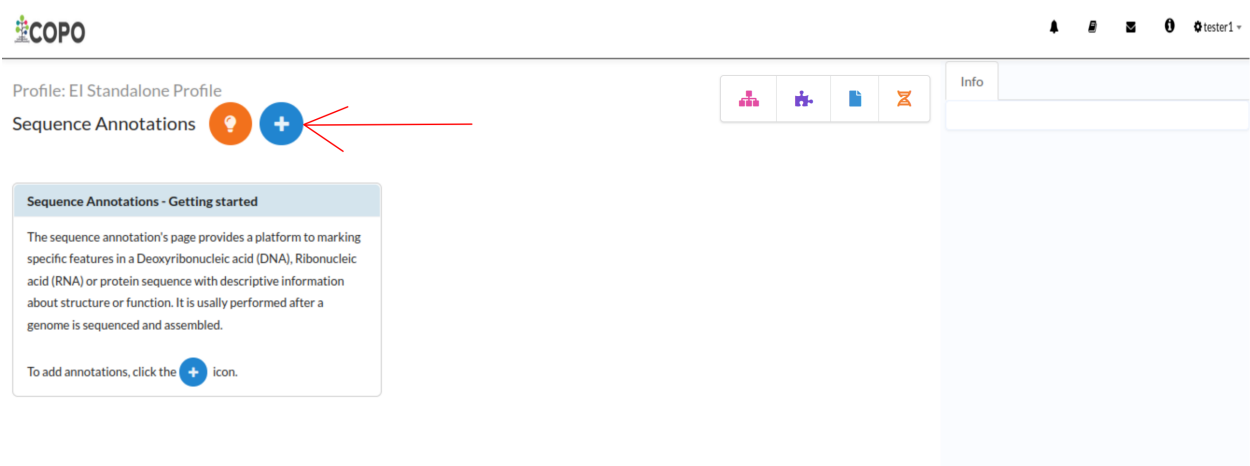


Fig. 3: Sequence Annotations’ submission: Click ‘Add Record’ button

Add Sequence Annotation

Submit annotation

Upload annotation files and fill in metadata, you must have already created a study in ENA and have uploaded samples and reads. You will be requested the relative accessions.

STUDY*

PRJEB66432

SAMPLE*

None

RUN

EXPERIMENT

ANNOTATION TITLE*

Annotation title user provided

DESCRIPTION

Free text description of the sequence annotationannotation

FILE*

None

TYPE*

None

FILE*

None

TYPE*

None

FILE*

None

TYPE*

None

Submit Annotation

Close

Fig. 4: Sequence Annotations’ submission: ‘Submit Annotation’ dialogue with no sample accession chosen from SAMPLE dropdown menu

Add Sequence Annotation

Submit annotation

Upload annotation files and fill in metadata, you must have already created a study in ENA and have uploaded samples and reads. You will be requested the relative accessions.

STUDY*

PRJEB66432

SAMPLE*

ERS16431676

RUN

ERR12080504

EXPERIMENT

ERX11462871

ANNOTATION TITLE*

Annotation title user provided

DESCRIPTION

Free text description of the sequence annotation

FILE*

None

TYPE*

None

FILE*

None

TYPE*

None

FILE*

None

TYPE*

None

Submit Annotation

Close

Fig. 5: Sequence Annotations’ submission: ‘Submit Annotation’ dialogue with sample accession chosen from SAMPLE dropdown menu

submission. The records will be highlighted **green** after a successful automatic submission.

Profile: El Standalone Profile
Sequence Annotations

Select all Select filtered Clear selection Export CSV + Add Edit Delete Submit

Showing 1 to 1 of 1 records Click beside a record to view extra details

STUDY	SAMPLE	RUN	EXPERIMENT	TITLE	DESCRIPTION	FILES	ACCESSION	SUBMISSION ERROR
PRJEB6432	ERS16431676			Test Annotation		Cafeteria_transcriptome_1.fastq.gz		

show 10 records

Previous 1 Next

Sequence annotation submitting...

Annotation submission has been scheduled, you will be notified when it is complete

Fig. 6: Sequence Annotations' submission: Sequence Annotations' web page displaying the (pending) uploaded sequence annotation(s)

Profile: El Standalone Profile
Sequence Annotations

Select all Select filtered Clear selection Export CSV + Add Edit Delete Submit

Showing 1 to 1 of 1 records Click beside a record to view extra details

STUDY	SAMPLE	RUN	EXPERIMENT	TITLE	DESCRIPTION	FILES	ACCESSION	SUBMISSION ERROR
PRJEB6432	ERS16431676			Test Annotation		Cafeteria_transcriptome_1.fastq.gz	ERZ21822618	

show 10 records

Previous 1 Next

Last Sequence Annotation Submitted - Seq Annotation Access: ERZ21822618

Annotation submission has been scheduled, you will be notified when it is complete

Sequence Annotations' submission: Sequence Annotations' web page displaying the submitted sequence annotation(s)

19.2 How to Delete Sequence Annotations

Note: Sequence annotations can only be deleted **before** they have been submitted.

Click the desired sequence annotation from the list of sequence annotations displayed on the **Sequence Annotations** web page. Then, click the **Delete** button (located in the top-right corner of the table) as shown below:

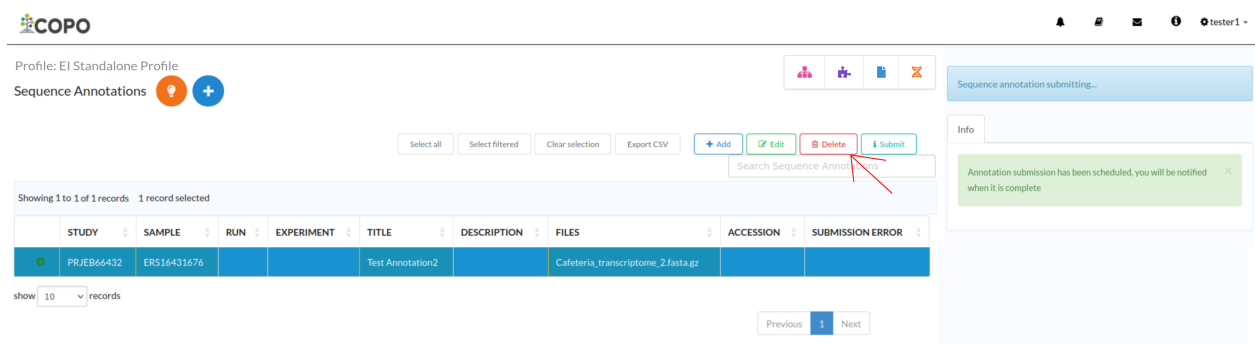


Fig. 7: Sequence annotation deletion: Click the “Delete” button to remove the highlighted sequence annotation from the profile

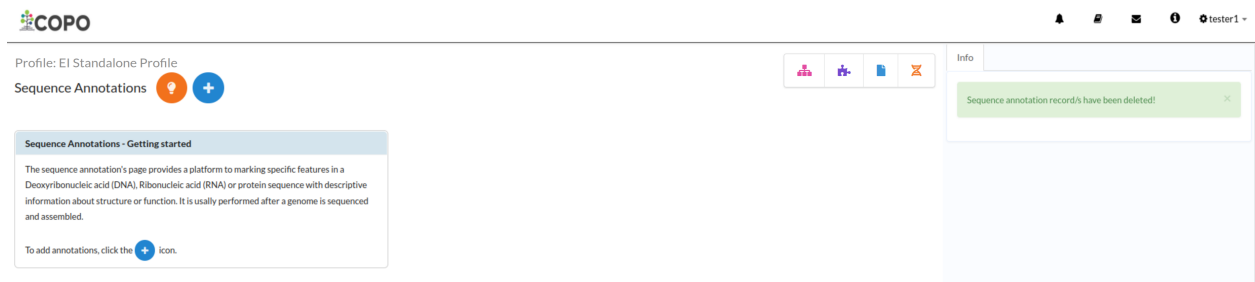



Fig. 8: Sequence annotation deletion: Sequence annotation record has been deleted

UPDATING PROFILES

Warning: Profile types cannot be changed or updated once they have been created. If you need to change the profile type, you will need to delete the profile and create a new one.

See also:

Deleting Profiles

To edit a profile, click the  icon that is associated with the desired profile. The option to edit or delete a profile record will be displayed once clicked.

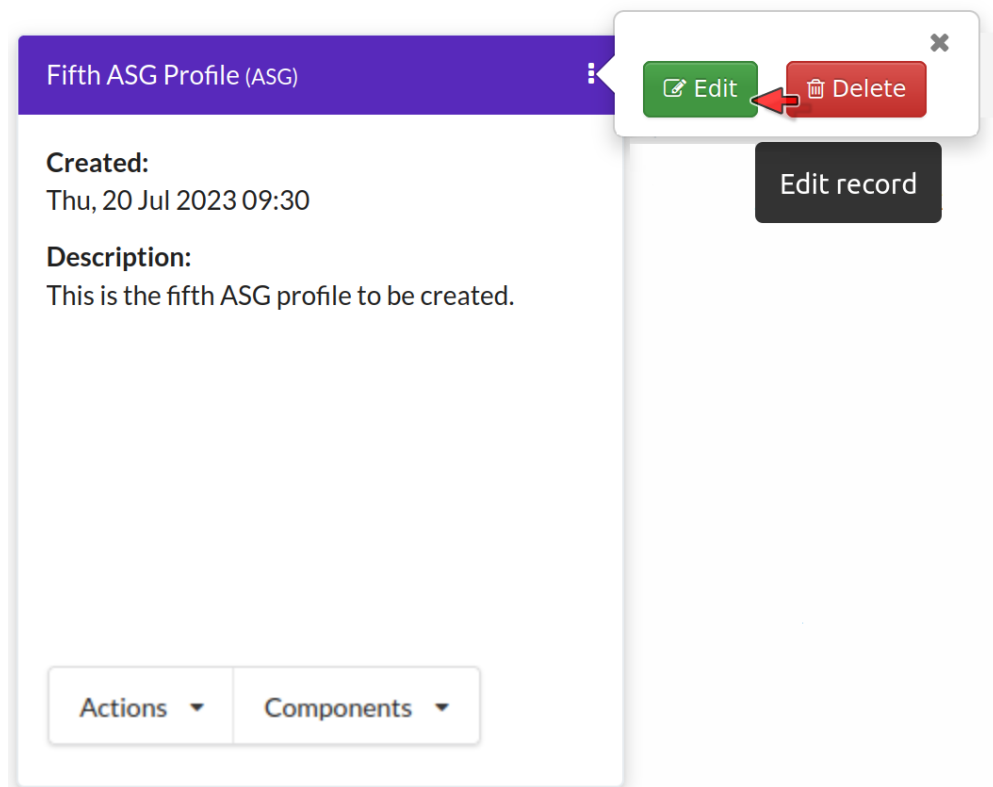


Fig. 1: COPO Profile: Click the Edit button

Edit Profile

Title required ⓘ

Fifth ASG Profile

Description required ⓘ

This is the fifth ASG profile to be created today.

Profile Type ⓘ

Aquatic Symbiosis Genomics (ASG) ▾

Associated Profile Type ⓘ

Select associated type(s)

Cancel

Save

Fig. 2: COPO Profile: Edit the existing details. Click the Save button to update the profile.

COPO

Work Profiles

Sort by: Date Created ▾

Eighteenth ERGA Profile (ERGA)

Created: Thu, 20 Jul 2023 23:38
Description: This is the eighteen ERGA profile to be created.
View more...

Actions ▾ Components ▾

Fifth ASG Profile (ASG)

Created: Thu, 20 Jul 2023 09:30
Description: This is the fifth ASG profile to be created.

Actions ▾ Components ▾

Seventeen ERGA Profile (ERGA)

Created: Thu, 29 Jun 2023 13:02
Description: This is the seventeen profile to be created

Actions ▾ Components ▾

Sixteen ERGA Profile (ERGA)

Created: Thu, 29 Jun 2023 10:49
Description: This is the sixteen ERGA profile to be created.

Actions ▾ Components ▾

Info

Record updated!

Web page will refresh in 3 seconds.

Profile Types Legend

ERGA

ASG

Fig. 3: COPO Profile: Profile record has been updated. Wait 3 seconds for the web page to be automatically reloaded.


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Chapter 20. Updating Profiles

20.1 Deleting Profiles

Note:

- Deleting a profile will **not** delete the associated COPO user account. The user account will still be able to log into the system.
- Only profiles that have no associated research objects such as samples, reads, assemblies or files etc. can be deleted.
- If you need to have a profile deleted that has associated research objects, please contact the .

To delete a profile, click the  icon that is associated with the desired profile. The option to edit or delete a profile record will be displayed once clicked.

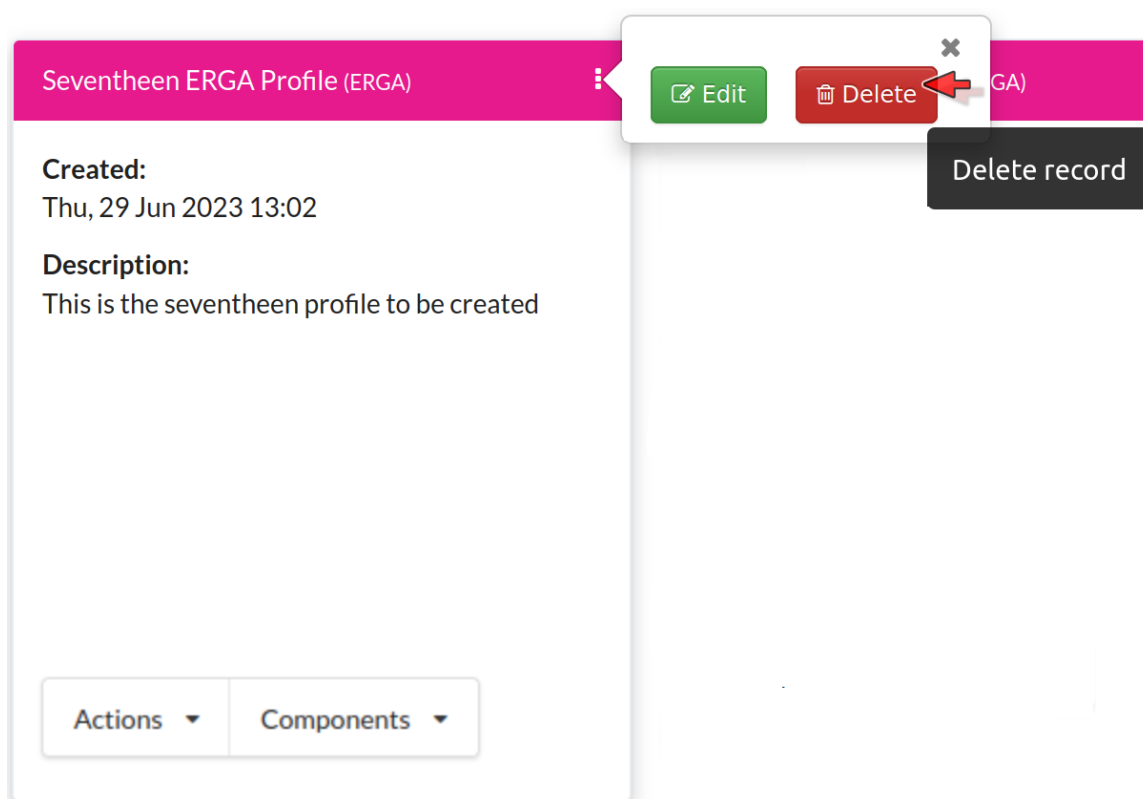


Fig. 4: COPO Profile: Click the Delete button

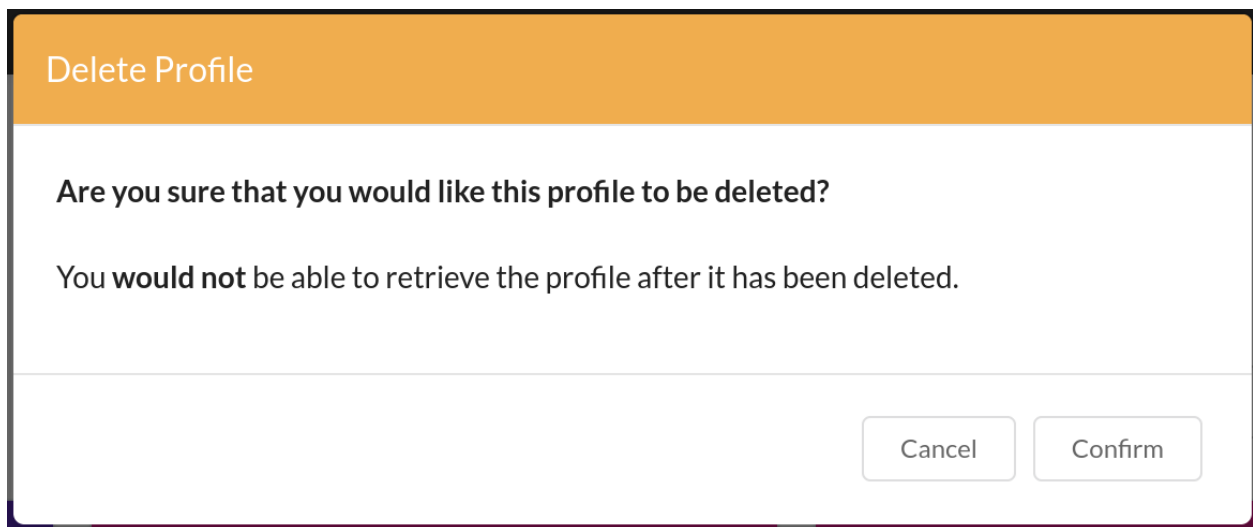


Fig. 5: COPO Profile: A confirmation dialog will appear. Click the Confirm button to confirm the deletion.

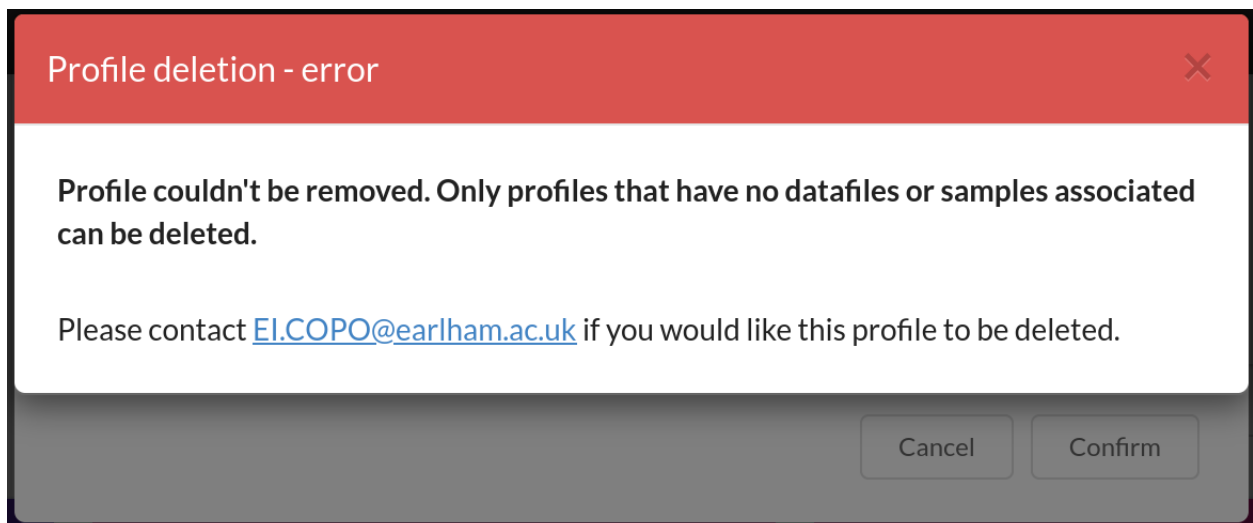


Fig. 6: COPO Profile: An error will occur if you try to remove a profile that that has associated samples or datafiles.

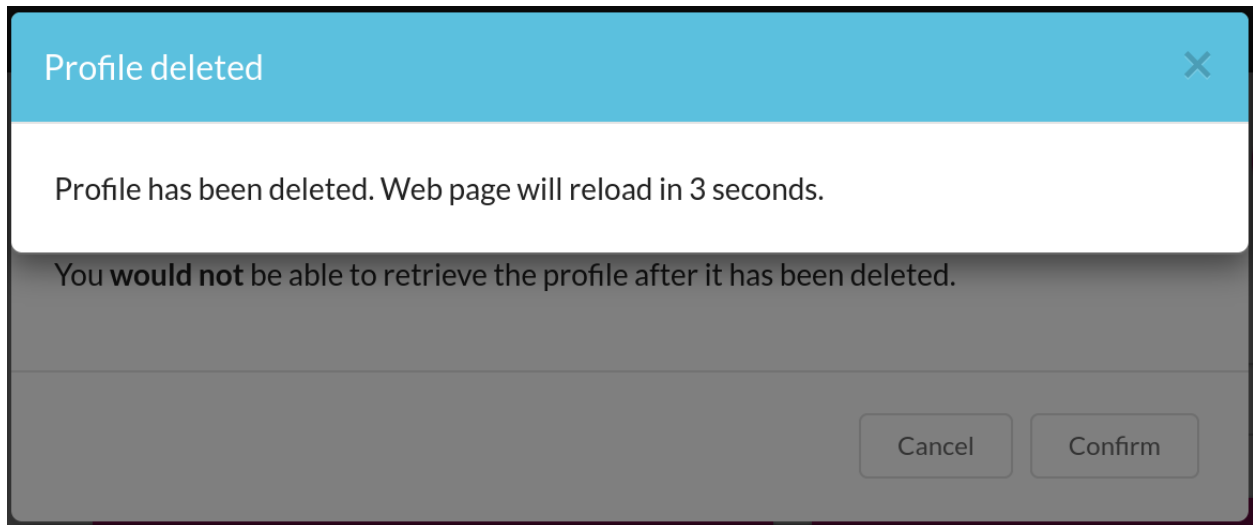


Fig. 7: COPO Profile: Profile record has been deleted. Wait 3 seconds for the web page to be automatically reloaded.

UPDATING SAMPLES

Samples can be updated by reuploading/resubmitting the manifest that was used to create them with the amended changes **before** or **after** the samples have been accepted by a sample manager and submitted to ENA¹.

Please note that not all field values of existing samples can be updated via the manifest resubmission update method. The fields that can be updated with that method are listed below. Those fields are known as *non-compliance fields* while the fields that are not listed or cannot be updated are known as *compliance fields*².

See the [How to Download Submitted Sample Manifest](#) section for guidelines about how to download a manifest that was already submitted.

Hint: To view a list of fields that can be updated for a particular project, collapse the list of fields by clicking the ► button below.

Important: The amended manifest or updated spreadsheet file **must** be uploaded to the same profile that was initially used to upload the manifest (before any modifications were done).

An error will occur if you perform one of the following actions:

- Upload the amended manifest to a different profile³ (other than the one used to upload the manifest to initially)
 - Upload the amended manifest to a new profile
 - Delete a profile that already has samples associated with it
-

Note:

- The manifest must be uploaded again with the amendments included for the change or update to occur.
 - You **cannot** reupload a manifest with some of the existing samples removed. The removed samples (from the reuploaded manifest) will not be automatically removed from the manifest sample record. If you would like existing samples to be removed or deleted from the manifest record, please contact for assistance detailing the profile title and reason for the removal.
 - Fields are also referred to as columns in the manifest.
-

- BARCODE_HUB
- BARCODE_PLATE_PRESERVATIVE
- COLLECTOR_SAMPLE_ID

- CULTURE_OR_STRAIN_ID
- DATE_OF_PRESERVATION
- DEPTH

¹ See term: [ENA](#).

² See term: [Compliance field](#).

³ Also known as COPO profile. See term: [COPO profile](#).

- DIFFICULT_OR_HIGH_PRIORITY_SAMPLE
- ELEVATION
- HAZARD_GROUP
- IDENTIFIED_BY
- IDENTIFIED_HOW
- IDENTIFIER_AFFILIATION
- INFRASPECIFIC_EPITHET
- LIFESTAGE
- PARTNER_SAMPLE_ID
- PLATE_ID_FOR_BARCODING
- PRESERVED_BY
- PRESERVER_AFFILIATION
- PURPOSE_OF_SPECIMEN
- RELATIONSHIP
- SEX
- SIZE_OF_TISSUE_IN_TUBE
- SPECIMEN_ID_RISK
- TIME_ELAPSED_FROM_COLLECTION_TO_PRESERVATION
- TIME_OF_COLLECTION
- TISSUE_FOR_BARCODING
- TISSUE_REMOVED_FOR_BARCODING
- TUBE_OR_WELL_ID_FOR_BARCODING
- VOUCHER_ID
- BARCODE_HUB
- BARCODE_PLATE_PRESERVATIVE
- COLLECTOR_SAMPLE_ID
- CULTURE_OR_STRAIN_ID
- DATE_OF_PRESERVATION
- DEPTH
- DIFFICULT_OR_HIGH_PRIORITY_SAMPLE
- ELEVATION
- GAL_SAMPLE_ID
- HAZARD_GROUP
- IDENTIFIED_BY
- IDENTIFIED_HOW
- IDENTIFIER_AFFILIATION
- INFRASPECIFIC_EPITHET
- LIFESTAGE
- PLATE_ID_FOR_BARCODING
- PRESERVED_BY
- PRESERVER_AFFILIATION
- PURPOSE_OF_SPECIMEN
- RELATIONSHIP
- SEX
- SIZE_OF_TISSUE_IN_TUBE
- SPECIMEN_IDENTITY_RISK
- TIME_ELAPSED_FROM_COLLECTION_TO_PRESERVATION
- TIME_OF_COLLECTION
- TISSUE_FOR_BARCODING
- TISSUE_REMOVED_FOR_BARCODING
- TUBE_OR_WELL_ID_FOR_BARCODING
- VOUCHER_ID
- ASSOCIATED_TRADITIONAL_KNOWLEDGE_CONTACT
- ASSOCIATED_TRADITIONAL_KNOWLEDGE_OR_BIOCULTURE
- ASSOCIATED_TRADITIONAL_KNOWLEDGE_OR_BIOCULTURE
- BARCODE_HUB
- BARCODING_STATUS
- BARCODE_PLATE_PRESERVATIVE
- BIOBANKED_TISSUE_PRESERVATIVE
- COLLECTED_BY
- COLLECTION_LOCATION
- COLLECTOR_AFFILIATION
- COLLECTOR_SAMPLE_ID
- COMMON_NAME
- CULTURE_OR_STRAIN_ID
- DATE_OF_COLLECTION
- DATE_OF_PRESERVATION
- DECIMAL_LATITUDE
- DECIMAL_LONGITUDE
- DEPTH
- DESCRIPTION_OF_COLLECTION_METHOD
- DIFFICULT_OR_HIGH_PRIORITY_SAMPLE
- DNA_REMOVED_FOR_BIOBANKING
- DNA_VOUCHER_ID_FOR_BIOBANKING
- ELEVATION
- ETHICS_PERMITS_DEF
- ETHICS_PERMITS_FILENAME
- ETHICS_PERMITS_REQUIRED
- FAMILY
- GAL_RIGHTS_APPLICABLE
- GAL_SAMPLE_ID
- GENUS
- GRID_REFERENCE
- HABITAT
- HAZARD_GROUP
- IDENTIFIED_BY
- IDENTIFIED_HOW
- IDENTIFIER_AFFILIATION
- IDENTIFIER_AFFILIATION
- INDIGENOUS_RIGHTS_APPLICABLE
- INDIGENOUS_RIGHTS_DEF
- INDIGENOUS_RIGHTS_DEF
- INFRASPECIFIC_EPITHET
- LIFESTAGE
- NAGOYA_PERMITS_DEF
- NAGOYA_PERMITS_FILENAME
- NAGOYA_PERMITS_REQUIRED
- ORDER_OR_GROUP
- ORGANISM_PART

- ORIGINAL_COLLECTION_DATE
- ORIGINAL_GEOGRAPHIC_LOCATION
- OTHER_INFORMATION
- PRESERVATION_APPROACH
- PRESERVATIVE_SOLUTION
- PRESERVED_BY
- PRESERVER_AFFILIATION
-
- PROXY_TISSUE_VOUCHER_ID_FOR_BIOBANKING
- PROXY_VOUCHER_ID
- PROXY_VOUCHER_LINK
- PURPOSE_OF_SPECIMEN
- REGULATORY_COMPLIANCE
- RELATIONSHIP
- SAMPLE_COORDINATOR
- SAMPLE_COORDINATOR_AFFILIATION
- SAMPLE_COORDINATOR_ORCID_ID
- SAMPLING_PERMITS_FILENAME
- SAMPLING_PERMITS_REQUIRED
- SCIENTIFIC_NAME
- SEX
- SIZE_OF_TISSUE_IN_TUBE
- SPECIMEN_IDENTITY_RISK
- TAXON_ID
- TAXON_REMARKS
-
- TIME_ELAPSED_FROM_COLLECTION_TO_PRESERVATION
- TIME_OF_COLLECTION
- TISSUE_FOR_BARCODING
- TISSUE_FOR_BIOBANKING
- TISSUE_REMOVED_FOR_BARCODING
- TISSUE_REMOVED_FOR_BIOBANKING
- TISSUE_REMOVED_FROM_BARCODING
- TISSUE_VOUCHER_ID_FOR_BIOBANKING
- TUBE_OR_WELL_ID_FOR_BARCODING
- VOUCHER_ID
- VOUCHER_INSTITUTION
- VOUCHER_LINK

UPDATING SEQUENCE ANNOTATIONS

This section describes how to update **Sequence Annotations**¹. The **Sequence Annotations** update process is similar to the **Sequence Annotations** submission process. Therefore, please refer to the [Sequence Annotations Submission](#) section for more information.

Note:

- Sequence Annotations must be uploaded before they can be updated.

See also:

- [How to Submit Sequence Annotations](#)
- [How to Delete Sequence Annotations](#)

1. Click the desired sequence annotation from the table of uploaded sequence annotations to highlight it.

Then, click the **Edit** button to update or edit the annotation as shown below:

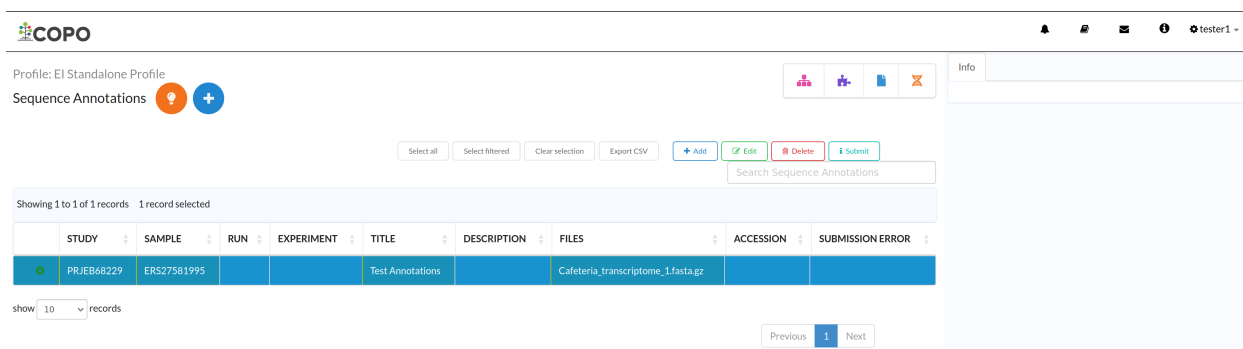


Fig. 1: **Sequence Annotations’ update: Click ‘Edit’ button after having clicked the desired sequence annotation**

2. An **Add Sequence Annotation** dialogue is displayed. Provide the updated details then, click the **Submit Annotation** button.
3. The updated sequence annotation(s) will be displayed on the **Sequence Annotations** web page after a successful update.

¹ See: [Sequence Annotation](#).

Add Sequence Annotation

Submit annotation

Upload annotation files and fill in metadata, you must have already created a study in ENA and have uploaded samples and reads. You will be requested the relative accessions.

STUDY*

PRJEB68229

SAMPLE*

ERS27581995

RUN

ERR12208020

EXPERIMENT

ERX11618893

ANNOTATION TITLE*

Test Annotations

DESCRIPTION

This sequence annotation describes sites of interest in the protein sequence namely post-translational modifications and binding sites.

FILE*

Cafeteria_transcriptome_1.fasta.v

TYPE*

fasta

FILE*

None

TYPE*

None

FILE*

None

TYPE*

None

FILE*

None

TYPE*

None

Submit Annotation

Close

Fig. 2: Sequence Annotations’ update: ‘Submit Annotation’ dialogue with updated information

Hint: Sequence annotation records that are highlighted **yellow** indicate that the records are pending submission. The records will be highlighted **green** after a successful automatic submission.

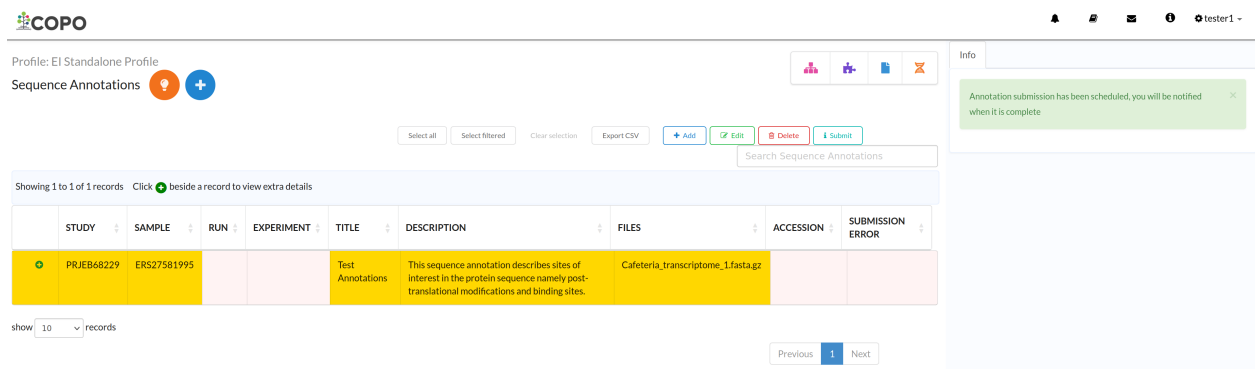
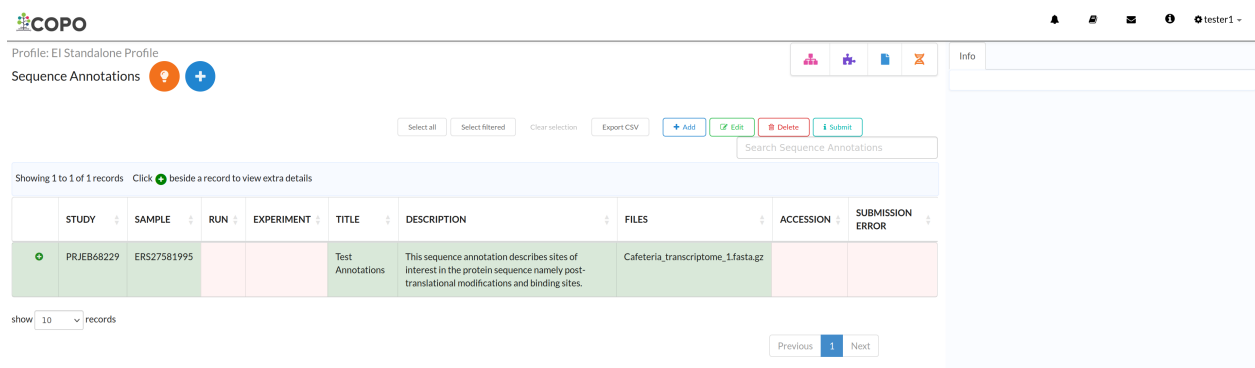


Fig. 3: Sequence Annotations’ update: Sequence Annotations’ web page displaying the (pending) updated sequence annotation(s)



Sequence Annotations’ update: Sequence Annotations’ web page displaying the updated sequence annotation(s) after it has been submitted

UPDATING READS

This section describes how to update **Reads** for a given checklist. The **Reads** update process is similar to the **Reads** submission process. Therefore, please refer to the [Reads Submission](#) section for more information.

Note:


- Reads must be uploaded before they can be updated.

See also:

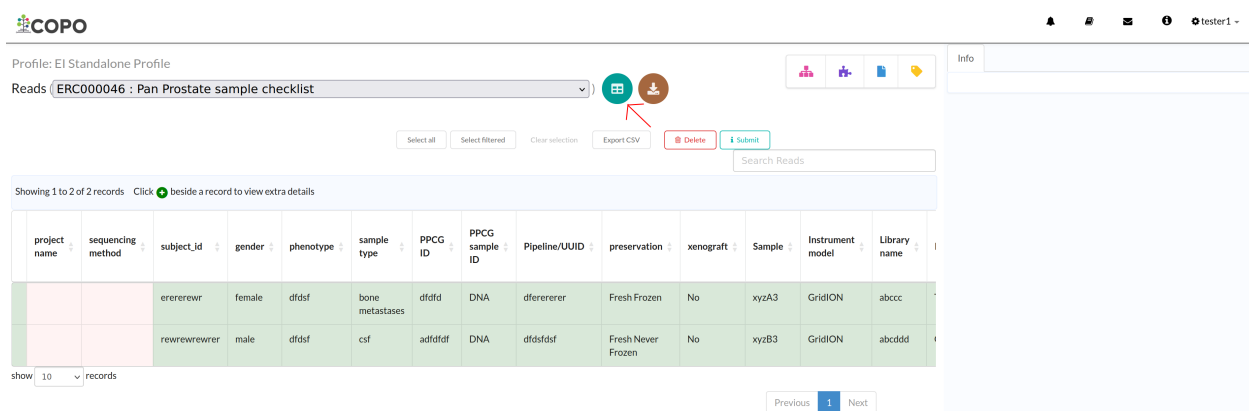
- [How to Submit Reads](#)
- [Explore Various Types of Reads Checklist](#)
- [How to Submit Files](#)

1. On the **Reads** web page, click the checklist dropdown then, choose a desired checklist from the list of available checklists that you would like to update a **Reads** for.

Then, click the  button as shown below to update a Reads for the chosen checklist as shown below:

Note: The colour of the  button is based on the type of profile that you are updating a Reads for.

See the [Profile Types Legend](#) section regarding the colour code for the various types of project profiles on COPO.




COPO

Profile: EI Standalone Profile

Reads (ERC000046 : Pan Prostate sample checklist)

Select all Select filtered Clear selection Export CSV Delete Submit

Showing 1 to 2 of 2 records Click  beside a record to view extra details

project name	sequencing method	subject_id	gender	phenotype	sample type	PPCG ID	PPCG sample ID	Pipeline/UUID	preservation	xenograft	Sample	Instrument model	Library name
		erererwr	female	dfdsf	bone metastases	dfdfdf	DNA	dfdfdfdf	Fresh Frozen	No	xyzA3	GridION	abccc
		rewrewrewr	male	dfdsf	csf	adfdfdf	DNA	dfdsfdfd	Fresh Never Frozen	No	xyzB3	GridION	abccdd

show 10 records

Previous 1 Next

Fig. 1: Reads' update: Click 'Add Reads' from Spreadsheet' button to upload an amended reads manifest

- An **Upload Read Manifest** dialogue is displayed. Click the **Upload Read Manifest** button to choose an updated file from your local system.

The uploaded manifest is shown in a table in the **Upload Read Manifest** dialogue as shown below. Click the **Finish** button to complete the update process of the reads manifest.

Upload Read Manifest

ENA Reads Manifest Validation
for **ERC000046 : Pan Prostate sample checklist**

Upload a completed manifest for validation

Spreadsheet is valid

Show 10 entries Search:

CG nple	Pipeline/UUID	Sample	gender	phenotype	preservation
JA	dferererer	xyzA3	female	dfdsf	Fresh Frozen
JA	dfdsfdf	xyzB3	female	dfdsf	Fresh Never Frozen

Showing 1 to 2 of 2 entries Previous 1 Next

Upload Read Manifest Finish Close

Fig. 2: **Reads' update: 'Upload Read Manifest' dialogue with updated manifest**

- The update read(s) will be displayed on the **Reads** web page after a successful update.

Hint: Reads records that are highlighted **yellow** indicate that the records are pending submission. The records will be highlighted **green** after a successful submission.

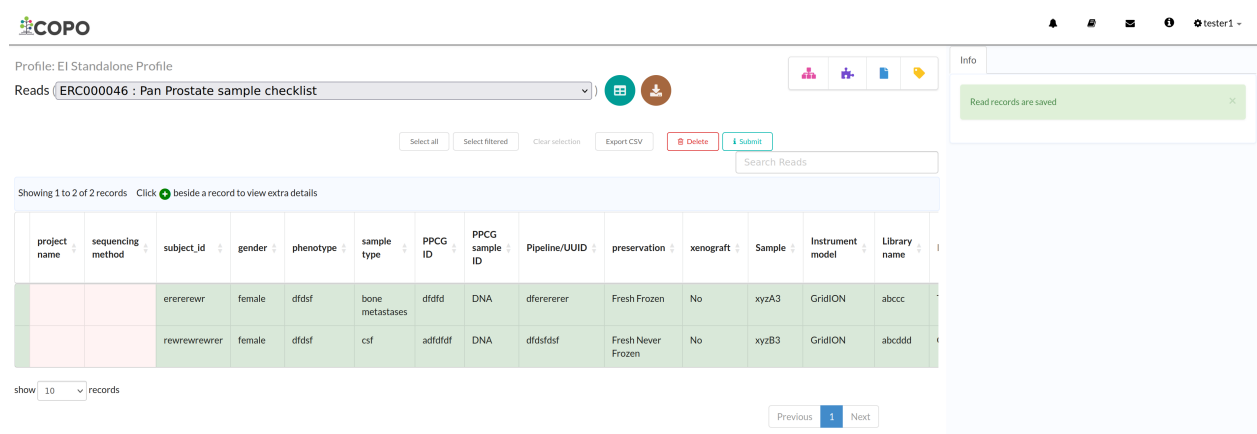


Fig. 3: Reads' update: Reads' web page displaying the updated read(s)

ADDING CHILDREN PROJECTS TO PARENT PROJECTS

24.1 In COPO

See *Choose associated profile type(s)* section when creating a profile for more details.

24.2 In Public Repositories

Please contact the if you would like child projects (subprojects) to be added to parent (main) projects in public repositories like ENA¹ or NCBI².

Please provide the parent project accession and the child project accession(s) when making the email request.

¹ See term: *ENA*.

² See term: *NCBI*.

DOWNLOADING MANIFEST TEMPLATES & STANDARD OPERATING PROCEDURES (SOPS)

In COPO, *manifests* refer to Microsoft Excel spreadsheets that are used to record metadata about a biological research.

25.1 Downloading Manifest Templates

Blank manifest templates are available for download below or on the [Manifests web page](#).

In addition, click the  button located on the COPO **Samples** web page to download a manifest template. See samples-component component for more details about accessing the **Samples** web page.

ASG manifest template¹

DTOL manifest template²

ERGA manifest template³

Barcoding manifest template (within Tree of Life profiles)

Reads manifest template (within Tree of Life profiles)

Note:

- The manifest templates for reads within Stand-alone profiles are available for download on the **Reads web page** for those profiles. See *Reads Submission* section for more details.
- Barcoding manifest templates are available for download on the Barcoding manifest web page. See *Barcoding Manifest Submission* section for more details.

¹ See term: *ASG (Aquatic Symbiosis Genomics)*.


² See term: *DTOL (Darwin Tree of Life)*.

³ See term: *ERGA (European Reference Genome Atlas)*.

25.2 Recording Data in Manifests

Each manifest follow a manual known as *Standard Operating Procedure (SOP)*⁴ which provides a detailed guidance on how to record metadata in the manifest.

The SOP for the various manifests are available below.

In addition, click the  button located on the COPO **Samples** web page to download the SOP. See samples-component component for more details about accessing the **Samples** web page.

25.2.1 ASG SOP

This follows most of the instructions outlined in the DToL SOP, with some minor changes and omissions.

ASG SOP

[ASG Project](#)

25.2.2 DToL (Darwin Tree of Life) SOP

DToL SOP

[DToL SOP GitHub repository](#)

[DToL Project](#)

25.2.3 DToL_ENV (Darwin Tree of Life Environmental Samples) SOP

This will be made available soon.

25.2.4 ERGA SOP

ERGA SOP

[ERGA SOP GitHub repository](#)

25.2.5 POP_GENOMICS (Population Genomics) SOP

POP_GENOMICS SOP

[ERGA SOP GitHub repository](#)


See also:

- *Using manifest wizard to prefill manifests*

⁴ See term: *SOP*.

USING COPO API

The **COPO API** is a RESTful website service that allows users to interact with the COPO system. The API is built using the Django REST (REpresentational State Transfer)¹ Framework.

Hint: The button, , indicates that the API method endpoints will produce results from the website host server i.e. if the live COPO website is used to query the endpoint, then, the live results will be retrieved while the opposite occurs if one uses the demo website to query the API method endpoints.

26.1 API End-points

The COPO API (Application Programming Interface)² comprises manifest, sample, statistics and profile endpoints. Their results are available for download in csv, json or ro-crate³ file formats depending on the record type as shown in the table below.

Each endpoint results contain metadata provided by the submitter.

Table 1: Available Result Formats for Records

File Format	Available Record Types
csv	Audit, Sample, Manifest
json	Audit, Sample, Manifest
ro-crate	Sample

Note: The live COPO website API endpoints are used in the examples below.

To use the demo website API endpoints, replace `https://copo-project.org/api/` with `https://demo.copo-project.org/api/` in the examples below.

¹ See term: *REST*

² See term: *API*

³ See term: *RO-Crate*

26.1.1 Audit Endpoints

Fetch Sample Updates Between Dates

```
https://copo-project.org/api/audit/sample/{from}/{to}
```

OR

```
$ curl -X GET "https://copo-project.org/api/audit/sample/{from}/{to}" -H "accept:↵↵application/json"
```

This results in a list of sample updates that occurred between a given date period.

Fetch Sample Updates by Manifest ID

```
https://copo-project.org/api/audit/sample/manifest_id/{manifest_id}
```

OR

```
$ curl -X GET "https://copo-project.org/api/audit/sample/manifest_id/{manifest_id}" -H↵↵"accept: application/json"
```

This results in a list of sample updates by manifest IDs (Identifications)⁴.

Fetch Sample Updates by COPO ID

```
https://copo-project.org/api/audit/sample/{copo_id}
```

OR

```
$ curl -X GET "https://copo-project.org/api/audit/sample/copo_id/{copo_id}" -H "accept:↵↵application/json"
```

This results in a list of sample updates based on {copo_id}.

Fetch Sample Updates by Update Type

```
https://copo-project.org/api/audit/sample/update_type/{update_type}
```

OR

```
$ curl -X GET "https://copo-project.org/api/audit/sample/update_type/{update_type}" -H↵↵"accept: application/json"
```

This results in a list of sample updates based who performed the update. The `update_type` can be **system** or **user**.

A **system** update occurs when the update was performed by COPO while a **user** update occurs when a user reuploads a manifest with amended sample metadata.

Please note that not all sample information that has been uploaded already can be updated when the manifest is reuploaded. Only fields that are updatable are updated when a manifest is reuploaded.

⁴ See term: *Manifest ID*

See the *Updating Samples* section for more information as well as the *Fetch updatable fields by project* API method.

Fetch Sample Updates by Field and Field Value

```
https://copo-project.org/api/audit/sample/{field}/{field_value}
```

OR

```
$ curl -X GET "https://copo-project.org/api/audit/sample/{field}/{field_value}" -H
↪ "accept: application/json"
```

This results in a list of sample updates based on a sample field value and one of the following sample fields:

- RACK_OR_PLATE_ID
- SPECIMEN_ID
- TUBE_OR_WELL_ID
- biosampleAccession
- public_name
- sraAccession

Fetch Sample Updates by ASG Sample Type

```
https://copo-project.org/api/audit/sample/asg
```

OR

```
$ curl -X GET "https://copo-project.org/api/audit/sample/asg" -H "accept: application/
↪ json"
```

This results in a list of updates for ASG⁸. sample types.

Fetch Sample Updates by DTOL Sample Type

```
https://copo-project.org/api/audit/sample/dtol
```

OR

```
$ curl -X GET "https://copo-project.org/api/audit/sample/dtol" -H "accept: application/
↪ json"
```

This results in a list of updates for DTOL⁹. sample types.

⁸ See term: *DTOL*

⁹ See term: *ENA*

Fetch Sample Updates by ERGA Sample Type

```
https://copo-project.org/api/audit/sample/erga
```

OR

```
$ curl -X GET "https://copo-project.org/api/audit/sample/erga" -H "accept: application/
↪ json"
```

This results in a list of updates for ERGA¹⁰ sample types.

26.1.2 Manifest Endpoints

Fetch Manifests

```
https://copo-project.org/api/manifest
```

OR

```
$ curl -X GET "https://copo-project.org/api/manifest" -H "accept: application/json"
```

This results in a list of all manifest IDs^{Page 136, 4}. The manifest identification can be used to retrieve records in the other endpoints.

Fetch Manifests by Sequencing Centre

```
https://copo-project.org/api/manifest/sequencing_centre?sequencing_centre=<sequencing-
↪ centre>
```

OR

```
$ curl -X GET "https://copo-project.org/api/manifest/sequencing_centre?sequencing_centre=
↪ <sequencing-centre>" -H "accept: application/json"
```

This results in a list of manifest IDs^{Page 136, 4} that are associated with the given sequencing_centre. In the API URL, replace <sequencing-centre> with the name of the sequencing centre.

The manifest identification can be used to retrieve records in the other endpoints.

Fetch Current Manifest Versions

```
https://copo-project.org/api/manifest/current_version
```

OR

```
$ curl -X GET "https://copo-project.org/api/manifest/current_version" -H "accept:
↪ application/json"
```

This displays the current or latest manifest version of each manifest project brokered through COPO.

¹⁰ See term: *Sample manager*

Validate Manifest by Profile ID

Note: Authentication is required in order to use this API method. Obtain an API token from the following endpoint before using this method:

```
https://copo-project.org/api/manifest/validate
```

This results in the ID of the validation report to be queried.

Validate Manifest by Report ID

Note: Authentication is required in order to use this API method. Obtain an API token from the following endpoint before using this method:

```
https://copo-project.org/api/manifest/validate/report/
```

OR

```
$ curl -X POST "https://copo-project.org/api/manifest/validate/report/" -H "accept: */*"
↪ -H "Content-Type: application/x-www-form-urlencoded" -d "validation_report_id=
↪ {report-id}
```

This gives the status and/or validation errors for a manifest based on the manifest report ID.

Validate Manifest

Note: Authentication is required in order to use this API method. Obtain an API token from the following endpoint before using this method:

```
https://copo-project.org/api/apiKey
```

```
https://copo-project.org/api/manifest/validations
```

OR

```
$ curl -X POST "https://copo-project.org/api/manifest/validations/" -H "accept: */*" -d
↪ ""
```

This checks whether a given manifest passes or fails validation for the authorised user.

26.1.3 Sample Endpoints

Fetch Sample Records by Project

```
https://copo-project.org/api/sample/{project}
```

OR

```
$ curl -X GET "https://copo-project.org/api/sample/{project}" -H "accept: application/
↪ json"
```

This results in a list of all the samples of a project in COPO.

Fetch Sample Records by Associated Project Type

Hint: The associated project type is the project type that the sample is subproject of. For example, a sample may be associated with a project type of “BGE” but the sample itself may be an “ERGA” sample.

In sample records, the associated project type is referred to as **associated_tol_project** whereas in profile records, it is referred to as **associated_type**.

```
https://copo-project.org/api/sample/associated_tol_project/{values}
```

OR

```
$ curl -X GET "https://copo-project.org/api/sample/associated_tol_project/{values}" -H
↪ "accept: application/json"
```

This results in a list of all sample records of a given associated project type(s) in COPO.

Fetch Sample Project Fields by Manifest Version

```
https://copo-project.org/api/sample/project/manifest_version/fields
```

OR

```
$ curl -X GET "https://copo-project.org/api/sample/project/manifest_version/fields" -H
↪ "accept: application/json"
```

This results in a list of sample fields by project and manifest version.

If no manifest version is provided, the latest manifest version is used. If no project is provided, all project types are used.

Fetch Sample Records between Dates

```
https://copo-project.org/api/sample/project/manifest_version/fields
```

OR

```
$ curl -X GET "https://copo-project.org/api/sample/project/manifest_version/fields" -H  
↪ "accept: application/json"
```

This results in a list of fields of a project for a given manifest version.

Fetch Sample Records between Dates

```
https://copo-project.org/api/sample/{from}/{to}
```

OR

```
$ curl -X GET "https://copo-project.org/api/sample/{from}/{to}" -H "accept: application/  
↪ json"
```

This results in a list of all samples recorded in the given date period.

Fetch Updatable Fields by Project

```
https://copo-project.org/api/sample/updatable_fields/{project}
```

OR

```
$ curl -X GET "https://copo-project.org/api/sample/updatable_fields/{project}" -H  
↪ "accept: */*"
```

This results in list of fields that can be updated when a manifest is reuploaded/resubmitted in COPO based on the given {project}.

Fetch Sample Records by COPO ID

Hint:

- Sample records IDs are referred to as `copo_id` in COPO and `alias` in ENA.
 - Multiple `copo_id` can be provided as a comma separated list in this endpoint.
-

```
https://copo-project.org/api/sample/copo_id/{copo_ids}
```

OR

```
$ curl -X GET "https://copo-project.org/api/sample/copo_id/{copo_ids}" -H "accept:  
↪ application/json"
```

This results in full sample information for the sample records returned from the given {copo_ids}.

Fetch Sample Records by Biosample ID

Note:

- Biosample accession IDs are assigned to sample records by ENA^{Page 137, 9} after the samples have been approved by a sample manager^{Page 138, 10}.
- The biosample_id is referred to as biosampleAccession in COPO and biosample_id in ENA.

```
https://copo-project.org/api/sample/biosample_id/{biosample_ids}
```

OR

```
$ curl -X GET "https://copo-project.org/api/sample/biosample_id/{biosample_ids}" -H
  ↳ "accept: application/json"
```

This results in full sample information for the sample records returned from the given {biosample_ids}.

Fetch Sample Records by Field and Values

Hint:

- Multiple values can be provided as a comma separated list in this endpoint.

```
https://copo-project.org/api/sample/sample_field/{field}/{values}
```

OR

```
$ curl -X GET "https://copo-project.org/api/sample/sample_field/{field}/{values}" -H
  ↳ "accept: application/json"
```

This results in full sample information for the sample records returned from the given {field}/{values}.

Fetch Sample Records by Sequencing Centre

```
https://copo-project.org/api/sample/sequencing_centre?sequencing_centre=<sequencing-
  ↳ centre>
```

OR

```
$ curl -X GET "https://copo-project.org/api/sample/sequencing_centre?sequencing_centre=
  ↳ <sequencing-centre>" -H "accept: application/json"
```

This results in full sample information for the sample records based on the given sequencing_centre. In the API URL, replace <sequencing-centre> with the name of the sequencing centre.

Fetch Study Records by Sample ID

Hint:

- Multiple `sample_ids` can be provided as a comma separated list in this endpoint.
-

```
https://copo-project.org/api/sample/StudyFromSampleAccession/{sample_ids}
```

OR

```
$ curl -X GET "https://copo-project.org/api/sample/StudyFromSampleAccession/{sample_ids}" -H "accept: application/json"
```

This results in full sample information for the sample records returned from the given `{sample_ids}`.

Fetch Sample Records by Study ID

Hint:

- Multiple `biostudyAccessions` can be provided as a comma separated list in this endpoint.
-

```
https://copo-project.org/api/sample/SampleFromStudyAccession/{biostudyAccessions}
```

OR

```
$ curl -X GET "https://copo-project.org/api/sample/SampleFromStudyAccession/{biostudyAccessions}" -H "accept: application/json"
```

This results in full sample information for the sample records returned from the given `{biostudyAccessions}`.

26.1.4 Profile Endpoints

Create Profile Record

Note: Authentication is required in order to use this API method. Obtain an API token from the following endpoint before using this method:

```
https://copo-project.org/api/apiKey
```

```
https://copo-project.org/api/profile/make_profile
```

OR

```
$ curl -X POST "https://copo-project.org/api/profile/make_profile" -H "accept: */*" -d ""
```

This creates a profile record for the authenticated user.

Fetch Profile Records

Note: Authentication is required in order to use this API method. Obtain an API token from the following endpoint before using this method:

```
https://copo-project.org/api/apiKey
```

```
https://copo-project.org/api/profile/get_for_user
```

OR

```
$ curl -X POST "https://copo-project.org/api/profile/get_for_user" -H "accept: */*" -d "
```

This results in a list of all profiles for the authenticated user.

26.1.5 Statistics' Endpoints

Fetch Number of COPO Users

```
https://copo-project.org/api/stats/number_of_users
```

OR

```
$ curl -X GET "https://copo-project.org/api/stats/number_of_users" -H "accept: application/json"
```

This results in the total number of registered users in COPO.

Fetch Number of Sample Records by Sample Type and Date

```
https://copo-project.org/api/stats/number_of_samples
```

OR

```
$ curl -X GET "https://copo-project.org/api/stats/number_of_samples" -H "accept: application/json"
```

This results in the total number of registered sample records in COPO by a given sample type and date.

If no sample type is provided and no start date and end date are provided, COPO will return the total number of samples.

Fetch Tree of Life (ToL) Projects Brokered by COPO

```
https://copo-project.org/api/stats/tol_projects
```

OR

```
$ curl -X GET "https://copo-project.org/api/stats/tol_projects" -H "accept: application/↵json"
```

This results in a list of all main/primary projects brokered by COPO.

Fetch Associated Tree of Life (ToL) Projects Brokered by COPO

```
https://copo-project.org/api/stats/associated_tol_projects
```

OR

```
$ curl -X GET "https://copo-project.org/api/stats/associated_tol_projects" -H "accept:↵application/json"
```

This results in a list of all child projects/ subprojects brokered by COPO.

EXPLORING MANIFEST WIZARD

The manifest wizard is a tool to help you populate a manifest with common data values. It is a simple wizard that will ask a few questions then, generate the manifest file for you.

The manifest wizard can be accessed via the **Prefilled template** download dropdown menu option on the [Manifests web page](#).

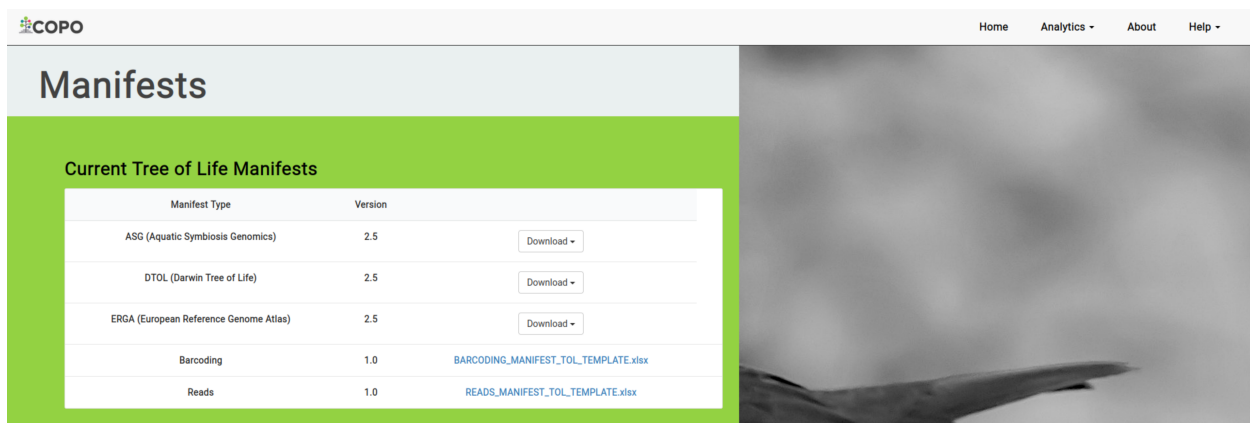


Fig. 1: Manifests web page: Tabular information for various manifest types and their current versions

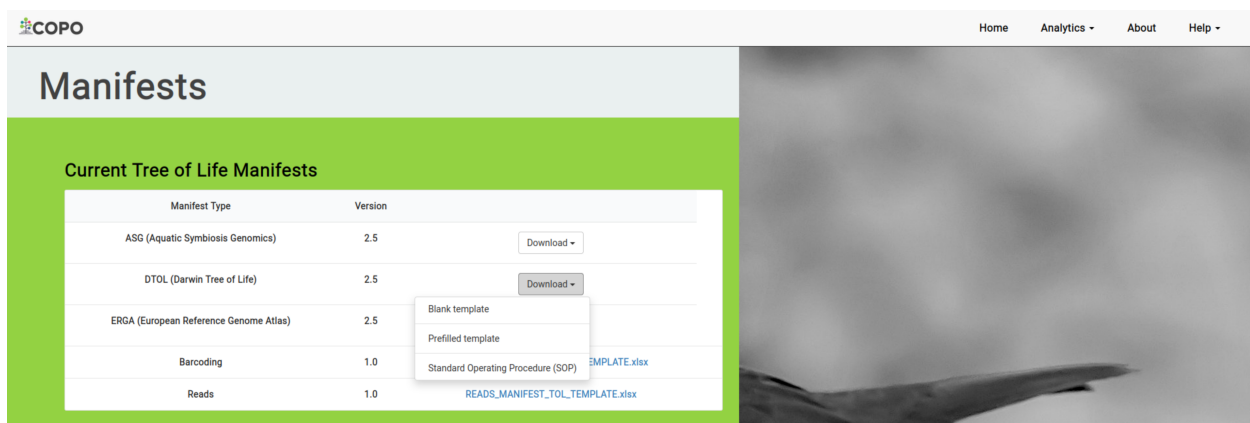


Fig. 2: Manifests web page: Manifest download template options - Blank template and Prefilled template with option to download, Standard Operating Procedure (SOP)

Blank manifest templates can be downloaded via the **Blank template** dropdown menu option or from the [Download Manifest Templates](#) section.

27.1 Prefill Manifests

1. Navigate to the [Manifests web page](#). Then, click the **Prefilled template** option from the dropdown menu.

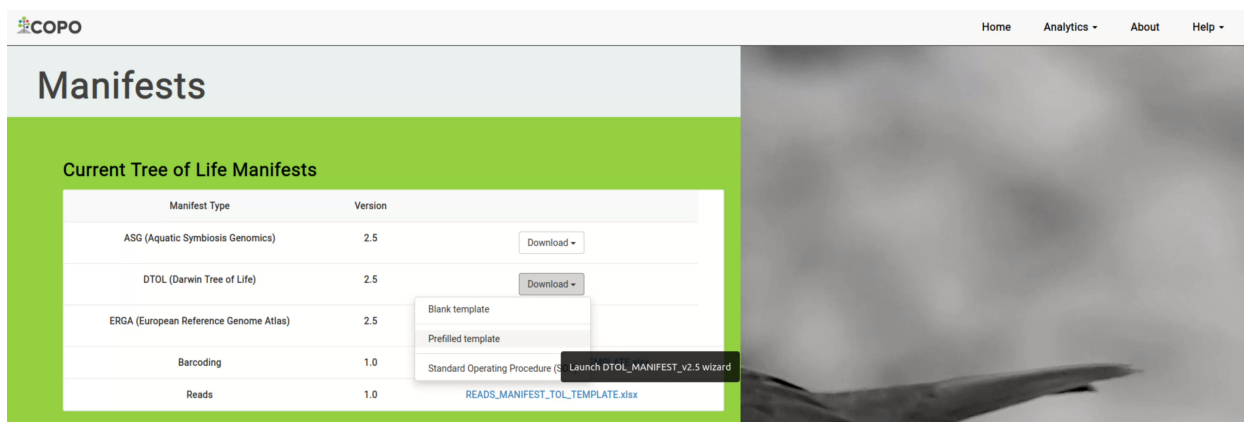




Fig. 3: Manifests web page: Click ‘Prefilled template’ dropdown menu option

2. In the **Tree of Life Manifest Wizard** displayed, enter the number samples that you would like to describe then, input a common value for a field by selecting the field name from the dropdown list.

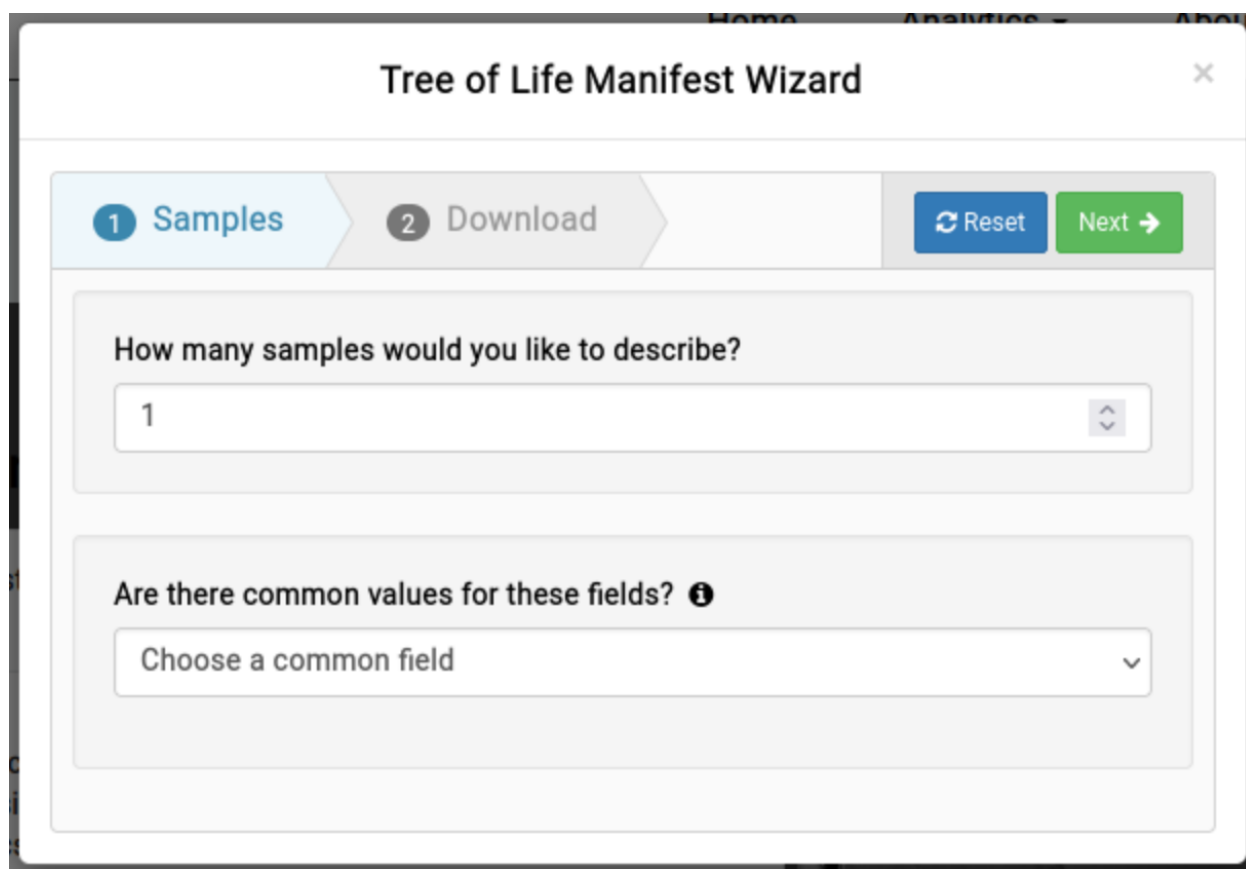
Note: The manifest wizard will only display fields that are associated with the type of manifest that you would like to prefill.

Once you have inputted a value for a common field, that value will be prefilled according to the number of samples that you have inputted.

3. Click the  to proceed to the next step of the manifest wizard.
4. Click the  button to download the prefilled manifest file.
5. Preview of downloaded manifest with prefilled metadata

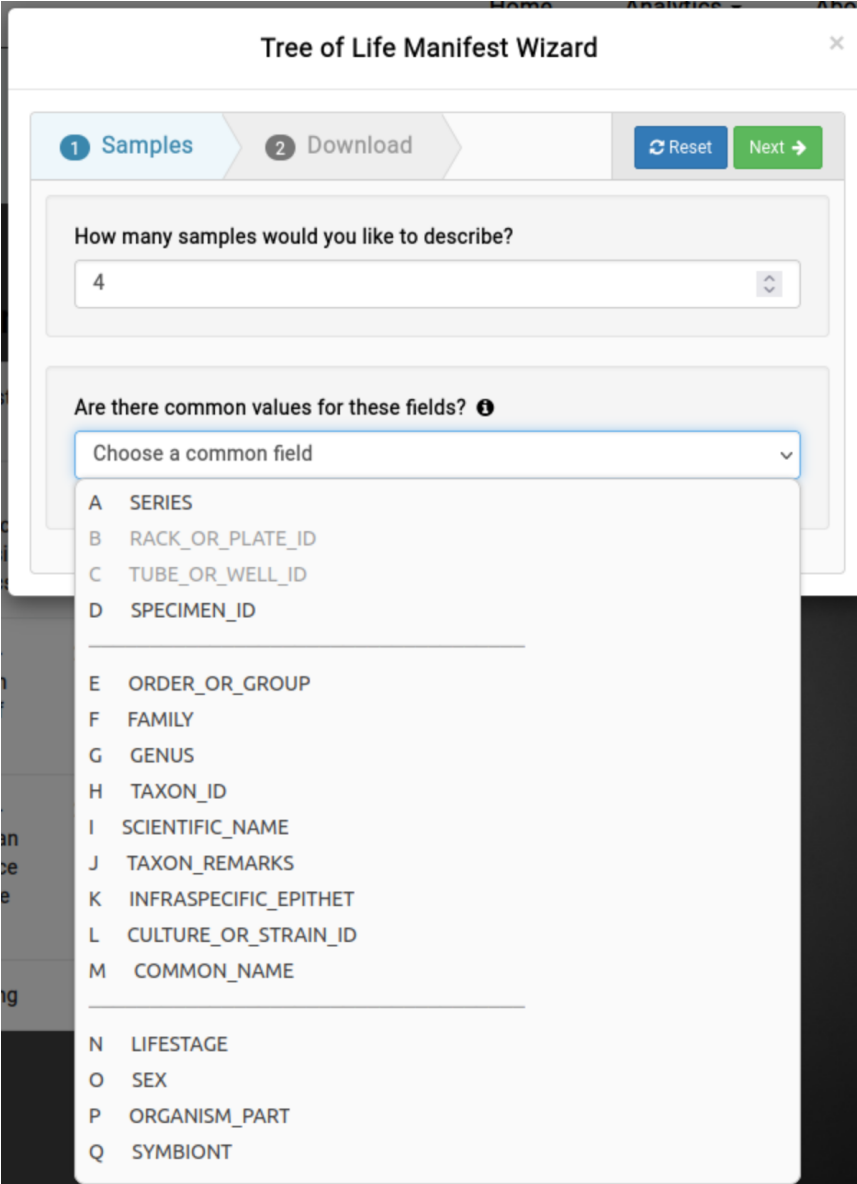
See also:

- [Standard Operating Procedure \(SOP\) guidelines](#) for manifests
- [Download Manifest Templates](#)



The image shows a web browser window displaying the 'Tree of Life Manifest Wizard'. The window has a title bar with a close button (X) in the top right corner. The main content area is divided into two steps: '1 Samples' (highlighted in light blue) and '2 Download' (in grey). To the right of the steps are two buttons: a blue 'Reset' button with a circular arrow icon and a green 'Next →' button. Below the steps, there are two input sections. The first section asks 'How many samples would you like to describe?' and features a text input field containing the number '1' and a small up/down arrow icon on the right. The second section asks 'Are there common values for these fields?' followed by an information icon (i). Below this question is a dropdown menu with the text 'Choose a common field' and a downward-pointing chevron icon.

Fig. 4: Manifests web page: Tree of Life Manifest wizard



The screenshot shows the 'Tree of Life Manifest Wizard' interface. At the top, there are two steps: '1 Samples' and '2 Download'. The 'Download' step is active. Below the steps, there are two main sections. The first section asks 'How many samples would you like to describe?' with a dropdown menu showing the value '4'. The second section asks 'Are there common values for these fields?' with a dropdown menu showing 'Choose a common field'. A list of common fields is displayed below the dropdown menu, including SERIES, RACK_OR_PLATE_ID, TUBE_OR_WELL_ID, SPECIMEN_ID, ORDER_OR_GROUP, FAMILY, GENUS, TAXON_ID, SCIENTIFIC_NAME, TAXON_REMARKS, INFRASPECIFIC_EPITHET, CULTURE_OR_STRAIN_ID, COMMON_NAME, LIFESTAGE, SEX, ORGANISM_PART, and SYMBIONT.

Tree of Life Manifest Wizard

1 Samples 2 Download

Reset Next →

How many samples would you like to describe?

4

Are there common values for these fields? ⓘ

Choose a common field

- A SERIES
- B RACK_OR_PLATE_ID
- C TUBE_OR_WELL_ID
- D SPECIMEN_ID

- E ORDER_OR_GROUP
- F FAMILY
- G GENUS
- H TAXON_ID
- I SCIENTIFIC_NAME
- J TAXON_REMARKS
- K INFRASPECIFIC_EPITHET
- L CULTURE_OR_STRAIN_ID
- M COMMON_NAME

- N LIFESTAGE
- O SEX
- P ORGANISM_PART
- Q SYMBIONT

Fig. 5: Tree of Life Manifest wizard: Common field dropdown menu

Tree of Life Manifest Wizard

1 Samples 2 Download

Reset Next

How many samples would you like to describe?

4

Are there common values for these fields? ⓘ

Choose a common field

ORDER_OR_GROUP	Lepidoptera	
FAMILY	Lyonetiidae	
GENUS	Lyonetia	
TAXON_ID	753195	
SCIENTIFIC_NAME	Lyonetia clerkella	
LIFESTAGE	ADULT	
SEX	MALE	

Fig. 6: Tree of Life Manifest wizard: Inputted common field values

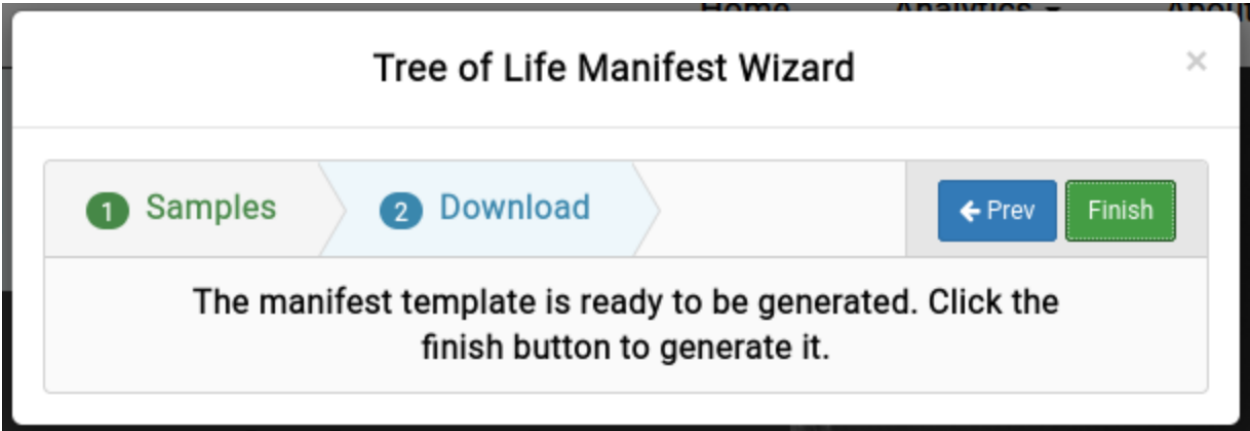


Fig. 7: Tree of Life Manifest wizard: Download prefilled manifest by clicking the ‘Finish’ button

SERIES	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY	GENUS	TAXON_ID	SCIENTIFIC_NAME	TAXON_REMARKS	INFRASPECIFIC_EPITHET
				Lepidoptera	Lyonetidae	Lyonetia	753195	Lyonetia clerkella		
				Lepidoptera	Lyonetidae	Lyonetia	753195	Lyonetia clerkella		
				Lepidoptera	Lyonetidae	Lyonetia	753195	Lyonetia clerkella		
				Lepidoptera	Lyonetidae	Lyonetia	753195	Lyonetia clerkella		

Fig. 8: Tree of Life Manifest wizard: Prefilled manifest

TREE OF LIFE DASHBOARD

The Tree of Life (ToL) dashboard can be explored on the [ToL dashboard web page](#).

Note: Few information will be displayed on the Tree of Life dashboard if you are not logged into COPO.

Hint:

- The Tree of Life dashboard provides an overview of COPO statistics, abbr:*ToL(Tree of Life)*¹ inspection, manifest submission and world map of Genome Acquisition Labs (GAL)s and partners.
- Click a card item on the dashboard to explore the data further.
- Click a map location on the world map to view more details about a GAL or Partner.

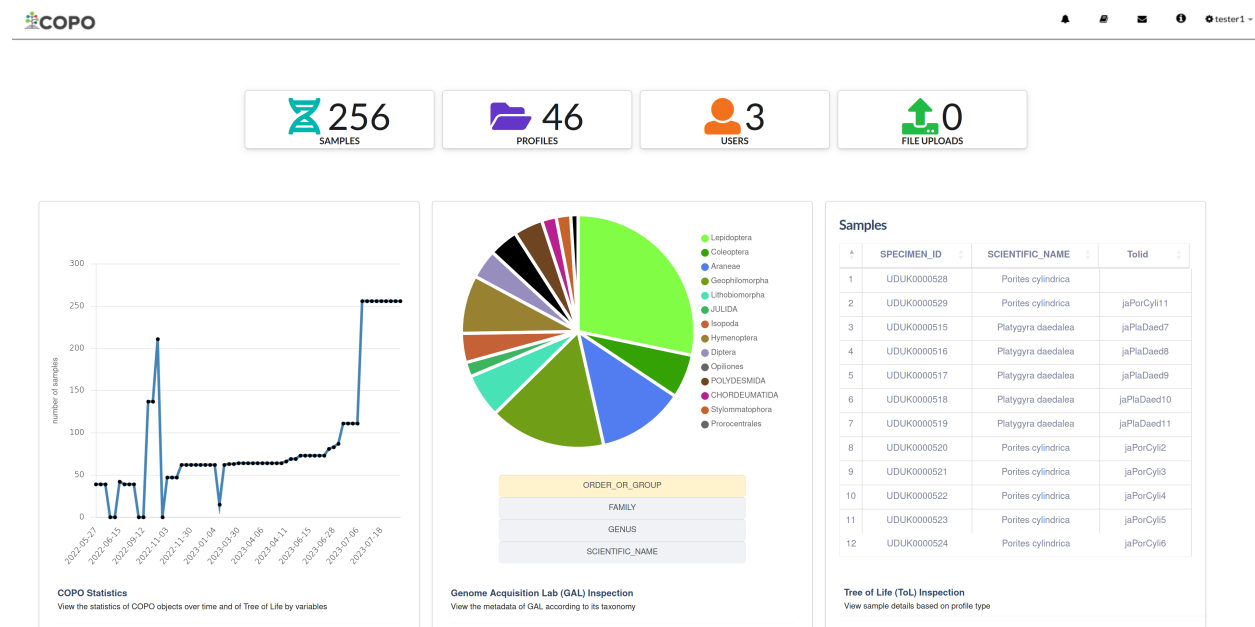


Fig. 1: ToL Dashboard: Overview of COPO statistics and ToL inspection

¹ See term: *Tree of Life (ToL)*

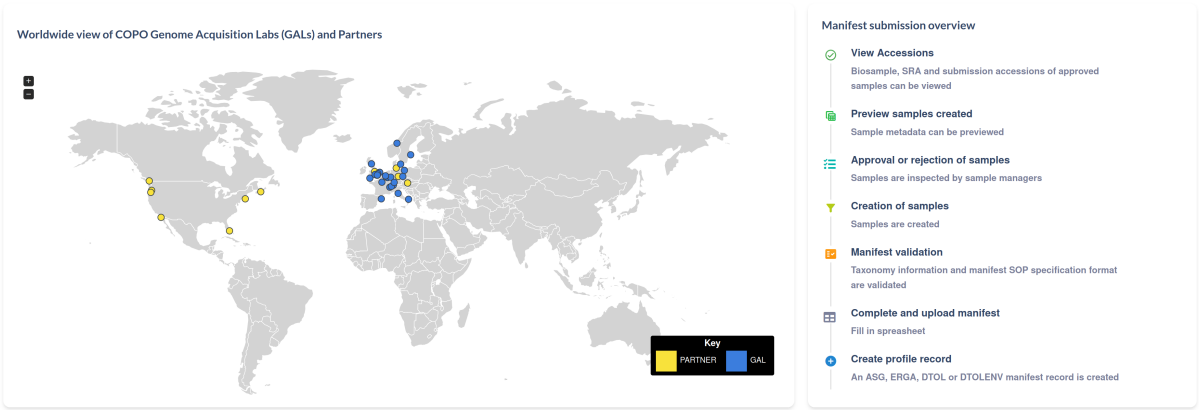


Fig. 2: ToL Dashboard: Geographical location of all GALs and Partners and an overview of manifest submissions

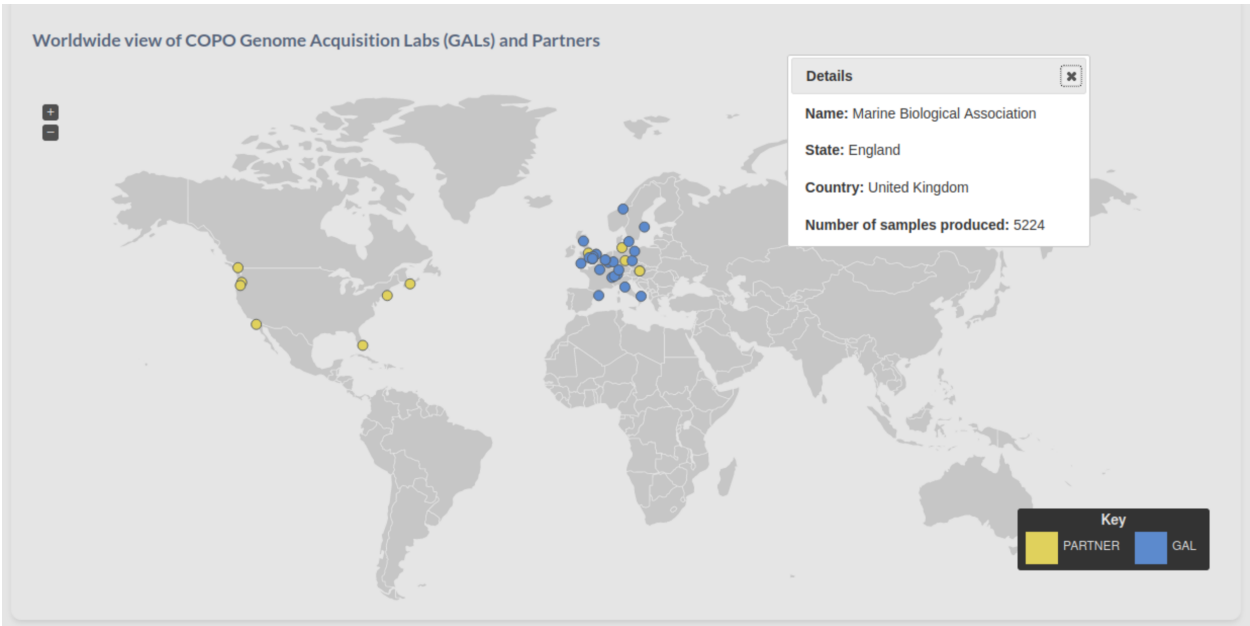


Fig. 3: ToL Dashboard: Popup dialogue with more information about one of the GALs

To view more details about a GAL or Partner, click one of the map locations on the world map. A popup dialogue will be displayed information about the GAL or Partner such as name, state, country, and number of samples produced.

28.1 Tree of Life Inspection

A **ToL inspection** analyses the sample metadata of COPO profile records and facilitates search faceting and data discovery of the results.

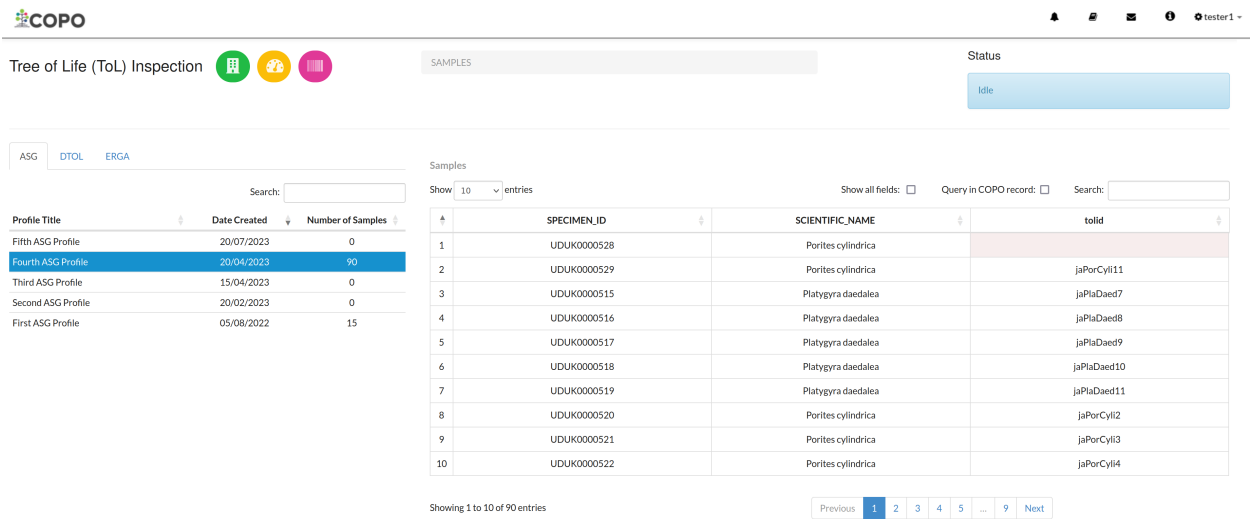


Fig. 4: Tree of Life (ToL) Inspection web page

28.2 Tree of Life Inspection by Genome Acquisition Lab

A **ToL inspection by GAL** analyses the sample metadata of COPO profile records by GALs² based on their taxonomy.

See also:

- *COPO statistics section*

² See term: *Genome Acquisition Lab (GAL)*. Also referenced as Partner.

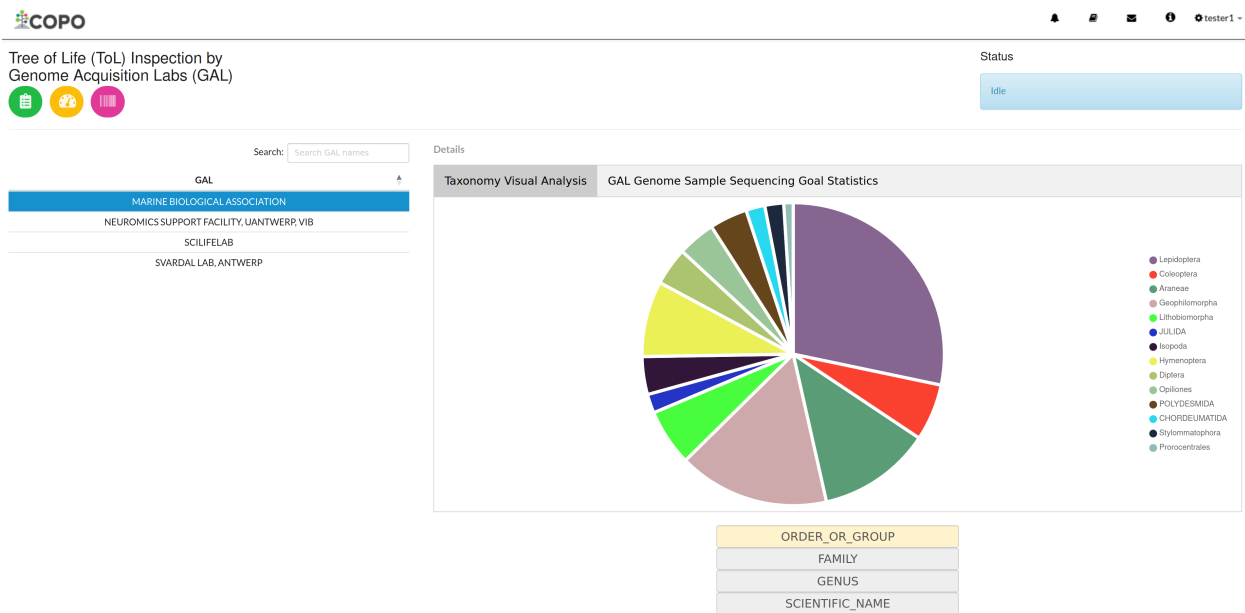


Fig. 5: Tree of Life (ToL) Inspection by Genome Acquisition Lab (GAL) web page


RETRIEVING ACCESSIONS

Approved submissions result in accessions being created. The accessions can be explored on the [Accessions' dashboard](#), on the [ENA browser](#)¹ or [NCBI Biosamples](#)² (after they become public).

The types of accessions that are created are:

- **Stand-alone submissions**
 - Project accessions
 - Experiment accessions
 - Run accessions
 - Read accessions
 - Assembly accessions
 - Sequence annotation accessions
- **ToL** Page 157, 3 **submissions**
 - Biosample accessions
 - SRA accessions
 - Submission accessions

Note:

- The  button will only appear on the web page if you are granted permission to be a sample manager.

See also:

- *Stand-alone profile components*
- *ToL profile components*
- Accessions profile component

¹ See term: *ENA*.

² See term: *NCBI*.

³ See term: *Tree of Life (ToL)*.

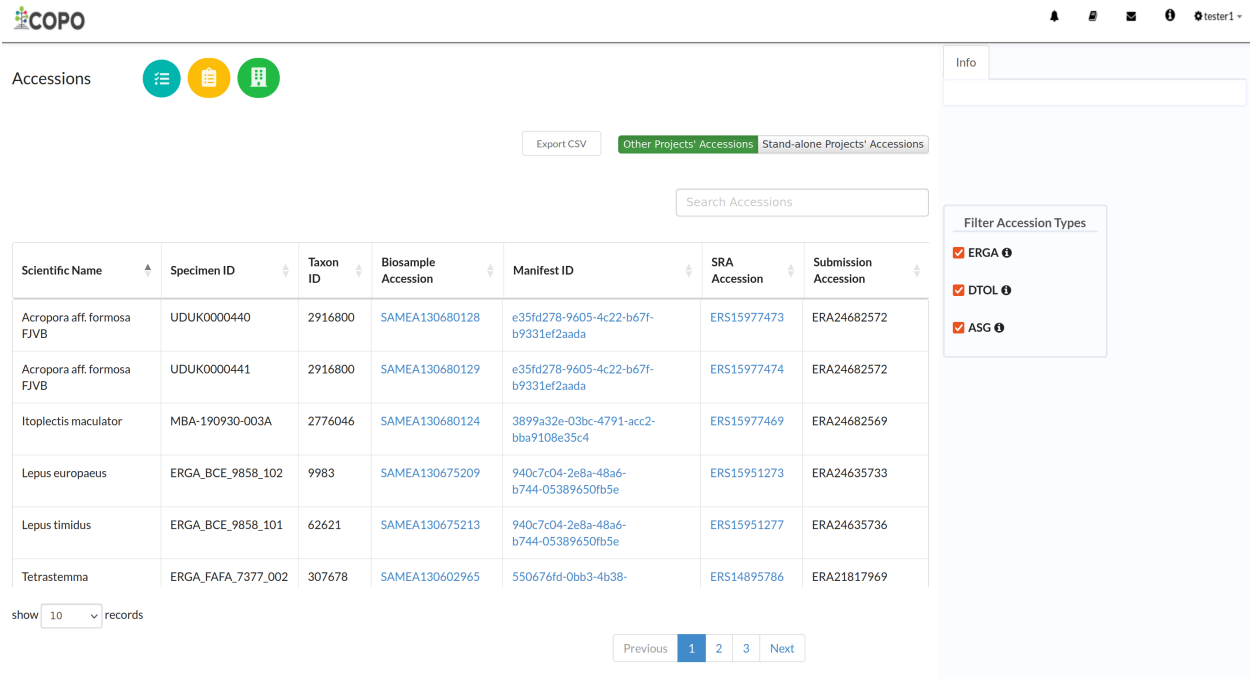


Fig. 1: Accessions Dashboard: Tree of Life projects' accessions

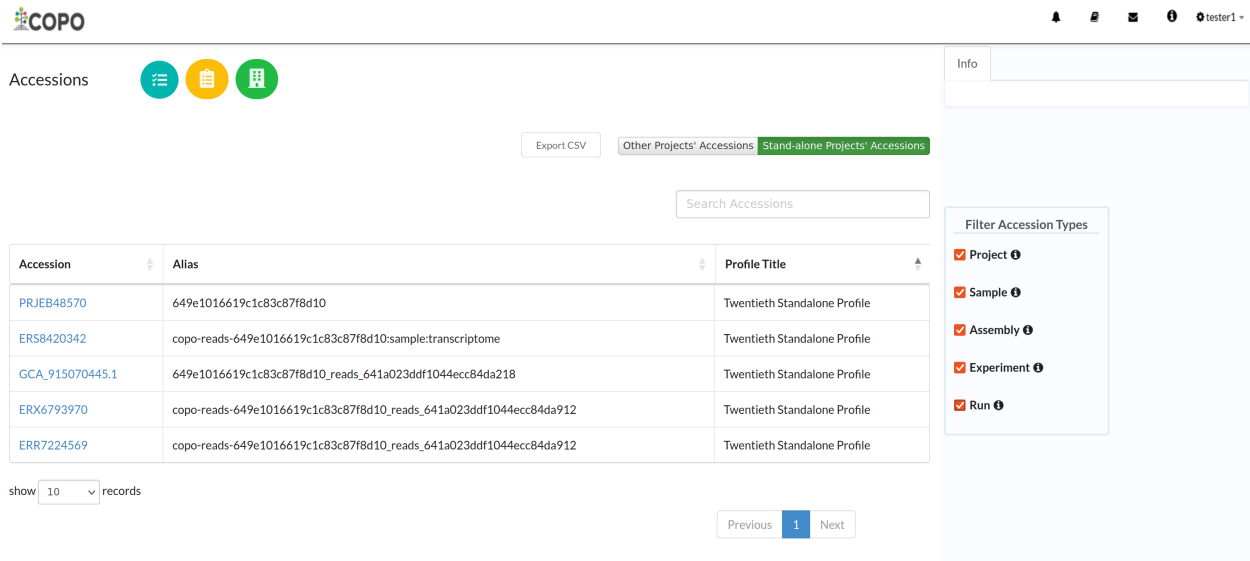


Fig. 2: Accessions Dashboard: Stand-alone projects' accessions

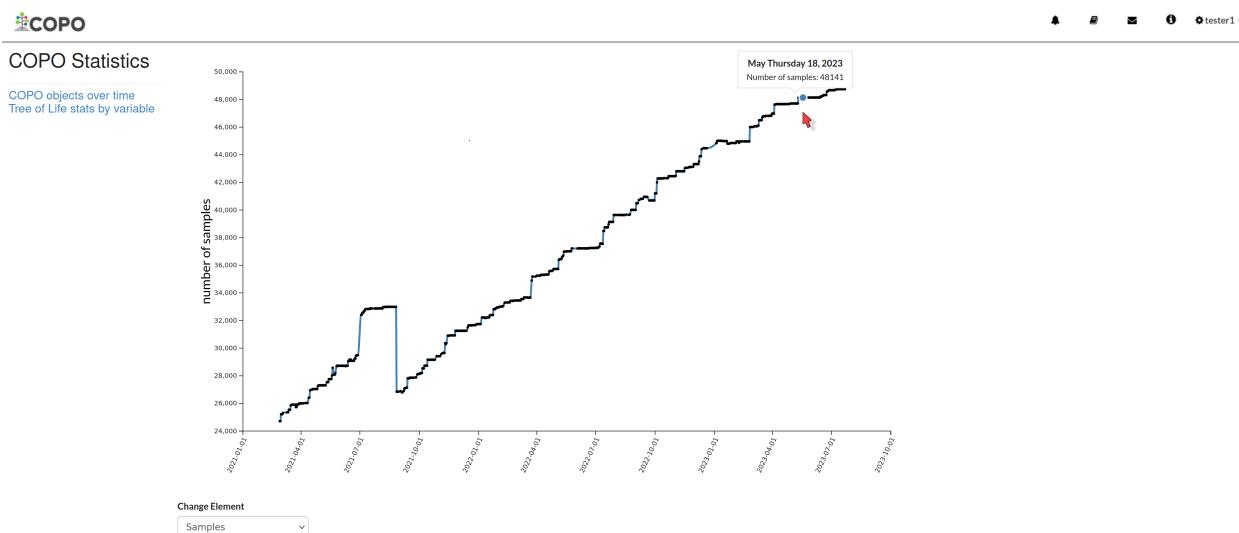
COPO STATISTICS

Statistics are generated for each COPO instance over time and by a variable. The statistics are automatically updated and can be accessed on the [Statistics web page](#).

30.1 Statistics over Time

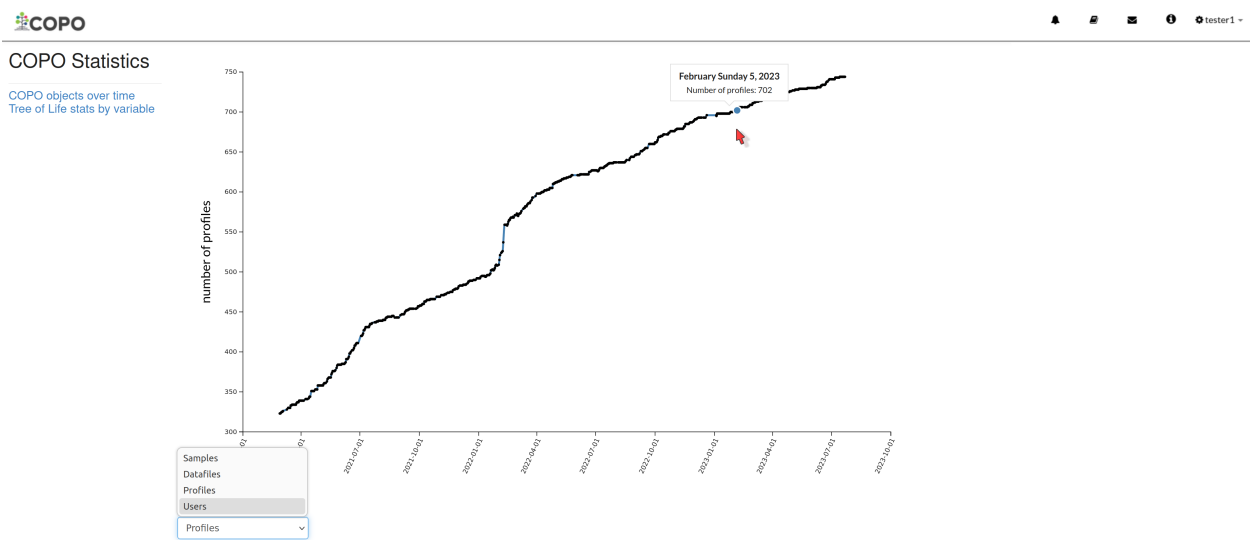
Statistics can be generated for the following research object elements over time:

- Samples
- Datafiles
- Profiles
- Users



COPO Statistics: Line graph illustrating the number of samples recorded over time

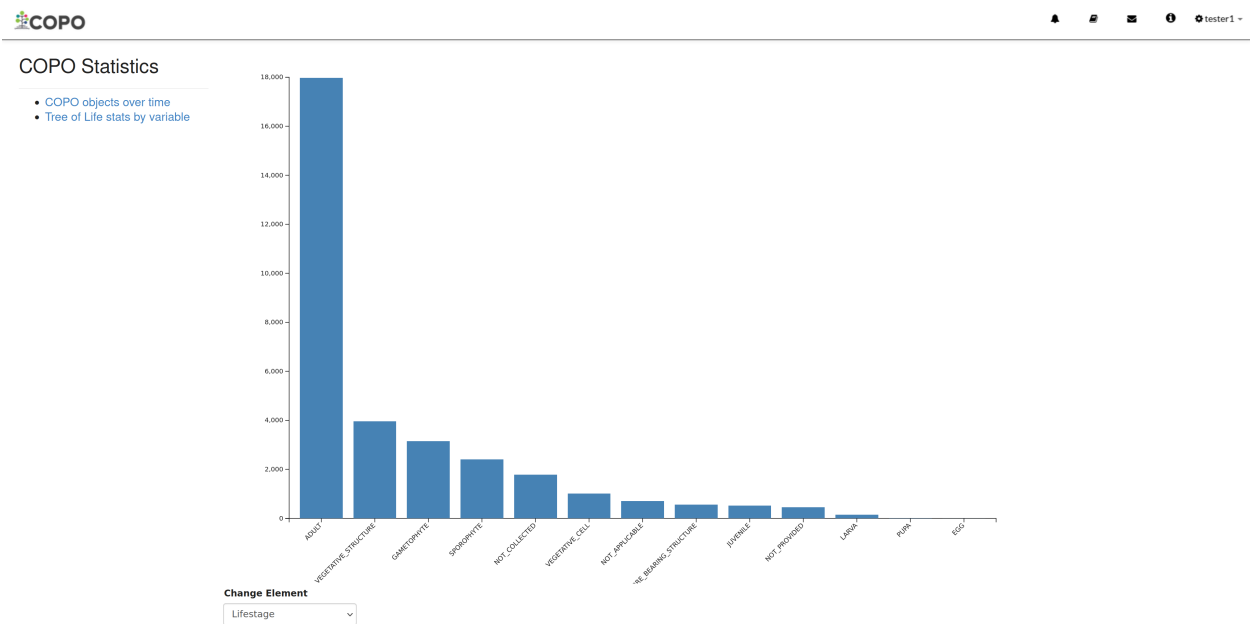
COPO Statistics: Dropdown menu of research object elements that can be queried to get statistics of the number of samples over time



30.2 Statistics by Variable

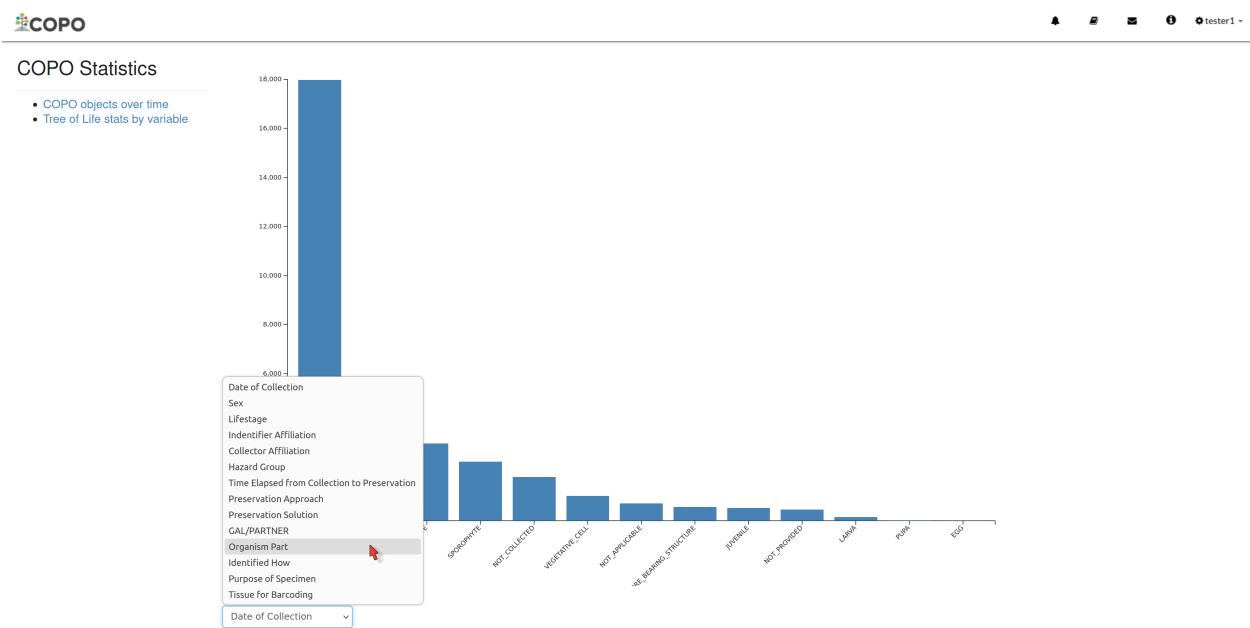
Statistics can be generated for the number of samples submitted based on the research elements or variables such as -

- Date of Collection
- Sex
- Harzard Group
- Organism Part



COPO Statistics: Bar graph illustrating total number of samples recorded for various Lifestage elements

COPO Statistics: Dropdown menu of elements/variables that can be queried to get statistics of the number of samples



MANIFEST CHECKLIST

Hint: To view the entire description of a checklist, collapse the description by clicking the ► button below.

The manifest checklist¹ is a combination of the default European Nucleotide Archive (ENA)² checklist and additional checklists that are specific to projects. The manifest checklist is used to generate the manifest file which can be a Microsoft Excel (MS) spreadsheet file, Comma-separated values (CSV) file or a form that is required to be uploaded to ENA.

An overview of each manifest checklist is given below. It was adapted from ENA [sample checklists](#) and [annotation checklists](#).

31.1 Barcoding Manifest Checklists

For mitochondrial cytochrome oxidase subunit 1 genes.

For ribosomal RNA genes from prokaryotic, nuclear or organellar DNA. All rRNAs are considered partial.

31.2 Sample Manifest Checklists

Minimum information required for the sample

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

¹ See term: *Manifest checklist*.

² See term: *ENA*.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

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Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Minimum information about a Micro B3 sample. A checklist for reporting metadata of marine microbial samples associated with genomics data. NOTE: Non-genomics data, i.e. oceanographic environmental data and morphology-based biodiversity data, should be submitted to the appropriate National Oceanographic Data Centre according to established reporting practices maintained by oceanographic community experts. Major National Oceanographic Data Centres from countries bordering the North-East Atlantic, and its adjacent seas: the Mediterranean, the Black Sea, the Baltic, the North Sea and the Arctic are listed at <http://www.seadatanet.org/Overview/Partners>.

For the Ocean Sampling Day campaign, non-genomics data shall be reported to the PANGAEA (<http://www.pangaea.de/submit/>).

Minimum information required for a prokaryotic pathogen sample

Minimum Data for Matching (MDM). A checklist for reporting metadata of pathogen samples for the Global Microbial Identifier (GMI) reporting system. More about GMI can be found here

Minimum information about a Tara Oceans sample. A checklist for reporting metadata of oceanic plankton samples associated with genomics data from the Tara Oceans Expedition.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Minimum information about an Influenza virus sample. A checklist for reporting metadata of Influenza virus samples associated with genomic data. This minimum metadata standard supports submission of avian, human and mammalian

surveillance data as well as serology and virus isolate information (where available). The ENA Influenza sample checklist is based on standards in use at the Influenza Research Database.

Minimum information about a virus pathogen. A checklist for reporting metadata of virus pathogen samples associated with genomic data. This minimum metadata standard was developed by the COMPARE platform for submission of virus surveillance and outbreak data (such as Ebola) as well as virus isolate information.

Minimum Information required for reporting samples associated with genomic data, derived from carcinogen induced animal tumours. This minimum metadata standard was developed in collaboration with Duncan Odom lab for the Mouse Liver Cancer Evolution Project.

The ENA Crop sample enhanced checklist has been developed in collaboration with a number of EMBL-EBI teams to capture enriched annotation of published crop plant samples that lack sufficient reported metadata and are typically associated with systematic transcriptomic realignment-based analyses.

Minimum information about sewage samples. A checklist for reporting of sewage surveillance samples associated with sequence data from metagenomic sequencing projects. This minimum metadata standard was developed by the COMPARE platform.

ENA implementation of plant specimen contextual information associated with molecular data. The checklist has been developed in collaboration with the NCBI-GenBank and iPlant data resources under the umbrella of the Genomic Standards Consortium.

Shellfish contextual information associated with molecular data. The checklist has been developed in collaboration with EMBRIC Project partners.

Minimum information about parasite samples. A checklist for reporting metadata of parasite samples associated with molecular data. This standard was developed by the COMPARE platform and can be used for submission of sample metadata derived from protozoan parasites (e.g. *Cryptosporidium*) and also multicellular eukaryotic parasites (e.g. *Platyhelminthes* and *Nematoda*).

Minimum information required for reporting samples associated with the UniEuk EukBank initiative. This checklist aims to capture contextual metadata associated with V4 18S SSU rRNA molecular data.

Minimum information to standardise metadata related to samples used in GMI PT (Global Microbial Identifier Proficiency Test). A checklist for reporting metadata of GMI PT samples associated with molecular data. This minimum metadata standard was developed by the COMPARE platform and can be used for submission of sample metadata derived from *Campylobacter coli*, *Campylobacter jejuni*, *Listeria monocytogenes*, *Klebsiella pneumoniae*, *Salmonella enterica*, *Escherichia coli* and *Staphylococcus aureus*.

Marine microalgae contextual information. The checklist has been developed in collaboration with EMBRIC Project partners and is suitable for reporting metadata related to environmental samples and those in culture collections.

A checklist for reporting metadata of human-associated pathogen samples for the COMPARE-ECDC-EFSA reporting system.

A checklist for reporting metadata of food-borne pathogen samples for the COMPARE-ECDC-EFSA reporting system.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Minimum information to standardise metadata of binned metagenome samples. Ensures binned and MAG metagenome assembly metadata is compatible.

Minimum information required for reporting samples associated with patient-derived xenograft (PDX) models or patient samples

Minimum information required for reporting HoloFood samples. HoloFood is a ‘hologenomic’ approach that will improve the efficiency of food production systems by understanding the biomolecular and physiological processes affected by incorporating feed additives and novel sustainable feeds in farmed animals

Minimum information required for reporting samples associated with the Tree of Life Programme.

SETTING UP COPO PROJECT LOCALLY WITH DOCKER

The central instance of COPO runs on a pool of three virtual machines. The following set up instructions are structured in a similar manner using one node. Feel free to make changes for a bigger or smaller pool.

Clone the [GitHub COPO project repository](#).

Visual Studio Code (VSCode) is recommended for running the COPO project after having set up the Docker environment. You can download VSCode from [here](#) for your local machine.

Note: There are a number of parameters in the command below that need to be updated or you may want to change for your local deployment. Please read through carefully.

Hint: A Python virtual environment is not required to run the COPO project application locally since the project is running via Docker containers. However, if you would like to run the project locally without Docker and within a Python virtual environment, please refer to the [COPO project setup with PyCharm documentation](#).

Warning: The `ENA_SERVICE` environment variable is set to the ENA development server. All submission to this server will be deleted after 24 hours. To submit to the production ENA server remove `dev` and set `prod`.

32.1 Install Docker

Follow the official [Docker installation documentation](#) for your distribution.

Make changes to your firewall, iptables and security groups to serve a website, use Docker swarm and redis. The port number will depend on your setup and if you choose to use the default ports for each service.

32.2 Initialise Docker Swarm

Listing 1: Start a Docker swarm

```
docker swarm init --advertise-addr <the IP of the machine you want to advertise>
```

e.g. `$ docker swarm init 127.0.0.1` where `127.0.0.1` is the IP address of localhost.

This command will return a token. You need this token to make the other VMs join the swarm if you plan to use more than one node. On the other machines run:

Listing 2: Command to make other VMs join the swarm manager

```
docker-swarm join --token <the token returned by the previous command> <the IP_↵
↵advertised previously>:2377
```

Check out the Docker documentation if you want to change the default port.

Note: You may need to change the following instructions depending on the server you are deploying to. Please consider which services need to run in the backend or frontend network.

32.2.1 Add Docker Node Labels

Label the node as a web service, nginx service, mongo service, postgres service and backup service. The web service and nginx service will be deployed on the frontend network. The mongo service, postgres service and backup service will be deployed on the backend network.

Adding One Docker Node Label

Hint: \$HOSTNAME is a bash variable that returns the hostname of the machine. You can use the hostname of the machine instead of the variable. In a Linux OS, you can run `$ echo $HOSTNAME` to get the hostname.

If you are using more than one node, you will need to label the other nodes as well.

Listing 3: Documentation for the Docker swarm command

```
docker node update \
  --label-add web-service=true \
  --label-add nginx-service=true \
  --label-add mongo-service=true \
  --label-add postgres-service=true \
  --label-add backup-service=true \
  $HOSTNAME
```

Adding More than Docker One Node Labels

If you are using more than one Docker node, you can label the other nodes as follows:

Node 1

Listing 4: Node 1 Docker label command

```
docker node update \
  --label-add web-service=true \
  --label-add nginx-service=true \
  --label-add mongo-service=false \
  --label-add postgres-service=false \
  --label-add backup-service=false \
  copo-0
```

Node 2

Listing 5: Node 2 Docker label command

```
docker node update \
  --label-add web-service=false \
  --label-add nginx-service=false \
  --label-add mongo-service=false \
  --label-add postgres-service=true \
  --label-add backup-service=true \
  copo-1
```

Node 3

Listing 6: Node 3 Docker label command

```
docker node update \
  --label-add web-service=false \
  --label-add nginx-service=false \
  --label-add mongo-service=true \
  --label-add postgres-service=false \
  --label-add backup-service=false \
  copo-2
```

Create Docker Volumes

Docker volumes are used to persist data via the plugin, **local-persist**. This ensures that the data is not lost when the containers are restarted. Volumes are created on the swarm manager.

Substitute the paths in commands before running it.

Hint: You may need to install curl before running the command below. You can install curl by running `$ sudo apt-get install curl`.

You may need to install the **local-persist** plugin to persist volumes before running the command below. You can install it by running: `$ curl -fsSL https://raw.githubusercontent.com/MatchbookLab/local-persist/master/scripts/install.sh | sudo docker`

Listing 7: Commands to create Docker volumes

```
docker volume create -d local-persist -o mountpoint=/path/to/web-data --name=web-data
docker volume create -d local-persist -o mountpoint=/path/to/static-data --name=static-
↪data
docker volume create -d local-persist -o mountpoint=/path/to/submission-data --
↪name=submission-data
docker volume create -d local-persist -o mountpoint=/path/to/logs-data --name=logs-data
docker volume create -d local-persist -o mountpoint=/path/to/mongo-data --name=mongo-
↪backup
docker volume create -d local-persist -o mountpoint=/path/to/postgres-data --
↪name=postgres-backup

docker volume create mongo-data
docker volume create postgres-data
```

Create Networks on Docker Swarm Manager

On the swarm manager create two networks - one for the frontend and one for the backend. The front-end network will be used by the web service and the nginx service while the backend network will be used by the database services.

Listing 8: Commands to create Docker networks on the swarm manager

```
docker network create -d overlay copo-frontend-network
docker network create -d overlay copo-backend-network
```

Listing 9: View networks created on Docker swarm manager

```
docker network ls
```

Create Secrets on Docker Swarm Manager

All secrets are file based. You will need to create some of the keys with third parties and choose passwords before proceeding with the COPO setup.

Listing 10: Commands to create secrets on Docker swarm manager

```
docker secret create copo_mongo_initdb_root_password copo_mongo_initdb_root_password
docker secret create copo_mongo_user_password copo_mongo_user_password
docker secret create copo_postgres_user_password copo_postgres_user_password
docker secret create copo_web_secret_key copo_web_secret_key
docker secret create copo_orcid_secret_key copo_orcid_secret_key
docker secret create copo_orcid_client_id copo_orcid_client_id
docker secret create copo_figshare_consumer_secret_key copo_figshare_consumer_secret_key
docker secret create copo_figshare_client_id_key copo_figshare_client_id_key
docker secret create copo_figshare_client_secret_key copo_figshare_client_secret_key
docker secret create copo_google_secret_key copo_google_secret_key
docker secret create copo_twitter_secret_key copo_twitter_secret_key
docker secret create copo_facebook_secret_key copo_facebook_secret_key
docker secret create copo_webin_user copo_webin_user
docker secret create copo_webin_user_password copo_webin_user_password
docker secret create copo-project.crt copo-project.crt
docker secret create copo-project.key copo-project.key
docker secret create copo_nih_api_key copo_nih_api_key
docker secret create copo_public_name_service_api_key copo_public_name_service_api_key
docker secret create copo_mail_password copo_mail_password
docker secret create copo_bioimage_path copo_bioimage_path
docker secret create ecs_secret_key ecs_secret_key
```

Listing 11: View secrets created on Docker swarm manager

```
docker secret ls
```

Build COPO Project Docker Image

Download the Dockerfile `Dockerfile_local`. for your local machine.

Place the downloaded Dockerfile in the COPO project root directory.

Alternatively, you can use the Dockerfile present in the root project directory `Dockerfile for demonstration environment`.

Note: The Dockerfile is configured to build the `local_copo_web` container image with the tag, `v1.0.1`. If you have a different tag and container name, you will need to change the Dockerfile accordingly.

If you are using a Mac OS, download the `Dockerfile_mac`.

Visit [here](#) for more information on how to build an application with a Docker image.

Listing 12: Navigate to COPO project root directory

```
cd <path-to-project-root-directory>/COPO
```

Listing 13: Build Docker image

```
docker build . -f Dockerfile_local -t local_copo_web:v1.0.1
```

Deploy Docker Image on Docker Swarm Manager

The `redis`, `postgres` and `mongo` Docker services are created on the swarm manager. Download the `local compose file` to create the services.

Alternatively, you can download `compose file for demonstration environment`.

Replace the `<path-to-project-root-directory>` with the absolute path to the COPO project root directory.

Note: The Docker compose file is configured to use the secrets and volumes created above. If you have used different names for the secrets and volumes, you will need to change the compose file accordingly.

If you are using a Mac OS, download the `Mac compose file`.

The following commands should be run from the root directory of the COPO project.

Warning: The `ENA_SERVICE` environment variable is set to the ENA development server. All submission to this server will be deleted after 24hours. To submit to the production ENA server remove "dev"

Listing 14: Edit Compose file to container tag e.g. local_copo_web:v1.0.1

```
nano local_copo.compose.yaml
```

Update the tag, save the file then, exit by inputting: CTRL + O then, ENTER then, CTRL + X

Listing 15: Command to deploy Docker image, local_copo_web:v1.0.1

```
docker stack deploy --compose-file '<path-to-file>/local_copo.compose.yaml' copo
```

Listing 16: Local Compose file for COPO project application

```
version: "3.8"
services:
  web:
    image: local_copo_web:v1.0.1
    command: >
      bash -c "code-server serve-local --disable-telemetry --auth none --host 0.0.0.0 --
↩port 8100"
    ports:
      - "8000:8000"
      - "8100:8100"
    volumes:
      - <path-to-project-root-directory>/COPO:/copo
    environment:
      - ENVIRONMENT_TYPE=prod
      - ASPERA_PLUGIN_DIRECTORY=aspera_linux_plugin
      - SECRET_KEY_FILE=/run/secrets/copo_web_secret_key
      - MEDIA_PATH=media/
      - DEBUG=true
      - REDIS_HOST=copo_redis
      - REDIS_PORT=6379
      - WEBIN_USER_FILE=/run/secrets/copo_webin_user
      - WEBIN_USER_PASSWORD_FILE=/run/secrets/copo_webin_user_password
      - ENA_SERVICE=https://wwwdev.ebi.ac.uk/ena/submit/drop-box/submit/
      - MONGO_USER=copo_user
      - MONGO_USER_PASSWORD_FILE=/run/secrets/copo_mongo_user_password
      - MONGO_DB=copo_mongo
      - MONGO_HOST=copo_mongo
      - MONGO_PORT=27017
      - MONGO_MAX_POOL_SIZE=100
      - POSTGRES_DB=copo
      - POSTGRES_USER=copo_user
      - POSTGRES_PORT=5432
      - POSTGRES_SERVICE=copo_postgres
      - POSTGRES_PASSWORD_FILE=/run/secrets/copo_postgres_user_password
      - ORCID_SECRET_FILE=/run/secrets/copo_orcid_secret_key
      - ORCID_CLIENT_FILE=/run/secrets/copo_orcid_client_id
      - FIGSHARE_CONSUMER_SECRET_FILE=/run/secrets/copo_figshare_consumer_secret_key
      - FIGSHARE_CLIENT_ID_FILE=/run/secrets/copo_figshare_client_id_key
      - FIGSHARE_CLIENT_SECRET_FILE=/run/secrets/copo_figshare_client_secret_key
      - GOOGLE_SECRET_FILE=/run/secrets/copo_google_secret_key
```

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```

- TWITTER_SECRET_FILE=/run/secrets/copo_twitter_secret_key
- FACEBOOK_SECRET_FILE=/run/secrets/copo_facebook_secret_key
- NIH_API_KEY_FILE=/run/secrets/copo_nih_api_key
- PUBLIC_NAME_SERVICE_API_KEY_FILE=/run/secrets/copo_public_name_service_api_key
- MAIL_PASSWORD_FILE=/run/secrets/copo_mail_password
- MAIL_PORT=587
- MAIL_ADDRESS=data@earlham.ac.uk
- MAIL_SERVER=outlook.office365.com
- MAIL_USERNAME=eidata@nbi.ac.uk
- ALLOWED_HOSTS=
- PUBLIC_NAME_SERVICE=https://id.tol.sanger.ac.uk/api/v2/
- ENA_ENDPOINT_REPORT=https://wwwdev.ebi.ac.uk/ena/submit/report/samples
- ASPERA_PATH=/root/.aspera/cli
- BIOIMAGE_PATH_FILE=/run/secrets/copo_bioimage_path
- BIOIMAGE_SERVER=bsaspera_w@hx-fasp-1.ebi.ac.uk
- ECS_SECRET_KEY_FILE=/run/secrets/ecs_secret_key
- ECS_ACCESS_KEY_ID=copo@nbi.ac.uk
- ECS_ENDPOINT=http://ei-copo.obj-data.nbi.ac.uk
- ENA_V2_SERVICE_SYNC=https://wwwdev.ebi.ac.uk/ena/submit/webin-v2/submit
- ENA_V2_SERVICE_ASYNC=https://wwwdev.ebi.ac.uk/ena/submit/webin-v2/submit/queue
- B2DROP_PERMITS=/copo/b2drop/permits
depends_on:
- redis
- postgres
- mongo
networks:
- copo-frontend-network
- copo-backend-network
deploy:
  replicas: 1
  restart_policy:
    condition: on-failure
  placement:
    constraints:
      - "node.labels.web-service==true"
resources:
  limits:
    cpus: '4'
    memory: 7GB
  reservations:
    cpus: '2'
    memory: 2GB
update_config:
  parallelism: 1
  delay: 10s
secrets:
- copo_web_secret_key
- copo_postgres_user_password
- copo_mongo_user_password
- copo_google_secret_key
- copo_facebook_secret_key
- copo_twitter_secret_key

```

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```

- copo_orcid_secret_key
- copo_orcid_client_id
- copo_figshare_client_id_key
- copo_figshare_client_secret_key
- copo_figshare_consumer_secret_key
- copo_webin_user
- copo_webin_user_password
- copo_nih_api_key
- copo_public_name_service_api_key
- copo_mail_password
- copo_bioimage_path
- ecs_secret_key

```

redis:

```
image: copo/copo-redis:redis-v6.2.6.18
```

networks:

```
- copo-frontend-network
```

deploy:

```
replicas: 1
```

```
endpoint_mode: dnsrr
```

restart_policy:

```
condition: on-failure
```

placement:**constraints:**

```
- "node.labels.web-service==true"
```

update_config:

```
parallelism: 1
```

```
delay: 10s
```

resources:**limits:**

```
cpus: "0.5"
```

```
memory: 1GB
```

reservations:

```
cpus: "0.3"
```

```
memory: 512mb
```

postgres:

```
image: postgres:9.6
```

networks:

```
- copo-backend-network
```

volumes:

```
- postgres-data:/var/lib/postgresql/data
```

secrets:

```
- copo_postgres_user_password
```

ports:

```
- "5432:5432"
```

environment:

```
- POSTGRES_DB=copo
```

```
- POSTGRES_USER=copo_user
```

```
- POSTGRES_PASSWORD_FILE=/run/secrets/copo_postgres_user_password
```

deploy:

```
replicas: 1
```

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```

    endpoint_mode: dnsrr
    restart_policy:
      condition: on-failure
    placement:
      constraints:
        - "node.labels.postgres-service==true"
    update_config:
      parallelism: 1
      delay: 10s
    resources:
      limits:
        cpus: "0.5"
        memory: 1GB
      reservations:
        cpus: "0.3"
        memory: 512mb

mongo:
  image: copo/copo-mongo:20
  networks:
    - copo-backend-network
  volumes:
    - mongo-data:/data/db
  secrets:
    - copo_mongo_initdb_root_password
    - copo_mongo_user_password
  ports:
    - "27017:27017"
  environment:
    - MONGO_INITDB_ROOT_USERNAME=copo_admin
    - MONGO_INITDB_ROOT_PASSWORD_FILE=/run/secrets/copo_mongo_initdb_root_password
    - MONGO_USER=copo_user
    - MONGO_USER_PASSWORD_FILE=/run/secrets/copo_mongo_user_password
    - MONGO_DB=copo_mongo
  deploy:
    replicas: 1
    #endpoint_mode: dnsrr
    restart_policy:
      condition: on-failure
    placement:
      constraints:
        - "node.labels.mongo-service==true"
    update_config:
      parallelism: 1
      delay: 10s
    resources:
      limits:
        cpus: "0.8"
        memory: 2GB
      reservations:
        cpus: "0.4"
        memory: 512mb

```

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```
networks:
  copo-backend-network:
    external: true
  copo-frontend-network:
    external: true
secrets:
  copo_web_secret_key:
    external: true
  copo_postgres_user_password:
    external: true
  copo_mongo_user_password:
    external: true
  copo_google_secret_key:
    external: true
  copo_figshare_client_id_key:
    external: true
  copo_facebook_secret_key:
    external: true
  copo_twitter_secret_key:
    external: true
  copo_orcid_secret_key:
    external: true
  copo_orcid_client_id:
    external: true
  copo_figshare_client_secret_key:
    external: true
  copo_figshare_consumer_secret_key:
    external: true
  copo_webin_user:
    external: true
  copo_webin_user_password:
    external: true
  copo_nih_api_key:
    external: true
  copo_public_name_service_api_key:
    external: true
  copo_mail_password:
    external: true
  copo_mongo_initdb_root_password:
    external: true
  copo-project.crt:
    external: true
  copo-project.key:
    external: true
  copo_bioimage_path:
    external: true
  ecs_secret_key:
    external: true
volumes:
  web-data:
    external: true
```

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```
static-data:
  external: true
submission-data:
  external: true
logs-data:
  external: true
mongo-backup:
  external: true
postgres-backup:
  external: true
mongo-data:
  external: true
postgres-data:
  external: true
b2drop-permits:
  external: true
```

Listing 17: View services created on Docker swarm manager

```
docker service ls
docker ps
docker ps -a
```

Listing 18: Inspect created image and check if it is running

```
docker image inspect local_copo_web:v1.0.1
```

Listing 19: Start copo_web Docker container (if it is not started)

```
docker service scale copo_web=1
```

Listing 20: Command to stop copo_web Docker container

```
docker service scale copo_web=0
```

Set up PostgreSQL database

In the terminal, navigate to the root directory of the COPO project application then, run the following commands.:

Hint: Retrieve the `local_copo_web` container ID by running the `$ docker ps` command below in the root project directory of the COPO project application in the terminal for the `local_copo_web:v1.0.1` Docker image.

Listing 21: Install PostgreSQL database version 9.6 in terminal

```
docker run --name postgresql -e POSTGRES_USER=<postgres-username> -e POSTGRES_PASSWORD=
-><postgres-password> -p 5432:5432 -v /data:/var/lib/postgresql/data -d postgres:9.6
```

Replace `<postgres-username>` and `<postgres-password>` with the username and password for PostgreSQL database respectively.

Listing 22: Enter the **local_copo_web** container

```
docker exec -it <local_copo_web-container-id> bash
```

Listing 23: Setup scripts to be run in the **local_copo_web** Docker container

```
python manage.py makemigrations
python manage.py makemigrations chunked_upload
python manage.py makemigrations allauth
python manage.py migrate
python manage.py setup_groups
python manage.py setup_schemas
python manage.py createcachetable
python manage.py social_accounts
```

Listing 24: Install Python requirements for the project

```
python manage.py makemigrations
python manage.py makemigrations chunked_upload
python manage.py makemigrations allauth
python manage.py migrate
python manage.py setup_groups
python manage.py setup_schemas
python manage.py createcachetable
python manage.py social_accounts
```

Listing 25: Create a Django admin/superuser

```
python3 manage.py createsuperuser
```

Enter the required details to create the Django admin/superuser. The Django admin/superuser can log into the COPO project application from the local [Django admin website](#).

Listing 26: Exit the **local_copo_web** Docker container

```
CTRL + P
CTRL + Q
exit
```

The commands above can be accessed in the `3_db_setup.sh` script. This file is located in the **set_up_scripts** directory of the COPO project root directory.

In the following steps, we will create the PostgreSQL database for the COPO project application in the root directory of the project.

Hint: Retrieve the PostgreSQL container ID by running the command below in the root project directory of the COPO project application in the terminal for the **postgres:9.6** Docker image: `$ docker ps`

Listing 27: Enter the PostgreSQL container

```
docker exec -it <postgres-container-id> bash
```

Listing 28: Run setup scripts in the PostgreSQL Docker container

```
psql -h 'localhost' -U $POSTGRES_USER -d 'copo' -c 'DELETE FROM socialaccount_socialapp_
↪sites'
psql -h 'localhost' -U $POSTGRES_USER -d 'copo' -c 'DELETE FROM django_site'
psql -h 'localhost' -U $POSTGRES_USER -d 'copo' -c 'DELETE FROM socialaccount_socialapp'
psql -h 'localhost' -U $POSTGRES_USER -d 'copo' -c "INSERT INTO django_site (id, domain,
↪ name) VALUES (1, 'www.copo-project.org', 'www.copo-project.org')"
psql -h 'localhost' -U $POSTGRES_USER -d 'copo' -c "INSERT INTO socialaccount_socialapp_
↪(id, provider, name, client_id, secret, key) VALUES (1, 'orcid', 'Orcid', '$ORCID_
↪CLIENT_ID', '$ORCID_SECRET', '')"
psql -h 'localhost' -U $POSTGRES_USER -d 'copo' -c 'INSERT INTO socialaccount_socialapp_
↪sites (id, socialapp_id, site_id) VALUES (1, 1, 1)'
```

The commands above can be accessed in the `3_db_setup.sh` script. This file is located in the `set_up_scripts` directory of the COPO project root directory.

32.2.2 Updating COPO Website Service

The COPO project is updated frequently and as such is under active development. To update your instance to a newer (or the latest) version, download the local `compose` file or the `compose` file for demonstration environment on the swarm manager or root directory of the project if you have one node.

Then, run the following commands in the terminal:

Note: The Docker tag below needs to be changed to reflect the most recent version available in DockerHub. Please check the latest version there. You can safely ignore the `*feature` tags as they are not stable releases. For stable releases look for `*rc`.

Hint:

- Retrieve the **copo-web** container ID by running the `$ docker ps` command below in the root project directory of the COPO project application in the terminal for the **copo/copo-web:v1.0.1** Docker image.
- To check if the web service is running, run the command below in the root project directory of the COPO project application in the terminal for the **copo/copo-web:v1.0.2** Docker image: `$ docker logs -f <container-ID-for-updated-copo-web>`
- If you update often we recommend taking care of removing old docker images regularly.

Listing 29: Edit Compose file by updating the Docker container tag on the Docker swarm manager

```
nano local_copo.compose.yaml
```

Update the Docker tag, save the file then, exit it by inputting: `CTRL + O` then, `ENTER` then, `CTRL + X`

Listing 30: Command to deploy updated Docker image: local_copo_web:v1.0.2 on the Docker swarm manager

```
docker stack deploy --compose-file '<path-to-file>/local_copo.compose.yaml' copo
```

32.2.3 Launch COPO Website

The COPO project application can be accessed locally on port 8100 via the VSCode browser extension.

Within the VSCode IDE browser, add a new configuration by following the steps below:

1. Navigate to Run -> Add Configuration
2. Edit the **launch.json** file that is created with the following file contents:

Listing 31: VSCode **launch.json** configuration file contents

```
{
  "version": "0.2.0",
  "configurations": [
    {
      "name": "Python: Django",
      "type": "python",
      "request": "launch",
      "program": "${workspaceFolder}/manage.py",
      "env": {
        "PYTHONPATH": "${workspaceFolder}/lib:${PYTHONPATH}"
      },
      "args": [
        "runserver",
        "0.0.0.0:8000"
      ],
      "django": true,
      "justMyCode": false
    },
    {
      "name": "Python: Django makemigration",
      "type": "python",
      "request": "launch",
      "program": "${workspaceFolder}/manage.py",
      "env": {
        "PYTHONPATH": "${workspaceFolder}/lib:${PYTHONPATH}"
      },
      "args": [
        "makemigration"
      ],
      "django": true,
      "justMyCode": false
    },
    {
      "name": "Python: Celery Workers",
      "type": "python",
```

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```

        "request": "launch",
        "module": "celery",
        "console": "integratedTerminal",
        "env" : {
            "GEVENT_SUPPORT": "True"
        },
        "args": ["-A", "web", "worker", "-l", "debug", "-P", "gevent", "--
→ concurrency", "10", "-Q", "celery", "-E"],
        "justMyCode": true
    },
    {
        "name": "Python: Celery Beat",
        "type": "python",
        "request": "launch",
        "module": "celery",
        "console": "integratedTerminal",
        "args": ["-A", "web", "beat", "-l", "debug"]
    }
]
}

```

The COPO project application can be accessed locally on [on port 80000](#) or [on port 81000](#).

Note: Install required VSCode extensions for the COPO project application by following the steps below:

1. Navigate to the **Extensions** tab on the left-hand side of the VSCode IDE
2. Search for and install the following extensions:
 - Python (required)

If your local machine is restarted, you will need to start the Docker container again at startup. To do this, run the following command in the terminal: `$ docker start <container-ID-for-copo-web>`. You can retrieve the container ID by running the command below in the root project directory of the COPO project application in the terminal for the **copo/copo-web:v1.0.2** Docker image: `$ docker ps`

32.2.4 Tips

- Enable **Manage Unsafe Repositories** in **Source Control** in VSCode browser application to allow VSCode to access the COPO GitHub project repository.
- Install the following VSCode extensions:
 - GitHub Copilot
 - Prettier - Code formatter
 - Git Extension Pack

Listing 32: Set GitHub configuration in terminal

```

git config --global user.name "<GitHub-username>"
git config --global user.email "<GitHub-email-address>"

```

Listing 33: Create a tag via the terminal

```
git tag <tagname>
```

Listing 34: Push a particular tag to GitHub via the terminal

```
git push origin <tagname>
```

Listing 35: Remove an existing tag from GitHub via the terminal

```
git tag -d <tag-name>
```

Listing 36: Docker command used to list all the running Docker containers

```
docker ps
```

Listing 37: Docker command used to start, stop and restart a Docker service

```
sudo systemctl start docker  
sudo systemctl stop docker  
sudo systemctl restart docker
```

Listing 38: Docker command used to start, stop and restart a container respectively

```
docker start  
docker stop  
docker restart
```

Listing 39: Docker command used to execute a command in a running container

```
docker exec it <container-ID> bash
```

Listing 40: Docker command used to find the installed version of docker

```
docker version
```

Listing 41: Docker command used to know the details of all the running, stopped, or exited containers

```
docker ps -a
```

Listing 42: Docker command used to create a volume so that the docker container can use it to store data

```
docker volume create <volume-name>
```

SETTING UP COPO PROJECT LOCALLY WITHOUT DOCKER

The COPO project is built on the Django framework and uses MongoDB, Redis, and PostgreSQL databases. Python is the main programming language used in the project.

The open source project is hosted on [GitHub](#).

According to your OS, please choose the appropriate link below for instructions on how to set up the project on your local machine:

33.1 Set Up COPO Project on Linux

Note: If you are using a different OS (Operating system) other than Ubuntu, you can skip this step. See *[COPO project guidelines for Windows users](#)* if Windows is your preferred OS.

33.1.1 Install Python

```
sudo apt -y install software-properties-common
sudo add-apt-repository ppa:deadsnakes/ppa
sudo apt update
sudo apt -y install python3.8
```

33.1.2 Install Python Development Tools

```
sudo apt -y install python3.8-distutils
sudo apt -y install build-essential libssl-dev libffi-dev
sudo apt -y install libxml2-dev libxslt1-dev python3-django
sudo apt update && sudo apt install -y default-jre rsync git nano libxml2-dev python_
↪ build-essential make gcc python3-dev locales python3-pip ruby-dev rubygems poppler-
↪ utils
```

33.1.3 Install Required Packages

Listing 1: Install required packages and enable the databases to start on boot

```
sudo apt -y install supervisor
sudo gem install sass
sudo apt -y install redis mongodb postgresql
sudo systemctl enable mongodb
sudo systemctl enable postgresql
sudo systemctl enable redis
```

Listing 2: Install MongoDB on your local machine

```
sudo apt-key adv --keyserver hkp://keyserver.ubuntu.com:80 --recv 7F0CEB10
echo "deb http://repo.mongodb.org/apt/ubuntu "$(lsb_release -sc)"/mongodb-org/3.0_
↳multiverse" | sudo tee /etc/apt/sources.list.d/mongodb-org-3.0.list
sudo apt update
sudo apt -y install mongodb-org
```

33.1.4 Install Integrated Development Environment (IDE)

Any IDE (Integrated Development Environment) can be used to work on the project. However, we recommend using one of the following IDEs:

PyCharm Professional

A cross-platform IDE that provides consistent experience on the Windows, macOS, and Linux operating systems.

```
sudo snap install pycharm-professional --classic
```

OR

Visit [PyCharm website](#) to download an appropriate version for your OS or download it from the [Ubuntu Software Center](#).

Visual Studio Code

VSCODE (Visual Studio Code) is a lightweight but powerful source code editor which runs on your desktop and is available on Windows, macOS and Linux.

It comes with built-in support for JavaScript, TypeScript and Node.js and has a rich ecosystem of extensions for other languages (such as C++, C#, Java, Python, PHP, Go) and runtimes (such as .NET and Unity).

Visit [VSCode website](#) to download an appropriate version for your OS or download it from the [Ubuntu Software Center](#)

33.1.5 Configure IDE

PyCharm

Note: If using VSCode IDE, you can skip this step.

Warning: If you encounter the error, Error: Please enable Django support for the project, navigate to File->Settings->Languages & Frameworks->Django->Enable Django to enable Django support for the project.

If using PyCharm IDE, add a new configuration by following the steps below: #. Navigate to Add New Configuration
#. Select **Django server** #. Click **Save**

Visit [Run/debug configurations](#) to learn how to create a configuration in PyCharm.

VSCode

If using VSCode IDE, add a new configuration by following the steps below: #. Navigate to Run -> Add Configuration
#. Edit the **launch.json** file that is created with the following file contents:

Listing 3: VSCode **launch.json** configuration file contents

```
{
  "version": "0.2.0",
  "configurations": [
    {
      "name": "Python: Django",
      "type": "python",
      "request": "launch",
      "program": "${workspaceFolder}/manage.py",
      "env": {
        "PYTHONPATH1": "${workspaceFolder}/lib:${PYTHONPATH}"
      },
      "args": [
        "runserver",
        "0.0.0.0:8000"
      ],
      "django": true,
      "justMyCode": false
    },
    {
      "name": "Python: Django makemigration",
      "type": "python",
      "request": "launch",
      "program": "${workspaceFolder}/manage.py",
      "env": {
        "PYTHONPATH": "${workspaceFolder}/lib:${PYTHONPATH}"
      },
      "args": [
```

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```

        "makemigration"
    ],
    "django": true,
    "justMyCode": false
},
{
    "name": "Python: Celery Workers",
    "type": "python",
    "request": "launch",
    "module": "celery",
    "console": "integratedTerminal",
    "env" : {
        "GEVENT_SUPPORT": "True"
    },
    "args": ["-A", "web", "worker", "-l", "debug", "-P", "gevent", "--
↪ concurrency", "10", "-Q", "celery", "-E"],
    "justMyCode": true
},
{
    "name": "Python: Celery Beat",
    "type": "python",
    "request": "launch",
    "module": "celery",
    "console": "integratedTerminal",
    "args": ["-A", "web", "beat", "-l", "debug"]
}
]
}

```

33.1.6 Declare Environment Variables

Set secrets in the environment variables in your **.bashrc** file. Activate **.bashrc** file by running the command: `source .bashrc`

If using PyCharm IDE, declare the environment variables in the following places: * Edit Configurations > Environment variables * File->Settings->Build, Execution, Deployment->Console->Python console * File->Settings->Build, Execution, Deployment->Console->Django console * File->Settings->Languages & Frameworks->Django->Enable Django

33.1.7 Set up Python virtual environment

Run the following commands within the project directory to set up a Python virtual environment for the project

Alternatively, you can create a virtual environment for the project with the command: `python3 -m venv venv`

Listing 4: Install packages with pip3 and Python3

```

sudo apt install -y python3-virtualenv
source venv/bin/activate
pip3 install -r requirements/base.txt
pip3 install celery

```

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```
python manage.py migrate && python manage.py social_accounts && python manage.py setup_
↪groups && python manage.py setup_schemas && python manage.py createcachetable &&↪
↪supervisord -c celery.conf && supervisorctl -c celery.conf start all
python manage.py createsuperuser
```

Warning: Here are solutions to possible errors that you might encounter after having ran the above commands:

- **Possible error #1:** `TypeError: 'Collection' object is not callable`. If you meant to call the `'authenticate'` method on a `'Database'` object it is failing because no such method exists.

Solution #1: Run the command: `$ pip3 install pymongo==3.11.4` **Reason:** pymongo versions >4 is incompatible with the COPO project

- **Possible error #2:** Issues related to **importlib**, **rdlib**, **lxml**, **numpy**, **pandas** and **cffi** Python packages

Solution #2: #. In the `requirements/base.txt` file located in the project directory, change the version numbers for the following packages so that all packages can be compatible with each other

```
- asgiref==3.7.2
- cffi==1.15.1
- importlib-metadata==1.6.1
- lxml==4.9.3
- numpy==1.20.0
- pandas==1.2.2
```

1. Change line 12 in **wizard_helper.py** file from `pandas.io.json import json_normalize` to `from pandas import json_normalize`

2. Run the command: `pip3 install -r requirements/base.txt` again to install the packages

- **Possible error #2:** `text index required for $text query`

Solution #3: Create an index in the `SampleCollection` in `mongoDB`: `db.SampleCollection.createIndex({ "$**": "text" })`

33.1.8 Set Up Mongo Database in COPO Project

Note: Replace the username and password for MongoDB with your own username and password

Run the `4_mongo_setup.sh` [MongoDB set up script](#) to configure the MongoDB database on your machine

Set up MongoDB in Studio3T

Note: Replace the <username> and <password> for MongoDB with your MongoDB username and password. By default, the username for MongoDB is `copo_user`. The hostname, `localhost`, can also be substituted with the IP address of `127.0.0.1`.

Create a new MongoDB connection manually with the following details: * **Connection Name:** `copo_mongo` * **Connection Type:** Standalone Connection * **Hostname:** `localhost` * **Port:** `27017` * **Authentication:** Username and Password * **Username:** `copo_user` * **Password:** <password> * **Authentication Database:** `admin`

OR

MongoDB **URI:** `mongodb://copo_user:password@localhost:27017/copo_mongo?retryWrites=true&connectTimeoutMS=10000&authSource=admin&authMechanism=SCRAM-SHA-1`

33.1.9 Set Up PostgreSQL Database in COPO Project

Note: Replace the username and password of PostgreSQL with your own username and password

Run the `3_db_setup.sh` PostgreSQL set up script to configure the PostgreSQL database on your machine

33.1.10 Launch COPO Website

Listing 5: Launch COPO website using the following command

```
python manage.py runserver
```

Alternatively, click on the **Run** button (i.e the green play button) on the top-right corner of the PyCharm IDE to launch the website.

33.2 Set Up COPO Project on Windows

33.2.1 Option 1: Using Ubuntu Terminal

Set up Ubuntu terminal on Windows by enabling the **Windows Subsystem for Linux** through the following steps.

Navigate to Control Panel->Programs-> Turn Windows Features On Or Off # Enable the **Windows Subsystem for Linux** option in the list # Click the **OK** button # Click **Restart now** when you're prompted to restart your computer # Open Microsoft Store (MS) from the **Start** menu, and search for **Linux** in the store or open this [link](#) to find the Ubuntu app on MS store: # Click **Get the apps** under the **Linux on Windows?** banner. # Search and click Ubuntu Linux distribution to get "Get" or "Install" it # Launch Ubuntu app

Note: The first time that the Linux environment is launched, one is prompted to enter a UNIX username and password. These don't have to match your Windows username and password, but will be used within the Linux environment.

Hint: In the Ubuntu terminal (which can be found in the Microsoft Store or from the **Start** menu or by searching for **Ubuntu** using the search bar): * To copy text: highlight desired text then, **right-click** * To paste text: **right-click**

Warning:

- **Error #1:** 0x800701bc WSL 2 requires an update to its kernel component. For information please visit <https://aka.ms/wsl2kernel> **Solution:** Go to Manual installation steps for older versions of WSL | Microsoft Docs to download WSL 2Set WSL 2 as default version: `wsl --set-default-version 2`
- **Error #2:** WslRegisterDistribution failed with error: 0x80370102. Error: 0x80370102 The virtual machine could not be started because a required feature is not installed. **Solution:** * Run Windows PowerShell under Administrator rights (Right-click on the Windows 10 Start button and select “Windows PowerShell (Admin)”) * Copy-paste the following command: * `Enable-WindowsOptionalFeature -Online -FeatureName VirtualMachinePlatform` * Restart the PC or laptop

33.2.2 Option 2: Using Windows Terminal

Note:

- Commands are entered in the command prompt
 - Cloning a GitHub repository enables the branches to show and gives access to committing, pushing etc to the remote repository
 - Repeat steps 1 to 19 under Ubuntu section in setting up COPO project on Ubuntu
-

Hint:

- To open the command prompt in Windows, open the **Start menu** and search for `cmd`.. Press **Enter** or click the result to open a command window or **right-click** the option to run it as an administrator
 - To view all environment variables in the terminal:`C:\Users<username> SET`
-

1. Download and install Python:
2. Download PyCharm: Python IDE for Professional Developers by JetBrains
3. Install Django: `>`py -m pip3 install Django``
4. Download [PyCharm IDE for Professional Edition](#):
5. Setup PyCharm Professional with a JetBrains account and a school email
6. Add/Authorise GitHub account to PyCharm
7. Clone the [COPO project GitHub repository](#) instead of downloading it as a .zip file from the GitHub repository
8. Open the cloned COPO project in PyCharm
9. In PyCharm, add a new configuration by navigating to - Add Configurations->Add new->Django Server
10. Set up or copy and paste environment variables in the following four places in PyCharm: * Edit Configurations * File->Settings->Build, Execution, Deployment->Console->Python console * File->Settings->Build, Execution, Deployment->Console->Django console * File->Settings->Languages & Frameworks->Django->Enable Django

11. Set system environment variables * On the Windows taskbar, right-click the Windows icon and select **System**.
* In the **Settings** window, under **Related Settings**, click **Advanced system settings**. * On the **Advanced** tab, click **Environment Variables** * Click **New** * to create a new environment variable * Click **Edit** to modify an existing environment variable * After creating or modifying the environment variable, click **Apply** and then, **OK** to have the change take effect

OR

Set environment variables in the terminal * To set environment variables in the terminal replace “export” with “set”

e.g. Replace `> export ENVIRONMENT_TYPE="dev"` with `> set ENVIRONMENT_TYPE="dev"`

BROKERING DATA IN COPO WITH FAIR DATA PRINCIPLES

Findable, Accessible, Interoperable and Reusable (FAIR) data enables data consumers (people or machines) to find, aggregate and analyse data that would otherwise be private or invisible, building on the existing web of linked data.

In COPO, the FAIR principles are applied as follows:

34.1 Findable

34.1.1 Using DataTables' search engine

COPo uses *DataTables* to display tabular data. The data are indexed in the DataTables' *smart* search engine and the search box is accessible within each table of data; it is located at the top right of the table. The search engine is updated automatically when metadata is added or updated.

The search box provides the following abilities:

- Match words out of order
- Partial word matching
- Preserved text

See [here](#) for more information about searching for data in DataTables.

34.1.2 Using COPO API

Metadata can also be found via the *COPO API*.

34.2 Accessible

The required data can be retrieved freely with unrestricted access or via authentication and authorisation mechanisms, where necessary.

34.3 Interoperable

Data are integrated and available on ENA and NCBI. Data can be exported in csv, json or ro-crate format using the COPO API.

34.4 Reusable

Metadata are well-described with a plurality of accurate and relevant attributes. They are published to public repositories and can be accessed with the COPO API via a clear and accessible data usage.

34.5 FAIR Webinars

Webinar: COPO: Extending the frontiers of “FAIR” Data in Agriculture as part of RDA/IGAD webinar series

Date: February 12th July, 2020.

Host: Research Data Alliance/Improving Global Agricultural Data (RDA/IGAD)

Featured:

- [Dr. Anthony Etuk](#) , former Research Software Engineer of the COPO team
- [Dr. Felix Shaw](#) , Research Software Engineer of the COPO team

<https://youtu.be/33Ozdpdfyh0>

See also:

Visit [FAIR website](#) for more information about FAIR principles.

LICENCE

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END OF TERMS AND CONDITIONS

35.1 How to apply the Apache Licence to your work

To apply the Apache Licence to your work, attach the following boilerplate notice, with the fields enclosed by brackets “[]” replaced with your own identifying information. (Don’t include the brackets!) The text should be enclosed in the appropriate comment syntax for the file format. We also recommend that a file or class name and description of purpose be included on the same “printed page” as the copyright notice for easier identification within third-party archives.

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CONTRIBUTOR COVENANT CODE OF CONDUCT

36.1 Our Pledge

We as members, contributors, and leaders pledge to make participation in our community a harassment-free experience for everyone, regardless of age, body size, visible or invisible disability, ethnicity, sex characteristics, gender identity and expression, level of experience, education, socio-economic status, nationality, personal appearance, race, religion, or sexual identity and orientation.

We pledge to act and interact in ways that contribute to an open, welcoming, diverse, inclusive, and healthy community.

36.2 Our Standards

Examples of behaviour that contributes to a positive environment for our community include:

- Demonstrating empathy and kindness toward other people
- Being respectful of differing opinions, viewpoints, and experiences
- Giving and gracefully accepting constructive feedback
- Accepting responsibility and apologising to those affected by our mistakes, and learning from the experience
- Focusing on what is best not just for us as individuals, but for the overall community

Examples of unacceptable behaviour include:

- The use of sexualised language or imagery, and sexual attention or advances of any kind
- Trolling, insulting or derogatory comments, and personal or political attacks
- Public or private harassment
- Publishing others' private information, such as a physical or email address, without their explicit permission
- Other conduct which could reasonably be considered inappropriate in a professional setting

36.3 Enforcement Responsibilities

Community leaders are responsible for clarifying and enforcing our standards of acceptable behaviour and will take appropriate and fair corrective action in response to any behaviour that they deem inappropriate, threatening, offensive, or harmful.

Community leaders have the right and responsibility to remove, edit, or reject comments, commits, code, wiki edits, issues, and other contributions that are not aligned to this Code of Conduct, and will communicate reasons for moderation decisions when appropriate.

36.4 Scope

This Code of Conduct applies within all community spaces, and also applies when an individual is officially representing the community in public spaces. Examples of representing our community include using an official e-mail address, posting via an official social media account, or acting as an appointed representative at an online or offline event.

36.5 Enforcement

Instances of abusive, harassing, or otherwise unacceptable behaviour may be reported to the community leaders responsible for enforcement at . All complaints will be reviewed and investigated promptly and fairly.

All community leaders are obligated to respect the privacy and security of the reporter of any incident.

36.6 Enforcement Guidelines

Community leaders will follow these Community Impact Guidelines in determining the consequences for any action they deem in violation of this Code of Conduct:

36.6.1 1. Correction

Community Impact: Use of inappropriate language or other behaviour deemed unprofessional or unwelcome in the community.

Consequence: A private, written warning from community leaders, providing clarity around the nature of the violation and an explanation of why the behaviour was inappropriate. A public apology may be requested.

36.6.2 2. Warning

Community Impact: A violation through a single incident or series of actions.

Consequence: A warning with consequences for continued behaviour. No interaction with the people involved, including unsolicited interaction with those enforcing the Code of Conduct, for a specified period of time. This includes avoiding interactions in community spaces as well as external channels like social media. Violating these terms may lead to a temporary or permanent ban.

36.6.3 3. Temporary Ban

Community Impact: A serious violation of community standards, including sustained inappropriate behaviour.

Consequence: A temporary ban from any sort of interaction or public communication with the community for a specified period of time. No public or private interaction with the people involved, including unsolicited interaction with those enforcing the Code of Conduct, is allowed during this period. Violating these terms may lead to a permanent ban.

36.6.4 4. Permanent Ban

Community Impact: Demonstrating a pattern of violation of community standards, including sustained inappropriate behaviour, harassment of an individual, or aggression toward or disparagement of classes of individuals.

Consequence: A permanent ban from any sort of public interaction within the community.

36.7 Attribution

This Code of Conduct is adapted from the [Contributor Covenant](https://www.contributor-covenant.org/version/2/0/code_of_conduct.html), version 2.0, is available at https://www.contributor-covenant.org/version/2/0/code_of_conduct.html.

Community Impact Guidelines were inspired by [Mozilla's code of conduct enforcement ladder](#).

For answers to common questions about this code of conduct, see the [FAQ](#) or [Translations](#).

Last reviewed on: 08-01-2024

PRIVACY NOTICE

This Privacy Notice explains what data is collected by the **Collaborative OPen Omics (COPO)** website service, its purposes, how the data is processed and how COPO keeps it secure.

Please view our [Terms of Use](#) regarding the rules and requirements for the use of the service.

37.1 Consent

Processing your data is necessary for our legitimate interest of allowing the operation and functioning of COPO. By using our website, you hereby consent to our Privacy Notice and agree to its terms.

37.1.1 Data Collected

COPO adopts appropriate data collection, validation, storage and processing practices as well as security measures to protect against unauthorised access, alteration, disclosure or destruction of your personal information, [Orcid](#) credentials and metadata provided on our service.

Information collected:

- Internet Protocol (IP) address
- Operating system
- Browser
- First name, last name and username after you sign into the service with your Orcid credentials
- Email address (after you input it in the dialog shown after a first-time access to the service)
- Date and time when a profile record and manifests are created or updated
- Metadata submitted. Metadata is the essential information about when, where, how and why data has been collected. It can relate to research elements like samples, assemblies, sequencing annotations, barcoding, experiments, reads or runs
- If you contact us via email, we may receive additional information about you such as the contents of the message and/or attachments you may send us and any other information you may choose to provide

Usage of information collected:

- To utilise Google Fonts, an interactive web directory via Cascading Style Sheets (CSS), which is embedded in the service
- To provide the user access to the service
- To answer support request sent by the user
- To monitor errors and exceptions that may occur during metadata submission
- To register your email address with your COPO user account and to submit your email address to public repositories after manifest submissions
- To send email notifications when submitted samples have been accepted or rejected by a sample manager

37.2 Data Access

- Authorised COPO team developers
- Public metadata repositories that COPO relies on to provide the service. They are:
 - [BioImage Archive \(BIA\)](#)
 - [ENA](#)¹
 - [NCBI](#)²

37.3 Data Retention

- Any personal data (name and email address) and metadata obtained from you will be retained as long as the service is live, even if you stop using the service.
- COPO obscures your email address and omits your name from the [COPO Application Programming Interface \(API\)](#) method results after a manifest submission. However, your email address will be submitted to public repositories and will be visible on public records as a metadata submitter.
- Access to the web and security logs containing personal data are restricted to the relevant COPO team developers

37.4 Cookies

This service uses “cookies” to store information about the web pages that the visitor has accessed or visited.

The information is used to log any errors or exceptions that may occur and user sessions.

¹ See term: [ENA](#).

² See term: [NCBI](#).

37.5 Questions

Any questions or comments concerning this Privacy Notice can be addressed to us by

Published on: 28-10-2023

TERMS OF USE

- The **Collaborative OPen Omics (COPO)** website service promotes *Findable, Accessible, Interoperable and Reusable (FAIR)* metadata brokerage through the submission of research objects (raw or processed data, reads, samples, images etc.) which are made public to the research community and public repositories like -
 - BioImage Archive (BIA)
 - ENA¹
 - NCBI²

- This service uses cookies to record information about your website session to enable the website to function well. You can control your use of cookies from your web browser but if you choose not to accept cookies from the COPO website service, you will not be able to take full advantage of all of the website's features.

- This service also uses Google Fonts, a website font service that is owned by Google LLC or by Google Ireland Limited, to provide an interactive web directory via Cascading Style Sheets (CSS) throughout the service.

The Google server needs to collect your Internet Protocol (IP) address in order to send you the Google Font files from the Google servers when you access the service. Through the use of Google Fonts, the website performance is optimised and is displayed more beautiful.

Even though our service self-host Google Fonts on some web pages in order to eliminate violating General Data Protection Regulation (GDPR), there are other web pages in our service that do not. By using the service, you consent for the service to use your IP address so that it can load the Google Fonts from the Google servers.

- COPO will make all reasonable effort to maintain continuity of its service and provide adequate warning of any changes or discontinuities. However, COPO accepts no responsibility for the consequences of any temporary or permanent discontinuity of the service.
- If you email or submit offensive, inappropriate or objectionable content on our website or to us, or engage in any disruptive behaviour on our service, we may use your personal information from our security logs to stop such behaviour. We may also use your personal information to inform relevant third parties about the content and your behaviour where we reasonably believe that you are or may be in breach of any applicable laws.
- COPO imposes no additional restrictions on the use of the submitted data available on our service after they have been provided by the metadata submitter other than those provided by the metadata submitters like embargoed metadata.

However, there are restrictions imposed on the metadata submitter on the metadata after the metadata have been uploaded and submitted on the COPO service.

Some of these metadata submitter restrictions include but are not limited to the following:

- Profile records cannot be deleted after they have associated research objects like samples, reads, files, sequencing annotations, accessions, barcoding manifests etc..

¹ See term: *ENA*.

² See term: *NCBI*.

- Samples cannot be deleted after they have been submitted; they can only be updated. More details about what field values can be updated can be found in the [Updating Samples](#) section in our documentation.
- Please see our documentation on the various profile components for [Stand-alone Profile](#) and [Tree of Life Profile](#) for more information concerning the restrictions and possibilities of the various research objects.
- All scientific metadata will be made publicly available after data submission and we may store it permanently.
- The metadata submitted and the [COPO Application Programming Interface \(API\) methods](#) are generated in part from the data contributed by the community who remain the data submitters.
- COPO does not guarantee the accuracy of any provided metadata for any purpose. We, however, make all reasonable effort to ensure that the metadata submitted are validated according to the Standard Operating Procedure (SOP)³ for each manifest type.

Please see our documentation regarding the [SOP requirements](#) for each manifest type for more information.

- The metadata submitted may be subject to embargoed rights or permits rights. It is the responsibility of users of this service to ensure that their exploitation of the data does not infringe any of the rights of such parties.
- We reserve the right to update these terms of use at any time. We will attempt to give reasonable notice of any changes by placing a notice on our website or by sending an email to any email address you may have provided to us, but you may wish to check the terms of use each time you use the website.

The date of the most recent revision will appear at the bottom of this web page, the ‘Terms of Use’ web page. If you do not agree to these changes, please do not continue to use our service.

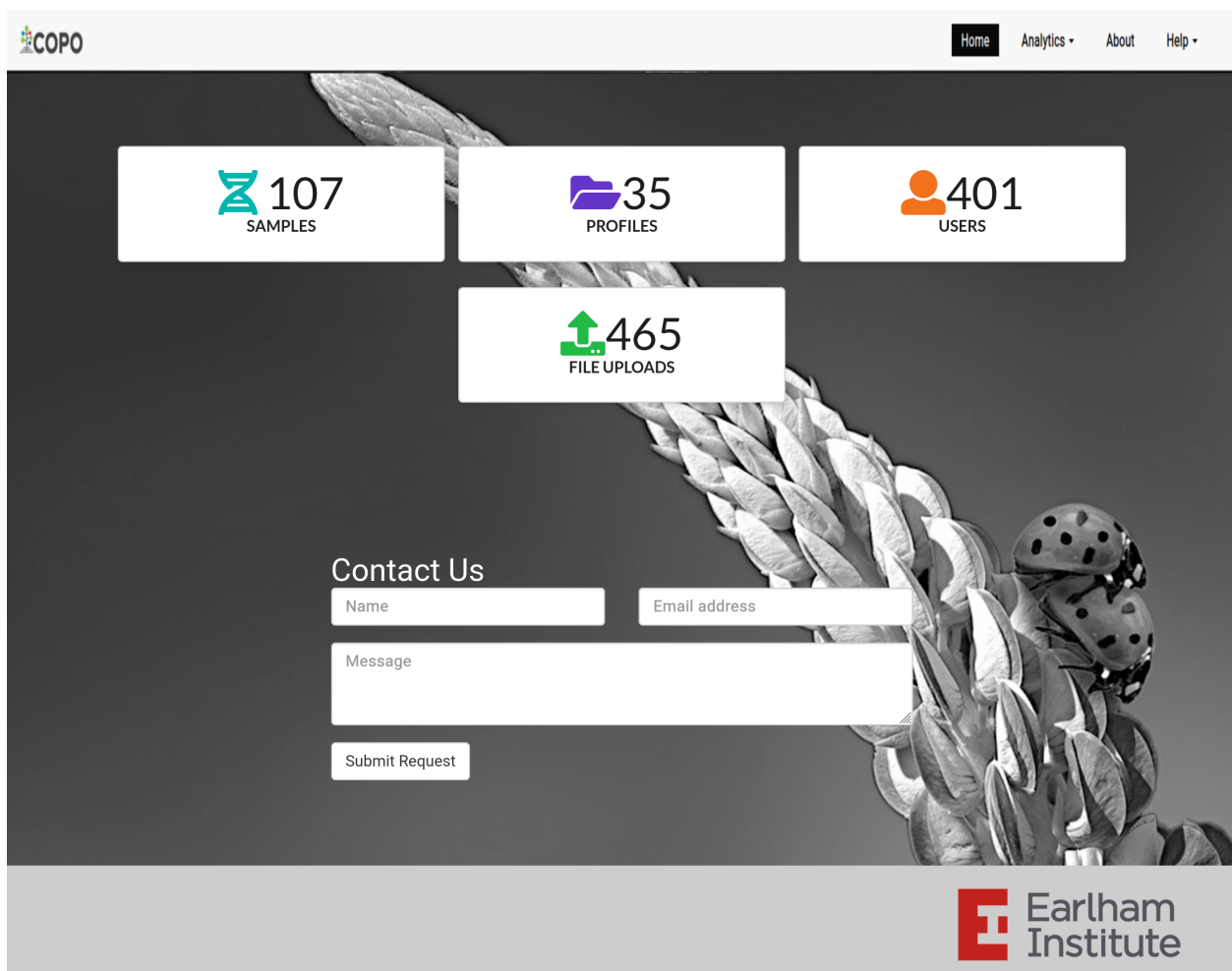
- Any feedback provided to COPO about its service will be treated as non-confidential unless the individual or organisation providing the feedback states otherwise.
- Any questions or comments concerning these terms of use can be addressed to us by . More details about the data that we collect from you when you browse the website, make manifest submissions and how we process the data are detailed in our [Privacy Notice](#).

Last revised: 28-10-2023

³ See term: [SOP](#).

CONTACT COPO

Send an email to the COPO team at copo@earlham.ac.uk, indicating your enquiry or request. The COPO team will respond as soon as possible.



The screenshot shows the COPO homepage with a navigation bar at the top containing links for Home, Analytics, About, and Help. The main content area features four statistics cards: 107 Samples, 35 Profiles, 401 Users, and 465 File Uploads. Below these is a 'Contact Us' form with fields for Name, Email address, and Message, and a 'Submit Request' button. The background of the page features a close-up image of a ladybug on a leaf. The Earlham Institute logo is visible in the bottom right corner.

Alternatively, you can input your enquiry or request in the Contact form on the COPO homepage



Alternatively, click the envelope icon located in the top-right section of the top navigation bar to be redirected to the contact form on the COPO homepage (if you are already logged into COPO)

FREQUENTLY ASKED QUESTIONS

Hint: To view the entire answer to a question, collapse the answer by clicking the ► button below.

40.1 Assemblies

40.1.1 What are the types of files that are required for assembly submissions in COPO?

See the [European Nucleotide Archive's \(ENA's\) documentation](#) for details about the types of files that can be submitted for assembly submissions.

40.1.2 How can I assign my own locus tag to assemblies?

Hint: Each profile in COPO is known as a study or project in ENA (after reads have been submitted).

Note: Reads submission **must** be done in order for a locus tag to be assigned to the project.

This is because a project submission is done to European Nucleotide Archive (ENA) once reads submission has been completed.


Contact the with the request indicating the locus tag that you would like to assign.

If not, ENA will automatically assign a locus tag to your assembly after it has been submitted in COPO and deposited to ENA.

See [ENA's documentation](#) for more details. The documentation outlines rules that the locus tag prefix should conform to.

40.2 Dashboard

40.2.1 How can I view accessions after I have submitted samples, reads, or experiments in COPO?

- Click the  button.
- The accessions dashboard will be displayed.
- Alternatively, navigate to the [Accessions dashboard](#).

40.2.2 Is there a way to analyse metadata submissions?

1. Tree of Life dashboard

- Alternatively, click the  button.

2. Tree of Life inspection web page

- Alternatively, click the  button.

3. Tree of Life inspection by Genome Acquisition Lab web page

- Alternatively, click the  button.

4. Statistics web page

40.3 Files

40.3.1 How do I know when data files that have been uploaded to COPO are public on European Nucleotide Archive (ENA)?

See [Checking ENA File Upload Status](#) section for more information.

40.4 Permits


40.4.1 Can I view or download permits that I have uploaded in COPO?

Yes, permits can be retrieved and downloaded by selecting the desired sample record(s) on the **Samples** web page

Then, clicking the  button on the web page.

40.4.2 Why am I unable to upload permit one after the other?

Warning:

- If you have more than one permit file to upload, they **must** be uploaded at the same time i.e. after you have clicked the  button, navigate to the directory where the permits are stored and CTRL + click all of the permits so that all the permits are highlighted and uploaded at the same time.

- All permit files have to be selected/opened from the directory and uploaded together not one after the other.

40.5 Profiles

40.5.1 How can I be added to a profile group?

40.5.2 How can I create a profile on COPO?

- View the following video to see how to create a profile.

<https://youtu.be/7xiVTNw6pPc>

40.5.3 How can I upload/submit research objects to a profile owned by another user or how can I create a group or how can I share my profile with others?

See *Sharing Profiles* section for more information.


40.5.4 How can I add a subproject to a profile on COPO?

- In the **Add Profile** form, choose the desired subproject(s) from the list of associated projects as shown below.
- See the *Secondary Projects* section for information about the available subprojects.

40.5.5 How can I add a subproject or secondary project to a primary project in ENA/Biosamples?

- Contact the with the request providing the project accession of the child/subproject and the project accession of the parent/primary project.

40.5.6 How can I edit or delete a profile that I have created in COPO?

- Click the  icon that is associated with the desired profile.
- The option to edit or delete a profile record will be displayed once clicked.
- The web page will refresh after the task has been completed successfully.

Add Profile

Title required ⓘ

Description required ⓘ

Profile Type ⓘ

Darwin Tree of Life (DTOL)

Associated Profile Type ⓘ

Select associated type(s)

Aquatic Symbiosis Genomics (ASG)

Biodiversity Genomics Europe (BGE)

European Reference Genome Atlas (ERGA)

European Reference Genome Atlas - Pilot (ERGA_PILOT)

Fig. 1: Add Profile form: Selecting Associated Profile Type dropdown menu

40.5.7 How many profiles can I have in COPO?

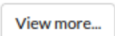
- For instance, you can create a profile to represent work done as part of a grant, subproject within a project or a PhD (Doctorate of Philosophy) project.

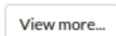
40.5.8 How can I view more profiles that I have created in COPO?

- More profiles that you have created will be loaded.


40.5.9 How can I view more information about a profile that I have created in COPO?

Note:


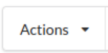
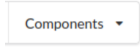
- The  button will only be associated with a profile if the profile has at least one of the following information.

- Click the  button associated with the profile.
- After the button is clicked, a popup dialog will show at least one of the following information if it is available:
 - **Release Status** (if applicable)
 - **Release Date** (if applicable)
 - **Associated Profile Type(s)**
 - **Sequencing Centre**

40.5.10 How can I navigate to the top of the web page after having loaded several work profiles?

- Alternatively, click the  button which automatically navigates to the top of the web page.

40.5.11 How can I create components for a profile?

1. Navigate to the work profile web page
2. Click the  button
3. Fill in then, save the form that is displayed
4. Click the  button associated with the created profile record to view a dropdown list of tasks that can be performed for that profile
5. Complete the action/task
6. Click the  button associated with the profile record to view the component of the action that was performed

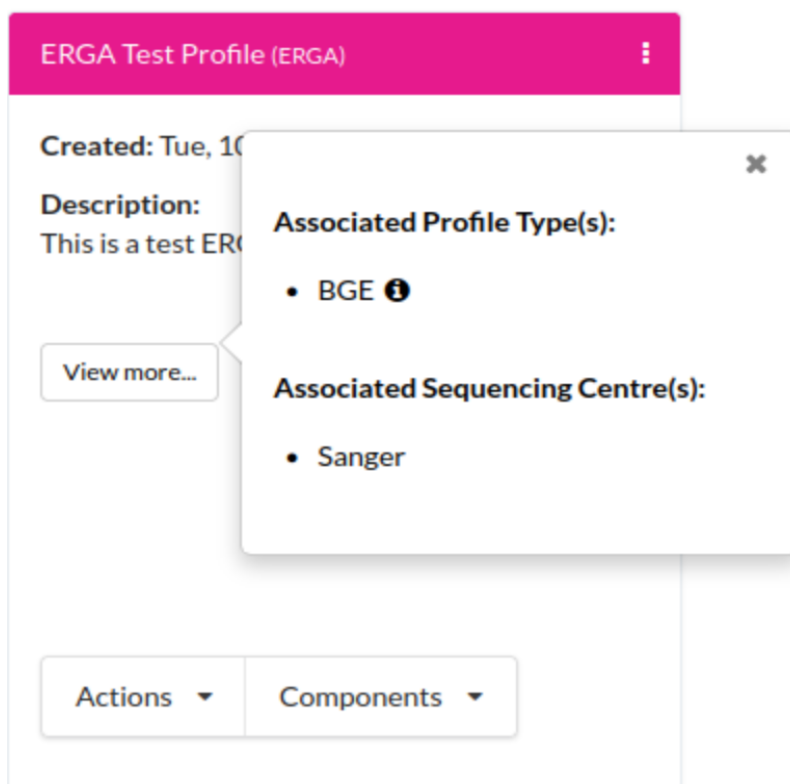


Fig. 2: Profile: View more information popup dialog

40.5.12 How can I make profiles or projects public or visible in European Nucleotide Archive (ENA)?

See *Releasing Profiles (Studies)* section for more information.

40.5.13 What are the names of the sequencing centres whose samples are brokered through COPO?

Currently, there are 20 sequencing centres whose samples are brokered through COPO.

Each COPO ERGA profile should be associated with a sequencing centre.

The following are the names of the sequencing centres:

- CENTRO NACIONAL DE ANÁLISIS GENÓMICO
- DNA SEQUENCING AND GENOMICS LABORATORY, HELSINKI GENOMICS CORE FACILITY
- EARLHAM INSTITUTE
- FUNCTIONAL GENOMIC CENTER ZURICH
- GENOSCOPE
- HANSEN LAB, DENMARK
- INDUSTRY PARTNER
- LAUSANNE GENOMIC TECHNOLOGIES FACILITY
- LEIBNIZ INSTITUTE FOR THE ANALYSIS OF BIODIVERSITY CHANGE, MUSEUM
- KOENIG, BONN
- NEUROMICS SUPPORT FACILITY, UANTWERP, VIB
- NGS BERN
- NGS COMPETENCE CENTER TÜBINGEN
- NORWEGIAN SEQUENCING CENTRE
- Other_ERGA_Associated_GAL
- SANGER INSTITUTE
- SCILIFELAB
- SVARDAL LAB, ANTWERP
- UNIVERSITY OF BARI
- UNIVERSITY OF FLORENCE
- WEST GERMAN GENOME CENTRE

40.6 Reads

40.6.1 How do I fill in the Reads manifest to submit paired reads?

- Ensure that the **Reads** manifest contains the following:
 - **PAIRED** as the value for the **Library layout** column
 - File names in the **File name** column separated by a comma

See below for a snapshot of a **Reads** manifest for paired reads:

File name	Instrument model	Library layout
small1_r1.fastq.gz, small2_r2.fastq.gz	GridION	PAIRED
small3_r3.fastq.gz, small4_r4.fastq.gz	GridION	PAIRED

Fig. 3: Reads' manifest for paired reads

40.6.2 What are the types of files that are required for read submissions in COPO?

See the [European Nucleotide Archive's \(ENA's\) documentation](#) for details about the types of files that can be submitted for read submissions.

40.7 Samples

40.7.1 How can I update values for samples that I have submitted in COPO?

Note:

- The manifest **must** be reuploaded in the same profile that the samples were submitted in.
- The desired value(s) will be updated once the field value is not a compliance field¹.
- See the [Updating Samples](#) section for information about which field values can be updated.

40.7.2 Can I delete samples that have submitted?

No, samples cannot be deleted after the manifest have been submitted.

40.7.3 Can I retrieve samples or the manifest that have been submitted?

Yes, see the [How to Download Submitted Sample Manifest](#) section for more information.

40.7.4 How can I view images that have been uploaded?

See the [View Submitted Images](#) section for more information.

40.7.5 How can I download permits that have been uploaded?

See the [Download Submitted Permits](#) section for more information.

40.7.6 What are the formats that I can download samples in?

The following are the formats that samples can be downloaded in:

- Microsoft Excel Spreadsheet format (.xlsx)
See the [Downloading manifest in spreadsheet format](#) section for more information.
- Comma-separated values (csv) format (.csv)

On the **Samples** web page, click the  button to download a manifest in csv format.

See [How to access Samples web page](#) section for guidance.

¹ See term: [Compliance field](#)

40.7.7 How can I submit virtual samples in COPO?

Virtual samples are research objects that are submitted to COPO under a Stand-alone profile.


See the *Submitting Virtual Samples* section for more information.

40.8 Sample Managers

40.8.1 How can I be assigned as a sample manager?

- Make a request to the indicating the type of profile group that you would like to be assigned as a sample manager.
- The permission will be granted after the request has been approved.

40.8.2 How can I know if I have been assigned as a sample manager?

- The  button will be displayed on the web page.
- The **accept/reject samples** web page will be displayed once the button is clicked.
- Alternatively, if you can navigate to the [Accept/Reject Samples' web page](#) with an **Unauthorisation** error web page being displayed then, you are a sample manager.

40.8.3 How can I accept or reject samples that users have submitted?


Note: See *Accessing the Accept or Reject Samples web page* section for guidelines on accessing the **Accept or Reject Samples** web page.

See *Accepting or Rejecting Samples* section for more information.

40.8.4 How can I download sample manifests that have been submitted by manifest providers or sample submitters?


See *Downloading submitted sample manifest* section for more information.

40.8.5 Can I download permits that users have uploaded in COPO?

Yes, on the **Accept or Reject Samples** web page, permits can be downloaded by selecting the desired sample record(s) then, clicking the  button on the web page.

See *Downloading permits* section for more information.


40.8.6 Can I view images that users have uploaded in COPO?

Yes, on the **Accept or Reject Samples** web page, images can be viewed by selecting the desired sample record(s) then, clicking the  button on the web page.

See *Viewing images* section for more information.

40.8.7 If I belong to more than one sample manager manifest group, how can I view or accept samples that belong to them?

Note:

- The manifest dropdown menu will only be displayed on the **Accept or Reject samples** web page if you as a sample manager, belongs to more than one sample manager manifest group.
 - If the *dtol* sample manager group dropdown menu option is selected, both Aquatic Symbiosis Genomics (ASG) profiles and Darwin Tree of Life (DTOL) profiles will be displayed in the **All profiles** tab and/or **Profiles for My Sequencing Centre** the **Accept or Reject samples** web page will be displayed (if any exists).
-
- Choose desired sample manager group from the manifest group dropdown menu.
 - Click the  button to accept or reject samples.

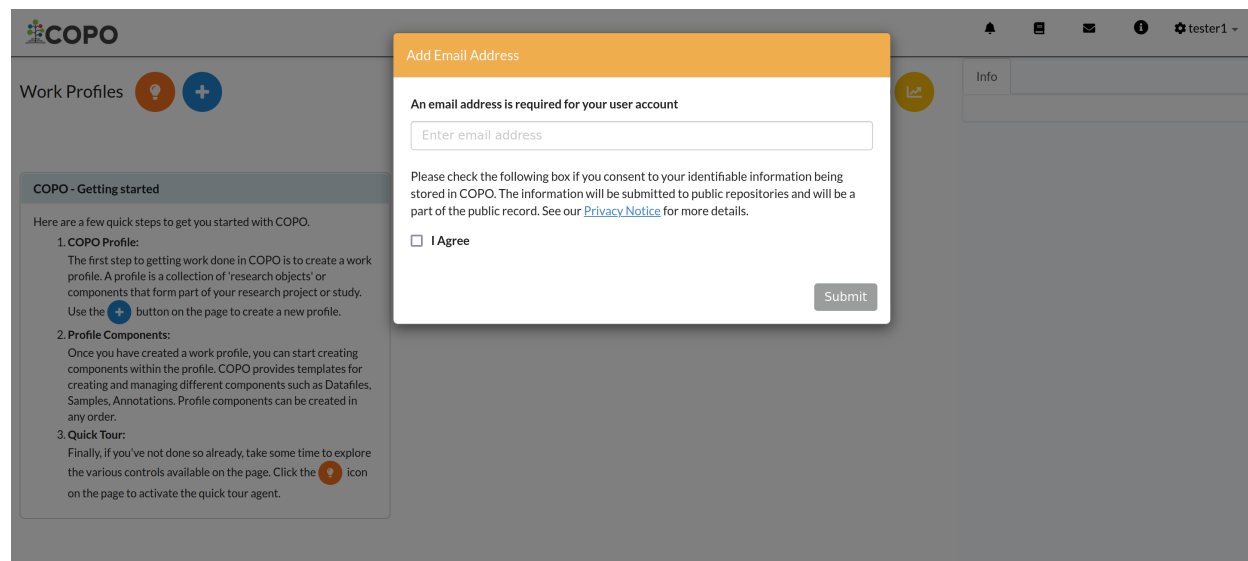


Fig. 4: Accept or Reject samples: Email address prompt shown when a user logs into COPO for the first time

See *Viewing images* section for more information.

GLOSSARY

API

A [software interface](#) that allows two or more applications to communicate with each other.

ASG

A [project](#) that aims to provide the genomic foundations needed by scientists to answer key questions about the ecology and evolution of symbiosis in marine and freshwater species, where at least one partner is a microbe.

Assembly

Any sequence records from coding or non-coding regions to full assembled chromosomes.

Barcoding manifest

In COPO, barcoding manifest submissions contain short assembled and annotated sequences that represent interesting features or gene regions. In ENA, the barcoding manifests are referred to as *targeted sequences*.

BGE

A [project](#) that undertakes a comprehensive application of genomic science to biodiversity research will drive fundamental advances in conservation science and policy.

Biocuration

The extraction of unstructured biological data from manifests into a structured, computable form.

Compliance field

A compliance field in COPO is a mandatory field that cannot be updated after a manifest has been uploaded or submitted before or after the samples have been accepted or rejected by a sample manager.

COPO (Collaborative OPen Omics)

[COPO](#) is a web-based tool for creating and managing metadata for research objects.

COPO profile

Also known as work profile. A collection of ‘research objects’ or components that contain data generated on a biological research project or study.

There are two general types of profiles in COPO: *Stand-alone* profiles and ToL profiles. ASG, DToL and ERGA are the ToL (primary) projects brokered through COPO.

CRUD (Create, Read, Update and Delete) operations

Comprises posting data (creating and/or updating data), reading data (e.g. making queries) and deleting data.

DataTables

A jQuery library plug-in that displays tabular data. They are used in COPO to display a list of research objects. See [DataTables](#) for more information.

DB (Database)

A [database](#) is an organised collection of data, generally stored and accessed electronically from a computer system.

DNA (Deoxyribonucleic acid)

The molecule inside cells that contains the genetic information responsible for the development and function of an organism.

Docker

A set of platform as a service (PaaS) products that use OS-level virtualisation to deliver software in packages called containers. Containers are isolated from one another and bundle their own software, libraries and configuration files; they can communicate with each other through well-defined channels.

Docker Engine is the software that oversees the hosting of the containers.

Dockerfile

A text-based file with no file extension that contains a script of instructions. Docker uses this script to build a container image. See [Dockerfile reference](#)

DTOL

Aims to sequence the genomes of 70,000 species of eukaryotic organisms in Britain and Ireland.

It is one of the ToL projects brokered through COPO. The [project](#) is a collaboration between biodiversity, genomics and analysis partners that is transforming the manner by which biology, conservation and biotechnology are conducted.

DTOL may sometimes be referred to as *DTOL*.

EBI (European Bioinformatics Institute)

[EBI](#) is a UK (United Kingdom) government-funded public repository for biological data that provides free access to biomedical and genomic information.

EI (Earlham Institute)

The [Earlham Institute](#) is a hub of life science research, training, and innovation focused on understanding the natural world through the lens of genomics. EI supports several projects including COPO project.

EI is one of four [Norwich BioScience Institutes \(NBI\)](#) international centres that is based in the Norwich Research Park in Eastern England. It is also one of eight institutes that receive strategic funding from the [Biotechnology and Biological Sciences Research Council \(BBSRC\)](#), part of UKRI (United Kingdom Research and Innovation), as well as support from other research funders.

The other NBI (Norwich BioScience Institutes) centres are [John Innes Centre \(JIC\)](#), [Sainsbury Laboratory \(TSL\)](#) and [Quadram Institute Bioscience \(QIB\)](#).

EMBL (European Molecular Biology Laboratory)

[EMBL](#) is a EU (European Union) intergovernmental organisation that performs basic research in molecular biology and provides services to the scientific community in its member states.

ENA

[ENA](#) is a repository for nucleotide sequence data that provides annotated DNA and RNA sequences. It also provides free and unrestricted access stores complementary information such as experimental procedures that details sequence assemblies and other metadata related to sequencing projects.

ENA is part of the [International Nucleotide Sequence Database Collaboration \(INSDC\)](#), which comprises the [DNA DataBank of Japan \(DDBJ\)](#), the [European Molecular Biology Laboratory \(EMBL\)](#), and [GenBank](#) at the [National Center for Biotechnology Information \(NCBI\)](#).

ERGA

A [project](#) that revolves around a pan-European scientific response to current threats to biodiversity by studying reference genomes which provide the most complete insight into the genetic basis that forms each species and represent a powerful resource in understanding how biodiversity functions.

FAIR

The ability to find, access, interoperate and reuse data with no or minimal human intervention.

GAL (Genome Acquisition Lab)

Partners or companies that perform genome sequencing.

Genome

A complete set of genetic material stored in long molecules of DNA in living organisms such as virus, oak tree or an elephant.

Genomics

The study of all or a substantial portion of the genes of an organism as a dynamic system, over time, to determine how those genes interact and influence biological pathways, networks, and physiology.

HTTP (Hypertext Transfer Protocol)

A [protocol](#) that allows communication between different systems. Similar to HTTPS (Hypertext Transfer Protocol Secure).

See also: [HTTPS protocol](#)

IP (Internet Protocol)

A [protocol](#) that allows communication between different systems.

Locus tag

Adapted from [ENA's definition](#): Locus tags are identifiers applied systematically to every gene in a sequencing project.

MacOS

A series of proprietary graphical operating systems developed and marketed by Apple Inc. since 2001.

Manifest

A csv (comma-separated values) file or Microsoft (MS) Excel spreadsheet that contains metadata regarding a research object.

The manifest is used by scientists to upload metadata into COPO.

Manifest checklist

A list of fields that are required to be filled in for a sample to be considered valid.

Manifest ID

A unique identifier assigned to each manifest record in COPO.

Metadata

In-depth and controlled contextual information about when, where, how and why data has been collected like geographical location, time of collection, tube or well identification and specimen identification. Metadata can relate to a research elements such as samples, assemblies, annotations or experiments.

In life sciences, metadata facilitates [biocuration](#) which revolves around the structuring of datasets in a way that allows automated search, query and retrieval.

MIT (Massachusetts Institute of Technology) licence

A permissive free software license from the Massachusetts Institute of Technology that has limited restriction on the reuse of software.

MongoDB

A document-oriented database program that uses JSON-like documents with optional schemas.

NCBI (National Center for Biotechnology Information)

[NCBI](#) is a US (United States) government-funded public repository for biological data that provides free access to biomedical and genomic information.

Ontology field

An ontology field in COPO is an auto-complete control, that maps user input to semantically-enriched values, which are explicit formal specifications of terms and their relationship to other terms in a domain.

**Profile action**

A set of actions that can be performed on a profile. They are correlated with the profile components in COPO.

Profile component

Also known as *research object*. It forms part of a research project or study.

Templates for creating or describing research objects can be found [here](#).

Profile components are correlated with profile actions in COPO.

Profile Types legend

This describes the types of the profiles that have been created. It is located at the right of the * *Work Profiles** web page.

PyCharm

A Python IDE (Integrated Development Environment) that provides code analysis, a graphical debugger, an integrated unit tester, integration with version control systems and supports web development with Django.

Read the Docs

A documentation [hosting service](#) based around Sphinx. COPO documentation is hosted on [Read the Docs](#).

Reads

A research object that holds raw read files and sequencing methods that refer to the DNA sequence from a small section of DNA.

It can be associated with one or more files, assemblies and sequence annotations.

Research

Systematic investigation, including research development, testing, and evaluation, designed to develop or contribute to generalisable knowledge.

REST

Relies on a stateless, client-server and cacheable communications [HTTP](#) request protocol. In COPO, it is used to communicate with the COPO API to perform [CRUD operations](#) using HTTP requests.

RNA-SEQ (Ribonucleic acid sequencing)

Analysis based on next-generation sequencing (NGS) data has recently become the de facto standard for the analysis of gene expression at the level of the whole transcriptome.

RO-Crate (Research Object Crate)

RO-Crate is based on schema.org annotations in JSON-LD, and aims to make best-practice in formal metadata description accessible and practical for use in a wider variety of situations, from an individual researcher working with a folder of data, to large data-intensive computational research environments.

See more information about RO-Crate [here](#).

Sample

Also known as *biosample*. A research object that represents biological samples collected and sequenced in real life.

Sample checklist

The checklist of metadata that the sample was registered with.

Sample manager

A sample manager is a person who is responsible for accepting or rejecting samples in a research project.

This person can also upload manifest on behalf of sample submitters.

Sample submitter

A sample submitter is a person who submits or uploads samples to a research project.

Sample submitters may also be referred to as manifest providers or manifest submitters.

Sequence annotation

A research object that is used to describe the process of marking specific features in a DNA, RNA or protein sequence with descriptive information about structure or function.

It can be associated with one or more files, reads and assemblies.

Singular stage

In datafile description, a **singular stage** is a stage of the description wizard in which all the files in the description bundle are constrained (by the system) to share the same metadata.

SOP (Standard Operating Procedure)

A manual compiled by various profile groups to help scientists fill in a manifest correctly.

See the *SOPs* section for more information.

Specimen

Also known as biospecimen. It is a piece or portion of tissue, urine or other biologically derived material used for diagnosis and analysis.

SRA (Sequence Read Archive) accession

A unique identifier assigned to a sample by the Sequence Read Archive (SRA) database. It usually starts with 'ERS' followed by a number.

Studio3T

Studio3T, formerly known as Robo3T, is a GUI (Graphical User Interface) for MongoDB.

Visit [Studio3T](#) to download an appropriate version for your OS.

ToL

A worldwide collaborative effort of biologists and nature enthusiasts to provide information about biodiversity, the characteristics of different groups of organisms and their evolutionary history (phylogeny).

Ubuntu

A LINUX (Linux) distribution based on Debian and composed mostly of free and open-source software.

URI (Uniform Resource Identifier)

A string of characters that unambiguously identifies a particular resource.

See also: [Uniform Resource Identifier](#)

Virtual sample

A virtual sample is a research object that is submitted to COPO under a *Stand-alone profile*. It represents samples in a **run** sequencing file.

See the *Virtual sample submission* section for more information.

VSCODE

VSCode is a lightweight but powerful source code editor which runs on your desktop and is available on Windows, macOS and Linux.

COPO PRESENTATIONS

This section entails presentations and other materials that have been used to introduce COPO to various audiences.

42.1 Seminar presentations

1. Advancing Biodiversity Research: The Evolution of Collaborative OPen Omics (COPO) Project

- Presented at the Earlham Institute internal seminar
- **Date:** Tuesday 23rd April, 2024
- **Presenter:** Miss Aaliyah Providence, Junior Software Developer of the COPO team

- **Abstract:**

This seminar explores the evolution of the Collaborative OPen Omics (COPO) project as an open-source metadata broker in biodiversity research. With its capability to broker different data seamlessly, COPO has revolutionised the way by which researchers collaborate and share information.

An integral part of COPO's development involves standardising as well as enriching metadata and enabling the integration of diverse datasets for publication to the European Nucleotide Archive (ENA) which facilitates public dissemination.

Additionally, COPO's user-friendly Application Programming Interface (API) empowers users to query sample data efficiently, further enhancing accessibility and interoperability in biodiversity studies. Through its continuous evolution, COPO continues to drive innovation and collaboration in the field of bioscience research.

- [Download seminar presentation](#)

Hint: Click the download link above to access the presentation slides. View the presentation in slide show mode to see the animations.

42.2 Poster presentations

1. Collaborative OPen Omics (COPO) - Building, Testing and Deployment

- **Authors:** COPO team - Aaliyah Providence, Debby Ku and Felix Shaw

- **Abstract:**

Collaborative OPen Omics (COPO) is a user-friendly platform that allows scientists to easily upload, update, and publish metadata while adhering to community standards, promoting transparent data sharing. Built with cutting-edge technology, it utilises Docker Swarm for seamless service management, ensuring continuous availability, scalability, and ease of maintenance.

Security is prioritised in COPO's architecture, with distinct network layers preventing direct client access to back-end data repositories. Docker secrets are employed to enforce strict measures against unauthorised access, enhancing data protection and platform integrity.

Overall, COPO provides a sophisticated solution for scientific data management, integrating modern methodologies and security protocols to facilitate collaborative research efforts and promote scientific advancement.

- Download poster presentation

See also:

- *COPO FAIR webinar presentations*
- Download general Tree of Life visual submission documentation
- Download an illustration of samples submission and validation process in COPO

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