SyRF is a fully integrated online platform for performing systematic reviews of preclinical studies and can be accessed at syrf.org.uk

This guide has been developed to help users register and use the SyRF screening application for the management and performance of their systematic reviews – including the screening of large reference sets between multiple researchers. For more information or questions regarding this user guide, please contact us at syrf.info@ed.ac.uk

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Glossary of terms

**Project**
Your systematic review and meta-analysis including the studies you are reviewing.

**A public project**
Project that can be seen by anyone with an account on SyRF. Users can request to join and can be assigned roles such as administration (i.e. have editing rights to the design of the project), screening, data annotation, or data extraction roles.

**A private project**
Project that cannot be viewed on SyRF by other users unless they have requested and have been granted permission to join the project.

**Protocol**
Structured description of what you set out to do in your systematic review and meta-analysis, we recommend that this is published or shared publicly with [PROSPERO](https://www.crd梃) PROSPERO.

**Screen**
Include or exclude publications identified in your systematic search based on the inclusion/exclusion criteria defined in your protocol. Described in further detail in [section 5](#).

**Annotation**
You may want to annotate studies by labelling or extracting relevant information from them. This stage of a project is fairly flexible and therefore you can define your own annotation questions for your project. Annotation questions should address all questions you want to ask as specified in your protocol. You can choose at which stage of the project you want to answer specific annotation questions. This is described in further detail in [section 6](#).

**Data extraction**
Where you extract data from graphs or tables in the form of means/medians and corresponding error.

**Experiment**
Experiment refers to any grouping of cohorts where an experiment is carried out at the same time and any of them can be compared with each other.

**Cohort**
Refers to a group of animals - same species, strain, source, co-morbidities (if applicable) - which all receive the same procedure and treatments and can be compared to other cohorts. So an experiment may involve the following cohorts: Treatment, Sham and Control; or Control, Treatment 1 and Treatment 2.

Whereby the following comparisons may be made:
- e.g. Cohort 1 = Disease Model
  - Cohort 2 = Disease Model + Comorbidity
  - Cohort 3 = Sham or Disease Model Control
  - Cohort 4 = Disease Model + Treatment (Low Dose)
  - Cohort 5 = Disease Model + Treatment (High Dose)
  - Cohort 6 = Disease Model + Treatment Control (vehicle)
Section 1 Registration

When you start a review, register as a user to access the SyRF screening and data extraction application. All review authors will need to register independently and can be added to a project by the project administrator. Registering helps us keep your data secure and allows the project administrator to control who has access to the project data at different stages of the review. Read our Data Management and Sharing Policy here.

If you are a first time user

Access SyRF at syrf.org.uk.

Click on the ‘Launch SYRF’ button on the top left hand corner of the screen. On the SyRF home page click ‘Register’.

Here your options are to ‘Create a new account’ by using a generic email address or you can choose to ‘Register using Google’.

You will receive an email to complete your registration.

I don’t see an email in my inbox from SyRF
Logging in if you already have an account

Access SyRF at syrf.org.uk.

On the SyRF home page click ‘Sign In’.

Using the details you registered with, login using a generic email address or select ‘Sign in with Google’ if you have registered with a Google account.

Once you have logged in, you should be able to access projects by clicking on ‘Projects’.
Section 2 Join a Project

When logged in you should be able to see Projects you are a member of and also all other public projects, by clicking 'Public projects'.

To collaborate on a project, you will need to click 'Register to join' on the project’s homepage.

The administrator of the project will then need to grant you permission to access different stages of the project.

My collaborators can’t see my project

Section 3 Create a New Project

To create a new project, simply click on ‘Create Project’.

A form will then appear, where you can enter your project details.

URL link to your protocol
We strongly encourage you have a published protocol before you start your systematic review. We recommend that you publish with PROSPERO

Private/Non-private project
If you choose to set your project to private here, it won’t be visible on the Projects page to any other users (including anyone you may want to collaborate with).

Name of Your Project
It is helpful to make this concise, but descriptive too so that it is clear to others

Description of your project
This is mainly for other users and collaborators and there can be as detailed as you would like
On clicking ‘Next’ you will be asked to fill out a form where you specify the inclusion and exclusion criteria for your project.

Click ‘Create’ to finish creating the project.

**Section 4 Project Overview**

Once you have created your project, you can keep track of your project progress through the Project Details Page. If you are an administrator and need to edit any details you can also do that here by clicking on the pencil icon in each section.

It is important to be specific and detailed for these sections, but also to include the main points about what screeners should include and exclude as part of your project. Key points identified here will appear to screeners during the screener stage and therefore need to be concise, but informative.
Uploading a systematic search

You can upload a systematic search by scrolling to the ‘Systematic Searches’ section and clicking the ‘+’ button.

This will reveal the following form:

Upload citation library from EndNote

To upload your library to SyRF, you will need to export your library from EndNote in an XML format.

*In Endnote:* Select all records (Ctrl+Shift+A)
Then go to: File>Export
Make sure ‘Save as type’ is set to XML

In SyRF when uploading your file, please select ‘EndNote XML Library File’ and choose the file of interest. Clicking ‘Next’ will then prompt you to check the details of the upload before you begin the upload.
Please note, at current we support spreadsheets (i.e. csv/tsv - see below) or XML libraries directly exported from EndNote. So if you have your citations in another citation management program, you will have to transfer these to EndNote first or reformat your export file to look like those from EndNote or a spreadsheet with headings as shown in the example spreadsheet specified on our page.

I am trying to upload an EndNote XML file that was creating by importing from a place other than an electronic database and getting an error

Upload list of studies as a spreadsheet with or without screening decisions

If you have already screened your list of studies outside of SyRF, you can still upload your library and bring this existing information into SyRF for further steps of your project. You can do this by saving your study details in a csv or tsv file and selecting the appropriate upload option when uploading your search. Please check here for the format your file needs to be in before upload.

Next, if you want to add screening decisions, make sure to have “Toggle to include screening decisions with upload” on and fill out the appropriate information for SyRF to be able to attribute data correctly.

Please note, if you need to delete a systematic search from your SyRF project refresh the browser first.
If you require full-text for your studies

If you require full-text to be available at any stage of your project, it is important that you have already retrieved these before uploading your search file. In the systematic search file that you upload (csv/tsv spreadsheet or XML from Endnote) make sure the column “PDF Relative Path” contains relative path links (i.e. relative to the root of the folder you send to us) to your PDFs for each record.

<table>
<thead>
<tr>
<th>Title</th>
<th>Authors</th>
<th>Publication Name</th>
<th>Alternate Name</th>
<th>Abstract</th>
<th>Url</th>
<th>Author Address</th>
<th>Year</th>
<th>DOI</th>
<th>Keywords</th>
<th>Reference Type</th>
<th>PDF Relative Path</th>
</tr>
</thead>
<tbody>
<tr>
<td>Very interesting study</td>
<td>Author, A.; Author, B.</td>
<td>Best Journal</td>
<td></td>
<td>This is an abstract about a very interesting study.</td>
<td></td>
<td></td>
<td>2019</td>
<td>354759f. nvuyedi en</td>
<td>Journal Article</td>
<td>/first_batch/345_2019.pdf</td>
<td></td>
</tr>
</tbody>
</table>

You will then need to contact us with the name of your project and share the folder containing your PDFs via Google Drive or similar.

We will upload these PDFs to the SyRF database and these can be opened from the screening form.

You can use EndNote to retrieve PDFs accessible through your institution’s subscription

*In Endnote: Select all records > Right click > Select ‘Find full text’. You may need to authenticate your log in details for your institution. There is a limit of searching for 250 per go but it is worth going through this step multiple times if necessary as it is the quickest way of retrieving PDFs at present. Endnote will download, save and name the PDFs. These can then be found in your Endnote Data File in a folder named ‘PDF’.*

If you download your PDFs in this way, it is advisable to keep the PDF names and links specified by EndNote so that the links get matched to the appropriate record.

> I am performing a two-stage screening process and need to add PDFs only for my included studies for full-text screening
View project studies and study details

You can now view project studies by clicking on the ‘View Project Studies’ button. This will show you all the studies you have uploaded to your project.

If you have a PDF associated with a study, a PDF icon will appear for your record here.

If you have screening decisions for a study, they will appear here (i.e. Included, Excluded, or Insufficiently Screened).

If you have multiple searches uploaded, this is where you can see, which study is part of each search.
Section 5 Define screening project stage

A typical systematic review project might have the following stages: screening for inclusion, annotation of studies/data abstraction, reconciliation*, analysis*.

To define the stages of your project go to the Stages section of your project homepage and click on the ‘+’ button.

*As SyRF is under continuous development these stages have to be performed outside of SyRF at present. We can try to provide some assistance for these stages, but please note you will have to perform these outside of SyRF.

When adding a project stage, enter details to define the stage and click ‘Create’. If you would like to include screening make sure the ‘Include Screening in stage’ option is selected.

The ‘Include Screening in stage’ check box allows you to combine different stages with the screening process. This is useful if you want the option to exclude publications at any point in the reviewing process. E.g. Screen plus answer selected annotation questions. Always tick this box for your screening stage.

Stages created appear in the ‘Stages’ section of your project. To enter one simply click ‘Enter Stage’.
**Screening**

To start reviewing enter your screening stage and press ‘Start Reviewing’.

You will then be presented with the following screening form (if there are eligible studies left for you to screen) and be able to start screening. If you would like to include selected annotation questions at this screening stage then please move on to and follow the instructions below described in the next section about how to design and add annotation questions to a stage.

Inclusion/Exclusion criteria defined at the beginning of a project. This should be descriptive enough so that other screeners can understand exactly what you are trying to include and what you are trying to exclude from your overall project. This information can be edited on the project overview page.

Use these buttons to navigate and make decisions for inclusion on each study.

This bar shows your review progress. Green: represents studies that you have screened, Blue: the remaining number of studies that are available for you to screen, Orange: studies which are unavailable for you to screen (e.g. due to sufficiently being screened)

If there is an abstract for a study, this will appear here. If there is a full-text PDF linked to a study, this will appear as a link below the abstract.

This bar shows your annotation progress. Green: studies with sessions fully completed by you, Blue: available for annotation to you, Orange: unavailable for annotation to you (e.g. due to completion by others)
Screening decisions in SyRF explained

SyRF will automatically take care of discrepancies for you if you have enough screeners. Currently most projects are set to have a minimum number of 2 screeners, with a project agreement ratio of 0.333 (Information specified on your project home page, under 'Screening Details').

This means that publications are marked as 'Included', 'Excluded' or 'Insufficiently screened', whereby you need at least 2 screeners for each study to have agreed on their decision (both said include or exclude). A study will continuously be offered up for screening to other reviewers until this threshold has been met, and two reviewers have given a publication the same decision. If this threshold has not been met, then this will be marked as 'Insufficiently screened' and offered up to the next reviewer.

If you would like different criteria for sufficient screening, please contact us and don’t forget to include your project name.

My project only has two screeners, how can I see screening decisions?
Section 6 Define annotation questions

As part of the data abstraction process you can annotate studies within SyRF by specifying what question you want your reviewers to answer about each publication in your project.

In order to do this go to the ‘Design Annotation Questions’ button on the project overview page.

Questions may be nested to allow for hierarchy of conditional information entry (i.e. questions can become active, depending on answers to other questions).

Annotation questions are entered into the following categories:

Study

Enter any question that is relevant to the overall study

*e.g. Do the authors refer to a protocol? (Yes or No checkbox)*
Disease Model Induction

Control Question

Define questions that are specific to the Model control

* e.g. Do the control animals receive Sham surgery? (Yes or No checkbox)

Non-Control Question

Define questions that are specific to the Model

* e.g. What type of surgery was done to induce the model? (Dropdown list with defined options)

Both

Define questions that are relevant to both Model control and Model animals

* e.g. What anaesthetic is used for both the model and sham surgery? (Dropdown list with defined options)

Treatment

Control Question

Define questions that are specific to the Treatment control

* e.g. What is the vehicle given to the control animals? (Dropdown list with defined options)

Non-Control Question

Define questions that are specific to the Treatment group

* e.g. Specify the dose of treatment drug given in mg/kg (Integer input field)

Both

Define questions that are relevant to both Treatment control and Treatment animals

* e.g. What route of drug or vehicle administration is used in the experiment? (Dropdown list with defined options)

Outcome assessment

Define questions relevant to each outcome assessment procedure in the study

* e.g. What is the behavioural test used to measure outcome? (Dropdown list with defined options)
Cohort

Define questions relevant to each cohort procedure in the study

e.g. What is the sex of the animals included in the cohort?
(Dropdown list with options males, females, both, unknown)

I have cohorts with comorbidities and I'm not clear on how to differentiate between them

Experiment questions

Define questions relevant to each experimental procedure in the study

e.g. Was there a habituation period?
(Yes or No checkbox)
Nesting Questions

For each question you can choose to add related questions, if you want to get answers to additional questions, which are conditional on the answer to the previous question.

e.g. “What is the model type?”
(Drop down list with option of: Pharmacological or Surgical)

If Pharmacological is selected we could add a related question by selecting “Add Pharmacological Related”, which you will then be able to see nested under your previous question.

e.g. “What is the drug given?”
(Drop down list with options of different drugs)

You could then further subset this question, by clicking on it and selecting ‘Add Related’ and asking for each drug selected: “What is the dose and route of delivery?”

If Surgical is selected then we may ask the related questions: “What was the anaesthetic used?” or “What was the site of lesion?”
Section 7 Define annotation project stage

Once you have designed all annotation questions, you should specify the stage at which you want to answer each question. You can do this before you start screening or after you have finished screening.

To be able to add questions to your stage of interest go to the ‘Stages’ section of your project homepage and click ‘Enter Stage’.

You will then need to click on ‘Stage Design’ to start editing the stage.

To add questions you will need to turn on ‘Annotation’ for this stage of the project using the slider.

If you want to do screening and/or data extraction at the same time, you will also need to have these functionalities turned on (e.g. even if you have screened at a separate stage, you might want to have the functionality of being able to exclude a study at a later time point when you have read the full-text).
You will then be able to select the questions that you want to be included in this stage by checking the box next to the relevant questions.

Next time you enter a stage from the project homepage and click ‘Start Reviewing’, you should be able to see at the bottom of the page the questions you have enabled. The tabs named “Study”, “Disease Model induction”, “Treatment” etc. contain the different level annotation questions, depending on where you have included questions. Click on each tab to see the questions attributed to each.

Make sure you save your progress throughout the annotation process using this button.

Save and mark a study as ‘Complete’ process using this button.

Undo your changes.

Delete your annotations for the study.

Please note that for some levels questions will only show once you have given your entry a ‘label’ (i.e. a name) e.g. Cohort A or Model 1

In this example we have only added annotation questions at this level and therefore no other levels are visible.

Also please remember that questions are nested under the section you have created them. So if you have created a Control question for a section, then your question will only appear if you have identified your entry as a Control procedure.
Section 8 Define data extraction stage

If you would like to extract time-point data collected for outcomes from a publication, you need to have ‘Data Extraction’ enabled.

To have this at a separate stage, you will need to create a new project stage, by clicking ‘+’ on the project overview page under ‘Stages’.

When you enter into the stage, and press ‘Study Design’, you will need to make sure to turn ‘Data Extraction’. Please note ‘Annotations’ being enabled is a prerequisite for enabling ‘Data Extraction’. You may or may not want to perform these within the same stage, however.

Enabling ‘Data Extraction’ will activate a set of required system annotations (which are not defined by the project administrator).

You will need to pull some of the annotation information entered together to be able to start entering outcome information. For example, you will need to specify:

- procedures carried out on an animal,
- treatments administered (where appropriate)
- details about the outcomes that have been assessed
Once you have this information you can start combining these pieces of information to create ‘Cohort’s.’

Create cohorts by putting in the relevant information from each section

Once this has been done reviewers will be able to extract numerical data for reported outcomes in a publication being reviewed.

Add the cohorts involved in an experiment

Details about each cohort that you are extracting data for appear here

Enter time point data for a specific outcome

**Time** = Time of assessment, the time zero should be consistent across all studies included in the review. For example, time zero may equal time of model induction or may equal time of drug administration. If necessary, all reviewers within your project should be informed of this.

If ‘Annotations’ are enabled without ‘Data Extraction’ then only the annotation questions defined by the project administrator will be shown on the annotation form (see section 6 above).
Troubleshooting & FAQ’s

I have registered on SyRF, but I have not received my authentication email.

We advise that you check your Spam/Junk folder as sometimes the authentication emails might go here. If you are still having issues then please can you email us with your name and the email address you are trying to register with so we can get a better idea of what the issue may be.

I would like to invite collaborators to my project, however they cannot see the project I have created.

Have you set your project to “Private”? A private project can only be seen by the people already registered to the project. In order to allow your collaborators to see and join your project, you will have to make your project “Public” first, and then you can make it private once they have joined successfully.

I have made changes to my protocol, can I update the version you have for me on the website?

While we strongly encourage you to have a protocol registered before you begin your review, we acknowledge that protocols can change as a project goes on and therefore yes, it is possible to update your published protocol and if you would like to proceed with this could you please send an updated version of your protocol to us, specifying at the bottom of when and what changes were made to the original protocol.

I am having trouble uploading my EndNote library onto the SyRF application.

If you are uploading a literature search without screening results, you can export your bibliography straight from your reference management software. Currently we only support libraries exported from EndNote in an XML format. We also now additionally support csv/tsv files where you can bring into SyRF screening decisions made outside of the app. Please follow the instructions specified in ‘Section 3 Create a new project’.

I exported my EndNote file for editing in another software (eg. R Studio) before putting it back into EndNote and then exporting this edited version as an XML for upload into SYRF. I keep getting an error

This is to do with how EndNote codes your file up when exporting to XML, and so when you take it out and try to put it back in again, for publications where there are multiple authors, these will now default to one line and thus be recognised as a single author. EndNote recognises text on a new line as a separate author, therefore you will need to do Edit > Find and Replace, select the field “Author” and replace the indicator of an ending of an author (i.e. “.,”) with Special Insert > Carriage return to make sure each author is on a new line within a publication’s “Author” field. Finally, EndNote on exporting adds an “and” between the last two authors, so this will have to be similarly replaced using Edit > Find and Replace to make sure these authors are also on new lines and recognised as separate.

I am performing a two stage screening process, whereby I want to take all the included studies from abstract-level screening and screen them at a full-text level. How do I add my full-texts in order to do this?

Usually if you create another stage in your project, without screening just annotation, then SyRF should automatically present only your included studies for annotation. In order to
perform a second stage of screening, you will need to first identify your included studies, by going to the 'Project Studies' page. Here you can set the Rows per page option to “All” and then download all the studies to a spreadsheet, where you can filter out the ones that are labelled as “Included” in the ‘Inclusion Status’ column. You will then need to obtain PDFs for these studies and send them as described in the If you require full-text for your studies section of this document. Unfortunately there is no way to currently perform two screening levels within the same project, and therefore these full-texts will then be added to a new project in SyRF for you to screen a second time. Please get in contact with us if you would like to do this.

*My project only has two screeners, how do I view the discrepancies and conflicts from my project’s screening stage?*

As explained in the section Screening decisions in SyRF explained, screening works best for projects with more than 2 screeners and therefore if your project does have more than 2 screeners, then SYRF will have automatically resolved discrepancies for you once all reviewers have finished screening. If you only have 2 screeners on your project, then you can either involve a third Screener to see all the studies where your first two screeners disagreed, or simply click the ‘View Project Studies’ button on your project homepage to see a list of all your uploaded studies, and those that have “Insufficiently screened” as their ‘Inclusion Status’ will be the ones you disagreed on.

*If you would like to know specific screening decisions for each of your reviewers, please find your project on this page and paste the Link given into your browser’s URL. On this page you can find and download the specific data behind your project. To download screening decisions, the first link on the left-hand side should give you the final decisions for your studies and the second one should give you individual Screener decisions.*

*I want to make comparisons between the efficiency of different models, where all the models have the same main disease, but some groups are also given a co-morbidity; as well as look at the difference between models treated and not treated. How would I set my cohorts up in order to extract data for all these groups?*

You will need to enter your main disease under your ‘Disease Model’ details tab and describe how this model was created here. To be able to enter a comorbid animal, it’s best to add a tickbox at Cohort level, which says “Co-morbid animal” (Tick for Yes and Leave blank for No). You can then enter your cohorts as follows:

- **Cohort 1 - Naïve animals (for NMD calculations, where appropriate):** This cohort will have no disease model and therefore this field would be left blank for this cohort.
- **Cohort 2 - Sham animal (control for disease model animal):** This cohort would be a disease model as you are performing some sort of procedure (eg. doing surgery but not giving lesion), and you should tick control for this as this is a control for your disease model induction.
- **Cohort 3 - Disease model animals:** This cohort would have your disease model of interest only.
- **Cohort 4 - Disease model + Comorbidity animals:** This cohort will have the disease model of interest and answers to questions that you could nest under your question “Co-morbid animal”-Yes.
- **Cohort 5 - Stroke + Treatment:** Disease model of interest and your treatment as treatment
- **Cohort 6 - Stroke + Comorbidity + Treatment:** This will have the disease model of interest and answers to questions that you could nest under your question “Co-morbid animal”-Yes + Treatment.
I have finished data extraction and would like to move on to analysing my data.

SyRF is unable to perform analyses at this stage. The best way to start the analysis stage is to download your data from SyRF, by finding the link to your project here and copying and pasting it into your browser to see the data specific to your project and make sure it’s correct and there. Once you are happy with this, we have a meta-analysis app that is able to perform some calculations and draw some graphs for you, which you can find here. This has limited use as it was designed for standard meta-analyses, so does not work for all projects. The code behind the app can be found here. The user guide is available here. It’s important to make sure all the column names in your file match those specified. Please note, this app is still under development, and therefore it isn’t able to perform nesting just yet, so this has to be done outside of the app.

If there are any questions you have not found an answer to here, please feel free to get in touch, sending us the relevant information about the project you are working and your user information, to help us investigate and answer your query quicker. Screenshots and detailed descriptions help us a lot! We also welcome feedback, so would love to hear your thoughts!