**Species Submission Form**

Swedish Reference Genome Portal 🧬

Glad to see your interest in displaying your data on the Genome Portal!

Before proceeding, ensure your data meets the [service scope and requirements](https://genomes.scilifelab.se/contribute/) and the [terms of use](https://genomes.scilifelab.se/terms/).

This form has four sections:

* Sections 1-3: Provide information on the study and the species.
* Section 4: Download and complete the [Data Tracks Form](https://nextcloud.dc.scilifelab.se/s/sof3AJxDMAdYzXG) to provide information that will be displayed in the genome browser.

**Submission steps:**

1. Fill out the **Species Submission Form** (this Word file).
2. Complete the **Data Tracks Form** (linked Excel file).
3. Provide a species photo (see the Annex at the end of this document for recommendations).
4. **Send all three files via** **email** to: [dsn-eb@scilifelab.se](http://dsn-eb@scilifelab.se/), including the species name in the email subject or body.

Thanks! Tack så mycket!

# 1. Principal investigator (PI) information

Provide information about the responsible investigator for the genome project.

|  |  |
| --- | --- |
| First name: | Jane |
| Surname: | Doe |
| Institutional affiliation: | University of Life |
| E-mail address: | email@example.com |

### Submitter information

If the submitter is the PI, leave this section empty. Otherwise, provide the required information and select the role that best suits you from the drop-down menu.

|  |  |
| --- | --- |
| First name: | Click or tap here to enter text. |
| Surname: | Click or tap here to enter text. |
| Institutional affiliation: | Click or tap here to enter text. |
| E-mail address: | Click or tap here to enter text. |
| Role: | Choose an item. |

# 2. Species information

|  |  |
| --- | --- |
| Scientific name: | *Aspergillus nidulans* |
| English (common) name: | A filamentous fungi |

### Species description

Provide a brief description (max. 200 words) description of the source species of the genome data. Focus on key characteristics relevant to the genome project (e.g., biology, ecology, range). Use in-text citations as needed, following the [APA 7](https://apastyle.apa.org/) format.

* Italicize species scientific names using asterisks (e.g., \*Homo sapiens\*).
* Need help? If you do not have a species description, type “**need assistance with species description**” in the grey text box below and we will get back to you.

\_A. nidulans\_ is a filamentous fungi that forms mold.

#### References

(If applicable) List the references corresponding to the in-text citations in the Description section, following the [APA 7](https://apastyle.apa.org/) format.

* Separate each reference with a new line.
* Italicize species scientific names using asterisks (e.g., \*Homo sapiens\*).

ReftestDescription, T. (2025). Test of ref parsing. Journal. DOI.

# 3. Genome assembly information

### Publication

(If applicable) Provide the reference of the scientific article reporting the genome assembly, following the [APA 7](https://apastyle.apa.org/) format. The article should describe the source material, methods, and analyses used in generating the genome assembly.

* Italicize species scientific names using asterisks (e.g., \*Homo sapiens\*).

ReftestGenome, T. (2025). Test of ref parsing. Journal. DOI.

### Funding

List the funding source(s) for the genome assembly and annotation tracks, using a new line for each. Include grant numbers when applicable.

FundingTest

# 4. Data Tracks Form

Download the [Data Tracks Form](https://nextcloud.dc.scilifelab.se/s/sof3AJxDMAdYzXG) (Excel format) and provide as much information as possible about the data files you wish to display on the genome browser, even if they are unpublished. This information will allow us retrieve files from public repositories and customize data tracks in the genome browser. Refer to the “Instructions and table example” tab in the spreadsheet for guidelines and a prefilled example table.

For support on submitting data to public repositories, see the “Recommendations for unpublished data files” in the Annex.

# Annex

### Recommendations for unpublished data files

All genome data displayed on the Genome Portal must be publicly available in a repository at the time of deployment. However, we can begin building a private webpage for your species while the data is under embargo (e.g., associated with an article under review), or in the process of being made public in a repository. For this, we require that you provide the reserved [Digital Object Identifier (DOI)](https://www.doi.org/) for the data files.

**NOTE:** The private species page will be publicly available only after the data files are published.

**Publishing recommendations for specific data types**

* **Genome assembly and protein-coding genes (compulsory):** These files are the minimum requirements to create a species webpage and must be publicly available in a domain-specific repository (e.g., ENA, or NCBI)
  + For ENA submission assistance, contact the [National Bioinformatics Infrastructure Sweden, NBIS](https://nbis.se/services/data-management-support/apply).
* **Annotation data tracks (optional but highly recommended):** These include FST, Tajima’s D, nucleotide diversity, repeat regions, conserved elements, methylated regions, and other genomic features or metrics sharing the same coordinates as the reference genome assembly.
  + We offer free assistance for submitting annotation data to the [SciLifeLab Data Repository](https://www.scilifelab.se/data/repository/). To request help, type “need assistance” in the “link\_to\_repository” column of the Data Track Form.
  + Variant Call Format (VCF) files should be submitted to the [European Variation Archive (EVA)](https://www.ebi.ac.uk/eva/). For assistance, contact the [NBIS](https://nbis.se/services/data-management-support/apply).

**NOTE:** If you request to build a private species page while your data is being submitted for publication, we can provide you a web address (URL) for inclusion in the repository or in the scientific articles’ Data Availability Statement. For citation instructions, see the [Cite us page](https://genomes.scilifelab.se/cite_us/).

### Recommendations for species photo

Please provide an image of the source species associated with the genome data.

* **Preferred image aspect ratio:** 4:3 (if different, we can adjust it accordingly).
* **Image source and licensing:**
  + If applicable, indicate the [creative common license](https://creativecommons.org/share-your-work/cclicenses/) of the photo (e.g., Tangara seledon by Gloria Fuentes, CC BY-SA 3.0)
  + If using a photo with permission, credit the author(s) (e.g., Pyrocephalus rubinus by Humberto Alvarez, used with permission).