

# SWFSbase User Guide



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## Introduction

SWFSbase is a secure BLAST server developed for the wildlife forensic community. It centralises curated reference databases contributed by laboratories and links them to essential forensic metadata, while also incorporating selected publicly available reference data. SWFSbase is hosted on [SequenceServer™ Cloud](#). More information about the platform is available on the SWFSbase webpage: <https://www.wildlifeforensicscience.org/swfsbase/>

This User Guide provides an overview of how to use SWFSbase, including the different interfaces of SWFSbase, how to run BLAST searches, and how to submit sequences.

If you have any questions or issues, please contact: [SWFSbase@wildlifeforensicscience.org](mailto:SWFSbase@wildlifeforensicscience.org).

## Accessing SWFSbase:

SWFSbase can only be used for wildlife forensic casework. It cannot be used for research unless the relevant sequences are 1) owned by you, 2) are publicly available, or 3) you have obtained permission from the data owner to use them for research.

To access SWFSbase you must:

1. Be a member of the Society for Wildlife Forensic Science (SWFS).
2. Review and sign the SWFSbase Terms of Use.

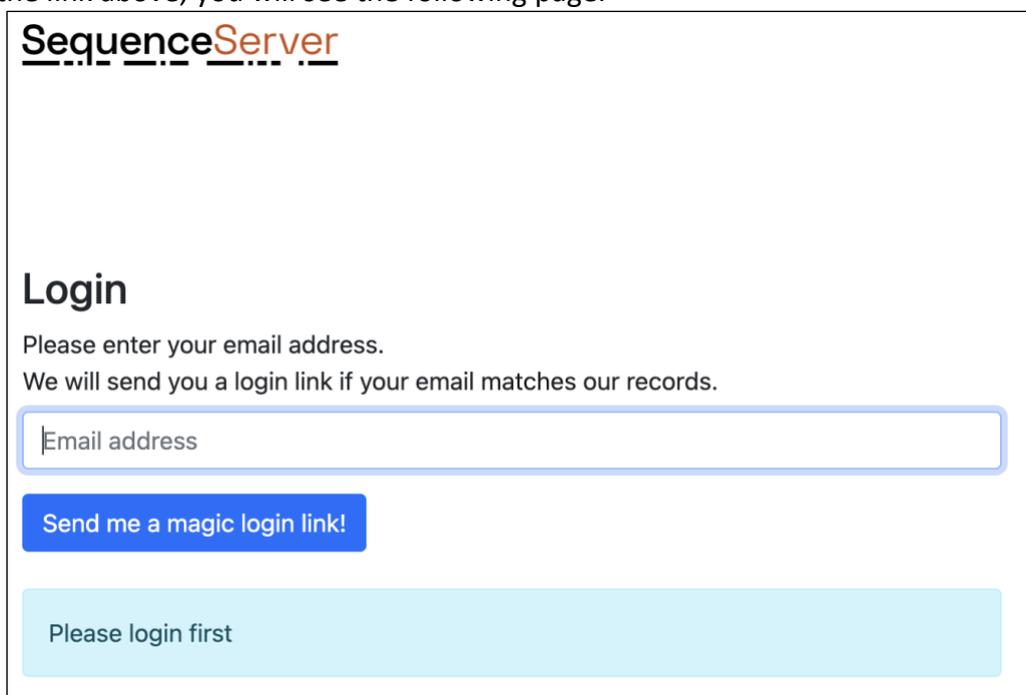
The Terms of Use can be downloaded from the [SWFSbase webpage](#). Signed agreements should be emailed to [SWFSbase@wildlifeforensicscience.org](mailto:SWFSbase@wildlifeforensicscience.org). Please also include your full name, institution, and the email address you would like associated with your login.

Once these requirements have been completed, you will be added as a SWFSbase user. You can then access the platform using the following link:

<https://wildlifeforensics.sequenceserver.com>

## Logging in to SWFSbase

SWFSbase uses a secure login system (two-step verification). When accessing the platform using the link above, you will see the following page:



**SequenceServer**

### Login

Please enter your email address.  
We will send you a login link if your email matches our records.

Send me a magic login link!

Please login first

To log in:

1. Enter your registered email address.
2. You will receive an email containing a login link.
3. Click the link (or copy and paste it into your browser).

The login link remains valid for up to 30 days, or until you click Logout within SWFSbase. After this, you will need to repeat the login process. For security reasons, it is recommended that you log out after each session. Additional information about platform security can be found [here](#).

## Running a BLAST with SWFSbase

Once you are logged in you will see the following BLAST interface:

The screenshot shows the SWFSbase BLAST interface. At the top, there's a navigation bar with 'SequenceServer Cloud' and links for 'Run BLAST', 'BLAST History', 'SRA BLAST', 'DNA Visualizer', 'Audit', 'Admin', 'Logout', and 'Help'. Below this is the 'SWFSbase For casework only' logo and a 'More information' link. The main area has a large text box for pasting query sequences, a section for selecting nucleotide databases (Core, Known erroneous, and SWFS member lab), and a settings section with tabs for 'Customize' and 'Advanced'. The settings include dropdowns for 'Task', 'E-value cutoff', and 'Maximum number of hits', a text input for 'Name', and a 'BLAST' button.

This interface functions similarly to an NCBI BLAST search. You can paste your sequence/s directly into the query box or drag and drop a FASTA file. Multiple sequences can be submitted in a single search.

### Included Databases

- **SWFS member lab database (verified sequences linked to metadata):** This is the key database within SWFSbase. It comprises vetted data contributed by multiple wildlife forensic laboratories, including data not available in other public repositories. Each sequence is linked to associated metadata to support assessment of specimen identification, sequence quality, and reliability (see image below). Laboratories may contribute sequences by following the submission instructions provided below.
- **Core nucleotide BLAST database:** This is the entire NCBI core nucleotide database ("core\_nt"), updated following NCBI's frequency (typically daily to fortnightly). These sequences are not curated within SWFSbase and are not linked to forensic metadata. The database is provided for convenience, allowing users to conduct searches without leaving the platform.
- **Known erroneous NCBI sequences (from the NCBI core nucleotide database above):** This is a small database that contains sequences from the NCBI core nucleotide database that have previously been identified as potentially erroneous. After conducting a search against the standard NCBI database, users may wish to query this database to determine whether top matches correspond to problematic records.

## Search Strategies

A useful strategy is to first search the '*SWFS member lab database*', which contains highly reliable and transparent reference data. You may then wish to search the '*NCBI nucleotide database*', which contains a much broader set of sequences. Finally, if your top matches come from NCBI, you can search the '*Known erroneous NCBI sequences*' database to determine whether any of those matches correspond to previously identified problematic records.

Note that the larger the database used, the longer the BLAST search will take. The '*NCBI core nucleotide database*' is by far the largest, and searches will therefore typically run slower than the other two databases. However, repeated searches against this database may run faster after the first search due to caching.

Once you enter a sequence, there are several BLAST presets available:

Settings

Choose a predefined setting or customize BLAST parameters.

- default:** Fast MEGABLAST algorithm for nucleotide query to nucleotide database searches. For highly similar sequences.
- discontiguous megablast:** Fast MEGABLAST algorithm for nucleotide query to nucleotide database searches. For more dissimilar sequences.
- discontiguous megablast excluding uncultured, environmental and unclassified:** Fast MEGABLAST algorithm for nucleotide query to nucleotide database searches. For more dissimilar sequences. Excluding uncultured, environmental and unclassified sequences.
- sensitive:** For nucleotide query to nucleotide database searches.
- oligos:** For short oligonucleotide alignments e.g. primers, microRNAs.

The '**default**' settings are appropriate for most searches, and are designed to quickly find highly similar sequences. If BLASTing against the '*NCBI nucleotide database*', it is useful to use the '**discontiguous megablast excluding uncultured, environmental and unclassified**' setting; this allows mismatches in the initial alignment seed, making the search more sensitive to distant sequence similarity, while excluding many low-quality or irrelevant sequences (searches may run slightly slower than the default preset).

Users may also click the 'Customize' and 'Advanced' settings to manually adjust BLAST parameters and filters.

## Viewing results

The BLAST results interface in SWFSbase is largely similar to NCBI BLAST. Several result fields are displayed by default; some fields may be irrelevant for your analysis and can be folded away using the minus signs. Your browser cookies should remember which fields you have folded, so they will remain folded in subsequent searches.

Below is an example of a BLAST result (the query is a tiger cytochrome-b sequence, searched against the '*SWFS member lab database*'), with some result fields already folded away:

SequenceServer Cloud Run BLAST BLAST History SRA BLAST DNA Visualizer Audit Admin Logout Help

SWFSbase For casework only [More information](#) | Questions? Email: [SWFSbase@wildlifeforensicscience.org](mailto:SWFSbase@wildlifeforensicscience.org)

**BLASTN: 1 query, 1 database**  
[Edit search](#) | [New search](#)

**Download FASTA, XML, TSV**  
 FASTA of all hits  
 FASTA of selected hit(s)  
 Alignment of all hits  
 Alignment of selected hit(s)  
 Standard tabular report  
 Full tabular report  
 Full XML report  
 Full Text report  
 Conserved Domains hits JSON

**Share results**  
[Copy URL to clipboard](#)  
[Send by email](#)

**Recommend SequenceServer**  
 Earn up to \$400 per signup

**Run Summary**  
 SequenceServer 3.1.3 using BLASTN 2.16.0+, query submitted on 2026-03-16 13:55:43 UTC  
 Databases: SWFS member lab database (verified sequences linked to metadata) (222 sequences, 217387 characters)  
 Parameters: task megablast, evalve 1e-20, max\_target\_seqs 50, sc-match 1, sc-mismatch -2, gap-open 0, gap-extend 0, filter L;m;  
 Please cite: <https://doi.org/10.1093/molbev/msz185>

**Graphical Overview**  
**Alignment Results**  
 Query= Query\_1 Length: 417  
 Graphical overview of aligning hit sequences to the query [SVG](#) [PNG](#)

**Length distribution of matching hit sequences**

**Hit sequences producing significant alignments**

#	Similar sequences	Query coverage (%)	Total score	E value	Identity (%)
1.	SWFS_00008 Panthera tigris cytochrome-b M.47626	98	387	0	98.3%
2.	SWFS_00002 Catopuma temminckii cytochrome-b M.39850	97	273	6.81×10 <sup>-145</sup>	89.1%
3.	SWFS_00104 Puma concolor Cytochrome b E21312	94	251	1.16×10 <sup>-132</sup>	88%
4.	SWFS_00103 Panthera uncia Cytochrome b D41147 MAM505	88	246	6.95×10 <sup>-130</sup>	89.1%
5.	SWFS_00105 Neofelis nebulosa Cytochrome b F30829	87	233	1.17×10 <sup>-122</sup>	88.1%
6.	SWFS_00063 Prionailurus bengalensis cytochrome-b FC-LC2	98	222	1.53×10 <sup>-116</sup>	84.8%
7.	SWFS_00106 Acinonyx jubatus Cytochrome b H20831	88	219	7.10×10 <sup>-115</sup>	86.6%
8.	SWFS_00107 Leopardus pardalis Cytochrome b J30443	79	204	1.55×10 <sup>-106</sup>	87.3%
9.	SWFS_00016 Cervus canadensis cytochrome-b QA1F38-QA1 G09	96	158	5.77×10 <sup>-81</sup>	79.9%
10.	SWFS_00188 Neofelis nebulosa Cytochrome b J20855	57	154	9.66×10 <sup>-79</sup>	88.2%
11.	SWFS_00187 Neofelis nebulosa Cytochrome b J20426	57	151	4.49×10 <sup>-77</sup>	87.8%
12.	SWFS_00186 Neofelis nebulosa Cytochrome b F30406	57	151	4.49×10 <sup>-77</sup>	87.8%

**Conserved Domains**  
 SWFS\_00008 Panthera tigris cytochrome-b M.47626 Hit 1. Length: 1,140  
[Select](#) | [Sequence](#) | [FASTA](#) | [Alignment](#) | [Explore DNA Features](#) | [Hit Metadata](#)  
 Graphical overview of aligning region(s)

Score: 715.77 (387), E value: 0, Identity: 401/408 (98.3%), Gaps: 0/408 (0%), Strand: + / +

```

Query      1  ACACCCCTTATCAAATTAATTAATCACTCATTTATTGACCTACCCGCCCATCCAATATTCAGCATGATGAAACTTTGGCTCTTACTAGGGGTGTGCTTAATC 106
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SWFSbase For casework only    [More information](#) | Questions? Email: [SWFSbase@wildlifeforensicscience.org](mailto:SWFSbase@wildlifeforensicscience.org)

### Sequence Metadata

Database: SWFS member lab database (verified sequences linked to metadata)  
Hit ID: SWFS\_00008

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General Information	Sample	Taxonomy
<p>Submitting Institute/Organisation <b>Australia Museum Research Institute</b></p> <p>Submitter's specimen identifier <b>M.47626</b></p> <p>Submitter's sequence identifier <b>M.47626_cyt-b</b></p> <p>Accession number, if available on a public database -</p> <p>Date added to SWFSbase <b>13/3/2026</b></p> <p>Additional notes <b>Sequenced as part of the Forcyt project</b> <a href="https://doi.org/10.1016/j.fsigs.2017.09.195">https://doi.org/10.1016/j.fsigs.2017.09.195</a></p>	<p>Institute/Organisation that has stewardship of the specimen or sample <b>Australia Museum</b></p> <p>Derived from voucher specimen or reference material? <b>Voucher</b></p> <p>Expert specimen identification carried out by? <b>Australian Museum Mammalogy Department</b></p> <p>Original collector of specimen or sample <b>Australia Zoo staff</b></p> <p>Collection date <b>Not provided</b></p> <p>Specimen photo available? <b>Yes</b></p> <p>Contact for specimen/sequence information <b>Australian Centre for Wildlife Genomics,</b> <b>tissue@australian.museum</b></p> <p>Additional specimen/sample information -</p>	<p>Phylum <b>Chordata</b></p> <p>Class <b>Mammalia</b></p> <p>Order <b>Carnivora</b></p> <p>Family <b>Felidae</b></p> <p>Genus <b>Panthera</b></p> <p>Species <b>tigris</b></p> <p>Subspecies/Variant <b>sumatrae</b></p> <p>Common name <b>Sumatran tiger</b></p> <p>Previous binomial -</p>
Location	Technical	Biology
<p>Wild, captive, or farmed? <b>Captive</b></p> <p>Latitude <b>Not provided</b></p> <p>Longitude <b>Not provided</b></p> <p>Country/Ocean <b>Australia</b></p> <p>State/Province <b>New South Wales</b></p> <p>Location <b>Captive, Australia Zoo, Previously, Melbourne Zoo, Dubbo Zoo, born Taronga Zoo</b></p>	<p>Submitting laboratory QMS Standards/Guidelines followed, if any <b>ISO17025</b></p> <p>Sequencing technology <b>MiSeq - shotgun sequencing</b></p> <p>Sample type <b>Biopsy sample</b></p> <p>Locus <b>Cytochrome b</b></p>	<p>Age class <b>Adult organism</b></p> <p>Sex <b>Male</b></p>

These metadata are intended to provide information about the reliability and provenance of the sequence hit, supporting interpretation of your results.

Sequences from the NCBI core nucleotide database are not linked to metadata within SWFSbase. To access additional information for these hits, you can click the NCBI link provided to view the sequence details on the NCBI website:

gi|373429553|gb|JN900475.1| Panthera tigris isolate KAU510 cytochrome b (cytb) gene, partial cds; mitochondrial Hit 1. Length: 417

Select | Sequence | FASTA | Alignment | Explore DNA Features | **NCBI** | NCBI GenBank

Graphical overview of aligning region(s)

Score: 771.17 (417), E value: 0, Identity: 417/417 (100%), Gaps: 0/417 (0%), Strand: + / +

```

Query 1 ACACCCCTTATCAAATTATTAATCACTCATTATTGACTACCCGCCCATCCAATATTTTCAGCATGATGAAACTTTGGCTCTTACTAGGGGTGTGCTTAATC 106
      |
Subject 1 ACACCCCTTATCAAATTATTAATCACTCATTATTGACTACCCGCCCATCCAATATTTTCAGCATGATGAAACTTTGGCTCTTACTAGGGGTGTGCTTAATC 106
Query 107 TTACAAATCCTCACTGGCCTCTTCTAGCCATACACTACACATCAGACACAATAACCGCTTCTCATCAGTTACCCACATTTGCCGCGACGTAACACTACGGCTGGA 212
      |
Subject 107 TTACAAATCCTCACTGGCCTCTTCTAGCCATACACTACACATCAGACACAATAACCGCTTCTCATCAGTTACCCACATTTGCCGCGACGTAACACTACGGCTGGA 212
Query 213 TTATCCGATATCTACATGCCAACGGAGCCTCCATATTTCTTATCTGTCTATACATGCACGTAGGACGAGGAATATACTACGGCTCTACACCTTCTCAGAAACATG 318
      |
Subject 213 TTATCCGATATCTACATGCCAACGGAGCCTCCATATTTCTTATCTGTCTATACATGCACGTAGGACGAGGAATATACTACGGCTCTACACCTTCTCAGAAACATG 318
Query 319 AAACATCGGGATTGTGCTATTGTTACGGTCATGGCTACAGCCTTCATAGGATATGCTTACCATGAGGACAAATATCATTCTGAGGGGCTGCAGTTTA 417
      |
Subject 319 AAACATCGGGATTGTGCTATTGTTACGGTCATGGCTACAGCCTTCATAGGATATGCTTACCATGAGGACAAATATCATTCTGAGGGGCTGCAGTTTA 417

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## Submitting sequences to SWFSbase

Laboratories that contribute data to SWFSbase play a vital role in enhancing the platform and supporting its mission.

To contribute to the ‘*Known erroneous NCBI sequence*’ database, please report any identified erroneous NCBI sequences to [SWFSbase@wildlifeforensicscience.org](mailto:SWFSbase@wildlifeforensicscience.org).

To contribute your laboratory’s sequence data and associated metadata suitable for forensic analysis, please follow the instructions below.

Each submission consists of two files: (1) a FASTA file containing sequences (.fasta, .fa, .fas, or .fsa), and (2) a metadata file prepared in Excel using the metadata template available on the SWFSbase webpage.

### Metadata entry

Information about each metadata field is provided on the first tab of the template. Please contact the SWFSbase team if you are unsure about any field.

### Linking metadata to your FASTA

A key field in the metadata is ‘**SWFSbase submission ID**’, which links each metadata row to its corresponding sequence. Each row of metadata in the Excel sheet must have a unique ‘SWFSbase submission ID’ that matches the **sequence ID** in the FASTA file.

**Note:** In a FASTA file, the sequence ID is the text immediately following the > symbol in the header, up to the first space. Anything after the first space is ignored.

For example, the top row of this metadata excel template screenshot has a ‘SWFSbase submission ID’ **ARS\_0001.1**:

Submission details					
Required	Required	Required	Optional	Optional	Optional
SWFSbase submission ID	Submitting Institute/Organisation	Submitter's specimen identifier	Submitter's sequence identifier	Accession number, if available on a public database	Additional notes
ARS_00001.1	Australia Museum Resear M.39850		M.39850_CO1		Sequenced as part of the Forcyt project <a href="https://doi.org/10.1016/j.fsigs">https://doi.org/10.1016/j.fsigs</a> .
ARS_00001.2	Australia Museum Resear M.39850		M.39850_cyt-b		Sequenced as part of the Forcyt project <a href="https://doi.org/10.1016/j.fsigs">https://doi.org/10.1016/j.fsigs</a> .



This should match the associated sequence in the FASTA file (the full sequence isn't displayed here):

```
>ARS_0001.1 M.39850 C01 Catopuma temmincki AustMus  
ATGTTCATAAACCGCTGACTATTTTCAACCAATCATAAAGATATTGGTACTCTTTA ... →
```

Note, any labelling system can be used for your 'SWFSbase submission IDs', as long as they are unique within that submission. You may use existing sequence IDs from your database (in this case, the 'SWFSbase submission ID' might be the same as the 'Submitter's specimen identifier' and/or 'Submitter's sequence identifier').

Alternatively, you can assign sequential IDs for your sequences. In the example below, the sequences are both from specimen M.39850, but for different loci, so `seq01`, and `seq02` have been used as the 'SWFSbase submission IDs' in both the FASTA and metadata files:

```
>seq01 M.39850 C01 Catopuma temmincki AustMus  
ATGTTCATAAACCGCTGACTATTTTCAACCAATCATAAAGATATTGGTACTCTTTA ... →  
  
>seq02 M.39850 cyt-b Catopuma temmincki AustMus  
ATGACCAACATTCGAAAATCACACCCCTTATTAATAATTATTAACCACTCATTTCAT ... →
```

**Important:**

- Ensure that all 'SWFSbase submission IDs' are unique and match exactly between the metadata and sequence files.
- Contact the SWFSbase team if you are unsure about formatting or any field in the template.

Once your sequences and metadata are prepared:

- Open the submission form here:  
<https://docs.google.com/forms/d/e/1FAIpQLSfKaROuBi3QilkBdS3xsBclujdTgFhFb304JcMC5LAVPeFIWA/viewform>
- Fill in the required fields.
- Attach your FASTA sequence file and metadata Excel file to the form.
- Submit the form.

The SWFSbase team will review each submission and contact you if there are any issues