

Whiteflybase - Getting Started

Register

Before you can begin using the identification tools in Whiteflybase you will need to create an account. To create an account Click the [1] Register Button.



To get started click the blue login button above

Welcome to Whiteflybase

Whiteflybase is a *Bemisia tabaci* species identification tool designed at the University of Western Australia.

All 5' mtCOI sequences that are used for identification are sourced from Genbank and are identified using Blast and Bayesian Phylogenetic methods.

For more information about the methods please see [Updated mtCOI reference dataset for the Bemisia tabaci species complex](#).

To use the application you will need to login and create an account. You can [Register Here](#).

Once you have logged in use the "Quick Start Guide".

Whiteflybase - [Open Access Policy](#)



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Account Details

On the register screen you will need to complete your First Name, Surname, Email Address and Password. Please ensure your email address is correct as it will be used to login and send you email communications. The submit button will become active once you have correctly filled to form.

Whiteflybase

Account Creation

Registration Confirmation

Once your registration has been completed you will be able to login to whiteflybase immediately using the password you have supplied. You will also receive a welcome email with your account details and information.

Logging In

Once you have a registered your account and when you visit the site you will need to login. To login, click the [1] Login Button



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Enter your Email address and password to login. If there is an issue with your account you will receive a message. If you have any issues with this process contact the administrator for assistance.

Login

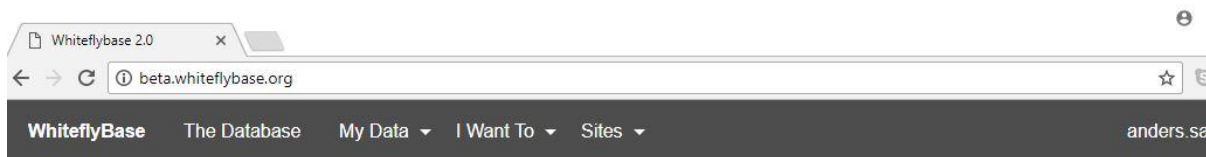
Don't have an account? [Register Here](#)

Uploading Sequences

Once logged in you will be presented with the process window. You will need your sequences ready on your computer in FASTA format. To get started click the [1] UPLOAD FASTA Button.



On the next screen you need to click the [1] Choose File button. Locate the [2] file in the finder window. [3] Select Open. Then [4] Upload



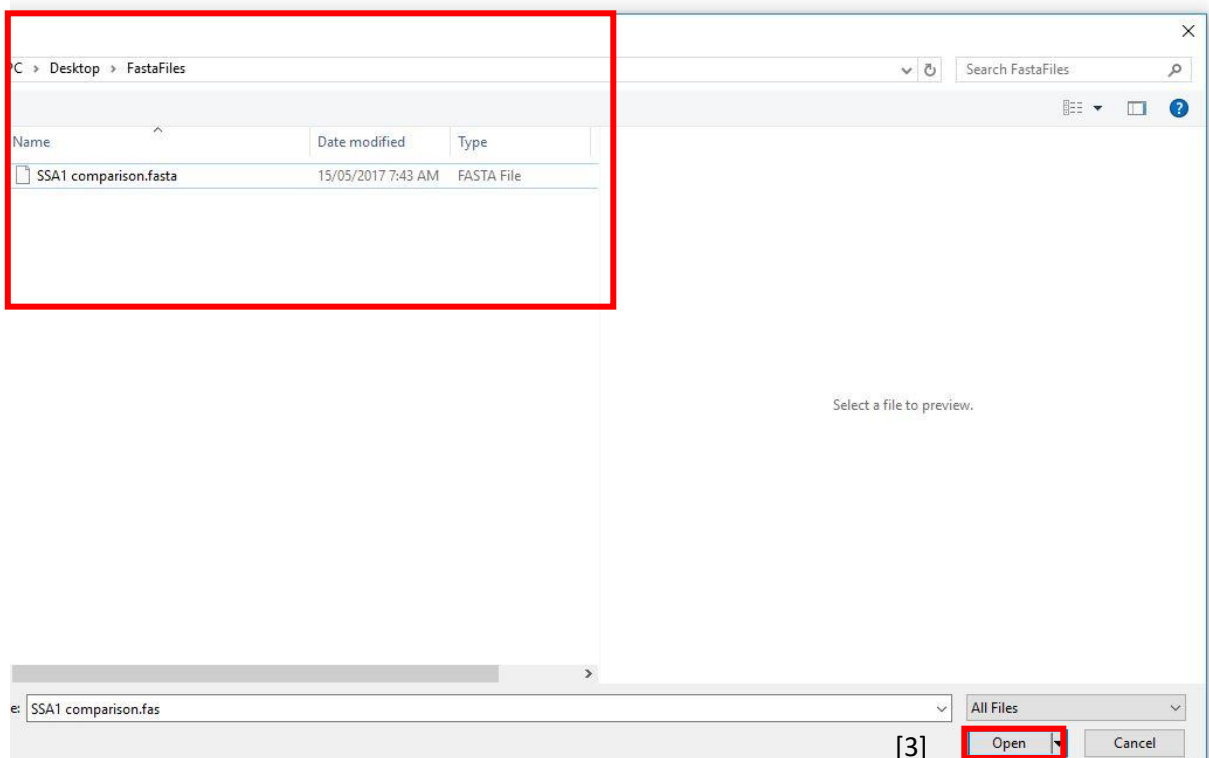
Upload New Sequence

Choose a fasta file containing your sequence or sequences to upload.

[1] Choose file No file chosen

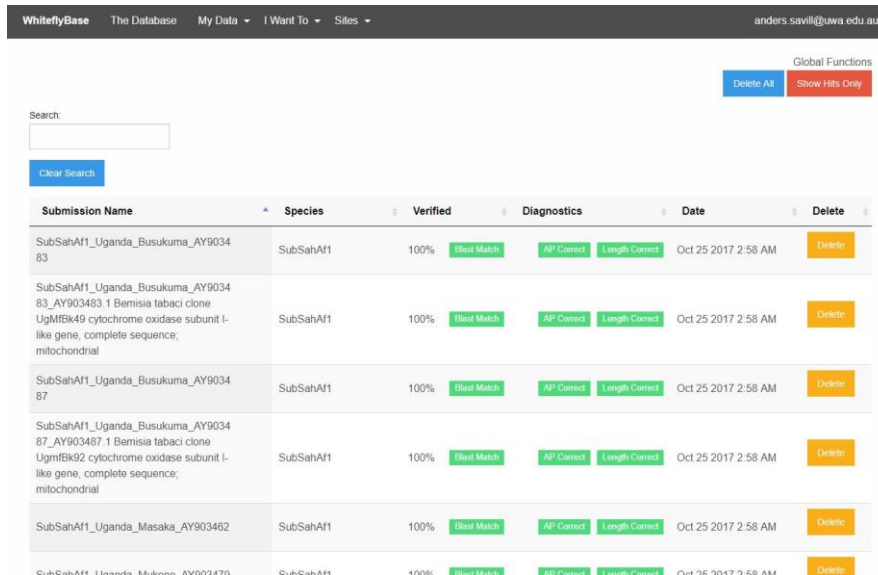
[4] Upload

[2]



Reviewing Sequences

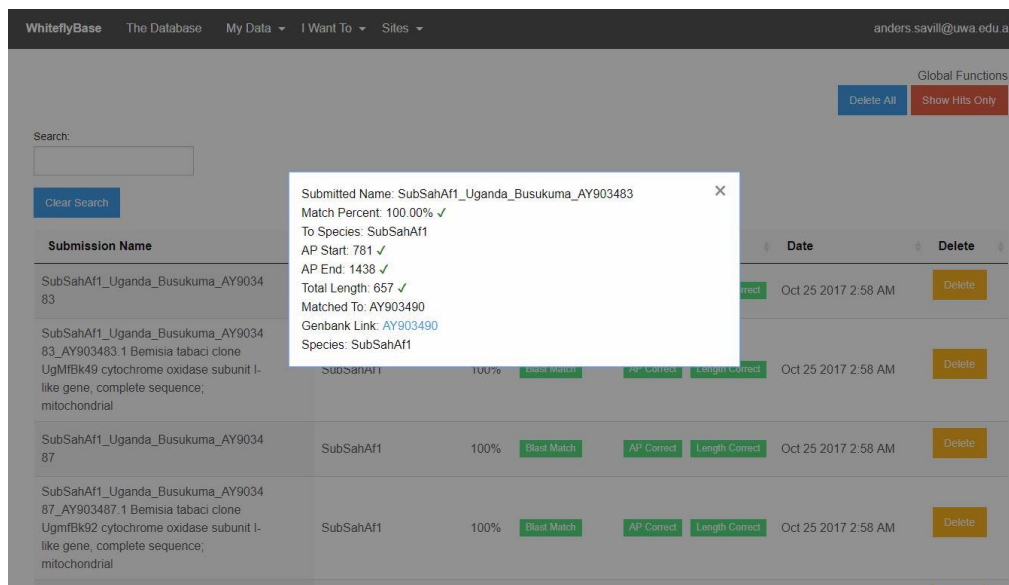
Once the sequences upload you will see the following screen. The most important part of this screen is the Verified Column. It shows the Blast Percentage Identity must sequences will return within 98-100% and indicates a strong possibility that the sequence is a particular species. Further tests can be run outside of whiteflybase to give a definitive species identification. The Diagnostics information is specific to further species delimitation methods and indicates the sequence is within the parameters for inclusion in the global dataset.



The screenshot shows the WhiteflyBase web interface. At the top, there is a navigation bar with 'WhiteflyBase', 'The Database', 'My Data', 'I Want To', and 'Sites'. On the right, the user email 'anders.savill@uwa.edu.au' is displayed. Below the navigation bar, there are 'Global Functions' buttons: 'Delete All' (blue) and 'Show Hits Only' (red). A search bar is present with a 'Clear Search' button. The main content is a table with the following columns: Submission Name, Species, Verified, Diagnostics, Date, and Delete. The table contains several rows of sequence submissions, all with a 'Verified' status of 100%. The 'Diagnostics' column for each row shows 'Blast Match', 'AP Correct', and 'Length Correct'.

Submission Name	Species	Verified	Diagnostics	Date	Delete
SubSahAf1_Uganda_Busukuma_AY903483	SubSahAf1	100%	Blast Match AP Correct Length Correct	Oct 25 2017 2:58 AM	Delete
SubSahAf1_Uganda_Busukuma_AY903483_AY903483.1 Bemisia tabaci clone UgMfBk49 cytochrome oxidase subunit I-like gene, complete sequence, mitochondrial	SubSahAf1	100%	Blast Match AP Correct Length Correct	Oct 25 2017 2:58 AM	Delete
SubSahAf1_Uganda_Busukuma_AY903487	SubSahAf1	100%	Blast Match AP Correct Length Correct	Oct 25 2017 2:58 AM	Delete
SubSahAf1_Uganda_Busukuma_AY903487_AY903487.1 Bemisia tabaci clone UgMfBk92 cytochrome oxidase subunit I-like gene, complete sequence, mitochondrial	SubSahAf1	100%	Blast Match AP Correct Length Correct	Oct 25 2017 2:58 AM	Delete
SubSahAf1_Uganda_Masaka_AY903462	SubSahAf1	100%	Blast Match AP Correct Length Correct	Oct 25 2017 2:58 AM	Delete
SubSahAf1_Hondas_Mukono_AY903470	SubSahAf1	100%	Blast Match AP Correct Length Correct	Oct 25 2017 2:58 AM	Delete

Clicking on a sequence row will provide you more details regarding the sequence. Most of this information is diagnostic in nature however the Matched To: and Genbank Link can be particularly useful.



The screenshot shows the WhiteflyBase web interface with a detailed view of a sequence submission. A modal window is open over the table, displaying the following information:

- Submitted Name: SubSahAf1_Uganda_Busukuma_AY903483
- Match Percent: 100.00% ✓
- To Species: SubSahAf1
- AP Start: 781 ✓
- AP End: 1438 ✓
- Total Length: 657 ✓
- Matched To: AY903490
- Genbank Link: AY903490
- Species: SubSahAf1

The background table is partially visible, showing the same columns as in the previous screenshot. The 'Delete' button for the selected row is highlighted.