DATABASE TEMPLATE v. 1.0

by

Michael Black, Tim White, Kyle Brudvik, Denise Su, Henry Gilbert, J.R. Boisserie

---

USER MANUAL

The **RHOI Database Template** was created by the NSF-HOMINID-funded **Revealing Hominid Origins Initiative** (RHOI, **http://rhoi.berkeley.edu**). One goal of the initiative is to standardize data management and to facilitate the sharing of comparable and accurate specimen-level paleontological data within a global scientific consortium. A history and rationale for these efforts is provided in Appendix A of this manual.

This manual is a comprehensive guide to all aspects of the RHOI Database Template. Even inexperienced users should be able to explore the RHOI Database Template without reading the manual thoroughly, but we strongly recommend that you read the manual first to discover the many hidden features of the template.

The RHOI Database Template, along with the necessary peripherals, is available for free download over the Internet at:

http://rhoi.berkeley.edu/informatics/RHOI_Database_Template/downloads.php

We invite you to download an Example database containing real, pre-entered data. Open it, explore it, and evaluate how it might work for you.

We anticipate that RHOI member projects, as well as other interested institutions, projects, and individuals will wish to adopt this template to digitally manage and archive curatorial, taxonomic, and spatial data on individual specimens, and on the localities from which they are collected.

The RHOI Database Template is a relational database structure created using **FileMaker Pro** software (Version 8), a standard databasing program that is entirely *PC and Mac compatible*. FileMaker Pro works well with Microsoft Excel, making data transfer quick and easy.

The software spreadsheet program **Excel** is widely used as a specimen catalog by RHOI members. Excel has its uses, but because it is a spreadsheet rather than a database, it lacks the presentation and data manipulation features and flexibility possible with a true database program. We encourage RHOI members to experiment with the RHOI Database Template (FileMaker) format before deciding to abandon Excel. It is our hope that when you see the functionality of the RHOI Database Template, you will be eager to abandon Excel for your cataloging needs.

The RHOI Database Template is designed to accommodate a wide spectrum of informatics needs and computing hardware preferences. RHOI members seeking modifications necessary to conform to their particular needs may contact Kyle Brudvik at kbrudvik@berkeley.edu for assistance, to report bugs, or to recommend improvements. RHOI member projects will be sent their own commercial FileMaker Pro software upon request.

We have designed the RHOI Database Template to suit the needs of most projects, but you may also wish to customize it for your particular needs. To do this, you will need to log into the Template as an "Administrator." To do this, navigate to the toolbar (at the top of the screen), and select "Administrator login" from the Scripts menu. Type in "**Admin**" in the Account Name field, and "**danger**" in the Password field. You will be alerted that you are now logged in as the Administrator. Click OK to proceed. Be warned, the password was chosen to remind you that with opportunity (to customize the database), comes risk (of breaking links that make it function). Full instructions on working with logins are found in Section **B.2.c.** of this manual.

We begin with v. 1.0, but you should regularly check back at the RHOI website for upgrades.

TABLE OF CONTENTS

A. NAVIGATING THE DATABASE LAYOUTS (SCREENS)

In FileMaker, "**Layouts**," are the screen pages that display data contained in **Fields** organized on the screen in different configurations. In the RHOI Database Template, there are **10 major layouts** (plus 2 for data and image importing), easily accessed via the **Navigational Buttons** at the bottom of each screen, or the **Pull-down Menu** on the top left of the screen (see box below). Additional **Directional Arrow Buttons** atop each page provide a convenient way to return to whichever screen you last used, or to jump back and forth between screens.

Layout: Specimen

Record: 1

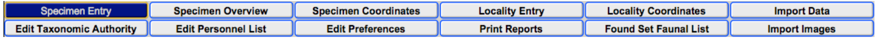
Total: 26

Unsorted

• Different layouts are accessible via the pull-down menu in the gray bar (the **Status Area**) on the top left of the screen.

ALTERNATIVELY,

• Rectangular buttons at the base of your screen allow easy movement between different layouts. The buttons turn dark blue to indicate the current open layout.



• These buttons take you to related records, so if there are no related records, they are inactive.

Certain fields appear in multiple layouts. When data are entered or changed in any layout, all other layouts will automatically display the new data.

Other Color Conventions:

- Light yellow boxes 🟨 indicate basic specimen, element, and collection information.
- Light blue boxes 🟦 indicate taxonomic information.
- Light gray boxes ⬜ indicate chronostratigraphic information.
- Light brown boxes 🟫 indicate curatorial information.
- Boxes with cross-hatching (e.g., ▨) denote the use of pull-down menus for data entry.

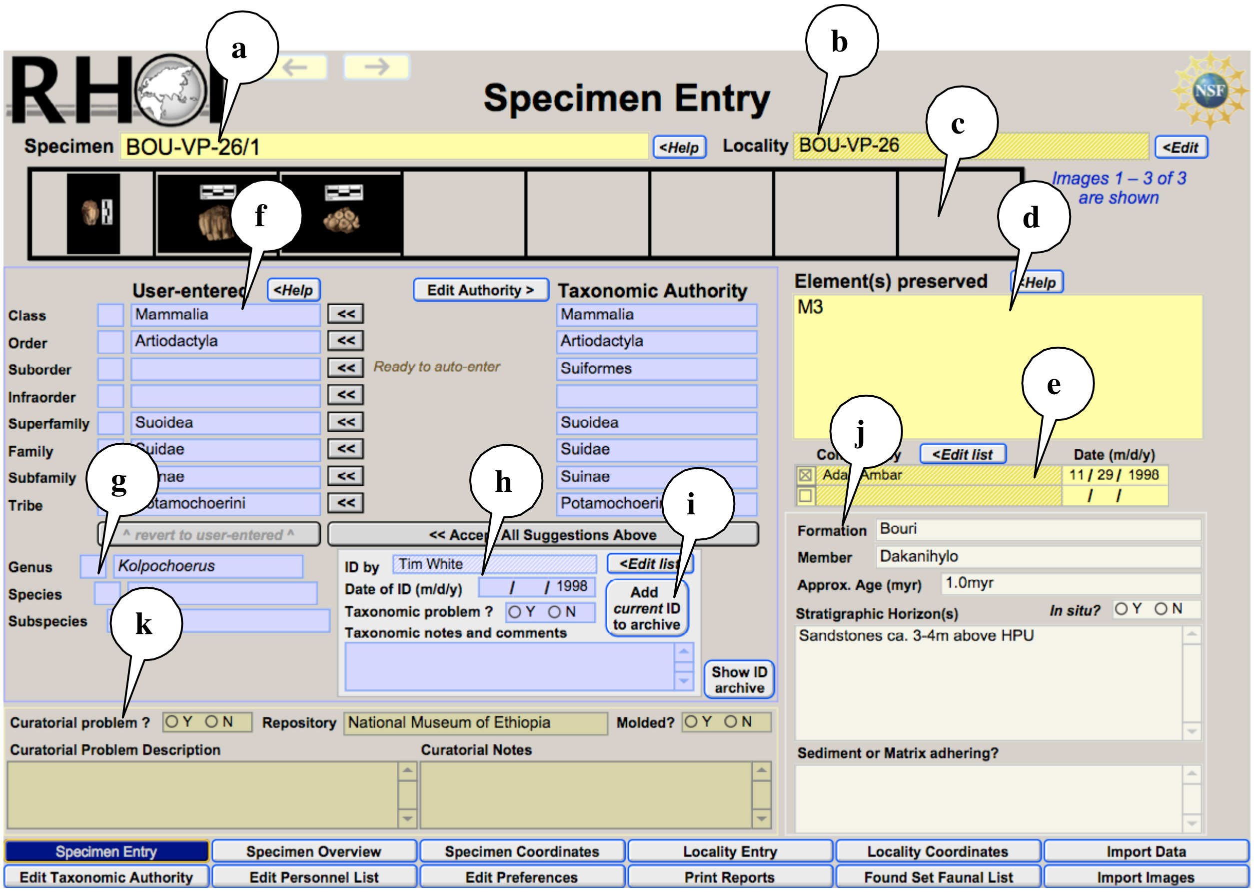
The following sections describe the various layouts used in the RHOI Database Template.

1. SPECIMEN ENTRY LAYOUT

Specimen Entry

This layout is designed for the entry and display of data pertaining to individual fossil specimens. Specimens are viewed one-at-a-time on this layout.

It is important that each specimen you enter into the RHOI Database Template has a unique specimen number associated with it. The Specimen Entry page allows you to enter data on new specimens, and to review the identification, locality, taxonomic, geological, and curatorial information associated with each specimen.



Specimen BOU-VP-26/1
Locality BOU-VP-26
Images 1 – 3 of 3 are shown

	User-entered	Taxonomic Authority
Class	Mammalia	Mammalia
Order	Artiodactyla	Artiodactyla
Suborder		Suiformes
Infraorder		
Superfamily	Suoidea	Suoidea
Family	uidae	Suidae
Subfamily	nae	Suinae
Tribe	otamochoerini	Potamochoeri

Ready to auto-enter

Genus *Kolpochoerus*
Species
Subspecies

ID by Tim White
Date of ID (m/d/y) / / 1998
Taxonomic problem ? ○ Y ○ N
Taxonomic notes and comments

Element(s) preserved
M3

☒	Ada Ambar	11 / 29 / 1998
☐		/ /

Formation Bouri
Member Dakanihylo
Approx. Age (myr) 1.0myr
Stratigraphic Horizon(s) *In situ?* ○ Y ○ N
Sandstones ca. 3-4m above HPU
Sediment or Matrix adhering?

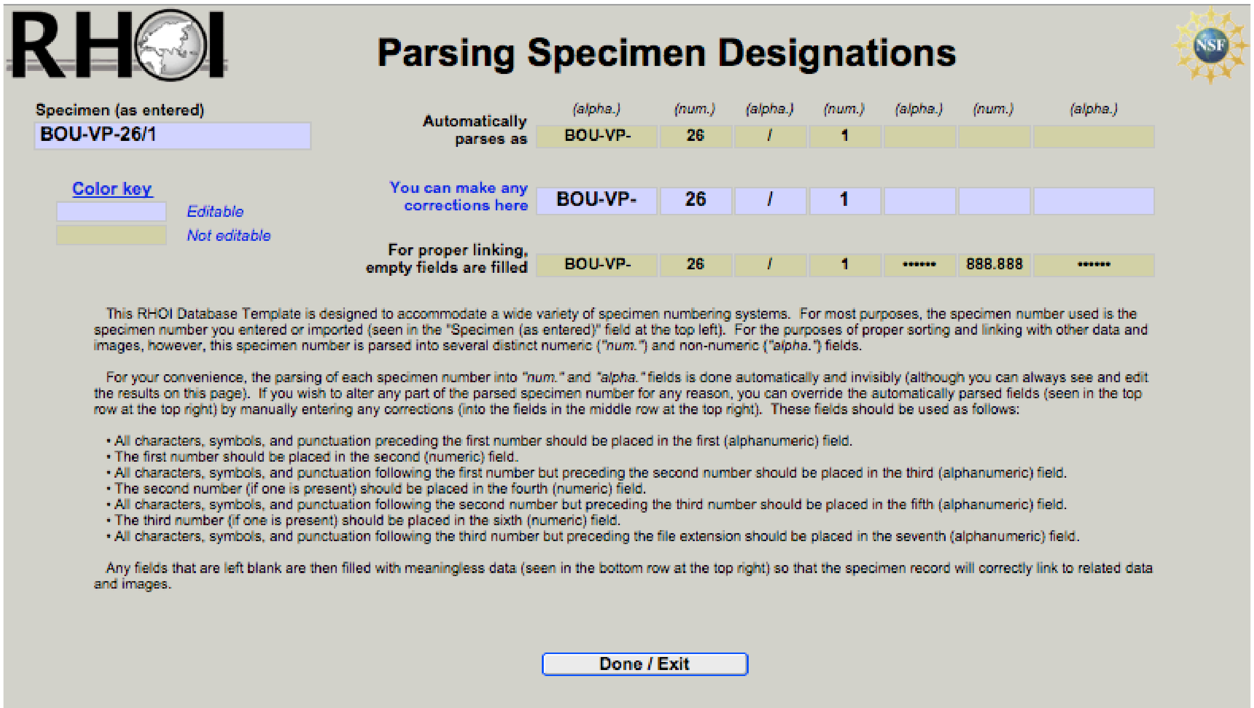
Curatorial problem ? ○ Y ○ N Repository National Museum of Ethiopia Molded? ○ Y ○ N
Curatorial Problem Description
Curatorial Notes

The following sections refer to the letters in the figure above.

a. Specimen Number

Specimen BOU-VP-26/1

Each project has its own cataloging and numbering conventions. To maximize flexibility, The RHOI Database Template is designed to accommodate a wide variety of specimen numbering systems. This design is revealed by clicking on the <Help box to the immediate right of the specimen number field of the Specimen Entry layout. This brings up the following screen:



RHOI

Parsing Specimen Designations

Specimen (as entered)
BOU-VP-26/1

	(alpha.)	*(num.)*	*(alpha.)*	*(num.)*	*(alpha.)*	*(num.)*	*(alpha.)*
Automatically parses as	BOU-VP-	26	/	1			
You can make any corrections here	BOU-VP-	26	/	1			
For proper linking, empty fields are filled	BOU-VP-	26	/	1	••••••	888.888	••••••

Color key

▭	*Editable*
▨	*Not editable*

This RHOI Database Template is designed to accommodate a wide variety of specimen numbering systems. For most purposes, the specimen number used is the specimen number you entered or imported (seen in the "Specimen (as entered)" field at the top left). For the purposes of proper sorting and linking with other data and images, however, this specimen number is parsed into several distinct numeric ("*num.*") and non-numeric ("*alpha.*") fields.

For your convenience, the parsing of each specimen number into "*num.*" and "*alpha.*" fields is done automatically and invisibly (although you can always see and edit the results on this page). If you wish to alter any part of the parsed specimen number for any reason, you can override the automatically parsed fields (seen in the top row at the top right) by manually entering any corrections (into the fields in the middle row at the top right). These fields should be used as follows:

- All characters, symbols, and punctuation preceding the first number should be placed in the first (alphanumeric) field.
- The first number should be placed in the second (numeric) field.
- All characters, symbols, and punctuation following the first number but preceding the second number should be placed in the third (alphanumeric) field.
- The second number (if one is present) should be placed in the fourth (numeric) field.
- All characters, symbols, and punctuation following the second number but preceding the third number should be placed in the fifth (alphanumeric) field.
- The third number (if one is present) should be placed in the sixth (numeric) field.
- All characters, symbols, and punctuation following the third number but preceding the file extension should be placed in the seventh (alphanumeric) field.

Any fields that are left blank are then filled with meaningless data (seen in the bottom row at the top right) so that the specimen record will correctly link to related data and images.

For most purposes, the specimen number used is the specimen number you entered or imported (seen in the **Specimen (as entered)** field at the top left). For the purposes of proper sorting and linking with other data and images, however, this specimen number is parsed on this layout into several distinct numeric ("*num.*") and non-numeric ("*alpha.*") fields.

For your convenience, the parsing of each specimen number into "num." and "alpha." fields is done automatically and invisibly (although you can always see and edit the results on this page). If you wish to alter any part of the parsed specimen number for any reason, you can override the automatically parsed fields (seen in the top row at the top right) by manually entering any corrections (into the fields in the middle row at the top right). These fields should be used as follows:

- All characters, symbols, and punctuation preceding the first number should be placed in the first (alphanumeric) field.
- The first number should be placed in the second (numeric) field.
- All characters, symbols, and punctuation following the first number but preceding the second number should be placed in the third (alphanumeric) field.
- The second number (if one is present) should be placed in the fourth (numeric) field.
- All characters, symbols, and punctuation following the second number but preceding the third number should be placed in the fifth (alphanumeric) field.
- The third number (if one is present) should be placed in the sixth (numeric) field.

- All characters, symbols, and punctuation following the third number but preceding the file extension should be placed in the seventh (alphanumeric) field.

Any fields that are left blank are then filled with meaningless data (seen in the bottom row at the top right) so that the specimen record will correctly link to related data and images.

The parsing of specimen numbers makes it possible for the RHOI Database Template to work perfectly, either with or without digital images, and to import a variety of specimen number formats used by different projects and museums. We explain how to import your data in section **C.2.a.**

Important Note: *You will frequently want to "sort" your data sequentially by specimen number. We have included a special script called* ***Sort by Specimen Number*** *to make this easy. Navigate to the FileMaker toolbar, at the top of your screen, and select Scripts>Sort by Specimen Number. The specimens in any "found" set will then be automatically sorted in the correct order.*

b. Locality Information

Locality BOU-VP-26

Various projects and museums use a variety of locality designations. In the Locality field, you are given a pull-down menu of various localities. You cannot manually enter the locality name into this field. Rather, you must use the pull-down menu. The locality name can be imported from an Excel spreadsheet (see below), or you can add or delete Localities and their common names by clicking on the **<Edit** button. This will bring up the Locality List as a separate screen page:

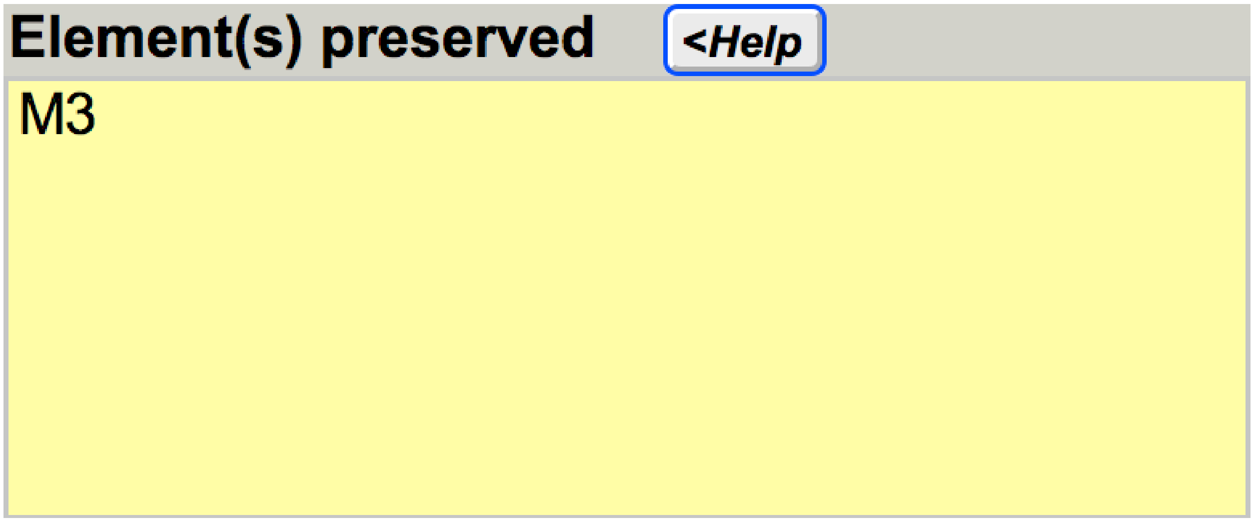
Locality List

Locality:	Common Name:	
BOU-VP-26	HPU Type Locality	Delete
XXX-EG 123	Example locality or site 1	Delete

c. The Photo Frame

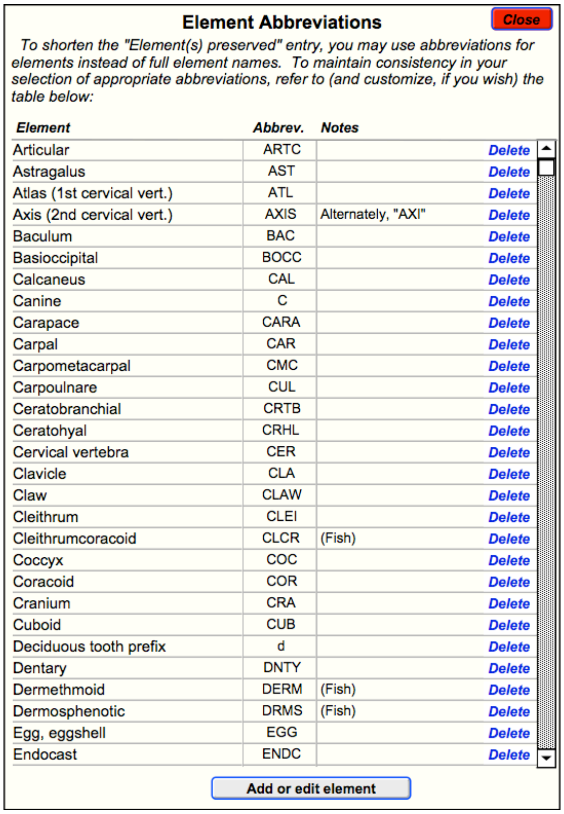
This feature is a handy way to see whether digital images of the specimen being browsed have been imported or linked to your database.

d. Element(s) Preserved



M3

Different projects and museums employ different conventions for identifying skeletal elements. The RHOI Database Template allows projects the flexibility of using either a code-based (abbreviated names), or a longhand method to characterize the skeletal or dental element(s) that make up a single specimen (usually an individual). If a longhand method (e.g., "mandible with left third premolar, broken first molar and intact third molar") is preferred, just enter this into the field. However, if you prefer a code-based system, click on the <Help button just above the field, and the skeletal element code set used by the Middle Awash project appears:



Element Abbreviations

To shorten the "Element(s) preserved" entry, you may use abbreviations for elements instead of full element names. To maintain consistency in your selection of appropriate abbreviations, refer to (and customize, if you wish) the table below:

Element	*Abbrev.*	*Notes*	
Articular	ARTC		Delete
Astragalus	AST		Delete
Atlas (1st cervical vert.)	ATL		Delete
Axis (2nd cervical vert.)	AXIS	Alternately, "AXI"	Delete
Baculum	BAC		Delete
Basioccipital	BOCC		Delete
Calcaneus	CAL		Delete
Canine	C		Delete
Carapace	CARA		Delete
Carpal	CAR		Delete
Carpometacarpal	CMC		Delete
Carpoulnare	CUL		Delete
Ceratobranchial	CRTB		Delete
Ceratohyal	CRHL		Delete
Cervical vertebra	CER		Delete
Clavicle	CLA		Delete
Claw	CLAW		Delete
Cleithrum	CLEI		Delete
Cleithrumcoracoid	CLCR	(Fish)	Delete
Coccyx	COC		Delete
Coracoid	COR		Delete
Cranium	CRA		Delete
Cuboid	CUB		Delete
Deciduous tooth prefix	d		Delete
Dentary	DNTY		Delete
Dermethmoid	DERM	(Fish)	Delete
Dermosphenotic	DRMS	(Fish)	Delete
Egg, eggshell	EGG		Delete
Endocast	ENDC		Delete

This set of codes can be ignored, modified, or replaced by other codes. There is also the built-in flexibility of editing or adding **Add or edit element** codes for additional elements or element portions used by your project.

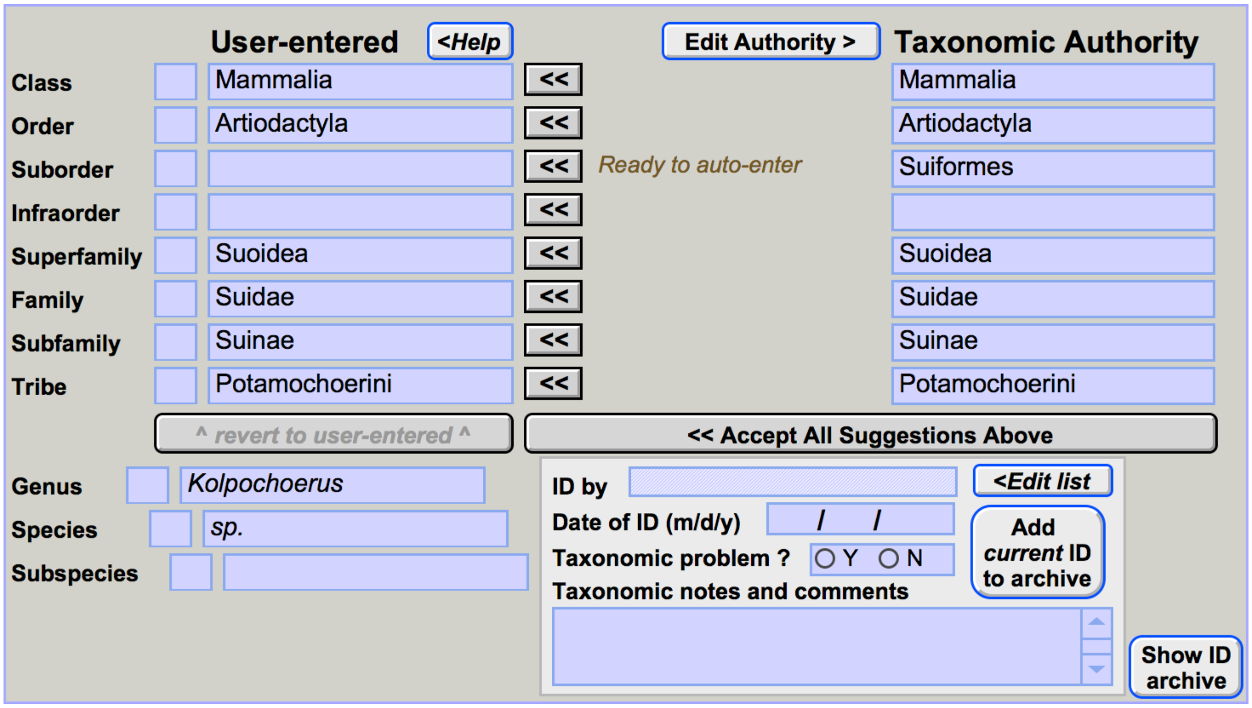
Clicking the red ***Close*** button at the top of the code window returns you to the full **Specimen Entry** layout when help is no longer needed.

e. Collection Information

These fields allow you to enter specimen-by-specimen information about the discoverer/collector, and date of acquisition. The **Collected by** field is entered via a pull-down menu and relies on the **Personnel List**, a separate table used to identify all personnel involved in collection, identification, and photography of specimens. This layout can be accessed and edited by clicking on the ***<Edit list*** button above the **Collected by** field. You will see a screen similar to the following:

Last name	First name	Name to be displayed in lists:	To be included in which lists?			
Gilbert	Henry	Henry Gilbert	☒ Collectors	☐ Identifiers	☒ Photographers	Delete
Group		Group	☒ Collectors	☐ Identifiers	☐ Photographers	Delete

f. Taxonomic User-Entered and Taxonomic Authority Columns



	User-entered	Taxonomic Authority
Class	Mammalia	Mammalia
Order	Artiodactyla	Artiodactyla
Suborder		Suiformes
Infraorder		
Superfamily	Suoidea	Suoidea
Family	Suidae	Suidae
Subfamily	Suinae	Suinae
Tribe	Potamochoerini	Potamochoerini

Genus *Kolpochoerus*
Species *sp.*
Subspecies
ID by
Date of ID (m/d/y) / /
Taxonomic problem ? ○ Y ○ N
Taxonomic notes and comments

This is the only place in the RHOI Database Template where you are allowed to modify the taxonomic identification of any specimen.

The **User-entered** column is the operational record for the most current taxonomic identification of each specimen. You will rely on the information here to generate faunal lists of various kinds (see below).

The **Taxonomic Authority** column is designed to help you reduce entry fatigue and error by relying on a pre-programmed look-up table. This internal **Taxonomic Authority** is where the hierarchical taxonomic designations for your fauna reside.

In the **User-entered** column, you will need to enter the lowest-level taxonomic identification available for your specimen (e.g., genus, "*Ceratotherium*"). The **Taxonomic Authority** column to the right then provides suggestions for higher-level names (i.e., Tribe and above). These are merely suggestions that are available for automatic entry. You may override these suggestions by simply typing a different name in the **User-entered** column.

If you choose to accept a **Taxonomic Authority** suggestion, simply click on an intervening grey double arrow button << Ready to auto-enter, and each suggested name will automatically enter into the **User-entered** column.

You also have the option of accepting all suggestions with one click. Just click on the << Accept All Suggestions Above button. If you make a mistake in the process of accepting the **Suggested** auto-entries, you can easily revert to your user-entered taxonomy by clicking the ^ revert to user-entered ^ button.

Please note that the automatic taxonomic entry function does not apply at or below the species level. The higher-level taxonomic standards, set in the **Taxonomic Authority**, are pre-entered in the RHOI Database. This particular hierarchy was built by Middle Awash project paleontologists, and basically follows McKenna and Bell (1997) and BirdLife International (2000). You are free to modify or delete any parts of it, or delete it and create your own taxonomic authority.

If you enter a genus name not pre-entered in the **Taxonomic Authority** into the **User-entered** column, the red words "***Genus not in Taxonomic Authority. Click the "Edit Authority" button to add it.***" will appear. Clicking on the Edit Authority > button automatically opens a window that allows the genus name to be added to the **Taxonomic Authority** (see below for more).

You may choose to delete names pre-entered in the **Taxonomic Authority**, not to use them, or to supplement them. You are free to edit the taxonomic standards to your own specifications.

When you click on the Edit Authority > button, you are taken to the **Taxonomic Authority** screen page, arranged as a spreadsheet (also accessible by clicking the Edit Taxonomic Authority button at the bottom of the screen).


Taxonomic Authority

Class	Order	Suborder	Infraorder	Superfamily	Family	Subfamily	Tribe	Genus	
Aves	Anseriformes		Anserides		Anatidae	Anatinae	Anserini	*Plectropterus*	Delete
Aves	Apodiformes				Apodidae				Delete
Aves	Charadriiformes								Delete
Aves	Ciconiiformes	Ciconii	Ciconiides	Ardeoidea	Ardeidae				Delete
Aves	Ciconiiformes	Ciconii	Ciconiides	Ciconioidea	Ciconiidae	Ciconiinae		*Leptoptilos*	Delete
Aves	Ciconiiformes	Ciconii	Ciconiides	Ciconioidea	Ciconiidae	Ciconiinae		*Mycteria*	Delete
Aves	Ciconiiformes	Ciconii	Ciconiides	Threskiornithoidea	Threskiornithidae				Delete
Aves	Ciconiiformes	Ciconii	Falconides		Accipitridae			*Aquila*	Delete
Aves	Ciconiiformes	Ciconii	Falconides		Accipitridae			*Buteo*	Delete
Aves	Ciconiiformes	Ciconii	Falconides		Accipitridae	Accipitrinae		*Accipiter*	Delete
Aves	Coliiformes				Coliidae				Delete
Aves	Columbiformes				Columbidae			*Streptopelia*	Delete
Aves	Columbiformes				Columbidae			*Treron*	Delete
Aves	Coraciiformes				Bucorvidae			*Bucorvus*	Delete
Aves	Galliformes				Numididae			*Numida*	Delete
Aves	Galliformes				Phasianidae			*Coturnix*	Delete
Aves	Galliformes				Phasianidae			*Excalfactoria*	Delete
Aves	Galliformes				Phasianidae			*Gutterea*	Delete
Aves	Galliformes				Phasianidae			*Pavo*	Delete
Aves	Galliformes				Phasianidae	Phasianinae	Perdicini	*Francolinus*	Delete
Aves	Gruiformes				Otididae			*Eupodotis*	Delete
Aves	Gruiformes				Otididae			*Rupodotis*	Delete
Aves	Gruiformes				Rallidae				Delete
Aves	Passeriformes				Corvidae				Delete
Aves	Pelecaniformes				Anhingidae			*Anhinga*	Delete
Aves	Pelecaniformes				Phalacrocoracidae			*Phalacrocorax*	Delete
Aves	Podicipediformes				Podicipedidae			*Podiceps*	Delete
Aves	Psittaciformes				Psittacidae	Psittacinae		*Agapornis*	Delete
Aves	Psittaciformes				Psittacidae	Psittacinae		*Poicephalus*	Delete
Aves	Strigiformes				Strigidae	Buboninae		*Otus*	Delete
Aves	Strigiformes	Strigi			Tytonidae	Tytoninae		*Tyto*	Delete
Aves	Struthioniformes	Struthioni	Struthionides		Struthionidae			*Struthio*	Delete
Mammalia	Artiodactyla	Ruminantia		Bovoidea	Bovidae	Alcelaphinae	Aepycerotini	*Aepyceros*	Delete
Mammalia	Artiodactyla	Ruminantia		Bovoidea	Bovidae	Alcelaphinae	Alcelaphini	*Alcelaphus*	Delete
Mammalia	Artiodactyla	Ruminantia		Bovoidea	Bovidae	Alcelaphinae	Alcelaphini	*Awashia*	Delete
Mammalia	Artiodactyla	Ruminantia		Bovoidea	Bovidae	Alcelaphinae	Alcelaphini	*Beatragus*	Delete
Mammalia	Artiodactyla	Ruminantia		Bovoidea	Bovidae	Alcelaphinae	Alcelaphini	*Connochaetes*	Delete
Mammalia	Artiodactyla	Ruminantia		Bovoidea	Bovidae	Alcelaphinae	Alcelaphini	*Damaliscus*	Delete
Mammalia	Artiodactyla	Ruminantia		Bovoidea	Bovidae	Alcelaphinae	Alcelaphini	*Damalops*	Delete
Mammalia	Artiodactyla	Ruminantia		Bovoidea	Bovidae	Alcelaphinae	Alcelaphini	*Megalotragus*	Delete
Mammalia	Artiodactyla	Ruminantia		Bovoidea	Bovidae	Alcelaphinae	Alcelaphini	*Parmularius*	Delete

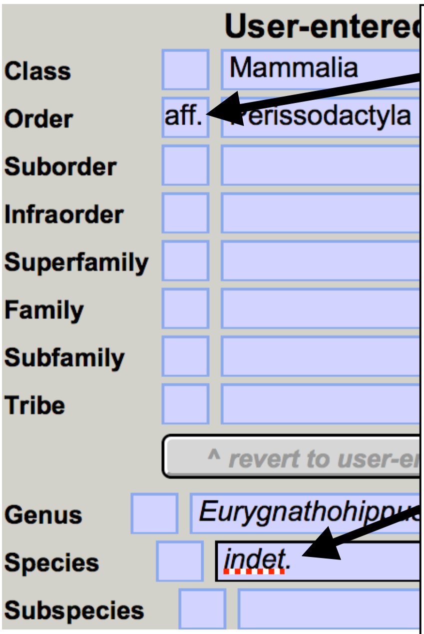
Any name or level on this hierarchy may be altered. Once entered here, your modifications will, from then on, be available in the auto-entry functions on the **Specimen Entry** layout.

The list of pre-entered taxa available in the RHOI Database Template is not comprehensive because ONLY the taxa currently present in the overall Middle Awash collection have been pre-entered. Virtually all projects will have a different taxonomic set, and you will therefore be customizing the **Taxonomic Authority** list to your specifications.

If the auto-entry function is of no interest to you, just ignore it. You can always override it by entering data directly into the **User-entered** column.

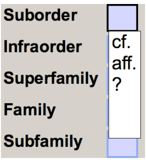
g. Taxonomic Abbreviations

Many taxonomy-related sorting features of the RHOI Database Template (e.g., creation of faunal lists) rely on the names being unencumbered by prefixes or suffixes such as "cf." or "sp." For this reason, the template provides you with designated fields to hold this information, and a guide to their recommended use.

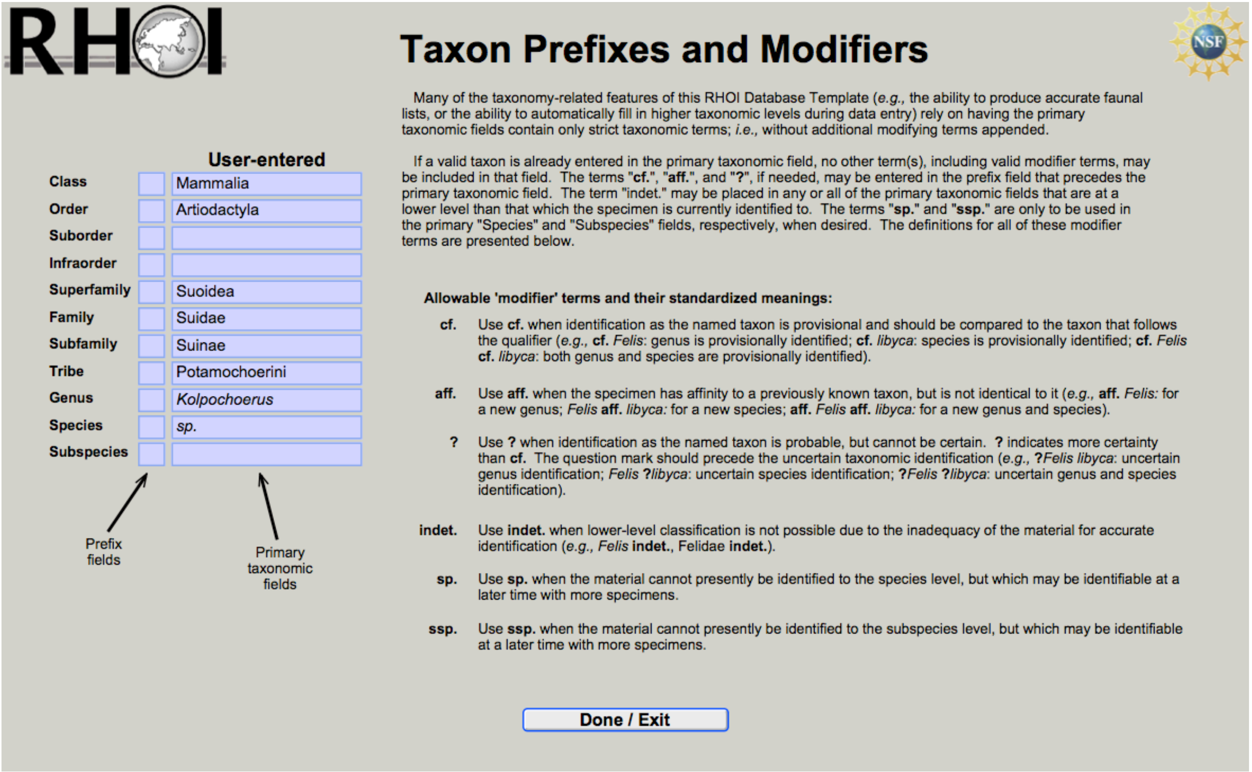


The small boxes located to the left of each taxonomic category are for taxonomic abbreviations, where needed.

The **<Help** button takes you to a window outlining the recommended conventions regarding "aff.", "cf.", and "?" all of which can be entered via the automatic menus



associated with each box. The terms "gen. nov. et sp. nov.", "indet.", "sp.", and "ssp." are also defined in Appendix B. Where appropriate, these may be entered in the relevant (longer) "Genus", "Species" and "Subspecies" entry boxes.



Taxon Prefixes and Modifiers

Many of the taxonomy-related features of this RHOI Database Template (*e.g.*, the ability to produce accurate faunal lists, or the ability to automatically fill in higher taxonomic levels during data entry) rely on having the primary taxonomic fields contain only strict taxonomic terms; *i.e.*, without additional modifying terms appended.

If a valid taxon is already entered in the primary taxonomic field, no other term(s), including valid modifier terms, may be included in that field. The terms "**cf.**", "**aff.**", and "**?**", if needed, may be entered in the prefix field that precedes the primary taxonomic field. The term "indet." may be placed in any or all of the primary taxonomic fields that are at a lower level than that which the specimen is currently identified to. The terms "**sp.**" and "**ssp.**" are only to be used in the primary "Species" and "Subspecies" fields, respectively, when desired. The definitions for all of these modifier terms are presented below.

Allowable 'modifier' terms and their standardized meanings:

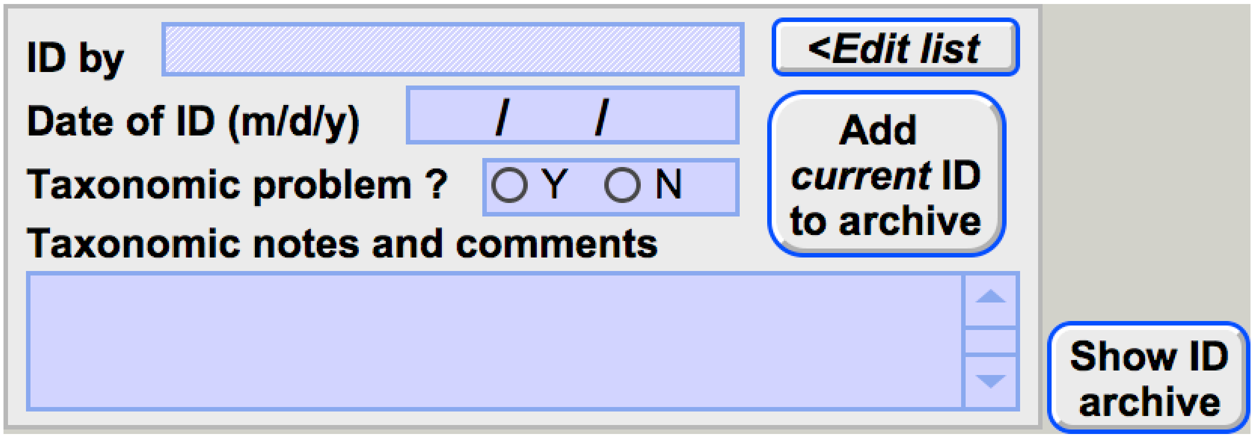
cf.	Use **cf.** when identification as the named taxon is provisional and should be compared to the taxon that follows the qualifier (*e.g.*, **cf.** *Felis*: genus is provisionally identified; **cf.** *libyca*: species is provisionally identified; **cf.** *Felis* **cf.** *libyca*: both genus and species are provisionally identified).
aff.	Use **aff.** when the specimen has affinity to a previously known taxon, but is not identical to it (*e.g.*, **aff.** *Felis:* for a new genus; *Felis* **aff.** *libyca:* for a new species; **aff.** *Felis* **aff.** *libyca:* for a new genus and species).
?	Use **?** when identification as the named taxon is probable, but cannot be certain. **?** indicates more certainty than **cf.** The question mark should precede the uncertain taxonomic identification (*e.g.*, **?***Felis libyca*: uncertain genus identification; *Felis* **?***libyca*: uncertain species identification; **?***Felis* **?***libyca*: uncertain genus and species identification).
indet.	Use **indet.** when lower-level classification is not possible due to the inadequacy of the material for accurate identification (*e.g.*, *Felis* **indet.**, Felidae **indet.**).
sp.	Use **sp.** when the material cannot presently be identified to the species level, but which may be identifiable at a later time with more specimens.
ssp.	Use **ssp.** when the material cannot presently be identified to the subspecies level, but which may be identifiable at a later time with more specimens.

Note that the **Taxon Prefixes and Modifiers** screen page is "live." You can use this page to directly enter names and prefixes for the specimen that is being viewed on the **Specimen Entry** layout, provided that none of these fields is "selected" (i.e., surrounded by a black rectangle) on that layout. To edit a selected field in the Taxon Prefixes and Modifiers screen page, you should click on the <Help button only AFTER clicking somewhere else on the **Specimen Entry** page. This feature helps you assign the appropriate prefixes, and allows the entries to be directly incorporated into the database. These will automatically appear on the **Specimen Entry** screen page when the **Help** screen page has been closed by clicking on its **Done/Exit** button (or by closing the **Help** page).

h. Taxonomic Identification Notes

The taxonomy of record for each specimen appears in the **User-entered** taxonomic hierarchy column in the Database Template. This is always the most **current** identification for any particular specimen.

It is important to identify the analyst who makes the lowest taxonomic identification in the **User-entered** column, as well as the date of that identification, and any notes regarding the identification. This information is entered here:



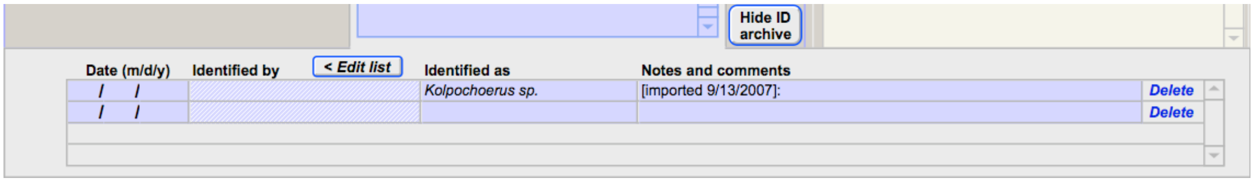
The **ID by** field is a pull-down list associated with the **Personnel List** for the Database Template. You can view and edit the list by clicking on the <Edit list button.

Information in the **ID by**, **Date of ID**, and **Taxonomic notes and comments** fields should always correspond to the **current** taxonomic identification in the **User-entered** column.

i. Taxonomic Identification Archive

Taxonomic identifications change over time, and it is important for projects and museums to be able to track those changes by creating archives. Therefore, the RHOI Database Template is designed to allow projects and museums to easily record these changes, and to allow the capture of multiple analyst opinions regarding taxonomic identifications.

Whenever identifications are changed in the **User-entered** column, you should archive that information by clicking on the Add *current* ID to archive button. The information you entered (identifier, date, and comments) will immediately appear in the **Taxonomic ID Archive**. You can see that archive by clicking on the Show ID archive button. The **Archive** will display as follows:

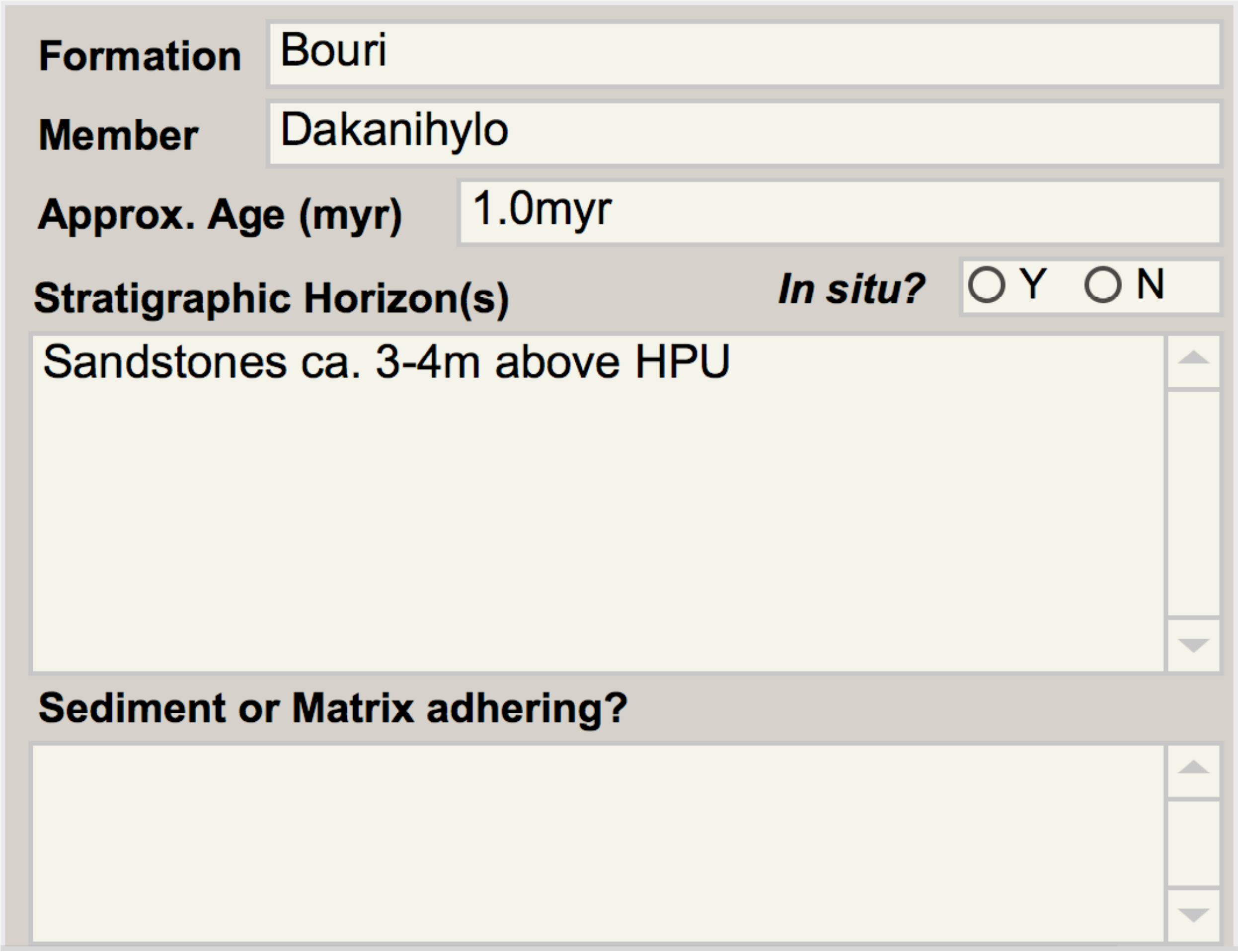


Date (m/d/y)	Identified by	Identified as	Notes and comments	
/ /		*Kolpochoerus sp.*	[imported 9/13/2007]:	*Delete*
/ /				*Delete*

It will automatically sort in reverse chronological order. Unresolved taxonomic problems (usually disagreements between different analysts) can be flagged for easy access and compilation by using the radio buttons Taxonomic problem ? ○ Y ○ N immediately above the taxonomic entry boxes.

j. Chronostratigraphic Information

This information is entered on a specimen-by-specimen basis in the lower right hand quadrant of the **Specimen Entry** layout.



Formation Bouri

Member Dakanihylo

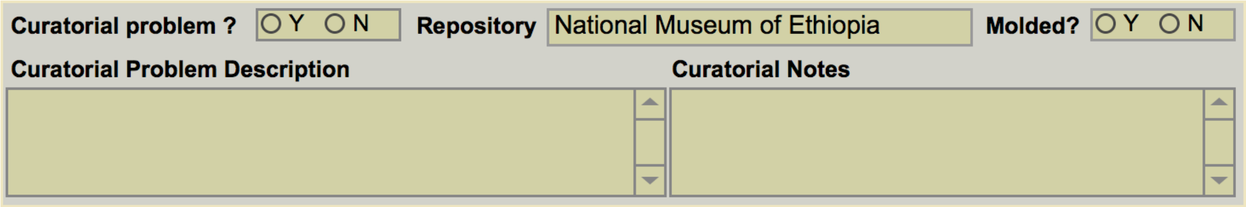
Approx. Age (myr) 1.0myr

Stratigraphic Horizon(s) ***In situ?*** ○ Y ○ N

Sandstones ca. 3-4m above HPU

Sediment or Matrix adhering?

k. Curatorial Information



Curatorial problem ? ○ Y ○ N **Repository** National Museum of Ethiopia **Molded?** ○ Y ○ N

Curatorial Problem Description

Curatorial Notes

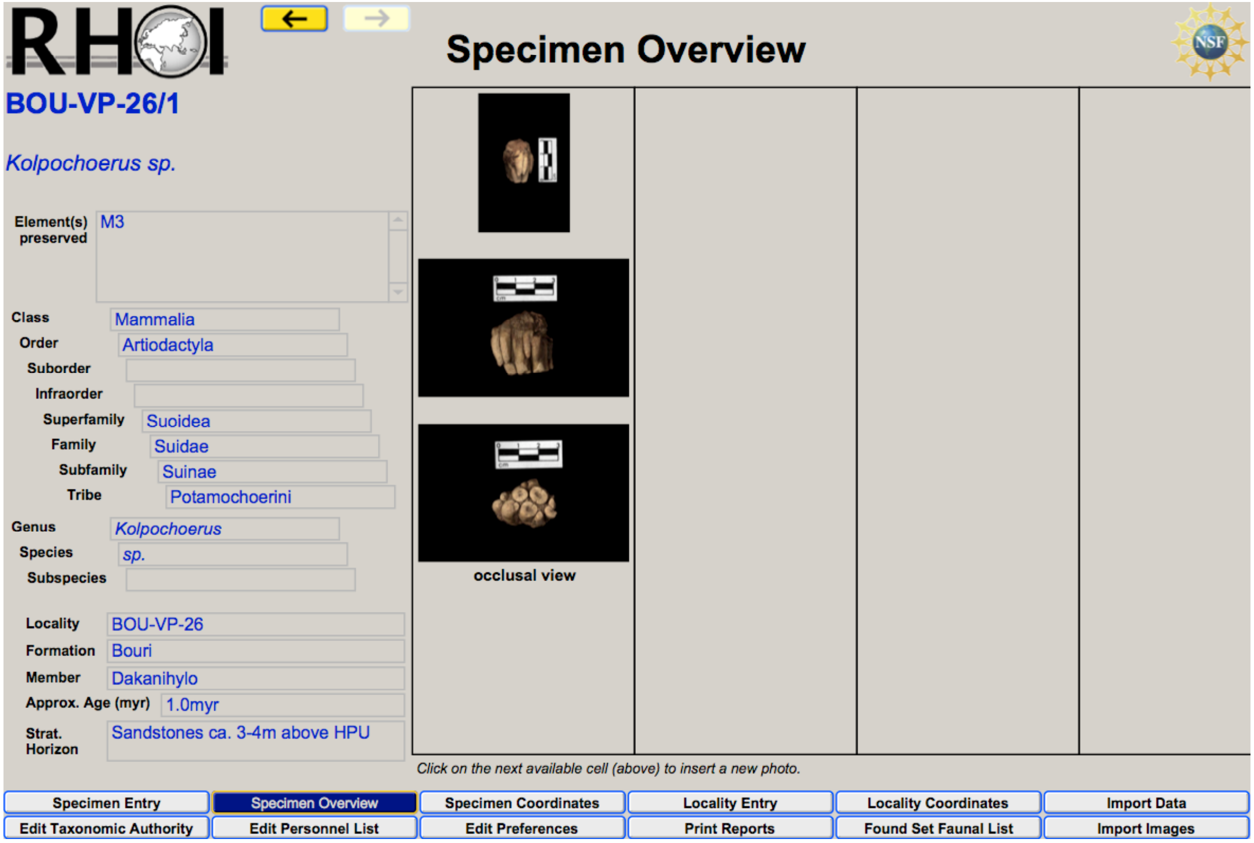
The RHOI Database Template allows you to make notations about particular problems involving individual specimens. For example, information about misplaced specimens, or specimens requiring further preparation can be entered here, along with archival notes on storage location, loan status, mold availability, or treatment history.

2. SPECIMEN OVERVIEW LAYOUT

Specimen Overview

This layout is for specimen assessment and viewing. The RHOI Database Template is designed to work either with or without digital images of specimens. If you choose not to include digital images of specimens, this **Specimen Overview** layout page works simply as a quick view of a specimen's identification and provenience.

You cannot alter taxonomic names or any other information on this layout (except for adding images. Refer to section **D** for a full explanation). All entry and editing must be done on the **Specimen Entry** layout. The **Specimen Overview** layout mirrors (repeats) information entered on the **Specimen Entry** layout, but formats it differently to make browsing your records easier.



BOU-VP-26/1

Kolpochoerus sp.

Element(s) preserved	M3
Class	Mammalia
Order	Artiodactyla
Suborder	
Infraorder	
Superfamily	Suoidea
Family	Suidae
Subfamily	Suinae
Tribe	Potamochoerini
Genus	*Kolpochoerus*
Species	*sp.*
Subspecies	
Locality	BOU-VP-26
Formation	Bouri
Member	Dakanihylo
Approx. Age (myr)	1.0myr
Strat. Horizon	Sandstones ca. 3-4m above HPU

Click on the next available cell (above) to insert a new photo.

When available, digital photos for the specimen appear as thumbnails, arranged in columns. To see a larger version of a particular image, click on the small thumbnail.

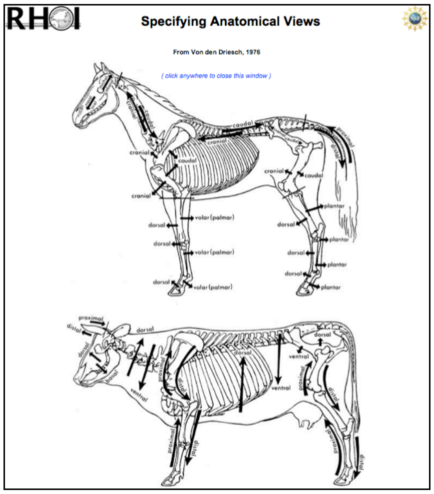
When you click on one of the thumbnail images, the following screen page opens:

On this Image viewer screen page, a pull-down menu ▨ allows you to label the anatomical view that each image represents. The **Edit views** button allows you to edit the views available on this menu.

Photographic Views

View Name	Notes	
unspecified view	use if view is unknown	Delete
anterior view		Delete
apical view		Delete
basal view		Delete
buccal view		Delete
caudal view		Delete
cranial view		Delete
dorsal view		Delete
distal view		Delete
distal or proximal view	use when unsure	Delete
ectocranial view		Delete
endocranial view		Delete
labial view		Delete
lingual view		Delete
left lateral view		Delete
lateral view		Delete
medial view		Delete
medial or lateral view	use when unsure	Delete
mesial view		Delete
nasal view		Delete
nuchal view		Delete
oblique view		Delete
occlusal view		Delete
palmar view		Delete
proximal view		Delete
right lateral view		Delete
ventral view		Delete
plantar view		Delete

The **Anatomical conventions** button opens a window to show conventional directional terms from Von den Driesch (1976).



Specifying Anatomical Views

From Von den Driesch, 1976

(click anywhere to close this window)

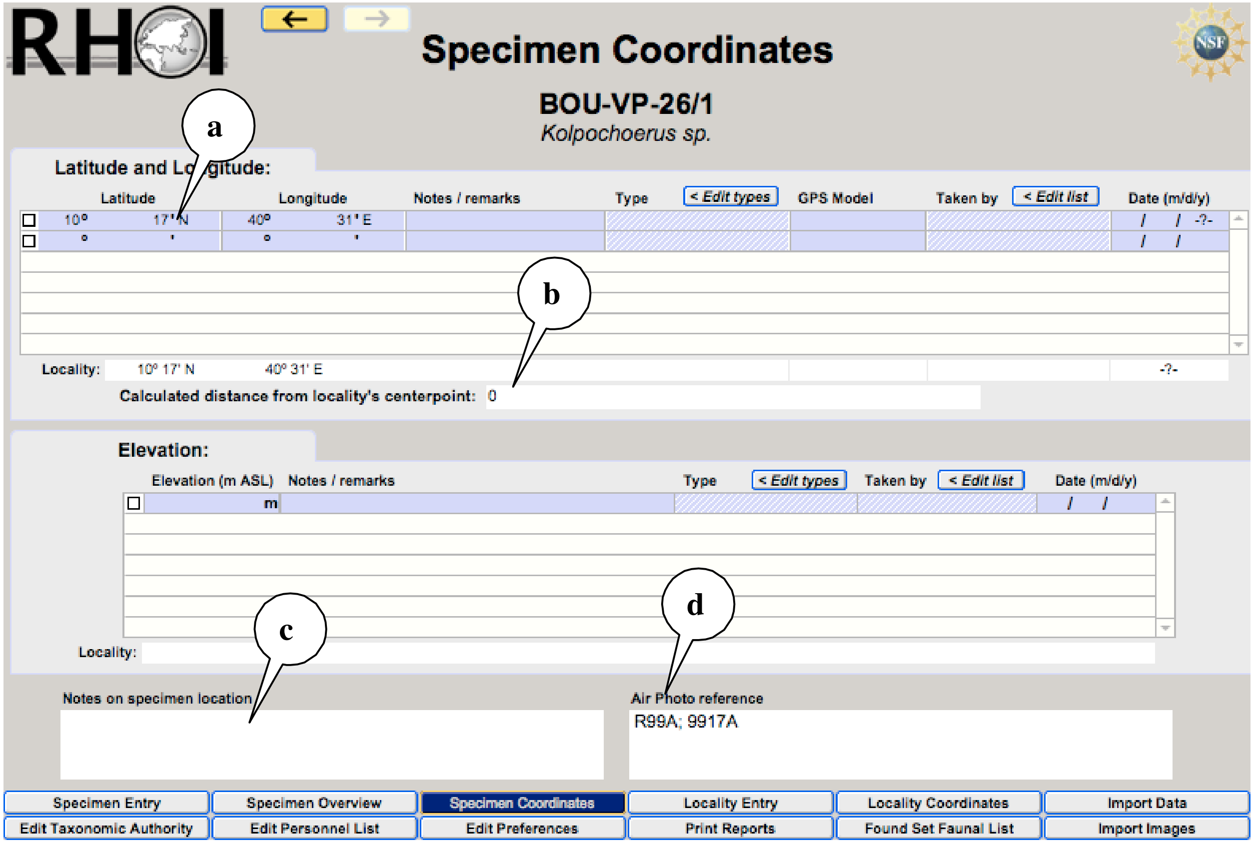
A **Delete this image >>** button is also included to allow you to delete the image being viewed.

For instructions and help in implementing the photo import functions, click on the **Import Images** button on the bottom right hand corner of the screen.

3. SPECIMEN COORDINATES LAYOUT

Specimen Coordinates

This layout allows you to enter and display spatial data pertaining to individual specimens. You may enter a variety of specimen-specific spatial information here; latitude and longitude, elevation, notes, and air photo references.



BOU-VP-26/1
Kolpochoerus sp.

Latitude and Longitude:

	Latitude	Longitude	Notes / remarks	Type	GPS Model	Taken by	Date (m/d/y)
☐	10° 17' N	40° 31' E					/ / -?-
☐	° '	° '					/ /
Locality:	10° 17' N	40° 31' E					-?-

Calculated distance from locality's centerpoint: 0

Elevation:

	Elevation (m ASL)	Notes / remarks	Type	Taken by	Date (m/d/y)
☐	m				/ /
Locality:					

Notes on specimen location:

Air Photo reference: R99A; 9917A

The following sections refer to the letters in the figure above.

a. Multiple Readings

You may list multiple position readings for the same specimen, and may designate the most accurate reading (reported at the top of the list) by clicking the small white box to the left.

b. Locality Centerpoint Readings

Some projects record locality center-point spatial information rather than individual coordinate data for each specimen. Locality-based center-point data entered on the **Locality Entry** layout appear here under the **Locality** field, which is auto-entered from spatial data recorded on the individual locality forms. The **Calculated distance from locality's centerpoint** field automatically calculates the distance between the actual specimen position (when recorded individually) and any locality centerpoint already separately entered on the **Locality Entry** layout. For specimens with individual spatial placement, this is a handy way to verify record accuracy and/or establish locality size.

c. Notes

Other positional notes, such as stratigraphic level, can be entered in the white text boxes at the bottom of the layout.

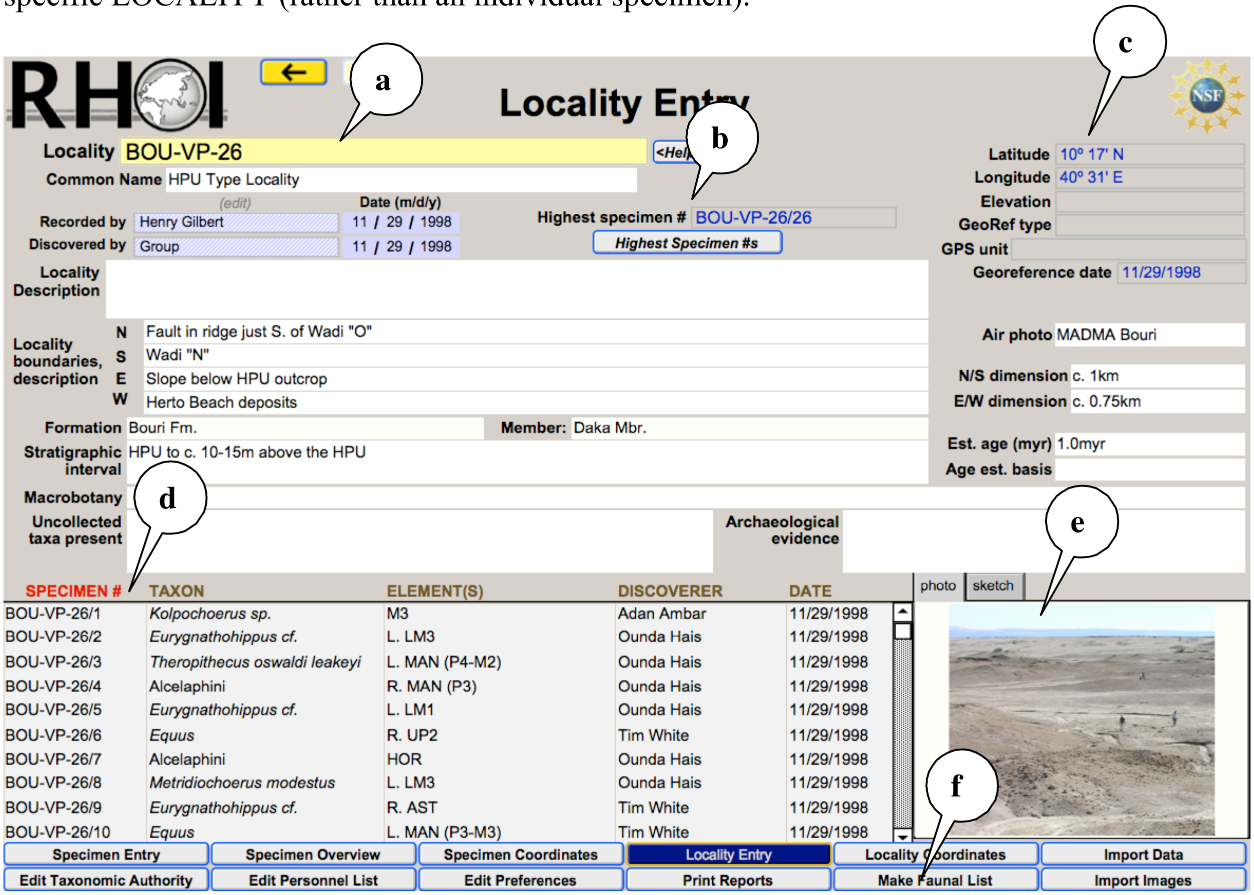
d. Air Photo Reference

If you have aerial photographs or satellite imagery (either hard-copy or digital) you used in the field to plot specimen locations, you can refer to that information here.

4. LOCALITY ENTRY LAYOUT

Locality Entry

This layout allows you to enter and display spatial and descriptive information pertaining to a specific LOCALITY (rather than an individual specimen).



Locality BOU-VP-26
Common Name HPU Type Locality
Recorded by Henry Gilbert — **Date (m/d/y)** 11 / 29 / 1998
Discovered by Group — 11 / 29 / 1998
Highest specimen # BOU-VP-26/26
Highest Specimen #s
Locality Description
Locality boundaries, description
N Fault in ridge just S. of Wadi "O"
S Wadi "N"
E Slope below HPU outcrop
W Herto Beach deposits
Formation Bouri Fm. — **Member:** Daka Mbr.
Stratigraphic interval HPU to c. 10-15m above the HPU
Macrobotany
Uncollected taxa present
Archaeological evidence
Latitude 10° 17' N
Longitude 40° 31' E
Elevation
GeoRef type
GPS unit
Georeference date 11/29/1998
Air photo MADMA Bouri
N/S dimension c. 1km
E/W dimension c. 0.75km
Est. age (myr) 1.0myr
Age est. basis

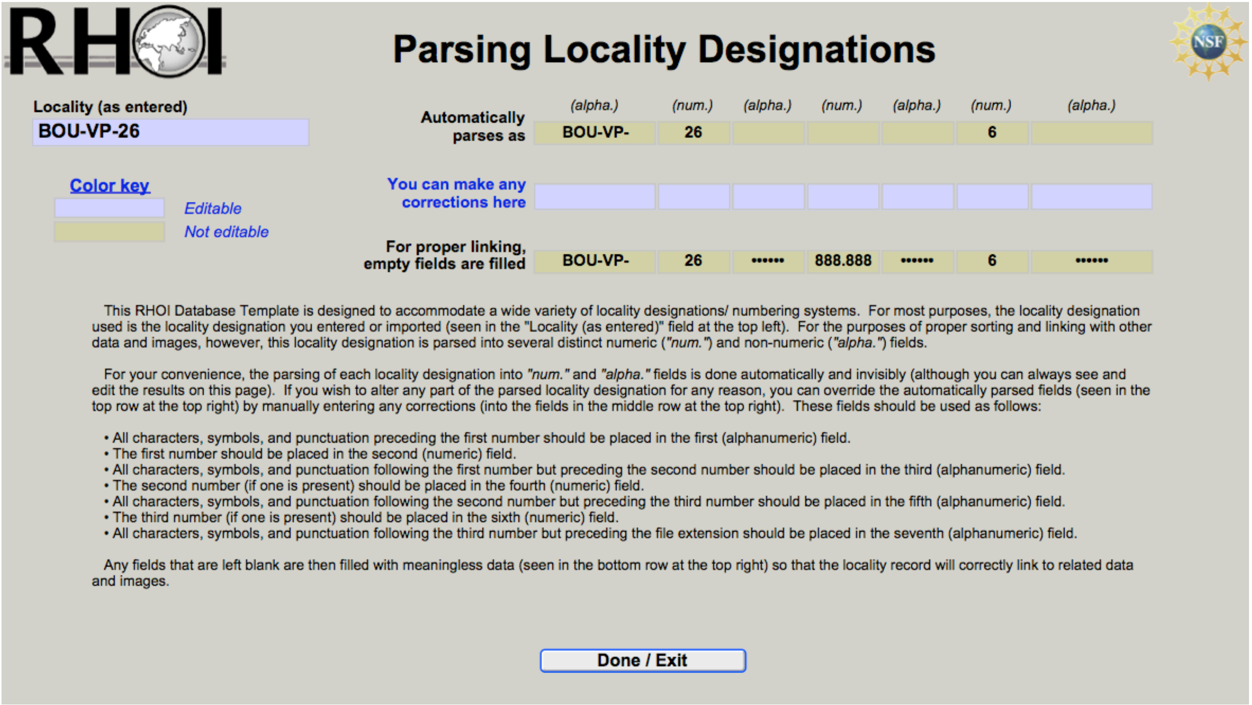
SPECIMEN #	TAXON	ELEMENT(S)	DISCOVERER	DATE
BOU-VP-26/1	*Kolpochoerus sp.*	M3	Adan Ambar	11/29/1998
BOU-VP-26/2	*Eurygnathohippus cf.*	L. LM3	Ounda Hais	11/29/1998
BOU-VP-26/3	*Theropithecus oswaldi leakeyi*	L. MAN (P4-M2)	Ounda Hais	11/29/1998
BOU-VP-26/4	Alcelaphini	R. MAN (P3)	Ounda Hais	11/29/1998
BOU-VP-26/5	*Eurygnathohippus cf.*	L. LM1	Ounda Hais	11/29/1998
BOU-VP-26/6	*Equus*	R. UP2	Tim White	11/29/1998
BOU-VP-26/7	Alcelaphini	HOR	Ounda Hais	11/29/1998
BOU-VP-26/8	*Metridiochoerus modestus*	L. LM3	Ounda Hais	11/29/1998
BOU-VP-26/9	*Eurygnathohippus cf.*	R. AST	Tim White	11/29/1998
BOU-VP-26/10	*Equus*	L. MAN (P3-M3)	Tim White	11/29/1998

The following sections refer to the letters in the figure above.

a. Locality Designations

Different projects use different **Locality** designation systems for their collection localities. You may enter the locality name and common name in the indicated fields. The RHOI Database Template is designed to accommodate a wide variety of locality designations and numbering systems. For most purposes, the locality designation used will be the locality designation you entered or imported (seen in the **Locality** field at the top left).

However, since locality designations may sometimes be integrated into the individual specimen numbers, for the purposes of proper sorting and linking with other data and images, some locality designations may have to be parsed into distinct numeric ("*num.*") and non-numeric ("*alpha.*") fields. By clicking on the <Help button provided, you are taken to a window entitled **Parsing Locality Designations**:



Parsing Locality Designations

Locality (as entered): BOU-VP-26

	(alpha.)	(num.)	(alpha.)	(num.)	(alpha.)	(num.)	(alpha.)
Automatically parses as	BOU-VP-	26				6	
You can make any corrections here							
For proper linking, empty fields are filled	BOU-VP-	26	••••••	888.888	••••••	6	••••••

This RHOI Database Template is designed to accommodate a wide variety of locality designations/ numbering systems. For most purposes, the locality designation used is the locality designation you entered or imported (seen in the "Locality (as entered)" field at the top left). For the purposes of proper sorting and linking with other data and images, however, this locality designation is parsed into several distinct numeric (*"num."*) and non-numeric (*"alpha."*) fields.

For your convenience, the parsing of each locality designation into *"num."* and *"alpha."* fields is done automatically and invisibly (although you can always see and edit the results on this page). If you wish to alter any part of the parsed locality designation for any reason, you can override the automatically parsed fields (seen in the top row at the top right) by manually entering any corrections (into the fields in the middle row at the top right). These fields should be used as follows:

- All characters, symbols, and punctuation preceding the first number should be placed in the first (alphanumeric) field.
- The first number should be placed in the second (numeric) field.
- All characters, symbols, and punctuation following the first number but preceding the second number should be placed in the third (alphanumeric) field.
- The second number (if one is present) should be placed in the fourth (numeric) field.
- All characters, symbols, and punctuation following the second number but preceding the third number should be placed in the fifth (alphanumeric) field.
- The third number (if one is present) should be placed in the sixth (numeric) field.
- All characters, symbols, and punctuation following the third number but preceding the file extension should be placed in the seventh (alphanumeric) field.

Any fields that are left blank are then filled with meaningless data (seen in the bottom row at the top right) so that the locality record will correctly link to related data and images.

For your convenience, the parsing of each locality designation into "*num.*" and "*alpha.*" fields is done automatically and invisibly (although you can always see and edit the results on this page). If you wish to alter any part of the parsed locality designation, you can override the automatically parsed fields (seen in the top row at the top right) by manually entering any corrections (into the fields in the middle row at the top right). These fields should be used as follows:

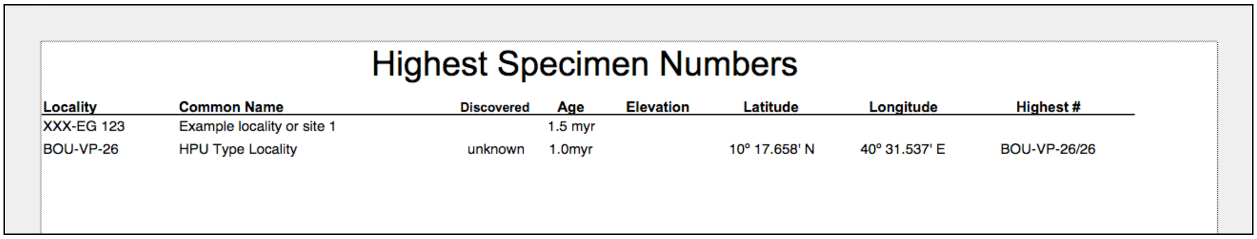
- All characters, symbols, and punctuation preceding the first number should be placed in the first (alphanumeric) field.
- The first number should be placed in the second (numeric) field.
- All characters, symbols, and punctuation following the first number but preceding the second number should be placed in the third (alphanumeric) field.
- The second number (if one is present) should be placed in the fourth (numeric) field.
- All characters, symbols, and punctuation following the second number but preceding the third number should be placed in the fifth (alphanumeric) field.
- The third number (if one is present) should be placed in the sixth (numeric) field.
- All characters, symbols, and punctuation following the third number but preceding the file extension should be placed in the seventh (alphanumeric) field.

Any fields that are left blank are then filled with meaningless data (seen in the bottom row at the top right) so that the locality record will correctly link to related data and images.

b. Highest Specimen Number

A field is provided to keep track of the highest specimen number assigned for a given locality, which is shown in blue letters.

Clicking on the **Highest Specimen #s** button creates a separate, time-stamped list of highest specimen numbers for ALL of the localities in your database.



Highest Specimen Numbers

Locality	Common Name	Discovered	Age	Elevation	Latitude	Longitude	Highest #
XXX-EG 123	Example locality or site 1		1.5 myr				
BOU-VP-26	HPU Type Locality	unknown	1.0myr		10° 17.658' N	40° 31.537' E	BOU-VP-26/26

You may find this feature useful for printing a hard copy prior to fieldwork, so that specimen numbers stay sequential, and non-repeating, from season to season.

c. Locality Coordinates

These fields automatically mirror the Latitude, Longitude, Elevation, and GPS data entered in the **Locality Coordinates** layout, described below. Clicking on any of these fields will take you to the **Locality Coordinates** layout, where you may edit as needed.

d. List of Specimens

This area of the **Locality Entry** layout allows you to view a complete list of specimens from each locality. This list can be sorted by specimen number, taxon, element(s), discoverer, or discovery date. Simply click on any one of the red titles atop the columns.

e. Photos and Sketches

The box in the lower right hand corner of this layout is designed to hold an imported archival photograph and/or sketch that shows the geographic placement and local stratigraphy of the locality. To import either a photo or sketch, click the appropriate tab at the upper left hand corner of the box:

Click anywhere in the frame where the new photo or sketch will appear. A new window called either **Photo of Locality for…** or **Sketch of Locality for…** will appear.

Click on the **Import/Replace Photo** button. Navigate to the file location on your hard drive for the image desired. Highlight that image, and click **Choose**. Your image should copy directly to the Database Template. You may wish to use a JPEG rather than a TIFF image to save on file size (see section **D.1.** for suggestions on managing file sizes). Use the same procedure to import sketches.

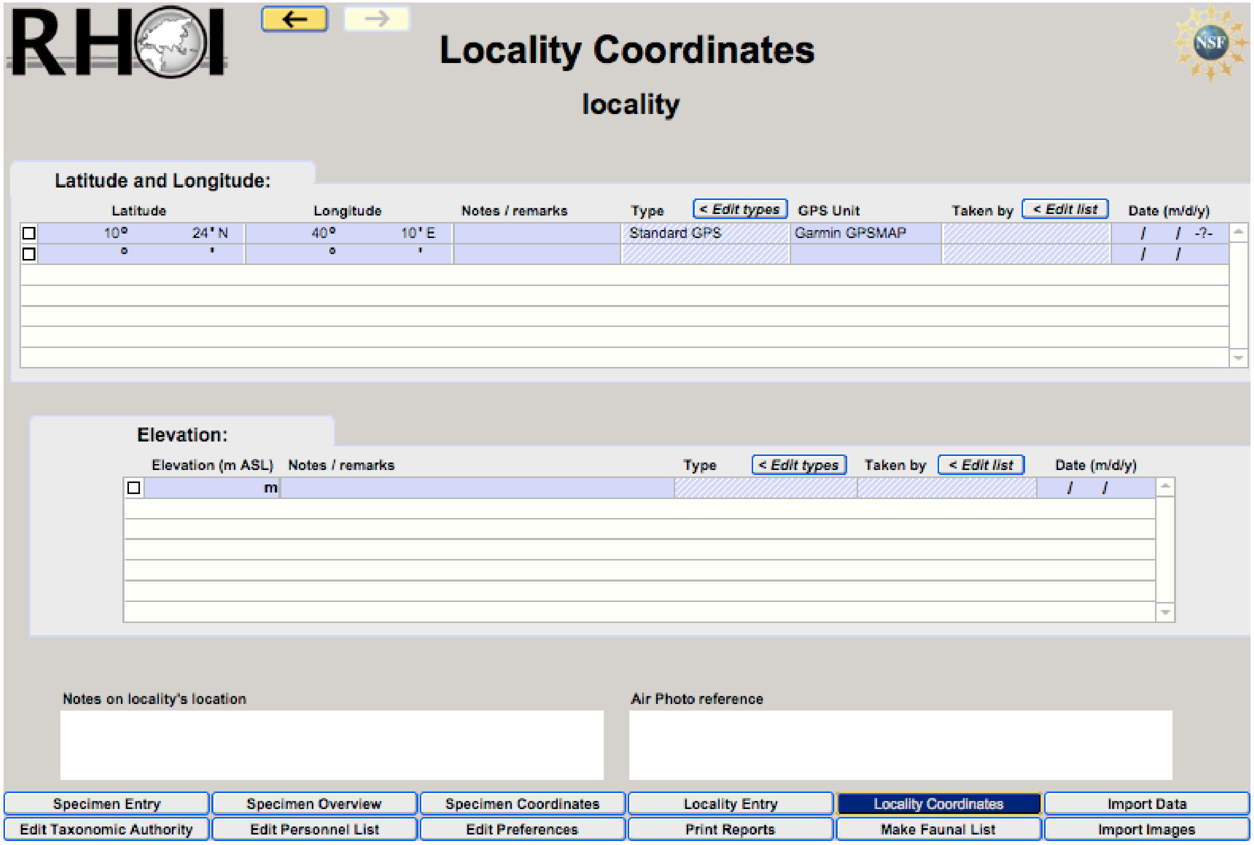
f. Faunal List

Additionally, you can generate an automatically-formatted faunal list for each locality by clicking the **Make Faunal List** button at the bottom right of the layout.

5. LOCALITY COORDINATES LAYOUT

Locality Coordinates

This layout allows you to enter and display spatial data pertaining to localities.



Locality Coordinates

locality

Latitude and Longitude:

	Latitude	Longitude	Notes / remarks	Type	GPS Unit	Taken by	Date (m/d/y)
☐	10° 24' N	40° 10' E		Standard GPS	Garmin GPSMAP		/ / -?-
☐	° '	° '					/ /

Elevation:

	Elevation (m ASL)	Notes / remarks	Type	Taken by	Date (m/d/y)
☐	m				/ /

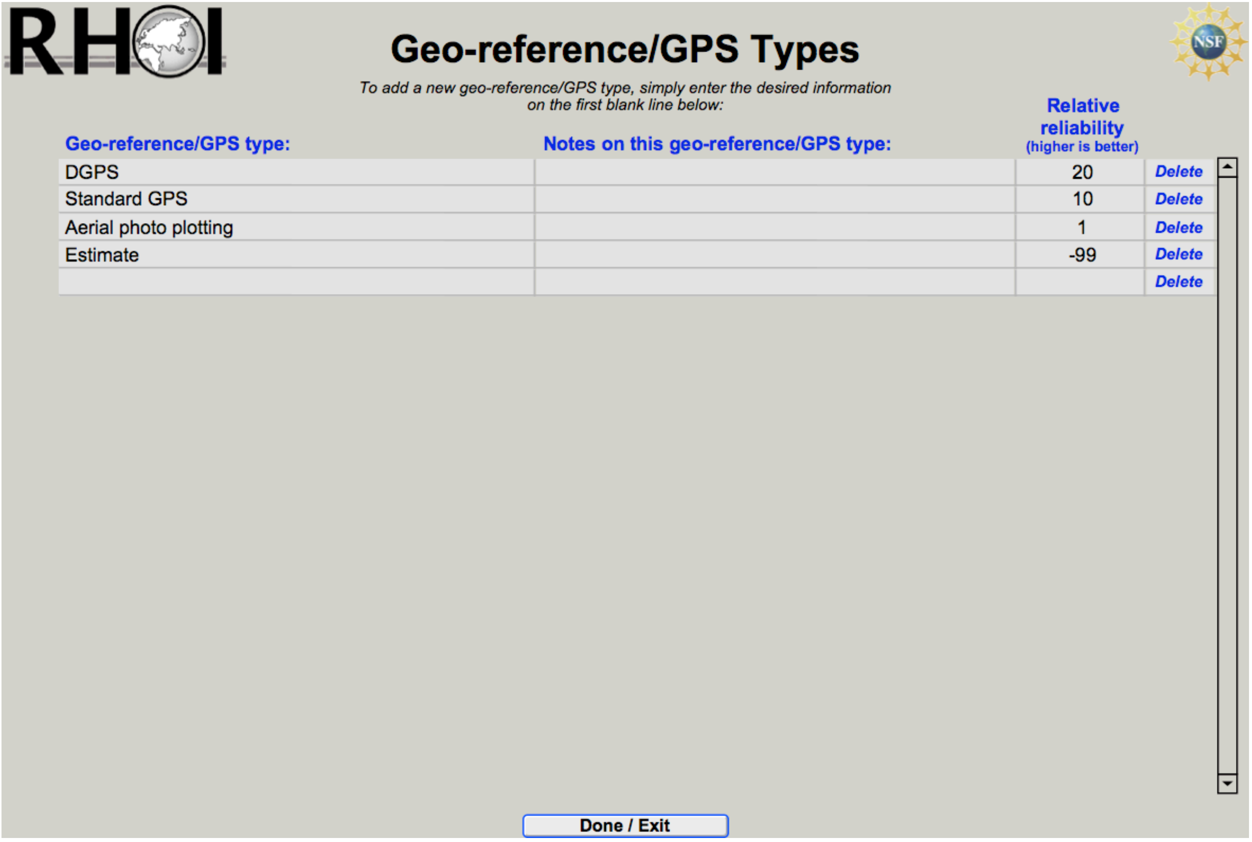
Notes on locality's location

Air Photo reference

The information entered here will be automatically entered into the provenience fields in the **Locality Entry** layout described above. You control this by designating the spatial data set(s) that you consider the most accurate by clicking the small white box to the left of the entry. This most accurate reading will then rise to the top of the list, and will appear automatically on the **Locality Entry** layout.

In the **Type** column, you may enter (via pull-down menu) the model of GPS or other instrument used to acquire the spatial coordinates. Click on the *< Edit types* button to edit the **Geo-reference/GPS Types** list of instruments. This list is the basis for the **Type** pull-down menu.

You may rank the reliability (accuracy) of any instrument in your list on this screen page:



Geo-reference/GPS Types

To add a new geo-reference/GPS type, simply enter the desired information on the first blank line below:

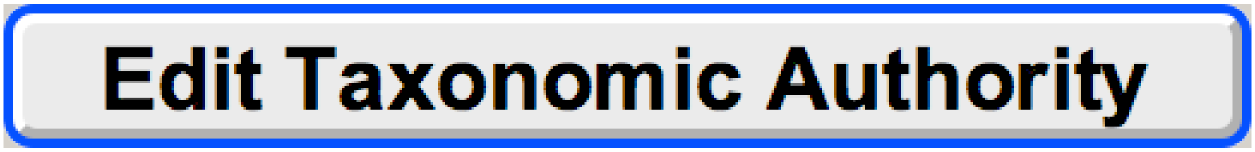
Geo-reference/GPS type:	Notes on this geo-reference/GPS type:	Relative reliability (higher is better)	
DGPS		20	Delete
Standard GPS		10	Delete
Aerial photo plotting		1	Delete
Estimate		-99	Delete
			Delete

Additionally, you can click the **<Edit list** button to edit the **Personnel List**. Select the check box next to **Collectors** to activate that person in the **Taken by** pull-down menu on the Locality Coordinates layout.

Personnel List

Last name	First name	Name to be displayed in lists:	To be included in which lists?			
Gilbert	Henry	Henry Gilbert	☒ Collectors	☐ Identifiers	☒ Photographers	Delete
Group		Group	☒ Collectors	☐ Identifiers	☐ Photographers	Delete

6. EDIT TAXONOMIC AUTHORITY LAYOUT



This layout is a complete summary of all taxa that have been entered at the genus level or above. The information is presented in a "spreadsheet" format, and can be edited here. These functions are described above under section **A.1.f.**

Class	Order	Suborder	Infraorder	Superfamily	Family	Subfamily	Tribe	Genus	
Aves	Anseriformes		Anserides		Anatidae	Anatinae	Anserini	*Plectropterus*	Delete
Aves	Apodiformes				Apodidae				Delete
Aves	Charadriiformes								Delete
Aves	Ciconiiformes	Ciconii	Ciconiides	Ardeoidea	Ardeidae				Delete
Aves	Ciconiiformes	Ciconii	Ciconiides	Ciconioidea	Ciconiidae	Ciconiinae		*Leptoptilos*	Delete
Aves	Ciconiiformes	Ciconii	Ciconiides	Ciconioidea	Ciconiidae	Ciconiinae		*Mycteria*	Delete
Aves	Ciconiiformes	Ciconii	Ciconiides	Threskiornithoidea	Threskiornithidae				Delete
Aves	Ciconiiformes	Ciconii	Falconides		Accipitridae			*Aquila*	Delete
Aves	Ciconiiformes	Ciconii	Falconides		Accipitridae			*Buteo*	Delete
Aves	Ciconiiformes	Ciconii	Falconides		Accipitridae	Accipitrinae		*Accipiter*	Delete
Aves	Coliiformes				Coliidae				Delete
Aves	Columbiformes				Columbidae			*Streptopelia*	Delete
Aves	Columbiformes				Columbidae			*Treron*	Delete
Aves	Coraciiformes				Bucorvidae			*Bucorvus*	Delete
Aves	Galliformes				Numididae			*Numida*	Delete
Aves	Galliformes				Phasianidae			*Coturnix*	Delete
Aves	Galliformes				Phasianidae			*Excalfactoria*	Delete
Aves	Galliformes				Phasianidae			*Gutterea*	Delete
Aves	Galliformes				Phasianidae			*Pavo*	Delete
Aves	Galliformes				Phasianidae	Phasianinae	Perdicini	*Francolinus*	Delete
Aves	Gruiformes				Otididae			*Eupodotis*	Delete
Aves	Gruiformes				Otididae			*Rupodotis*	Delete
Aves	Gruiformes				Rallidae				Delete
Aves	Passeriformes				Corvidae				Delete
Aves	Pelecaniformes				Anhingidae			*Anhinga*	Delete
Aves	Pelecaniformes				Phalacrocoracidae			*Phalacrocorax*	Delete
Aves	Podicipediformes				Podicipedidae			*Podiceps*	Delete
Aves	Psittaciformes				Psittacidae	Psittacinae		*Agapornis*	Delete
Aves	Psittaciformes				Psittacidae	Psittacinae		*Poicephalus*	Delete
Aves	Strigiformes				Strigidae	Buboninae		*Otus*	Delete
Aves	Strigiformes	Strigi			Tytonidae	Tytoninae		*Tyto*	Delete
Aves	Struthioniformes	Struthioni	Struthionides		Struthionidae			*Struthio*	Delete
Mammalia	Artiodactyla	Ruminantia		Bovoidea	Bovidae	Alcelaphinae	Aepycerotini	*Aepyceros*	Delete
Mammalia	Artiodactyla	Ruminantia		Bovoidea	Bovidae	Alcelaphinae	Alcelaphini	*Alcelaphus*	Delete
Mammalia	Artiodactyla	Ruminantia		Bovoidea	Bovidae	Alcelaphinae	Alcelaphini	*Awashia*	Delete
Mammalia	Artiodactyla	Ruminantia		Bovoidea	Bovidae	Alcelaphinae	Alcelaphini	*Beatragus*	Delete
Mammalia	Artiodactyla	Ruminantia		Bovoidea	Bovidae	Alcelaphinae	Alcelaphini	*Connochaetes*	Delete
Mammalia	Artiodactyla	Ruminantia		Bovoidea	Bovidae	Alcelaphinae	Alcelaphini	*Damaliscus*	Delete
Mammalia	Artiodactyla	Ruminantia		Bovoidea	Bovidae	Alcelaphinae	Alcelaphini	*Damalops*	Delete
Mammalia	Artiodactyla	Ruminantia		Bovoidea	Bovidae	Alcelaphinae	Alcelaphini	*Megalotragus*	Delete
Mammalia	Artiodactyla	Ruminantia		Bovoidea	Bovidae	Alcelaphinae	Alcelaphini	*Parmularius*	Delete

You may use this layout to edit the **Taxonomic Authority** (as described above), or to view the entire authority as a single faunal list (by clicking the **View as Faunal List** button). Please note, faunal lists for individual localities are best compiled from the **Make Faunal List** command on the Locality Entry layout, described above, or from the **Found Set Faunal List** layout, described in section **A.10.**, rather than via the **Taxonomic Authority**.

The RHOI Database Template comes pre-populated with the Middle Awash faunal hierarchy, so you will need to modify it to fit your project's needs.

If you do not wish to use the auto-entry features of the **Specimen Entry** layout, you may simply ignore the **Taxonomic Authority**. This list serves only to provide the foundation for the auto-entry functions on the **Specimen Entry** layout.

The RHOI Database Template works fine without any of the taxa listed on this spreadsheet, but the auto-entry functions on the **Specimen Entry** layout will not work without any data entered here.

7. EDIT PERSONNEL LIST LAYOUT

Edit Personnel List

This layout allows you to keep track of personnel, sorted by first and last names.

Personnel List

Last name	First name	Name to be displayed in lists:	To be included in which lists?			
Gilbert	Henry	Henry Gilbert	☒ Collectors	☐ Identifiers	☒ Photographers	*Delete*
Group		Group	☒ Collectors	☐ Identifiers	☐ Photographers	*Delete*

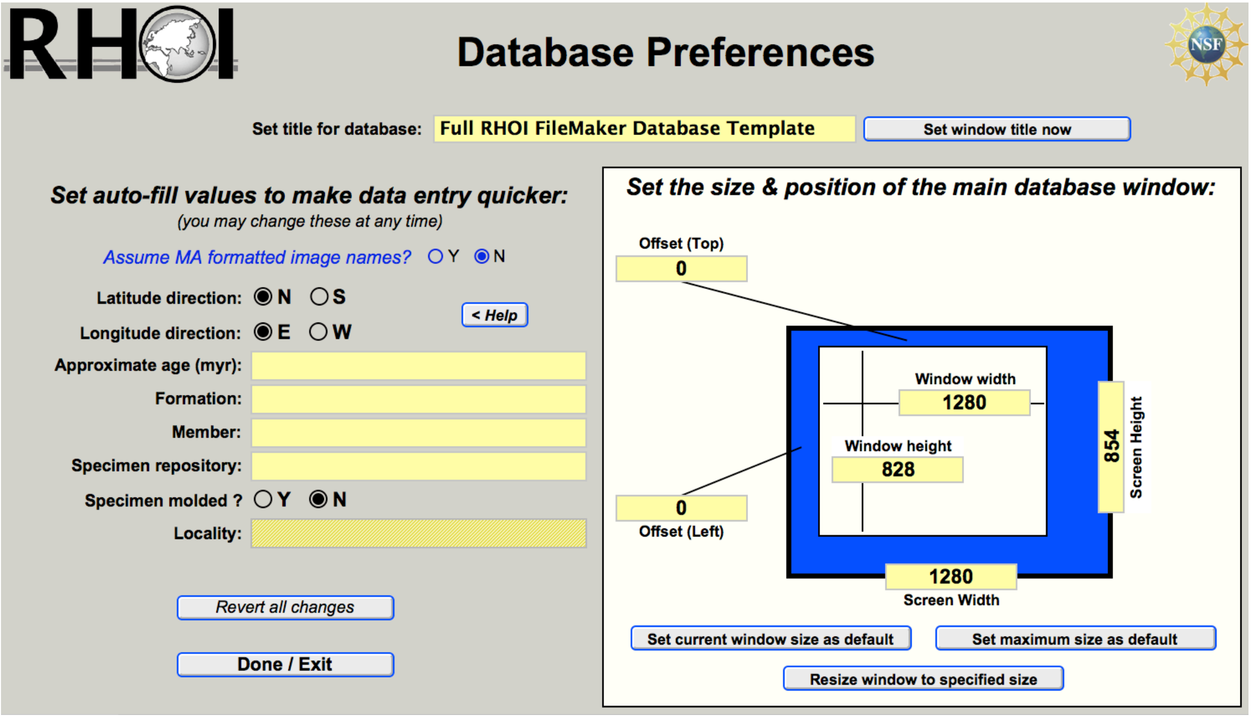
This is a useful tool for identifying investigators who find and collect the fossils, identify them, and/or take digital photographs for your project.

To add or subtract people from the list, click on the appropriate buttons. When the boxes are checked, these names appear in the corresponding pull-down menus throughout the database.

8. EDIT PREFERENCES LAYOUT

Edit Preferences

This layout allows you to customize the RHOI Database Template to make it specific to your own museum's or project's needs and preferences. These steps are described in section **B.2.b.**, below.



Database Preferences

Set title for database: Full RHOI FileMaker Database Template

Set auto-fill values to make data entry quicker:
(you may change these at any time)

Assume MA formatted image names? ○ Y ● N

Latitude direction:	● N ○ S
Longitude direction:	● E ○ W
Approximate age (myr):	
Formation:	
Member:	
Specimen repository:	
Specimen molded ?	○ Y ● N
Locality:	

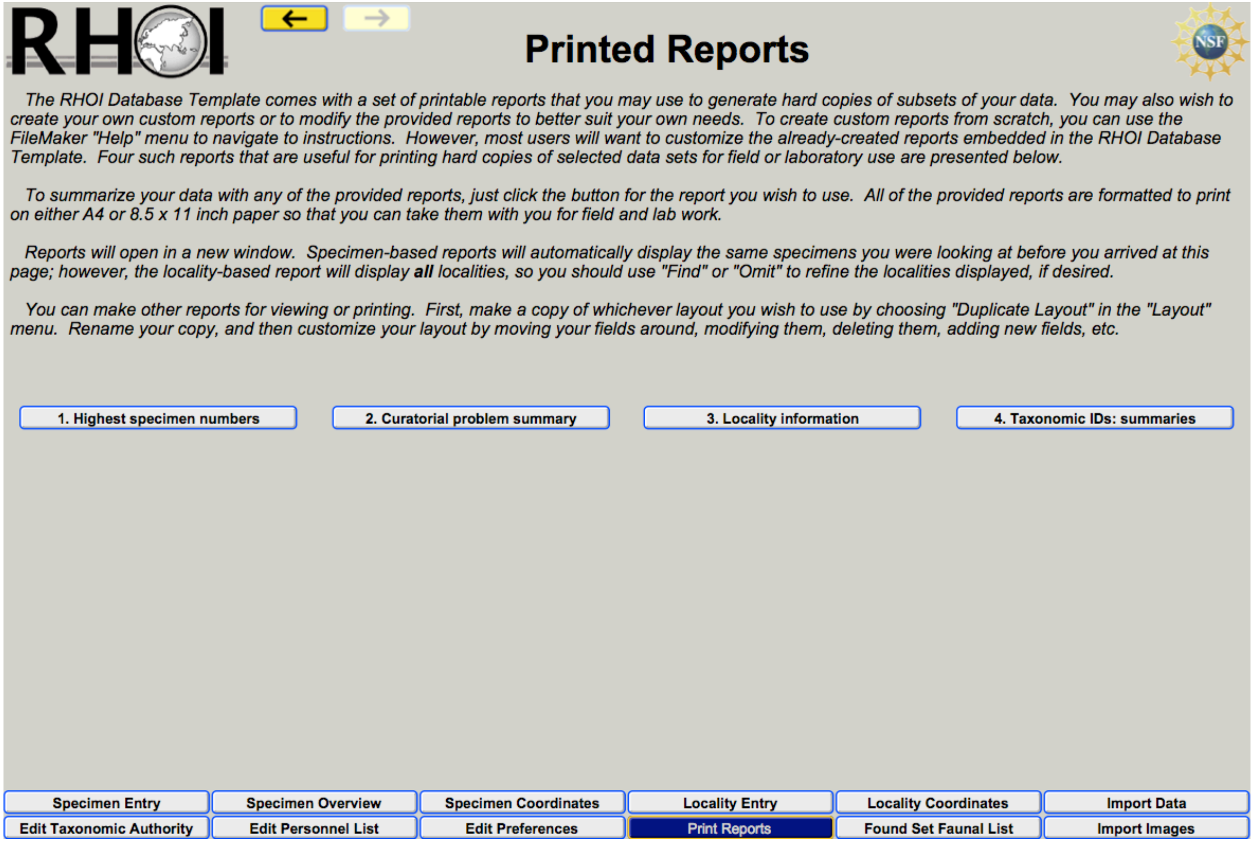
Set the size & position of the main database window:

Offset (Top)	0
Window width	1280
Window height	828
Offset (Left)	0
Screen Width	1280
Screen Height	854

9. PRINT REPORTS LAYOUT

Print Reports

The RHOI Database Template comes with a set of print-ready report forms, which you can use to make hard (printed) copies of subsets of your data. You may also wish to create your own custom reports, or modify the provided reports to better suit your own museum's/project's needs. Consult the **Help** feature of FileMaker to guide you. You can also print hard copies of any of these reports for use by your project's workers in field or museum contexts, for later digital entry. Just add a couple of new, empty records, and print these with all the fields empty.



Printed Reports

The RHOI Database Template comes with a set of printable reports that you may use to generate hard copies of subsets of your data. You may also wish to create your own custom reports or to modify the provided reports to better suit your own needs. To create custom reports from scratch, you can use the FileMaker "Help" menu to navigate to instructions. However, most users will want to customize the already-created reports embedded in the RHOI Database Template. Four such reports that are useful for printing hard copies of selected data sets for field or laboratory use are presented below.

To summarize your data with any of the provided reports, just click the button for the report you wish to use. All of the provided reports are formatted to print on either A4 or 8.5 x 11 inch paper so that you can take them with you for field and lab work.

*Reports will open in a new window. Specimen-based reports will automatically display the same specimens you were looking at before you arrived at this page; however, the locality-based report will display **all** localities, so you should use "Find" or "Omit" to refine the localities displayed, if desired.*

You can make other reports for viewing or printing. First, make a copy of whichever layout you wish to use by choosing "Duplicate Layout" in the "Layout" menu. Rename your copy, and then customize your layout by moving your fields around, modifying them, deleting them, adding new fields, etc.

To generate any of the provided reports for printing (illustrated on this page), click on the button of the report you wish to use.

Individual reports will open in a new window.

- The **Highest Specimen Numbers** report is described in section **A.4.b.** and is useful for keeping track of specimen numbers for given localities between collection periods (seasons).

- The **Curatorial Problem Summary** is useful for quickly identifying problems and working within museum collections.
- The **Locality Information** report is useful to have when conducting field work.
- The **Taxonomic IDs: summaries** report is the most effective way to allow project paleontologists to proceed with their identifications and make their revisions available for entry into the database. It is highly recommended (see section **B.2.**) that a single person on each project/in each museum take responsibility for entry of **ALL** taxonomic identifications and revisions in order to keep a working database.

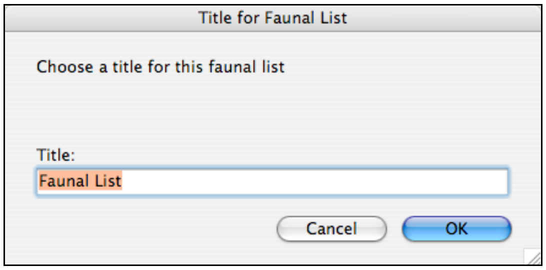
All of the specimen-based reports will automatically display the same specimens you were looking at before you arrived at this page, in the same sorting order in which you were viewing them. It is therefore useful to check that you have *found* and *sorted* the records you intend to print before opening these reports (layouts) via this page.

Note that the "Locality" Report will display **ALL** localities unless you use **Find** or **Omit** to limit the set of localities displayed (or printed).

10. FOUND SET FAUNAL LIST LAYOUT

This layout is a preformatted faunal list for whatever set of specimens has been **found** by searching within the database. You can search for localities, taxa, stratigraphic horizons, or any other subset of your data for which a faunal list is useful.

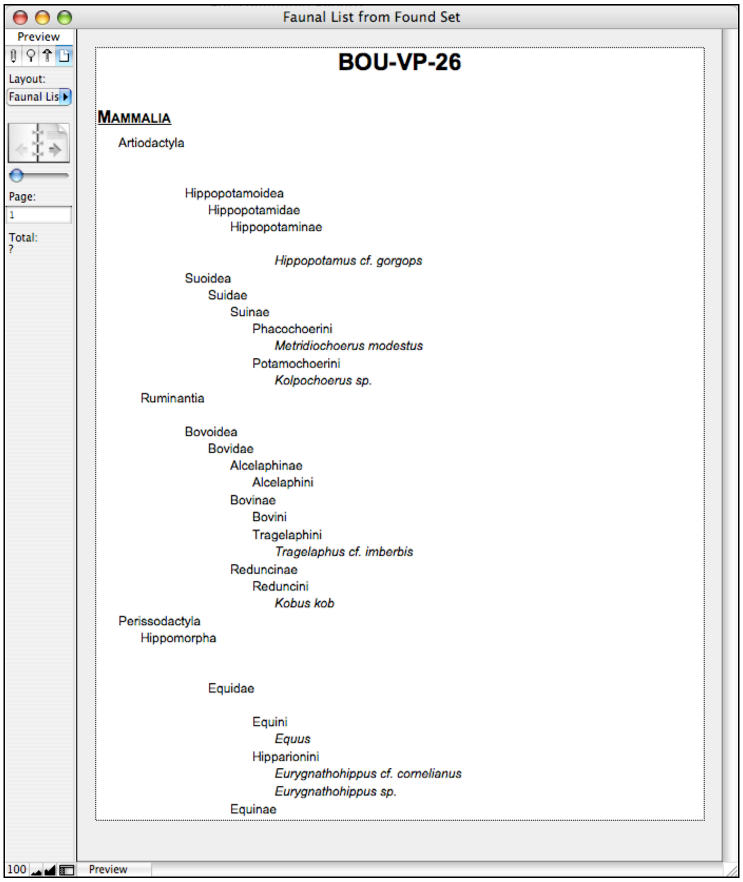
When you click on this button, the RHOI Database Template automatically creates another FileMaker file representing a complete, preformatted faunal list for whatever set of records that you have searched for (called the "**found set**"). You will first be asked to name this list, which you are about to create and save:


Title for Faunal List

Choose a title for this faunal list

Title: Faunal List

Name this faunal list file and click **OK**.



BOU-VP-26

MAMMALIA

- Artiodactyla
    - Hippopotamoidea
        - Hippopotamidae
            - Hippopotaminae
                - *Hippopotamus cf. gorgops*
    - Suoidea
        - Suidae
            - Suinae
                - Phacochoerini
                    - *Metridiochoerus modestus*
                - Potamochoerini
                    - *Kolpochoerus sp.*
    - Ruminantia
        - Bovoidea
            - Bovidae
                - Alcelaphinae
                    - Alcelaphini
                - Bovinae
                    - Bovini
                    - Tragelaphini
                        - *Tragelaphus cf. imberbis*
                - Reduncinae
                    - Reduncini
                        - *Kobus kob*
- Perissodactyla
    - Hippomorpha
        - Equidae
            - Equini
                - *Equus*
            - Hipparionini
                - *Eurygnathohippus cf. cornelianus*
                - *Eurygnathohippus sp.*
            - Equinae

The list then appears for viewing and printing. To save your current Faunal List, use your FileMaker toolbar at the top of your computer screen. Navigate to **File>Save/Send Records As** and choose either **Excel...** or **PDF...**

Under **Save as:** name your file and choose where on your computer you want it to go. Make sure that under the **Save:** option, you select "Records being browsed". This will save your entire Faunal List rather than just a subset of it. Click **Save** and wait for the action to process. You can now return to your database.

B. DOWNLOADING AND CUSTOMIZING YOUR DATABASE

1. INTRODUCTION

The software spreadsheet program **Excel** is widely used as a catalog by RHOI members. Excel has its uses, but because it is a spreadsheet rather than a database, it lacks the presentation and data manipulation features and flexibility possible with a true database program. We encourage RHOI members to experiment with the RHOI Database Template (FileMaker) format before deciding to abandon Excel. It is our hope that when you see the functionality of the RHOI Database Template, you will be eager to abandon Excel for your cataloging needs.

After experimentation, if you choose to adopt the RHOI Database Template described here (and we hope that you do, because of its many advantages), you will find that transferring data to and from Excel is quick, easy, and accurate. Here are the steps you should take:

• **INSTALL** FileMaker software. To open, view, and use either the example database or the empty copy described below, you will need to have FileMaker Pro Advanced loaded on your computer. RHOI Project leaders are eligible to obtain the software from the NSF-funded RHOI project. Please contact Tim White (timwhite@berkeley.edu) if you need help securing this software. You may download a free version of FileMaker for a 30 day trial period at: **http://filemakertrial.com/**

• **TEST DRIVE** the fully functional RHOI Database Template with real data and images. **DOWNLOAD** the example database (containing actual specimen and locality data and images from the Middle Awash project, with spatial placements degraded). This is available on the RHOI website (**http://rhoi.berkeley.edu/RHOI_Database_Template/downloads.php**). This working example version will allow you to explore the features of the database.

• **DOWNLOAD** the "RHOI Database Template: Empty Copy" electronic file document from the RHOI website: **http://rhoi.berkeley.edu/RHOI_Database_Template/downloads.php**

Use this to create your project's new database file. Rename the file so that it is recognizable as yours. We recommend making the words "MASTER" or "ARCHIVE" part of your downloaded empty file's new name in order to indicate that this is your primary catalog of record (see below).

You are now ready to **import** your existing records from Excel into your new FileMaker database file.

It is very important that **ALL** your records originally in Excel be imported into the **CORRECT** fields in FileMaker. The RHOI Database Template has been designed to give you complete control over this process.

Note that the "Empty" RHOI Database file you downloaded from the RHOI website comes with some information already pre-entered. These are the previously described Taxonomic Authority data and element and image codes that are used by the Middle Awash project. These were left in because they may be of value to other projects. If you don't want them, simply remove whatever pre-populated data you wish. Just click on the Edit Taxonomic Authority, *Edit views*, Edit Personnel List, and/or Add or edit element, and edit. Refer to the sections below for more detailed instructions.

2. NAMING AND CUSTOMIZING

a. Renaming Your Database

Rename the empty FileMaker file that you have downloaded to your computer.

- We recommend the term "*your project*_MASTER" or "*your project*_ARCHIVE," to indicate that this file (instead of some other copy) will become your project's working or archival document.

- We recommend that a single individual, often the project leader or PI, or their direct designate, be responsible for all modifications to this file.

- We recommend these two steps to prevent "cladogenesis" of your project's database. It is a nightmare to track and integrate changes made to "phylogenetically" differentiated database files in the hands of multiple individuals entering data simultaneously or at different times/places.

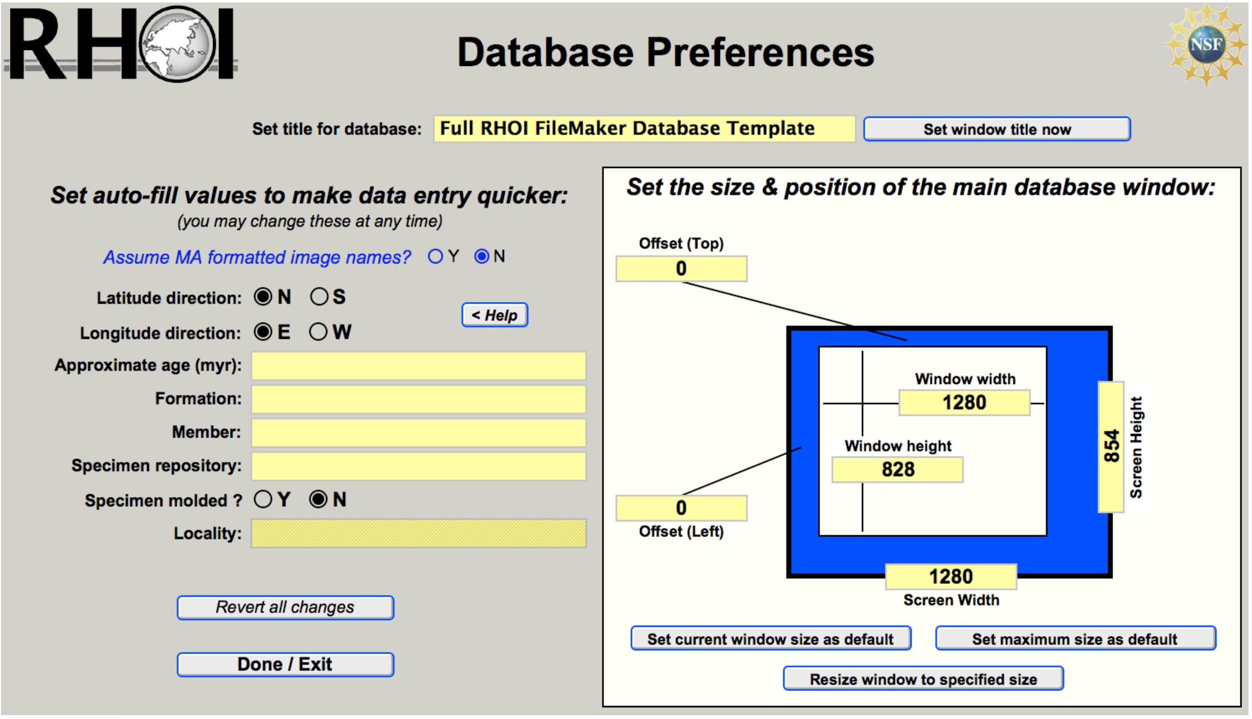
  This operational problem is addressed by several features of the RHOI Database Template. For example, by using the "Print Reports" feature, you can generate hard copy printouts for your project's various faunal analysts. They can make their identifications on these printouts, and then the person responsible for the museum/project's MASTER can make the entries digitally. If each analyst reports his/her taxonomic identifications via these printouts, entry is facilitated, the MASTER digital database catalog always remains the most current version, and a new printout can be made for the analyst as soon as their new handwritten data on the printouts have been digitally entered into your MASTER. Other approaches are possible, but difficult to implement operationally, and more prone to "cladogenesis."

  The most important aspect of a project's paleontological database management is the maintenance of a single MASTER database administered by a single individual.

b. Customizing Your Database

Open your new, empty MASTER file.

Click the Edit Preferences button on the lower right hand corner of ANY Layout. This action gives you a layout that allows you to custom-set the characteristics of your database, including the way it will appear on your computer's desktop.



Database Preferences

Set title for database: Full RHOI FileMaker Database Template

Set auto-fill values to make data entry quicker:
(you may change these at any time)

Assume MA formatted image names? ○ Y ● N

Latitude direction: ● N ○ S

Longitude direction: ● E ○ W

Approximate age (myr):

Formation:

Member:

Specimen repository:

Specimen molded ? ○ Y ● N

Locality:

Set the size & position of the main database window:

Offset (Top): 0

Window width: 1280

Window height: 828

Screen Height: 854

Offset (Left): 0

Screen Width: 1280

Setting default values here will make entering new data quicker. You may always re-set these preferences at a later time.

When you are satisfied with your preferences, click the **Done / Exit** button on this layout.

c. Administering Your Database: Safety Precautions

You should make every effort to secure the integrity of the data in your database. One of the best ways to do this is to designate ONE person as the "official keeper" of the MASTER database. Consider this person, probably you, the official Project Recorder. Having only ONE person physically entering all data directly into your MASTER database and storing this MASTER on only ONE computer, with a designated back-up hard-drive, will ensure that your data are neither lost nor corrupted.

Remember, your database is the ultimate digital record of the physical specimens in your project/museum collection. As such, it is imperative that you safeguard the integrity of these data as much as possible.

Keeping complete control of your database can seem challenging at times. This is especially so if you sometimes find it useful to share your database, in its entirety, with others. You may, for example, want feedback on some aspect of your data, or need a colleague's expertise in identifying specimens. You may want other users to be able to view your database as you do, so the data are easy to discuss. You may prefer this to printing out hard-copy pages for your selected users. In such circumstances, giving others a read-only version of your database, in the form of a PDF, will allow them to view your data without frustration, because there is no way for them to "mess it up."

Take make a PDF, first select the layout you wish to display your data in. You may find the pre-set layouts (forms) in the "**Print Reports**" area (see Section **A.9.** above) useful for this purpose. Then, find the set of specimens you would like to share as a PDF. Do this by performing a find (e.g., by locality or taxon). You probably will want to sort this "found set" by specimen number or some other field(s). See FileMaker "Help" for more on how to "find" and "sort."

Once you have your layout chosen, and your set found and sorted, navigate to **File>Save/Send Records As** and choose **PDF…** Under **Save as:** name your file and direct it to where on your computer you would like to save it. Choose "Records being browsed" under **Save:** and click the **Save** button. You can now attach this PDF to an email to a colleague.

To help you keep your MASTER database as secure as possible, the Empty Database you downloaded has a key security feature built-in; **logins**.

There are 2 **login** settings, **Administrator**, and **Regular User**. Each has unique access privileges, because each will be used differently.

The **Administrator** login enables you to DO ANYTHING to the database, such as add or delete fields, add or delete specimen records, import new images, define the various fields, and add or delete whole tables. When you are logged in as **Administrator**, you have complete control over ALL aspects of your database.

The Administrator login is special, so it is password protected. The pre-loaded password is "**danger**". The reason for this password is that when you are operating the database in this mode, your actions can have hidden consequences. We therefore recommend this mode only be used by experienced database managers.

The other login setting is the **Regular User** login. This is like the Administrator, but has fewer access privileges. When you access your database as Regular User, you can change or enter any and all data in your database, but you cannot move fields around on layouts, define fields, or add and delete tables. The Regular User login is handy because you can work on your database without fear of accidentally "messing it up."

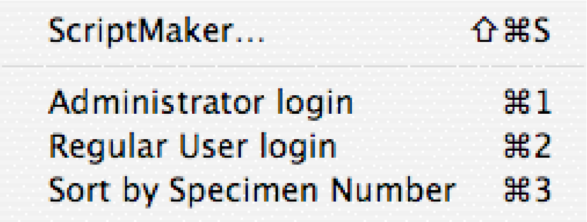
There is NO PASSWORD needed for the Regular User login.

To apply either the Administrator or Regular User login, do the following.

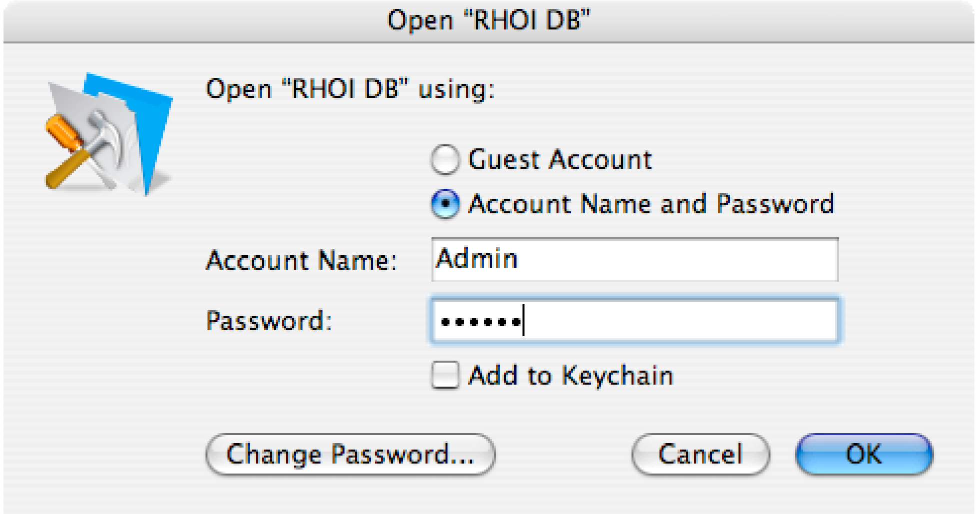
Administrator

1) In the FileMaker Toolbar, at the top of the screen, click on Scripts.

2) Select the **Administrator login** from the choices.



The following screen appears:



Open "RHOI DB" using:

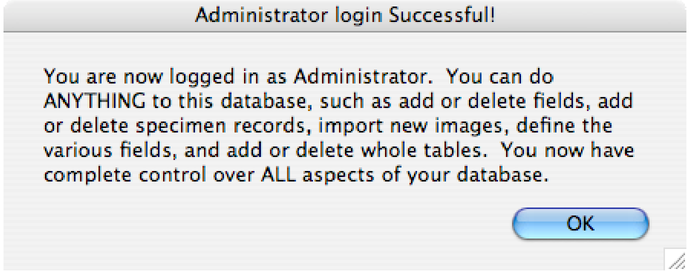
○ Guest Account
● Account Name and Password

Account Name: Admin
Password: ••••••
☐ Add to Keychain

3) "Admin" will be already entered in the Account Name field. Type your password in the Password field. The initial password is “danger”, but change this as soon as possible.

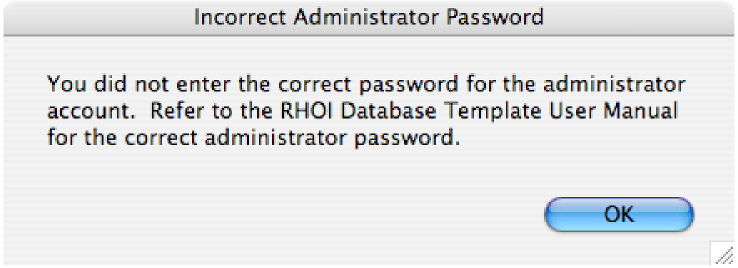
4) Click **OK**.

5) The following screen will appear to confirm you as **Administrator**:



You are now logged in as Administrator. You can do ANYTHING to this database, such as add or delete fields, add or delete specimen records, import new images, define the various fields, and add or delete whole tables. You now have complete control over ALL aspects of your database.

If you type in an INCORRECT password, you will see the following dialogue box:



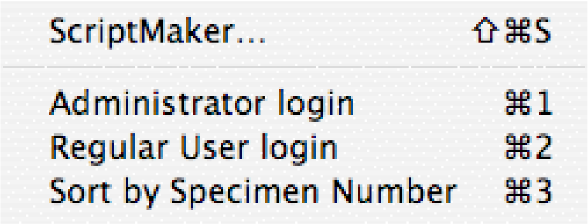
You did not enter the correct password for the administrator account. Refer to the RHOI Database Template User Manual for the correct administrator password.

Click **OK** and type in the correct password.

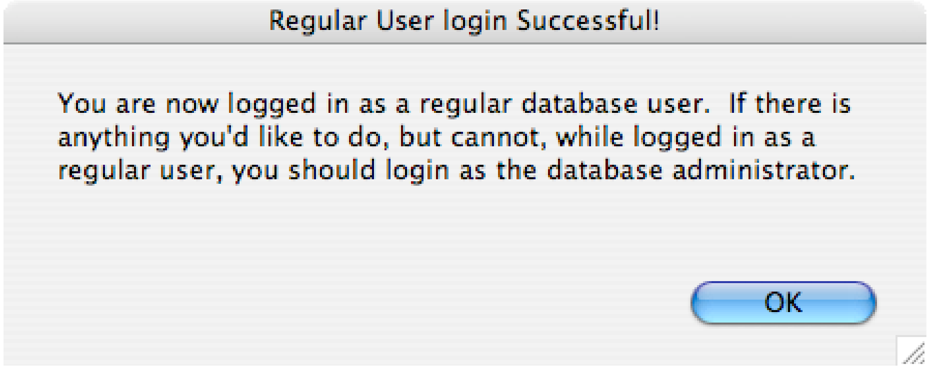
Regular User

1) In the FileMaker Toolbar, at the top of the screen, click on Scripts.

2) Select the **Regular User login** from the choices.



You will be logged in automatically and the following screen will appear:



You are now logged in as a regular database user. If there is anything you'd like to do, but cannot, while logged in as a regular user, you should login as the database administrator.

C. IMPORTING DATA INTO YOUR CUSTOMIZED DATABASE

You may ignore this section if you are going to be entering all of your data by hand, on a specimen-by-specimen basis. Simply follow the instructions in the preceding section if this is the case.

The RHOI Database Template is designed to allow you to accurately download your data from previously existing spreadsheets and databases. Just follow these steps:

1. PREPARE YOUR FILES

Before you begin your data transfer you should:

a. Make a backup copy of the electronic catalog (spreadsheet or database) you are currently using.

b. Rename this "back-up" file. Choose a name that you can easily identify as the *pre-import version* of your catalog(s) (e.g., "My_Old_Catalog(s))."

c. Archive this back-up in a secure place.

d. If you have not downloaded the RHOI Database Template Empty Copy yet, please visit the RHOI website at **http://rhoi.berkeley.edu/RHOI_Database_Template/downloads.php** and do so.

e. Rename the downloaded "**RHOI_DB_Empty**" FileMaker file. Choose a name like "*yourproject'sname*_MASTER", where "*yourproject'sname*" is the name of your specific project or museum collection.

f. Open your newly re-labeled FileMaker database. On the **Specimen Entry** layout, click the **Edit Preferences** button found on the bottom of the screen (see section **A.8.** for more). Re-label the header of your new database as "**xxx_MASTER"** (assign your own appropriate name).

g. Download the Excel file **Import Staging.xls** from the RHOI website. THIS FILE **MUST** BE PLACED in THE SAME FOLDER as your "MASTER" file.

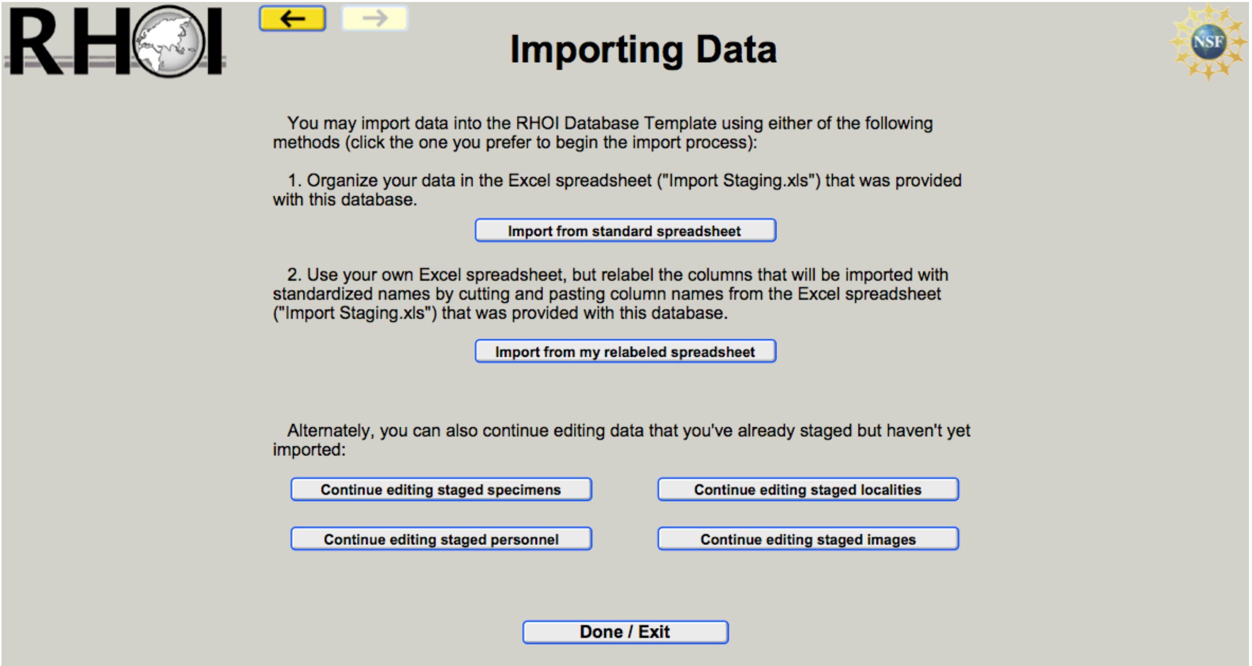
2. OPEN YOUR NEW MASTER DATABASE

Using the instructions in the previous section, you can now customize your version of the database so that it fits optimally on your computer screen and so that any auto-fill features are set. You may return to this page to readjust any of these values at a later time.

a. Importing Data

Click on the **Import Data** button, located in the bottom right hand corner of the **Specimen Entry** page of your MASTER database.

This opens the following **Importing Data** window, from which you will be doing all of your importing.



Importing Data

You may import data into the RHOI Database Template using either of the following methods (click the one you prefer to begin the import process):

1. Organize your data in the Excel spreadsheet ("Import Staging.xls") that was provided with this database.

2. Use your own Excel spreadsheet, but relabel the columns that will be imported with standardized names by cutting and pasting column names from the Excel spreadsheet ("Import Staging.xls") that was provided with this database.

Alternately, you can also continue editing data that you've already staged but haven't yet imported:

This window is designed to allow you to import your data accurately and efficiently. You have two options for data entry in this window:

- **OPTION 1:** Importing data via the standard RHOI-provided **Import Staging.xls** spreadsheet, which contains pre-entered column names.

If you choose to import data from the standard spreadsheet provided by the RHOI, click the **Import from standard spreadsheet** button (the top one). Make sure that the **Import Staging.xls** file is located in the SAME FOLDER as the RHOI Database Template MASTER file (which you have already re-named according to your own needs) on your hard drive. **NEVER** change the file name of the "**Import Staging.xls"** spreadsheet. The RHOI Database Template will NOT recognize the standard spreadsheet if its name has been changed.

IMPORTANT NOTE: *If the **Import Staging.xls** and your new RHOI Database Template MASTER are not together in the same folder, your data will NOT import.*

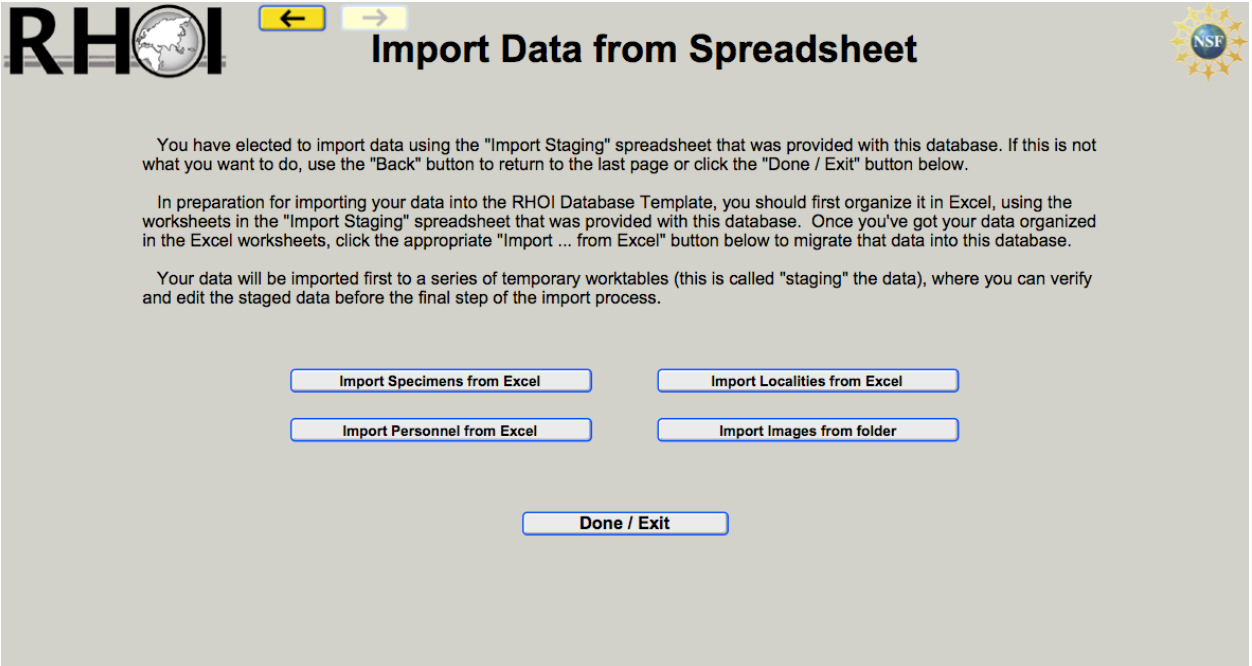
- **OPTION 2:** Importing data directly from your own project's/museum's Excel spreadsheet. To do this, you must first re-label the column headings in **your** project's Excel file to match the ones in the **Import Staging.xls** spreadsheet. Do this re-labeling of **your** project's Excel file by cutting and pasting the pre-provided column names from the RHOI-provided **Import Staging.xls** spreadsheet.

If you choose to work directly from your own Excel spreadsheet, you will have to label the columns yourself to insure that your data are transferred to the correct fields in your MASTER. After you have done this, click on the **Import from my relabeled spreadsheet** button (see Section **c** below).

The **Importing Data** window also allows you to continue editing data in the staging area in the event that you have saved data there for later editing.

b. OPTION 1: Importing Data from the Standard Spreadsheet

Upon clicking the **Import from standard spreadsheet** button, the following window appears:



You have elected to import data using the "Import Staging" spreadsheet that was provided with this database. If this is not what you want to do, use the "Back" button to return to the last page or click the "Done / Exit" button below.

In preparation for importing your data into the RHOI Database Template, you should first organize it in Excel, using the worksheets in the "Import Staging" spreadsheet that was provided with this database. Once you've got your data organized in the Excel worksheets, click the appropriate "Import ... from Excel" button below to migrate that data into this database.

Your data will be imported first to a series of temporary worktables (this is called "staging" the data), where you can verify and edit the staged data before the final step of the import process.

This window provides you with an explanation of the process, and allows you to import four different sets of data: **specimen-related**, **locality-related**, **personnel-related**, and **images**.

The four buttons on this page let you handle each set of data individually. Some projects and museums will have only specimen-related data to import. If you have **ONLY** specimen-related data, but no digital images, you can ignore the Import Images from folder button.

If you **DO** have locality- and/or personnel-related data, import those **FIRST**, so that they link properly to the specimen-related data you will enter next. The procedure for importing Locality and/or Personnel-related data is the same as that for specimen-related data (see below).

Before you can import any data, you must first fill your empty **Import Staging.xls** spreadsheet with the data from your original catalog spreadsheet. In this process, make sure that each data type goes into the correct columns, correctly matching across all rows. YOU **MUST** LEAVE ALL COLUMN POSITIONS AND THEIR TITLES UN-ALTERED DURING THIS OPERATION. This is because the import from your project's Excel catalog to your new FileMaker database depends upon column name AND column position.

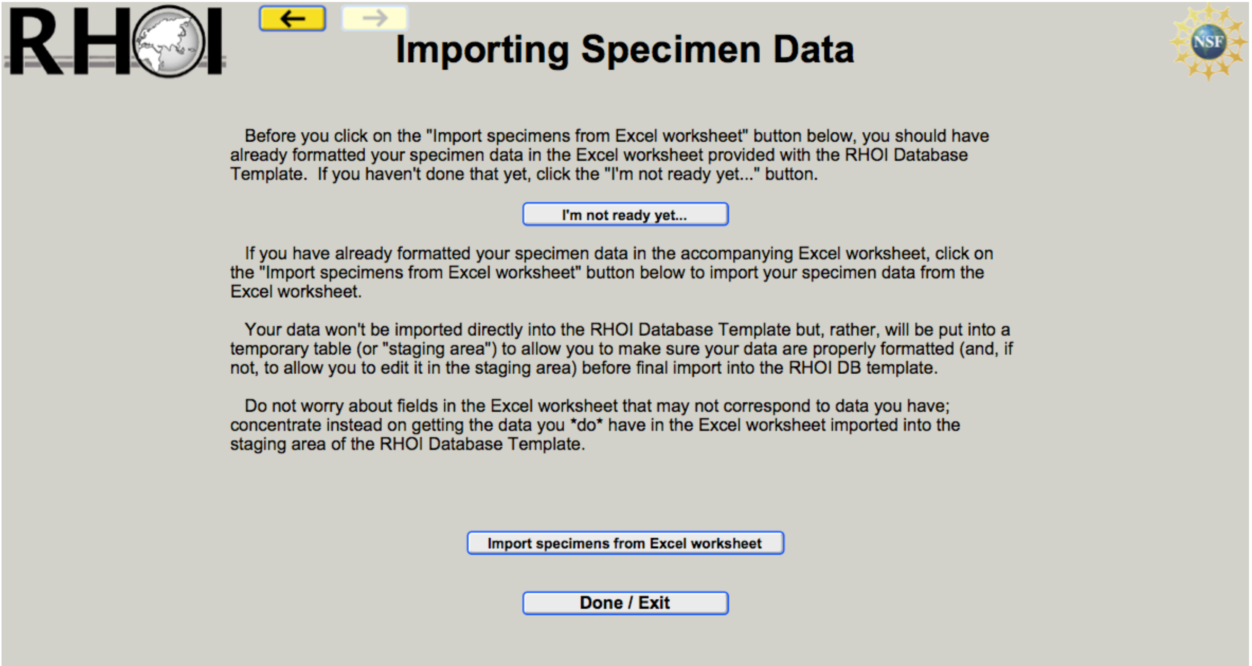
BE VERY CAREFUL in your cutting and pasting, to make sure that all specimen numbers align horizontally with their stratigraphic and taxonomic information.

After you are satisfied, be sure to "**Save**" the **Import Staging.xls** spreadsheet.

Rather than cutting and pasting your data into the **Import Staging.xls** spreadsheet, you may find it easier to re-label the columns of your project's original catalog Excel spreadsheet with the labels from the **Import Staging.xls** spreadsheet. If so, proceed to Section **C.2.c.** below.

When you are ready to import your main specimen-related data, click the Import Specimens from Excel button. This will automatically import your specimen data into the **Staging Area** (see section **C.2.c.** below).

When you click the Import Specimens from Excel button, the following window appears:



Importing Specimen Data

Before you click on the "Import specimens from Excel worksheet" button below, you should have already formatted your specimen data in the Excel worksheet provided with the RHOI Database Template. If you haven't done that yet, click the "I'm not ready yet..." button.

If you have already formatted your specimen data in the accompanying Excel worksheet, click on the "Import specimens from Excel worksheet" button below to import your specimen data from the Excel worksheet.

Your data won't be imported directly into the RHOI Database Template but, rather, will be put into a temporary table (or "staging area") to allow you to make sure your data are properly formatted (and, if not, to allow you to edit it in the staging area) before final import into the RHOI DB template.

Do not worry about fields in the Excel worksheet that may not correspond to data you have; concentrate instead on getting the data you *do* have in the Excel worksheet imported into the staging area of the RHOI Database Template.

Once you click the **Import specimens from Excel worksheet** button, FileMaker will automatically read your **Import Staging.xls** file and begin the data import. You will get a window that looks like this:

Import

Importing from:
"[Import Staging.xls] Specimens".

Records Remaining: 1251

This process may take several minutes, but you will be able to monitor the progress via the loading bar..

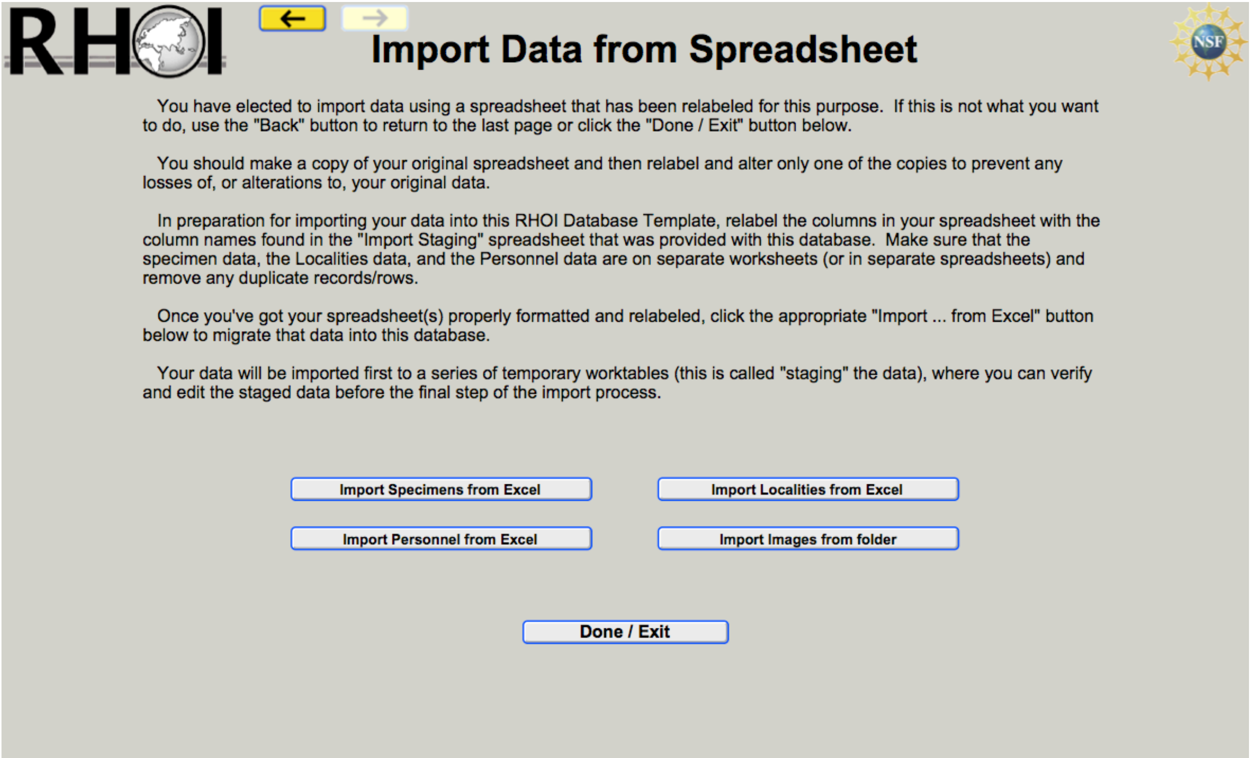
Once done, your data will be "staged" in the database and the following window will appear:

If you do not see any data in this window (as in the image above), your data import was not successful. Please make sure you have all of your data in a file labeled **Import Staging.xls**. Be sure that this file has properly labeled columns. Be sure that it is stored in the same folder on your hard drive as your new database (e.g., "xxx_MASTER"). Once you are satisfied that all these conditions are met, repeat the instructions in section **C.2.b.**, above.

If you are not importing data from your own re-labeled spreadsheet, skip forward to section **C.2.d.** for further instructions on how to edit your data in the staging area.

c. OPTION 2: Importing Data from your own spreadsheet

If you choose to import your data from your own re-labeled spreadsheet, click on the Import from my relabeled spreadsheet button in the **Importing Data** window (see above). The following window will appear:



Import Data from Spreadsheet

You have elected to import data using a spreadsheet that has been relabeled for this purpose. If this is not what you want to do, use the "Back" button to return to the last page or click the "Done / Exit" button below.

You should make a copy of your original spreadsheet and then relabel and alter only one of the copies to prevent any losses of, or alterations to, your original data.

In preparation for importing your data into this RHOI Database Template, relabel the columns in your spreadsheet with the column names found in the "Import Staging" spreadsheet that was provided with this database. Make sure that the specimen data, the Localities data, and the Personnel data are on separate worksheets (or in separate spreadsheets) and remove any duplicate records/rows.

Once you've got your spreadsheet(s) properly formatted and relabeled, click the appropriate "Import ... from Excel" button below to migrate that data into this database.

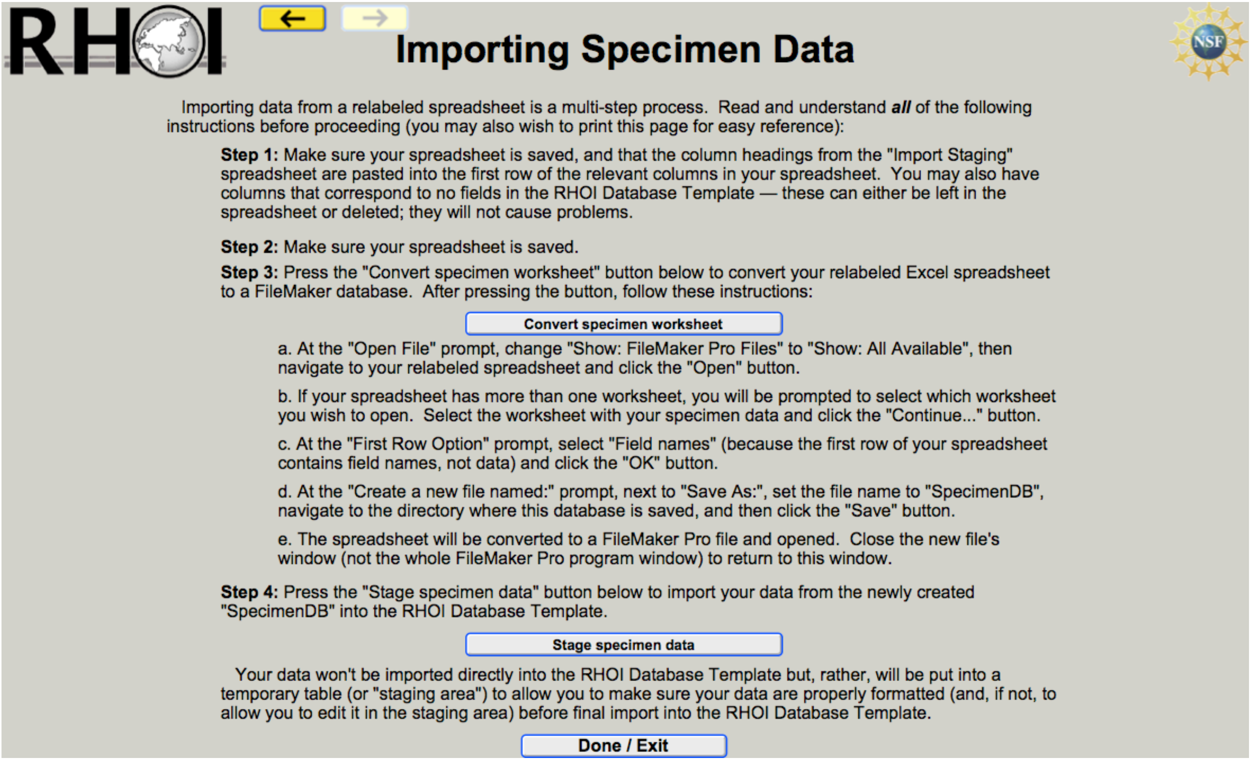
Your data will be imported first to a series of temporary worktables (this is called "staging" the data), where you can verify and edit the staged data before the final step of the import process.

Please carefully read ALL the instructions on this window to check that you've set up your spreadsheet correctly. The column names for your data must be the same as those from the **Import Staging.xls** spreadsheet provided with this database template (see the website).

Make sure that Specimen, Locality, and Personnel are on separate worksheets (or spreadsheets), and remove any duplicate records or rows.

When you are ready to import data, **FIRST** import your **localities**- and/or **personnel**-related data, if you have them. The procedure for importing locality and/or personnel-related data is the same as that for specimen-related data.

Next, move on to the **specimen**-related data. Click the **Import Specimens from Excel** button. The following window will appear:



Importing Specimen Data

Importing data from a relabeled spreadsheet is a multi-step process. Read and understand ***all*** of the following instructions before proceeding (you may also wish to print this page for easy reference):

Step 1: Make sure your spreadsheet is saved, and that the column headings from the "Import Staging" spreadsheet are pasted into the first row of the relevant columns in your spreadsheet. You may also have columns that correspond to no fields in the RHOI Database Template — these can either be left in the spreadsheet or deleted; they will not cause problems.

Step 2: Make sure your spreadsheet is saved.

Step 3: Press the "Convert specimen worksheet" button below to convert your relabeled Excel spreadsheet to a FileMaker database. After pressing the button, follow these instructions:

a. At the "Open File" prompt, change "Show: FileMaker Pro Files" to "Show: All Available", then navigate to your relabeled spreadsheet and click the "Open" button.

b. If your spreadsheet has more than one worksheet, you will be prompted to select which worksheet you wish to open. Select the worksheet with your specimen data and click the "Continue..." button.

c. At the "First Row Option" prompt, select "Field names" (because the first row of your spreadsheet contains field names, not data) and click the "OK" button.

d. At the "Create a new file named:" prompt, next to "Save As:", set the file name to "SpecimenDB", navigate to the directory where this database is saved, and then click the "Save" button.

e. The spreadsheet will be converted to a FileMaker Pro file and opened. Close the new file's window (not the whole FileMaker Pro program window) to return to this window.

Step 4: Press the "Stage specimen data" button below to import your data from the newly created "SpecimenDB" into the RHOI Database Template.

Your data won't be imported directly into the RHOI Database Template but, rather, will be put into a temporary table (or "staging area") to allow you to make sure your data are properly formatted (and, if not, to allow you to edit it in the staging area) before final import into the RHOI Database Template.

It is a two-step process to import your data into the staging area if you are using your own re-labeled spreadsheet. In this option, your Excel spreadsheet needs to be converted to a FileMaker Pro file, and then imported to the staging area in your MASTER. It is essential that you follow the instructions in this window very carefully. You will first click the **Convert specimen worksheet** button and follow the instructions (Step 3, a-e) exactly as given. These are:

a. At the "Open File" prompt, change "Show: FileMaker Pro Files" to "Show: All Available," then navigate to your relabeled spreadsheet and click the "Open" button.

b. If your spreadsheet has more than one worksheet, you will be prompted to select which worksheet you wish to open. Select the worksheet with your specimen data and click the "Continue..." button.

c. At the "First Row Option" prompt, select "Field names" (because the first row of your spreadsheet contains field names, not data) and click the "OK" button.

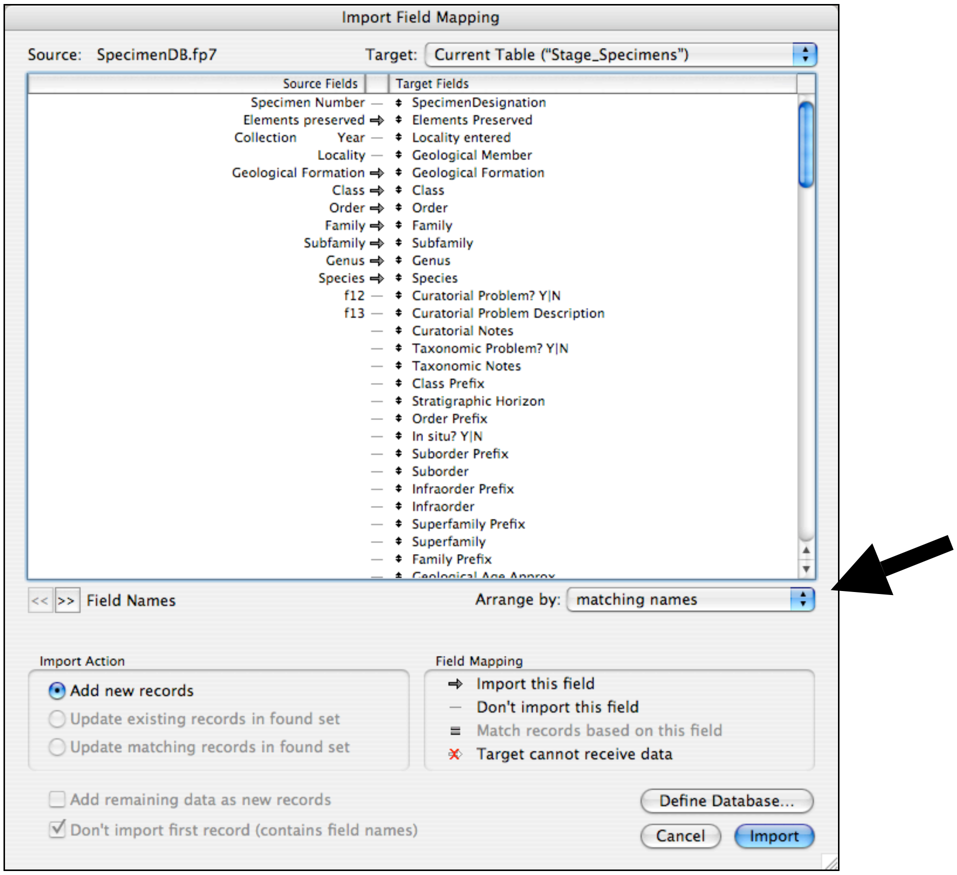
d. At the "Create a new file named:" prompt, next to "Save As:", set the file name to "Specimen DB", navigate to the directory where this database is saved, and click the "Save" button.

e. The spreadsheet will be converted to a FileMaker Pro file and opened. Close the new file's window (not the whole FileMaker Pro program window) and return to this window.

Following these instructions exactly is important. For example, if you get a dialog box saying that the FileMaker file is damaged, *be sure* that you have followed instruction "a" about clicking on the "**Show: All Available**" box.

Be sure that you follow the directions in step "d," in which you *must* navigate (using the "Where" pull-down menu in the dialog box) to the folder in which your MASTER database resides.

When you are finished with Step 3, proceed to Step 4 and click the **Stage specimen data** button. The "Import Field Mapping" window will appear:



Import Field Mapping

Source: SpecimenDB.fp7

Target: Current Table ("Stage_Specimens")

Source Fields		Target Fields
Specimen Number	—	SpecimenDesignation
Elements preserved	➡	Elements Preserved
Collection Year	—	Locality entered
Locality	—	Geological Member
Geological Formation	➡	Geological Formation
Class	➡	Class
Order	➡	Order
Family	➡	Family
Subfamily	➡	Subfamily
Genus	➡	Genus
Species	➡	Species
f12	—	Curatorial Problem? Y|N
f13	—	Curatorial Problem Description
	—	Curatorial Notes
	—	Taxonomic Problem? Y|N
	—	Taxonomic Notes
	—	Class Prefix
	—	Stratigraphic Horizon
	—	Order Prefix
	—	In situ? Y|N
	—	Suborder Prefix
	—	Suborder
	—	Infraorder Prefix
	—	Infraorder
	—	Superfamily Prefix
	—	Superfamily
	—	Family Prefix
	—	Geological Age Approx

Arrange by: matching names

Import Action
- ● Add new records
- ○ Update existing records in found set
- ○ Update matching records in found set

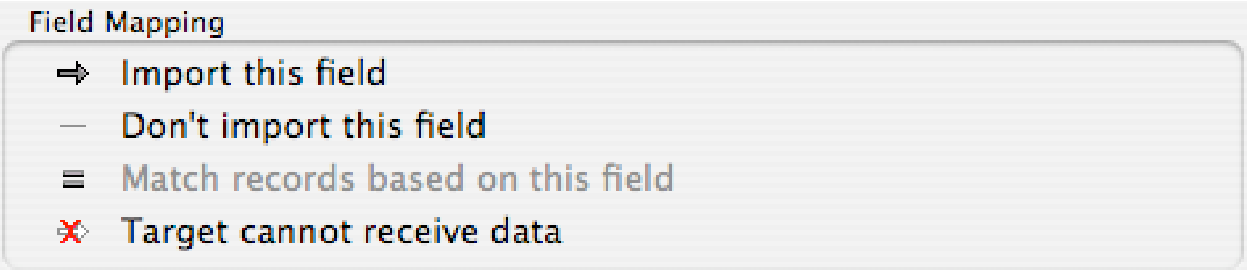
☐ Add remaining data as new records
☑ Don't import first record (contains field names)

In the **Arrange by:** pull-down menu (see arrow), Arrange by: matching names two-thirds of the way down this page, on the right, click the "matching names" option. This will align most of the fields from your old Excel catalog (the "**Source Fields**") with the fields in your new FileMaker database (the "**Target Fields**").

You may have to vertically align your old **Source Fields** and new **Target Fields** manually by dragging the double-arrow ⬍, to the left of the specific **Target Field**, with your cursor. Matching source and target fields allows the RHOI Database Template to place your data into the correct fields.

For example, in the window above, the Specimen Number (**Source Field**) is vertically aligned correctly with the Specimen Designation (**Target Field**), even though the names do not exactly match. To make sure that your data are transfered into the correct field, not only do the relevant fields need to align vertically, they need to be linked with an arrow ⇨.

Once the fields are correctly aligned, you will need to change the dash separating them into an arrow by clicking on it. The key to the "Field Mapping" symbols, in the bottom right of the Field Mapping Window, looks like this:



Field Mapping

⇨ Import this field

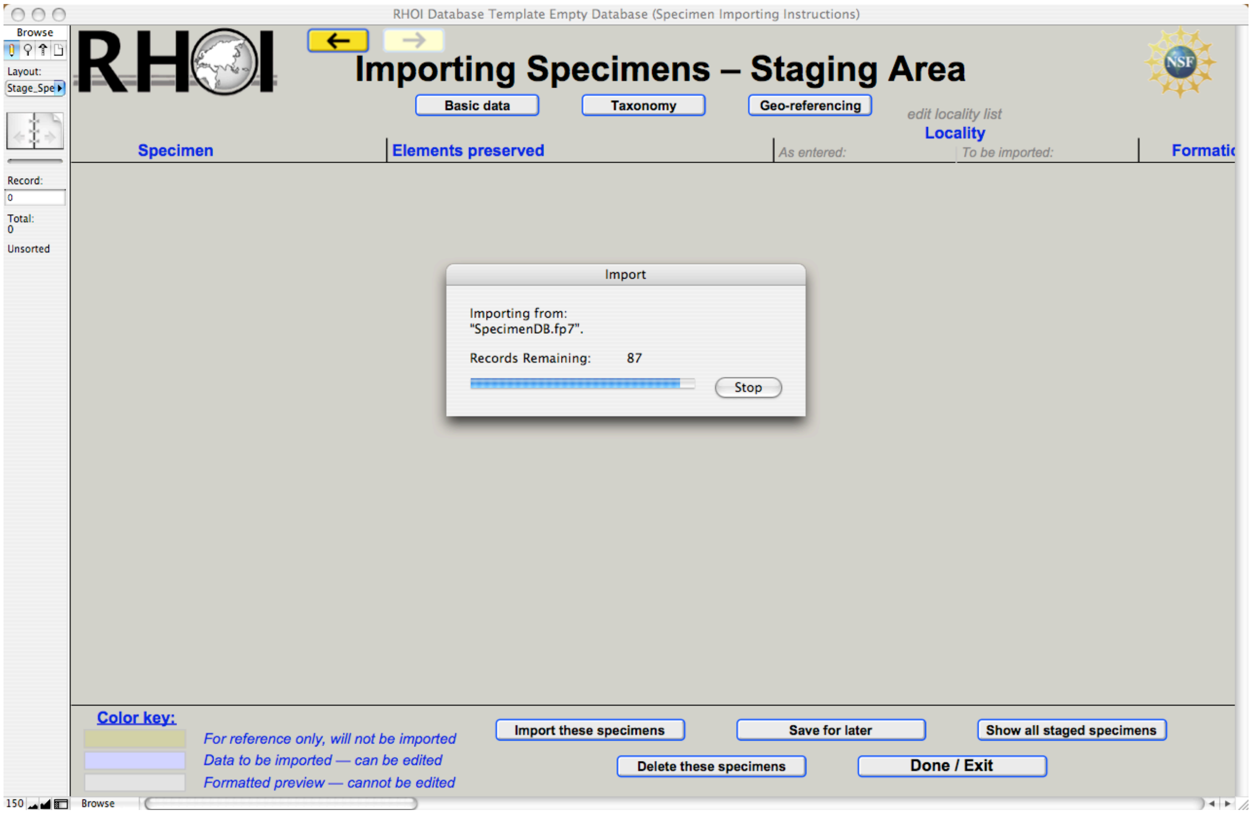
— Don't import this field

≡ Match records based on this field

✗ Target cannot receive data

Once all of your **Source Fields** are aligned correctly with their corresponding **Target Fields**, and they are all accompanied by directional linking arrows, click on the **Import** button.

In the next small "Import Options" dialogue window that appears, check the box to the left of the text "Perform auto-enter options while importing." Click **Import**. Your data will now import into the staging area and the following window will appear:

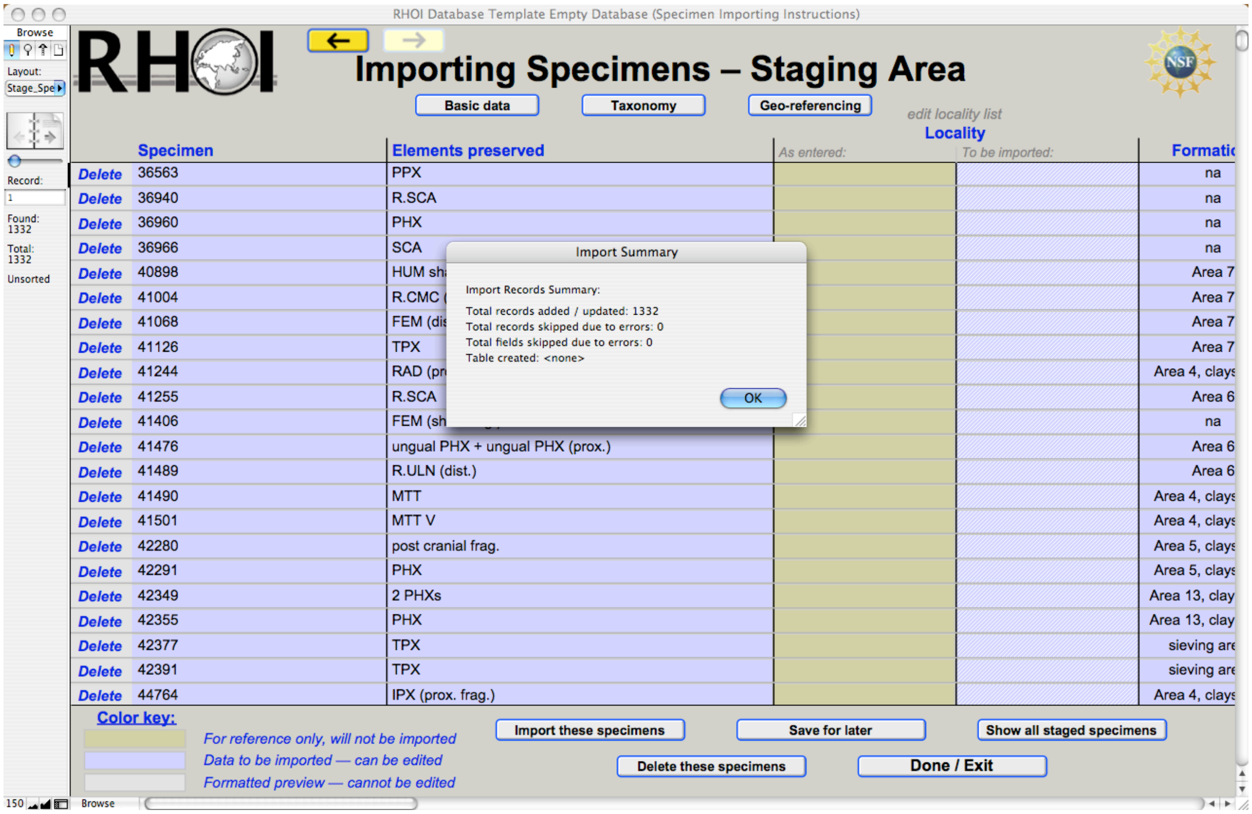


Importing from:
"SpecimenDB.fp7".

Records Remaining: 87

While your data are importing, you will see a small "Import" window overtop your main staging area window. This may take a few minutes.

When your data are finished importing, you will see the following "Import Summary" window:



	Specimen	Elements preserved	Formatio
Delete	36563	PPX	na
Delete	36940	R.SCA	na
Delete	36960	PHX	na
Delete	36966	SCA	na
Delete	40898	HUM sh	Area 7
Delete	41004	R.CMC (	Area 7
Delete	41068	FEM (dis	Area 7
Delete	41126	TPX	Area 7
Delete	41244	RAD (pr	Area 4, clays
Delete	41255	R.SCA	Area 6
Delete	41406	FEM (sh	na
Delete	41476	ungual PHX + ungual PHX (prox.)	Area 6
Delete	41489	R.ULN (dist.)	Area 6
Delete	41490	MTT	Area 4, clays
Delete	41501	MTT V	Area 4, clays
Delete	42280	post cranial frag.	Area 5, clays
Delete	42291	PHX	Area 5, clays
Delete	42349	2 PHXs	Area 13, clay
Delete	42355	PHX	Area 13, clay
Delete	42377	TPX	sieving are
Delete	42391	TPX	sieving are
Delete	44764	IPX (prox. frag.)	Area 4, clays

Import Summary

Import Records Summary:

Total records added / updated: 1332
Total records skipped due to errors: 0
Total fields skipped due to errors: 0
Table created: <none>

OK

The "Import Summary" window gives you a brief summary of how the data import went. If you see that any records or fields were "skipped due to errors", you will have to go back and re-import your data.

Click **OK**.

The following window appears:

Check that this staging area window displays your data. If it does not (as in the image above) you will need to re-do your data preparation and make sure your spreadsheet is in the same folder as your new FileMaker database.

Also check that your data are displayed in the correct columns. If they are not, you did not match your **Source** and **Target** fields correctly in the "Import Field Mapping" window.

d. Import Staging

When you imported your data into the RHOI Database Template using the steps above, you did not import directly into the database. Instead, you first imported your data into the **Staging Area** (see picture above). This allows you to check the quality of your data and to make any changes necessary before the final import step.

Use the **Basic data**, **Taxonomy**, and **Geo-referencing** buttons, near the top of the window, to check over your data before making final imports.

IMPORTANT NOTE: *Some PC users may occasionally experience difficulty staging their collection day, month, and/or year fields. Please be sure to double-check these are filled in properly in the Collection Date columns in the Staging Area. Use two-digit day and month numbers and two- or four-digit year numbers. Check that the "To be imported:" column displays your collection date information correctly.*

You will be able to delete specimens in the staging area by clicking on the **Delete these specimens** button, or to import them into the database by clicking on the **Import these specimens** buttons. You will also be able to save the specimens in the staging area for later editing by clicking on the **Save for later** button.

IMPORTANT NOTE: *If you do not have any locality- or personnel-related data to import, the **To be imported** columns for locality- and any personnel-related columns (e.g., Collector or Discoverer) will be blank, even if the **As entered** columns are filled in.*

If no data are in the **To be imported** columns, nothing will be imported. To enable your new MASTER database to recognize the locality or personnel names in the **As entered** column, the names must be in their respective lists (i.e., **Locality List**, **Personnel List**).

There are two options to do this:

1. You may import Locality and Personnel data by using the procedures described in sections **C.2.b.** and **C.2.c.** (i.e., from Excel spreadsheets).

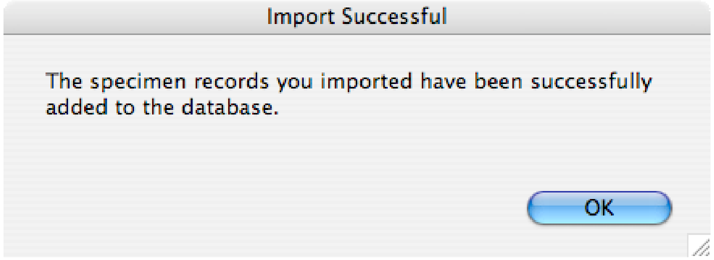
2. You may add names into these lists manually by clicking on the gray **edit locality list** or **edit personnel list** text in the staging area. This will take you to the **Locality List** or **Personnel List** where you can add names as needed. The **Personnel List** can also be accessed by clicking on the **Edit Personnel List** button at the bottom of the screen (you must exit the staging area), see Section **A.7.** Use this method if you do not already have locality or personnel-related data entered somewhere else.

Once your Locality and Personnel names are in their respective lists, FileMaker will be able to recognize and link your Locality and Personnel names to your specimen data and the **To be imported** column will be filled in automatically.

IMPORTANT NOTE: *If you do not import your Locality and Personnel names into their respective lists BEFORE you import your Specimen data into the database, the program will NOT link your Specimen data with Locality and Personnel names, and these fields will therefore appear as blank. At this point, your only option will be to start over, or to manually enter the Locality or Personnel names via the pull-down menu for each specimen. Therefore, make sure that your "To be imported" column matches your "As entered" column in the staging area before you click on the "Import" button.*

When you are satisfied with how your data are displayed in the staging area, click on the **Import these specimens** button to import your data into the RHOI Database Template. This may take several minutes to complete, depending on how much data you have. While your data are importing, you will see an **Import Progress** screen that counts down how many records you have left to import. This will give you a good indication of your wait time.

Once the import is finished, you should see the following dialogue box, indicating that your import was a success:



Import Successful

The specimen records you imported have been successfully added to the database.

If you do NOT see this dialogue, something went wrong. Go back through the steps listed in this section to correct the error.

D. IMPORTING IMAGES

You have two options for importing your specimen images: 1) from your pre-labeled **Images** folder or 2) one-by-one, using your **Specimen Entry** or **Specimen Overview** layout as your gateway. Whichever method you choose, the RHOI Database Template makes image importing easy.

IMPORTANT NOTE: IMAGES FOLDER

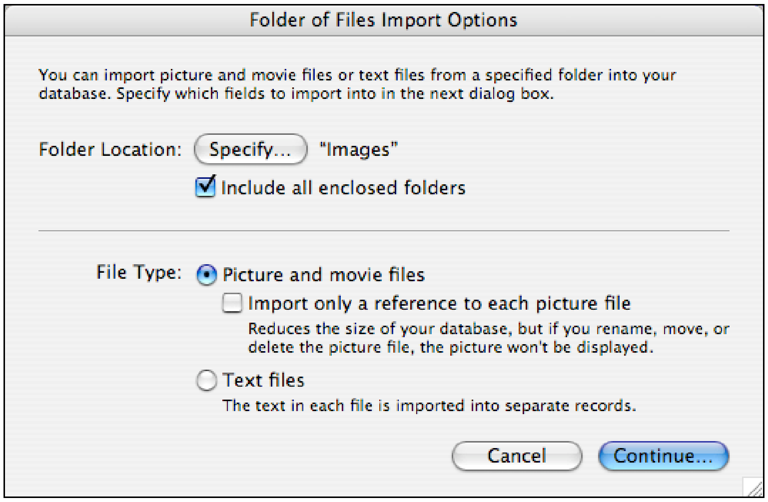
*If you have not already done so, take the time now to put all of your images into a single folder labeled **Images**. Your images may already be sub-divided into folders by taxon, locality, year, etc. If you prefer to leave your images the way you have them, that is fine. Just make sure you have a single folder labeled **Images** into which all your sub-folders can go. Then, make sure that your **Images** folder is nested within the same overall folder as your database.*

IMPORTANT NOTE: IMAGE NAMES

Your new RHOI Database Template can accept images with any kind of names. Your project/museum may have its own established protocols for naming specimen images (e.g., according to the specimen number, the locality, the photographer, etc.). These are all fine. Even if your image files have no formal names, but are instead labeled arbitrarily, based on your camera's settings (e.g., "DSC 20058"...), this is fine too. The associations between image and specimen can be made manually. Just follow the image importing instructions below and you will be able to merge your specimen images with your new database.

1. IMPORTING A FOLDER OF SPECIMEN IMAGES

To import specimen images from your pre-labeled **Images** folder, click on the Import Images button at the bottom of the screen. You are taken to the following dialog box:



You can import picture and movie files or text files from a specified folder into your database. Specify which fields to import into in the next dialog box.

Folder Location: "Images"
☑ Include all enclosed folders

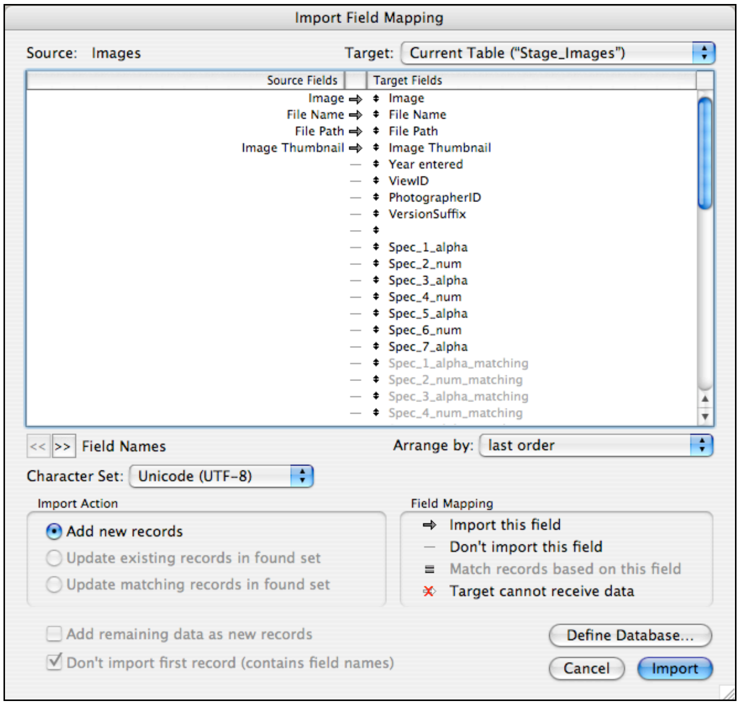
File Type:
● Picture and movie files
  ☐ Import only a reference to each picture file
  Reduces the size of your database, but if you rename, move, or delete the picture file, the picture won't be displayed.
○ Text files
  The text in each file is imported into separate records.

You are asked to "Specify" the folder containing the images you wish to import (i.e., your **Images** folder). If your **Images** folder contains several sub-folders (see the "IMPORTANT NOTE" above), be sure to check the box to the left of "Include all enclosed folders".

You also have the option to import the entire image into your database or to import only a "reference" of your image. Choosing the "Import only a reference to each picture file" option will mean that they are only "linked" to your database and not physically embedded within it. This keeps the size of your database small, but with a consequence--if you choose to move your images or re-label them in the future, your images will not appear in your database. This is because your FileMaker database will look for the original file path and image name you used in creating its "link" to your remote image. If you move the file or re-label it, you will break that "link."

If you are concerned with the overall file size of your database, you may want to import only links to your images, or import only size-reduced images (particularly if your individual images are large). For most purposes however, embedding your images directly in your database will cause you fewer problems and potentially save you from having to repeat image imports.

After you specify the folder, the **Import Field Mapping** dialog will pop up (see below). Line up your Source and Target fields and click **Import**.


Import Field Mapping

Source: Images   Target: Current Table ("Stage_Images")

Source Fields		Target Fields
Image	⇒	Image
File Name	⇒	File Name
File Path	⇒	File Path
Image Thumbnail	⇒	Image Thumbnail
	—	Year entered
	—	ViewID
	—	PhotographerID
	—	VersionSuffix
	—	
	—	Spec_1_alpha
	—	Spec_2_num
	—	Spec_3_alpha
	—	Spec_4_num
	—	Spec_5_alpha
	—	Spec_6_num
	—	Spec_7_alpha
	—	Spec_1_alpha_matching
	—	Spec_2_num_matching
	—	Spec_3_alpha_matching
	—	Spec_4_num_matching

<< >> Field Names   Arrange by: last order

Character Set: Unicode (UTF-8)

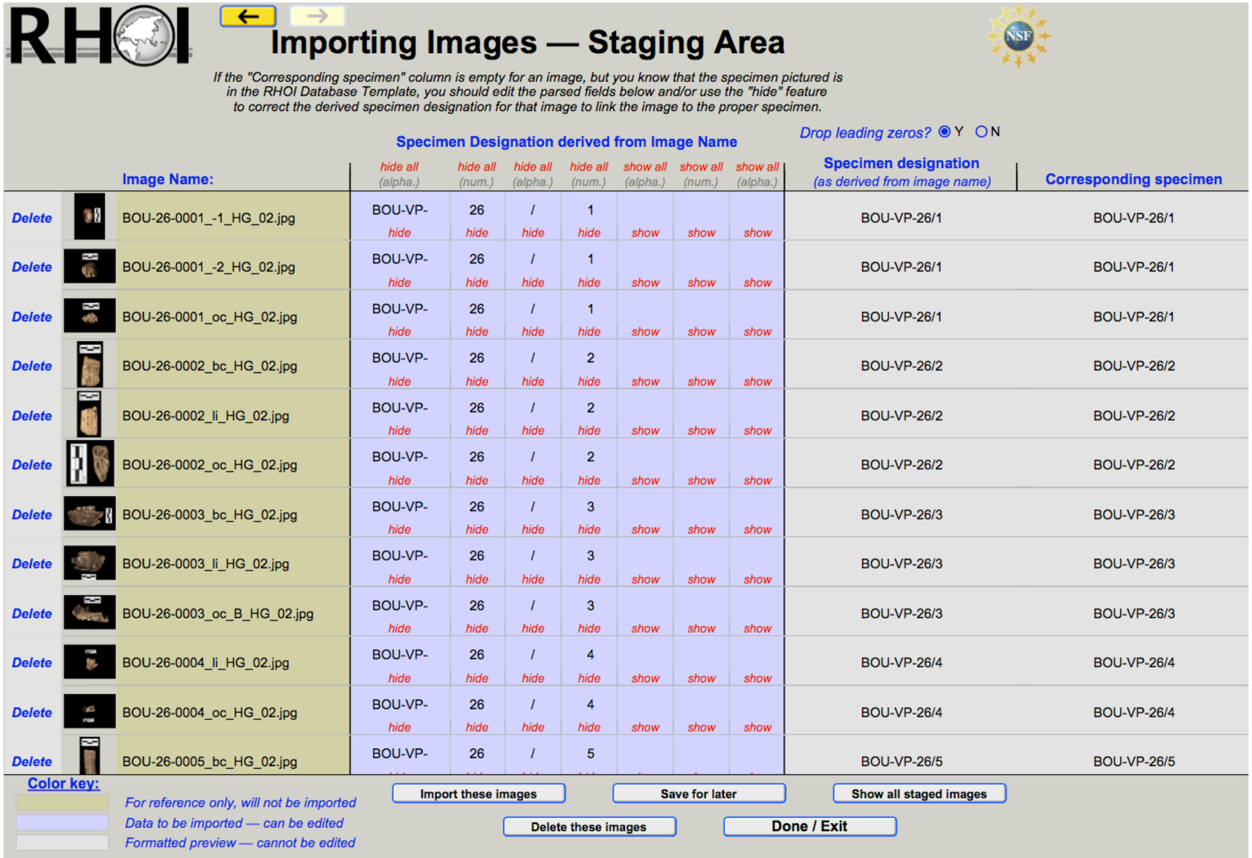
Import Action
- ● Add new records
- ○ Update existing records in found set
- ○ Update matching records in found set

Field Mapping
- ⇒ Import this field
- — Don't import this field
- ≡ Match records based on this field
- ✗ Target cannot receive data

☐ Add remaining data as new records

☑ Don't import first record (contains field names)

Your images will be imported into the **Importing Images – Staging Area** (see below). This staging area works in the same manner as the staging area for data. It allows you to make sure that the specimen images correspond with the correct specimen numbers. If no specimen number appears in the **Corresponding specimen** column, no image will import. This happens because the RHOI Database Template had trouble parsing the Image Name. You will need to manipulate the **Specimen Designation derived from Image Name** columns by hiding or showing them, or by changing the letters, numbers, and symbols in the alpha-numeric fields. Once the images correspond to the correct specimen numbers, you can click on the **Import these images** button to import the images to the database. Or, you can delete or save the images for later edits in the staging area.



Importing Images — Staging Area

If the "Corresponding specimen" column is empty for an image, but you know that the specimen pictured is in the RHOI Database Template, you should edit the parsed fields below and/or use the "hide" feature to correct the derived specimen designation for that image to link the image to the proper specimen.

Drop leading zeros? ● Y ○ N

Specimen Designation derived from Image Name

	Image Name:	*hide all* (alpha.)	*hide all* (num.)	*hide all* (alpha.)	*hide all* (num.)	*show all* (alpha.)	*show all* (num.)	*show all* (alpha.)	**Specimen designation** *(as derived from image name)*	**Corresponding specimen**
Delete	BOU-26-0001_-1_HG_02.jpg	BOU-VP- *hide*	26 *hide*	/ *hide*	1 *hide*	*show*	*show*	*show*	BOU-VP-26/1	BOU-VP-26/1
Delete	BOU-26-0001_-2_HG_02.jpg	BOU-VP- *hide*	26 *hide*	/ *hide*	1 *hide*	*show*	*show*	*show*	BOU-VP-26/1	BOU-VP-26/1
Delete	BOU-26-0001_oc_HG_02.jpg	BOU-VP- *hide*	26 *hide*	/ *hide*	1 *hide*	*show*	*show*	*show*	BOU-VP-26/1	BOU-VP-26/1
Delete	BOU-26-0002_bc_HG_02.jpg	BOU-VP- *hide*	26 *hide*	/ *hide*	2 *hide*	*show*	*show*	*show*	BOU-VP-26/2	BOU-VP-26/2
Delete	BOU-26-0002_li_HG_02.jpg	BOU-VP- *hide*	26 *hide*	/ *hide*	2 *hide*	*show*	*show*	*show*	BOU-VP-26/2	BOU-VP-26/2
Delete	BOU-26-0002_oc_HG_02.jpg	BOU-VP- *hide*	26 *hide*	/ *hide*	2 *hide*	*show*	*show*	*show*	BOU-VP-26/2	BOU-VP-26/2
Delete	BOU-26-0003_bc_HG_02.jpg	BOU-VP- *hide*	26 *hide*	/ *hide*	3 *hide*	*show*	*show*	*show*	BOU-VP-26/3	BOU-VP-26/3
Delete	BOU-26-0003_li_HG_02.jpg	BOU-VP- *hide*	26 *hide*	/ *hide*	3 *hide*	*show*	*show*	*show*	BOU-VP-26/3	BOU-VP-26/3
Delete	BOU-26-0003_oc_B_HG_02.jpg	BOU-VP- *hide*	26 *hide*	/ *hide*	3 *hide*	*show*	*show*	*show*	BOU-VP-26/3	BOU-VP-26/3
Delete	BOU-26-0004_li_HG_02.jpg	BOU-VP- *hide*	26 *hide*	/ *hide*	4 *hide*	*show*	*show*	*show*	BOU-VP-26/4	BOU-VP-26/4
Delete	BOU-26-0004_oc_HG_02.jpg	BOU-VP- *hide*	26 *hide*	/ *hide*	4 *hide*	*show*	*show*	*show*	BOU-VP-26/4	BOU-VP-26/4
Delete	BOU-26-0005_bc_HG_02.jpg	BOU-VP-	26	/	5				BOU-VP-26/5	BOU-VP-26/5

Color key:

🟨	*For reference only, will not be imported*
🟪	*Data to be imported — can be edited*
⬜	*Formatted preview — cannot be edited*

IMPORTANT NOTE: FILE SIZE

Your RHOI Database Template can store a lot of data, including images, but you should always be aware of your overall file size. This may become important if you begin embedding thousands of specimen images. A large batch of images at file sizes bigger than 1 or 2 MB, for example, might cause your database to perform sub-optimally. To make sure your database runs smoothly, we suggest that each image you import be smaller than 2 MB. Depending on the program you use to manipulate your images (e.g., Photoshop, Illustrator, Microsoft Digital Image, etc.), you will have some options for decreasing file size. Look in your program's HELP menu for instructions about reducing the sizes of your image files.

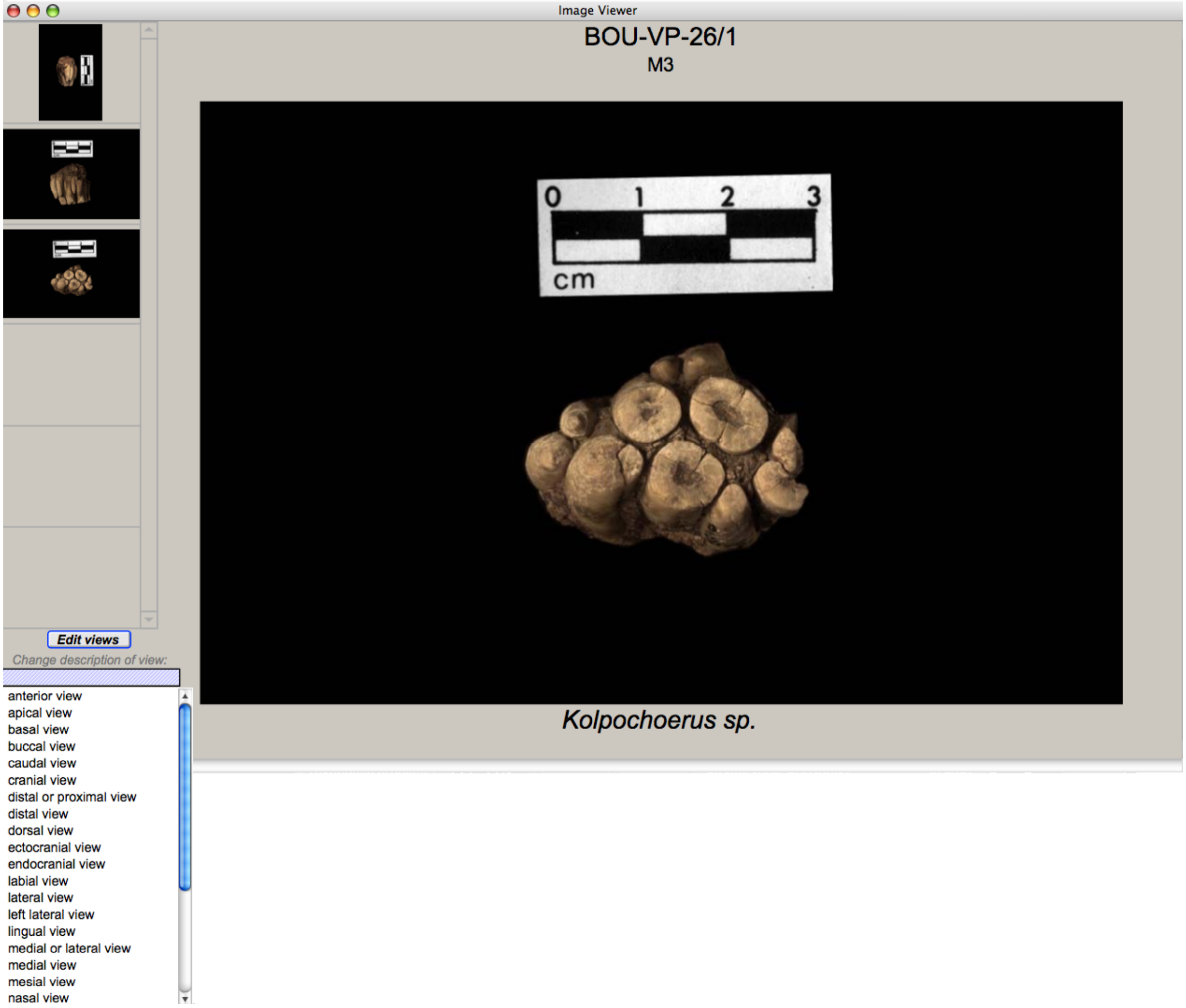
2. IMPORTING YOUR IMAGES SPECIMEN-BY-SPECIMEN

You also have the option to import your images on a specimen-by-specimen basis. Do this from the Specimen Entry or Specimen Overview layout. Click on the image strip (Specimen Entry) or image grid (Specimen Overview). You will be asked: "Would you like to import an additional photo for this specimen?" Click "Yes".

Next, you will be guided to your hard drive where you will be asked to find and select an image you want to insert. Once you select an image you want, click "Open".

Your image will automatically import into your database.

Once your image appears (visible in the image strip or image grid), you can modify it as needed. Click on the thumbnail version of your image to be taken to the **Image Viewer** page:



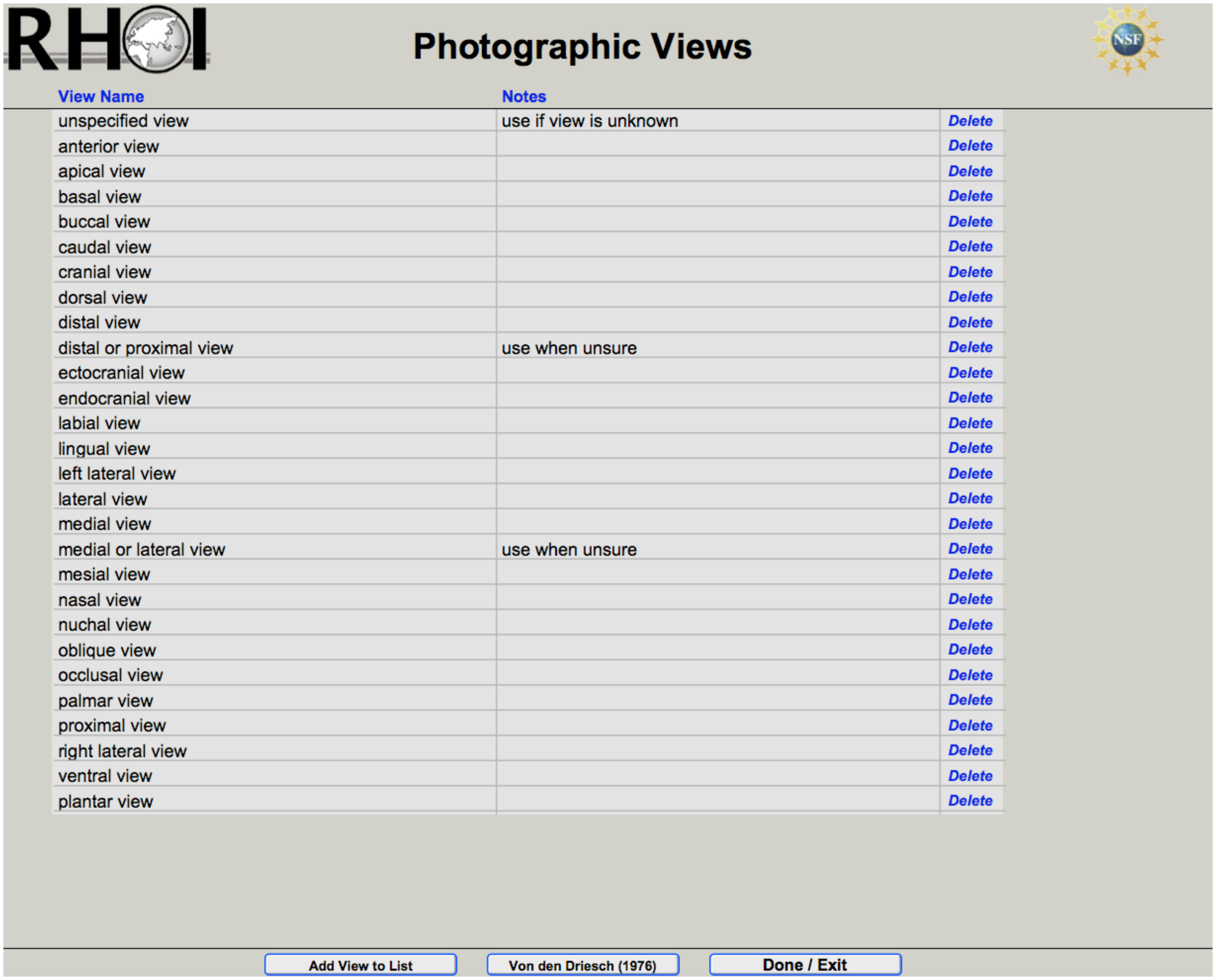
BOU-VP-26/1

M3

Kolpochoerus sp.

Here, you can add information about the view (e.g., occlusal, anterior, etc.) or delete the image entirely (e.g., if you imported the wrong image into your specimen record by mistake).

While on the **Image Viewer** page, you will be able to edit the pre-programmed photographic views. The RHOI has compiled a fairly comprehensive list of views for most taxa,



Photographic Views

View Name	Notes	
unspecified view	use if view is unknown	Delete
anterior view		Delete
apical view		Delete
basal view		Delete
buccal view		Delete
caudal view		Delete
cranial view		Delete
dorsal view		Delete
distal view		Delete
distal or proximal view	use when unsure	Delete
ectocranial view		Delete
endocranial view		Delete
labial view		Delete
lingual view		Delete
left lateral view		Delete
lateral view		Delete
medial view		Delete
medial or lateral view	use when unsure	Delete
mesial view		Delete
nasal view		Delete
nuchal view		Delete
oblique view		Delete
occlusal view		Delete
palmar view		Delete
proximal view		Delete
right lateral view		Delete
ventral view		Delete
plantar view		Delete

but you should feel free to modify it to suit your needs.

Appendix A. BACKGROUND AND HISTORY

The **Revealing Hominid Origins Initiative** (RHOI; NSF-HOMINID; http://rhoi.berkeley.edu/) was created by the late F. Clark Howell and Tim White in 2002, and funded by the U.S. National Science Foundation in 2003. It is a global paleoanthropological effort to recover, interpret, and disseminate information pertinent to the origin of the hominid clade.

RHOI Goals

- To provide funding for ongoing field-based projects with currently insufficient support in order to rapidly and efficiently recover, curate, analyze, and disseminate primary research results via publication and shared databases
- To thereby accelerate the entire scientific community's access to original fossils and other data
- To explore unknown terrain in the search for new fossil-bearing sites
- To foster cross-project communication, collaboration, and integration
- To support the development of paleoanthropological infrastructure
- To use informatics to facilitate the sharing of accurate, comparable data

RHOI Principles

RHOI is structured to enhance and to expand normal scientific research. Each research project affiliated with the initiative is fully autonomous in its operations. The RHOI does not mandate such matters as post-analysis publication of results, or access to fossils or other datasets. Each project retains full and independent responsibility for conducting its ongoing investigations within local and national regulations. These projects maintain complete autonomy in personnel, publication/announcement scheduling, and research agenda.

The sharing of unpublished or partially published research results within RHOI and beyond is voluntary, and entirely at the discretion of individual investigators and/or research projects. The initiative imposes no deadlines for such data sharing. However, all consortium members are expected and strongly encouraged to make their results accessible through publication and other means--to the widest community--at the fastest possible pace. A key RHOI objective is to accelerate the rate at which newly acquired data becomes available to the entire scientific community.

RHOI does not seek to alter the normal discovery/analysis/peer-review publication cycle that is fundamental to modern science. This process is responsible for the ultimate dissemination of research results. However, a central goal of the initiative is to improve the science and speed the normal publication process by supporting and facilitating cross-project collaborations. By taking active steps in informatics, the RHOI aims to extend and foster such collaborations.

RHOI Informatics

As originally envisioned, the initiative's success would depend on the coordination of research efforts (field and laboratory) and the sharing of information via electronic technology, with information flow in multiple directions. Initial efforts to implement a flexible, web-based, distributed information infrastructure to serve the needs of paleontologists within and beyond the initiative resulted in the prototype (designed by John Damuth, Ray Bernor, and Henry Gilbert) presently available at: **http://herc.berkeley.edu/rhoi/_rhoi_specimen_db.php**

The initial concept anticipated that each RHOI project (active or curatorial) would provide the high-quality, detailed empirical data produced by their field and analytical teams. These data are foundational to more widely-adopted summaries based primarily on literature compilations or secondary sources. To avoid the pitfalls (including geometric propagation of error) associated with the latter data sets (lack of standardization, lack of currency, lack of substantiation/reliability), RHOI was designed to make available the specimen-level data that ultimately underlie all species occurrences. It was not an attempt to replace the posting of rapidly outdated faunal lists reported in the literature or via web-based platforms such as PDB, ETE, NOW, etc. Indeed, among the tasks of the RHOI's working groups were the augmentation, revision, and standardization of the seemingly empirical, yet effectively unverifiable data that underlie such faunal lists. RHOI sought to make these specimen-level data, including specimen images, widely and promptly available on a web-based platform.

The RHOI's needs presented a technical challenge not met by conventional database approaches in paleontology, which rely on a monolithic central database (ordinarily of faunal lists or stratigraphic ranges) and a traditional client-server model. With the start of the project in 2003, the RHOI canvassed its participants in an effort to gather data that would be assembled and distributed via the latest technology in distributed computing, including peer-to-peer web services, cross-architecture web service platforms, and XML, SOAP, and MySQL/PHP standards.

The RHOI launched bibliographic and news functions that continue at the time of writing. The RHOI established a specimen-based, digital-image-incorporating, open-access website. Unpublished data from the Middle Awash and Çorakyerler projects were hosted: **http://herc.berkeley.edu/rhoi/_rhoi_specimen_db.php**

However, after establishing those mechanisms, our attempts to include the datasets from other projects were less successful, owing to a variety of factors. The most important of these were researcher concerns about priority, pre-publication versus post-publication availability, and institutional constraints. The RHOI continued to work with all its member projects and institutions in order to better understand their informatics infrastructures (often an Excel spreadsheet or handwritten notes) and concerns. Although all projects desired and welcomed access to better-quality specimen-level data, a variety of technical and administrative hurdles prevented universal participation in the single-forum approach originally envisioned for the RHOI.

At the same time, the information technology revolution has moved very fast, outpacing the informatics programs of even the most technologically-progressive projects associated with the RHOI. It is now technologically simple to globally serve large, image-associated databases. However, the barriers to global access linger, and the RHOI has revealed a great deal about the disposition of these barriers within paleoanthropology. In addition to the overemphasized (but still real) issues with priority lies the more basic issue of standardization. The range of different approaches to data management employed by RHOI-affiliated projects was found to be very wide. These differences transcend differences between software or operating preferences, and most of them involved a lack of standardization. At the onset of the RHOI, the use of data fields among projects was disjunct, and this led the RHOI to initiate discussions to establish the range of data acquisition and management practices, and to deliberate on establishing some basic standards that would be helpful in any downstream information sharing programs.

During these communications and deliberations, and with the advice of its Advisory Committee, the RHOI began to investigate an alternative means for projects to make their data freely available. This effort was aided substantially by the rapid development of FileMaker software, as well as database serving technologies, increasing bandwidths, and general improvements in computing infrastructure during the last few years. Consultations with member projects and individuals allowed the RHOI to identify and prioritize their informatics status and needs, and to articulate a solution consistent with original RHOI goals. This led to the development of the current specimen-based RHOI Database Template.

We encourage all RHOI projects to adopt the RHOI Database Template for several reasons:

- It is user-friendly
- It is flexible
- It has powerful data management and manipulation capabilities
- It has been designed to accommodate and standardize the most basic and most important specimen-based and locality-based information that each project is collecting or responsible for managing
- It will allow each project to maintain up-to-date records and to share these with other projects and investigators.
- It prompts you to acquire and maintain basic data important to any paleobiological endeavor

Appendix B. TAXONOMIC CONVENTIONS

? = *identification probable but not certain*
Use **?** when identification as the named taxon is probable, but cannot be certain. **?** indicates more certainty than cf. The **?** should precede the uncertain taxonomic identification (e.g., **?***Felis libyca*: uncertain genus identification; *Felis* **?***libyca*: uncertain species identification; **?***Felis* **?***libyca*: uncertain genus and species identification).

aff. = *having affinity, with but not identical to*
Use **aff.** when the specimen has affinity to a previously known taxon, but is not identical to it (e.g., **aff.** *Felis*: for a new genus; *Felis* **aff.** *libyca*: for a new species; **aff.** *Felis* **aff.** *libyca*: for a new genus and new species).

blank = *identification pending*
Leave the identification empty (blank) for all cases in which further study is expected to result in a better identification.

cf. = *to be compared to*
Use **cf.** when identification as the named taxon is provisional and should be compared to the taxon that follows the qualifier (e.g., **cf.** *Felis*: genus is provisionally identified; **cf.** *libyca*: species is provisionally identified; **cf.** *Felis* **cf.** *libyca*: both genus and species are provisionally identified).

gen. nov. et sp. nov. = *new genus and new species*
Use **gen. nov. et sp. nov.** during the interim between recognition of a new taxon (genus and species) and formal publication.

indet. = *indeterminate*
Use **indet.** when lower level classification is not possible due to the inadequacy of the material for accurate identification (e.g., *Felis* **indet.**, Felidae **indet.**).

sp. = *species*
Use **sp.** when the material cannot presently be identified to the species level but may be identifiable at a later date with more specimens (e.g., *Felis* **sp.**).

ssp. = *subspecies*
Use **ssp.** when the material cannot presently be identified to the subspecies level, but which may be identifiable at a later time with more specimens (e.g., *Felis libyca* **ssp.**).

REFERENCES

Bengtson, P. (1988). Open Nomenclature. Palaeontology 31, 223-227.

BirdLife International (2000). Threatened birds of the world. Lynx Editions and BirdLife International, Cambridge, United Kingdom.

Kornicker, L. S. (1979). The Question Mark in Taxonomic Literature. Journal of Paleontology 53, 761.

Matthews, S. C. (1973). Notes on Open Nomenclature and on Synonymy Lists. Palaeontology 16, 713-719.

McKenna, M. C. and S. K. Bell (1997). Classification of mammals above the species level. Columbia University Press, New York.

ACKNOWLEDGEMENTS

The authors thank the following individuals for their support of this endeavor: F. Clark Howell, Ray Bernor, Maia Bukhsianidze, Brianne Daniels, David DeGusta, Gerald Eck, Yohannes Haile-Selassie, Leslea Hlusko, Ben Mersey, and Scott Simpson.