


Galaxy Portal User Guide

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Galaxy Portal



A quick and easy way to check the status of biomedical research on Galaxy.

Completely free and open-source.

Galaxy Portal - 5 items		
Main History		>
test		>
Second History		>
Empty History		>
MyHistory		>

About Galaxy Portal

The Galaxy Portal app aims to be a convenient way to check the status and review histories from Galaxy biomedical research instances.

The Galaxy Portal app was designed to be intuitive to use, but this guide explains the main features and how to get the most out of it.

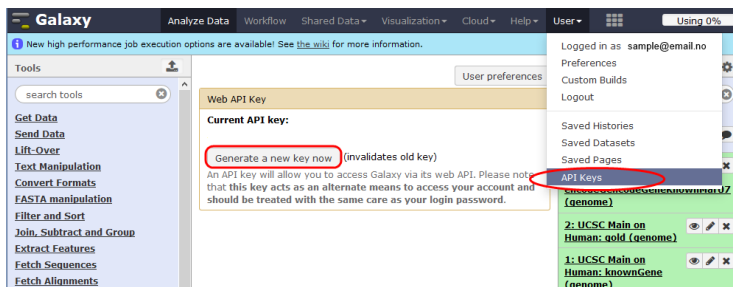
Galaxy Instance

To use the app you will need to have an account on a Galaxy instance, such as <https://usegalaxy.org>. If you do not already have an account you can get one by visiting the Galaxy instance using a web browser.

You can log into Galaxy Portal with your normal username and password. The app does not remember your password, but instead retrieves a secret API Key. If you do not already have one the key is automatically generated when you first log in from the app.

Changing API Key

You can change the Galaxy API key by logging into the Galaxy instance, selecting **User** from the menu and choosing **API Keys**. You will then need to log into the Galaxy Portal app again for access.



First Time Use

When you first open the Galaxy Portal app you will be greeted with a welcome message similar to that shown below.

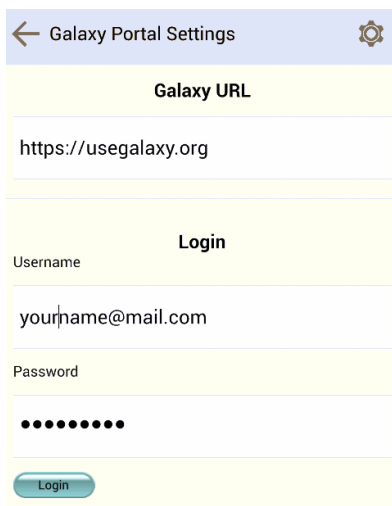



It shows the current Galaxy URL, which will default to the “*Use Galaxy*” instance. Below that is a message in red telling you to set the Galaxy URL and API Key. This is done by opening the settings by tapping the cog wheel seen top right and circled in red, and logging in with your username and password.

This process is described in detail in the next section titled “Initial Setup”.

Initial Setup

The first **Galaxy URL** field determines the Galaxy instance you wish to connect to. The default is <https://usegalaxy.org>, but you can enter the url to any Galaxy instance you have an account with – including your own local instance.



← Galaxy Portal Settings 

Galaxy URL

https://usegalaxy.org

Login

Username

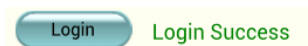
yourname@mail.com

Password

●●●●●●●●●●

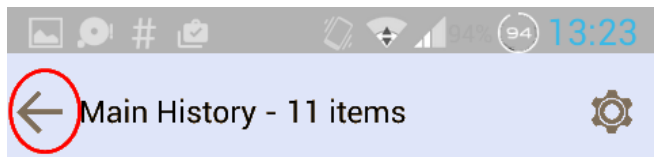
Login

Simply type in your username and password and tap the “Login” button. This will connect to the Galaxy instance and you should see a success message.

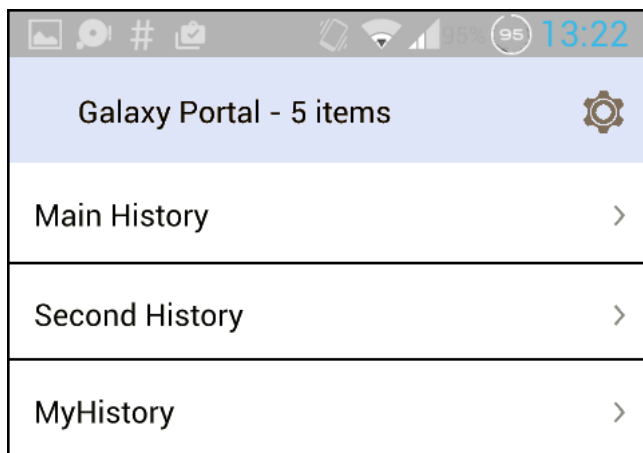


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This is all you need and you can now click the back arrow on the left in the top action bar to go to the main history list.



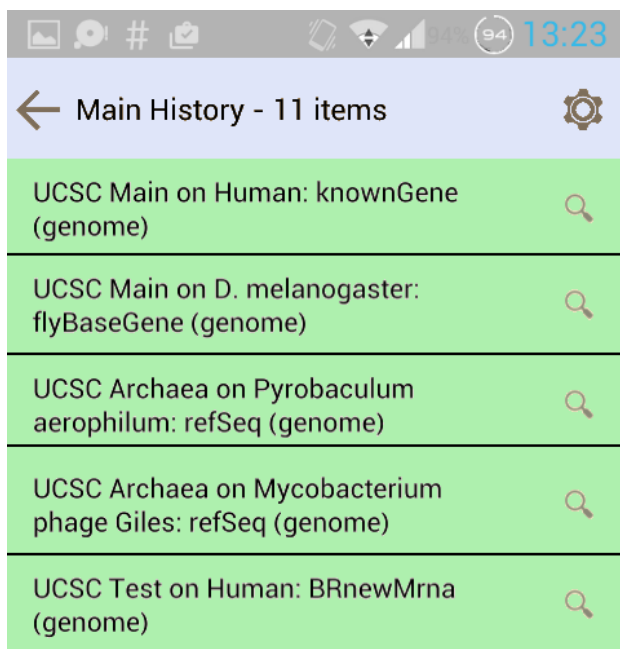
This will bring you to the history list which will be automatically populated with your history items using the names you created in the Galaxy web interface.



If the list is empty then either you do not have any histories or the app was unable to connect. Check the network status of your device, any firewalls and confirm that the url and API is correct. You can confirm that you can reach the url by typing it into a web browser.

History Items

Click on one of your histories to open it and show all the job data for that history. The title in the top action bar will change to show the name of the history and number of items. Each item will be displayed with its name and a magnifying glass on the right.






Items are colour coded to show the status of that item.

Job Status Colour Coding




Ok		green
Running		lemon
Paused		yellow
Queued		light gray
Error		red
Discarded		gray
Empty		blue
New		snow white
Resubmitted		cyan

Example of three items with one queued job:










UCSC Main on Lancelet: blastHg18KG (genome)	
UCSC Main on C. elegans: pubsBingBlat (genome)	
UCSC Main on Squirrel monkey: genscan (genome)	

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Example of two items flipped, one with a running job:

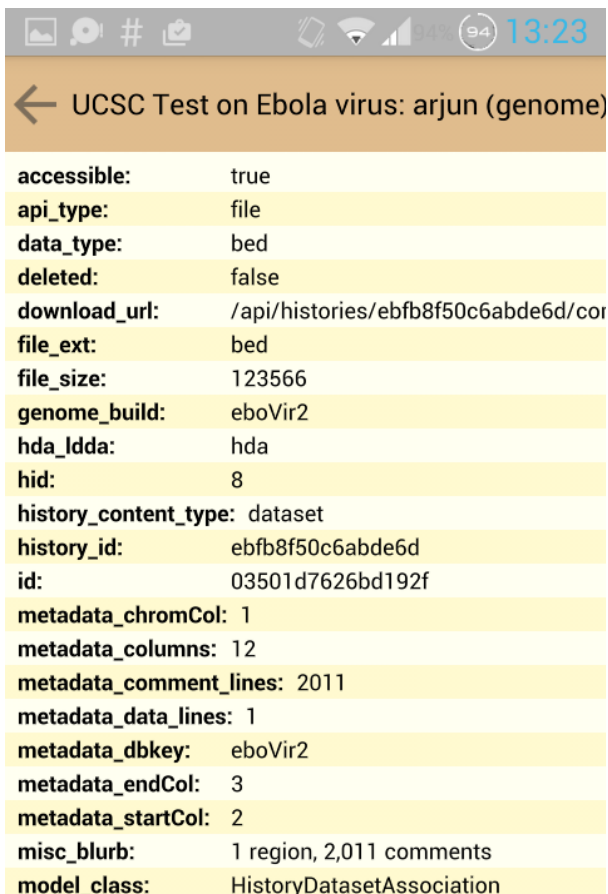
UCSC Main on Gorilla: xenoRefGene (genome)	
Status: ok Content: dataset Type: file	
Status: running Content: dataset Type: file	

Clicking on a history item will flip it to show additional data, including the status. You can click the item again to flip it back to its name. See the *Settings* section on *Field Configuration* for how to configure which fields are shown.

#     89%  11:54	
← HistoryOne - 3 items	
Status: ok hda_ldda: hda genome_build: hg17 update_time: 2014-09-22T16:19:09.508441 file_size: 354019 file_size: 354019	
UCSC Main on Lancelet: blastHg18KG (genome)	
Status: ok hda_ldda: hda genome_build: ce10 update_time: 2014-09-22T16:19:57.551381 file_size: 719821 file_size: 719821	

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Click the magnifying glass to zoom in on all the details of the item. This will retrieve all available fields - usually including a peek at your data.

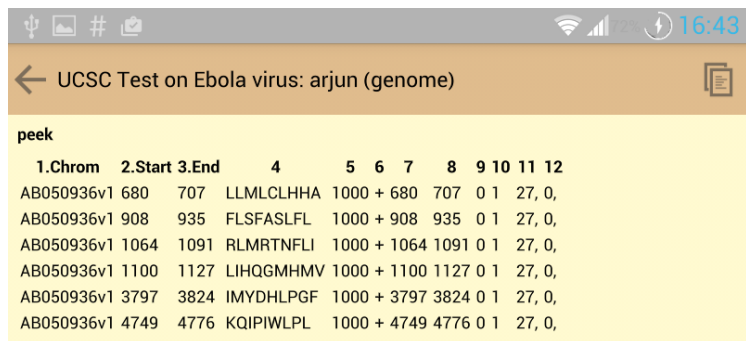


The screenshot shows a mobile application interface. At the top is an Android-style status bar with icons for camera, gallery, home, and other functions, along with the time 13:23. Below the status bar is a header bar with a back arrow and the title 'UCSC Test on Ebola virus: arjun (genome)'. The main content area displays a list of key-value pairs for a dataset, with each pair on a separate row. The keys are in bold, and the values are in regular text. The background of the rows alternates between light yellow and white.

accessible:	true
api_type:	file
data_type:	bed
deleted:	false
download_url:	/api/histories/ebfb8f50c6abde6d/cor
file_ext:	bed
file_size:	123566
genome_build:	eboVir2
hda_ldda:	hda
hid:	8
history_content_type:	dataset
history_id:	ebfb8f50c6abde6d
id:	03501d7626bd192f
metadata_chromCol:	1
metadata_columns:	12
metadata_comment_lines:	2011
metadata_data_lines:	1
metadata_dbkey:	eboVir2
metadata_endCol:	3
metadata_startCol:	2
misc_blurb:	1 region, 2,011 comments
model_class:	HistoryDatasetAssociation

Field View

You can open any of these fields by clicking on the field and if the opened data is larger than your screen you can drag it around to see everything. You can always go back by hitting the back arrow in the top action bar.



1.Chrom	2.Start	3.End	4	5	6	7	8	9	10	11	12
AB050936v1	680	707	LLMLCLHHA	1000	+	680	707	0	1	27,	0,
AB050936v1	908	935	FLSFASLFL	1000	+	908	935	0	1	27,	0,
AB050936v1	1064	1091	RLMRTNFLI	1000	+	1064	1091	0	1	27,	0,
AB050936v1	1100	1127	LIHQGMHMY	1000	+	1100	1127	0	1	27,	0,
AB050936v1	3797	3824	IMYDHLPGF	1000	+	3797	3824	0	1	27,	0,
AB050936v1	4749	4776	KQIPIWLPL	1000	+	4749	4776	0	1	27,	0,

Copy

You can copy the data in the field view to the clipboard by clicking the copy icon.



Landscape and Portrait View

If your device supports it, rotate it to get a landscape view. Any part of the Galaxy Portal app can be viewed in both portrait and landscape mode, and you can rotate between the two at any time.

Settings

The settings can be reached from the main history lists by clicking the cog on the far right of the top action bar (same as shown for initial setup).

Field Configuration

You can configure the fields shown when a history item is flipped.

☒ Enable Advanced Fields

hda_ldda

genome_build

update_time

none

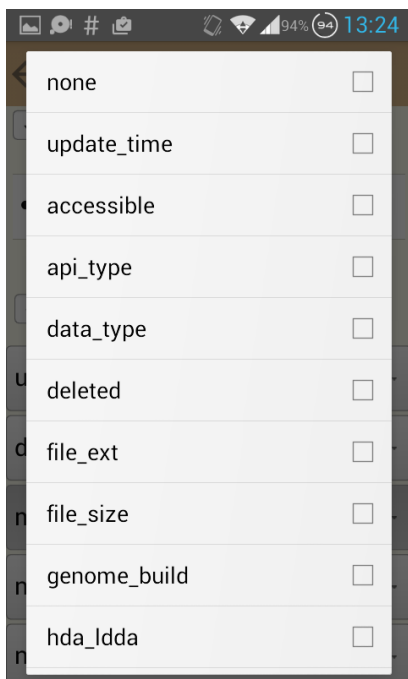
none

Advanced field data is enabled by default and allows you to select up to five fields retrieved from the list of fields provided by your

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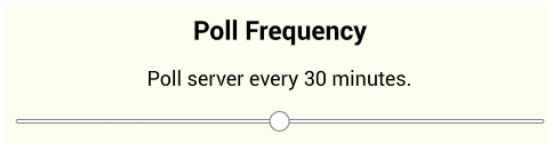
Galaxy instance. If you prefer to only see the basic fields uncheck the advanced fields button. This also eliminates an extra call to the Galaxy instance for the advanced field data and so can improve performance and will use less bandwidth (see *polling* below for how to control how often the app retrieves data).

Choose the field in the list by clicking the drop down box. You can see less data by selecting “none” for some of the fields.



Polling

You can change how frequently the Galaxy instance is polled to update the data in your Galaxy Portal app. By pulling the slider you can change the frequency from zero (never) to every 60 minutes.

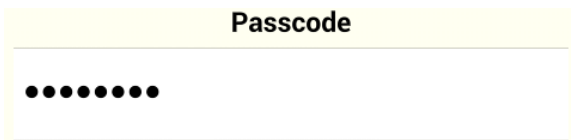


The Galaxy instance is always polled when you open the app, you select a new item in your histories or you open the detail view of an item. However, if you set the polling interval to zero then this is the only time the Galaxy instance is polled.

If you set it to 'X' minutes then the data will be automatically updated every 'X' minutes.

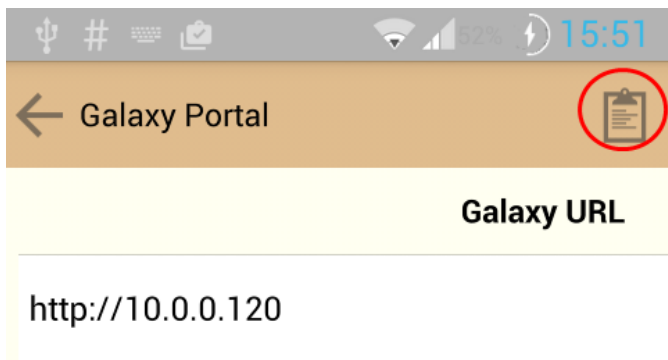
Passcode

As extra security you can enable a passcode to start the app with your API key. If enabled then the passcode must be entered to login to your Galaxy histories with the app. If the wrong passcode is typed an option to bypass the passcode is offered, but doing so will delete the API key and passcode and must be entered again.



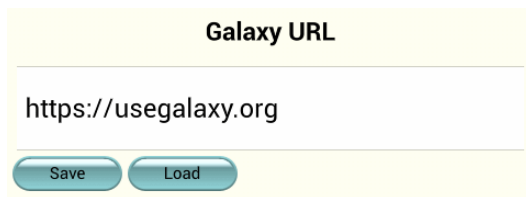
Paste

If you copy the url or Galaxy API from your browser you can paste it into the Galaxy Portal app by selecting the field and then clicking the paste icon which will appear. This is particularly useful to avoid having to type the long Galaxy API sequence.



Saving Multiple Instance

The Galaxy Portal app can remember multiple instances to make it easy to switch between them. Once you have logged into an instance a “Save” button will appear. Tap it to save the connection.



Loading an Instance

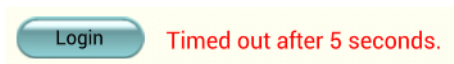
When you have saved one or more instances you can load any of them using the “Load” button that appears under the Galaxy URL. When you tap the “Load” button a list will appear with all stored connections.



You can simply click a url to connect to that Galaxy instance. If you wish to remove it from the list tap the trash button icon on the right side.

Troubleshooting

If you get a message that the login timed out as shown below, then the Galaxy Portal app was unable to connect to the specified Galaxy url.

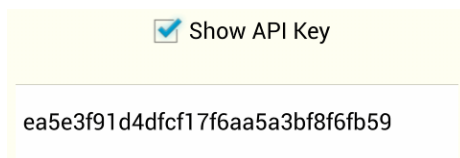


If you get an error message as shown below your connection was refused. This is often because you typed the wrong username or password.



Manually Entering API Key

When you log in using a username and password the Galaxy Portal app automatically retrieves the API Key for you (one is generated if you did not have one). However, if you instead wish to type or paste an API key manually you can do shown by checking “Show API Key” in the settings and the API Key field will be revealed. This works exactly the same as logging in with a username and password, and the connection can be saved just like any other connection.



Wide Screen Mode

A new wide screen mode has been added (will be available in version 1.2 and onwards). If the width of the screen is 1000 pixels or greater the selected history will be displayed in together with the list of histories. This generally affects computer monitors and some tablets or phones when held vertically, while smaller devices will still show only one list and let the user navigate between the lists by clicking on histories and the back arrow.

An example of wide screen display:

Main Data Collection - 33 Items		
Main Data Collection	>	Chimp
Project X	>	UCSC Main on Cow: genome (genome)
Additional Analysis Data	>	UCSC Main on Dolphin: genome (genome)
Genome History	>	UCSC Main on Dog: genome (genome)
	>	UCSC Main on Heliophaga: genome (genome)
	>	UCSC Main on Human: genome (genome)
	>	WormBase on D10484472_1063384

View Dataset

On the job item details view accessed through the magnifying glass there is in version 1.2 a new “View Dataset” button. This can be clicked to download a paged list of the dataset. Most datasets are large so this can take some time.

Because the dataset is so large it is of limited use at the moment, but is mostly intended as a proof of concept. In future this could be downloadable or searchable. However, a copy button is provided at the top to allow putting the dataset into the clipboard for pasting into another program for review, emailing or storing.