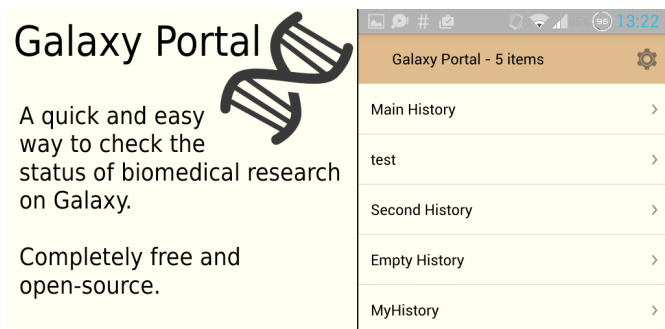


# Galaxy Portal User Guide

This document was last updated: 2<sup>nd</sup> November 2014.

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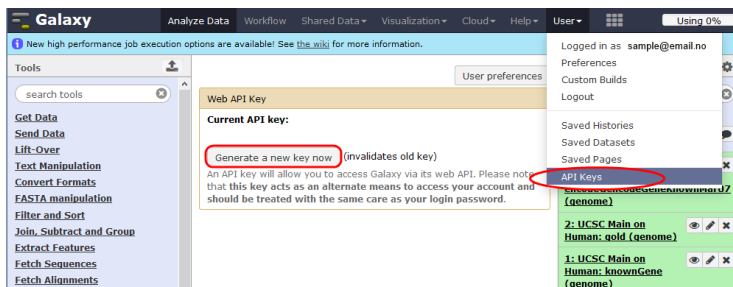
## About Galaxy Portal

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. If something is not intuitive please provide feedback even if it was explained in this guide.

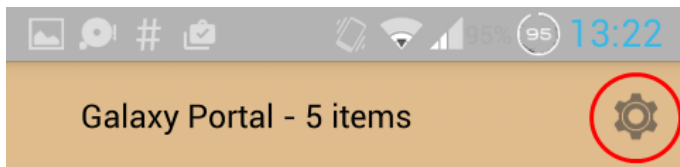
# Galaxy Instance

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 will also need to have a Galaxy API which you can create by selecting **User** from the menu and choosing **API Keys**. This key is your authentication for interacting with your histories through the Galaxy Portal app.



## Initial Setup

Open the configuration page clicking on the cog on the far right in the top action bar.

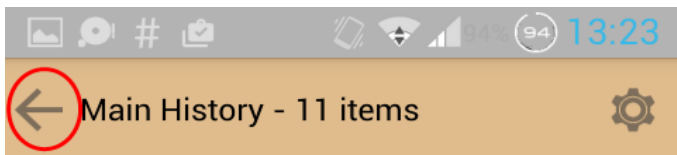


In the first url field type the path to your galaxy instance, e.g. <https://usegalaxy.org>. In the Galaxy API field type or paste the API code you created in your Galaxy user account.

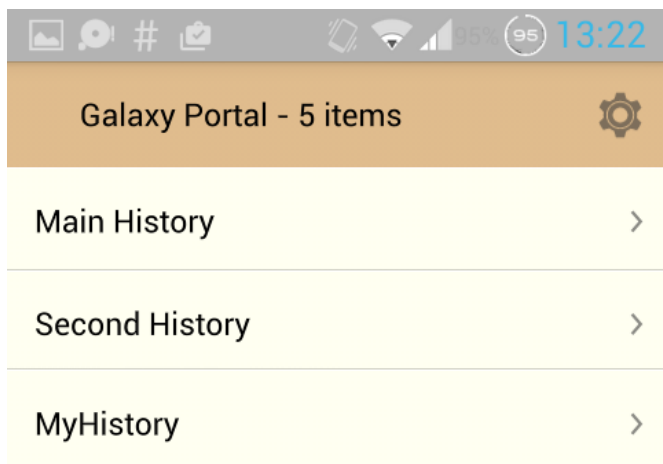
A screenshot of the Galaxy Portal configuration screen. At the top is a tan header bar with a back arrow and the text "Galaxy Portal". Below this is a yellow section titled "Galaxy URL" containing a text input field with the value "https://usegalaxy.org". Below that is another yellow section titled "API Key" with the subtitle "(Generate 'API Keys' in the Galaxy User menu)". This section contains a text input field that is currently empty and filled with black dots, indicating a password or sensitive information. The status bar at the top shows icons for camera, speech bubble, hash, envelope, smartphone, Wi-Fi, cellular signal, 94% battery, and the time 13:24.

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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.



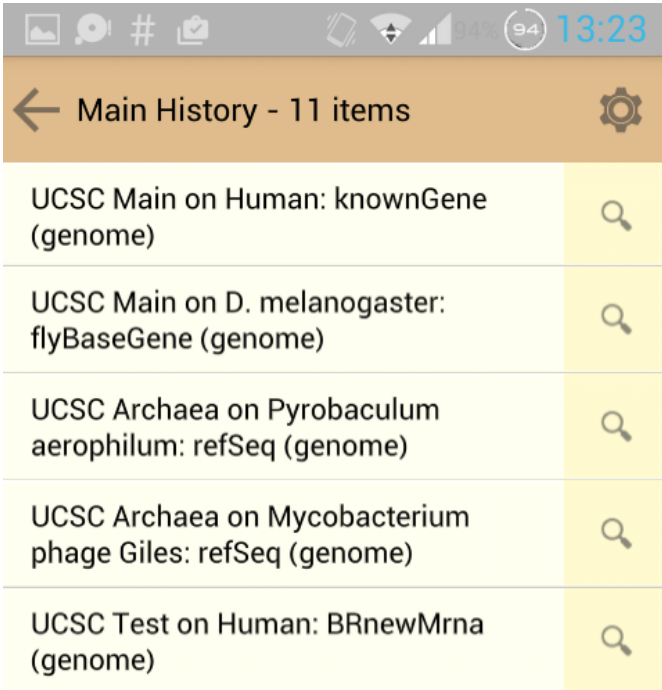
This will bring you to the history list which will be automatically populated with your history items using the names you created in the Galaxy web interface.








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.






Main History - 11 items	
UCSC Main on Human: knownGene (genome)	
UCSC Main on D. melanogaster: flyBaseGene (genome)	
UCSC Archaea on Pyrobaculum aerophilum: refSeq (genome)	
UCSC Archaea on Mycobacterium phage Giles: refSeq (genome)	
UCSC Test on Human: BRnewMrna (genome)	

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

## Job Status Colour Coding




<b>Ok</b>		<b>ivory</b>
<b>Running</b>		<b>aquamarine</b>
<b>Paused</b>		<b>yellow</b>
<b>Queued</b>		<b>sky blue</b>
<b>Error</b>		<b>red</b>
<b>Discarded</b>		<b>gray</b>
<b>Empty</b>		<b>lemon</b>
<b>New</b>		<b>snow white</b>
<b>Resubmitted</b>		<b>cyan</b>

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:

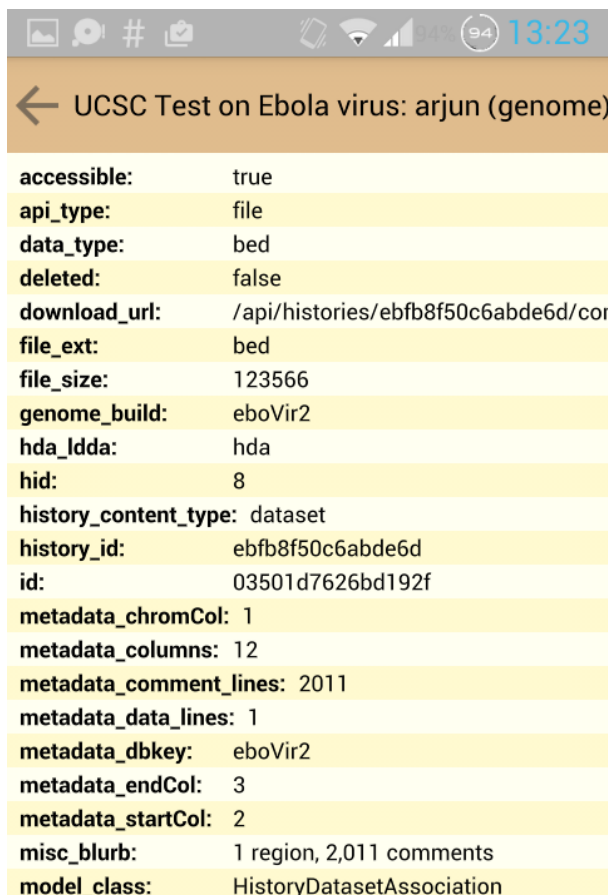
UCSC Main on Gorilla: xenoRefGene (genome)	
<b>Status:</b> ok <b>Content:</b> dataset <b>Type:</b> file	
<b>Status:</b> running <b>Content:</b> dataset <b>Type:</b> file	

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%  89 11:54	
 HistoryOne - 3 items 	
<b>Status:</b> ok <b>hda_idda:</b> hda <b>genome_build:</b> hg17 <b>update_time:</b> 2014-09-22T16:19:09.508441 <b>file_size:</b> 354019 <b>file_size:</b> 354019	
UCSC Main on Lancelet: blastHg18KG (genome)	
<b>Status:</b> ok <b>hda_idda:</b> hda <b>genome_build:</b> ce10 <b>update_time:</b> 2014-09-22T16:19:57.551381 <b>file_size:</b> 719821 <b>file_size:</b> 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.



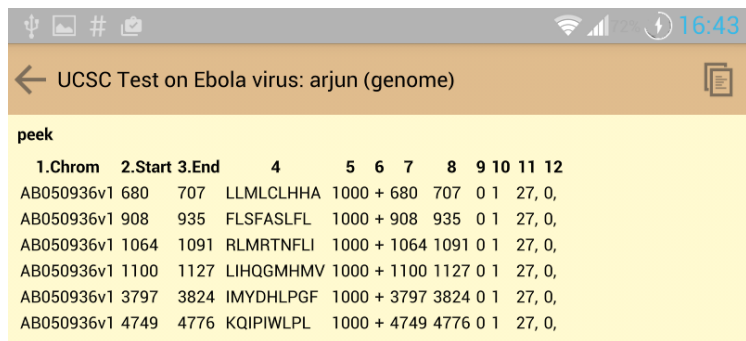
The screenshot shows a mobile application interface. At the top is an Android-style status bar with icons for camera, gallery, home, and other functions, along with the time 13:23. Below the status bar is a header bar with a back arrow and the title 'UCSC Test on Ebola virus: arjun (genome)'. The main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

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



UCSC Test on Ebola virus: arjun (genome)

peek

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

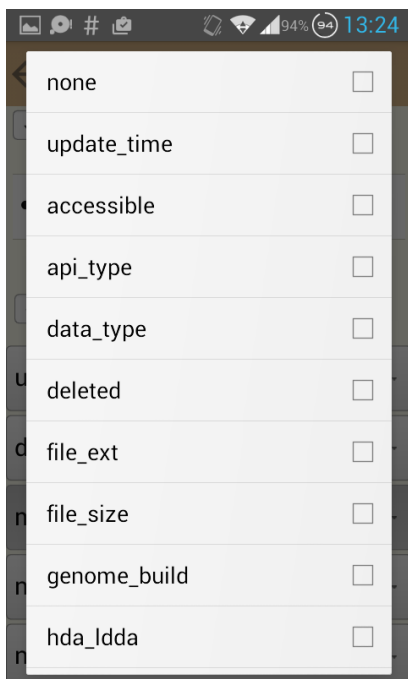
none

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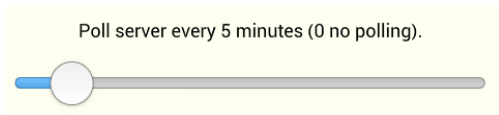
Galaxy instance. If you prefer to only see the basic fields uncheck the advanced fields button. This also eliminates an extra call to the Galaxy instance for the advanced field data and so can improve performance and will use less bandwidth (see *polling* below for how to control how often the app retrieves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

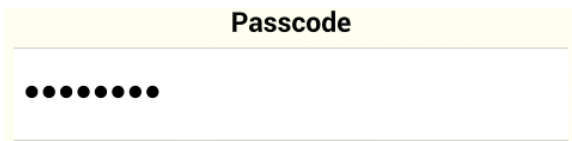


The Galaxy instance is always polled when you open the app, you select a new item in your histories or you open the detail view of an item. However, if you set the polling interval to zero then this is the only time the Galaxy instance is polled.

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

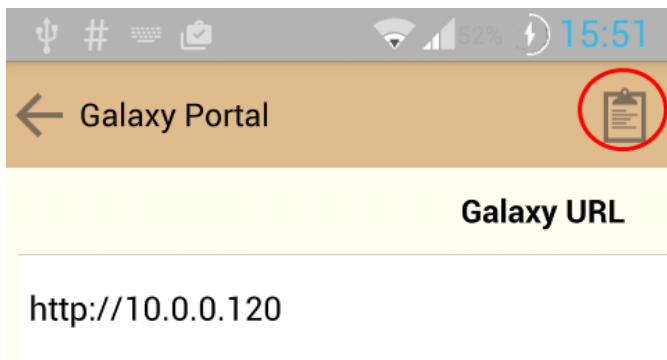
### Passcode

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.



## **Feedback**

Thank you for taking an interest in the Galaxy Portal app. Please send any constructive feedback to the contact on the first page. Your feedback is essential to improve the app and learn what works and what doesn't and so is much appreciated. Even just a quick email that you have tried the app and found it useful is helpful.