

Long Term Archive Howto

This is a short manual on how to search for and retrieve data from the Long Term Archive.

User Access

To access the LTA you need to have an account in MoM that is enabled for the archive.

1. This automatically happens if you were a member of the original project proposal in MoM.
2. Otherwise Science Support needs to add you to the project to which you need access.
3. For public data you can use an anonymous account.

If you were not originally a member of the project in MoM and Science Support adds you to it, you might get an email asking you to set a new password in [ASTRON Web Applications Password Self Service](#). Please note that this will set a new password not just for the LTA *but for MoM (LOFAR/WSRT) and Northstar as well*.

Finding data

Once your account is set up, you can navigate to [LTA Catalog site](#)

Login into the website by clicking in 'login' (third item in the menu):

[Home](#) | [Help](#) | [login \(AWANONYMOUS\)](#) | [project \(ALL\)](#) | [Search](#) | [Show Latest](#)

Currently you can only search the LTA catalogue per project. This means you need to select a project first by clicking on the 'project' link. Projects which you do not have access to will be grayed out in the resulting list.

[login \(awsciencesupport\)](#) | [project \(Commissioning2012\)](#) | [Search](#) | [Show Latest](#)

Once you have selected your project, you can use either:

1. The *Search* screen which allows you to search by RA/Dec, ObservationId, Frequency, etc.
2. The *Show Latest* screen which shows you the most recently added data for this project.

The result of either query will be a list of data products or observations similar to this:

Interferometric Data 1 to 256 (showing 256 of total 44709)

[edit columns](#) | [stage](#) [uris](#)

#	<input type="checkbox"/>	DataProduct Identifier	Target Name	Right Ascension [degrees]	Declination [degrees]	Central Frequency [MHz]	Chann Width [
1	<input type="checkbox"/>	3400453	3C218	139.523541667	-12.0955555556	155.859375	3051.7578
2	<input type="checkbox"/>	3400408	Hercules-A	252.784166667	4.9925	156.25	3051.7578
3	<input type="checkbox"/>	3400429	3C218	139.523541667	-12.0955555556	130.6640625	3051.7578
4	<input type="checkbox"/>	3400445	3C218	139.523541667	-12.0955555556	146.09375	3051.7578
5	<input type="checkbox"/>	3400450	3C218	139.523541667	-12.0955555556	151.171875	3051.7578
6	<input type="checkbox"/>	3400462	3C218	139.523541667	-12.0955555556	165.8203125	3051.7578
7	<input type="checkbox"/>	3400442	3C218	139.523541667	-12.0955555556	145.5078125	3051.7578
8	<input type="checkbox"/>	3400463	3C218	139.523541667	-12.0955555556	166.015625	3051.7578
9	<input type="checkbox"/>	3400465	3C218	139.523541667	-12.0955555556	166.40625	3051.7578
10	<input type="checkbox"/>	3400469	3C218	139.523541667	-12.0955555556	171.2890625	3051.7578
11	<input type="checkbox"/>	3400464	3C218	139.523541667	-12.0955555556	166.2109375	3051.7578

If you have a list of observations, you can navigate to the data products by clicking on the relevant link in the 'Number of Correlated/BeamFormed DataProducts' column. For navigating to data for only one particular sub-array pointing (SAP), select first the relevant SAP from the list obtained by clicking on the relevant link in the 'Number of Sub-Array Pointings' column.

Retrieving data

Once you have a list of dataproducts, observations or pipelines, you can use the check boxes to select which files you want to download. The first check box can be used to select or deselect all files or observations on a page.

[edit columns](#) | [stage](#) [uris](#)

#	<input type="checkbox"/>	DataProduct Identifier	Target Name	Right Ascensi [degree
1	<input checked="" type="checkbox"/>	3400453	3C218	139.52354
2	<input checked="" type="checkbox"/>	3400408	Hercules-A	252.78416
3	<input checked="" type="checkbox"/>	3400429	3C218	139.52354
4	<input checked="" type="checkbox"/>	3400445	3C218	139.52354
5	<input type="checkbox"/>	3400450	3C218	139.52354
6	<input checked="" type="checkbox"/>	3400462	3C218	139.52354
7	<input type="checkbox"/>	3400442	3C218	139.52354
8	<input checked="" type="checkbox"/>	3400463	3C218	139.52354
9	<input checked="" type="checkbox"/>	3400465	3C218	139.52354
10	<input type="checkbox"/>	3400469	3C218	139.52354
11	<input type="checkbox"/>	3400464	3C218	139.52354

When you have made your selection of files, you click on *stage*. This shows you the following message. It means that a request has been sent to the LTA staging service to start retrieving the requested files from tape storage and make them available. You will get an e-mail when this tape retrieval is complete.

The following file(s) are requested for download. You will receive an email when the files can be retrieved.

Size	Filename
758.2 MB	L75432_SAP004_SB215_uv.MS_f6b663ca.tar

The e-mail that you get when the tape retrieval is complete gives you a list of files and has two attachments, `html.txt` and `srm.txt`:

Your data retrieval request with id 25 has been staged and is ready for retrieval.




List of files:

`srm://lofar-srm.fz-juelich.de:8443/pnfs/fz-juelich.de/data/lofar/ops/projects/commissionin_04d3730c.tar`

The attached files can be used to retrieve the staged files.

For more information visit http://www.lofar.org/wiki/doku.php?id=public:lta_howto

This mail has been automatically generated by the ASTRON/LOFAR LTA staging service. Do not reply to this message. If you have any questions or remarks, please contact sciencesupport@astron.nl and provide the id of the request in your message.

Name	Size	Type
 Message	4KB	Message Attachment
 html.txt	214 Bytes	File Attachment
 srm.txt	189 Bytes	File Attachment

There are two ways you can use this list to retrieve the files: `http` and `srm`

Please take note of the following

1. Unless you have an extremely fast connection (10 Gbit/s or more), it is in general advisable to stage no more than 10 TB at a time (see also point 4). At maximum efficiency a 1 Gbit/s connection will already take 24 hours to retrieve 10 TB of data, in practice it will often take quite a bit more.
2. On a 1 Gbit/s connection as a general rule of thumb, you should be able to retrieve data at about 100-500 GB/hour, especially if you try to retrieve 4-8 files concurrently. If you see speeds much lower than this, you might have some kind of network problem and should in general contact your IT staff.
3. Staging the data from tape to disk might take quite a bit of time. In the large data centres that the LTA uses, the tape drives are shared with all users and requests are queued. This is not just users of LOFAR but large data other projects like the LHC. This might mean that it takes anywhere from a few hours to a day or more to stage a copy of your data from tape to disk.
4. The amount of space available for staging data is limited although quite large. This space is however shared between all LOFAR LTA users. This includes LTA operations for buffering data from CEP to the LTA before it gets moved to tape. If many users are staging data at the same time, and/or LOFAR operations is transferring large amounts of data, the system might temporarily run low on disk space. You might then get a message that your request was only

partially successful. In general the request will still finish 1-2 days later and we do monitor if requests don't get stuck and restart if needed.

5. We strive to keep a copy of data that was staged on disk for 1-2 weeks so you have some time to download it. After that it might get removed to make space for more recent requests. The the copy of the data on tape is only read and will still be available if you need to access the data again at a later stage but you might need to stage a copy to disk again.
6. We are continuously trying to improve the reliability and speed of the available services. Please contact Science Support if you have any problems or suggestions for improvement.
7. The data centres the LTA uses also have maintenance or small outages sometimes. Science Support can advice you if this is the case and when it is planned to end, if you are having trouble accessing data. In general this will not be at the same dates as the LOFAR stop days.

HTTP download

If you open `html.txt` this file contains a list of http links that you can feed to a unix commandline tool like `wget` or `curl` or even use in a browser.

For `wget` you can use the following command line:

```
wget -i html.txt
```

This will download the files in `html.txt` to the current directory. Do not set the username and password on the `wget` command line because this allows other users on the system to view them in the process list. Instead you should create a file `~/.wgetrc` with two lines according to the following example:

```
user=lofaruser  
password=secret
```

Set access authorizations of the `.wgetrc` file to user only so that the credentials are not exposed to anybody else, e.g.:

```
chmod 600 .wgetrc
```

There is no easy way to have `wget` rename the files as part of the command directly. It does not accept the `-O` flag inside a file it gets with `-i`. You can either rename files afterward, or add the `-O` option to each line in `html.txt` but then feed each line to `wget` separately like this: `cat html.txt | xargs wget`. By default the `html.txt` file does not contain such options.

SRM download

If you open the file `srm.txt` this file contains a list of srm locations which you would feed to `srmcp`. SRM is a GRID specific protocol that is currently supported for data at the SARA and Jülich locations. It is faster, especially if you have significantly more than 1 GB/s bandwidth. It requires a valid [GRID certificate](#) and installation of the [GRID srm software](#). NB There is an [alternative installation that does not require root privileges](#). Contact Science Support if you think you might need a GRID account but it can not be provided by your own institute. An example command line would be:

```
srncp -server_mode=passive -copyjobfile=srm.txt
```

to retrieve all requested files contained in srm.txt or e.g.

```
srncp -server_mode=passive srm://lofar-srm.juelich.de:8443/pnfs/fz-  
juelich.de/data/lofar/ops/projects/commissioning2012/file.tar  
file:////data/files/file.tar
```

to retrieve a single file. You need `--server_mode=passive` if you are behind a firewall or on an internal network. Omitting this option may result in improved transfer speed as it will attempt to use multiple streams when retrieving a file. An alternative strategy to improve the overall transfer speed is to run multiple srncp requests in parallel, e.g. by splitting the provided srm.txt file and feeding the partial lists to separate srncp commands.

Troubleshooting

- If you download files with http/wget and then have trouble extracting the data from the tar file, check if the files are much smaller than you expect. Something might have gone wrong with the transfer. One thing you can do to check, is just try to read the tar file with something like `less`. Instead of the data, it might contain an error. Depending on the error you might need to contact Science Support.
- We have seen the error “All Ready slots are taken and Ready Thread Queue is full”, which means the system is overloaded and you should try again in a few hours.

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