# SCARF Web Portal – A quick guide

To login to SCARF portal, you don't need any additional accounts. If you are registered to use SCARF, you should be able to login. The URL is <a href="http://portal.scarf.rl.ac.uk">http://portal.scarf.rl.ac.uk</a>

As there are two types of users that access SCARF, so there are two different types of login methods.

- 1) Login using STFC federal ID. This option is for users who are internal to STFC
- 2) Login using x509 certificate. This option is for external users who currently login using GSISSH term or other mechanisms.





**SCARF Portal Welcome page** 

### SCARF Portal User guide

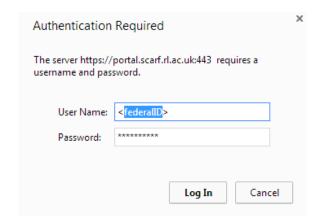
Once you click on the relevant button, you may see a message similar to that below depending on which browser you are using to access the portal.



Certificate not trusted warning screen

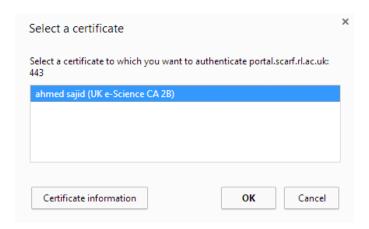
This screen can safely be ignore and you can continue the login process by clicking on "Proceed anyway".

If you are logging in using your federal ID and password, you will see a similar pop-up to the one below.



Federal ID prompt pop-up

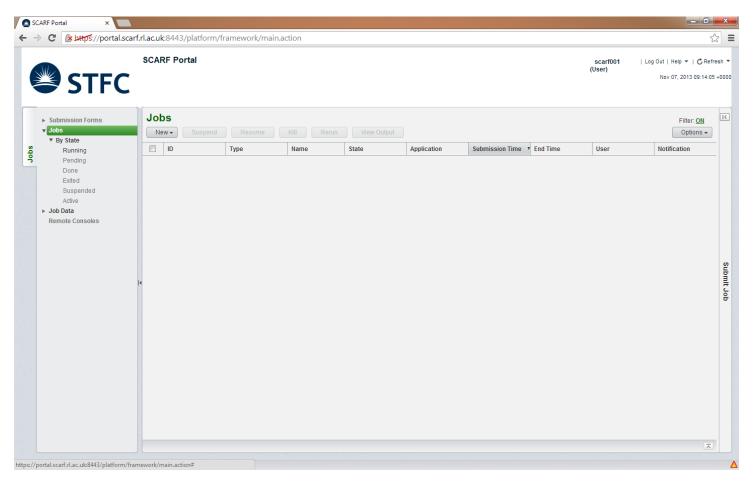
If you wish to login using your x509 certificate, you need to make sure is that your certificate is loaded in your browser. You will see a pop-up similar to the following one:



Select a certificate pop-up

## **Submitting job**

Once your authentication is successful, you should be able to see the screen below.

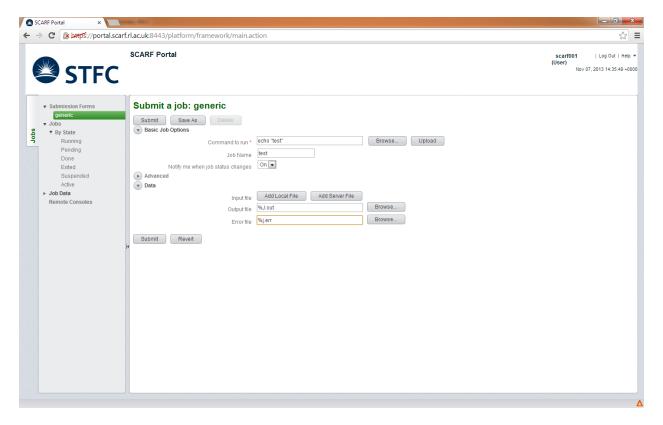


**SCARF Portal screen** 

If you have any jobs submitted to the queue you can see them by clicking on the relevant state.

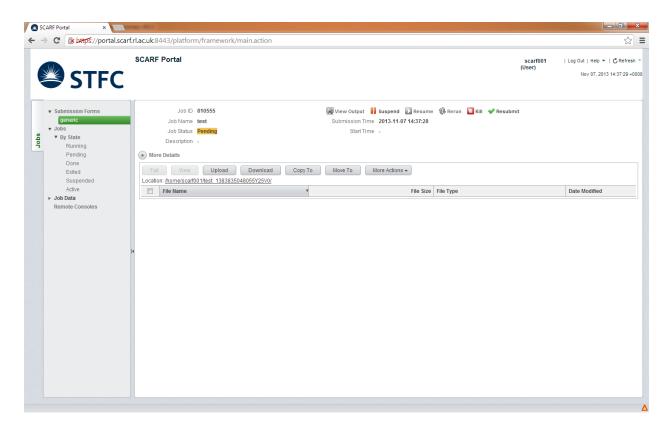
A number of templates are provided under Submission Forms in the menu on the left hand side. If the job does not match any of the application specific templates then the generic template should be used.

The image below shows how bsub -J test -o %J.out -e %J.err echo "test" which submits a very simple job would be implemented in the portal

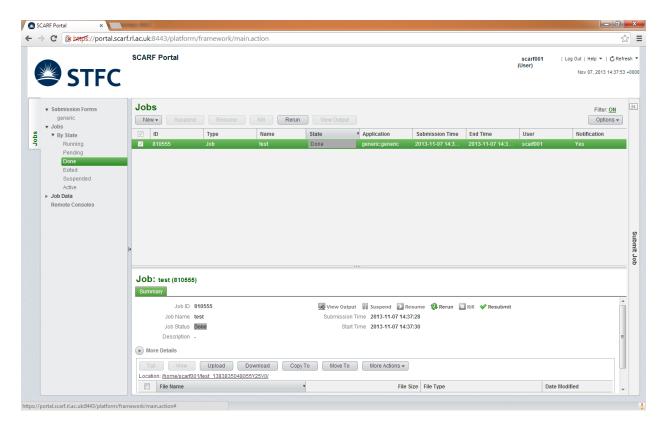


Job example - Submission page

### SCARF Portal User guide



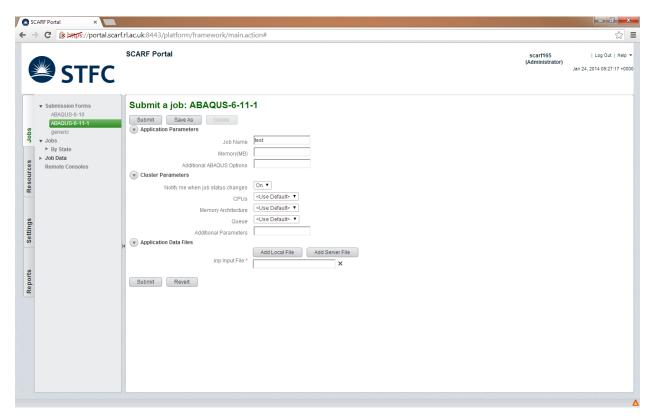
Job example – showing the status of job



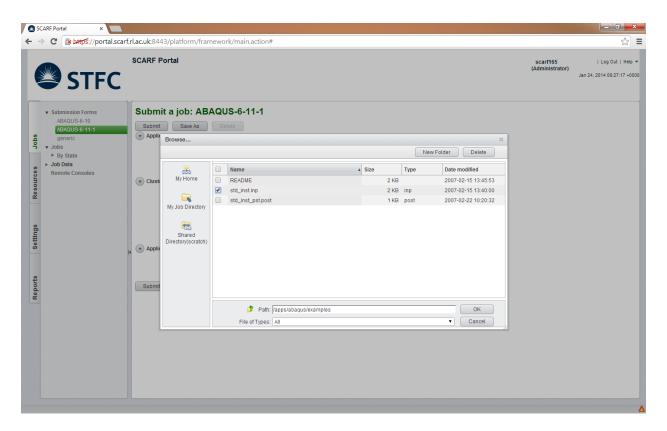
Job example – showing completed job

## **Abaqus Example:**

There are several Abaqus job submission forms corresponding to the different versions available on SCARF.

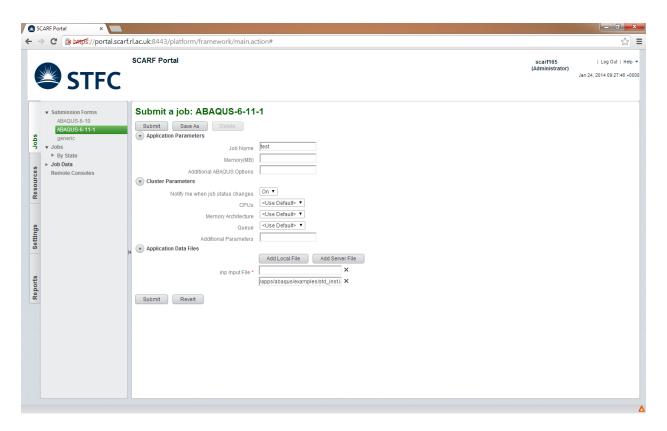


Abaqus job submission form



**Selecting Input file** 

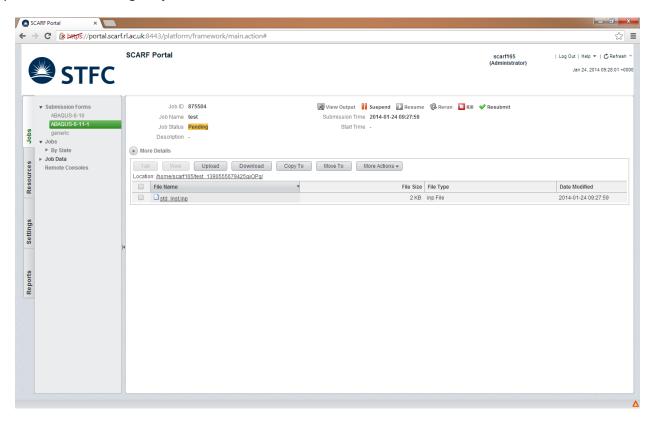
You can either upload file from your machine by clicking on "Add Local File" or use one that already exists on SCARF by clicking on "Add Server File". In the screenshot shown, the example input file is chosen located under /apps/abaqus/examples.



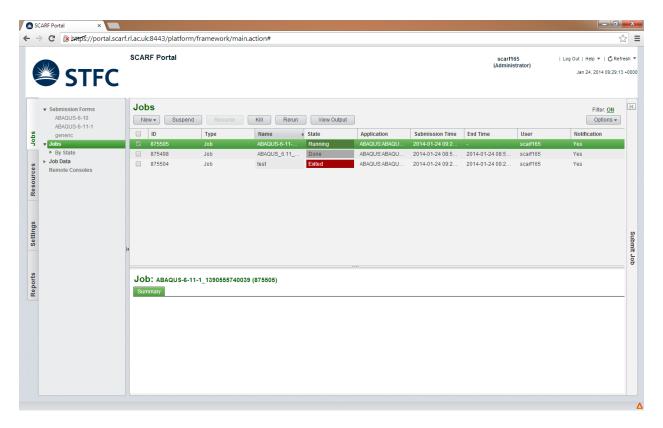
Abaqus job submission form

If no additional parameters are specified, the job will be submitted with the default ones.

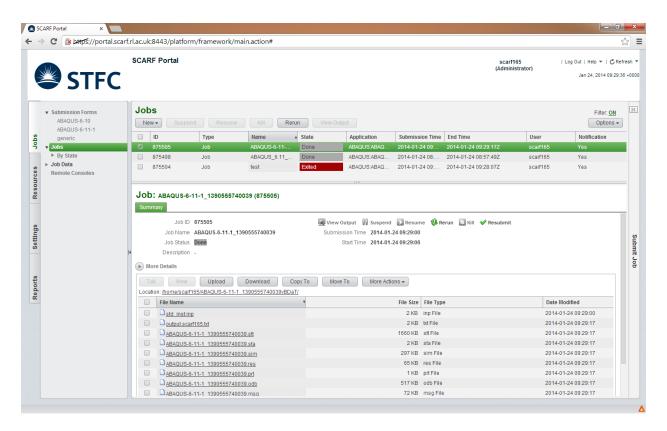
The following screen appears after submitting the job.



Job pending status page



Job status main page



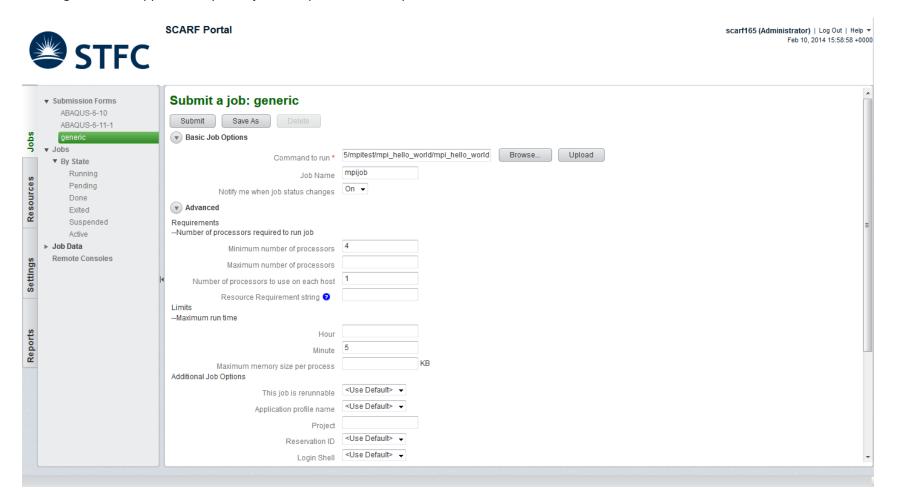
Job status page with output files

After the job gets completed you can view the output files by clicking on the job id from the list.

If you want a submission form created, do send us an email and we will be happy to help.

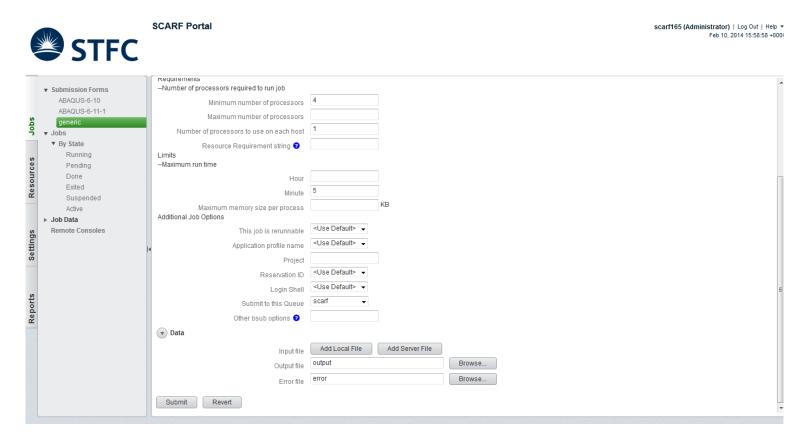
### **Submitting MPI job:**

In addtion to generic and application specific jobs, the portal also accepts MPIJobs.



MPI job submission page

To submit mpijob the command is, /opt/platform\_mpi/bin/mpirun -lsf -np <numberofprocesses> <mpicommand>

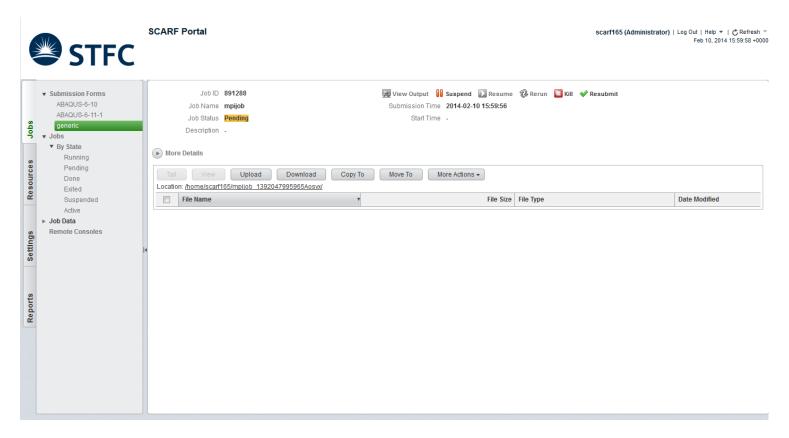


MPI job submission page - Advanced options

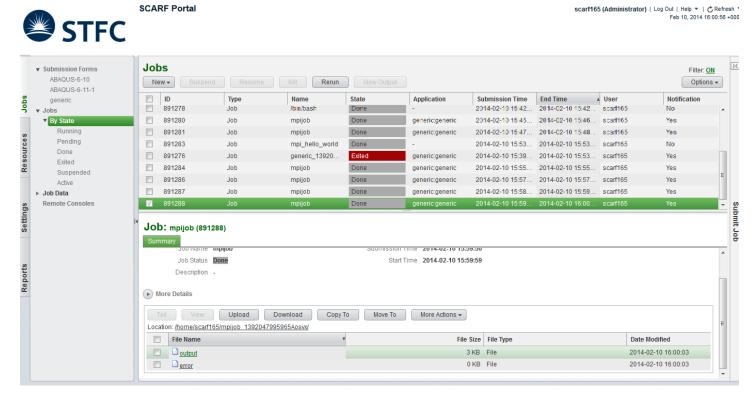
The advanced section of job submission can be expanded to specify extra arguments. For example, selecting the number of job slots/processors required to run the job, run time of the job or how many job slots to use per host. In this particular example 4 processors are being requested, 1 per host.

There will not be any output or error files generated unless specified during the submission process.

In other bsub options you can specify '-x' for exclusive access, if needed.



Job pending status page



Job status page with output files

#### Following is the output file from the submitted job.

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```
</home/scarf165/mpijob 1392047995965Aosvx> was used as the working directory.
Started at Mon Feb 10 \overline{15:59:59} 2014
Results reported at Mon Feb 10 16:00:03 2014
Your job looked like:
# LSBATCH: User input
/opt/platform mpi/bin/mpirun -lsf -np 4 /home/escq/scarf165/mpitest/mpi hello world/mpi hello world
_____
Successfully completed.
Resource usage summary:
   CPU time : 10.68 sec.
   Max Memory : 2 MB
   Max Swap : 24 MB
   Max Processes : 1
   Max Threads : 1
The output (if any) follows:
Hello world from processor cn214.scarf.rl.ac.uk, rank 0 out of 4 processors
Hello world from processor cn228.scarf.rl.ac.uk, rank 1 out of 4 processors
Hello world from processor cn212.scarf.rl.ac.uk, rank 2 out of 4 processors
Hello world from processor cn238.scarf.rl.ac.uk, rank 3 out of 4 processors
PS:
Read file <error> for stderr output of this job.
```

As the output shows, the job used 4 processors and each of them was on a different system.