

PowerOmics FAQ

How to Use PowerOmics

[Getting Started on PowerOmics](#) : An overview of po.rice.edu including a description of the system, its filesystems and quotas, example job submission scripts, instructions on how to customize your environment, and information on getting help.

[How do I get a research account?](#) Step-by-step instructions on how to get a research sponsor account for faculty, or a login account for Rice users and guests of Rice.

[How do I get a class account?](#) Step-by-step instructions for faculty and students on how to set up accounts for a class.

[How do I use the system for a class?](#) Guide for students and instructors who are using the system for a class.

[How do I use Linux?](#) Basic description of Linux and links to Linux tutorials and resources.

[How do I get help?](#) Web form for requesting help.

Policies

[User Fee Schedule and Explanation](#)

[Account Retention, Data Retention, and Data Backup, Recovery, and Archiving](#)

[Software Installation Policy](#)

Access to PowerOmics

[What is the password for my new account?](#)

[How do I change my password?](#)

[How do I login using SSH from Unix/Linux?](#)

[How do I login using SSH from Windows?](#)

[How do I login from off-campus?](#)

[How do I transfer files to the cluster?](#)

[How do I transfer large data sets from off-campus?](#)

Submitting Jobs and Job Scheduling

[How do I submit a job with SLURM?](#)

[Submitting Jobs on NOTS with SLURM?](#)

[How do I submit a job to a specific partition via SLURM?](#)

[How do I use the Interactive partition via SLURM?](#)

[How do I run graphical applications on a compute node via SLURM?](#)

[How do I enable or disable email notifications for my jobs using SLURM?](#)

[How do I submit a parallel \(MPI\) job with SLURM?](#)

[How do I submit a job with mpiexec or mpirun via SLURM?](#)

[How do I force jobs to run in sequence via SLURM?](#)

[How do I submit large numbers of single core jobs via SLURM?](#)

[How do I get exclusive access to a node via SLURM?](#)

[How do I set environment variables with module in SLURM batch scripts?](#)

Software Development, Performance, and Debugging

[Building, Porting, and Deploying Linux Applications on Power Architecture](#)

[Power 8 Performance FAQ](#)

[Why is the default compiler mode 32 bit?](#)

[How Do I Compile My Program?](#)

[Handling Symmetric Multithreading \(SMT\) on PowerOmics](#)

[How Do I use BLAS and LAPACK Libraries on PowerOmics?](#)

[Which Filesystem Should I Use for Job Output?](#)

[How Do I Use Scratch Storage?](#)

[Why Is My Program Running Slow?](#)

[How Do I Improve Job Efficiency and Performance?](#)

[How Do I Use HPCToolkit to Profile the Performance of My Code?](#)

[How Do I Ensure My Job Has Enough Memory To Run Using SLURM?](#)

[How do I determine how much memory my job needs?](#)

[How do I change the stack size for my processes?](#)

[How do I set environment variables with module in batch scripts?](#)

Software Tools

Nothing at the moment.

General HowTo Questions and Answers

[How do I use Linux?](#)

[How do I change my password?](#)

[How do I use /projects?](#)

[How do I use passwordless SSH?](#)

[How do I change my default shell?](#)

[How do I change my stack size for my processes?](#)

[How do I use turnin to submit my homework assignment?](#)