

## BioLockJ commands are located under \$BLJ/script

Command	Description
<a href="#">biolockj</a> [config_path]	Start a pipeline using the [[Configuration]] properties in [config_path]. Pipeline output directory is created under <a href="#">\$BLJ_PROJ</a> .
<a href="#">blj_build</a>	Run <a href="#">build.xml</a> ant script to build BioLockJ.jar from Java source code.
<a href="#">blj_complete</a>	Manually completes the current module and pipeline status.
<a href="#">blj_config</a>	The <a href="#">install</a> script updates ~/.bash_profile to call <a href="#">blj_config</a> . Adds BioLockJ [[Commands]] into your \$PATH & sets program variables: \$BLJ: BioLockJ application directory. \$BLJ_SCRIPT: BioLockJ script directory containing executable script files. \$BLJ_PROJ: Root pipeline directory used in multiple [[Commands]].
<a href="#">blj_downlaod</a>	If on cluster, print command syntax to download current or most recent <a href="#">\$BLJ_PROJ</a> pipeline analysis to your local workstation directory: <i>pipeline.downloadDir</i> .
<a href="#">blj_functions</a>	This script contains common functions used in BioLockJ.
<a href="#">blj_go</a>	Go to most recent <a href="#">\$BLJ_PROJ</a> pipeline & list contents.
<a href="#">blj_log</a>	Tail last 1K lines from current or most recent <a href="#">\$BLJ_PROJ</a> pipeline log file.
<a href="#">blj_reset</a>	Reset pipeline status to incomplete. If restarted, execution will start with the current module.
<a href="#">blj_summary</a>	Print current or most recent <a href="#">\$BLJ_PROJ</a> pipeline summary.