NOTE: This information has been superseded by a newer version of Skyline. For current documentation, run SkylineRunner.exe or SkylineCmd.exe without any command-line arguments. The same information can be found in the Skyline user interface at Help > Documentation > Command Line.

Skyline Command-Line Interface

The command-line interface for Skyline is called SkylineRunner.exe. It is a tiny shim executable less than 10 KB in size. It requires a full Skyline installation on the computer on which it is run. SkylineRunner simply starts Skyline running without any user interface, pipes the parameter options from the command-line to the running Skyline instance, and prints output from Skyline to the command console. At present, only one instance of SkylineRunner may be executed at a time.

The Skyline instance started by SkylineRunner is independent of any other instances that may already be running on the same machine. It is not necessary to have a visible instance of Skyline running on your computer for SkylineRunner to work.

SkylineRunner is intended for automating tasks, such as quality control, scheduling and refinement, during acquisition. SkylineRunner can open a Skyline document, import a newly acquired data file, and export a report or new method.

Parameter Options:

The current implementation of SkylineRunner offers the following options:

General input/output

--in=path/to/file.sky	Open a Skyline file
--save	Saves any changes to the file
--out=path/to/file.sky	Same as save except writes to the specified file
--batch-commands =path/to/file	Runs a file line by line treating each line like a SkylineRunner input. Useful for automating the execution of multiple commands. The open Skyline file remains active through all commands.
--dir=path/to/folder	Used to specify a default root directory for all other path arguments, other than the directory in which the command is run.
--timestamp	All logging output will be preceded by a time and date.

Until the section titled Settings Customization all other command line parameters rely on the "in" parameter because they all rely on having a Skyline document open.

Importing results replicates

--import-file=path/to/file	Attach a replicate to the open document
--import-replicate-name=<name>	Name to give the new replicate in an –import-file

	operation.
--import-optimizing=<ce | dp>	Indicates the data being imported contains extra transitions for detecting optimal collision energy or declustering potential.
--import-append	Append the import-file to the given replicate. This is an intention check in case the document already has a replicate with the given name. By default this is set to false. This option only works with the –import-file option.
--import-all=path/to/folder	Imports from a folder all files or sub-folders which are not already in the document, naming each with the base-name of the file or sub-folder, unless the --import-naming-pattern parameter is also supplied.
--import-naming-pattern=reg-ex	A regular expression from which the first group will be used to name replicates in an --import-all operation (e.g. [^_]_(.*) for everything after the first underscore).
--import-before=<date>	When importing from a folder, only import from files with modified time before the given date.
--import-on-or-after=<date>	When importing from a folder, only import from files with modified time after the given date.
--import-no-join	Import results files to individual .skyd files without joining them to the main document .skyd file. This is useful for distributed processing, as on HPC cluster.
--import-lockmass-positive	Waters lockmass correction *m/z* for positive ion scans.
--import-lockmass-negative	Waters lockmass correction *m/z* for negative ion scans.
--import-lockmass-tolerance	Waters lockmass correction tolerance (Da).

Reintegrate with advanced peak picking models

--reintegrate-model-name=<name>	The name of a scoring model to use for the reintegrate operation. The model can either be pre-defined (e.g. using the Edit > Refine > Reintegrate form) or created automatically during this operation by using --reintegrate-create-model.
--reintegrate-create-model	This option will cause a new model to be created, using the mProphet algorithm with all

	available scores for the results found in the document. (requires --reintegrate-model-name)
--reintegrate-annotate-scoring	Peaks will be annotated with q value and score annotations. (requires --reintegrate-model-name)
--reintegrate-overwrite-peaks	Existing manually integrated peaks will be overwritten with peaks chosen by the reintegration model. (requires --reintegrate-model-name)

Removing results replicates

--remove-before=<date>	Remove all results from the open document with an acquired time before the given date.
--remove-all	Remove all results from the open document.

Importing FASTA files

--import-fasta=path/to/file	Import a FASTA file into the open document.
--keep-empty-proteins	Keeps any empty proteins in the open document after importing a FASTA file.

Importing peptide searches

--import-search-file=path/to/file	Import a peptide search results file into the open document, building a document-specific spectral library. This may be specified multiple times for multiple files. Use –import-fasta argument to add matched peptides as targets.
--import-search-cutoff-score=<cutoff>	Defines a cutoff score (between 0 and 1) to be used when building a spectral library from peptide search results files, where 1 is for highest confidence matches and 0 includes everything. [default 0.95]
--import-search-add-mods	Adds all modifications found in peptide search results files to the open document.

Adding spectral libraries

--add-library-path=path/to/file	Specify a spectral library to be added to the open document.
--add-library-name=<name>	Name to give the spectral library in an –add-library-path operation.

Exporting reports

--report-name=<name>	The name of a report to export as it appears in the Skyline Export Report form
--report-file=path/to/file.csv	The path to export the report to. Required if --

	report-name is specified.
--report-format=<CSV | TSV>	CSV for comma-separated reports (or semicolon separated, depending on your localization) or TSV for tab separated reports [default CSV]
--report-invariant	Exports the report with the “Invariant” language setting, using English (US) number formats and header text without spaces, ideal for use with the R statistical programming environment.

Exporting chromatograms

--chromatogram-file=path/to/file.tsv	The path to the tab delimited file where to export chromatograms.
--chromatogram-precursors	Export precursor ion chromatograms.
--chromatogram-products	Export product ion chromatograms.
--chromatogram-base-peaks	Export base peak chromatograms.
--chromatogram-tics	Export total ion current chromatograms.

Exporting transition lists

--exp-translist-instrument=<AB Sciex | Agilent | Thermo | Waters>	Export a transition list. This option is required for exporting a transition list and has no default. This option cannot be used with --exp-method-instrument, because you cannot export a method and transition list simultaneously.

Vendor-specific transition list options

AB Sciex	--exp-dwell-time=<millis>	Dwell time per transition. This option is required for unscheduled transition lists.
Agilent	--exp-dwell-time=<millis>	Same as above.
Thermo Scientific	--exp-add-energy-ramp	Adds an extra column for energy ramp to the transition list. Optional. Defaults to false.
Waters	--exp-run-length=<minutes>	Run length of the entire gradient in minutes. This option is required for unscheduled experiments.

Exporting native instrument methods

--exp-method-instrument=<AB SCIEX QTRAP |	Export a method. This option is

Agilent 6400 Series | Thermo TSQ | Thermo LTQ | Waters Xevo | Waters Quattro Premier>	required for exporting a method and has no default. This option cannot be used with --exp-translist-instrument, because you cannot export a method and transition list simultaneously.
--exp-template=path/to/file.meth|exp|dam|m	Path of the method template. This can be a file or a directory depending on your instrument. This option is required for method export.

Vendor-specific method options

AB Sciex Qtrap	--exp-dwell-time=<millis>	Dwell time per transition. This option is required for standard (unscheduled) methods.
Agilent (all instruments)	--exp-dwell-time=<millis>	Same as above
Thermo (all but LTQ)	--exp-run-length=<minutes>	Run length of the entire gradient in minutes. This option is required for unscheduled experiments.
Waters (all instruments)	--exp-run-length=<minutes>	Same as run length above

Method and transition list options

--exp-file=path/to/file	Path to the method or transition list file (or directory) to export to. This option is required for method and transition list export.
--exp-strategy=<single | protein | buckets>	Strategy for dividing a method into injections. The default is “single”.
--exp-method-type=<standard | scheduled | triggered>	Sets a standard, scheduled or triggered method. The default is “standard”.
--exp-max-trans=<number>	Maximum number of transitions per injection for export strategies “protein” and “buckets” OR maximum number of simultaneous transitions for scheduled methods. The default is 100.
--exp-optimizing=<ce | dp>	Export a method with extra transitions for finding optimal collision energy or

	declustering potential.
--exp-scheduling-replicate=<name>	Use this only if creating a scheduled or triggered method. The default is to schedule based on an average of all replicates, but if you specify one, the method will be scheduled based on that replicate.
--exp-ignore-proteins	Ignore protein boundaries in creating methods.
--exp-primary-count=<number>	For --exp-method-type=triggered specifies the number of transitions to make primary.

Publishing to Panorama

--panorama-server=<server url>	URL of the Panorama server to which the --in file is to be published. The URL should contain the protocol (http or https), hostname and port, if required. Examples: https://panoramaweb.org or http://localhost:8080
--panorama-username=<username>	The username/email address for a user with access to publish to the Panorama server.
--panorama-password=<password>	The password for a user with access to publish to the Panorama server.
--panorama-folder=path/to/folder	The path to a folder on the Panorama server to which the file is to be published (e.g. MyProject/MyFolder).

If the parameters above are used along with parameters to import results files into the document (--import-file or –import-all) the Skyline document will be uploaded to the given Panorama server only if new results are added to the document.

Settings Customization

The below commands do not rely on the "in" parameter because they modify the user settings that are independent of a specific Skyline document.

--full-scan-precursor-res=<resolving power>	Resolving power of the precursor mass analyzer.

--full-scan-precursor-res-mz=<m/z value>	The m/z value at which the precursor mass analyzer resolving power is specified. (applies only to orbitrap and ft_icr mass analyzers)
--full-scan-product_res=<resolving power>	Resolving power of the product mass analyzer.
--full-scan-precursor-res-mz=<m/z value>	The m/z value at which the product mass analyzer resolving power is specified. (applies only to orbitrap and ft_icr mass analyzers)
--full-scan-rt-filter-tolerance=<minutes>	The number of minutes on either side of the predicted time or MS/MS IDs, i.e. ± minutes. Defaults to.
--tool-arguments="<arguments>"	Optional command-line arguments for the tool to be added, used when the tool is executed. (Not applicable to web URL commands)
--tool-initial-dir=path/to/dir	Optional initial directory for the tool to be added, used when the tool is executed. (Not applicable to web URL commands)
--tool-conflict-resolution=<overwrite | skip>	Tells the SkylineRunner how to resolve a tool name conflict, by either overwriting an existing installation or skipping installation of the new tool.
--tool-report=<report-name>	The name of a report in the settings to use as the input report for the tool.
--tool-output-to-immediate-window	When present the tool output is piped to the Immediate Window at runtime.
--report-add=path/to/file.skyr	Adds the report formats from a skyr file. If there are name conflicts the --report-conflict-resolution parameter is required.
--report-conflict-resolution=<overwrite | skip>	Tells the SkylineRunner how to resolve a report name conflict, by either overwriting the existing report or skipping adding the new report.
--tool-add-zip=path/to/file.zip	Import tools from a tool installation ZIP file.
--tool-zip-conflict-resolution=<overwrite |	Specify whether tool conflicts from the provided ZIP file should be resolved by

parallel>	overwriting or installing in parallel. This is for conflicts related to tool versioning and report names.
--tool-zip-overwrite-annotations=<true | false>	Specify whether conflicting custom annotations from the provided ZIP file should overwrite (true) existing annotations or be skipped (false).
--tool-program-macro=<programTitle> Or --tool-program-macro=<programTitle>,<programVersion> Eg. --tool-program-macro=R,2.15.2	Specifies a program title and version to use with the –tool-program-path command. Together these commands are for importing tools from a ZIP file that use the $(ProgramPath()) macro as their command. For more information see the documentation on External Tools.
--tool-program-path=path/to/file	Specifies the path to an executable on the local machine for the program title and version specified by the –tool-program-macro flag.
--tool-ignore-required-packages	Ignore required packages when installing a tool from a ZIP file.