

## PerkinElmer Wallac1445



**Manufacturer:** PerkinElmer Life Sciences  
**Model Number:** Wallac1445  
**Web Address:** [www.perkinelmer.com](http://www.perkinelmer.com)

Wallac1445 is a PE Sciex mass spectrometer which is used to analyze samples.

### Mass Spectrometer: Commands

▶ **SubmitBatch( )** - Submits all samples into Analyst's queue for acquisition. If the queue status is 'waiting', the acquisition will begin immediately.

▶ **GetAutosampler( )** - Retrieve the current type of the autosampler.

▶ **SetAutosampler( autosampler )** - Set the type of the autosampler.

autosampler	Integer	Type of the autosampler. -1: None, 0: PE200, 200: Gilson215, 201: Gilson233, 400: HP1100
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▶ **SetScriptName( script )** - Set the full path for the batch script including the file extension.

script	String	Full path for the batch script.
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▶ **OpenBatch( batchFile )** - Creates the batch object based on the specified batch file. You must specify the full path-name of the file including the extension ('.dab').

batchFile	String	Name of the batch file.
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▶ **SaveBatch( batchFile )** - Saves the batch object into the specified batch file. You must specify the full path-name of the file including the extension ('.dab').

batchFile	String	Name of the batch file.
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▶ **CreateBatch( sampleNumber )** - Create a new batch on the analyst server.

sampleNumber	Integer	Number of samples in the batch.
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▶ **CreateSets( setNumber )** - Create the specified number of sets on the Analyst server.

setNumber	Integer	Number of sets in the batch.
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▶ **SetBatchName( batchName )** - Set the name of the current batch.

batchName	String	Name of the current batch.
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▶ **SetProjectName( projectName )** - Set the name of the current project.

projectName	String	Name of the current project.
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▶ **SetOwnerName( ownerName )** - Set the name of the current owner of the batch.

ownerName	String	Name of the current owner of the batch.
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▶ **SetAcquisFolder( directory )** - Set the directory in which the acquisition methods are located, including the trailing '\' of the directory name.

directory	String	Directory in which the acquisition methods are located.
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▶ **SetOutputFolder( directory )** - Set the directory in which data will be acquired including the trailing '\' of the directory name. This should be the 'Data' folder of the associated project.

directory	String	Directory in which the data files are located.
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▶ **SetSample( index, sampleName, sampleID, rackCode, rackPosition, plateType, platePosition, vialPosition, sampleType, methodName, dataFile, setNumber )** - Set the sample information for the current batch.

index	Integer	Sample index.
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sampleName	String	Name of the sample.
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sampleID	String	Unique identifier for the sample.
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rackCode	String	Type of the autosampler rack.
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rackPosition	Integer	Number of the autosampler rack.
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plateType	String	Type of the microplate.
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platePosition	Integer	Index of the microplate on the rack.
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vialPosition	String	Index of the well on the microplate.
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sampleType	Integer	Sample type, when quantitating. The type is one of: '0' for unknowns, '1' for standards, '2' for QCs, '3' for blanks, '4' for double blanks and '5' for solvents.
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methodName	String	Acquisition method for the sample.
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dataFile	String	Name of the data file for the specified sample, including the file extension ('.wiff'). If you wish to place data in a sub-folder of the project's 'Data' folder you can specify a '\' separated name, for example 'SubFolder\MyData.wiff'.
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setNumber	Integer	Set number associated with the specified sample.
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▶ **SetSet( index, setName, acquisMethod, quantMethod )** - Set the set information for the current batch.

index	Integer	Set index.
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setName	String	Name of the set.
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acquisMethod	String	Acquisition method for the set.
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quantMethod	String	Quantitation method for the set.
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