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# Command Reference: WritePenmanMonteithToStateCU()

**Write Penman-Monteith crop coefficients data to a StateCU file**

**StateCU Command**

Version 3.10.00, 2010-04-02

The `WritePenmanMonteithToStateCU()` command writes Penman-Monteith crop coefficients that have been defined to a StateCU Penman-Monteith crop coefficients file.

The following dialog is used to edit the command and illustrates the syntax of the command.

**Edit WritePenmanMonteithToStateCU() Command**

This command writes the StateCU Penman-Monteith data to a StateCU Penman-Monteith file.  
It is recommended that the file be specified using a path relative to the working directory.  
The working directory is:  
C:\Develop\StateDMI\_SourceBuild\StateDMI\test\regression\UserManualRef\ReadPenmanMonteithFromHydroBase

Output file:

Precision:  Optional - digits after decimal (default=3).

Write how:  Optional - indicate whether to overwrite/update (default=OverwriteFile).

Command:  

```
WritePenmanMonteithToStateCU (OutputFile="rg2007.kpm")
```

WritePenmanMonteithToStateCU

**WritePenmanMonteithToStateCU() Command Editor**

The command syntax is as follows:

```
WritePenmanMonteithToStateCU(Parameter=value,...)
```

### Command Parameters

Parameter	Description	Default
OutputFile	The name of the output file to write, surrounded by double quotes.	None – must be specified.
Precision	The number of digits after the decimal for curve values, used for backward compatibility with older file versions.	3
WriteHow	OverwriteFile if the file should be overwritten or UpdateFile if the file should be updated, resulting in the previous header being carried forward.	OverwriteFile

The following example command file illustrates how to read Penman-Monteith coefficients from HydroBase, sort the data, create a StateCU file, and check the results:

```
StartLog(LogFile="Crops_KPM.StateDMI.log")
#
# StateDMI commands to create the Penman-Monteith crop coefficients file
#
# Step 1 - read data from HydroBase
#
# Read the general ASCE standardized coefficients
ReadPenmanMonteithFromHydroBase(PenmanMonteithMethod="PENMAN-MONTEITH_ALFALFA")
#
# Step 3 - write the file
#
SortPenmanMonteith()
WritePenmanMonteithToStateCU(OutputFile="rg2007.kpm")
#
# Check the results
#
CheckPenmanMonteith(ID="*")
WriteCheckFile(OutputFile="Crops_KPM.StateDMI.check.html")
```