

# Phase Command-Line Pharmacophore Modeling

This document summarizes the complete command-line pharmacophore model development workflow. The starting point is one or more Maestro files containing multiconformer models for the ligands of interest. A Phase project is created from these ligands, after which a series of steps is followed, directly analogous to the Develop Pharmacophore Model workflow in Maestro. The full description of the commands is given in [Chapter 12](#) of the *Phase User Manual*. On Windows, you can run these commands in a Schrödinger Command Prompt window, which you open from the **Start** menu; you do not need to include `$SCHRODINGER` or `$SCHRODINGER/utilities` in the command when running in this window.

## Create/Add to a Project:

```
$SCHRODINGER/utilities/pharm_project {-new|-add} -mae maefile [-ignoreTitles] [-stereo]
    [-act actProp] [-conf confProp]
```

## Modify Master Data:

```
$SCHRODINGER/utilities/pharm_data [-log|-exp] [-multiply scale] [-commit] [-restore]
    [-active aboveVal] [-inactive belowVal] [-train numTrain] [-rand seed] [-pharm_set] [-sort]]]
    [-conf confProp] [-group [titles]|-ungroup]
```

## Create Pharmacophore Sites:

```
$SCHRODINGER/utilities/pharm_create_sites -setup [-fd fdFile]
$SCHRODINGER/phase_feature create_sites [job-options]
$SCHRODINGER/utilities/pharm_create_sites -cleanup
```

## Find Common Pharmacophores:

```
$SCHRODINGER/utilities/pharm_find_common -setup -sites numSites [-match minMatch] [-freq]
$SCHRODINGER/phase_partition find_common [job-options]
$SCHRODINGER/phase_multiPartition find_common [-minSites n] [job-options]
$SCHRODINGER/utilities/pharm_find_common -cleanup
```

## Score Hypotheses with Respect to Actives:

```
$SCHRODINGER/utilities/pharm_score_actives -setup [-tol] [-act|-prop weight] [-conf weight]
$SCHRODINGER/phase_scoring score_actives [job-options]
$SCHRODINGER/utilities/pharm_score_actives -cleanup
```

## Score Hypotheses with Respect to Inactives:

```
$SCHRODINGER/utilities/pharm_score_inactives -setup -w weight
$SCHRODINGER/phase_inactive score_inactives [job-options]
$SCHRODINGER/utilities/pharm_score_inactives -cleanup
```

## Cluster Hypotheses by Geometric Similarity:

```
$SCHRODINGER/utilities/pharm_cluster_hypotheses -setup [-link method]
$SCHRODINGER/phase_hypoCluster cluster_hypotheses [job-options]
$SCHRODINGER/utilities/pharm_cluster_hypotheses -cleanup [-report level]
```

## Build QSAR Models:

```
$SCHRODINGER/utilities/pharm_build_qsar -setup [-model type] [-grid spacing] [-factors n]
    [-tvalue tmin] [-exclude n] [-rand seed]] [-atomTypeVol]
$SCHRODINGER/phase_multiQsar build_qsar [job-options]
$SCHRODINGER/utilities/pharm_build_qsar -cleanup
```

**Preserve Project Data in a Tar Archive:**

```
$SCHRODINGER/utilities/pharm_archive -step stepName -tar tarFile [-gzip]
```

Once pharmacophore hypotheses and QSAR models have been developed, a number of other command-line utilities may be run:

**Align Project Ligands or New Molecules to a Pharmacophore Hypothesis:**

```
$SCHRODINGER/phase_find_matches [options]
```

**Align/Merge a Pair of Hypotheses:**

```
$SCHRODINGER/utilities/align_hypoPair -fixed fixedHypoID -free freeHypoID -new newHypoID
  [-dtol deltaDist] [-match minSites] [-mix] [-equiv equivFile] [-merge method] [-keep maxAlign]
  [-rmsd rmsdFile] [-sim [simFile] [-rmsdMax rmsdMax]]
```

**Create Excluded Volumes Automatically:**

```
$SCHRODINGER/utilities/create_xvolShell -hypo hypoID [-ref maeFile] [-buff dist] [-grid spacing]
  [-partial atoms [-mask dist]] [-hydrogens] [-append] [-cut]
$SCHRODINGER/utilities/create_xvolClash -hypo hypoID -pos maeFilePos -neg maeFileNeg
  [-freq minClash] [-buff dist] [-grid spacing] [-hydrogens] [-append]
$SCHRODINGER/utilities/create_xvolReceptor -hypo hypoID -receptor maeFileRec
  [-ligand maeFileLig] [-radius r|-rprop rpropName] [-scale s|-sprop spropName]
  [-buff dmin] [-limit dmax] [-hydrogens] [-append]
```

**Analyze QSAR Predictions within Hit Files:**

```
$SCHRODINGER/utilities/phase_qsar_stats -hypo hypoID [-hits hitFile [-act actProp] [-plot csvFile]]
  [-out outFile]
```

**Visualize QSAR Models:**

```
$SCHRODINGER/utilities/qsarVis -hyp hypoID -mol molname [-volume_qsar] [-class name]
  [-pc posThresh] [-nc negThresh] [-trans value] [-npls plsFactors]
```

In the above commands, *job-options* represents the standard Job Control options:

-HOST <i>host</i>	Run the job on the specified host.
-LOCAL	Run the job in the current directory, rather than in a temporary scratch directory.
-TMPDIR <i>tmpdir</i>	Use <i>tmpdir</i> for temporary files.
-WAIT	Do not return control to the shell until the job finishes.
-INTERVAL <i>N</i>	Interval in seconds between output updates.
-NICE	Run the job at reduced priority.