



## Alphabetical list of Ahelp files for CIAO 3.4

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	<b>Topic</b>	<b>Context</b>	<b>Summary</b>
<b>A</b>	<a href="#">abs</a>	<a href="#">slangrtl</a>	Compute the absolute value of a number
	<a href="#">acisreadcorr</a>	<a href="#">tools</a>	Flag and relocate out-of-time CCD events
	<a href="#">acisspec</a>	<a href="#">tools</a>	(1) Extract source and/or background ACIS imaging spectra for both point-like and extended sources; (2) coadd ACIS spectra; (3) build weighted ARFs and RMFs.
	<a href="#">acis_bkgrnd_lookup</a>	<a href="#">tools</a>	Find the matching ACIS "blank-sky" dataset for an observation
	<a href="#">acis_build_badpix</a>	<a href="#">tools</a>	Create an observation-specific bad-pixel file
	<a href="#">acis_classify_hotpix</a>	<a href="#">tools</a>	Determine whether a suspicious pixel is hot or affected by an afterglow.
	<a href="#">acis_detect_afterglow</a>	<a href="#">tools</a>	Identify and flag cosmic ray afterglows (L1)
	<a href="#">acis_expmap</a>	<a href="#">tools</a>	Generate ACIS exposure maps for celldetect recursive blocking
	<a href="#">acis_fef_lookup</a>	<a href="#">tools</a>	Find the FITS Embedded Function file for use by mkrmf
	<a href="#">acis_find_hotpix</a>	<a href="#">tools</a>	Identify pixels that have an unusually large (or small) number of events.
	<a href="#">acis_process_events</a>	<a href="#">tools</a>	Produce or update TIME, coordinates, PI, GRADE, and STATUS information in ACIS event files
	<a href="#">acis_run_hotpix</a>	<a href="#">tools</a>	Identify and flag "hot" pixels and cosmic-ray "afterglows."
	<a href="#">acis_set_arclib</a>	<a href="#">tools</a>	

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<a href="#">aconvolve</a>	<a href="#">tools</a>	Sets the bad pixel parameters of the ardlib file to the given file
<a href="#">acos</a>	<a href="#">slangrtl</a>	Convolve an N-dimensional image with a kernel
<a href="#">acos</a>	<a href="#">slangrtl</a>	Compute the inverse cosh of an number
<a href="#">acrosscorr</a>	<a href="#">tools</a>	Cross-correlate two N-dimensional images or autocorrelate an image
<a href="#">add_grating_orders</a>	<a href="#">tools</a>	Add positive and negative diffraction orders of a grating PHA spectra and the corresponding ARFs
<a href="#">add_grating_spectra</a>	<a href="#">tools</a>	Add two, source and background, grating PHA spectra, averages the corresponding ARFs, and group the coadded spectrum.
<a href="#">ahelp</a>	<a href="#">ahelp</a>	Access the CIAO help documentation.
<a href="#">analysis-menu</a>	<a href="#">gui</a>	The "Analysis" menu in CIAO GUIs allows users to run command-line tools.
<a href="#">analysis</a>	<a href="#">sherpa</a>	Specifies whether to analyze datasets in energy, wavelength, or channel space.
<a href="#">analyze_ltcv</a>	<a href="#">tools</a>	analyze_ltcv.sl – An algorithm for cleaning lightcurves
<a href="#">apowerspectrum</a>	<a href="#">tools</a>	Compute the power spectrum of an N-dimensional input array, or from two columns (independent/dependent variable) in an input file
<a href="#">append_to_slang_load_path</a>	<a href="#">slangrtl</a>	Append a directory to the load-path S-Lang function to find defined symbols (functions and variables)
<a href="#">apropos</a>	<a href="#">varmm</a>	
<a href="#">ardlib</a>	<a href="#">calibration</a>	Analysis Reference Data Library
<a href="#">arestore</a>	<a href="#">tools</a>	restore image resolution using deconvolution techniques
<a href="#">array_info</a>	<a href="#">slangrtl</a>	Returns information about an array
<a href="#">array_map</a>	<a href="#">slangrtl</a>	Apply a function to each element of an array
<a href="#">array_sort</a>	<a href="#">slangrtl</a>	Sort an array
<a href="#">array_to_bstring</a>	<a href="#">slangrtl</a>	Convert an array to a binary string
<a href="#">ascii2fits</a>	<a href="#">tools</a>	Convert simple ASCII files to FITS format files
<a href="#">asinh</a>	<a href="#">slangrtl</a>	

<a href="#"><u>asin</u></a>	<a href="#"><u>slangrtl</u></a>	Compute the inverse-sinh of an number
<a href="#"><u>asphist</u></a>	<a href="#"><u>tools</u></a>	Compute the arc-sine of an number Bin the aspect solution into a 3D histogram of duration vs pointing offset and roll offset.
<a href="#"><u>assoc delete key</u></a>	<a href="#"><u>slangrtl</u></a>	Delete a key from an Associative Array
<a href="#"><u>assoc get keys</u></a>	<a href="#"><u>slangrtl</u></a>	Return all the key names of an Associative Array
<a href="#"><u>assoc get values</u></a>	<a href="#"><u>slangrtl</u></a>	Return all the values of an Associative Array
<a href="#"><u>assoc key exists</u></a>	<a href="#"><u>slangrtl</u></a>	Check to see whether a key exists in an Associative Array
<a href="#"><u>atanh</u></a>	<a href="#"><u>slangrtl</u></a>	Compute the inverse-tanh of an number
<a href="#"><u>atan</u></a>	<a href="#"><u>slangrtl</u></a>	Compute the arc-tangent of an number
<a href="#"><u>atof</u></a>	<a href="#"><u>slangrtl</u></a>	Convert a string to a double precision number
<a href="#"><u>atten</u></a>	<a href="#"><u>sherpa</u></a>	Attenuation by ISM. Integration OFF.
<a href="#"><u>autoest</u></a>	<a href="#"><u>sherpa</u></a>	Automatic estimation of initial parameter values in Sherpa models
<a href="#"><u>autoload</u></a>	<a href="#"><u>slangrtl</u></a>	Load a function from a file
<a href="#"><u>autoname</u></a>	<a href="#"><u>concept</u></a>	Autonaming is a feature available in various tools for automatically naming an output file based upon the name of an input file.
<a href="#"><u>axbary</u></a>	<a href="#"><u>tools</u></a>	Apply barycentric corrections to event times, GTIs, and header values.
<a href="#"><u>axes</u></a>	<a href="#"><u>chips</u></a>	Specifies the appearance of the bounding box surrounding a drawing area. The command AXIS is equivalent.

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<b>B</b>	<a href="#"><u>background</u></a>	<a href="#"><u>sherpa</u></a>	Defines a model expression to be used for the background. The command BG is an abbreviated equivalent.
	<a href="#"><u>back</u></a>	<a href="#"><u>sherpa</u></a>	Inputs the contents of one or more background data files.
	<a href="#"><u>batch</u></a>	<a href="#"><u>chips</u></a>	Turns on/off use of a plotting device.
	<a href="#"><u>bayes</u></a>	<a href="#"><u>sherpa</u></a>	

## Ahelp (alphabetical) – CIAO 3.4

<a href="#"><u>bbodyfreq</u></a>	<a href="#"><u>sherpa</u></a>	A Bayesian maximum likelihood function.
<a href="#"><u>bbody</u></a>	<a href="#"><u>sherpa</u></a>	Blackbody as a function of frequency. Integration ON.
<a href="#"><u>berrors</u></a>	<a href="#"><u>sherpa</u></a>	Blackbody as a function of energy. Integration ON.
<a href="#"><u>beta1d</u></a>	<a href="#"><u>sherpa</u></a>	Defines an expression to be used to specify the statistical errors for background data. The commands BACKERRORS and BSTATERRORS are equivalent.
<a href="#"><u>beta2d</u></a>	<a href="#"><u>sherpa</u></a>	1-D surface brightness beta-model. Integration OFF
<a href="#"><u>box1d</u></a>	<a href="#"><u>sherpa</u></a>	2-D Lorentzian with varying power law. Integration OFF. The LORPOW2D model is equivalent.
<a href="#"><u>box2d</u></a>	<a href="#"><u>sherpa</u></a>	1-D box function. Integration OFF.
<a href="#"><u>bp11d</u></a>	<a href="#"><u>sherpa</u></a>	2-D box function. Integration OFF.
<a href="#"><u>bpl1d</u></a>	<a href="#"><u>sherpa</u></a>	Broken power law function. Integration ON.
<a href="#"><u>browse</u></a>	<a href="#"><u>chips</u></a>	Launches the CIAO file-browsing GUI, Prism. The command PRISM is equivalent.
<a href="#"><u>bstring_to_array</u></a>	<a href="#"><u>slangrtl</u></a>	Convert a binary string to an array of characters
<a href="#"><u>bstrlen</u></a>	<a href="#"><u>slangrtl</u></a>	Get the length of a binary string
<a href="#"><u>bsyserrors</u></a>	<a href="#"><u>sherpa</u></a>	Defines an expression or file to be used to specify the systematic errors for background data.
<a href="#"><u>bye</u></a>	<a href="#"><u>sherpa</u></a>	Terminates the Sherpa program. Other equivalent termination commands are EXIT and QUIT.
<a href="#"><u>byte_compile_file</u></a>	<a href="#"><u>slangrtl</u></a>	Compile a file to byte-code for faster loading.

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<b>C</b>	<a href="#"><u>calCreateInfo</u></a>	<a href="#"><u>caldb</u></a>	Create a CALDB structure for use in other CALDB calls.
	<a href="#"><u>calc_kcorr</u></a>	<a href="#"><u>sherpa</u></a>	Calculate the k correction for a spectral model, redshift, and energy range.
	<a href="#"><u>caldb</u></a>	<a href="#"><u>calibration</u></a>	CALibration DataBase (CALDB)
	<a href="#"><u>caldb</u></a>	<a href="#"><u>modules</u></a>	The S-Lang interface to the CXC CALDB library
	<a href="#"><u>calFindFile</u></a>	<a href="#"><u>caldb</u></a>	Query the Calibration Database for a file
	<a href="#"><u>calGetData</u></a>	<a href="#"><u>caldb</u></a>	

<a href="#"><u>calGetDate</u></a>	<a href="#"><u>caldb</u></a>	Returns the code name stored in the CALDB structure.
<a href="#"><u>calGetDetector</u></a>	<a href="#"><u>caldb</u></a>	Returns the observation start date stored in the CALDB structure.
<a href="#"><u>calGetError</u></a>	<a href="#"><u>caldb</u></a>	Returns the name of the detector stored in the CALDB structure.
<a href="#"><u>calGetFilter</u></a>	<a href="#"><u>caldb</u></a>	Returns the severity of the last CALDB error.
<a href="#"><u>calGetInstrument</u></a>	<a href="#"><u>caldb</u></a>	Returns the name of the filter stored in the CALDB structure.
<a href="#"><u>calGetQuery</u></a>	<a href="#"><u>caldb</u></a>	Returns the name of the instrument stored in the CALDB structure.
<a href="#"><u>calGetTelescope</u></a>	<a href="#"><u>caldb</u></a>	Returns the value of the query expression stored in the CALDB structure.
<a href="#"><u>calGetTime</u></a>	<a href="#"><u>caldb</u></a>	Returns the name of the telescope stored in the CALDB structure.
<a href="#"><u>calPrintInfo</u></a>	<a href="#"><u>caldb</u></a>	Returns the observation start time stored in the CALDB structure.
<a href="#"><u>calSetData</u></a>	<a href="#"><u>caldb</u></a>	Display the contents of the CALDB structure
<a href="#"><u>calSetDate</u></a>	<a href="#"><u>caldb</u></a>	Sets the data product code name for the next CALDB query.
<a href="#"><u>calSetDetector</u></a>	<a href="#"><u>caldb</u></a>	Sets the date for the next CALDB query.
<a href="#"><u>calSetExpression</u></a>	<a href="#"><u>caldb</u></a>	Sets the name of the detector in the CALDB structure.
<a href="#"><u>calSetFilter</u></a>	<a href="#"><u>caldb</u></a>	Sets the boundary condition(s) for the CALDB query.
<a href="#"><u>calSetInstrument</u></a>	<a href="#"><u>caldb</u></a>	Sets the filter to be used in a CALDB query.
<a href="#"><u>calSetTelescope</u></a>	<a href="#"><u>caldb</u></a>	Sets the name of the instrument in the CALDB structure.
<a href="#"><u>calSetTime</u></a>	<a href="#"><u>caldb</u></a>	Sets the name of the telescope in the CALDB structure.
<a href="#"><u>cash</u></a>	<a href="#"><u>sherpa</u></a>	Sets the time for the next CALDB query.
<a href="#"><u>cast</u></a>	<a href="#"><u>sherpa</u></a>	A maximum likelihood function.
<a href="#"><u>celldetect</u></a>	<a href="#"><u>tools</u></a>	[REMOVED AS OF CIAO 3.0.2]
<a href="#"><u>chart_spectrum</u></a>	<a href="#"><u>tools</u></a>	Casts a dataset to single or double precision.
		Use a "sliding cell" to search for sources
		chart_spectrum.sl – Create a source spectrum for input to ChaRT

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<a href="#"><u>char</u></a>	<a href="#"><u>slangrtl</u></a>	Convert an ascii value into a string
<a href="#"><u>chdir</u></a>	<a href="#"><u>slangrtl</u></a>	Change the current working directory.
<a href="#"><u>chicvar</u></a>	<a href="#"><u>sherpa</u></a>	Chi-square statistic with constant variance computed from the counts data.
<a href="#"><u>chidvar</u></a>	<a href="#"><u>sherpa</u></a>	Chi-square statistic with variance computed from the data.
<a href="#"><u>chigehrels</u></a>	<a href="#"><u>sherpa</u></a>	Chi-square statistic with the Gehrels variance function.
<a href="#"><u>chimvar</u></a>	<a href="#"><u>sherpa</u></a>	Chi-square statistic with variance computed from model amplitudes.
<a href="#"><u>chiprimini</u></a>	<a href="#"><u>sherpa</u></a>	Chi-square statistic with Primini variance function.
<a href="#"><u>chips auto redraw</u></a>	<a href="#"><u>chips</u></a>	Set the automatic redrawing mode.
<a href="#"><u>chips clear</u></a>	<a href="#"><u>chips</u></a>	Removes all plotting objects, creating a new blank drawing area.
<a href="#"><u>chips color name</u></a>	<a href="#"><u>chips</u></a>	Converts a color number to a string.
<a href="#"><u>chips color value</u></a>	<a href="#"><u>chips</u></a>	Converts the name of a color to its numeric value.
<a href="#"><u>chips eval</u></a>	<a href="#"><u>chips</u></a>	Call ChIPS commands from S-Lang
<a href="#"><u>chips get pane</u></a>	<a href="#"><u>chips</u></a>	Get the current pane/drawing area.
<a href="#"><u>chips get xrange</u></a>	<a href="#"><u>chips</u></a>	Get the upper and/or lower x-axis limits of the plot
<a href="#"><u>chips get xscale</u></a>	<a href="#"><u>chips</u></a>	Get the x-axis scale
<a href="#"><u>chips get yrange</u></a>	<a href="#"><u>chips</u></a>	Get the upper and/or lower y-axis limits of the plot
<a href="#"><u>chips get yscale</u></a>	<a href="#"><u>chips</u></a>	Get the y-axis scale
<a href="#"><u>chips get zrange</u></a>	<a href="#"><u>chips</u></a>	Get the upper and/or lower z-axis limits of the plot
<a href="#"><u>chips get zscale</u></a>	<a href="#"><u>chips</u></a>	Get the z-axis scale
<a href="#"><u>chips label</u></a>	<a href="#"><u>chips</u></a>	Adds a label to a drawing area.
<a href="#"><u>chips line</u></a>	<a href="#"><u>chips</u></a>	Adds a line to a drawing area.
<a href="#"><u>chips pickpoints</u></a>	<a href="#"><u>chips</u></a>	Read 1 or more cursor positions from ChIPS.
<a href="#"><u>chips redraw</u></a>	<a href="#"><u>chips</u></a>	Redraws all plotting objects.
<a href="#"><u>chips set pane</u></a>	<a href="#"><u>chips</u></a>	Set the current pane/drawing area.
<a href="#"><u>chips set xrange</u></a>	<a href="#"><u>chips</u></a>	Set the upper and/or lower x-axis limits of the plot
<a href="#"><u>chips set xscale</u></a>	<a href="#"><u>chips</u></a>	Set the x-axis scale
<a href="#"><u>chips set yrange</u></a>	<a href="#"><u>chips</u></a>	Set the upper and/or lower y-axis limits of the plot
<a href="#"><u>chips set yscale</u></a>	<a href="#"><u>chips</u></a>	Set the y-axis scale

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<a href="#"><u>chips_set_zrange</u></a>	<a href="#"><u>chips</u></a>	Set the upper and/or lower z–axis limits of the plot
<a href="#"><u>chips_set_zscale</u></a>	<a href="#"><u>chips</u></a>	Set the z–axis scale
<a href="#"><u>chips_split</u></a>	<a href="#"><u>chips</u></a>	Creates multiple drawing areas.
<a href="#"><u>chips_version</u></a>	<a href="#"><u>chips</u></a>	Report the version of ChIPS as a number or string.
<a href="#"><u>chips</u></a>	<a href="#"><u>chips</u></a>	Introduction to ChIPS, CIAO's plotting package.
<a href="#"><u>chisquare</u></a>	<a href="#"><u>sherpa</u></a>	Chi–square statistic.
<a href="#"><u>chmod</u></a>	<a href="#"><u>slangrtl</u></a>	Change the mode of a file
<a href="#"><u>chown</u></a>	<a href="#"><u>slangrtl</u></a>	Change the owner of a file
<a href="#"><u>ciao.par</u></a>	<a href="#"><u>gui</u></a>	Parameter file to configure options for CIAO applications.
<a href="#"><u>ciaoshmem</u></a>	<a href="#"><u>gui</u></a>	Provides information on and configuration of CIAO sessions.
<a href="#"><u>ciao</u></a>	<a href="#"><u>concept</u></a>	Chandra Interactive Analysis of Observations
<a href="#"><u>clearerr</u></a>	<a href="#"><u>slangrtl</u></a>	Clear the error of a file stream
<a href="#"><u>clearstack</u></a>	<a href="#"><u>varmm</u></a>	S–Lang function to clear the stack.
<a href="#"><u>clear</u></a>	<a href="#"><u>chips</u></a>	Removes all plotting objects and creates a new blank drawing area.
<a href="#"><u>close</u></a>	<a href="#"><u>sherpa</u></a>	Closes the image display window.
<a href="#"><u>close</u></a>	<a href="#"><u>slangrtl</u></a>	Close an open file descriptor
<a href="#"><u>colden</u></a>	<a href="#"><u>proposaltools</u></a>	Interactive program to evaluate the neutral hydrogen column density at a given direction on the sky
<a href="#"><u>colorsys</u></a>	<a href="#"><u>chips</u></a>	Sets the color system for hardcopy plots.
<a href="#"><u>color_image</u></a>	<a href="#"><u>tools</u></a>	Run dmimg2jpg to make a color JPEG image
<a href="#"><u>compute_errors</u></a>	<a href="#"><u>sherpa</u></a>	Module function to estimate errors for an array of data
<a href="#"><u>compute_statistic</u></a>	<a href="#"><u>sherpa</u></a>	Module function to estimate a statistic given arrays of data, model amplitudes, and errors, etc.
<a href="#"><u>configure</u></a>	<a href="#"><u>concept</u></a>	Configuration and customization of CIAO
<a href="#"><u>Conj</u></a>	<a href="#"><u>slangrtl</u></a>	Compute the complex conjugate of a number
<a href="#"><u>const1d</u></a>	<a href="#"><u>sherpa</u></a>	1–D constant amplitude model. Integration ON.
<a href="#"><u>const2d</u></a>	<a href="#"><u>sherpa</u></a>	2–D constant amplitude model. Integration ON.
<a href="#"><u>contour</u></a>	<a href="#"><u>chips</u></a>	Adds a contour plot to a drawing area.

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<a href="#"><u>coords</u></a>	<a href="#"><u>chandra</u></a>	Coordinate systems used in Chandra analysis
<a href="#"><u>coord</u></a>	<a href="#"><u>sherpa</u></a>	Specifies the coordinate system for use in fits to 2-D images.
<a href="#"><u>cosh</u></a>	<a href="#"><u>slangrtl</u></a>	Compute the hyperbolic cosine of an number
<a href="#"><u>cos</u></a>	<a href="#"><u>sherpa</u></a>	Cosine function. Integration OFF.
<a href="#"><u>cos</u></a>	<a href="#"><u>slangrtl</u></a>	Compute the cosine of an number
<a href="#"><u>covariance</u></a>	<a href="#"><u>sherpa</u></a>	Computes covariance matrices, and provides an estimate of confidence intervals for selected thawed parameters.
<a href="#"><u>cplot</u></a>	<a href="#"><u>sherpa</u></a>	Causes the specified 2-D data to be displayed, with a contour plot, via ChIPS.
<a href="#"><u>createparamset</u></a>	<a href="#"><u>sherpa</u></a>	To be especially efficient, one may establish and assign a name to a model component, as well as set model parameters and their ranges, all at one time using a single command:
<a href="#"><u>create delimited string</u></a>	<a href="#"><u>slangrtl</u></a>	Concatenate strings using a delimiter
<a href="#"><u>create model</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to instantiate new source or instrument models.
<a href="#"><u>create</u></a>	<a href="#"><u>sherpa</u></a>	Establishes a model component and its parameters, for use in the current Sherpa session.
<a href="#"><u>csmooth</u></a>	<a href="#"><u>tools</u></a>	Adaptively smooth a 2-D image
<a href="#"><u>cstat</u></a>	<a href="#"><u>sherpa</u></a>	A maximum likelihood function.
<a href="#"><u>ctime</u></a>	<a href="#"><u>slangrtl</u></a>	Convert a calendar time to a string
<a href="#"><u>cumsum</u></a>	<a href="#"><u>slangrtl</u></a>	Compute the cumulative sum of an array
<a href="#"><u>current namespace</u></a>	<a href="#"><u>slangrtl</u></a>	Get the name of the current namespace
<a href="#"><u>curve</u></a>	<a href="#"><u>chips</u></a>	Plots a curve or change its attributes (PLOT is equivalent).
<a href="#"><u>c</u></a>	<a href="#"><u>chips</u></a>	Defines the current curve.

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<b>D</b>	<a href="#"><u>dataspace</u></a>	<a href="#"><u>sherpa</u></a>	Creates a data grid on which models may be evaluated.
	<a href="#"><u>data</u></a>	<a href="#"><u>sherpa</u></a>	Inputs the contents of one or more source data files.
	<a href="#"><u>dates</u></a>	<a href="#"><u>proposaltools</u></a>	DATES is an interactive calendar and time conversion tool.

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<a href="#"><u>dcounts</u></a>	<a href="#"><u>sherpa</u></a>	Calculates the sum of observed counts data for source or background datasets.
<a href="#"><u>define_case</u></a>	<a href="#"><u>slangrtl</u></a>	Define upper-lower case conversion.
<a href="#"><u>delete</u></a>	<a href="#"><u>chips</u></a>	Deletes plotting objects (drawing area, curves, lines and labels) from a plot.
<a href="#"><u>delta1d</u></a>	<a href="#"><u>sherpa</u></a>	1-D delta function. Integration ON.
<a href="#"><u>delta2d</u></a>	<a href="#"><u>sherpa</u></a>	2-D delta function. Integration ON.
<a href="#"><u>dered</u></a>	<a href="#"><u>sherpa</u></a>	Dereddening function. Integration OFF.
<a href="#"><u>describe</u></a>	<a href="#"><u>guide</u></a>	Describe is a GUIDE command that prints out detailed information about either one or two energy levels and, if two levels are input, any atomic transitions between them.
<a href="#"><u>destreak</u></a>	<a href="#"><u>tools</u></a>	Remove streak events from ACIS data
<a href="#"><u>devaucouleurs</u></a>	<a href="#"><u>sherpa</u></a>	DeVaucouleurs profile. Integration OFF.
<a href="#"><u>display</u></a>	<a href="#"><u>chips</u></a>	Causes the specified 2-D data to be displayed, using the default imaging display tool (i.e. ds9)
<a href="#"><u>dither_region</u></a>	<a href="#"><u>tools</u></a>	Compute fraction of region area that covers chips
<a href="#"><u>dmappend</u></a>	<a href="#"><u>tools</u></a>	Append multiple blocks/extensions to an existing output file.
<a href="#"><u>dmarfadd</u></a>	<a href="#"><u>tools</u></a>	Add multiple ARF files together, weighting by exposure.
<a href="#"><u>dmbinning</u></a>	<a href="#"><u>dm</u></a>	The CIAO binning syntax
<a href="#"><u>dmcols</u></a>	<a href="#"><u>dm</u></a>	Selecting columns in a table
<a href="#"><u>dmcontour</u></a>	<a href="#"><u>tools</u></a>	Make contour regions from a 2-D image
<a href="#"><u>dmcoords</u></a>	<a href="#"><u>tools</u></a>	Convert between Chandra coordinate systems
<a href="#"><u>dmcopy</u></a>	<a href="#"><u>tools</u></a>	Filter and bin tables and images.
<a href="#"><u>dmdiff</u></a>	<a href="#"><u>tools</u></a>	Compare values in two FITS files.
<a href="#"><u>dmextract</u></a>	<a href="#"><u>tools</u></a>	Make a histogram table file (e.g. PHA file, lightcurve file) from a table column. Generate count histogram on supplied regions for a spatial table or image file.
<a href="#"><u>dmfiltering</u></a>	<a href="#"><u>dm</u></a>	The CIAO filtering syntax
<a href="#"><u>dmfilth</u></a>	<a href="#"><u>tools</u></a>	Replace pixel values in source regions of an image with values

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<a href="#"><u>dmgroupreg</u></a>	<a href="#"><u>tools</u></a>	interpolated from surrounding background regions
<a href="#"><u>dmgroup</u></a>	<a href="#"><u>tools</u></a>	Translates DS9 regions and groups to CIAO format.
<a href="#"><u>dmgti</u></a>	<a href="#"><u>tools</u></a>	Group a specified column in a table with various options
<a href="#"><u>dmhedit</u></a>	<a href="#"><u>tools</u></a>	Create a Good Time Interval from limits placed on time-based files (event and Mission Time Line files).
<a href="#"><u>dmhistory</u></a>	<a href="#"><u>tools</u></a>	Edit datamodel file headers
<a href="#"><u>dmimages</u></a>	<a href="#"><u>dm</u></a>	Extracts the tool history from the file header
<a href="#"><u>dmimfiltering</u></a>	<a href="#"><u>dm</u></a>	Images in CIAO: logical and physical coordinate systems
<a href="#"><u>dmimg2jpg</u></a>	<a href="#"><u>tools</u></a>	The CIAO filtering syntax for images
<a href="#"><u>dmimgcalc</u></a>	<a href="#"><u>tools</u></a>	Make a color JPEG image (or EPS) from three image files
<a href="#"><u>dmimghist</u></a>	<a href="#"><u>tools</u></a>	Perform arithmetic on images
<a href="#"><u>dmimgpick</u></a>	<a href="#"><u>tools</u></a>	Create a histogram of the pixel values in a 2-D image
<a href="#"><u>dmimgthresh</u></a>	<a href="#"><u>tools</u></a>	Maps image values to rows in a table
<a href="#"><u>dmintro</u></a>	<a href="#"><u>dm</u></a>	Set low (or high) intensity or exposure regions of an image to a constant value.
<a href="#"><u>dmjoin</u></a>	<a href="#"><u>tools</u></a>	The Data Model library underlies most of the CXC tools.
<a href="#"><u>dmkeypar</u></a>	<a href="#"><u>tools</u></a>	Join two files whose sampling is different.
<a href="#"><u>dmlist</u></a>	<a href="#"><u>tools</u></a>	Retrieve information about a keyword from an input file
<a href="#"><u>dmmakepar</u></a>	<a href="#"><u>tools</u></a>	List contents or structure of a file.
<a href="#"><u>dmmakereg</u></a>	<a href="#"><u>tools</u></a>	Write header keywords to a parameter file
<a href="#"><u>dmmerge</u></a>	<a href="#"><u>tools</u></a>	Convert a region string to a CXC FITS region file
<a href="#"><u>dmopt</u></a>	<a href="#"><u>dm</u></a>	Merge two or more compatible tables (e.g. event files) into one.
<a href="#"><u>dmpaste</u></a>	<a href="#"><u>tools</u></a>	Controlling data model internal options
<a href="#"><u>dmreadpar</u></a>	<a href="#"><u>tools</u></a>	Add new columns to a table.
<a href="#"><u>dmregions</u></a>	<a href="#"><u>dm</u></a>	Create header keywords from a parameter file
		CIAO region filtering syntax

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<a href="#"><u>dmregrid</u></a>	<a href="#"><u>tools</u></a>	Rebin a stack of 2-dimensional images.
<a href="#"><u>dmsort</u></a>	<a href="#"><u>tools</u></a>	Sort a table.
<a href="#"><u>dmstat</u></a>	<a href="#"><u>tools</u></a>	Compute statistics for images and columns in tables.
<a href="#"><u>dmsyntax</u></a>	<a href="#"><u>dm</u></a>	The Data Model syntax for filtering and binning files.
<a href="#"><u>dmtcalc</u></a>	<a href="#"><u>tools</u></a>	Modify and create columns in a table
<a href="#"><u>dmttype2split</u></a>	<a href="#"><u>tools</u></a>	Create a type 1 output file for specified rows of a type 2 file.
<a href="#"><u>dm</u></a>	<a href="#"><u>dm</u></a>	The CIAO Data Model
<a href="#"><u>dollarsign</u></a>	<a href="#"><u>sherpa</u></a>	Must precede any Unix command issued within Sherpa or ChIPS.
<a href="#"><u>double</u></a>	<a href="#"><u>slangrtl</u></a>	Convert an object to double precision
<a href="#"><u>drawarea</u></a>	<a href="#"><u>chips</u></a>	Specifies the location for a new drawing area.
<a href="#"><u>ds9_center</u></a>	<a href="#"><u>ds9</u></a>	Center image at position
<a href="#"><u>ds9_clear</u></a>	<a href="#"><u>ds9</u></a>	Erase a DS9 frame
<a href="#"><u>ds9_get_array</u></a>	<a href="#"><u>ds9</u></a>	Retrieve displayed image
<a href="#"><u>ds9_get_cmap</u></a>	<a href="#"><u>ds9</u></a>	Retrieve colormap from DS9
<a href="#"><u>ds9_get_coords</u></a>	<a href="#"><u>ds9</u></a>	Retrieve position of next mouseclick within any frame
<a href="#"><u>ds9_get_crosshair</u></a>	<a href="#"><u>ds9</u></a>	Retrieve position of crosshair cursor
<a href="#"><u>ds9_get_file</u></a>	<a href="#"><u>ds9</u></a>	Retrieve name of file being displayed
<a href="#"><u>ds9_get_regions</u></a>	<a href="#"><u>ds9</u></a>	Retrieve descriptions of regions applied to a displayed image
<a href="#"><u>ds9_get_scale</u></a>	<a href="#"><u>ds9</u></a>	Retrieve image scale
<a href="#"><u>ds9_get_zoom</u></a>	<a href="#"><u>ds9</u></a>	Retrieve zoom level
<a href="#"><u>ds9_launch</u></a>	<a href="#"><u>ds9</u></a>	Establish connection to a DS9 process
<a href="#"><u>ds9_pan</u></a>	<a href="#"><u>ds9</u></a>	Shift image position
<a href="#"><u>ds9_put_array</u></a>	<a href="#"><u>ds9</u></a>	Visualize an image pixel array
<a href="#"><u>ds9_put_crosshair</u></a>	<a href="#"><u>ds9</u></a>	Set position of crosshair cursor
<a href="#"><u>ds9_put_file</u></a>	<a href="#"><u>ds9</u></a>	Load FITS file
<a href="#"><u>ds9_put_regions</u></a>	<a href="#"><u>ds9</u></a>	Request that region descriptions be applied to the displayed image
<a href="#"><u>ds9_put_wcs_keys</u></a>	<a href="#"><u>ds9</u></a>	Apply WCS to displayed image, using pre-formatted FITS keywords
<a href="#"><u>ds9_put_wcs_struct</u></a>	<a href="#"><u>ds9</u></a>	Apply WCS to displayed image, using structure field values
<a href="#"><u>ds9_put_wcs</u></a>	<a href="#"><u>ds9</u></a>	Apply WCS to displayed image,

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<a href="#"><u>ds9_quit</u></a>	<a href="#"><u>ds9</u></a>	using raw numeric or string values
<a href="#"><u>ds9_set_cmap</u></a>	<a href="#"><u>ds9</u></a>	Terminate a DS9 process
<a href="#"><u>ds9_set_scale</u></a>	<a href="#"><u>ds9</u></a>	Change colormap of DS9
<a href="#"><u>ds9_set_zoom</u></a>	<a href="#"><u>ds9</u></a>	Change image scale
<a href="#"><u>ds9_view</u></a>	<a href="#"><u>ds9</u></a>	Zoom in or out
		Launch DS9 with file or image pixel array
<a href="#"><u>ds9</u></a>	<a href="#"><u>modules</u></a>	A simple S–Lang interface to ds9
<a href="#"><u>dup_fd</u></a>	<a href="#"><u>slangrtl</u></a>	Duplicate a file descriptor
<a href="#"><u>dup_struct</u></a>	<a href="#"><u>yarmm</u></a>	S–Lang function to duplicate a structured variable.
<a href="#"><u>dup</u></a>	<a href="#"><u>slangrtl</u></a>	Duplicate the value at the top of the stack
<a href="#"><u>d</u></a>	<a href="#"><u>chips</u></a>	Defines the current drawing area.

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<b>E</b>	<a href="#"><u>echo</u></a>	<a href="#"><u>sherpa</u></a>	Turns on/off reporting of user keystrokes.
	<a href="#"><u>edge</u></a>	<a href="#"><u>sherpa</u></a>	Photoabsorption edge model. Integration OFF.
	<a href="#"><u>eflux</u></a>	<a href="#"><u>sherpa</u></a>	Calculates the unconvolved energy flux for source or background datasets.
	<a href="#"><u>eqwidth</u></a>	<a href="#"><u>sherpa</u></a>	Computes the equivalent width of an emission or absorption line in source or background data.
	<a href="#"><u>erase</u></a>	<a href="#"><u>sherpa</u></a>	Erases user inputs and settings, and/or model components.
	<a href="#"><u>erfc</u></a>	<a href="#"><u>sherpa</u></a>	A 1–D complementary error function. Integration OFF.
	<a href="#"><u>erf</u></a>	<a href="#"><u>sherpa</u></a>	A 1–D error function. Integration OFF.
	<a href="#"><u>errno_string</u></a>	<a href="#"><u>slangrtl</u></a>	Return a string describing an errno.
	<a href="#"><u>errno</u></a>	<a href="#"><u>slangrtl</u></a>	Error code set by system functions.
	<a href="#"><u>errors</u></a>	<a href="#"><u>sherpa</u></a>	Defines an expression to be used to specify the statistical errors for source data.
	<a href="#"><u>error</u></a>	<a href="#"><u>slangrtl</u></a>	Generate an error condition
	<a href="#"><u>errs</u></a>	<a href="#"><u>chips</u></a>	Specifies the appearance of errorbars.
	<a href="#"><u>evalfile</u></a>	<a href="#"><u>slangrtl</u></a>	Interpret a file containing S–Lang code.
	<a href="#"><u>eval</u></a>	<a href="#"><u>slangrtl</u></a>	Interpret a string as S–Lang code
	<a href="#"><u>eventdef</u></a>	<a href="#"><u>chandra</u></a>	Column definition in Chandra event files

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<a href="#"><u>exch</u></a>	<a href="#"><u>slangrtl</u></a>	Exchange two items on the stack
<a href="#"><u>exit</u></a>	<a href="#"><u>chips</u></a>	Terminates the program. The command QUIT is equivalent.
<a href="#"><u>exp</u></a>	<a href="#"><u>slangrtl</u></a>	Compute the exponential of an number
<a href="#"><u>extract_element</u></a>	<a href="#"><u>slangrtl</u></a>	Extract the nth element of a string with delimiters
<b>F</b>		
<a href="#"><u>fakeit</u></a>	<a href="#"><u>sherpa</u></a>	Creates a simulated 1-D dataset.
<a href="#"><u>farf2d</u></a>	<a href="#"><u>sherpa</u></a>	A 2-D file-based ancillary response model. Alternate names include FEXPMAP and FEXPMAP2D.
<a href="#"><u>farf</u></a>	<a href="#"><u>sherpa</u></a>	A 1-D file-based ancillary response model.
<a href="#"><u>fclose</u></a>	<a href="#"><u>slangrtl</u></a>	Close a file
<a href="#"><u>fdopen</u></a>	<a href="#"><u>slangrtl</u></a>	Convert a FD_Type file descriptor to a stdio File_Type object
<a href="#"><u>feffile</u></a>	<a href="#"><u>sherpa</u></a>	Specifies the Fits Embedded Function (FEF) file whose contents will be displayed with FEFPLT.
<a href="#"><u>fefplot</u></a>	<a href="#"><u>sherpa</u></a>	Plots an instrument response stored in a Fits Embedded Function (FEF) file that is read in via FEFFILE.
<a href="#"><u>feof</u></a>	<a href="#"><u>slangrtl</u></a>	Get the end-of-file status
<a href="#"><u>ferror</u></a>	<a href="#"><u>slangrtl</u></a>	Determine the error status of an open file descriptor
<a href="#"><u>fflush</u></a>	<a href="#"><u>slangrtl</u></a>	Flush an output stream
<a href="#"><u>fgetlines</u></a>	<a href="#"><u>slangrtl</u></a>	Read all the lines from an open file
<a href="#"><u>fgets</u></a>	<a href="#"><u>slangrtl</u></a>	Read a line from a file.
<a href="#"><u>fileno</u></a>	<a href="#"><u>slangrtl</u></a>	Convert a stdio File_Type object to a FD_Type descriptor
<a href="#"><u>filtwin</u></a>	<a href="#"><u>gui</u></a>	GUI to perform interactive filtering of data
<a href="#"><u>firstlook</u></a>	<a href="#"><u>gui</u></a>	GUI to allow an efficient means of accessing Chandra data products
<a href="#"><u>fits_bitpix</u></a>	<a href="#"><u>varmm</u></a>	Converts S-Lang variables and data types to FITS BITPIX values.
<a href="#"><u>fit</u></a>	<a href="#"><u>sherpa</u></a>	Initiates fitting (optimization). The command [B]RUN is equivalent.
<a href="#"><u>flux</u></a>	<a href="#"><u>sherpa</u></a>	Calculates the unconvolved photon flux for source or background datasets.
<a href="#"><u>font</u></a>	<a href="#"><u>chips</u></a>	Changes the default global font.
<a href="#"><u>fopen</u></a>	<a href="#"><u>slangrtl</u></a>	Open a file
<a href="#"><u>fprintf</u></a>	<a href="#"><u>slangrtl</u></a>	

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<a href="#"><u>fpsf1d</u></a>	<a href="#"><u>sherpa</u></a>	Create and write a formatted string to a file
<a href="#"><u>fpsf</u></a>	<a href="#"><u>sherpa</u></a>	A 1-D file-based PSF instrument model.
<a href="#"><u>fputs</u></a>	<a href="#"><u>slangrtl</u></a>	Write a string to an open stream
<a href="#"><u>fread</u></a>	<a href="#"><u>slangrtl</u></a>	Read binary data from a file
<a href="#"><u>freeze</u></a>	<a href="#"><u>sherpa</u></a>	Prohibits model parameter(s) from varying.
<a href="#"><u>frmf</u></a>	<a href="#"><u>sherpa</u></a>	A 1-D file-based response matrix model.
<a href="#"><u>fseek</u></a>	<a href="#"><u>slangrtl</u></a>	Reposition a stream
<a href="#"><u>ftell</u></a>	<a href="#"><u>slangrtl</u></a>	Obtain the current position in an open stream
<a href="#"><u>ftest</u></a>	<a href="#"><u>sherpa</u></a>	Computes significance using the F test.
<a href="#"><u>fullgarf</u></a>	<a href="#"><u>tools</u></a>	Create a grating arf for a particular order and grating for a given observation.
<a href="#"><u>fwrite</u></a>	<a href="#"><u>slangrtl</u></a>	Write binary data to a file

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<b>G</b>	<a href="#"><u>gauss1d</u></a>	<a href="#"><u>sherpa</u></a>	1-D unnormalized Gaussian function. Integration ON.
	<a href="#"><u>gauss2d</u></a>	<a href="#"><u>sherpa</u></a>	2-D unnormalized Gaussian function. Integration OFF.
	<a href="#"><u>getcwd</u></a>	<a href="#"><u>slangrtl</u></a>	Get the current working directory
	<a href="#"><u>getegid</u></a>	<a href="#"><u>slangrtl</u></a>	Get the effective group id
	<a href="#"><u>getenv</u></a>	<a href="#"><u>slangrtl</u></a>	Get the value of an environment variable
	<a href="#"><u>geteuid</u></a>	<a href="#"><u>slangrtl</u></a>	Get the effective user-id of the current process
	<a href="#"><u>getgid</u></a>	<a href="#"><u>slangrtl</u></a>	Get the group id
	<a href="#"><u>getpid</u></a>	<a href="#"><u>slangrtl</u></a>	Get the current process id
	<a href="#"><u>getppid</u></a>	<a href="#"><u>slangrtl</u></a>	Get the parent process id
	<a href="#"><u>getuid</u></a>	<a href="#"><u>slangrtl</u></a>	Get the user-id of the current process
	<a href="#"><u>getx</u></a>	<a href="#"><u>sherpa</u></a>	Assigns x-axis values taken from a plot to model parameters.
	<a href="#"><u>gety</u></a>	<a href="#"><u>sherpa</u></a>	Assigns y-axis values taken from a plot to model parameters.
	<a href="#"><u>get_analysis</u></a>	<a href="#"><u>sherpa</u></a>	Module function to retrieve the current analysis setting.
	<a href="#"><u>get_arf_axes</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to retrieve the

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<a href="#"><u>get_axes</u></a>	<a href="#"><u>sherpa</u></a>	energy/wavelength grid of an ARF associated with source and background data
<a href="#"><u>get_coord</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to get the energy/wavelength/channel grid of source and background datasets.
<a href="#"><u>get_data</u></a>	<a href="#"><u>sherpa</u></a>	Module function to retrieve the current coordinate setting for 2-D image data.
<a href="#"><u>get_dcouncts_sum</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to get the amplitudes of source and background datasets.
<a href="#"><u>get_defined_models</u></a>	<a href="#"><u>sherpa</u></a>	Calculates the sum of observed counts in source and background datasets using module functions in Sherpa.
<a href="#"><u>get_dir</u></a>	<a href="#"><u>sherpa</u></a>	Module functions that return lists of defined Sherpa source and instrument models
<a href="#"><u>get_doc_string_from_file</u></a>	<a href="#"><u>slangrtl</u></a>	Module function to retrieve the current path.
<a href="#"><u>get_eflux</u></a>	<a href="#"><u>sherpa</u></a>	Read documentation from a file
<a href="#"><u>get_energy_axes</u></a>	<a href="#"><u>sherpa</u></a>	Calculate the energy flux (unconvolved) for source or background datasets using module functions in Sherpa.
<a href="#"><u>get_eqwidth</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to retrieve the energy grids of source and background datasets.
<a href="#"><u>get_errors</u></a>	<a href="#"><u>sherpa</u></a>	Module functions that compute the equivalent width of an emission or absorption line in source or background data.
<a href="#"><u>get_filename</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to get the error estimates of source and background datasets.
<a href="#"><u>get_filter_expr</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to retrieve filenames associated with a dataset.
<a href="#"><u>get_filter</u></a>	<a href="#"><u>sherpa</u></a>	Module function to retrieve the strings describing filters applied to source and background datasets.
<a href="#"><u>get_fit</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to get the filter arrays associated with source and background datasets.
<a href="#"><u>get_flux2d</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to get information about the quality of a fit.

<a href="#"><u>get_fluxed_spectrum</u></a>	<a href="#"><u>sherpa</u></a>	Module functions for computing fluxes/summing counts in 2-D images.
<a href="#"><u>get_flux_str</u></a>	<a href="#"><u>sherpa</u></a>	Retrieve a fluxed spectrum (counts divided by ARF) using module functions in Sherpa.
<a href="#"><u>get_ftest</u></a>	<a href="#"><u>sherpa</u></a>	Retrieves a default structure for use with <code>get_pflux()</code> , etc.
<a href="#"><u>get_groups</u></a>	<a href="#"><u>sherpa</u></a>	Module function that returns the statistical significance computed with the F test
<a href="#"><u>get_import_module_path</u></a>	<a href="#"><u>slangrtl</u></a>	Module functions for retrieving a grouping or quality array from source and background files.
<a href="#"><u>get_lfactorial</u></a>	<a href="#"><u>sherpa</u></a>	Get the search path for dynamically loadable objects
<a href="#"><u>get_mccounts_sum</u></a>	<a href="#"><u>sherpa</u></a>	Module function to compute the natural logarithm of the factorial of the input quantity
<a href="#"><u>get_metadata</u></a>	<a href="#"><u>sherpa</u></a>	Module functions for computing the sum of convolved model counts in source and background datasets.
<a href="#"><u>get_method_expr</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to retrieve metadata associated with source and background datasets.
<a href="#"><u>get_models</u></a>	<a href="#"><u>sherpa</u></a>	Module function to retrieve the name of the current optimization method.
<a href="#"><u>get_model_params</u></a>	<a href="#"><u>sherpa</u></a>	Module functions that return lists of available source and instrument models
<a href="#"><u>get_num_par</u></a>	<a href="#"><u>sherpa</u></a>	Access to the default model and instrument parameters of Sherpa from S-Lang.
<a href="#"><u>get_paramestint</u></a>	<a href="#"><u>sherpa</u></a>	Module functions that report the total number of parameters for all defined models, including instrument models
<a href="#"><u>get_paramestlim</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to retrieve the value and statistic arrays from the most recent run of a parameter estimation method
<a href="#"><u>get_paramestreg</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to determine confidence intervals, and retrieve the parameter bounds.

<a href="#"><u>get_paramest</u></a>	<a href="#"><u>sherpa</u></a>	most recent run of a parameter estimation method
<a href="#"><u>get_par</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to retrieve the output of parameter estimation methods.
<a href="#"><u>get_pflux</u></a>	<a href="#"><u>sherpa</u></a>	Module function for getting model parameter values, etc.
		get_flux(), get_pflux(), and get_bpflux() calculate the photon flux (unconvolved) for source and background datasets using the module functions in Sherpa.
<a href="#"><u>get_photon_axes</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to retrieve photon-space grids over which models are evaluated.
<a href="#"><u>get_photon_energy_axes</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to retrieve photon-space energy grids over which models are evaluated.
<a href="#"><u>get_photon_wave_axes</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to retrieve photon-space wavelength grids over which models are evaluated.
<a href="#"><u>get_qvalue</u></a>	<a href="#"><u>sherpa</u></a>	Module function that returns the statistical significance computed as a q-value.
<a href="#"><u>get_raw_axes</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to retrieve the raw channel number grids of source and background datasets.
<a href="#"><u>get_record</u></a>	<a href="#"><u>sherpa</u></a>	Module function to return a record of model parameter values at the end of each iteration of the fitting process.
<a href="#"><u>get_sky_limits</u></a>	<a href="#"><u>tools</u></a>	Find the region covered by an image in sky coordinates
<a href="#"><u>get_slang_load_path</u></a>	<a href="#"><u>slangrtl</u></a>	Get the value of the interpreter's load-path
<a href="#"><u>get_source_components</u></a>	<a href="#"><u>sherpa</u></a>	Return, as an array, the names of the model components in the source expression of a dataset.
<a href="#"><u>get_source</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to retrieve predicted source and background model photon amplitudes.
<a href="#"><u>get_src_region</u></a>	<a href="#"><u>tools</u></a>	Outputs regions that have counts higher than background
<a href="#"><u>get_stackexpr</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to retrieve a model stack expression.
<a href="#"><u>get_statistic</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to get the current value of the statistic comparing

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<a href="#"><u>get_stats</u></a>	<a href="#"><u>sherpa</u></a>	source and background data and model values.
<a href="#"><u>get_stat_expr</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to retrieve predicted model counts, statistics, residuals, sigma residuals, and ratios from source and background datasets.
<a href="#"><u>get_struct_field_names</u></a>	<a href="#"><u>slangrtl</u></a>	Module function to retrieve the name of the current statistic.
<a href="#"><u>get_struct_field</u></a>	<a href="#"><u>slangrtl</u></a>	Retrieve the field names associated with a structure
<a href="#"><u>get_syserrors</u></a>	<a href="#"><u>sherpa</u></a>	Get the value associated with a structure field
<a href="#"><u>get_verbose</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to get the systematic error estimates of source and background datasets.
<a href="#"><u>get_wave_axes</u></a>	<a href="#"><u>sherpa</u></a>	Module function to display Sherpa's current verbosity setting.
<a href="#"><u>get_weights</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to retrieve the wavelength grids of source and background datasets.
<a href="#"><u>get</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to get the statistical weights of source and background datasets.
<a href="#"><u>gmtime</u></a>	<a href="#"><u>slangrtl</u></a>	Summary of Sherpa/S–Lang module functions that retrieve settings or data.
<a href="#"><u>goodness</u></a>	<a href="#"><u>sherpa</u></a>	Break down a time in seconds to GMT timezone
<a href="#"><u>grid–powell</u></a>	<a href="#"><u>sherpa</u></a>	Reports information on the goodness–of–fit.
<a href="#"><u>gridmodel</u></a>	<a href="#"><u>sherpa</u></a>	A grid search utilizing the Powell method at each grid point.
<a href="#"><u>grids</u></a>	<a href="#"><u>chips</u></a>	N–D user–specified amplitude model. Integration OFF.
<a href="#"><u>grid</u></a>	<a href="#"><u>sherpa</u></a>	Adds grid lines to a drawing area and/or changes grid attributes.
<a href="#"><u>groupByCounts</u></a>	<a href="#"><u>sherpa</u></a>	A grid search of parameter space, with no minimization.
<a href="#"><u>group</u></a>	<a href="#"><u>modules</u></a>	Group a dataset by number of counts or signal–to–noise within Sherpa.
<a href="#"><u>group</u></a>	<a href="#"><u>sherpa</u></a>	The S–Lang interface to the CXC grouping library
		Causes Sherpa to apply a read–in bin grouping scheme to source or

<a href="#"><u>grpAdaptiveSnr</u></a>	<a href="#"><u>group</u></a>	background data. Adaptively group an array by signal to noise.
<a href="#"><u>grpAdaptive</u></a>	<a href="#"><u>group</u></a>	Group an array by the number of counts per group using an adaptive scheme.
<a href="#"><u>grpBinFile</u></a>	<a href="#"><u>group</u></a>	Group an array using the grouping applied to another dataset.
<a href="#"><u>grpBinWidth</u></a>	<a href="#"><u>group</u></a>	Group an array into a set of equal-width groups (by group width).
<a href="#"><u>grpBin</u></a>	<a href="#"><u>group</u></a>	Group an array using low and high boundaries.
<a href="#"><u>grpGetChansPerGroup</u></a>	<a href="#"><u>group</u></a>	Calculate the number of channels (elements) in each group.
<a href="#"><u>grpGetGroupSum</u></a>	<a href="#"><u>group</u></a>	Apply the supplied grouping to an array.
<a href="#"><u>grpGetGrpNum</u></a>	<a href="#"><u>group</u></a>	Calculate the group number for each element in the array.
<a href="#"><u>grpMaxSlope</u></a>	<a href="#"><u>group</u></a>	Group an array so that its absolute gradient is above a user-defined limit.
<a href="#"><u>grpMinSlope</u></a>	<a href="#"><u>group</u></a>	Group an array so that its absolute gradient is below a user-defined limit.
<a href="#"><u>grpNumBins</u></a>	<a href="#"><u>group</u></a>	Group an array into a set of equal-width groups (by number of groups).
<a href="#"><u>grpNumCounts</u></a>	<a href="#"><u>group</u></a>	Group an array by the number of counts per group.
<a href="#"><u>grpSnr</u></a>	<a href="#"><u>group</u></a>	Group an array by signal to noise.
<a href="#"><u>guess</u></a>	<a href="#"><u>sherpa</u></a>	Estimates initial parameter values and ranges, based on input data.
<a href="#"><u>guide</u></a>	<a href="#"><u>chandra</u></a>	Grating User Interactive Data Extension (GUIDE)
<a href="#"><u>gui</u></a>	<a href="#"><u>gui</u></a>	Graphical User Interface (GUI)

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<b>H</b>	<a href="#"><u>hrc_build_badpix</u></a>	<a href="#"><u>tools</u></a>	Create observation-specific bad pixel file for HRC
	<a href="#"><u>hrc_dftstats</u></a>	<a href="#"><u>tools</u></a>	Calculate statistics from hrc_calc_dead_time and a GTI
	<a href="#"><u>hrc_process_events</u></a>	<a href="#"><u>tools</u></a>	Correct HRC event positions, times, PHA, etc.
	<a href="#"><u>hubble</u></a>	<a href="#"><u>sherpa</u></a>	Hubble-Reynolds profile. Integration OFF. The REYNOLDS model is equivalent.

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<b>I</b>	<a href="#"><u>identify</u></a>	<a href="#"><u>guide</u></a>	List emission lines near given wavelength.
	<a href="#"><u>ignore</u></a>	<a href="#"><u>sherpa</u></a>	Specifies a data portion to be excluded, for 1– or 2–D data.
	<a href="#"><u>image</u></a>	<a href="#"><u>sherpa</u></a>	Causes the specified 2–D data to be displayed, via ds9.
	<a href="#"><u>Imag</u></a>	<a href="#"><u>slangrtl</u></a>	Compute the imaginary part of a number
	<a href="#"><u>implements</u></a>	<a href="#"><u>slangrtl</u></a>	Name a private namespace
	<a href="#"><u>import</u></a>	<a href="#"><u>slangrtl</u></a>	Dynamically link to a specified module
	<a href="#"><u>info</u></a>	<a href="#"><u>chips</u></a>	Prints summary information about the current plotting objects.
	<a href="#"><u>init_char_array</u></a>	<a href="#"><u>slangrtl</u></a>	Initialize an array of characters
	<a href="#"><u>instrument</u></a>	<a href="#"><u>sherpa</u></a>	Defines an expression to be used for modeling the instrument in source or background data analysis. The command RESPONSE is equivalent.
	<a href="#"><u>integer</u></a>	<a href="#"><u>slangrtl</u></a>	Convert a string to an integer
	<a href="#"><u>integrate</u></a>	<a href="#"><u>sherpa</u></a>	Controls the integration of model components.
	<a href="#"><u>interval–projection</u></a>	<a href="#"><u>sherpa</u></a>	Plots the fit statistic as a function of parameter value, using the PROJECTION algorithm. The commands INT–PROJ and INTPROJ are abbreviated equivalents.
	<a href="#"><u>interval–uncertainty</u></a>	<a href="#"><u>sherpa</u></a>	Plots the fit statistic as a function of parameter value, using the UNCERTAINTY algorithm. The commands INT–UNC and INTUNC are abbreviated equivalents.
	<a href="#"><u>int</u></a>	<a href="#"><u>slangrtl</u></a>	Typecast an object to an integer
	<a href="#"><u>ionbal</u></a>	<a href="#"><u>guide</u></a>	Calculate collisional ionization equilibrium ion balance.
	<a href="#"><u>isatty</u></a>	<a href="#"><u>slangrtl</u></a>	Determine if an open file descriptor refers to a terminal
	<a href="#"><u>isdigit</u></a>	<a href="#"><u>slangrtl</u></a>	Tests for a decimal digit character
	<a href="#"><u>isis</u></a>	<a href="#"><u>chandra</u></a>	Interactive Spectral Interpretation System (ISIS)
	<a href="#"><u>is_defined</u></a>	<a href="#"><u>slangrtl</u></a>	Indicate whether a variable or function defined.
	<a href="#"><u>is_list_element</u></a>	<a href="#"><u>slangrtl</u></a>	Test whether a delimited string contains a specific element

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<a href="#"><u>is_paramset</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to determine if whether the specified parameter(s) are thawed or frozen.
<a href="#"><u>is_struct_defined</u></a>	<a href="#"><u>varmm</u></a>	S–Lang function to see if a structure or field in a structure is defined
<a href="#"><u>is_struct_type</u></a>	<a href="#"><u>slangrtl</u></a>	Determine whether or not an object is a structure
<a href="#"><u>is_substr</u></a>	<a href="#"><u>slangrtl</u></a>	Test for a specified substring within a string.
<a href="#"><u>is_subtracted</u></a>	<a href="#"><u>sherpa</u></a>	Module function to determine if whether the specified dataset is background–subtracted.
<a href="#"><u>is</u></a>	<a href="#"><u>sherpa</u></a>	Summary of Sherpa/S–Lang module query functions.
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<b>J</b>	<a href="#"><u>jdpileup</u></a>	<a href="#"><u>sherpa</u></a> A CCD pileup model developed by John Davis of MIT.
	<a href="#"><u>jointmode</u></a>	<a href="#"><u>sherpa</u></a> Joint–mode models define the function argument, on which a model expression is evaluated, to be a particular data axis.
	<a href="#"><u>journal</u></a>	<a href="#"><u>sherpa</u></a> Turns on/off the writing of all commands to a file.
<hr/>		
<b>K</b>	<a href="#"><u>kernel</u></a>	<a href="#"><u>sherpa</u></a> Defines an expression to be used as a kernel in 1D source model convolution.
	<a href="#"><u>kill</u></a>	<a href="#"><u>slangrtl</u></a> Send a signal to a process
<hr/>		
<b>L</b>	<a href="#"><u>label</u></a>	<a href="#"><u>chips</u></a> Adds a label to a drawing area and/or changes label attributes.
	<a href="#"><u>lc_clean</u></a>	<a href="#"><u>tools</u></a> lc_clean.sl – Clean a lightcurve to match the ACIS "blank–sky" datasets
	<a href="#"><u>length</u></a>	<a href="#"><u>slangrtl</u></a> Get the length of an object
	<a href="#"><u>levels</u></a>	<a href="#"><u>chips</u></a> Sets the contour levels in a contour plot.
	<a href="#"><u>level</u></a>	<a href="#"><u>chandra</u></a> Describes the amount of processing performed to create a given product.
	<a href="#"><u>levenberg-marquardt</u></a>	<a href="#"><u>sherpa</u></a> The Levenberg–Marquardt optimization method.
	<a href="#"><u>lightcurve</u></a>	<a href="#"><u>tools</u></a> Bin source and background events by specified time intervals
	<a href="#"><u>limits</u></a>	<a href="#"><u>chips</u></a> Sets the ranges to be displayed in the axes.

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<a href="#"><u>linear</u></a>	<a href="#"><u>chips</u></a>	Changes one or more axes to linear scale.
<a href="#"><u>linebroad</u></a>	<a href="#"><u>sherpa</u></a>	Line broadening profile. Integration ON.
<a href="#"><u>lineid</u></a>	<a href="#"><u>sherpa</u></a>	Sets a user-defined line identification (or general model description) for the model in the MDL output.
<a href="#"><u>line</u></a>	<a href="#"><u>chips</u></a>	Adds a line to a drawing area and/or changes line attributes.
<a href="#"><u>linkparam</u></a>	<a href="#"><u>sherpa</u></a>	Parameter expressions are used to link model component parameters:
<a href="#"><u>listdir</u></a>	<a href="#"><u>slangrtl</u></a>	Get a list of the files in a directory
<a href="#"><u>list_paramest</u></a>	<a href="#"><u>sherpa</u></a>	Module functions listing the current and default values of the parameters used to configure each Sherpa parameter estimation method.
<a href="#"><u>list_par</u></a>	<a href="#"><u>sherpa</u></a>	Module function that lists information about all defined model parameters.
<a href="#"><u>list</u></a>	<a href="#"><u>chips</u></a>	Lists the contents of datafiles using the CIAO tool dmlist.
<a href="#"><u>list</u></a>	<a href="#"><u>sherpa</u></a>	Summary of Sherpa/S-Lang module list functions.
<a href="#"><u>ln</u></a>	<a href="#"><u>chips</u></a>	Defines the current line.
<a href="#"><u>load_arf</u></a>	<a href="#"><u>sherpa</u></a>	Module function to load data from an ARF file into Sherpa
<a href="#"><u>load_ascii</u></a>	<a href="#"><u>sherpa</u></a>	Module function to load ASCII data into Sherpa
<a href="#"><u>load_backset</u></a>	<a href="#"><u>sherpa</u></a>	Module function to load background data into Sherpa
<a href="#"><u>load_back_from</u></a>	<a href="#"><u>sherpa</u></a>	Module function to load background from a PHA file into Sherpa
<a href="#"><u>load_dataset</u></a>	<a href="#"><u>sherpa</u></a>	Module function to load data into Sherpa
<a href="#"><u>load_fitsbin</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to load source and background data from a FITS binary table into Sherpa
<a href="#"><u>load_image</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to load source and background data from a FITS image into Sherpa
<a href="#"><u>load_inst_from</u></a>	<a href="#"><u>sherpa</u></a>	Module function to load data from ARF and RMF files into Sherpa source or background instrument models.
<a href="#"><u>load_inst</u></a>	<a href="#"><u>sherpa</u></a>	Module function to load data from

<a href="#"><u>load_ph2</u></a>	<a href="#"><u>sherpa</u></a>	ARF and RMF files into Sherpa. load_instrument is an alternate name.	
<a href="#"><u>load_ph</u></a>	<a href="#"><u>sherpa</u></a>	Module function to load source and background data from PHA Type I files into Sherpa	
<a href="#"><u>load_rmf</u></a>	<a href="#"><u>sherpa</u></a>	Module function to load data from an RMF file into Sherpa	
<a href="#"><u>load</u></a>	<a href="#"><u>sherpa</u></a>	Summary of Sherpa/S–Lang module functions that load data into Sherpa	
<a href="#"><u>localtime</u></a>	<a href="#"><u>slangrtl</u></a>	Break down a time in seconds to local timezone	
<a href="#"><u>location</u></a>	<a href="#"><u>chips</u></a>	Specifies the location for an existing drawing area.	
<a href="#"><u>log10</u></a>	<a href="#"><u>slangrtl</u></a>	Compute the base–10 logarithm of an number	
<a href="#"><u>log</u></a>	<a href="#"><u>chips</u></a>	Changes one or more axes to logarithmic scale.	
<a href="#"><u>log</u></a>	<a href="#"><u>slangrtl</u></a>	Compute the logarithm of an number	
<a href="#"><u>lorentz1d</u></a>	<a href="#"><u>sherpa</u></a>	1–D normalized Lorentzian function. Integration ON.	
<a href="#"><u>lorentz2d</u></a>	<a href="#"><u>sherpa</u></a>	2–D unnormalized Lorentzian function. Integration OFF.	
<a href="#"><u>lplot</u></a>	<a href="#"><u>sherpa</u></a>	Causes the specified 1–D data to be displayed, via ChIPS.	
<a href="#"><u>lseek</u></a>	<a href="#"><u>slangrtl</u></a>	Reposition a file descriptor's file pointer	
<a href="#"><u>lstat_file</u></a>	<a href="#"><u>slangrtl</u></a>	Get information about a symbolic link	
<a href="#"><u>l</u></a>	<a href="#"><u>chips</u></a>	Defines the current label.	
<hr/>			
<b>M</b>	<a href="#"><u>make_printable_string</u></a>	<a href="#"><u>slangrtl</u></a>	Format a string suitable for parsing Mathematical operations in S–Lang.
	<a href="#"><u>math</u></a>	<a href="#"><u>slang</u></a>	
	<a href="#"><u>max</u></a>	<a href="#"><u>slangrtl</u></a>	Get the maximum value of an array
	<a href="#"><u>mcounts</u></a>	<a href="#"><u>sherpa</u></a>	Calculates the sum of convolved model amplitudes for source or background datasets.
	<a href="#"><u>mdl2latex</u></a>	<a href="#"><u>guide</u></a>	Output latex table of fitted emission lines and fluxes.
	<a href="#"><u>mdl</u></a>	<a href="#"><u>sherpa</u></a>	A Model Descriptor List (MDL) file stores a collection of datasets and

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<a href="#"><u>merge_all</u></a>	<a href="#"><u>tools</u></a>	model(s) in a structured format that can be read or written by Sherpa.
<a href="#"><u>merging_rules</u></a>	<a href="#"><u>concept</u></a>	Combine any number of observations. If desired, create corresponding exposure maps and exposure-corrected images.
<a href="#"><u>message</u></a>	<a href="#"><u>slangrtl</u></a>	A description of the merging rules used when combining header information.
<a href="#"><u>method</u></a>	<a href="#"><u>sherpa</u></a>	Print a string onto the message device
<a href="#"><u>min</u></a>	<a href="#"><u>slangrtl</u></a>	Specifies the optimization method. The command SEARCHMETHOD is equivalent.
<a href="#"><u>mkacisrmf</u></a>	<a href="#"><u>tools</u></a>	Get the minimum value of an array
<a href="#"><u>mkarf</u></a>	<a href="#"><u>tools</u></a>	Generate an RMF for Chandra imaging data
<a href="#"><u>mkgreg</u></a>	<a href="#"><u>tools</u></a>	Generate an ARF for Chandra imaging data (and grating 0-th order)
<a href="#"><u>mkdir</u></a>	<a href="#"><u>slangrtl</u></a>	Creates a stack of background regions for a given source list
<a href="#"><u>mkexpmap</u></a>	<a href="#"><u>tools</u></a>	Create a new directory
<a href="#"><u>mkfifo</u></a>	<a href="#"><u>slangrtl</u></a>	Generate a Chandra imaging exposure map (effective area vs. sky position)
<a href="#"><u>mkgarf</u></a>	<a href="#"><u>tools</u></a>	Create a named pipe
<a href="#"><u>mkgrmf</u></a>	<a href="#"><u>tools</u></a>	Generate a Chandra Grating ARF for one detector element.
<a href="#"><u>mkinstmap</u></a>	<a href="#"><u>tools</u></a>	Generate an RMF for Chandra grating data
<a href="#"><u>mkoif</u></a>	<a href="#"><u>tools</u></a>	Generate a Chandra instrument map (effective area vs. detector position)
<a href="#"><u>mkpsf</u></a>	<a href="#"><u>tools</u></a>	Create an OIF (observation index file) for a dataset
<a href="#"><u>mkrmf</u></a>	<a href="#"><u>tools</u></a>	Extract a point spread function (PSF) from the PSF library.
<a href="#"><u>mksubbgreg</u></a>	<a href="#"><u>tools</u></a>	Generate an RMF for Chandra imaging data
<a href="#"><u>mkwarf</u></a>	<a href="#"><u>tools</u></a>	Subtracts source regions from background regions
<a href="#"><u>mlr</u></a>	<a href="#"><u>sherpa</u></a>	Generate a weighted ARF for Chandra ACIS data
<a href="#"><u>modeexpr</u></a>	<a href="#"><u>sherpa</u></a>	Computes significance using the Maximum Likelihood Ratio test.

			Model components can be used to create model expressions, in conjunction with the SOURCE and BACKGROUND commands (which then are used to fit the data), or with model stacks:
<a href="#"><u>modelstack</u></a>	<a href="#"><u>sherpa</u></a>		A model stack assigns an arbitrary name to a model expression, for subsequent use in parameter expressions and/or nested models.
<a href="#"><u>models</u></a>	<a href="#"><u>sherpa</u></a>		Summary of Available Models
<a href="#"><u>monitor_photom</u></a>	<a href="#"><u>tools</u></a>		Generate a photometric lightcurve from ACA monitor data
<a href="#"><u>monte_lm</u></a>	<a href="#"><u>sherpa</u></a>		A Monte Carlo search utilizing the Powell method at each selected point.
<a href="#"><u>monte_powell</u></a>	<a href="#"><u>sherpa</u></a>		A Monte Carlo search utilizing the Powell method at each selected point.
<a href="#"><u>montecarlo</u></a>	<a href="#"><u>sherpa</u></a>		A Monte Carlo search of parameter space.
<a href="#"><u>mtl_build_gti</u></a>	<a href="#"><u>tools</u></a>		Create Good Time Interval from Mission Time Line and limits
<a href="#"><u>mtl</u></a>	<a href="#"><u>chandra</u></a>		A description of the Mission Time Line (MTL)
<a href="#"><u>mul2</u></a>	<a href="#"><u>slangrtl</u></a>		Multiply a number by 2
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<b>N</b>	<a href="#"><u>nbeta</u></a>	<a href="#"><u>sherpa</u></a>	1-D normalized beta function. Integration ON.
	<a href="#"><u>nestedmodel</u></a>	<a href="#"><u>sherpa</u></a>	Nested models define the function argument on which a model expression is evaluated to be another model expression. A nested model, <nested_model>, appears as an element of a model expression, <modelExpr>.
	<a href="#"><u>ngauss1d</u></a>	<a href="#"><u>sherpa</u></a>	1-D normalized Gaussian function. Integration ON.
	<a href="#"><u>noise</u></a>	<a href="#"><u>sherpa</u></a>	Defines an expression to be used for modeling detector noise in source and background datasets.
	<a href="#"><u>notice</u></a>	<a href="#"><u>sherpa</u></a>	Specifies a data portion to be included, for 1- or 2-D data.
	<a href="#"><u>numbersign</u></a>	<a href="#"><u>sherpa</u></a>	Denotes a comment. The symbol % also denotes a comment.

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<b>O</b>	<a href="#">obsvis</a>	<a href="#">proposaltools</a>	Observation Visualizer
	<a href="#">open</a>	<a href="#">sherpa</a>	Opens the image display window.
	<a href="#">open</a>	<a href="#">slangrtl</a>	Open a file
	<a href="#">oplot</a>	<a href="#">sherpa</a>	Causes multiple data curves to be displayed in the same drawing area, via ChIPS.
	<a href="#">overview</a>	<a href="#">slang</a>	Overview of the S–Lang programing language

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<b>P</b>	<a href="#">paccess</a>	<a href="#">paramio</a>	Returns the path to the specified parameter file.
	<a href="#">paccess</a>	<a href="#">tools</a>	Gives the location of a tool's parameter file
	<a href="#">pack</a>	<a href="#">chips</a>	Renumbers plotting objects after a delete operation.
	<a href="#">pack</a>	<a href="#">slangrtl</a>	Pack objects into a binary string
	<a href="#">pad_pack_format</a>	<a href="#">slangrtl</a>	Add padding to a pack format
	<a href="#">pagesize</a>	<a href="#">chips</a>	Sets the page dimensions for hardcopy plots.
	<a href="#">paramclose</a>	<a href="#">paramio</a>	Close a parameter file opened by paramopen.
	<a href="#">paramest</a>	<a href="#">sherpa</a>	An interactive interface to the parameter estimation routines in Sherpa.
	<a href="#">parameter</a>	<a href="#">concept</a>	Describes the parameter interface used by CIAO.
	<a href="#">paramio</a>	<a href="#">modules</a>	The S–Lang interface to the CXC parameter system
	<a href="#">paramopen</a>	<a href="#">paramio</a>	Open a parameter file.
	<a href="#">paramprompt</a>	<a href="#">sherpa</a>	Turns on/off prompting for model parameter values.
	<a href="#">paramset</a>	<a href="#">sherpa</a>	The model components that have been established in the current Sherpa session, and their parameter information, may be listed with the command SHOW MODELS. Values for these established model component parameters may be set individually using one of the following command syntax options:
	<a href="#">path_basename</a>	<a href="#">slangrtl</a>	Get the basename part of a pathname
	<a href="#">path_concat</a>	<a href="#">slangrtl</a>	Combine elements of a pathname
	<a href="#">path dirname</a>	<a href="#">slangrtl</a>	Get the directory name part of a pathname

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<a href="#"><u>path_extname</u></a>	<a href="#"><u>slangrtl</u></a>	Return the extension part of a pathname
<a href="#"><u>path_get_delimiter</u></a>	<a href="#"><u>slangrtl</u></a>	Get the value of a search-path delimiter
<a href="#"><u>path_is_absolute</u></a>	<a href="#"><u>slangrtl</u></a>	Determine whether or not a pathname is absolute
<a href="#"><u>path_sans_extname</u></a>	<a href="#"><u>slangrtl</u></a>	Strip the extension from a pathname
<a href="#"><u>pclose</u></a>	<a href="#"><u>slangrtl</u></a>	Close an object opened with popen
<a href="#"><u>pdump</u></a>	<a href="#"><u>tools</u></a>	Dumps the values of the parameters, with one parameter per line.
<a href="#"><u>peg</u></a>	<a href="#"><u>gui</u></a>	Parameter Editor Gui (for CXCDs parameter interface)
<a href="#"><u>pgets</u></a>	<a href="#"><u>paramio</u></a>	Read/write individual parameter values from S-Lang.
<a href="#"><u>pget</u></a>	<a href="#"><u>paramio</u></a>	Get a parameter value within S-Lang.
<a href="#"><u>pget</u></a>	<a href="#"><u>tools</u></a>	Get parameter values
<a href="#"><u>pickpoints</u></a>	<a href="#"><u>chips</u></a>	Starts the interactive cursor mode, which reads out the cursor position.
<a href="#"><u>pileup</u></a>	<a href="#"><u>chandra</u></a>	An overview of pileup in the Chandra ACIS detector.
<a href="#"><u>pileup</u></a>	<a href="#"><u>sherpa</u></a>	Defines the pileup model expression to be used for fitting a 1D dataset.
<a href="#"><u>pimms</u></a>	<a href="#"><u>proposaltools</u></a>	PIMMS (Portable, Interactive Multi-Mission Simulator) converts source fluxes and count rates between missions.
<a href="#"><u>pixlib</u></a>	<a href="#"><u>modules</u></a>	The S-Lang interface to the CXC pixlib library
<a href="#"><u>pix_apply_aspect</u></a>	<a href="#"><u>pixlib</u></a>	Convert from FPC to Sky tangent coordinates by applying an aspect solution.
<a href="#"><u>pix_chip_to_fpc</u></a>	<a href="#"><u>pixlib</u></a>	Convert from the Chip to Focal Plane coordinate (FPC) system.
<a href="#"><u>pix_chip_to_gdp</u></a>	<a href="#"><u>pixlib</u></a>	Convert from the Chip to Grating Dispersion Plane (GDP) coordinate system.
<a href="#"><u>pix_chip_to_tdet</u></a>	<a href="#"><u>pixlib</u></a>	Convert from the Chip to Tiled Detector (TDET) coordinate system.
<a href="#"><u>pix_close_pixlib</u></a>	<a href="#"><u>pixlib</u></a>	Convert between different Chandra coordinate systems in S-Lang
<a href="#"><u>pix_deapply_aspect</u></a>	<a href="#"><u>pixlib</u></a>	Convert from Sky tangent coordinates to FPC by reversing the aspect solution.
<a href="#"><u>pix_disp_config</u></a>	<a href="#"><u>pixlib</u></a>	Display the current settings of the pixlib module.

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<a href="#"><u>pix_dmTanPixToWorld</u></a>	<a href="#"><u>pixlib</u></a>	Convert from FPC to World (celestial) coordinates by applying an aspect solution.
<a href="#"><u>pix_dmTanWorldToPix</u></a>	<a href="#"><u>pixlib</u></a>	Convert from World (celestial) to FPC coordinates by applying an aspect solution.
<a href="#"><u>pix_fpc_to_chip</u></a>	<a href="#"><u>pixlib</u></a>	Convert from the Focal Plane (FPC) to Chip coordinate system.
<a href="#"><u>pix_fpc_to_gdp</u></a>	<a href="#"><u>pixlib</u></a>	Convert from the Focal Plane (FPC) to Grating Dispersion Plane (GDP) coordinate system.
<a href="#"><u>pix_fpc_to_msc</u></a>	<a href="#"><u>pixlib</u></a>	Convert from the Focal Plane (FPC) to Mirror Spherical (MSC) coordinate system.
<a href="#"><u>pix_gac_to_gdp</u></a>	<a href="#"><u>pixlib</u></a>	Convert from the Grating diffracted Angular coordinates (GAC) to Grating Dispersion Plane (GDP) coordinate system.
<a href="#"><u>pix_gdp_to_gac</u></a>	<a href="#"><u>pixlib</u></a>	Convert from the Grating Dispersion Plane (GDP) to Grating diffracted Angular coordinates (GAC) system.
<a href="#"><u>pix_get_energy</u></a>	<a href="#"><u>pixlib</u></a>	Return the photon energy corresponding to a given grating dispersion (GAC) value.
<a href="#"><u>pix_get_flength</u></a>	<a href="#"><u>pixlib</u></a>	Return the value of the telescope focal length used by the pixlib module.
<a href="#"><u>pix_get_grating_angle</u></a>	<a href="#"><u>pixlib</u></a>	Return the grating angle of the currently-selected grating arm.
<a href="#"><u>pix_get_grating_period</u></a>	<a href="#"><u>pixlib</u></a>	Return the grating period of the currently-selected grating arm.
<a href="#"><u>pix_get_grating_wavelength</u></a>	<a href="#"><u>pixlib</u></a>	Return the photon wavelength corresponding to a given grating dispersion (GAC) value.
<a href="#"><u>pix_get_rowland</u></a>	<a href="#"><u>pixlib</u></a>	Return the value of the Rowland Circle diameter used by the pixlib module.
<a href="#"><u>pix_init_pixlib</u></a>	<a href="#"><u>pixlib</u></a>	Initialize the pixlib library.
<a href="#"><u>pix_set_aimpoint</u></a>	<a href="#"><u>pixlib</u></a>	Set the aim point to be used by the pixlib module.
<a href="#"><u>pix_set_detector</u></a>	<a href="#"><u>pixlib</u></a>	Set the detector to use in the pixlib routines.
<a href="#"><u>pix_set_fpsys</u></a>	<a href="#"><u>pixlib</u></a>	Set the focal plane system for the pixlib module.
<a href="#"><u>pix_set_gdpsys</u></a>	<a href="#"><u>pixlib</u></a>	Set the grating dispersion plane (GDP) system for the pixlib module.

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<a href="#"><u>pix_set_grating</u></a>	<a href="#"><u>pixlib</u></a>	Set the grating arm and order to use in the pixlib module.
<a href="#"><u>pix_set_gzo</u></a>	<a href="#"><u>pixlib</u></a>	Set the grating zero-order position for the pixlib module.
<a href="#"><u>pix_set_simoffset</u></a>	<a href="#"><u>pixlib</u></a>	Set the stage position for the pixlib module.
<a href="#"><u>pix_set_tdetsys</u></a>	<a href="#"><u>pixlib</u></a>	Set the tiled detector plane system for the pixlib module.
<a href="#"><u>pix_tdet_to_chip</u></a>	<a href="#"><u>pixlib</u></a>	Convert from the Tiled Detector (TDET) to Chip coordinate system.
<a href="#"><u>pline</u></a>	<a href="#"><u>tools</u></a>	Display the parameter values, with all parameters on a single line
<a href="#"><u>plist_names</u></a>	<a href="#"><u>paramio</u></a>	List parameter names for a single tool from S-Lang.
<a href="#"><u>plist</u></a>	<a href="#"><u>tools</u></a>	List the contents of a parameter file.
<a href="#"><u>plotx</u></a>	<a href="#"><u>sherpa</u></a>	[REMOVED AS OF CIAO 3.0.2] Sets the unit type for the x-axis of a plot.
<a href="#"><u>ploty</u></a>	<a href="#"><u>sherpa</u></a>	Sets the unit type for the y-axis of a plot.
<a href="#"><u>plot_eprof</u></a>	<a href="#"><u>sherpa</u></a>	Display a radial profile (elliptical annuli) of 2D data, fit, and residuals.
<a href="#"><u>plot_rprof</u></a>	<a href="#"><u>sherpa</u></a>	Display a radial profile (circular annuli) of 2D data, fit, and residuals.
<a href="#"><u>poisson</u></a>	<a href="#"><u>sherpa</u></a>	Poisson function. Integration OFF.
<a href="#"><u>polynom1d</u></a>	<a href="#"><u>sherpa</u></a>	1-D polynomial function. Integration ON.
<a href="#"><u>polynom2d</u></a>	<a href="#"><u>sherpa</u></a>	2-D polynomial function. Integration ON.
<a href="#"><u>polynom</u></a>	<a href="#"><u>slangrtl</u></a>	Evaluate a polynomial
<a href="#"><u>popen</u></a>	<a href="#"><u>slangrtl</u></a>	Open a process
<a href="#"><u>pop</u></a>	<a href="#"><u>slangrtl</u></a>	Discard an item from the stack
<a href="#"><u>powell</u></a>	<a href="#"><u>sherpa</u></a>	The Powell optimization method.
<a href="#"><u>powlaw1d</u></a>	<a href="#"><u>sherpa</u></a>	1-D power law. Integration ON.
<a href="#"><u>pquery</u></a>	<a href="#"><u>paramio</u></a>	Query a parameter value from S-Lang.
<a href="#"><u>pquery</u></a>	<a href="#"><u>tools</u></a>	Query whether a parameter exists and, if so, get and return its value.
<a href="#"><u>precess</u></a>	<a href="#"><u>proposaltools</u></a>	Interactive astronomical coordinate conversion program that provides precession of equatorial coordinates and conversion between equatorial, ecliptic, galactic, and supergalactic coordinates
<a href="#"><u>prepend_to_slang_load_path</u></a>	<a href="#"><u>slangrtl</u></a>	Prepend a directory to the load-path

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<a href="#"><u>printf</u></a>	<a href="#"><u>slangrtl</u></a>	Create and write a formatted string to stdout
<a href="#"><u>print</u></a>	<a href="#"><u>chips</u></a>	Creates a hardcopy of the current plot.
<a href="#"><u>print</u></a>	<a href="#"><u>varmm</u></a>	S–Lang functions to print variables, arrays and structures
<a href="#"><u>prism</u></a>	<a href="#"><u>gui</u></a>	Format–independent file browsing GUI
<a href="#"><u>projection</u></a>	<a href="#"><u>sherpa</u></a>	Estimates confidence intervals for selected thawed parameters.
<a href="#"><u>prompt</u></a>	<a href="#"><u>sherpa</u></a>	Changes the Sherpa prompt.
<a href="#"><u>prop–coords</u></a>	<a href="#"><u>proposaltools</u></a>	Defines available coordinate systems for Chandra Proposal Tools
<a href="#"><u>prop–time</u></a>	<a href="#"><u>proposaltools</u></a>	Defines available calendars and timescales for Chandra Proposal Tools
<a href="#"><u>prop–tools</u></a>	<a href="#"><u>proposaltools</u></a>	Tools that aid in the preparation and submission of Chandra proposals
<a href="#"><u>provide</u></a>	<a href="#"><u>slangrtl</u></a>	Declare that a specified feature is available
<a href="#"><u>pset</u></a>	<a href="#"><u>paramio</u></a>	Set a parameter value within S–Lang.
<a href="#"><u>pset</u></a>	<a href="#"><u>tools</u></a>	Set parameter values on the command line
<a href="#"><u>psextract</u></a>	<a href="#"><u>tools</u></a>	Extract source and background ACIS spectra for point–like sources and build associated ARFs and RMFs.
<a href="#"><u>psf_project_ray</u></a>	<a href="#"><u>tools</u></a>	Project rays generated by ChaRT onto a semi–infinite detector plane.
<a href="#"><u>ptsrc1d</u></a>	<a href="#"><u>sherpa</u></a>	A 1–D file–based point–source fitting model.
<a href="#"><u>ptsrc2d</u></a>	<a href="#"><u>sherpa</u></a>	A 2–D file–based point–source fitting model.
<a href="#"><u>punlearn</u></a>	<a href="#"><u>paramio</u></a>	Restore the system defaults for a parameter file from S–Lang.
<a href="#"><u>punlearn</u></a>	<a href="#"><u>tools</u></a>	Restore system default parameter values
<a href="#"><u>putenv</u></a>	<a href="#"><u>slangrtl</u></a>	Add or change an environment variable

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<b>Q</b>	<a href="#"><u>quizcaldb</u></a>	<a href="#"><u>tools</u></a>	Find calibration files in the CALDB
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<b>R</b>	<a href="#"><u>readarf</u></a>	<a href="#"><u>varmm</u></a>	S–Lang function to read an Ancillary Response File (ARF)
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## Ahelp (alphabetical) – CIAO 3.4

<a href="#"><u>readascii</u></a>	<a href="#"><u>varmm</u></a>	S–Lang function to read in an ASCII data file.
<a href="#"><u>readbintab</u></a>	<a href="#"><u>varmm</u></a>	S–Lang function to read a FITS binary table.
<a href="#"><u>readfile</u></a>	<a href="#"><u>varmm</u></a>	S–Lang functions to read a data file into a S–Lang variable.
<a href="#"><u>readimage</u></a>	<a href="#"><u>varmm</u></a>	S–Lang function to read a FITS image.
<a href="#"><u>readlink</u></a>	<a href="#"><u>slangrtl</u></a>	Get the value of a symbolic link
<a href="#"><u>readpha</u></a>	<a href="#"><u>varmm</u></a>	S–Lang function to read a spectrum in PHA format (both type I and II)
<a href="#"><u>readrdb</u></a>	<a href="#"><u>varmm</u></a>	S–Lang function to read a file in RDB format.
<a href="#"><u>readrmf</u></a>	<a href="#"><u>varmm</u></a>	S–Lang function to read a Redistribution Matrix File (RMF)
<a href="#"><u>read</u></a>	<a href="#"><u>sherpa</u></a>	Inputs the contents of one or more files.
<a href="#"><u>read</u></a>	<a href="#"><u>slangrtl</u></a>	Read from an open file descriptor
<a href="#"><u>Real</u></a>	<a href="#"><u>slangrtl</u></a>	Compute the real part of a number
<a href="#"><u>record</u></a>	<a href="#"><u>sherpa</u></a>	Controls output of parameters values and statistics to an ASCII file.
<a href="#"><u>redo</u></a>	<a href="#"><u>chips</u></a>	Redoes the most recently undone plotting command.
<a href="#"><u>redraw</u></a>	<a href="#"><u>chips</u></a>	Redraws the plot or sets the redraw mode
<a href="#"><u>regArea</u></a>	<a href="#"><u>region</u></a>	Calculate the area enclosed by a region.
<a href="#"><u>regExtent</u></a>	<a href="#"><u>region</u></a>	Calculate the bounding box of a region.
<a href="#"><u>regInsideRegion</u></a>	<a href="#"><u>region</u></a>	Is a point (or set of points) inside a region?
<a href="#"><u>region–projection</u></a>	<a href="#"><u>sherpa</u></a>	Creates a contour plot of confidence regions using the PROJECTION algorithm. The commands REG–PROJ and REGPROJ are abbreviated equivalents.
<a href="#"><u>region–uncertainty</u></a>	<a href="#"><u>sherpa</u></a>	Creates a contour plot of confidence regions using the UNCERTAINTY algorithm. The commands REG–UNC and REGUNC are abbreviated equivalents.
<a href="#"><u>regions</u></a>	<a href="#"><u>tools</u></a>	regions.sl – Display the FEF regions covered by a source
<a href="#"><u>region</u></a>	<a href="#"><u>modules</u></a>	The S–Lang interface to the CXC region library

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<a href="#"><u>regParse</u></a>	<a href="#"><u>region</u></a>	Parse a region for use by the routines in the region library
<a href="#"><u>regPrintRegion</u></a>	<a href="#"><u>region</u></a>	Print out details about a region.
<a href="#"><u>regRegionString</u></a>	<a href="#"><u>region</u></a>	Print out details about a region.
<a href="#"><u>relativesize</u></a>	<a href="#"><u>chips</u></a>	Alters the relative size of drawing areas. The command RELSIZE is equivalent.
<a href="#"><u>remove</u></a>	<a href="#"><u>slangrtl</u></a>	Delete a file
<a href="#"><u>rename</u></a>	<a href="#"><u>sherpa</u></a>	Changes the name that has been given to a model component by the user.
<a href="#"><u>rename</u></a>	<a href="#"><u>slangrtl</u></a>	Rename a file
<a href="#"><u>reproject aspect</u></a>	<a href="#"><u>tools</u></a>	Modify aspect solution file RA, Dec, and roll or updfile WCS to minimize position differences between two source lists.
<a href="#"><u>reproject events</u></a>	<a href="#"><u>tools</u></a>	Regrid an event file (or stack) to a common tangent point
<a href="#"><u>reproject image grid</u></a>	<a href="#"><u>tools</u></a>	Projects image from one WCS to another
<a href="#"><u>reproject image</u></a>	<a href="#"><u>tools</u></a>	Projects image from one WCS to another
<a href="#"><u>require</u></a>	<a href="#"><u>slangrtl</u></a>	Make sure a feature is present, and load it if not
<a href="#"><u>reset</u></a>	<a href="#"><u>sherpa</u></a>	Restores settings and/or parameter values.
<a href="#"><u>reshape</u></a>	<a href="#"><u>slangrtl</u></a>	Reshape an array
<a href="#"><u>restore paramest</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to restore the default values of the parameters used to configure each Sherpa parameter estimation method.
<a href="#"><u>restore</u></a>	<a href="#"><u>chips</u></a>	Restores a plot with all attributes.
<a href="#"><u>reverse</u></a>	<a href="#"><u>varmm</u></a>	S–Lang function to reverse a 1D array
<a href="#"><u>rmdir</u></a>	<a href="#"><u>slangrtl</u></a>	Remove a directory
<a href="#"><u>rmfimg</u></a>	<a href="#"><u>tools</u></a>	Create a simple image of an RMF or ARF file
<a href="#"><u>rsp2d</u></a>	<a href="#"><u>sherpa</u></a>	A 2–D instrument model utilizing an exposure map and point–spread function.
<a href="#"><u>rsp</u></a>	<a href="#"><u>sherpa</u></a>	A 1–D instrument model.
<a href="#"><u>run_fit</u></a>	<a href="#"><u>sherpa</u></a>	Module function to fit datasets, and retrieve information about the final fit.
<a href="#"><u>run_paramestint</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to display statistics as a function of parameter

<a href="#"><u>run_paramestlim</u></a>	<a href="#"><u>sherpa</u></a>	value, and to retrieve the value and statistic arrays
<a href="#"><u>run_paramestreg</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to determine confidence intervals, and retrieve the parameter bounds.
<a href="#"><u>run_paramest</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to display contours of statistics as a function of parameter values, and to retrieve arrays of values and statistics
<a href="#"><u>run</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to run parameter estimation routines and retrieve information.
		Summary of Sherpa/S–Lang module run functions.
<hr/>		
<b>S</b>		
<a href="#"><u>save_state</u></a>	<a href="#"><u>sherpa</u></a>	The save_state() function
<a href="#"><u>save</u></a>	<a href="#"><u>sherpa</u></a>	Saves information to an ASCII file.
<a href="#"><u>schechter</u></a>	<a href="#"><u>sherpa</u></a>	Schechter function. Integration OFF.
<a href="#"><u>session</u></a>	<a href="#"><u>concept</u></a>	A session is a conceptual notion of how various CIAO applications interact with each other to form an integrated data analysis environment.
<a href="#"><u>setback</u></a>	<a href="#"><u>sherpa</u></a>	Sets attributes of a background dataset.
<a href="#"><u>setdata</u></a>	<a href="#"><u>sherpa</u></a>	Sets attributes of a source dataset.
<a href="#"><u>setgid</u></a>	<a href="#"><u>slangrtl</u></a>	Set the group–id of the current process
<a href="#"><u>setpgid</u></a>	<a href="#"><u>slangrtl</u></a>	Set the process group–id
<a href="#"><u>setplot</u></a>	<a href="#"><u>sherpa</u></a>	An alternative interface to the Sherpa plot customisation variables
<a href="#"><u>setuid</u></a>	<a href="#"><u>slangrtl</u></a>	Set the user–id of the current process
<a href="#"><u>set_analysis</u></a>	<a href="#"><u>sherpa</u></a>	Module function to set the units for 1–D spectral analysis.
<a href="#"><u>set_axes</u></a>	<a href="#"><u>sherpa</u></a>	Module functions for creating new source or background dataspaces.
<a href="#"><u>set_backscale</u></a>	<a href="#"><u>sherpa</u></a>	Module functions for setting source and background extraction region areas.
<a href="#"><u>set_coord</u></a>	<a href="#"><u>sherpa</u></a>	Module function to set the coordinate system for 2–D image analysis.
<a href="#"><u>set_dataspace</u></a>	<a href="#"><u>sherpa</u></a>	An alternative form of DATASPACE and set_axes().

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<a href="#"><u>set_data</u></a>	<a href="#"><u>sherpa</u></a>	Set source and background data using the S-lang module function in Sherpa.
<a href="#"><u>set_dir</u></a>	<a href="#"><u>sherpa</u></a>	Module function to change directories.
<a href="#"><u>set_eroff</u></a>	<a href="#"><u>sherpa</u></a>	Switch off the drawing of error bars in Sherpa plots
<a href="#"><u>set_eron</u></a>	<a href="#"><u>sherpa</u></a>	Switch on the drawing of error bars in Sherpa plots
<a href="#"><u>set_errors</u></a>	<a href="#"><u>sherpa</u></a>	Module functions for assigning source and background error estimates.
<a href="#"><u>set_exptime</u></a>	<a href="#"><u>sherpa</u></a>	Module functions for setting source and background exposure times.
<a href="#"><u>set_filter</u></a>	<a href="#"><u>sherpa</u></a>	Module functions for assigning source and background filters from an array.
<a href="#"><u>set_float_format</u></a>	<a href="#"><u>slangrtl</u></a>	Set the format for printing floating point values.
<a href="#"><u>set_groups</u></a>	<a href="#"><u>sherpa</u></a>	Module functions for grouping and setting quality to source and background files from an array.
<a href="#"><u>set_ignore2d</u></a>	<a href="#"><u>sherpa</u></a>	Module functions for ignoring source and background regions in 2-D datasets.
<a href="#"><u>set_ignore_all</u></a>	<a href="#"><u>sherpa</u></a>	Module functions for ignoring all source and background data.
<a href="#"><u>set_ignore_bad</u></a>	<a href="#"><u>sherpa</u></a>	Module functions for ignoring bad (quality > 0) channels.
<a href="#"><u>set_ignore</u></a>	<a href="#"><u>sherpa</u></a>	Module functions for ignoring source and background filter ranges in 1-D datasets.
<a href="#"><u>set_import_module_path</u></a>	<a href="#"><u>slangrtl</u></a>	Set the search path for dynamically loadable objects
<a href="#"><u>set_lin</u></a>	<a href="#"><u>sherpa</u></a>	Switch plotting axis to linear scale in Sherpa plots
<a href="#"><u>set_log</u></a>	<a href="#"><u>sherpa</u></a>	Switch axis to log in Sherpa plots
<a href="#"><u>set_notice2d</u></a>	<a href="#"><u>sherpa</u></a>	Module functions for noticing source and background regions in 2-D datasets.
<a href="#"><u>set_notice_all</u></a>	<a href="#"><u>sherpa</u></a>	Module functions for noticing all source and background data.
<a href="#"><u>set_notice</u></a>	<a href="#"><u>sherpa</u></a>	Module functions for noticing source and background filter ranges in 1-D datasets.
<a href="#"><u>set_paramset</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to thaw or freeze

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<a href="#"><u>set_par</u></a>	<a href="#"><u>sherpa</u></a>	the specified parameter(s).
<a href="#"><u>set_slang_load_path</u></a>	<a href="#"><u>slangrtl</u></a>	Module function for setting model parameter values, etc.
<a href="#"><u>set_stackexpr</u></a>	<a href="#"><u>sherpa</u></a>	Set the value of the interpreter's load-path
<a href="#"><u>set_state_defaults</u></a>	<a href="#"><u>varmm</u></a>	Module functions to set a model stack expression.
<a href="#"><u>set_state</u></a>	<a href="#"><u>varmm</u></a>	Restore the default values of state (configuration) variables
<a href="#"><u>set_struct_fields</u></a>	<a href="#"><u>slangrtl</u></a>	Set multiple fields of a state (configuration) variable
<a href="#"><u>set_struct_field</u></a>	<a href="#"><u>slangrtl</u></a>	Set the fields of a structure
<a href="#"><u>set_subtract</u></a>	<a href="#"><u>sherpa</u></a>	Set the value associated with a structure field
<a href="#"><u>set_subtract</u></a>	<a href="#"><u>sherpa</u></a>	Module functions to subtract background from a source dataset, or to undo subtraction.
<a href="#"><u>set_syserrors</u></a>	<a href="#"><u>sherpa</u></a>	Module functions for assigning source and background systematic error estimates.
<a href="#"><u>set_verbose</u></a>	<a href="#"><u>sherpa</u></a>	Module function to reset Sherpa's verbosity.
<a href="#"><u>set_weights</u></a>	<a href="#"><u>sherpa</u></a>	Module functions for assigning source and background statistical weights.
<a href="#"><u>set</u></a>	<a href="#"><u>sherpa</u></a>	Summary of Sherpa/S-Lang module functions that change settings or data.
<a href="#"><u>sherpa-module</u></a>	<a href="#"><u>sherpa</u></a>	Accessing data with the Sherpa/S-Lang module functions.
<a href="#"><u>sherpa-plot-hooks</u></a>	<a href="#"><u>sherpa</u></a>	Customizing Sherpa plots using the prefunc and postfunc fields of Sherpa State Objects
<a href="#"><u>sherpa.cov</u></a>	<a href="#"><u>sherpa</u></a>	Configure COVARIANCE in Sherpa.
<a href="#"><u>sherpa.dataplot</u></a>	<a href="#"><u>sherpa</u></a>	Configure appearance of Sherpa plots.
<a href="#"><u>sherpa.fitplot</u></a>	<a href="#"><u>sherpa</u></a>	Configure appearance of Sherpa plots.
<a href="#"><u>sherpa.intproj</u></a>	<a href="#"><u>sherpa</u></a>	Configure INTERVAL-PROJECTION in Sherpa.
<a href="#"><u>sherpa.intunc</u></a>	<a href="#"><u>sherpa</u></a>	Configure INTERVAL-UNCERTAINTY in Sherpa.
<a href="#"><u>sherpa.multiplot</u></a>	<a href="#"><u>sherpa</u></a>	

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<a href="#"><u>sherpa.output</u></a>	<a href="#"><u>sherpa</u></a>	Configure appearance of Sherpa plots.
<a href="#"><u>sherpa.plot</u></a>	<a href="#"><u>sherpa</u></a>	A Description of the sherpa.output State Object
<a href="#"><u>sherpa.proj</u></a>	<a href="#"><u>sherpa</u></a>	Configure appearance of Sherpa plots.
<a href="#"><u>sherpa.reproj</u></a>	<a href="#"><u>sherpa</u></a>	Configure PROJECTION in Sherpa.
<a href="#"><u>sherpa.regunc</u></a>	<a href="#"><u>sherpa</u></a>	Configure REGION–PROJECTION in Sherpa.
<a href="#"><u>sherpa.resplot</u></a>	<a href="#"><u>sherpa</u></a>	Configure REGION–UNCERTAINTY in Sherpa.
<a href="#"><u>sherpa.unc</u></a>	<a href="#"><u>sherpa</u></a>	Configure appearance of Sherpa plots.
<a href="#"><u>sherpa_eval</u></a>	<a href="#"><u>sherpa</u></a>	Configure UNCERTAINTY in Sherpa.
<a href="#"><u>sherpa_plotfn</u>s</a>	<a href="#"><u>sherpa</u></a>	Call Sherpa commands from S–Lang
<a href="#"><u>sherpa_utils</u></a>	<a href="#"><u>sherpa</u></a>	Plot–related functions for Sherpa.
<a href="#"><u>sherpa</u></a>	<a href="#"><u>sherpa</u></a>	Provides a number of S–Lang functions useful for Sherpa.
<a href="#"><u>shexp10</u></a>	<a href="#"><u>sherpa</u></a>	Command summary of Sherpa, CIAO's modeling and fitting engine.
<a href="#"><u>shexp</u></a>	<a href="#"><u>sherpa</u></a>	Exponential function, base 10.
<a href="#"><u>shift</u></a>	<a href="#"><u>slangrtl</u></a>	Integration OFF.
<a href="#"><u>shlog10</u></a>	<a href="#"><u>sherpa</u></a>	Exponential function. Integration OFF.
<a href="#"><u>shlog</u></a>	<a href="#"><u>sherpa</u></a>	Shift the elements of a 1–d array
<a href="#"><u>show_tgain_corr</u></a>	<a href="#"><u>tools</u></a>	Logarithm function, base 10.
<a href="#"><u>show_wgt</u></a>	<a href="#"><u>tools</u></a>	Integration OFF.
<a href="#"><u>show</u></a>	<a href="#"><u>sherpa</u></a>	Natural logarithm function.
<a href="#"><u>sigma-rejection</u></a>	<a href="#"><u>sherpa</u></a>	Integration OFF.
<a href="#"><u>show</u></a>	<a href="#"><u>tools</u></a>	Display the time–dependent gain correction for a given chip location.
<a href="#"><u>show_wgt.sl</u></a>		show_wgt.sl – Examine the weights file created by mkwarf
<a href="#"><u>sign</u></a>	<a href="#"><u>slangrtl</u></a>	Reports current status.
<a href="#"><u>simplex</u></a>	<a href="#"><u>sherpa</u></a>	The SIGMA–REJECTION optimization method for fits to 1–D data. Alternate names are SIG–REJ and SR.
<a href="#"><u>simspec</u></a>	<a href="#"><u>sherpa</u></a>	Compute the sign of a number
		A simplex optimization method.
		Create and fit a simulated PHA spectrum.

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<a href="#"><u>simul–ann–1</u></a>	<a href="#"><u>sherpa</u></a>	A simulated annealing search, with one parameter varied at each step.
<a href="#"><u>simul–ann–2</u></a>	<a href="#"><u>sherpa</u></a>	A simulated annealing search, with all parameters varied at each step.
<a href="#"><u>simul–pow–1</u></a>	<a href="#"><u>sherpa</u></a>	A combination of SIMUL–ANN–1 with POWELL.
<a href="#"><u>simul–pow–2</u></a>	<a href="#"><u>sherpa</u></a>	A combination of SIMUL–ANN–2 with POWELL.
<a href="#"><u>sinh</u></a>	<a href="#"><u>slangrtl</u></a>	Compute the hyperbolic sine of an number
<a href="#"><u>sin</u></a>	<a href="#"><u>sherpa</u></a>	Sine function. Integration OFF.
<a href="#"><u>sin</u></a>	<a href="#"><u>slangrtl</u></a>	Compute the sine of an number
<a href="#"><u>sizeof_pack</u></a>	<a href="#"><u>slangrtl</u></a>	Compute the size implied by a pack format string
<a href="#"><u>skip</u></a>	<a href="#"><u>chips</u></a>	Skips the designated number of lines from subsequent input files.
<a href="#"><u>skyfov</u></a>	<a href="#"><u>tools</u></a>	Make a field-of-view region in sky coordinates
<a href="#"><u>slangrtl</u></a>	<a href="#"><u>slangrtl</u></a>	S–Lang Run Time Library
<a href="#"><u>slang</u></a>	<a href="#"><u>slang</u></a>	The S–Lang programing language
<a href="#"><u>sleep</u></a>	<a href="#"><u>slangrtl</u></a>	Pause for a specified number of seconds
<a href="#"><u>slsh</u></a>	<a href="#"><u>slang</u></a>	Evaluate and run S–Lang code.
<a href="#"><u>slxpa_errno</u></a>	<a href="#"><u>xpa</u></a>	This variable stores the error status for the XPA commands.
<a href="#"><u>source</u></a>	<a href="#"><u>sherpa</u></a>	Defines the source model expression to be used for fitting a dataset. The command SRC is an abbreviated equivalent.
<a href="#"><u>specextract</u></a>	<a href="#"><u>tools</u></a>	Extract source and background ACIS spectra for point-like and extended sources and build associated WMAPs, ARFs and RMFs.
<a href="#"><u>spectrum</u></a>	<a href="#"><u>tools</u></a>	spectrum.sl – Calculate spectral weights for creating an instrument map
<a href="#"><u>split</u></a>	<a href="#"><u>chips</u></a>	Creates multiple drawing areas and/or arranges their locations.
<a href="#"><u>splot</u></a>	<a href="#"><u>sherpa</u></a>	Causes the specified 2-D data to be displayed, with a surface plot, via ChIPS.
<a href="#"><u>sprintf</u></a>	<a href="#"><u>slangrtl</u></a>	Format objects into a string
<a href="#"><u>sqrt</u></a>	<a href="#"><u>sherpa</u></a>	Square root function. Integration OFF.

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<a href="#"><u>sqrt</u></a>	<a href="#"><u>slangrtl</u></a>	Compute the square root of a number
<a href="#"><u>sqr</u></a>	<a href="#"><u>slangrtl</u></a>	Compute the square of a number
<a href="#"><u>sscanf</u></a>	<a href="#"><u>slangrtl</u></a>	Parse a formatted string
<a href="#"><u>sso_freeze</u></a>	<a href="#"><u>tools</u></a>	Reproject sky x and y coordinates into a Solar System Object centered reference frame.
<a href="#"><u>sstats</u></a>	<a href="#"><u>tools</u></a>	sstats.sl – Calculate statistics of images
<a href="#"><u>stackio</u></a>	<a href="#"><u>modules</u></a>	The S-Lang interface to the CXC stack library
<a href="#"><u>stack</u></a>	<a href="#"><u>concept</u></a>	How to set a parameter to more than one value using a stack.
<a href="#"><u>stataerrs</u></a>	<a href="#"><u>sherpa</u></a>	Defines an expression or file to be used to specify the statistical errors for source data.
<a href="#"><u>statistic</u></a>	<a href="#"><u>sherpa</u></a>	Specifies the fitting statistic.
<a href="#"><u>stat_file</u></a>	<a href="#"><u>slangrtl</u></a>	Get information about a file
<a href="#"><u>stat_is</u></a>	<a href="#"><u>slangrtl</u></a>	Parse the st_mode field of a stat structure
<a href="#"><u>stephi1d</u></a>	<a href="#"><u>sherpa</u></a>	1-D step function. Integration OFF. The command HIGHPASS is equivalent.
<a href="#"><u>stepl01d</u></a>	<a href="#"><u>sherpa</u></a>	1-D step function. Integration OFF. The command LOWPASS is equivalent.
<a href="#"><u>stk_append</u></a>	<a href="#"><u>stackio</u></a>	Add an item (or items) to a stack.
<a href="#"><u>stk_build</u></a>	<a href="#"><u>stackio</u></a>	Build a stack from text input (file name or regular expression).
<a href="#"><u>stk_build</u></a>	<a href="#"><u>tools</u></a>	stk_build is used to build a stack from a user-defined string. The output is to stdout, stderr, or a file.
<a href="#"><u>stk_change_current</u></a>	<a href="#"><u>stackio</u></a>	Change the current element of a stack.
<a href="#"><u>stk_change_num</u></a>	<a href="#"><u>stackio</u></a>	Change the given element of a stack.
<a href="#"><u>stk_close</u></a>	<a href="#"><u>stackio</u></a>	Close a stack.
<a href="#"><u>stk_count</u></a>	<a href="#"><u>stackio</u></a>	Returns the number of elements in a stack.
<a href="#"><u>stk_count</u></a>	<a href="#"><u>tools</u></a>	stk_count is used to count the number of items in a stack. The output is to the stk_count parameter file.
<a href="#"><u>stk_current</u></a>	<a href="#"><u>stackio</u></a>	Returns the current position of the stack.

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<a href="#"><u>stk_delete_current</u></a>	<a href="#"><u>stackio</u></a>	Deletes the current element from the stack.
<a href="#"><u>stk_delete_num</u></a>	<a href="#"><u>stackio</u></a>	Deletes the specified element from the stack.
<a href="#"><u>stk_disp</u></a>	<a href="#"><u>stackio</u></a>	Display the contents of a stack.
<a href="#"><u>stk_expand_n</u></a>	<a href="#"><u>stackio</u></a>	Create a numbered stack of N elements.
<a href="#"><u>stk_read_next</u></a>	<a href="#"><u>stackio</u></a>	Returns the next element from a stack.
<a href="#"><u>stk_read_num</u></a>	<a href="#"><u>stackio</u></a>	Returns the selected element from a stack.
<a href="#"><u>stk_read_num</u></a>	<a href="#"><u>tools</u></a>	stk_read_num is used to read one element of a user-defined stack. The output is to the outelement field of the stk_read_num parameter file.
<a href="#"><u>stk_rewind</u></a>	<a href="#"><u>stackio</u></a>	Rewind the stack to its starting position.
<a href="#"><u>stk_set_current</u></a>	<a href="#"><u>stackio</u></a>	Sets the current position of the stack.
<a href="#"><u>stk_where</u></a>	<a href="#"><u>tools</u></a>	stk_where finds the location of an item in a stack
<a href="#"><u>store</u></a>	<a href="#"><u>chips</u></a>	Saves a plot with all attributes.
<a href="#"><u>strcat</u></a>	<a href="#"><u>slangrtl</u></a>	Concatenate strings
<a href="#"><u>strchopr</u></a>	<a href="#"><u>slangrtl</u></a>	Chop or split a string into substrings.
<a href="#"><u>strchop</u></a>	<a href="#"><u>slangrtl</u></a>	Chop or split a string into substrings.
<a href="#"><u>strcmp</u></a>	<a href="#"><u>slangrtl</u></a>	Compare two strings
<a href="#"><u>strcompress</u></a>	<a href="#"><u>slangrtl</u></a>	Remove excess whitespace characters from a string
<a href="#"><u>string_match_nth</u></a>	<a href="#"><u>slangrtl</u></a>	Get the result of the last call to string_match
<a href="#"><u>string_match</u></a>	<a href="#"><u>slangrtl</u></a>	Match a string against a regular expression
<a href="#"><u>string</u></a>	<a href="#"><u>slangrtl</u></a>	Convert an object to a string representation.
<a href="#"><u>strjoin</u></a>	<a href="#"><u>slangrtl</u></a>	Concatenate elements of a string array
<a href="#"><u>strlen</u></a>	<a href="#"><u>slangrtl</u></a>	Compute the length of a string
<a href="#"><u>strlow</u></a>	<a href="#"><u>slangrtl</u></a>	Convert a string to lowercase
<a href="#"><u>strncmp</u></a>	<a href="#"><u>slangrtl</u></a>	Compare the first few characters of two strings
<a href="#"><u>strong</u></a>	<a href="#"><u>guide</u></a>	List "strong" emission lines at a given temperature, within specified wavelength bounds.

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<a href="#"><u>strreplace</u></a>	<a href="#"><u>slangrtl</u></a>	Replace one or more substrings
<a href="#"><u>strsub</u></a>	<a href="#"><u>slangrtl</u></a>	Replace a character with another in a string.
<a href="#"><u>strtok</u></a>	<a href="#"><u>slangrtl</u></a>	Extract tokens from a string
<a href="#"><u>strtrans</u></a>	<a href="#"><u>slangrtl</u></a>	Replace characters in a string
<a href="#"><u>strtrim_beg</u></a>	<a href="#"><u>slangrtl</u></a>	Remove leading whitespace from a string
<a href="#"><u>strtrim_end</u></a>	<a href="#"><u>slangrtl</u></a>	Remove trailing whitespace from a string
<a href="#"><u>strtrim</u></a>	<a href="#"><u>slangrtl</u></a>	Remove whitespace from the ends of a string
<a href="#"><u>strup</u></a>	<a href="#"><u>slangrtl</u></a>	Convert a string to uppercase
<a href="#"><u>str_delete_chars</u></a>	<a href="#"><u>slangrtl</u></a>	Delete characters from a string
<a href="#"><u>str_quote_string</u></a>	<a href="#"><u>slangrtl</u></a>	Escape characters in a string.
<a href="#"><u>str_replace</u></a>	<a href="#"><u>slangrtl</u></a>	Replace a substring of a string
<a href="#"><u>str_uncomment_string</u></a>	<a href="#"><u>slangrtl</u></a>	Remove comments from a string
<a href="#"><u>subspace</u></a>	<a href="#"><u>concept</u></a>	Describes the filtering applied to a file
<a href="#"><u>substr</u></a>	<a href="#"><u>slangrtl</u></a>	Extract a substring from a string
<a href="#"><u>subtract</u></a>	<a href="#"><u>sherpa</u></a>	Performs background subtraction.
<a href="#"><u>sum</u></a>	<a href="#"><u>slangrtl</u></a>	Sum over the elements of an array
<a href="#"><u>surface</u></a>	<a href="#"><u>chips</u></a>	Adds a surface plot to a drawing area.
<a href="#"><u>symbol</u></a>	<a href="#"><u>chips</u></a>	Specifies the appearance of symbols in a curve.
<a href="#"><u>syntax</u></a>	<a href="#"><u>tools</u></a>	Syntax used for writing mathematical operations in dmcalc, dmimgcalc, and dmgti
<a href="#"><u>syserrors</u></a>	<a href="#"><u>sherpa</u></a>	Defines an expression or file to be used to specify the systematic errors for source data.
<a href="#"><u>system</u></a>	<a href="#"><u>slangrtl</u></a>	Execute a shell command

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<b>T</b>	<a href="#"><u>tanh</u></a>	<a href="#"><u>slangrtl</u></a>	Compute the hyperbolic tangent of an number
	<a href="#"><u>tan</u></a>	<a href="#"><u>sherpa</u></a>	Tangent function. Integration OFF.
	<a href="#"><u>tan</u></a>	<a href="#"><u>slangrtl</u></a>	Compute the tangent of an number
	<a href="#"><u>taskmonitor</u></a>	<a href="#"><u>gui</u></a>	GUI to run a task as a background process and display the output
	<a href="#"><u>tgdetect</u></a>	<a href="#"><u>tools</u></a>	Detect and centroid the zero order image in a spatial sub-region of a grating event list.
	<a href="#"><u>tgextract</u></a>	<a href="#"><u>tools</u></a>	Bin event list grating wavelengths column into a one-dimensional

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<a href="#"><u>tgidselectsrc</u></a>	<a href="#"><u>tools</u></a>	counts histogram, by source, grating part, and diffraction order.
<a href="#"><u>tgmatchsrc</u></a>	<a href="#"><u>tools</u></a>	Filter an input source list based upon a SNR threshold.
<a href="#"><u>tg_bkg</u></a>	<a href="#"><u>tools</u></a>	Match sources between two source lists by their 2-D separation files.
<a href="#"><u>tg_create_mask</u></a>	<a href="#"><u>tools</u></a>	Creates a PHA background file for use in XSPEC
<a href="#"><u>tg_osort_img</u></a>	<a href="#"><u>tools</u></a>	Create a region file to define spectrum sky boundaries
<a href="#"><u>tg_resolve_events</u></a>	<a href="#"><u>tools</u></a>	Create an image that shows the density of events in different orders
<a href="#"><u>tg_scale_reg</u></a>	<a href="#"><u>tools</u></a>	Assign grating events to spectral orders; use detector energy resolution for order separation, if available.
<a href="#"><u>thaw</u></a>	<a href="#"><u>sherpa</u></a>	Create a region file that labels distances along the grating arm
<a href="#"><u>ticks</u></a>	<a href="#"><u>chips</u></a>	Allows model parameter(s) to vary.
<a href="#"><u>tickvals</u></a>	<a href="#"><u>chips</u></a>	Specifies the spacing of tick marks.
<a href="#"><u>tic</u></a>	<a href="#"><u>slangrtl</u></a>	Controls the appearance of numerical tick mark labels.
<a href="#"><u>times</u></a>	<a href="#"><u>chandra</u></a>	Start timing
<a href="#"><u>times</u></a>	<a href="#"><u>slangrtl</u></a>	"Times" used in Chandra datasets and Chandra data analysis
<a href="#"><u>time</u></a>	<a href="#"><u>slangrtl</u></a>	Get process times
<a href="#"><u>tips</u></a>	<a href="#"><u>slang</u></a>	Return the current data and time as a string
<a href="#"><u>title</u></a>	<a href="#"><u>chips</u></a>	S-Lang tips and example functions
<a href="#"><u>title</u></a>		Adds a title and/or changes the title attribute.
<a href="#"><u>toc</u></a>	<a href="#"><u>slangrtl</u></a>	Get elapsed CPU time
<a href="#"><u>tolower</u></a>	<a href="#"><u>slangrtl</u></a>	Convert a character to lowercase.
<a href="#"><u>toupper</u></a>	<a href="#"><u>slangrtl</u></a>	Convert a character to uppercase.
<a href="#"><u>tpsf1d</u></a>	<a href="#"><u>sherpa</u></a>	A 1-D TCD-model-based instrument model.
<a href="#"><u>tpsf</u></a>	<a href="#"><u>sherpa</u></a>	A 2-D TCD-model-based instrument model.
<a href="#"><u>transpose</u></a>	<a href="#"><u>slangrtl</u></a>	Transpose an array
<a href="#"><u>truncate</u></a>	<a href="#"><u>sherpa</u></a>	Resets negative model amplitudes to zero.
<a href="#"><u>typecast</u></a>	<a href="#"><u>slangrtl</u></a>	Convert an object from one data type to another.
<a href="#"><u>typeof</u></a>	<a href="#"><u>slangrtl</u></a>	Get the data type of an object.
<a href="#"><u>type</u></a>	<a href="#"><u>chips</u></a>	

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Reports the data that are associated with a curve.

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<b>U</b>	<a href="#"><u>umask</u></a>	<a href="#"><u>slangrtl</u></a>	Set the file creation mask
	<a href="#"><u>uname</u></a>	<a href="#"><u>slangrtl</u></a>	Get the system name
	<a href="#"><u>uncertainty</u></a>	<a href="#"><u>sherpa</u></a>	Estimates confidence intervals for selected thawed parameters.
	<a href="#"><u>undo</u></a>	<a href="#"><u>chips</u></a>	Undoes the most recently executed plotting command.
	<a href="#"><u>ungroup</u></a>	<a href="#"><u>sherpa</u></a>	Causes Sherpa to undo a grouping scheme that had been applied to source or background data.
	<a href="#"><u>unlink</u></a>	<a href="#"><u>sherpa</u></a>	Removes a link between model parameters.
	<a href="#"><u>unpack</u></a>	<a href="#"><u>slangrtl</u></a>	Unpack Objects from a Binary String
	<a href="#"><u>unsubtract</u></a>	<a href="#"><u>sherpa</u></a>	Undoes background subtraction.
	<a href="#"><u>usage</u></a>	<a href="#"><u>slangrtl</u></a>	Generate a usage error
	<a href="#"><u>usermethod</u></a>	<a href="#"><u>sherpa</u></a>	A user-defined method.
	<a href="#"><u>usermodel</u></a>	<a href="#"><u>sherpa</u></a>	User implemented model.
	<a href="#"><u>usermodel</u></a>	<a href="#"><u>slang</u></a>	Creating Sherpa Usermodels with S–Lang
	<a href="#"><u>username</u></a>	<a href="#"><u>varmm</u></a>	Returns the login name of the owner of the current process.
	<a href="#"><u>userstat</u></a>	<a href="#"><u>sherpa</u></a>	User implemented statistic.
	<a href="#"><u>use_namespace</u></a>	<a href="#"><u>slangrtl</u></a>	Change to another namespace
	<a href="#"><u>use</u></a>	<a href="#"><u>sherpa</u></a>	Calls and executes a Sherpa script.

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<b>V</b>	<a href="#"><u>variables</u></a>	<a href="#"><u>slang</u></a>	Variables in S–Lang
	<a href="#"><u>varmmrl</u></a>	<a href="#"><u>modules</u></a>	The Varmm readline module for S–Lang
	<a href="#"><u>varmm_rl_blink</u></a>	<a href="#"><u>varmmrl</u></a>	Sets the "blink" mode of the ChIPS and Sherpa command line.
	<a href="#"><u>varmm_rl_editmode</u></a>	<a href="#"><u>varmmrl</u></a>	Set the editing mode ("emacs" or "vi") of the ChIPS and Sherpa command line.
	<a href="#"><u>varmm</u></a>	<a href="#"><u>modules</u></a>	The Variable, Math and Macro S–Lang library
	<a href="#"><u>verbose</u></a>	<a href="#"><u>chips</u></a>	Regulates reporting of error and informational messages.
	<a href="#"><u>verror</u></a>	<a href="#"><u>slangrtl</u></a>	Generate an error condition
	<a href="#"><u>version</u></a>	<a href="#"><u>sherpa</u></a>	Reports the Sherpa version that is in use.

## Ahelp (alphabetical) – CIAO 3.4

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<a href="#"><u>viewpoint</u></a>	<a href="#"><u>chips</u></a>	Controls the rotation angle of a surface plot.	
<a href="#"><u>vmessage</u></a>	<a href="#"><u>slangrtl</u></a>	Print a formatted string onto the message device	
<a href="#"><u>vtpdetect</u></a>	<a href="#"><u>tools</u></a>	Voronoi Tessellation and Percolation (VTP) source detection	
<b>W</b>	<a href="#"><u>wavdetect</u></a>	<a href="#"><u>tools</u></a>	Mexican–Hat Wavelet source detection (wtransform+wrecon)
	<a href="#"><u>wcs_match</u></a>	<a href="#"><u>tools</u></a>	Create a frame transformation to minimize the aspect difference between data from the same sky region.
	<a href="#"><u>wcs_update</u></a>	<a href="#"><u>tools</u></a>	Modify aspect solution file RA, Dec, and roll or infile WCS based on a transformation matrix.
	<a href="#"><u>where</u></a>	<a href="#"><u>slangrtl</u></a>	Get indices where an integer array is non–zero
	<a href="#"><u>wrecon</u></a>	<a href="#"><u>tools</u></a>	Combine wavelet transform coefficients into sources
	<a href="#"><u>writeascii</u></a>	<a href="#"><u>varmm</u></a>	S–Lang function to create an ASCII output file from S–Lang arrays
	<a href="#"><u>writefits</u></a>	<a href="#"><u>varmm</u></a>	S–Lang function to create a FITS output file.
	<a href="#"><u>write</u></a>	<a href="#"><u>sherpa</u></a>	Causes the specified information to be written to the screen or to a file.
	<a href="#"><u>wtransform</u></a>	<a href="#"><u>slangrtl</u></a>	Write to an open file descriptor
		<a href="#"><u>tools</u></a>	Obtain wavelet transform coefficients for poisson image data
<b>X</b>	<a href="#"><u>xlabel</u></a>	<a href="#"><u>chips</u></a>	Adds a label along the X–axis of a drawing area and/or changes X–axis label attributes.
	<a href="#"><u>xpaaccess</u></a>	<a href="#"><u>xpa</u></a>	Find out how many XPA access points are available that match a given name.
	<a href="#"><u>xpaclose</u></a>	<a href="#"><u>xpa</u></a>	Close a persistent XPA connection created by XPAOpen().
	<a href="#"><u>xpagetb</u></a>	<a href="#"><u>xpa</u></a>	Retrieve binary data from one or more XPA servers.
	<a href="#"><u>xpagetofile</u></a>	<a href="#"><u>xpa</u></a>	Retrieve data from one or more XPA servers and write the results to a file.
	<a href="#"><u>xpaget</u></a>	<a href="#"><u>xpa</u></a>	Retrieve data from one or more XPA servers.

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## Ahelp (alphabetical) – CIAO 3.4

<a href="#"><u>xpaopen</u></a>	<a href="#"><u>xpa</u></a>	Create a persistent connection for XPA calls.
<a href="#"><u>xpaset</u></a>	<a href="#"><u>xpa</u></a>	Send a command or data to one or more XPA servers.
<a href="#"><u>xpa_maxhosts</u></a>	<a href="#"><u>xpa</u></a>	This variable stores the maximum number of hosts to be contacted in a XPA call.
<a href="#"><u>xpa_version</u></a>	<a href="#"><u>xpa</u></a>	The version of the XPA library being used by the S-Lang module.
<a href="#"><u>xpa</u></a>	<a href="#"><u>modules</u></a>	The S-Lang interface to the XPA library.
<a href="#"><u>xsabsori</u></a>	<a href="#"><u>sherpa</u></a>	Ionized absorber. XSpec model.
<a href="#"><u>xsacisabs</u></a>	<a href="#"><u>sherpa</u></a>	Decay in the ACIS quantum efficiency. XSpec model.
<a href="#"><u>xsappec</u></a>	<a href="#"><u>sherpa</u></a>	APEC thermal plasma model. XSpec model.
<a href="#"><u>xsbapec</u></a>	<a href="#"><u>sherpa</u></a>	APEC thermal plasma model with velocity broadening as a free parameter. XSpec model.
<a href="#"><u>xsbbbodyrad</u></a>	<a href="#"><u>sherpa</u></a>	Blackbody spectrum with norm proportional to surface area. XSpec model.
<a href="#"><u>xsbbbody</u></a>	<a href="#"><u>sherpa</u></a>	Blackbody spectrum. XSpec model.
<a href="#"><u>xsbxrav</u></a>	<a href="#"><u>sherpa</u></a>	E-folded broken power law reflected from neutral matter. XSpec model.
<a href="#"><u>xsbxriv</u></a>	<a href="#"><u>sherpa</u></a>	E-folded broken power law reflected from ionized matter. XSpec model.
<a href="#"><u>xsbkpower</u></a>	<a href="#"><u>sherpa</u></a>	Broken power law. XSpec model.
<a href="#"><u>xsbmc</u></a>	<a href="#"><u>sherpa</u></a>	Comptonization by relativistically moving matter. XSpec model.
<a href="#"><u>xsbremss</u></a>	<a href="#"><u>sherpa</u></a>	Thermal bremsstrahlung. XSpec model.
<a href="#"><u>xsbvappec</u></a>	<a href="#"><u>sherpa</u></a>	APEC thermal plasma model with variable abundances and velocity broadening as a free parameter. XSpec model.
<a href="#"><u>xsc6mekl</u></a>	<a href="#"><u>sherpa</u></a>	6th-order Chebyshev polynomial DEM using mekal. XSpec model.
<a href="#"><u>xsc6pmekl</u></a>	<a href="#"><u>sherpa</u></a>	Exponential of 6th-order Chebyshev polyn. DEM using mekal. XSpec model.
<a href="#"><u>xsc6pvmkl</u></a>	<a href="#"><u>sherpa</u></a>	Variable abundance version of c6pmekl. XSpec model.
<a href="#"><u>xsc6vmekl</u></a>	<a href="#"><u>sherpa</u></a>	

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<a href="#"><u>xscabs</u></a>	<a href="#"><u>sherpa</u></a>	Variable abundance version of c6mekl. XSpec model.
<a href="#"><u>xscemekl</u></a>	<a href="#"><u>sherpa</u></a>	Compton scattering (non-relativistic). XSpec model.
<a href="#"><u>xscevmkl</u></a>	<a href="#"><u>sherpa</u></a>	Multi-temperature mekal. XSpec model.
<a href="#"><u>xscflow</u></a>	<a href="#"><u>sherpa</u></a>	Multi-temperature vmeka. XSpec model.
<a href="#"><u>xscompbb</u></a>	<a href="#"><u>sherpa</u></a>	Cooling flow model. XSpec model.
		Comptonized blackbody spectrum after Nishimura et al. (1986). XSpec model.
<a href="#"><u>xscompls</u></a>	<a href="#"><u>sherpa</u></a>	Comptonization spectrum after Lamb and Sanford (1979). XSpec model.
<a href="#"><u>xscompst</u></a>	<a href="#"><u>sherpa</u></a>	Comptonization spectrum after Sunyaev and Titarchuk (1980). XSpec model.
<a href="#"><u>xscomptt</u></a>	<a href="#"><u>sherpa</u></a>	Comptonization spectrum after Titarchuk (1994). XSpec model.
<a href="#"><u>xsconstant</u></a>	<a href="#"><u>sherpa</u></a>	Energy-independent multiplicative factor. XSpec model.
<a href="#"><u>xscutoffpl</u></a>	<a href="#"><u>sherpa</u></a>	Power law with high energy exponential cutoff. XSpec model.
<a href="#"><u>xscyclabs</u></a>	<a href="#"><u>sherpa</u></a>	Cyclotron absorption line. XSpec model.
<a href="#"><u>xdiskbbb</u></a>	<a href="#"><u>sherpa</u></a>	Multiple blackbody disk model. XSpec model.
<a href="#"><u>xdiskline</u></a>	<a href="#"><u>sherpa</u></a>	Line emission from relativistic accretion disk. XSpec model.
<a href="#"><u>xdiskm</u></a>	<a href="#"><u>sherpa</u></a>	Disk model with gas pressure viscosity. XSpec model.
<a href="#"><u>xdisko</u></a>	<a href="#"><u>sherpa</u></a>	Modified blackbody disk model. XSpec model.
<a href="#"><u>xdiskpkn</u></a>	<a href="#"><u>sherpa</u></a>	Accretion disk around a black hole. XSpec model.
<a href="#"><u>xdisk</u></a>	<a href="#"><u>sherpa</u></a>	Disk model. XSpec model.
<a href="#"><u>xdust</u></a>	<a href="#"><u>sherpa</u></a>	Dust scattering out of the beam. XSpec model.
<a href="#"><u>xsedge</u></a>	<a href="#"><u>sherpa</u></a>	Absorption edge. XSpec model.
<a href="#"><u>xsequil</u></a>	<a href="#"><u>sherpa</u></a>	Equilibrium ionization collisional plasma model from Borkowski. XSpec model.
<a href="#"><u>xsexpabs</u></a>	<a href="#"><u>sherpa</u></a>	Low-energy exponential cutoff. XSpec model.

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<a href="#"><u>xsexpdec</u></a>	<a href="#"><u>sherpa</u></a>	An exponential decay. XSpec model.
<a href="#"><u>xsexpfac</u></a>	<a href="#"><u>sherpa</u></a>	Exponential factor. XSpec model.
<a href="#"><u>xsgabs</u></a>	<a href="#"><u>sherpa</u></a>	A multiplicative gaussian absorption line. XSpec model.
<a href="#"><u>xsgaussian</u></a>	<a href="#"><u>sherpa</u></a>	Simple gaussian line profile. XSpec model.
<a href="#"><u>xsgnei</u></a>	<a href="#"><u>sherpa</u></a>	Generalized single ionization NEI plasma model. XSpec model.
<a href="#"><u>xsgrad</u></a>	<a href="#"><u>sherpa</u></a>	GR accretion disk around a black hole. XSpec model.
<a href="#"><u>xsgrbm</u></a>	<a href="#"><u>sherpa</u></a>	Gamma-ray burst model. XSpec model.
<a href="#"><u>xshigecut</u></a>	<a href="#"><u>sherpa</u></a>	High energy cutoff. XSpec model.
<a href="#"><u>xshrefl</u></a>	<a href="#"><u>sherpa</u></a>	Simple reflection model good up to 15 keV. XSpec model.
<a href="#"><u>xslaor</u></a>	<a href="#"><u>sherpa</u></a>	Line from accretion disk around a black hole. XSpec model.
<a href="#"><u>xslorentz</u></a>	<a href="#"><u>sherpa</u></a>	Lorentzian line profile. XSpec model.
<a href="#"><u>xsmekal</u></a>	<a href="#"><u>sherpa</u></a>	Mewe–Kaastra–Liedahl thermal plasma (1995). XSpec model.
<a href="#"><u>xsmeka</u></a>	<a href="#"><u>sherpa</u></a>	Mewe–Gronenschild–Kaastra thermal plasma (1992). XSpec model.
<a href="#"><u>xsmkcfflow</u></a>	<a href="#"><u>sherpa</u></a>	Cooling flow model based on mekal. XSpec model.
<a href="#"><u>xsnei</u></a>	<a href="#"><u>sherpa</u></a>	Simple nonequilibrium ionization plasma model. XSpec model.
<a href="#"><u>xsnotch</u></a>	<a href="#"><u>sherpa</u></a>	Notch line absorption. XSpec model.
<a href="#"><u>xsnpshock</u></a>	<a href="#"><u>sherpa</u></a>	Plane-parallel shock with ion and electron temperatures. XSpec model.
<a href="#"><u>xsnsa</u></a>	<a href="#"><u>sherpa</u></a>	Spectra in the X-ray range (0.05–10 keV) emitted from a hydrogen atmosphere of a neutron star. XSpec model.
<a href="#"><u>xsnteea</u></a>	<a href="#"><u>sherpa</u></a>	Pair plasma model. XSpec model.
<a href="#"><u>xspcfabs</u></a>	<a href="#"><u>sherpa</u></a>	Partial covering fraction absorption. XSpec model.
<a href="#"><u>xspectabundan</u></a>	<a href="#"><u>sherpa</u></a>	Performs the XSPEC command abund.
<a href="#"><u>xspectxsect</u></a>	<a href="#"><u>sherpa</u></a>	Performs the XSPEC command xsect.

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<a href="#"><u>xspewrwlw</u></a>	<a href="#"><u>sherpa</u></a>	Power law with pegged normalization. XSpec model.
<a href="#"><u>xspexrav</u></a>	<a href="#"><u>sherpa</u></a>	Exponentially cutoff power law reflected from neutral matter. XSpec model.
<a href="#"><u>xspexriv</u></a>	<a href="#"><u>sherpa</u></a>	Exponentially cutoff power law reflected from ionized matter. XSpec model.
<a href="#"><u>xspheabs</u></a>	<a href="#"><u>sherpa</u></a>	Photo-electric absorption. XSpec model.
<a href="#"><u>xsplabs</u></a>	<a href="#"><u>sherpa</u></a>	Absorption model with power law dependence on energy. XSpec model.
<a href="#"><u>xsplcabs</u></a>	<a href="#"><u>sherpa</u></a>	Cutoff power law observed through dense, cold matter. XSpec model.
<a href="#"><u>xsposem</u></a>	<a href="#"><u>sherpa</u></a>	Positronium continuum. XSpec model.
<a href="#"><u>xspowerlaw</u></a>	<a href="#"><u>sherpa</u></a>	Simple photon power law. XSpec model.
<a href="#"><u>xspshock</u></a>	<a href="#"><u>sherpa</u></a>	Constant temperature, plane-parallel shock plasma model. XSpec model.
<a href="#"><u>xspwab</u></a>	<a href="#"><u>sherpa</u></a>	An extension of partial covering fraction absorption into a power-law distribution of covering fraction. XSpec model.
<a href="#"><u>xsraymond</u></a>	<a href="#"><u>sherpa</u></a>	Raymond-Smith thermal plasma. XSpec model.
<a href="#"><u>xsrreddens</u></a>	<a href="#"><u>sherpa</u></a>	IR/optical/UV extinction from Cardelli et al. (1989). XSpec model.
<a href="#"><u>xsredge</u></a>	<a href="#"><u>sherpa</u></a>	Recombination edge. XSpec model.
<a href="#"><u>xsrfsch</u></a>	<a href="#"><u>sherpa</u></a>	E-folded power law reflected from an ionized relativistic disk. XSpec model.
<a href="#"><u>xssedov</u></a>	<a href="#"><u>sherpa</u></a>	Sedov model with electron and ion temperatures. XSpec model.
<a href="#"><u>xssmedge</u></a>	<a href="#"><u>sherpa</u></a>	Smoothed absorption edge. XSpec model.
<a href="#"><u>xsspline</u></a>	<a href="#"><u>sherpa</u></a>	Spline multiplicative factor. XSpec model.
<a href="#"><u>xssrcut</u></a>	<a href="#"><u>sherpa</u></a>	Synchrotron radiation from cutoff electron distribution. XSpec model.
<a href="#"><u>xssresc</u></a>	<a href="#"><u>sherpa</u></a>	Synchrotron radiation from escape-limited electron distribution. XSpec model.
<a href="#"><u>xssssice</u></a>	<a href="#"><u>sherpa</u></a>	Einstein Observatory SSS ice

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<a href="#"><u>xsstep</u></a>	<a href="#"><u>sherpa</u></a>	absorption. XSpec model.
<a href="#"><u>xstbabs</u></a>	<a href="#"><u>sherpa</u></a>	Step function convolved with gaussian. XSpec model.
<a href="#"><u>xstbgrain</u></a>	<a href="#"><u>sherpa</u></a>	Calculates the absorption of X-rays by the ISM. XSpec model.
<a href="#"><u>xstbvarabs</u></a>	<a href="#"><u>sherpa</u></a>	Calculates the absorption of X-rays by the ISM, allowing user to vary all abundances, depletion factors, and grain properties. XSpec model.
<a href="#"><u>xsuvred</u></a>	<a href="#"><u>sherpa</u></a>	UV reddening. XSpec model.
<a href="#"><u>xsvapec</u></a>	<a href="#"><u>sherpa</u></a>	APEC thermal plasma model with variable abundances. XSpec model.
<a href="#"><u>xsvvarabs</u></a>	<a href="#"><u>sherpa</u></a>	Photoelectric absorption with variable abundances. XSpec model.
<a href="#"><u>xsvbremss</u></a>	<a href="#"><u>sherpa</u></a>	Thermal bremsstrahlung spectrum with variable H/He. XSpec model.
<a href="#"><u>xsvequil</u></a>	<a href="#"><u>sherpa</u></a>	Ionization equilibrium collisional plasma model with variable abundances. XSpec model.
<a href="#"><u>xsvgnei</u></a>	<a href="#"><u>sherpa</u></a>	Non-equilibrium ionization collisional plasma model with variable abundances. XSpec model.
<a href="#"><u>xsvmcflow</u></a>	<a href="#"><u>sherpa</u></a>	Cooling flow model based on vmekal. XSpec model.
<a href="#"><u>xsvmekal</u></a>	<a href="#"><u>sherpa</u></a>	M–K–L thermal plasma with variable abundances. XSpec model.
<a href="#"><u>xsvmeka</u></a>	<a href="#"><u>sherpa</u></a>	M–G–K thermal plasma with variable abundances. XSpec model.
<a href="#"><u>xsvnei</u></a>	<a href="#"><u>sherpa</u></a>	Non-equilibrium ionization collisional plasma model with variable abundances. XSpec model.
<a href="#"><u>xsvnpshock</u></a>	<a href="#"><u>sherpa</u></a>	Plane–parallel shock plasma model with separate ion and electron temperatures and variable abundances. XSpec model.
<a href="#"><u>xsvphabs</u></a>	<a href="#"><u>sherpa</u></a>	Photoelectric absorption with variable abundances. XSpec model.
<a href="#"><u>xsvpshock</u></a>	<a href="#"><u>sherpa</u></a>	Constant temperature, plane–parallel shock plasma model with variable abundances. XSpec model.
<a href="#"><u>xsvraymond</u></a>	<a href="#"><u>sherpa</u></a>	Raymond–Smith thermal plasma

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<a href="#"><u>xsvsedov</u></a>	<a href="#"><u>sherpa</u></a>	with variable abundances. XSpec model.
<a href="#"><u>xswabs</u></a>	<a href="#"><u>sherpa</u></a>	Sedov model with separate ion and electron temperatures and variable abundances. XSpec model.
<a href="#"><u>xswndabs</u></a>	<a href="#"><u>sherpa</u></a>	Photoelectric absorption (Morrison and McCammon). XSpec model.
<a href="#"><u>xsxion</u></a>	<a href="#"><u>sherpa</u></a>	Photoelectric absorption with low energy window. XSpec model.
<a href="#"><u>xszbbody</u></a>	<a href="#"><u>sherpa</u></a>	Reflected spectra of a photo-ionized accretion disk or ring. XSpec model.
<a href="#"><u>xszbremss</u></a>	<a href="#"><u>sherpa</u></a>	Redshifted blackbody. XSpec model.
<a href="#"><u>xszedge</u></a>	<a href="#"><u>sherpa</u></a>	Redshifted thermal bremsstrahlung. XSpec model.
<a href="#"><u>xszgauss</u></a>	<a href="#"><u>sherpa</u></a>	Redshifted gaussian. XSpec model.
<a href="#"><u>xszhighect</u></a>	<a href="#"><u>sherpa</u></a>	Redshifted high energy cutoff. XSpec model.
<a href="#"><u>xszpcfabs</u></a>	<a href="#"><u>sherpa</u></a>	Redshifted partial covering absorption. XSpec model.
<a href="#"><u>xszphabs</u></a>	<a href="#"><u>sherpa</u></a>	Redshifted photoelectric absorption. XSpec model.
<a href="#"><u>xszpowerlw</u></a>	<a href="#"><u>sherpa</u></a>	Redshifted power law. XSpec model.
<a href="#"><u>xsztbabs</u></a>	<a href="#"><u>sherpa</u></a>	Calculates the absorption of X-rays by the ISM for modeling redshifted absorption. Does not include a dust component. XSpec model.
<a href="#"><u>xszvarabs</u></a>	<a href="#"><u>sherpa</u></a>	Redshifted photoelectric absorption with variable abundances. XSpec model.
<a href="#"><u>xszvfeabs</u></a>	<a href="#"><u>sherpa</u></a>	Redshifted absorption with variable iron abundance. XSpec model.
<a href="#"><u>xszvphabs</u></a>	<a href="#"><u>sherpa</u></a>	Redshifted photoelectric absorption with variable abundances. XSpec model.
<a href="#"><u>xszwabs</u></a>	<a href="#"><u>sherpa</u></a>	Redshifted "Wisconsin absorption." XSpec model.
<a href="#"><u>xszwndabs</u></a>	<a href="#"><u>sherpa</u></a>	Redshifted photoelectric absorption with low energy window. XSpec model.
<a href="#"><u>xs</u></a>	<a href="#"><u>sherpa</u></a>	XSpec model functions.

## Ahelp (alphabetical) – CIAO 3.4

<b>Y</b>	<a href="#"><u>ylabel</u></a>	<a href="#"><u>chips</u></a>	Adds a label along the Y–axis of a drawing area and/or changes Y–axis label attributes.
<b>Z</b>	<a href="#"><u>zlabel</u></a>	<a href="#"><u>chips</u></a>	Adds a label along the Z–axis of a drawing area and/or changes Z–axis label attributes.
–	<a href="#"><u>apropos</u></a>	<a href="#"><u>slangrtl</u></a>	Generate a list of functions and variables
	<a href="#"><u>auto_declare</u></a>	<a href="#"><u>slangrtl</u></a>	Set automatic variable declaration mode
	<a href="#"><u>clear_error</u></a>	<a href="#"><u>slangrtl</u></a>	Clear an error condition
	<a href="#"><u>debug_info</u></a>	<a href="#"><u>slangrtl</u></a>	Configure debugging information
	<a href="#"><u>featurep</u></a>	<a href="#"><u>slangrtl</u></a>	Test whether or not a feature is present
	<a href="#"><u>function_name</u></a>	<a href="#"><u>slangrtl</u></a>	Returns the name of the currently executing function
	<a href="#"><u>get_namespaces</u></a>	<a href="#"><u>slangrtl</u></a>	Returns a list of namespace names
	<a href="#"><u>isnull</u></a>	<a href="#"><u>slangrtl</u></a>	Check array for NULL elements
	<a href="#"><u>NARGS</u></a>	<a href="#"><u>slangrtl</u></a>	The number of parameters passed to a function
	<a href="#"><u>pop_n</u></a>	<a href="#"><u>slangrtl</u></a>	Remove objects from the stack
	<a href="#"><u>print_stack</u></a>	<a href="#"><u>slangrtl</u></a>	print the values on the stack.
	<a href="#"><u>push_struct_field_values</u></a>	<a href="#"><u>slangrtl</u></a>	Push the values of a structure's fields onto the stack
	<a href="#"><u>reshape</u></a>	<a href="#"><u>slangrtl</u></a>	Copy an array to a new shape
	<a href="#"><u>slangtrace</u></a>	<a href="#"><u>slangrtl</u></a>	Turn function tracing on or off.
	<a href="#"><u>slang_doc_dir</u></a>	<a href="#"><u>slangrtl</u></a>	Installed documentation directory
	<a href="#"><u>slang_guess_type</u></a>	<a href="#"><u>slangrtl</u></a>	Guess the data type that a string represents.
	<a href="#"><u>slang_version_string</u></a>	<a href="#"><u>slangrtl</u></a>	The S–Lang library version number as a string
	<a href="#"><u>slang_version</u></a>	<a href="#"><u>slangrtl</u></a>	The S–Lang library version number
	<a href="#"><u>slxpa_version</u></a>	<a href="#"><u>xpa</u></a>	The version of the S–Lang XPA module.
	<a href="#"><u>stkdepth</u></a>	<a href="#"><u>slangrtl</u></a>	Get the number of objects currently on the stack.
	<a href="#"><u>stk_reverse</u></a>	<a href="#"><u>slangrtl</u></a>	Reverse the order of the objects on the stack.
	<a href="#"><u>stk_roll</u></a>	<a href="#"><u>slangrtl</u></a>	Roll items on the stack
	<a href="#"><u>time</u></a>	<a href="#"><u>slangrtl</u></a>	Get the current time in seconds
	<a href="#"><u>traceback</u></a>	<a href="#"><u>slangrtl</u></a>	Generate a traceback upon error
	<a href="#"><u>trace_function</u></a>	<a href="#"><u>slangrtl</u></a>	Set the function to trace

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<u>typeof</u>	<u>slangrtl</u>	Get the data type of an object
<u>class_id</u>	<u>slangrtl</u>	Return the class–id of a specified type
<u>class_type</u>	<u>slangrtl</u>	Return the class–type of a specified type
<u>eqs</u>	<u>slangrtl</u>	Test for equality between two objects
<u>exit</u>	<u>varmm</u>	S–Lang function to abort applications.
<u>get_defined_symbols</u>	<u>slangrtl</u>	Get the symbols defined by the preprocessor
<u>get_reference</u>	<u>slangrtl</u>	Get a reference to a global object
<u>is_initialized</u>	<u>slangrtl</u>	Determine whether or not a variable has a value
<u>pop_args</u>	<u>slangrtl</u>	Remove n function arguments from the stack
<u>push_args</u>	<u>slangrtl</u>	Remove n function arguments onto the stack
<u>uninitialize</u>	<u>slangrtl</u>	Uninitialize a variable

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