SIMPLE 2.0 command line dictionary

*acf* autocorrelation function

*amsklp* automask low-pass limit (in Å)

*bin* binarize (yes|no)

*box*  image size in pixels (image assumed to be *box\*box* array)

*boxpd* padded box size (default is *2\*box*)

*center* center(yes|no)

*clsdoc*  Spider format clustering document

*cure* cure or not (yes|no), for curing NaN:s and normalize

*cwd* current working directory

*debug* debug mode (yes|no)

*deterministic* deterministic search (yes|no)

*discrete* discrete option (yes|no)

*doalign* do alignment (yes|no)

*dopca* do PCA (yes|no)

*doprint* do print (yes|no)

*e1* first Euler angle

*e2* second Euler angle

*e3* third Euler angle

*edge* edge size for softening molecular envelope (in pixels)

*eo* even-odd test (yes|no)

*even* even (yes|no)

*fbody* file body (<body>.ext)

*filter* filter (yes|no)

*frac* fraction [0,1]

*fromp* from particle index

*froms* from state index

*gw* Gaussian half width (in pixels)

*hp* high-pass limit (in Å)

*kmeans* do kmeans (yes|no)

*local* local refinement (yes|no)

*lp* low-pass limit (in Å)

*matched* use matched Wiener filter (yes|no)

*maxits* maximum number of iterations

*minp* minimum number of particle images (in a cluster)

*moldiam* molecular diameter (in Å)

*msk* circular or spherical mask radius (in pixels)

*mskfile* external mask file (\*.spi)

*mul* multiplication (scaling) factor (for shifts)

*mw* molecular weight (in kD)

*navgs* number of averages

*ncls* number of clusters

*ndiscrete* number of discrete (orientations)

*ndocs* number of documents

*newbox* new box size

*noise* noise (yes|no)

*noris* number of orientations

*norm* normalize (yes|no)

*npart* number of partitions

*npeaks* number of peaks (=number of nonzero orientation weights)

*nptcls* number of particle images

*nran* number of images in random sample

*nspace* number of projection directions in search space

*nstates* number of discrete state groups

*nthr* number of openMP threads

*nvars* number of eigenvectors or hidden variables

*nvox* number of voxels

*oritab* SIMPLE orientations file (\*.txt)

*outfile* SIMPLE output file (\*.txt)

*outstk* output Spider image stack (\*.spi suffix required)

*outvol* output Spider volume (\*.spi suffix required)

*part* partition number

*pgrp* point-group symmetry (c1, c2, c3, …, or d1, d2, d3, …)

*phrand* phase randomize (yes|no)

*phranlp* phase randomization low-pass limit (in Å)

*ppca* probabilistic pca (yes|no)

*ring1* inner ring in polar image representation

*ring2* outer ring in polar image representation

*rnd* random (yes|no)

*roalgn* rotational alignment (yes|no)

*shalgn* shift alignment (yes|no)

*smpd*  sampling distance (in Å)

*snr* signal-to-noise ratio

*space* space (real|fourier)

*startit* starting iteration (if different than 1)

*state* discrete state group

*stk* spider image stack name (\*.spi suffix required)

*stk2* second spider image stack name (\*.spi suffix required)

*stk3* third spider image stack name (\*.spi suffix required)

*tau* temperature parameter

*time\_per\_image* per particle time indicator

*top* to particle index

*tos* to state index

*tres* threshold

*trs* origin shift search range parameter [-*trs*,*trs*]

*trsstep* translation step size

*utst* unit test number

*var* variance

*vol1* spider volume 1 name (\*.spi suffix required)

*wfun* weighting function or interpolation kernel

*winsz* window size for interpolation

*zero* zero (yes|no)