```
#           Removal of the rec. polar vect.: vdW radius probe
p15 1.83
#           Coulombic fast energy: 1=distance dept diel / grid margin / grid spacing
p16 1 20.0 0.5
#           van der Waals fast energy: grid margin / grid spacing
p17 20.0 0.3
#           accurate energy: Coulombic cutoff for formal charges is automatically
#                            set to 1.3 x van_der_Waals_cutoff
#           accurate energy (vdWaals): nonbonding cutoff / grid spacing
p18 12.0 1.0
#           Multiplicative factor (k) for apolar docking to skip evaluation of
#           electrostatics. The vdW energy cutoff is:
#           k x Number of fragment atoms, including hydrogen atoms
p19 -0.333333
#           Solvation grid: grid margin / grid spacing
p20 24.0 0.5
#           Solvation: water radius / # points per sphere to generate SAS /
#                      solvent dielectric constant
p21 1.4 500 78.5
#           Hydrophobicity maps: point densities (A^-2) on the SAS for apolar
#                    vectors on the receptor / on the fragment /
#                    probe radius to generate SAS for apolar vectors /
#                    scaling factor for desolvation and / vdW interactions
p22 1.0 1.0 1.4 1.0 1.0
#           Scaling factors for fast and also accurate energy evaluation:
#           van der Waals / electrostatic interaction / receptor desolvation /
#           fragment desolvation
p23 1.0 1.0 1.0 1.0
#      ------------------------------------------------------------------------
#           Clustering parameters
#           Clustering parameters
#           Clustering parameters
#      ------------------------------------------------------------------------
#           GSEAL : sim. weight factors (150 atom el.) 0 or # non-default + list
p24 4
6  6  2.0
7  7 10.0
8  8 10.0
16 16 10.0
#           The clustering with GSEAL proceeds in two steps: the
#           first clustering yields large clusters which contain almost
#           overlapping as well as more distant fragments; the second
#           clustering is done on each cluster found in the first clustering
#           to eliminate fragments which are very close in space.
#
#           First clustering:  overall clustering
#           GSEAL similarity exponential factor / cutoff factor
p25 0.9 0.4
#
#           Second clustering: to discard redundant positions
#           GSEAL similarity exponential factor / cutoff factor
p26 0.9 0.9
#           Maximal number of positions to be clustered
p27 20
#           Number of lines to be written in the output file for the sorted
#           energies and the two clustering procedures /
#           Printlevel (0=lean, 1=adds sorting before postprocessing, 2=adds 2nd
#           clustering)
p28 100 1
#      ------------------------------------------------------------------------
#           Forcefield parameters from now on
#           Forcefield parameters from now on
#           Forcefield parameters from now on
#      ------------------------------------------------------------------------
# Parameters are CGenFF v4 (2016) and param36 (2012) with water and ions as per
# toppar_water_ions.str
#
# NB: if the user includes metal ions in the binding site, appropriate hydrogen bond
# distances with these ions should be provided in the "Hydrogen bond distances
# between donor and acceptor" section below
```