```
#seed.param v4.0
#
#      ------------------------------------------------------------------------
#           PARAMETERS FORMERLY IN SEED.INP
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#      ------------------------------------------------------------------------
#            Dielectric constant of the solute (receptor and fragment)
p1  2.0
#            Ratio of kept vectors for docking : polar / apolar
p2  1.0 1.0
#            First value: write *_clus.mol2 file (y/n)
#            Second value: write *_best.mol2 file (y/n)
p3  n y
#          First value: write *_clus.dat summary table file (y/n)
#            Second value: write *_best.dat summary table file (y/n)
p4  y y
#            First value: maximum number of cluster members saved in *_clus*
#            output files. Note that this value determines the maximum number
#            of poses per cluster that go through slow energy evaluation.
#          Second value: maximum number of poses saved in *_best* output files.
p5  5 1
#            The docked fragments are saved in the dir ./outputs
#            Filename for output log file. This is the main SEED output file.
p6  ./outputs/seed.out
#            write (w) or read (r) Coulombic grid / grid filename
p7  w  ./scratch/coulomb.grid
#            write (w) or read (r) van der Waals grid / grid filename
p8  w  ./scratch/vanderwaals.grid
#            write (w) or read (r) receptor desolvation grid / grid filename
p9  w  ./scratch/desolvation.grid
#
#      ------------------------------------------------------------------------
#            PARAMETERS FOR DOCKING
#            DEFINITIONS:
#            fast energy: used only to preprocess, i.e., as a filter
#                         [Majeux et al, PROTEINS 42, 256-268, 2001]
#            accurate (and slower) energy: used to postprocess and should
#                                          NOT be turned off
#                         [Majeux et al, PROTEINS 37,  88-105, 1999]
#      ------------------------------------------------------------------------
#
#            Bump checking: used only if fast energy is switched off
#            n x atoms = maximum tolerated bumps /
#            scaling factor for interatomic distance /
#            severe overlap factor (beta factor in PROTEINS paper)
p10 2.0 0.89 0.6
#            van der Waals energy cutoff (kcal/mol):
#            used if fast energy is switched on
p11 1.0
#            Angle (deg) and number of points on the sphere around the HB vectors
p12 50.0 100
#            Number of fragment rotations around each axis
p13 72
#            Modification of February 2002:
#            Removal of rec. polar and apolar vectors using angle criterion
#            angle_rmin (deg)  angle_rmax   multipl_fact_rmin   multipl_fact_rmax
#            Method:
#            The minimal (minDist) and maximal (maxDist) distances
#            between the vectors and the points in the binding site
#            (as defined in the SEED input file) are evaluated.
#            A vector is discarded if the angle between the vector
#            and its closest point in the binding site is larger than
#            a cutoff angle value.
#            The cutoff angle value follows the following distribution:
#            -  angle_rmin  if distance <= (multipl_fact_rmin*minDist)
#            -  angle_rmax  if distance >= (multipl_fact_rmax*maxDist)
#            -  linear dependence (range between angle_rmin and angle_rmax)
#               for other distances
p14 70.0 10.0 1.2 0.8
```