PELE (Protein Energy Landscape Exploration) is one of NBD’s core simulation technologies. It has been developed over more than 10 years in one of the most reputed simulation groups in Europe (Barcelona Supercomputing Center), backed up by several international grants such as the Advanced European Research Council grant. It is a simulation program that combines a MonteCarlo stochastic approach with protein structure prediction and energy minimization algorithms. It can be used for solving a wide variety of molecular recognition problems.

**Features & Advantages**

- Extremely fast, able to be run on the most modern HPC multi-core infrastructures.
- Several algorithms for protein structure prediction and optimization available.
- Thoroughly tested in many academic and industrial projects, as the scientific references found below clearly demonstrate.
- Able to tackle molecular recognition problems that are unattainable by most in silico approaches.

**Applications**

PELE is one of the most advanced induced fit docking algorithms described. It has been recently ranked among the best programs for native pose prediction in the latest CSAR blind test carried out by the University of Michigan together with GSK. PELE can also be used as a fragment screening tool as it can reliably predict the binding mode of a fragment molecule even in the most flexible and promiscuous binding sites. In addition, PELE is extremely accurate at describing ligand migration pathways of binding and unbinding, opening up the rational design of optimized enzymes for industrial applications.

**Scientific References**

How does PELE work?

1) Localized perturbation. After an energy calculation for the initial structure, the procedure begins with the generation of a perturbation in the system.

2) Side chain sampling. The algorithm proceeds by placing all side chains local to the ligand with a rotamer library side chain optimization at a rotamer resolution of 10°. The side chain algorithm uses steric filtering and a clustering method to reduce the number of rotamers to be minimized (side chain minimization only).

3) Minimization. The last step involves the minimization of a user-defined region (typically we include the full protein) with a Truncated Newton minimizer.

These three steps compose a move that is accepted (defining a new minima) or rejected based on a Metropolis criterion. The procedure has been parallelized using the MPI communications protocol, with the option of interchanging coordinates between different trajectories. Whenever any trajectory is significantly further along a given reaction coordinate than any of the other trajectories, the trailing trajectory is abandoned and restarted from the position of the leading trajectory. This allows an efficient sampling of the configurational space towards one defined objective, increasing the speed and accuracy of sampling.