| Score | Frozen | Algorithm | Game | # conformations w/ RMSD <10 Å | RMSD range |
|---|---|---|---|---|---|
| **Lennard-Jones** | **No** | **EXP3** | **AA** | **2** | **6.82-15.40** |
| | | | OA | 0 | 12.1-15.65 |
| | | | OO | 3 | 7.96-12 |
| | | UCB | AA | 1 | 8.1-12.8 |
| | | | OA | 1 | 8.91-11.71 |
| | | | OO | 0 | 11.9-12.42 |
| | Yes | EXP3 | AA | 3 | 8.75-12.36 |
| | | | OA | 3 | 7.7-12.4 |
| | | | OO | 3 | 8.89-11.9 |
| | | UCB | AA | 2 | 8.41-12.02 |
| | | | OA | 1 | 8.67-12.69 |
| | | | OO | 2 | 8.89-12.92 |
| Modified Lennard-Jones | No | EXP3 | AA | 3 | 8.75-12 |
| | | | OA | 3 | 8.26-11.6 |
| | | | OO | 3 | 8.01-11.1 |
| | | UCB | AA | 2 | 8.26-15.21 |
| | | | OA | 1 | 8.14-14.9 |
| | | | OO | 0 | 11.9-11.9 |
| | Yes | EXP3 | AA | 3 | 8.75-12.36 |
| | | | OA | 4 | 7.71-9.33 |
| | | | OO | 4 | 8.75-9.33 |
| | | UCB | AA | 2 | 8.26-15.53 |
| | | | OA | 1 | 8.64-16.2 |
| | | | OO | 0 | 11.65-12.92 |
| Gauss | No | EXP3 | AA | 4 | 8.19-9.34 |
| | | | OA | 3 | 8.41-12.92 |
| | | | OO | 2 | 8.19-15.2 |
| | | UCB | AA | 2 | 8.41-11.88 |
| | | | OA | 2 | 8.37-10.88 |
| | | | OO | 0 | 11.9-11.9 |
| | Yes | EXP3 | AA | 4 | 8.75-9.34 |
| | | | OA | 1 | 8.9-11.88 |
| | | | OO | 1 | 8.75-12.92 |
| | | UCB | AA | 1 | 8.41-15.53 |
| | | | OA | 4 | 8.41-8.93 |
| | | | OO | 2 | 8.31-12.92 |
| $1/d^2$ | No | EXP3 | AA | 3 | 8.51-10.64 |
| | | | OA | 2 | 7.38-14.9 |
| | | | OO | 2 | 8.89-12.3 |
| | | UCB | AA | 4 | 8.08-9.81 |
| | | | OA | 4 | 6.66-8.72 |
| | | | OO | 2 | 8.81-11.9 |
| | Yes | EXP3 | AA | 4 | 8.19-9.33 |
| | | | OA | 1 | 8.64-11.6 |
| | | | OO | 2 | 8.26-16.2 |
| | | UCB | AA | 3 | 7.44-10 |
| | | | OA | 3 | 8.64-14.92 |
| | | | OO | 1 | 9.75-12.92 |

Table ST4: **Sampling results for the structure of the core of the ALU domain of the mammalian SRP (PDB ID 1E8O).** The molecule contains 49 nucleotides and 8 players. Six different parameter sets per game type are shown. Values shown in blue highlight combinations providing conformations with RMSD values below 8Å. Elements highlighted in yellow correspond to the default GARN options for the molecule.