

Score	Frozen	Algorithm	Game	# conformations w/ RMSD <7 Å	RMSD range
Lennard-Jones	No	EXP3	AA	1	6.84-11.62
			OA	6	4.61-11.67
			OO	7	4.71-11.23
		UCB	AA	5	5.24-11.23
			OA	10	4.46-9.31
			OO	12	7.64-16.6
Yes	EXP3	AA	2	6.84-11.17	
		OA	11	4.91-8.07	
		OO	9	4.22-9.58	
	UCB	AA	10	4.32-11.37	
		OA	8	4.27-10.12	
		OO	10	6.41-15.68	
Modified Lennard-Jones	No	EXP3	AA	3	5.43-11.85
			OA	7	5.25-8.72
			OO	13	4.46-8.68
		UCB	AA	12	4.32-8.86
			OA	12	4.4-9.38
			OO	6	4.27-11.23
Yes	EXP3	AA	4	5.92-10.07	
		OA	13	4.43-8.5	
		OO	10	5.25-9.72	
		UCB	AA	17	4.3-7.26
		OA	11	4.32-10.58	
		OO	6	4.32-11.85	
Gauss	No	EXP3	AA	6	5.21-10.07
			OA	12	5.72-8.98
			OO	8	5.34-9.72
		UCB	AA	8	4.3-11.85
			OA	5	5.68-11.72
			OO	10	4.88-9.58
Yes	EXP3	AA	6	8.49-16.92	
		OA	10	4.61-9.47	
		OO	9	4.46-10.07	
	UCB	AA	4	4.95-10.62	
		OA	5	4.81-11.08	
		OO	15	4.3-9.72	
1/d ²	No	EXP3	AA	6	5.69-10.07
			OA	1	5.77-11.85
			OO	10	4.27-8.3
		UCB	AA	2	5.84-10.07
			OA	2	6.34-11.67
			OO	19	3.63-9.14
Yes	EXP3	AA	6	5.3-10.07	
		OA	2	5.77-11.08	
		OO	8	5.24-8.64	
	UCB	AA	2	4.4-11.85	
		OA	2	4.79-10.52	
		OO	13	3.46-10.5	

Table ST5: **Sampling results for the structure of the L1 protuberance in the ribosome (PDB ID 1MZP).** The molecule contains 55 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 5Å. Elements highlighted in yellow correspond to the default GARN options for the molecule.