

PDB ID	# Nucleotides	GARN*		iFoldRNA		MC-SYM		FARNA*		NAST*	
		Time	# structures	Time	# structures	Time	# structures	Time	# structures	Time	# structures
1MZP	55	~ 5 min	50	~ 1 h 40	50	NA	NA	~ 5 min	50	~ 15 min	50
1E8O	49	~ 5 min	50	~ 1 h 30	50	~ 10 h	18	~ 5 min	50	~ 10 min	50
4FE5	67	~ 30 min	50	~ 2h30	50	NA	NA	~ 4 h	43	~ 20 min	50
4QJH	74	~ 30 min	50	~ 2h	50	NA	NA	~ 4 h 30	50	~ 20 min	50
4TS0	89	~ 1h	50	~ NA	NA	~ 8 h	50	~ 4 h	50	~ 25 min	50
1LNG	97	~ 1h	50	~ 3h	50	~ 8 h	50	~ 4 h	50	~ 25 min	50
4WFL	107	~ 2h	50	~ 3h	50	NA	NA	~4 h 30	50	~ 25 min	50
4QK8	124	~ 2h	50	~ 4h	50	NA	NA	~ 5 h	50	~ 25 min	50
1MFQ	127	~ 2 h	50	~ 4 h 30	50	~ 6 h	4	~ 5 h	8	~ 25 min	50
4GXY	172	~ 12 h	50	NA	NA	NA	NA	~ 30 h	6	~ 25 min	50

Table ST11: **Computation time and number of output pdb files generated for all the compared methods.** \* indicates that the computation was performed locally on an Intel Xeon E5607 2.27GHz CPU. NAST computation was also performed with OpenCL on a NVIDIA Quadro 5000 GPU. Other computations were performed on dedicated servers. NAST appears to be much faster than the other methods, but it calculates only secondary structure interactions: the lack on tertiary information as input only allows for extended structures as a result. The computation time for RNAJAG was not available from [30].