- The same method was used to find linker sequences for cyclic nonamer.

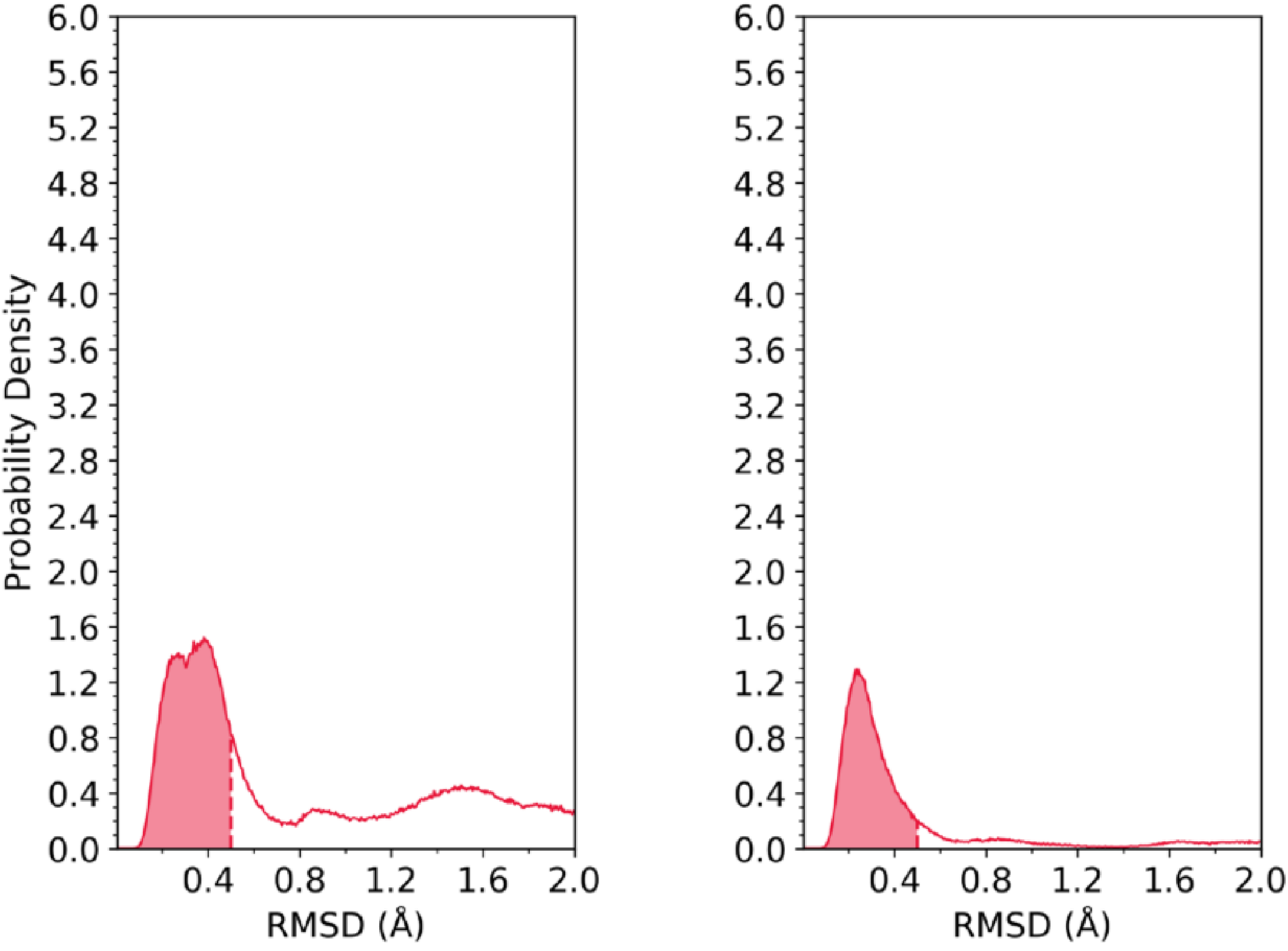
- 52 sequences were proposed in total.

- Molecular dynamics simulations were carried out.

- The results were analyzed.

Linker sequence selection is informed by aa's intrinsic propensity

cyclo-(SESEGGGG) as the starting point


Probability Density
6.0
5.6
5.2
4.8
4.4
4.0
3.6
3.2
2.8
2.4
2.0
1.6
1.2
0.8
0.4
0.0
0.4
0.8
1.2
1.6
2.0
RMSD (Å)
6.0
5.6
5.2
4.8
4.4
4.0
3.6
3.2
2.8
2.4
2.0
1.6
1.2
0.8
0.4
0.0
0.4
0.8
1.2
1.6
2.0
RMSD (Å)

cyclo-(SESEGGGG)

all conformations

conformations without clash