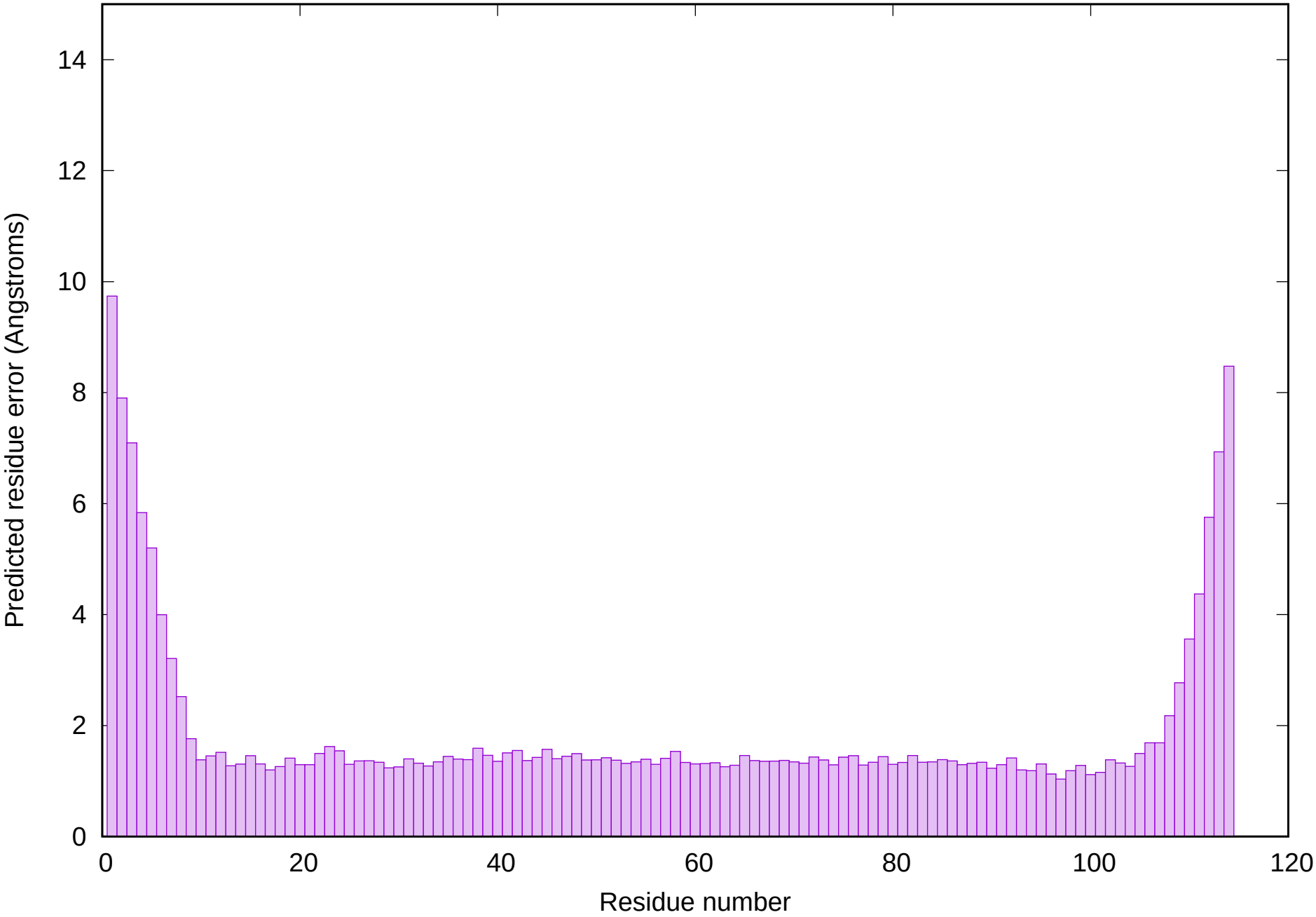
Predicted residue error (Angstroms)
0
2
4
6
8
10
12
14
0
20
40
60
80
100
120
Residue number