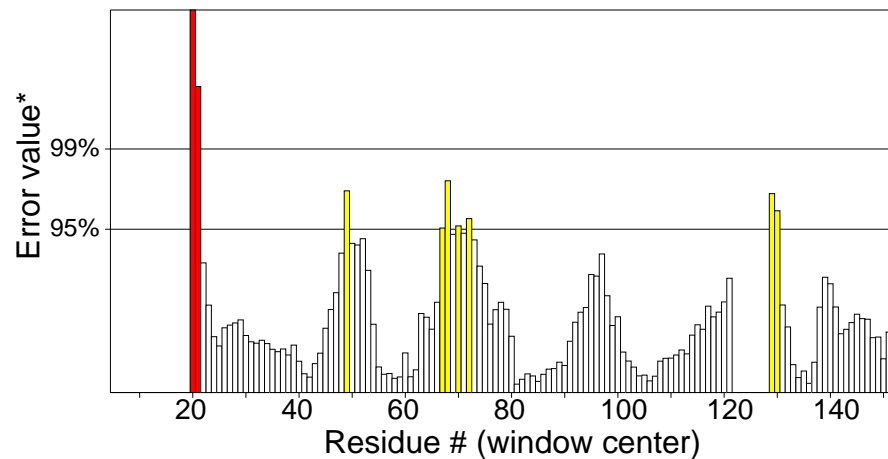


Program: ERRAT2

File: shread_fb977_unrelaxed_rank_001_alphafold2_model_1_seed_000.pdb

Chain#:A

Overall quality factor**: 92.800



*On the error axis, two lines are drawn to indicate the confidence with which it is possible to reject regions that exceed that error value.

**Expressed as the percentage of the protein for which the calculated error value falls below the 95% rejection limit. Good high resolution structures generally produce values around 95% or higher. For lower resolutions (2.5 to 3Å) the average overall quality factor is around 91%.