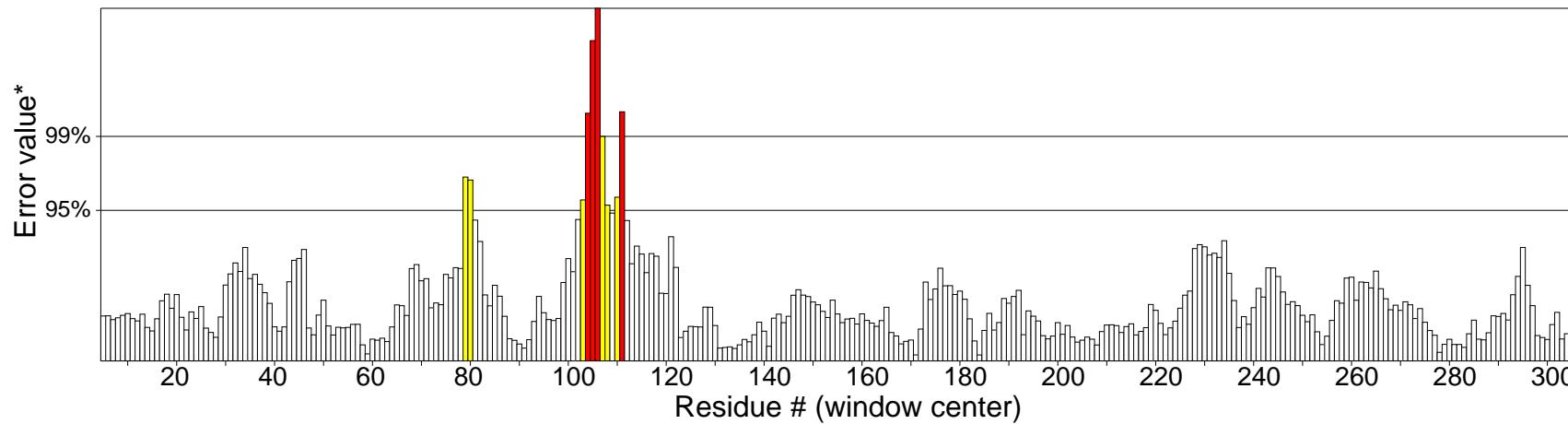


Program: ERRAT2

File: Hpyr004913

Chain#:A

Overall quality factor**: 95.858



*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.

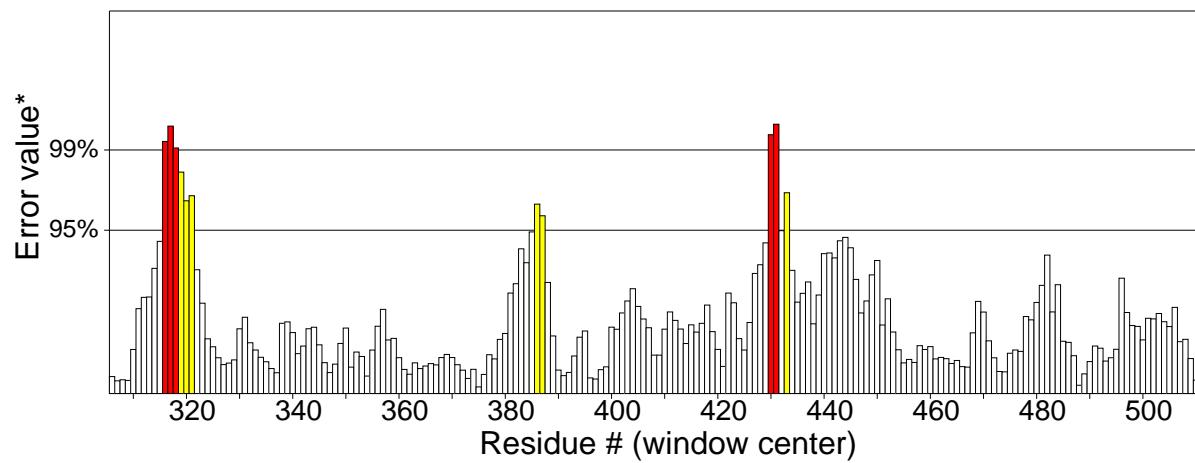
**Expressed as the percentage of the protein for which the calculated error value falls below the 95% rejection limit. Good high resolution structures generally produce values around 95% or higher. For lower resolutions (2.5 to 3A) the average overall quality factor is around 91%.

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