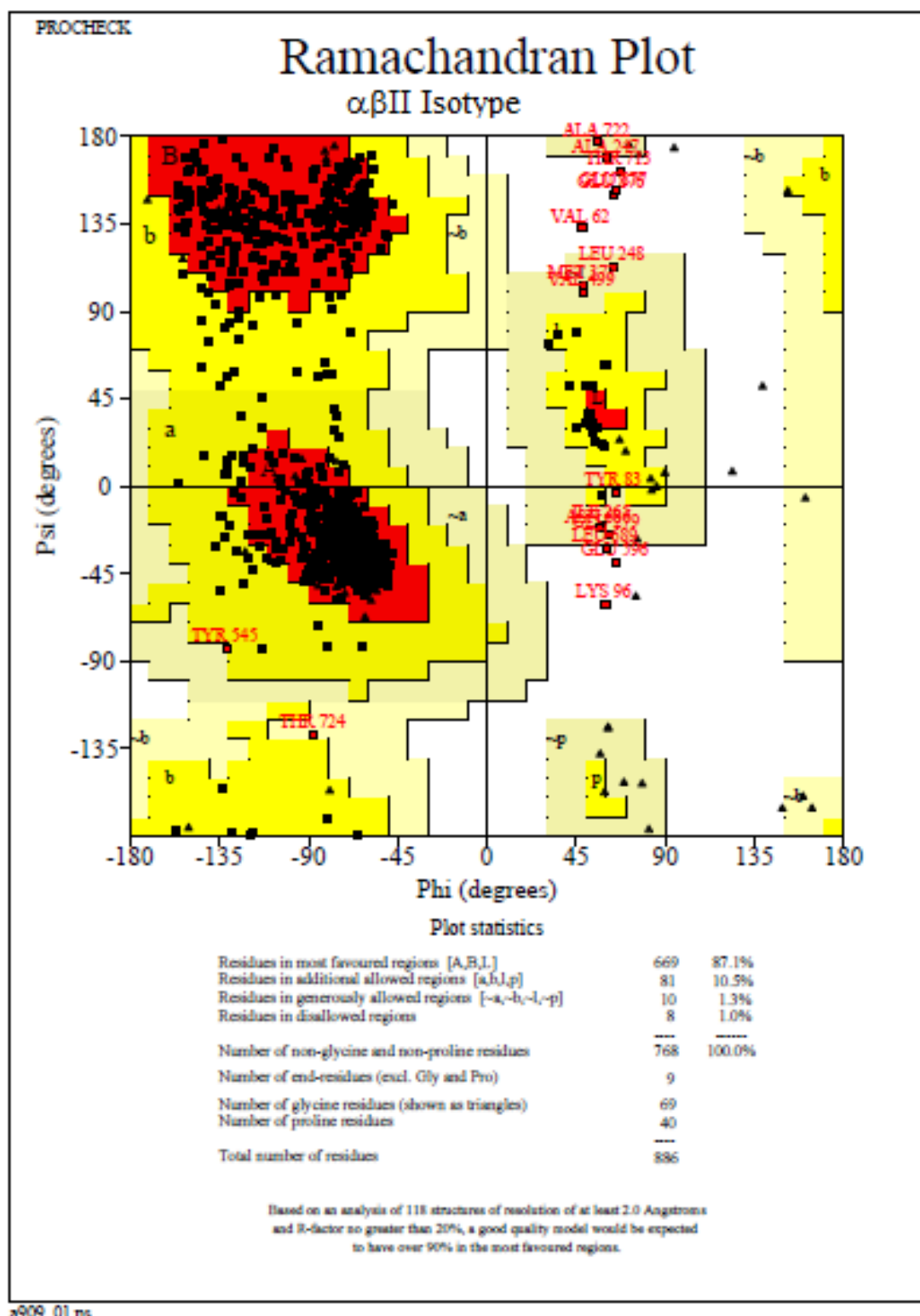
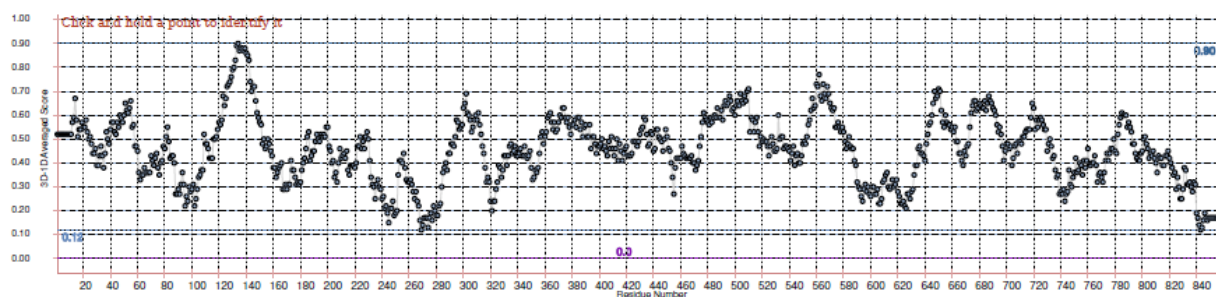


S2 Fig.



(A)

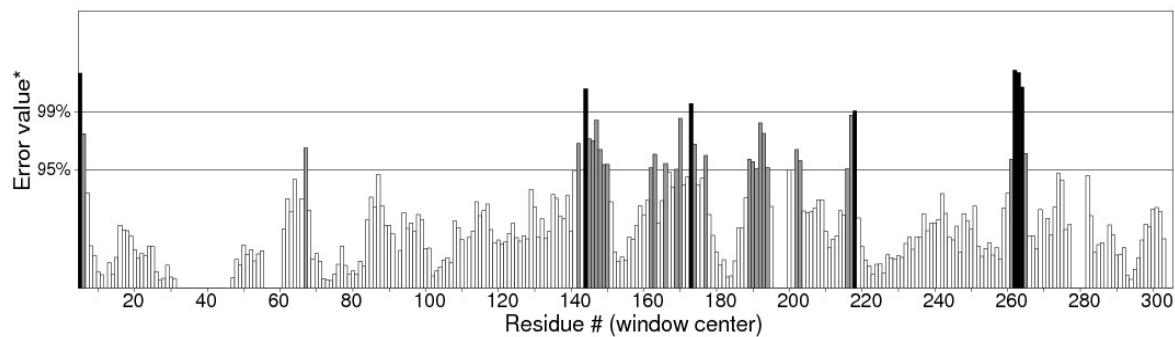
Verify-3D graph of $\alpha\beta$ II Isotype



(B)

Errat score of $\alpha\beta$ II Isotype

Program: ERRAT2
 File: /var/www/SAVES/Jobs/1720384/erratt.pdb
 Chain#:1
 Overall quality factor**: 88.052



*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%.

(C)