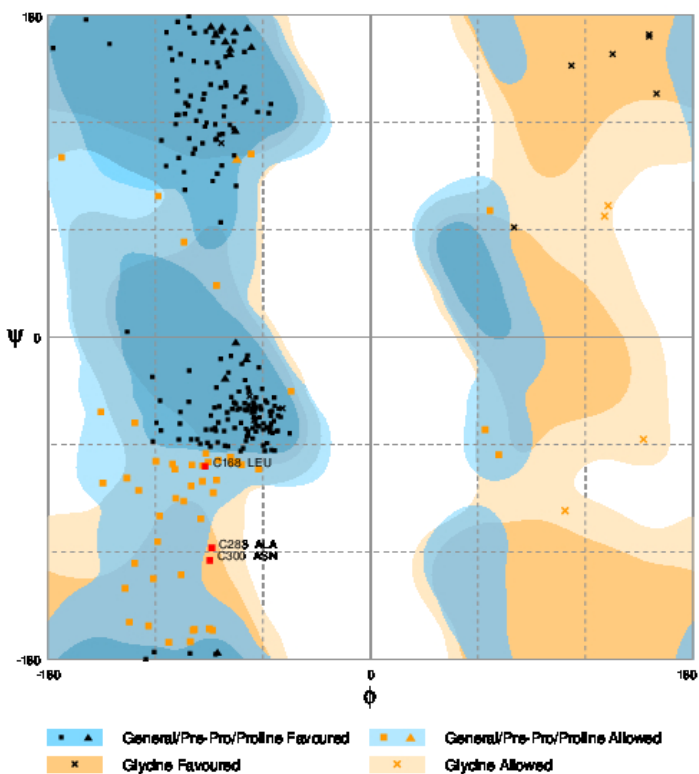
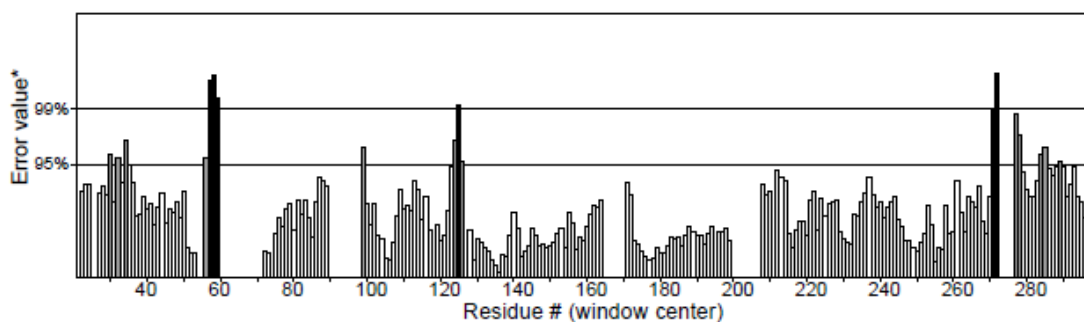


Supplementary information



S-1 Ramachandran plot of the amino acids that make up the receptor (PRR)

Program: ERRAT2  
File: /var/www/html/Services/ERRAT/DATA/3165393.pdb  
Chain#:1  
Overall quality factor\*\*: 92.140

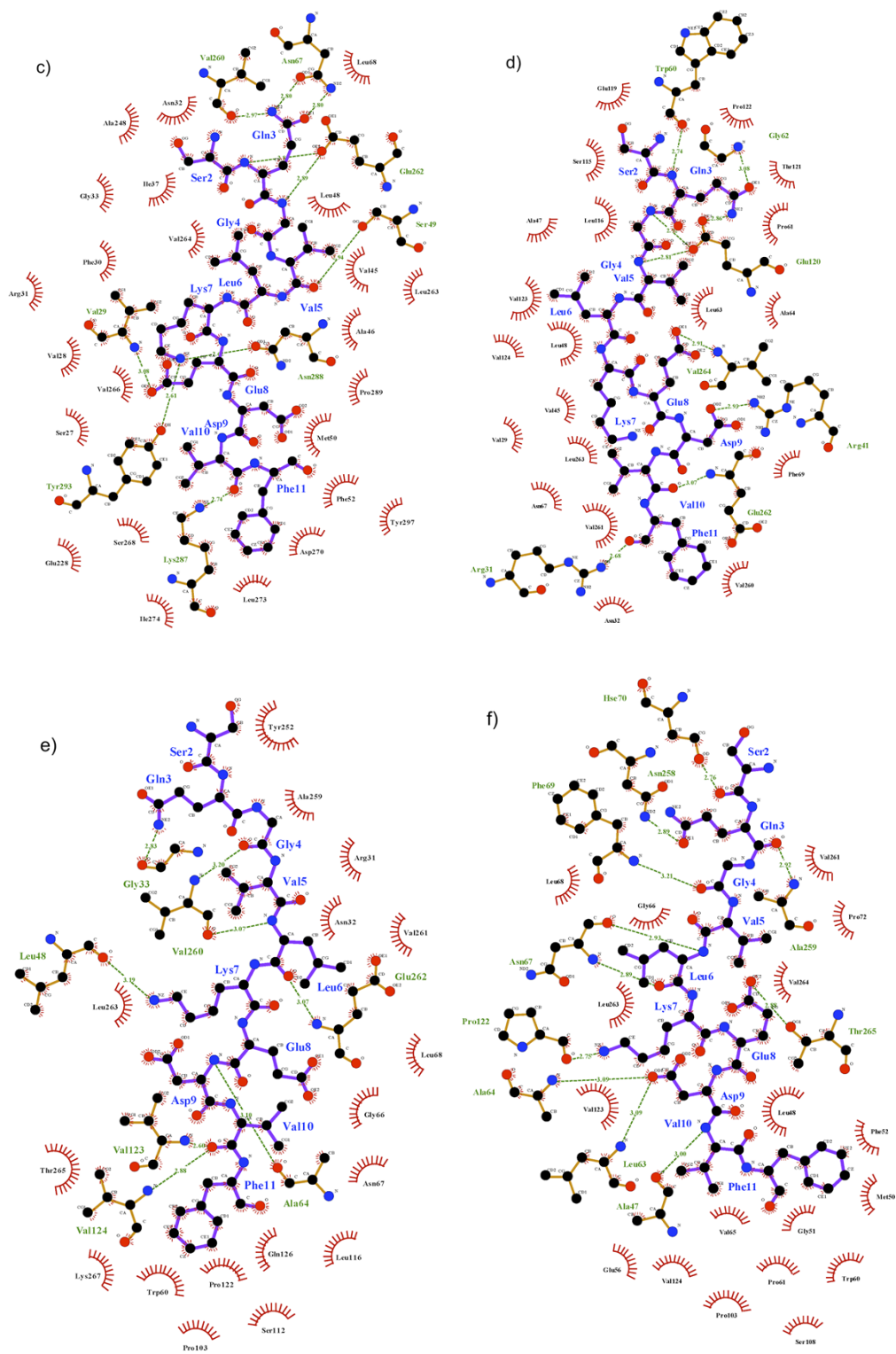


\*On the error axis, two lines are drawn to indicate the confidence with which it is possible to reject regions that exceed that error value.  
\*\*Expressed as the percentage of the protein for which the calculated error value falls below the 95% rejection limit. Good high resolution structures generally produce values around 95% or higher. For lower resolutions (2.5 to 3Å) the average overall quality factor is around 91%.

S-2. Plot ERRAT quality model (PRR) obtained by molecular modeling







S-4. Aminoacids residues that formed binding site predicted on the PRR and main interactions obtained for the peptide SQGLKEDVF with PRR.