XRD

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-Ramachandran plot

A Ramachandran plot (also known as a Ramachandran map or a Ramachandran diagram or a [φ,ψ] plot), deve
Gopalasamudram Narayana Ramachandran and Viswanathan Sasisekharan is a way to visualize dihedral angl
amino acid residues in protein structure. It shows the possible conformations of ψ and φ angles for a polypeptid

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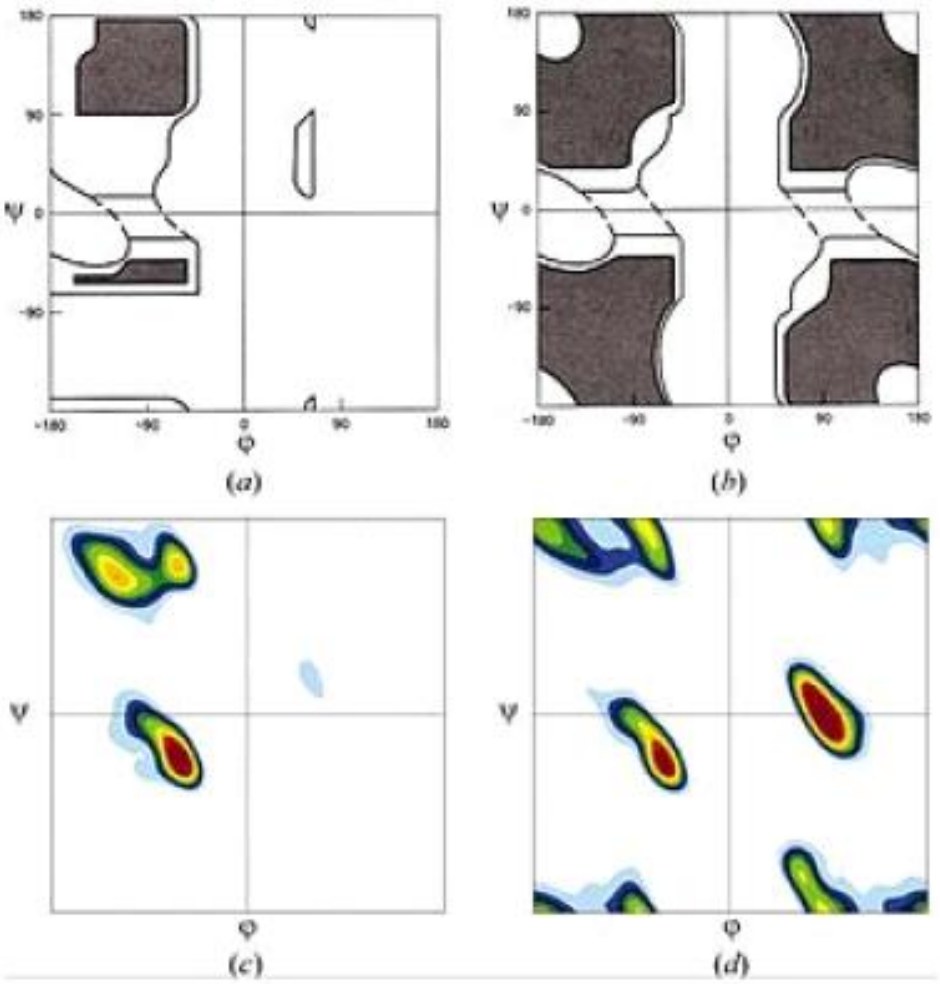
dihedral angles named φ and ψ by Ramachandran.



The classical version of the Ramachandran plot for (a) alanine and (b) glycine

According to Ramachandran & Sasisekharan (1968). The fully allowed regions are shaded; the partially allowed regio solid line. The connecting regions enclosed by the dashed lines are permissible with slight flexibility of bond angles. T arrived at by stereo-chemical modelling. Although some overall features of these plots are correct, the details differ fr experimentally observed Ramachandran plots for (c) all 19 non-glycines and (d) glycine.

The most remarkable differences are that most regions show a 45 degree slope rather than being parallel to any of the region is split into two distinct maxima and the two most populated regions (red) for glycine seen in (d) were predicte permissible as shown in (b). There are five areas in the glycine plot; two with psi 0 and three with psi 180.