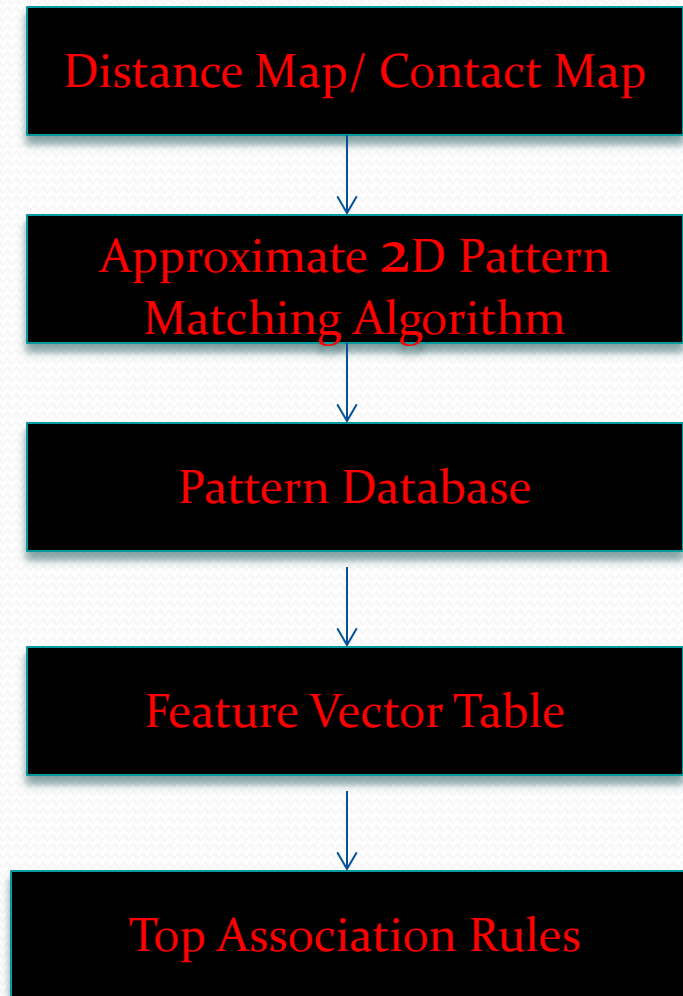


# Association Rule Mining of Protein Contact Maps from Protein 3D Structures

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# Proposed Methodology



# Results

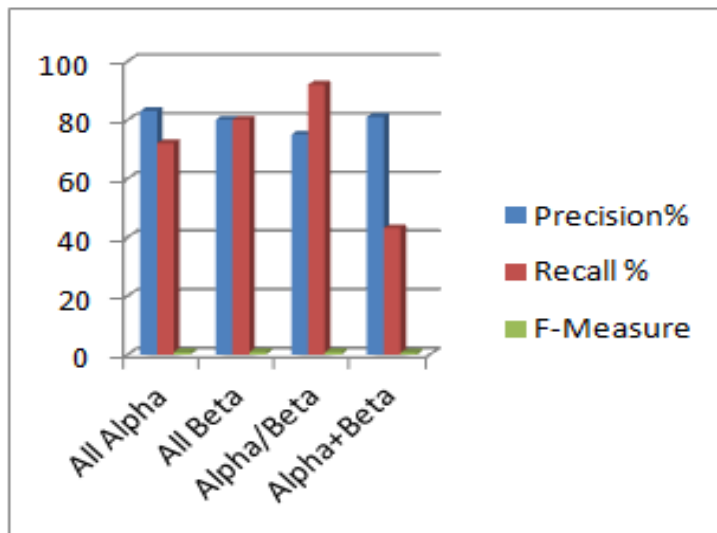


Fig1: Structural classification using diagonal features

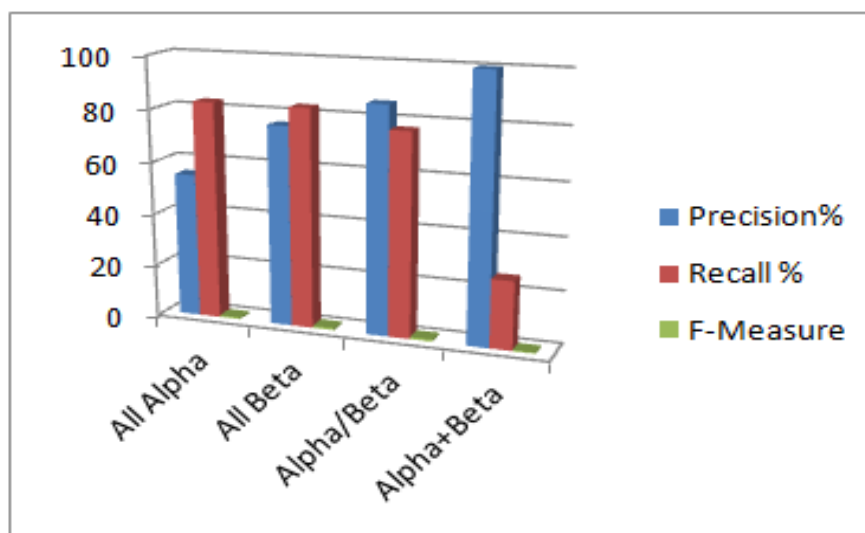


Fig 2: Structural classification using pattern features

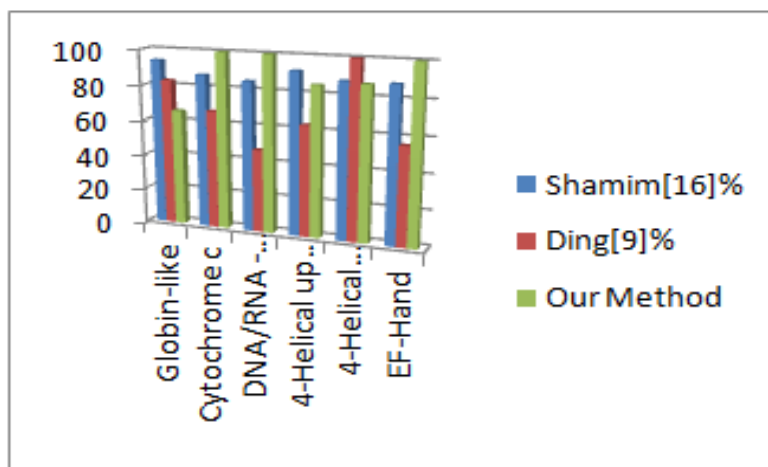


Fig3: Comparison of accuracy results obtained for All-alpha fold classification with results in literature

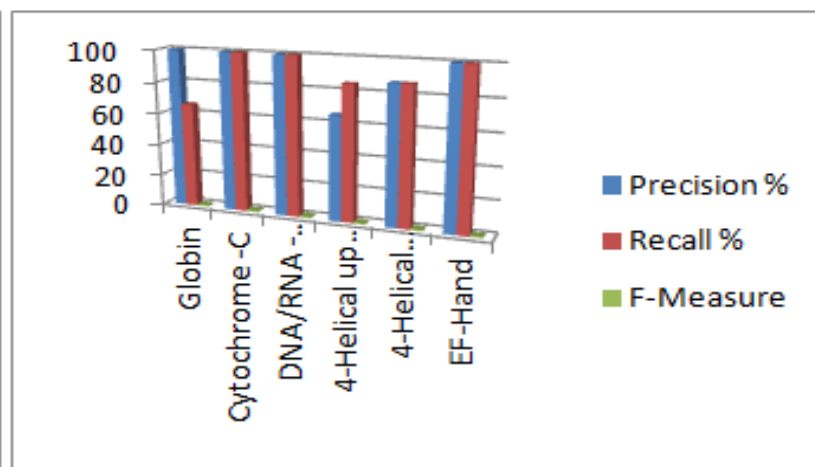


Fig4: All-Alpha classification in protein folds diagonal features + pattern features