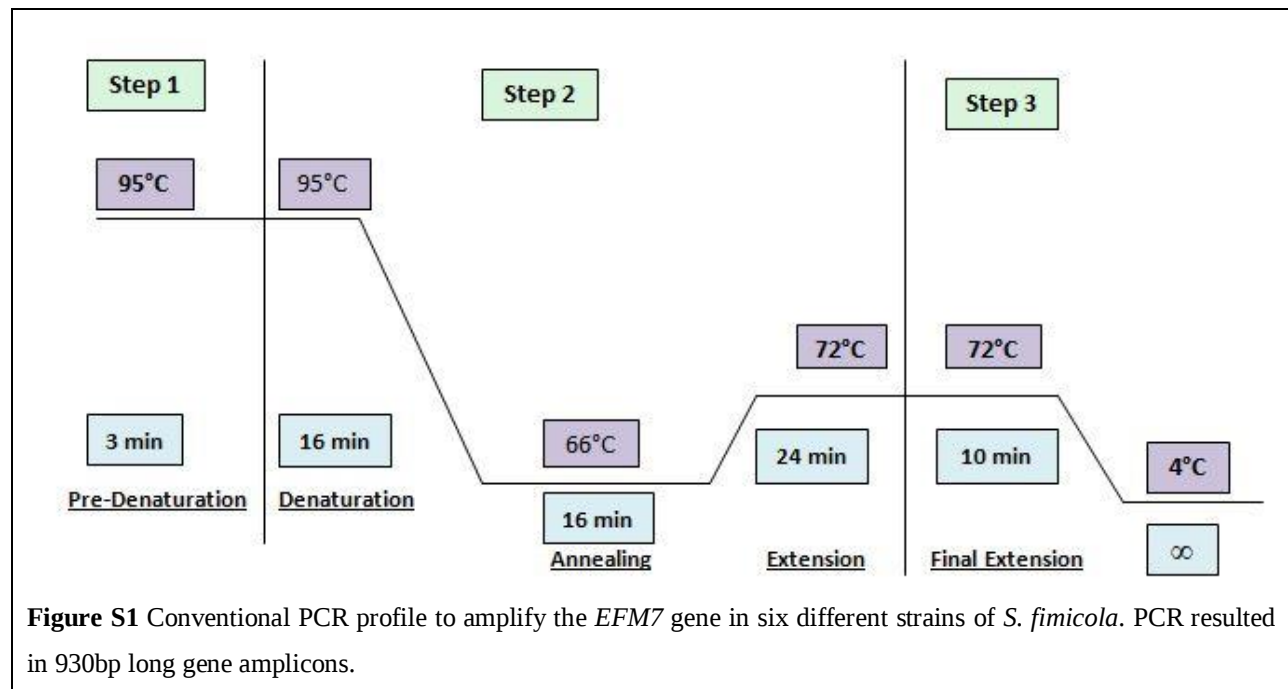
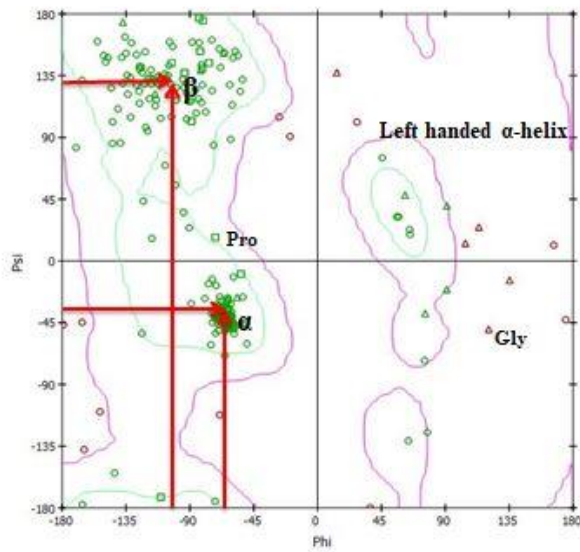
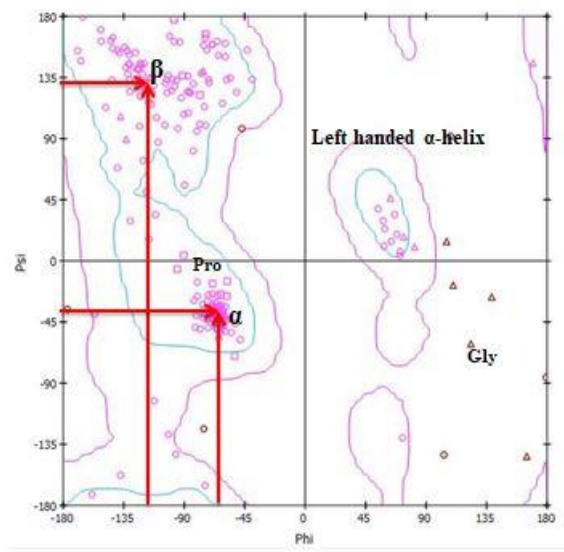


Supplementary Material

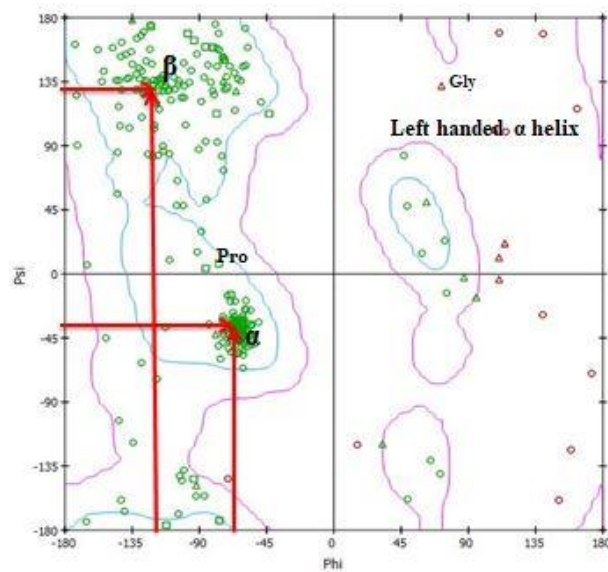




a: Amino acid density graph of *Sordaria fimicola* (S3)



b: Amino acid density graph of *Sordaria fimicola* (N5)



c: Amino acid density graph of *Sordaria macrospora*

Figure S1 Graphical representations of 3D protein models of S3 and N5 of *S. fimicola* and *S. macrospora*. The 3D protein structure of two representatives of SFS and NFS strains (S3 and N5) respectively of *S. fimicola* and *S. macrospora* were plotted in the form of a Ramachandran graph to check their stereochemistry and structural accuracy. The horizontal axis of the graphs presented Phi (ϕ) values up to 180° while the vertical axis presented with Psi (ψ) values up to 180° . The graphs are divided into four quadrants the right side bottom quadrant has a cluster of amino acids exposed to those residues which are involved in the making of α -helix while the top right quadrant has a cluster of residues involved in the making of β - sheets. These clusters mostly occur in bounded regions highlighted by sky blue colored boundaries in all three graphs where the steric hindrance between ϕ and ψ angles is the least and

these are called low-energy regions or favorable regions as they showed stable protein structure. In all three graphs, these regions can be seen clearly. The white portion of the graphs outside the boundaries of α -helix and β -sheet is known as a high-energy region where steric clashes between amino acids are at their peak and not favorable for stable protein structure. Here mostly Gly residue is found because it does not have side chains with it so it faced the least steric clashes like other amino acids. Another important structure residing in the top left quadrant is left-handed α -helix which is not common in all protein models. These graphs represented that the putative 3D protein models of EFM7 of two strains of *S. fimicola* are biologically active, have structural accuracy and this protein may be able to make further interactions with other proteins. From the graphs of S3 of *S. fimicola* and *S. macrospora*, it can be clearly seen that they are more resembling with each other as compared to the N5 strain of *S. fimicola* which showed that SFS strains are phylogenetically closer to *S. macrospora* than NFS strains. This fact is supported by Figures 1, 2 and 3 in the main paper.