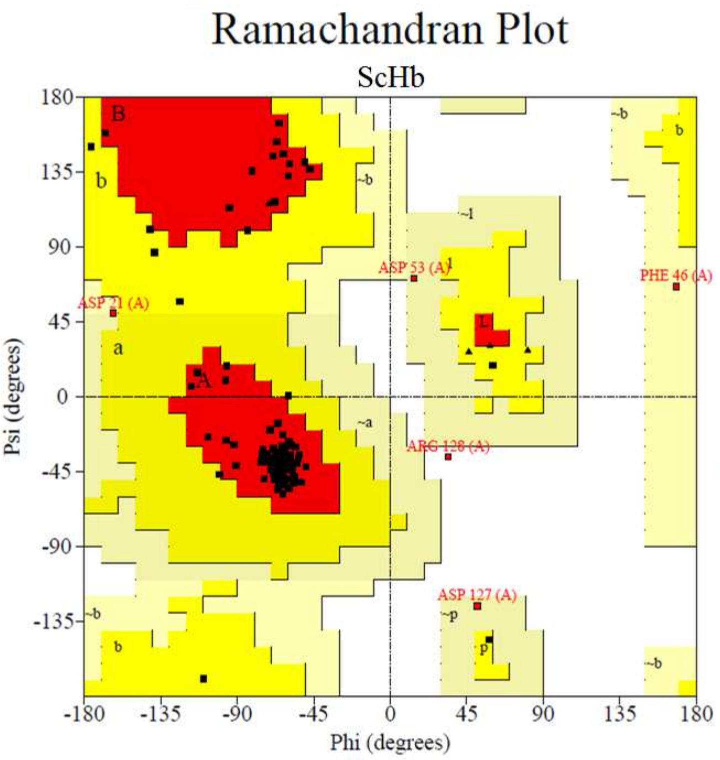
Corrêa (2014) Molecular cloning and protein folding characterization of a predicted heme-binding globin in a sugar cane EST database - Journal of Integrated Omics

Supplemental Figure 1. Ramachandran plot of the ScHb 3D model, which was based on the structure of ORYsa GLB1a (PDB: 1D8U-A). The plot shows the acceptability of the model.



Plot statistics

Residues in most favoured regions [A,B,L]	127	89.4%
Residues in additional allowed regions [a,b,l,p]	10	7.0%
Residues in generously allowed regions [~a,~b,~l,~p]	4	2.8%
Residues in disallowed regions	1	0.7%
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Number of non-glycine and non-proline residues	142	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	5	
Number of proline residues	4	

Total number of residues	153	

Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.