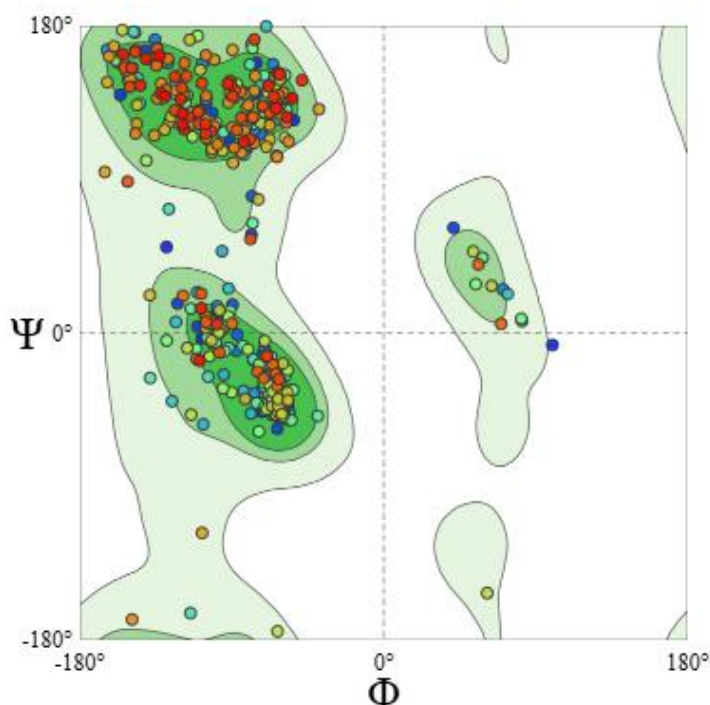




MolProbity Score	1.25
Clash Score (A149 TYR-A152 TYR), (A152 TYR-A152 TYR)	1.69
Ramachandran Favoured	96.06%
Ramachandran Outliers A316 GLY, A33 ASN	0.33%
Rotamer Outliers A556 SER, A569 VAL, A343 LEU, A602 CYS, A490 THR, A505 THR	1.21%
C-Beta Deviations A47 ASP, A590 SER, A489 THR	3
Bad Bonds	0 / 4682
Bad Angles A416 ASP, A353 PHE, A249 ASN, (A158 TRP-A159 PRO), A399 SER, (A219 ALA-A220 PRO), A411 GLN, A173 ASN, (A399 SER-A400 LEU), (A598 VAL-A599 PRO), (A308 TYR-A309 PRO), A195 HIS, (A481 THR-A482 THR), A439 TRP, (A509 THR-A510 PRO), (A352 PHE-A353 PHE), A287 PHE, A280 HIS, (A447 VAL-A448 PRO), (A95 ASN-A96 PRO)	22 / 6424
Cis Non-Proline (A25 GLY-A26 SER)	1 / 587
Cis Prolines (A47 ASP-A48 PRO), (A124 ARG-A125 PRO), (A591 ASP-A592 PRO)	3 / 23
Twisted Non-Proline (A490 THR-A491 LYS)	1 / 587

Supplementary Figure 5. Ramachandran plot of the structural model of *P. crustosum* G10 glucoamylase (UniProt A0A9P5L1K9). The results were obtained using MolProbity version 4.4 (ExpASY). The structural model was constructed with 100% coverage and a GMQE score of 93%, using the *A. niger* glucoamylase structure (AlphaFold G3Y7U0) as a template. The two proteins share 71.7% sequence identity, excluding the signal peptides.