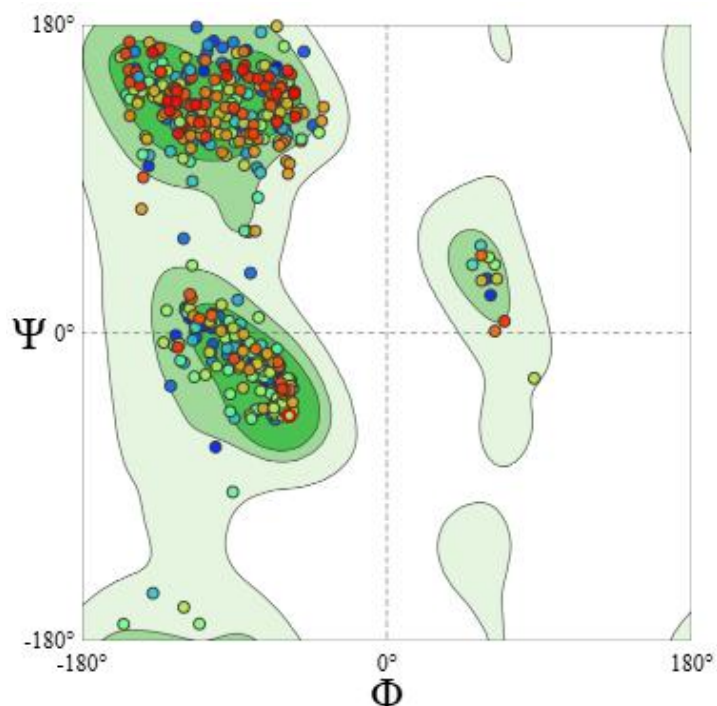




MolProbity Score	1.38
Clash Score	2.38
Ramachandran Favoured	94.8%
Ramachandran Outliers A391 SER, A480 THR, A482 THR	0.5%
Rotamer Outliers A476 THR, A322 HIS, A473 THR, A482 THR, A479 THR	0.98%
C-Beta Deviations A428 CYS, A434 ASP, A457 VAL, A390 SER, A207 THR	5
Bad Bonds	0 / 4654
Bad Angles (A252 TYR-A253 PRO), (A391 SER-A392 PRO), A328 ASP, A457 VAL, A233 ASP, (A216 TRP-A217 PRO), A259 ASP, A285 ASP, A175 ASP, A390 SER, A24 ASN, A256 SER, A453 LEU, A147 HIS, A284 HIS, A434 ASP, A286 ASN, (A596 SER-A597 TRP), A108 HIS, A425 MET, A304 SER, (A373 VAL-A374 PRO), A179 THR, A560 PHE, A301 ASN, (A441 VAL-A442 PRO), (A258 SER-A259 ASP), (A147 HIS-A148 PRO), A452 VAL, (A582 VAL-A583 PRO), A122 HIS, (A550 LEU-A551 PRO)	33 / 6375
Cis Prolines (A138 THR-A139 PRO), (A328 ASP-A329 PRO), (A575 ASP-A576 PRO)	3 / 24

Supplementary Figure 3. Ramachandran plot of the structural model of *P. crustosum* G10 α -amylase (UniProt A0A9P5KX09). The results were obtained using MolProbity version 4.4 (Expasy). The structural model was constructed with 100% coverage and a GMQE score of 94%, using the *P. oxalicum* α -amylase structure (AlphaFold S7Z6T2_PENO1) as a template. The two proteins share 77.35% sequence identity, excluding the signal peptides.