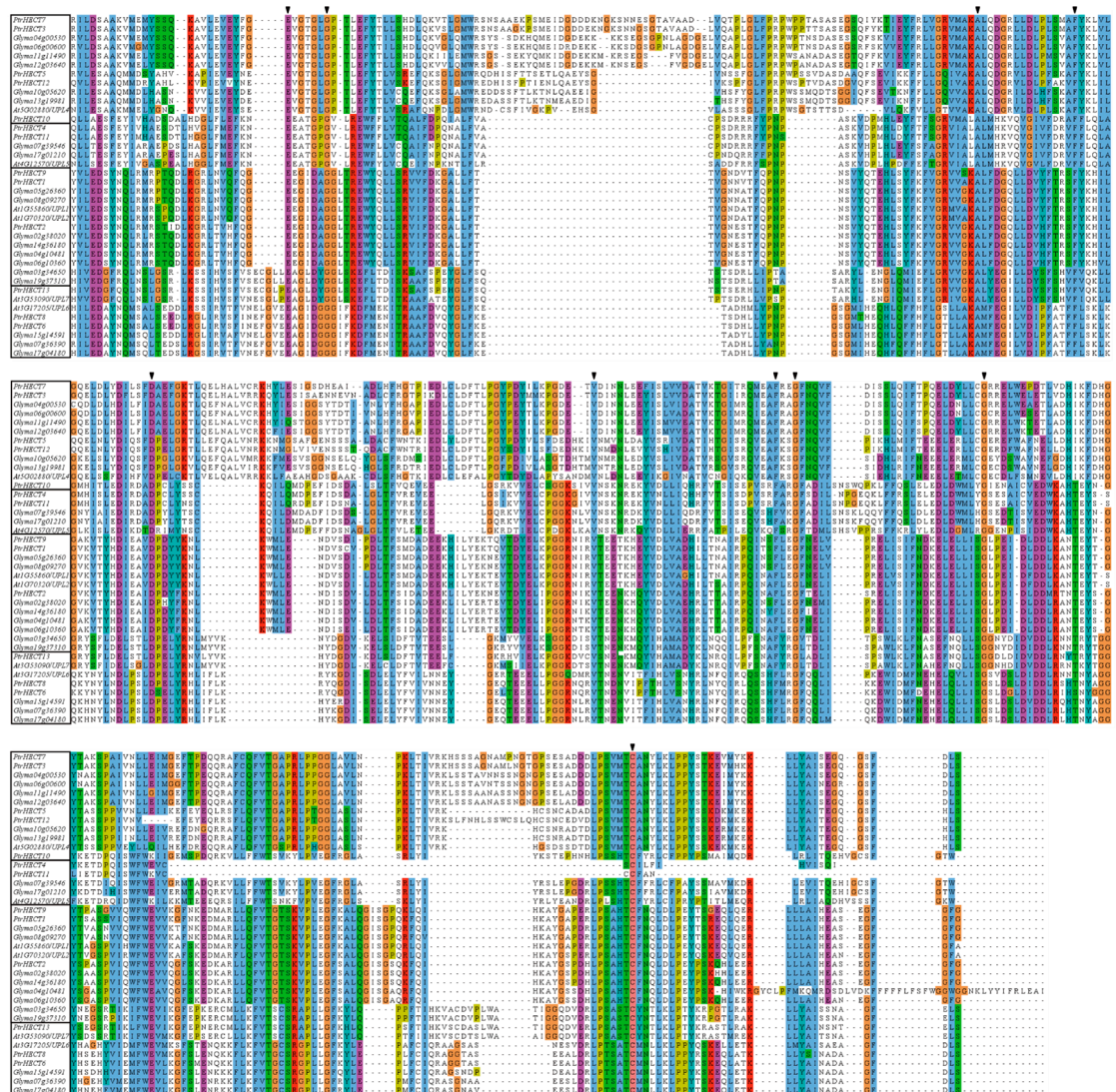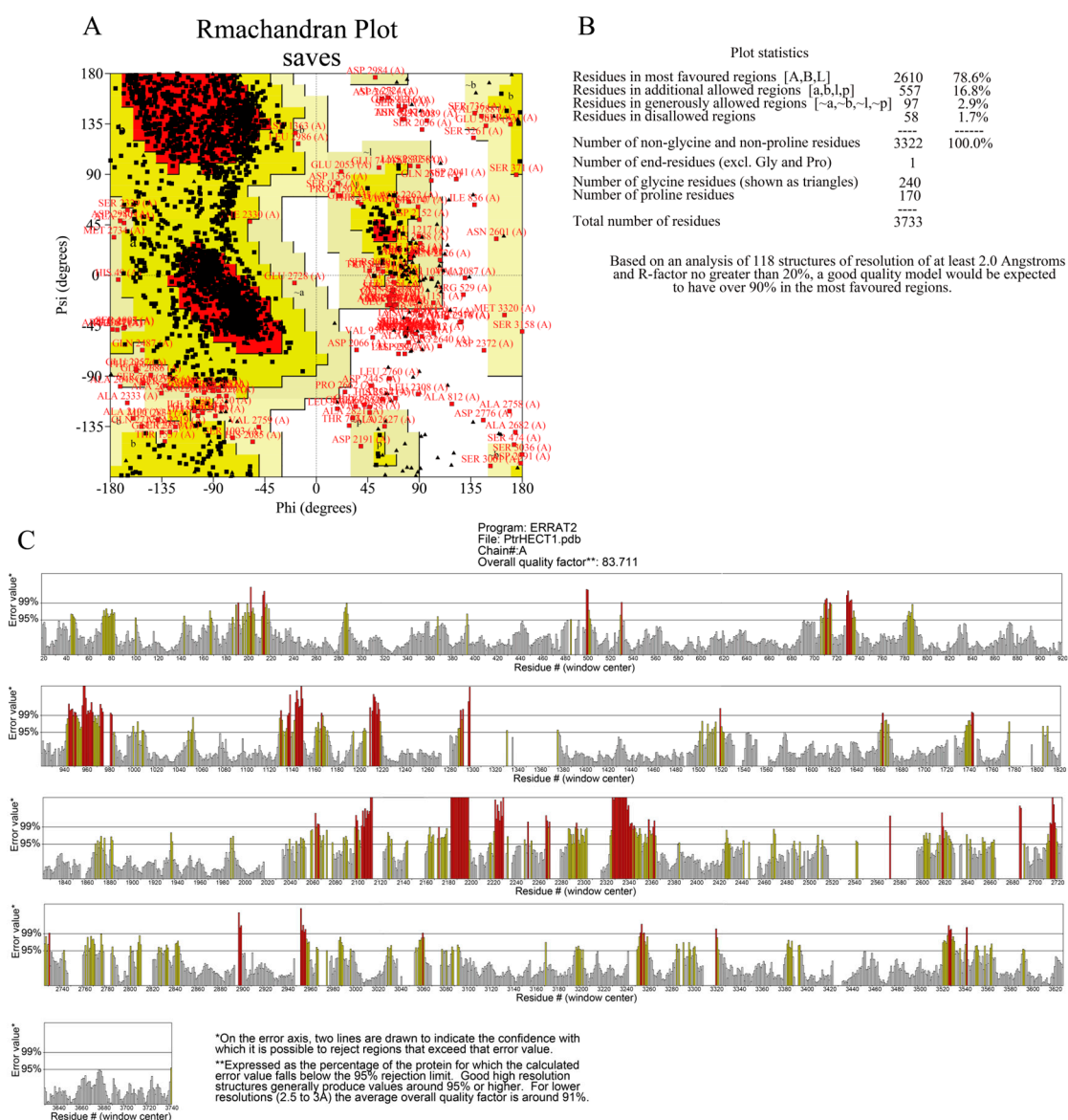**Supplementy Table S1.** The primers for qRT-PCR.

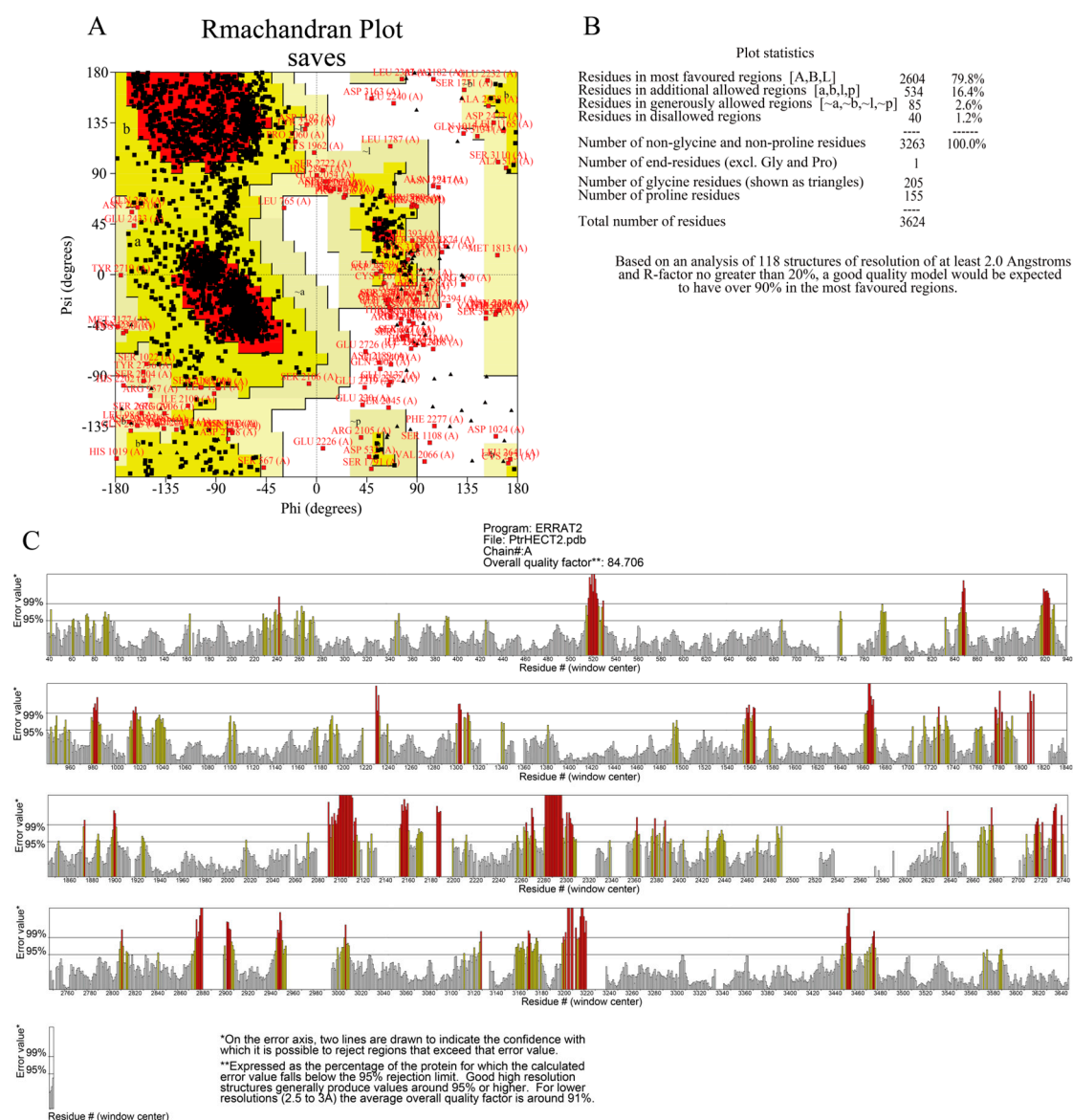| Primer name	Primer sequence (5'→3')
PtrActin.F	TGTTGCCCTTGACTATGAGCAGGA
PtrActin.R	ACGGAATCTCTCAGCTCCAATGGT
PtrHECT1.F	TGAGCAGCATCTTTCTAACCT
PtrHECT1.R	GGGTCACACCCATTTTGTGC
PtrHECT2.F	TGCCTCCTCGCATTCATTGT
PtrHECT2.R	GGTTCCCTGCAGCAAAACTG
PtrHECT3.F	AGCCAGGAGATGAAACTGTTGAT
PtrHECT3.R	GTTCTCTTCGCCCACAAAGC
PtrHECT4.F	TTGTGGAACTTTGCCCTGGT
PtrHECT4.R	CAAGATCTTCAAGCTCCAAGCT
PtrHECT5.F	CGAGGAGGAACTTGAGCGTT
PtrHECT5.R	CTCCTGTAGGTAGCCGAGGT
PtrHECT6.F	GAGGGAGAAAGGCAGTGGAG
PtrHECT6.R	ATCCCCACCAGCAAATAGGC
PtrHECT7.F	CAGAGAGTTGTGGGAGCCTG
PtrHECT7.R	GGGTTTAGGACAGCCAGACC
PtrHECT8.F	TCATGAGGGGCTTTCAGCAG
PtrHECT8.R	TCGCTATGATAACCACCCGC
PtrHECT9.F	CCTTGAGAGTGGTGGGGAAC
PtrHECT9.R	CCAGGAGGAAGAGGGGATGA
PtrHECT10.F	AGACGACACCGAATCATCCAC
PtrHECT10.R	GATTGAGACCGACGGAGAGG
PtrHECT11.F	TTTGATGGGGAGTGTGGTGG
PtrHECT11.R	GCCAACTTGTTCAGAGGCAT
PtrHECT12.F	GACGTCGCACGTCTTATCCA
PtrHECT12.R	GAGCTTGAGCAGCTGATTCT
PtrHECT13.F	ACACCATCTCGCAAGCATCA
PtrHECT13.R	TGAAGCGTCTCCAAACCCTC

Supplementary Figure S1. Sequence alignment of the HECT domain of all the identified HECT proteins in *Populus trichocarpa*, *Arabidopsis thaliana*, *Glycine max*, *Oryza sativa*, *Zea mays* and *Triticum aestivum*. The HECT conserved domain (PF00632) of all the putative HECT proteins were analyzed to identify the conserved active site residues. The triangle indicates the conserved active site cysteine residue.

Supplementary Figure S2. Homology modelled structure validation of PtrHECT1 using (A) Ramachandran plot; (B) Ramachandran plot statistics; and (C) ERRAT.

Supplementary Figure S3. Homology modelled structure validation of PtrHECT2 using (A) Ramachandran plot; (B) Ramachandran plot statistics; and (C) ERRAT.

Supplementary Figure S4. Homology modelled structure validation of PtrHECT3 using (A) Ramachandran plot; (B) Ramachandran plot statistics; and (C) Verify3D.

A

Rmachandran Plot
saves

B

Plot statistics

Residues in most favoured regions [A,B,L]	643	89.8%
Residues in additional allowed regions [a,b,l,p]	54	7.5%
Residues in generously allowed regions [~a,~b,~l,~p]	10	1.4%
Residues in disallowed regions	9	1.3%
	----	------
Number of non-glycine and non-proline residues	716	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	41	
Number of proline residues	34	

Total number of residues	793	

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
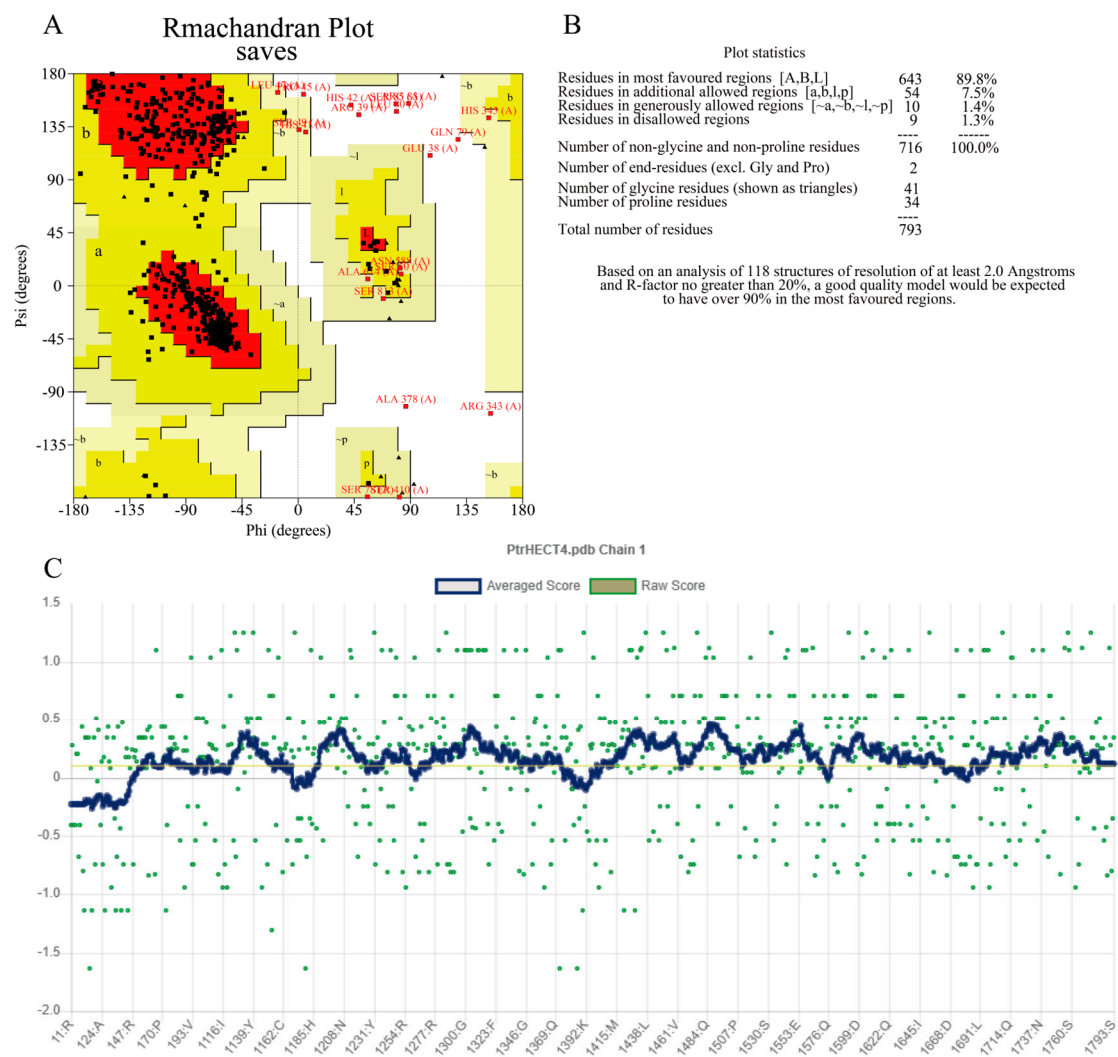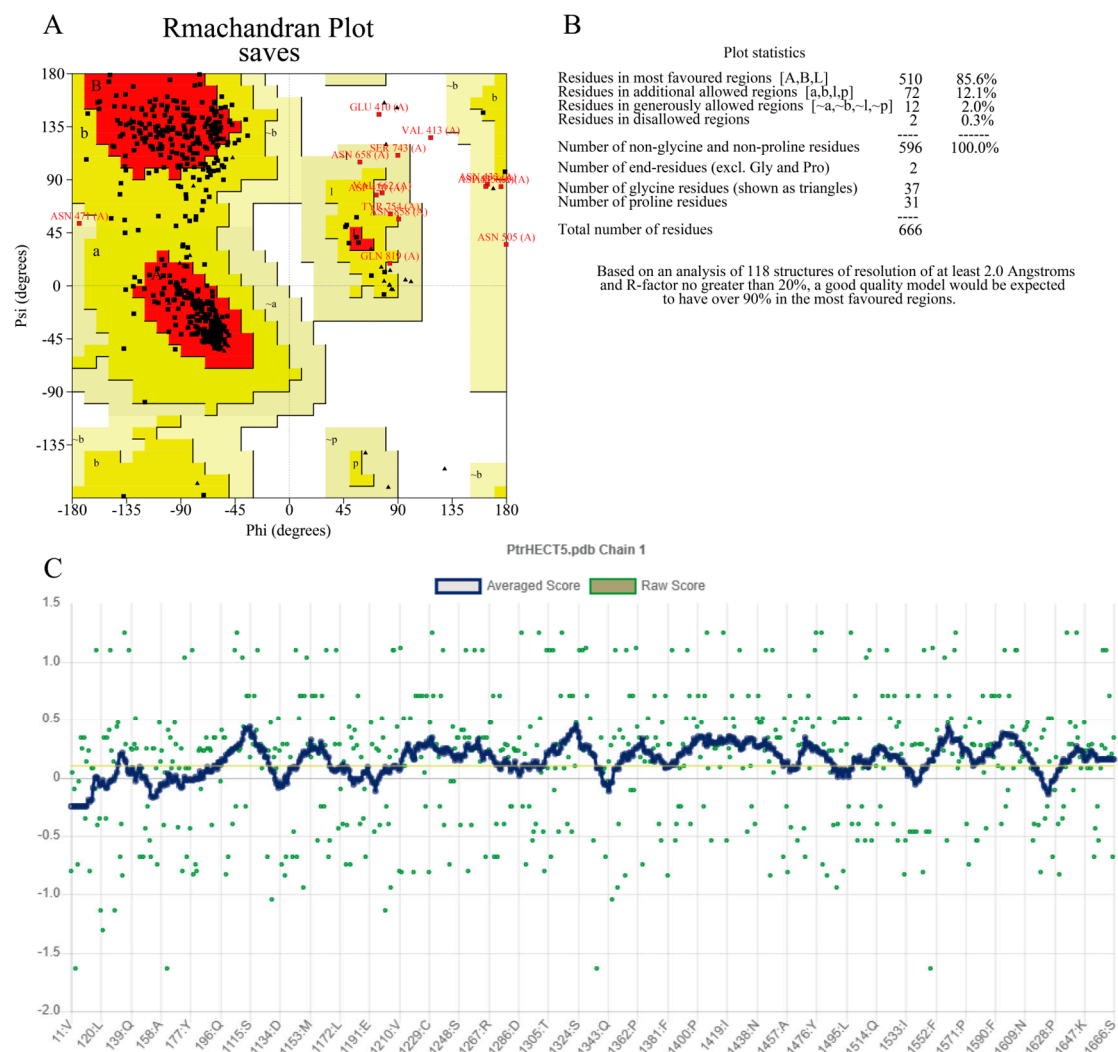to have over 90% in the most favoured regions.

C

Supplementary Figure S5. Homology modelled structure validation of PtrHECT4 using (A) Ramachandran plot; (B) Ramachandran plot statistics; and (C) Verify3D.

A Rmachandran Plot
saves

B Plot statistics

Residues in most favoured regions [A,B,L]	510	85.6%
Residues in additional allowed regions [a,b,l,p]	72	12.1%
Residues in generously allowed regions [~a,~b,~l,~p]	12	2.0%
Residues in disallowed regions	2	0.3%
	----	------
Number of non-glycine and non-proline residues	596	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	37	
Number of proline residues	31	

Total number of residues	666	

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.
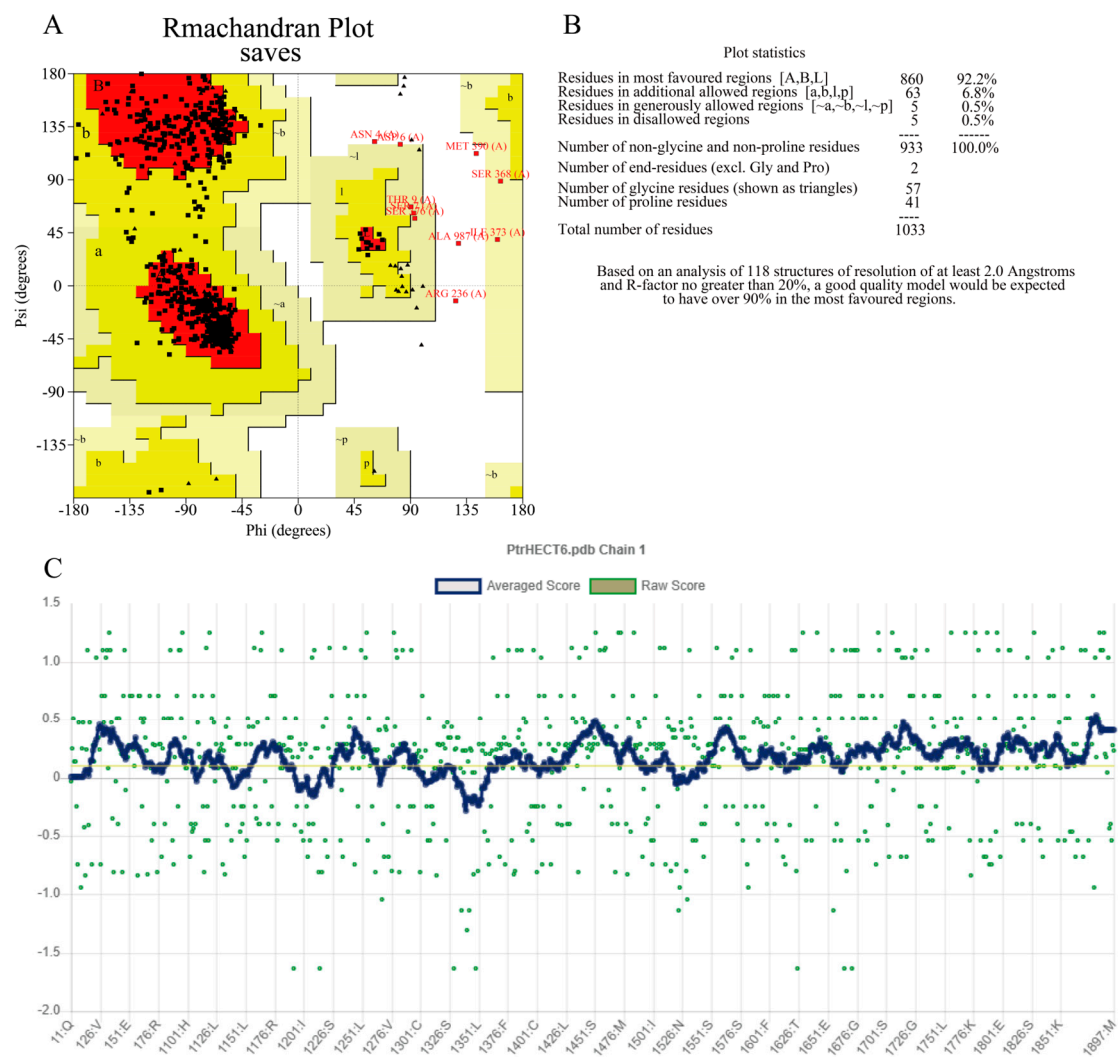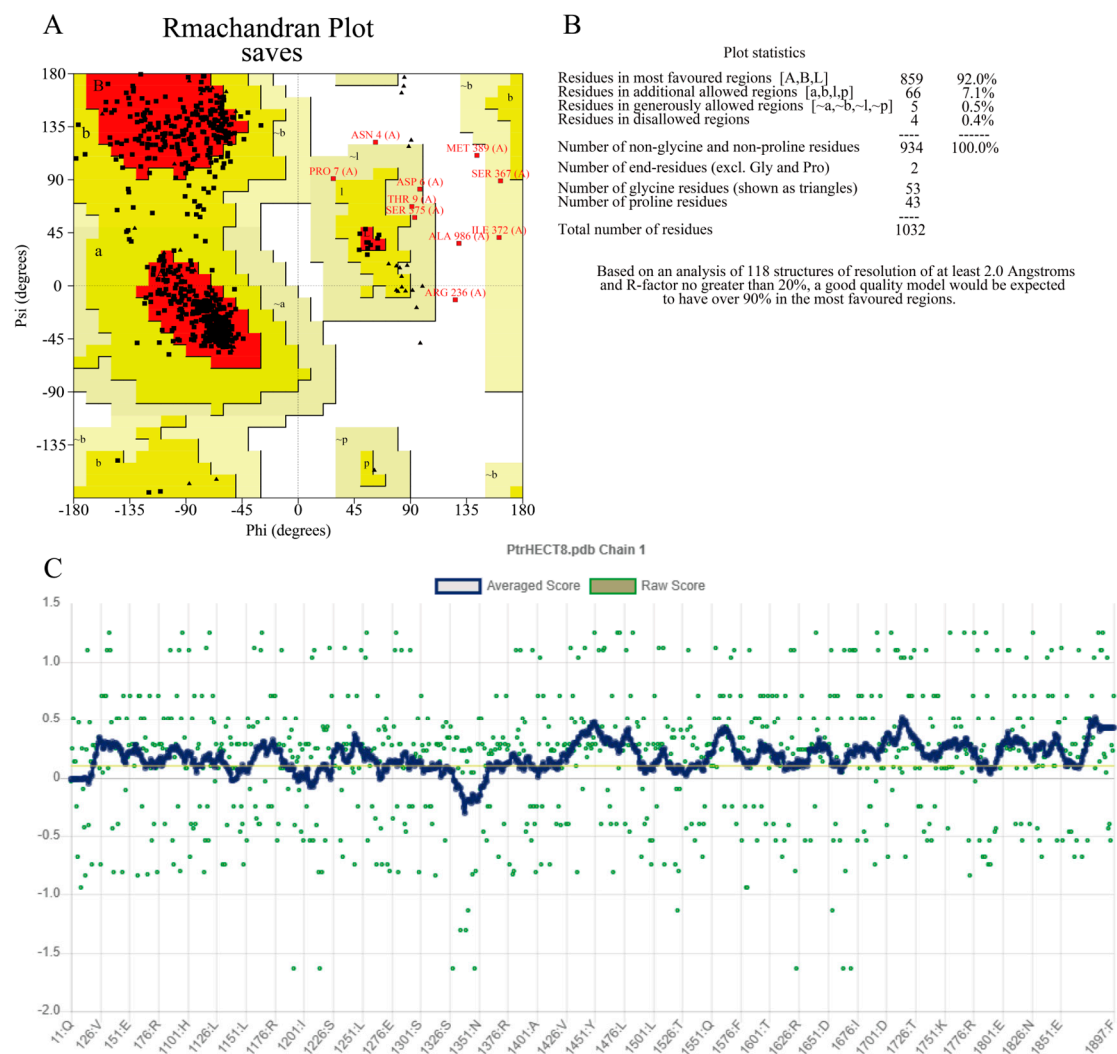
C

Supplementary Figure S6. Homology modelled structure validation of PtrHECT5 using (A) Ramachandran plot; (B) Ramachandran plot statistics; and (C) Verify3D.

A

Rmachandran Plot
saves

B

Plot statistics

Residues in most favoured regions [A,B,L]	860	92.2%
Residues in additional allowed regions [a,b,l,p]	63	6.8%
Residues in generously allowed regions [~a,~b,~l,~p]	5	0.5%
Residues in disallowed regions	5	0.5%
	----	------
Number of non-glycine and non-proline residues	933	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	57	
Number of proline residues	41	

Total number of residues	1033	

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
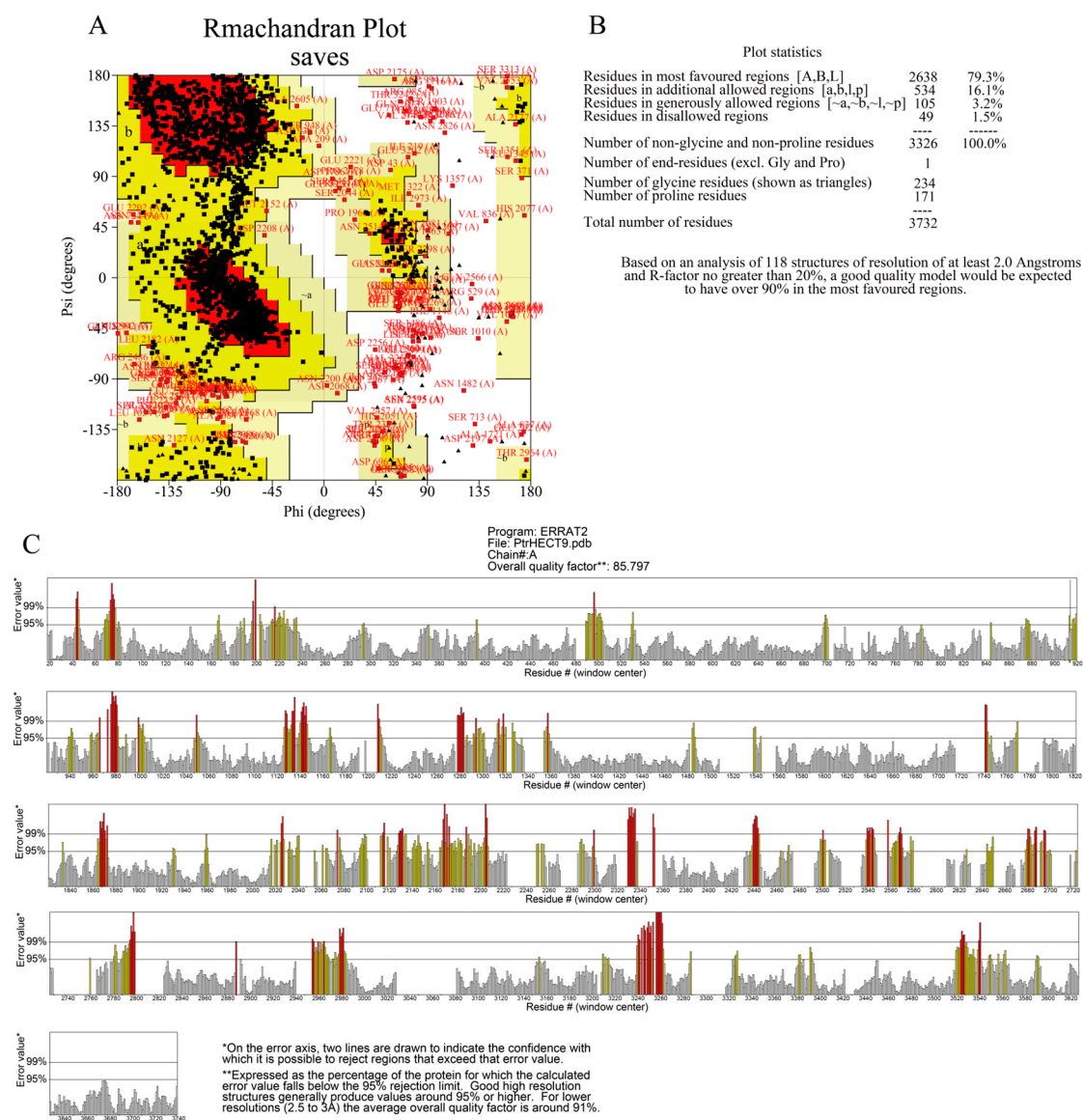to have over 90% in the most favoured regions.

C

Supplementary Figure S7. Homology modelled structure validation of PtrHECT6 using (A) Ramachandran plot; (B) Ramachandran plot statistics; and (C) Verify3D.
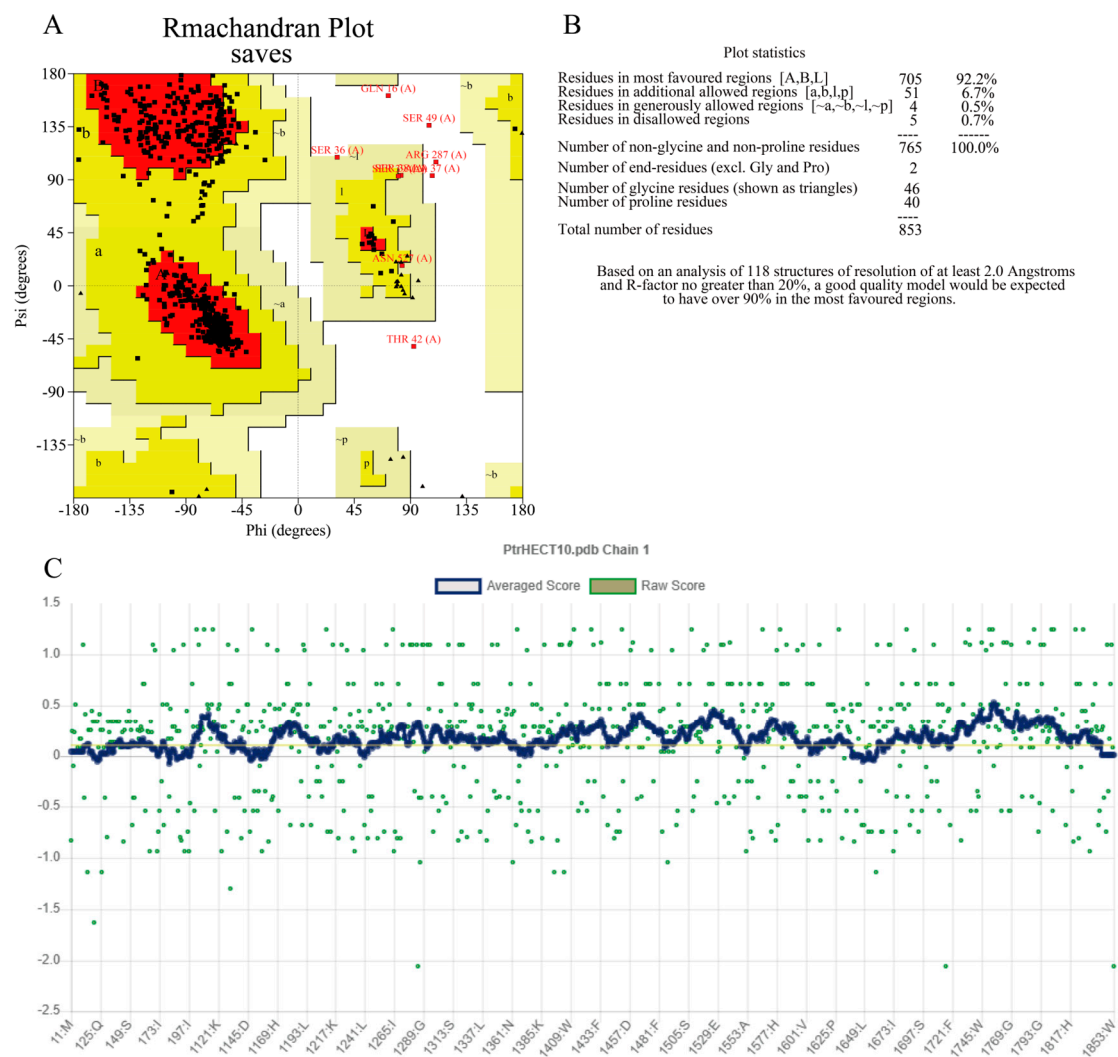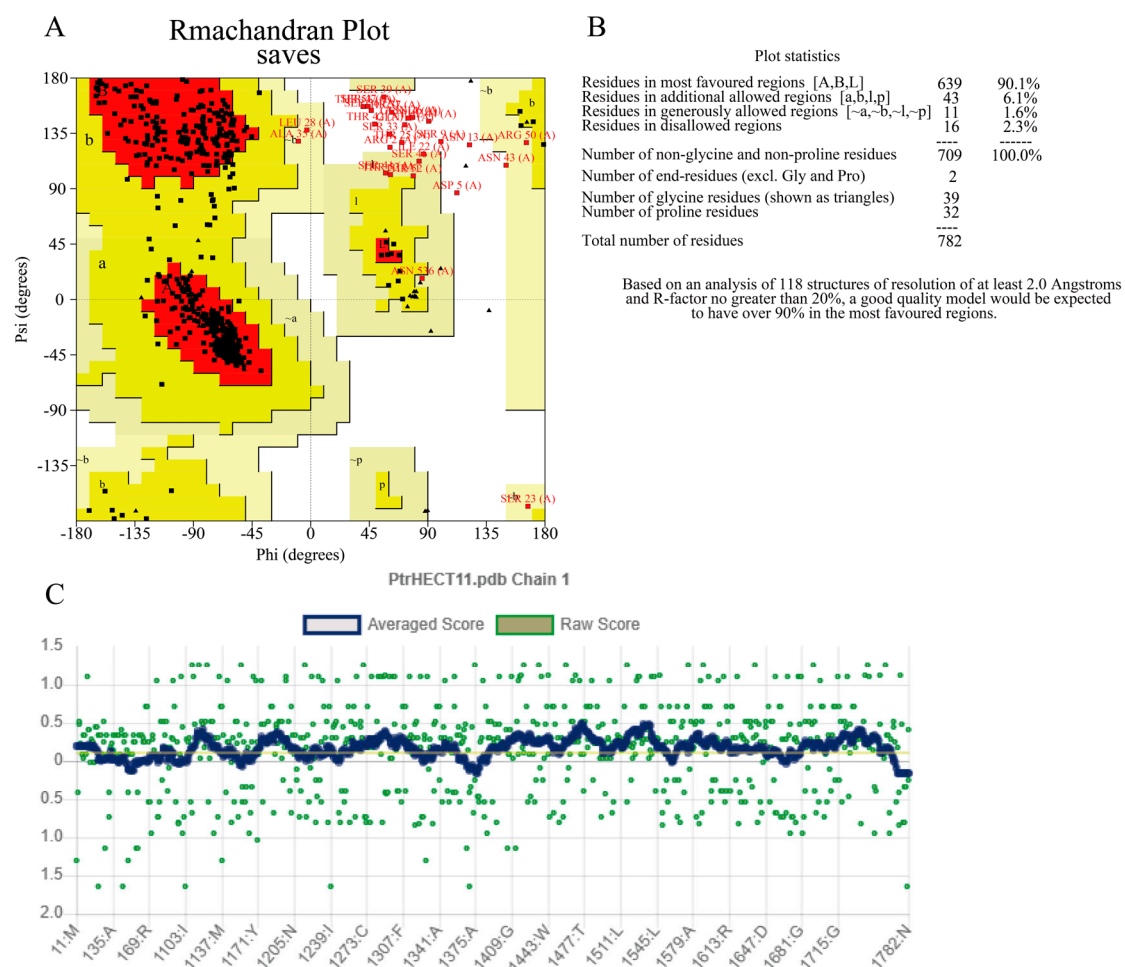
Supplementary Figure S8. Homology modelled structure validation of PtrHECT7 using (A) Ramachandran plot; (B) Ramachandran plot statistics; and (C) Verify3D.

A

Rmachandran Plot
saves

B

Plot statistics

Residues in most favoured regions [A,B,L]	859	92.0%
Residues in additional allowed regions [a,b,l,p]	66	7.1%
Residues in generously allowed regions [~a,~b,~l,~p]	5	0.5%
Residues in disallowed regions	4	0.4%
	----	------
Number of non-glycine and non-proline residues	934	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	53	
Number of proline residues	43	

Total number of residues	1032	

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.

C

PtrHECT8.pdb Chain 1

Supplementary Figure S9. Homology modelled structure validation of PtrHECT8 using (A) Ramachandran plot;
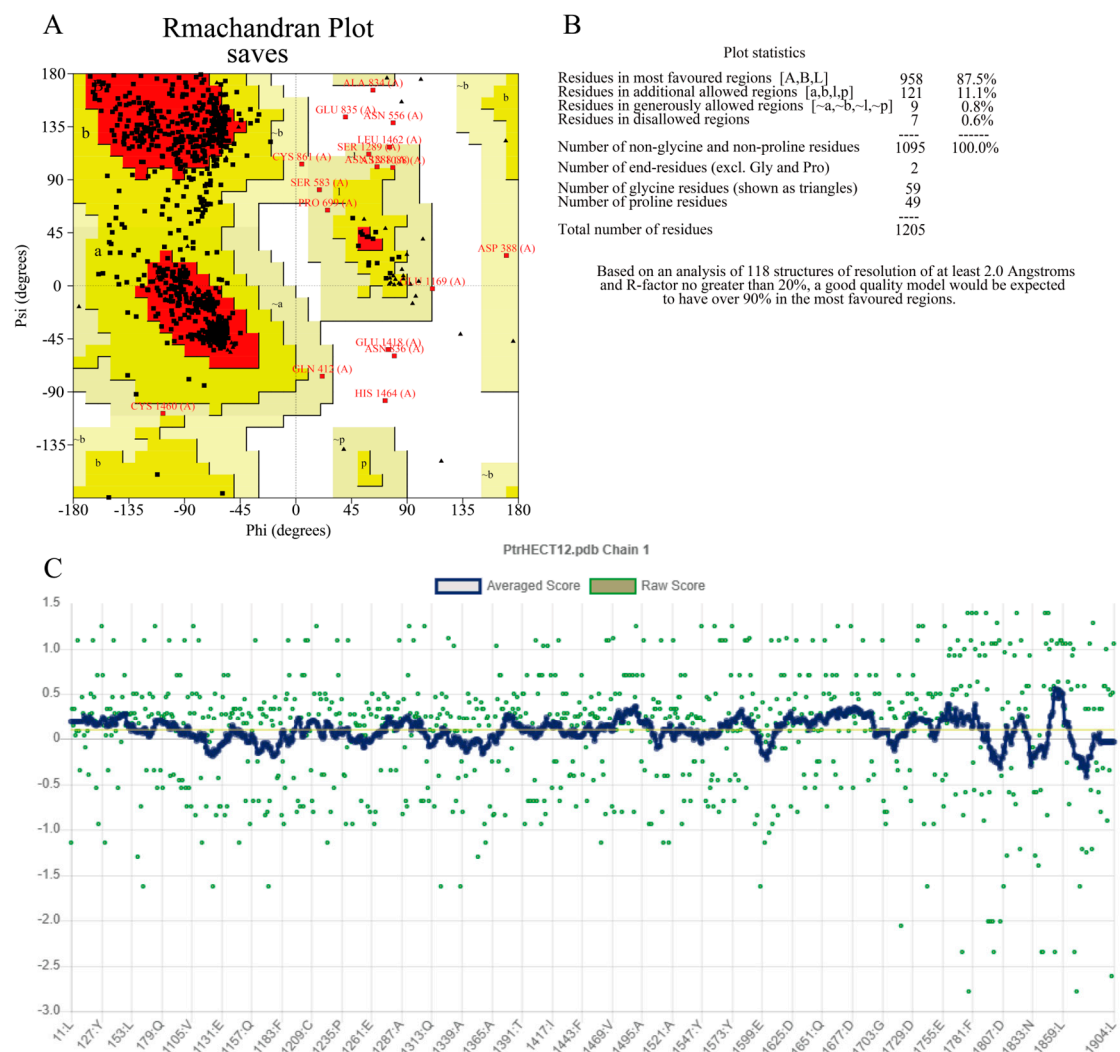(B) Ramachandran plot statistics; and (C) Verify3D.

Supplementary Figure S10. Homology modelled structure validation of PtrHECT9 using (A) Ramachandran plot; (B) Ramachandran plot statistics; and (C) ERRAT.
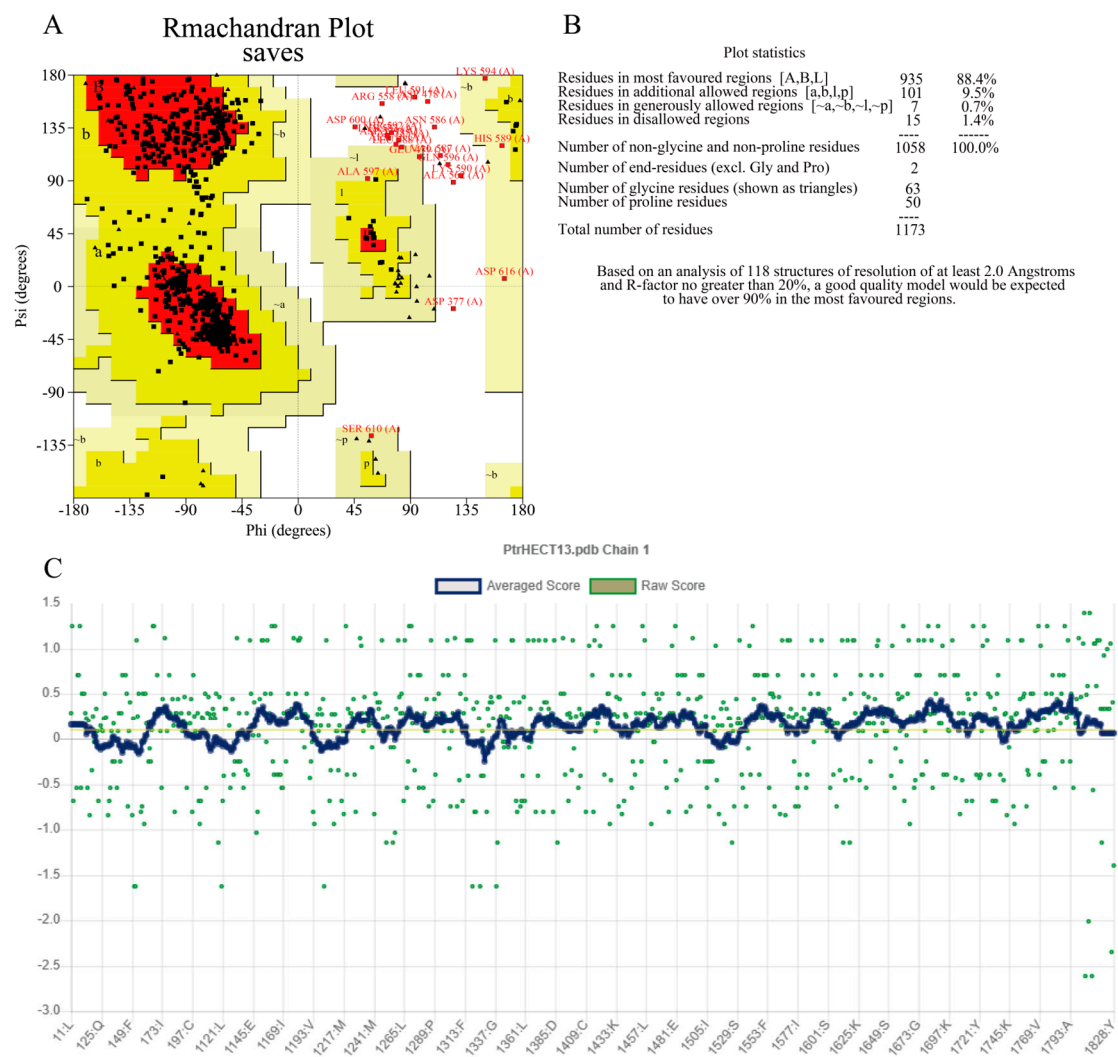
Supplementary Figure S11. Homology modelled structure validation of PtrHECT10 using (A) Ramachandran plot; (B) Ramachandran plot statistics; and (C) Verify3D.

Supplementary Figure S12. Homology modelled structure validation of PtrHECT11 using (A) Ramachandran plot; (B) Ramachandran plot statistics; and (C) Verify3D.

Supplementary Figure S13. Homology modelled structure validation of PtrHECT12 using (A) Ramachandran plot; (B) Ramachandran plot statistics; and (C) Verify3D.

Supplementary Figure S14. Homology modelled structure validation of PtrHECT13 using (A) Ramachandran plot; (B) Ramachandran plot statistics; and (C) Verify3D.