Appendix 0 Table 3. Model refinement statistics for ApoFtn atomic model.

	ApoFtn **7ohf**
Initial model used (PDB code)	2x17
Model resolution (Å, FSC = 0.5)	3.3
CC mask	0.776
Model composition	
Nonhydrogen atoms	24 x 1399
Protein residues	24 × 169
RMSD	
Bond lengths (Å)	0.008
Bond angles (°)	0.864
Validation	
MolProbity score	0.88
Clashscore	1.41
Rotamer outliers (%)	1
Ramachandran plot	
Favored (%)	99.4
Allowed (%)	0.6
Disallowed (%)	0