Supplementary

	VERIFY 3D	ERRAT	PROVE	PROCHECK					WHATCHECK			
Model	Amino acids (%) with averaged 3D-1D Score >= 0.2	Overall Quality Factor	Buried outlier protein atoms (%)	Residues in the most favored regions (%)	Residues in additiona l allowed regions (%)	Residues in generousl y allowed regions (%)	Residues in disallowe d regions (%)	G-Factors (Overall Average Scores)	Number of stereochem ical properties labeled "Pass"	Number of stereochem ical properties labeled "Warning"	Number of stereochem ical properties labeled "ERROR"	Overall summary report
i-TASSER	55.97	67.46	7.70	42.10	36.00	15.80	6.10	-1.30	20	18	10	Pass
MODELLE R	98.51	40.48	7.20	83.30	12.30	3.50	0.90	-0.31	28	11	7	Pass
Phyre2	55.97	67.20	8.40	71.90	22.80	3.50	1.80	-0.23	29	10	7	Pass
RaptorX	36.57	29.03	9.60	80.70	14.00	5.30	0.00	-0.20	29	10	7	Pass
Robetta	88.81	100.00	6.00	88.60	11.40	0.00	0.00	0.34	30	12	5	Pass
Notes: *Green means "Pass", yellow refers "Warning", and red states "ERROR". *PROCHECK's Ramachandran plot results can be interpreted as separating "allowed" and "disallowed" regions. *Number of WHATCHECK properties changes with the case. VERIFY 3D: *>= 80% of amino acids have scored >= 0.2 in 3D-1D profile for good quality. ("Pass") *< 80% of amino acids have scored >= 0.2 in 3D-1D profile for bad quality. ("ERROR") ERRAT: *Average overall quality factor for good high resolution structures is generally around 95% or higher. ("Pass")												
^Average overall quality factor for lower resolutions (2.5 to 3 A) is generally around 91%. ("Warning")												
*If buried outlier protein atoms > 5%, referring "ERROR". *If buried outlier protein atoms are from 1% to 5%, referring "Warning". *If buried outlier protein atoms < 1%, referring "Pass".												
PROCHECK: *The given results belong to Ramachandran plot and G-factor analyses. *>90% in the most favored regions for good quality. ("Pass") *G-factor > -0.5 for good quality structures. ("Pass")												
 WHATCHECK: *If a stereochemical feature analyzed in WHATCHECK refers to good quality, labeled as "Pass". *If a stereochemical feature analyzed in WHATCHECK refers to medium-level quality, labeled as "Warning". *If a stereochemical feature analyzed in WHATCHECK refers to bad quality, labeled as "ERROR". *See WHATCHECK's source (https://swift.cmbi.umcn.nl/gv/whatcheck/) for further information about the features. 												

Supplementary Table 1. Quality assessments from five different algorithms for validation of the homology models.



Supplementary Figure 1: Overall structures of **A**) the best quality Robetta model with **C**) the second-best quality MODELLER model of HriCFP to compare with each other and with **B**) a known common fluorescent protein structure, which is the enhanced cyan fluorescent protein of *Aequorea victoria* (PDB ID: 2wsn), here. Chromophore in 2wsn and chromophore-creating residues in HriCFP are represented as balls and sticks with cyan color and labels whilst others as rounded ribbon with orange alpha-helices, purple beta-sheets and gray loops.