W O R L D W I D E

wwPDB

PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

May 23, 2020 – 12:43 am BST

PDB ID	:	3HZE
Title	:	Crystal Structure of Ycf54 protein from Thermosynechococcus elongatus, Northeast Structural Genomics Consortium Target TeR59
Authors	:	Kuzin, A.; Abashidze, M.; Seetharaman, J.; Sahdev, S.; Xiao, R.; Ciccosanti, C.; Lee, D.; Everett, J.K.; Nair, R.; Acton, T.B.; Rost, B.; Montelione, G.T.; Tong, L.; Hunt, J.F.; Northeast Structural Genomics Consortium (NESG)
Deposited on	:	2009-06-23
Resolution	:	2.00 Å(reported)

The following versions of software and data (see references (i)) were used in the production of this report:

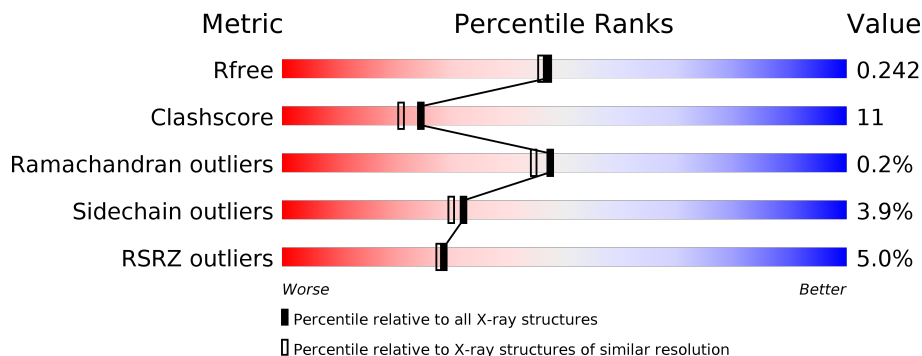|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1   Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.

Metric	Percentile Ranks	Value
Rfree		0.242
Clashscore		11
Ramachandran outliers		0.2%
Sidechain outliers		3.9%
RSRZ outliers		5.0%

Worse ... *Better*

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	114	75% 18% • 6%
1	B	114	% 77% 15% • 6%
1	C	114	5% 71% 21% • 6%
1	D	114	4% 71% 21% • 6%
1	E	114	7% 69% 21% • 5%
1	F	114	11% 68% 22% • 6%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5735 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Ycf54 protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	107	Total	C	N	O	S	Se	0	0	0
			892	579	146	165	1	1			
1	B	107	Total	C	N	O	S	Se	0	0	0
			892	579	146	165	1	1			
1	C	107	Total	C	N	O	S	Se	0	0	0
			892	579	146	165	1	1			
1	D	107	Total	C	N	O	S	Se	0	0	0
			892	579	146	165	1	1			
1	E	108	Total	C	N	O	S	Se	0	0	0
			900	584	147	166	1	2			
1	F	107	Total	C	N	O	S	Se	0	0	0
			892	579	146	165	1	1			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	107	LEU	-	EXPRESSION TAG	UNP Q8DIT2
A	108	GLU	-	EXPRESSION TAG	UNP Q8DIT2
A	109	HIS	-	EXPRESSION TAG	UNP Q8DIT2
A	110	HIS	-	EXPRESSION TAG	UNP Q8DIT2
A	111	HIS	-	EXPRESSION TAG	UNP Q8DIT2
A	112	HIS	-	EXPRESSION TAG	UNP Q8DIT2
A	113	HIS	-	EXPRESSION TAG	UNP Q8DIT2
A	114	HIS	-	EXPRESSION TAG	UNP Q8DIT2
B	107	LEU	-	EXPRESSION TAG	UNP Q8DIT2
B	108	GLU	-	EXPRESSION TAG	UNP Q8DIT2
B	109	HIS	-	EXPRESSION TAG	UNP Q8DIT2
B	110	HIS	-	EXPRESSION TAG	UNP Q8DIT2
B	111	HIS	-	EXPRESSION TAG	UNP Q8DIT2
B	112	HIS	-	EXPRESSION TAG	UNP Q8DIT2
B	113	HIS	-	EXPRESSION TAG	UNP Q8DIT2
B	114	HIS	-	EXPRESSION TAG	UNP Q8DIT2
C	107	LEU	-	EXPRESSION TAG	UNP Q8DIT2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	108	GLU	-	EXPRESSION TAG	UNP Q8DIT2
C	109	HIS	-	EXPRESSION TAG	UNP Q8DIT2
C	110	HIS	-	EXPRESSION TAG	UNP Q8DIT2
C	111	HIS	-	EXPRESSION TAG	UNP Q8DIT2
C	112	HIS	-	EXPRESSION TAG	UNP Q8DIT2
C	113	HIS	-	EXPRESSION TAG	UNP Q8DIT2
C	114	HIS	-	EXPRESSION TAG	UNP Q8DIT2
D	107	LEU	-	EXPRESSION TAG	UNP Q8DIT2
D	108	GLU	-	EXPRESSION TAG	UNP Q8DIT2
D	109	HIS	-	EXPRESSION TAG	UNP Q8DIT2
D	110	HIS	-	EXPRESSION TAG	UNP Q8DIT2
D	111	HIS	-	EXPRESSION TAG	UNP Q8DIT2
D	112	HIS	-	EXPRESSION TAG	UNP Q8DIT2
D	113	HIS	-	EXPRESSION TAG	UNP Q8DIT2
D	114	HIS	-	EXPRESSION TAG	UNP Q8DIT2
E	107	LEU	-	EXPRESSION TAG	UNP Q8DIT2
E	108	GLU	-	EXPRESSION TAG	UNP Q8DIT2
E	109	HIS	-	EXPRESSION TAG	UNP Q8DIT2
E	110	HIS	-	EXPRESSION TAG	UNP Q8DIT2
E	111	HIS	-	EXPRESSION TAG	UNP Q8DIT2
E	112	HIS	-	EXPRESSION TAG	UNP Q8DIT2
E	113	HIS	-	EXPRESSION TAG	UNP Q8DIT2
E	114	HIS	-	EXPRESSION TAG	UNP Q8DIT2
F	107	LEU	-	EXPRESSION TAG	UNP Q8DIT2
F	108	GLU	-	EXPRESSION TAG	UNP Q8DIT2
F	109	HIS	-	EXPRESSION TAG	UNP Q8DIT2
F	110	HIS	-	EXPRESSION TAG	UNP Q8DIT2
F	111	HIS	-	EXPRESSION TAG	UNP Q8DIT2
F	112	HIS	-	EXPRESSION TAG	UNP Q8DIT2
F	113	HIS	-	EXPRESSION TAG	UNP Q8DIT2
F	114	HIS	-	EXPRESSION TAG	UNP Q8DIT2

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).

PO4

O3

O⁻

O2   O⁻ — P = O   O1

P

O⁻

O4

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total 5	O 4	P 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	84	Total 84	O 84	0	0
3	B	66	Total 66	O 66	0	0
3	C	75	Total 75	O 75	0	0
3	D	60	Total 60	O 60	0	0
3	E	53	Total 53	O 53	0	0
3	F	32	Total 32	O 32	0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.
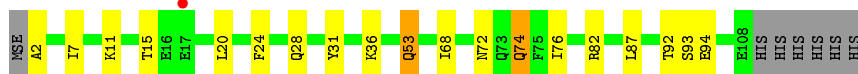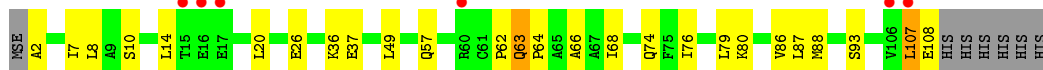
• Molecule 1: Ycf54 protein

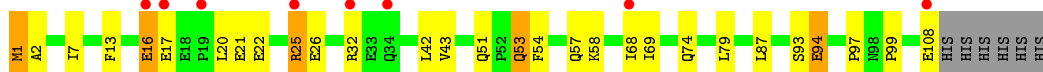• Molecule 1: Ycf54 protein

• Molecule 1: Ycf54 protein

• Molecule 1: Ycf54 protein

• Molecule 1: Ycf54 protein

• Molecule 1: Ycf54 protein

Chain F:

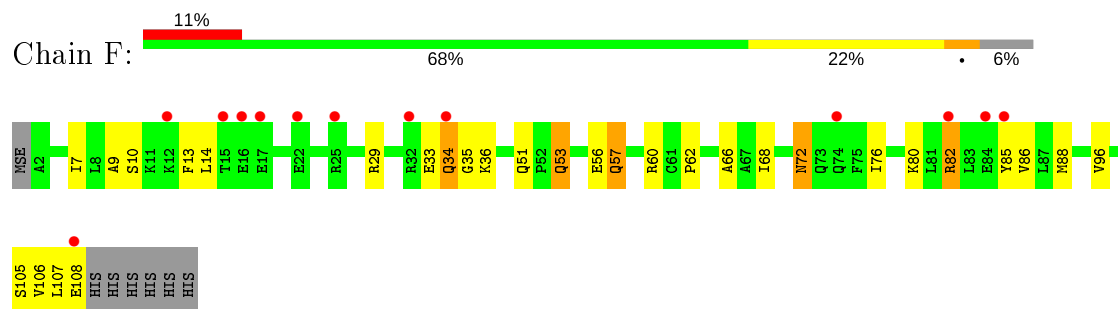# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	82.43Å 86.08Å 123.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00 39.08 – 1.90	Depositor EDS
% Data completeness (in resolution range)	93.8 (20.00-2.00) 98.4 (39.08-1.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	4.59 (at 1.89Å)	Xtriage
Refinement program	CNS 1.2, REFMAC	Depositor
R, R_{free}	0.207 , 0.232 0.219 , 0.242	Depositor DCC
R_{free} test set	6634 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å^2)	18.8	Xtriage
Anisotropy	0.326	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 50.3	EDS
L-test for twinning[2]	$<|L|> = 0.48, <L^2> = 0.31$	Xtriage
Estimated twinning fraction	0.017 for k,h,-l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	5735	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.44% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $<|L|>$, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5   Model quality (i)

5.1   Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section:
PO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value
is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an
outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or
angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#|Z|>5$	RMSZ	$\#|Z|>5$
1	A	0.37	0/915	0.58	0/1240
1	B	0.35	0/915	0.59	0/1240
1	C	0.35	0/915	0.57	0/1240
1	D	0.34	0/915	0.55	0/1240
1	E	0.36	0/923	0.56	0/1250
1	F	0.31	0/915	0.53	0/1240
All	All	0.35	0/5498	0.56	0/7450

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2   Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms
and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen
atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within
the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	892	0	874	16	0
1	B	892	0	874	18	0
1	C	892	0	874	21	0
1	D	892	0	874	20	0
1	E	900	0	886	27	0
1	F	892	0	874	26	0
2	C	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	84	0	0	2	0
3	B	66	0	0	0	0
3	C	75	0	0	1	0
3	D	60	0	0	0	0
3	E	53	0	0	0	0
3	F	32	0	0	0	0
All	All	5735	0	5256	116	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

The worst 5 of 116 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:21:GLU:HG2	1:A:25:ARG:HH12	1.24	1.01
1:C:10:SER:HB3	1:C:62:PRO:HG2	1.52	0.92
1:F:10:SER:HB3	1:F:62:PRO:HG2	1.51	0.91
1:B:74:GLN:HG3	1:E:13:PHE:HB2	1.55	0.87
1:D:17:GLU:HG3	1:E:58:LYS:HE3	1.57	0.86

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	105/114 (92%)	103 (98%)	2 (2%)	0	100	100
1	B	105/114 (92%)	103 (98%)	2 (2%)	0	100	100
1	C	105/114 (92%)	102 (97%)	3 (3%)	0	100	100
1	D	105/114 (92%)	103 (98%)	1 (1%)	1 (1%)	15	9
1	E	106/114 (93%)	99 (93%)	7 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	105/114 (92%)	102 (97%)	3 (3%)	0	100	100
All	All	631/684 (92%)	612 (97%)	18 (3%)	1 (0%)	47	44

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	17	GLU

5.3.2   Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	95/100 (95%)	91 (96%)	4 (4%)	30	27
1	B	95/100 (95%)	93 (98%)	2 (2%)	53	57
1	C	95/100 (95%)	93 (98%)	2 (2%)	53	57
1	D	95/100 (95%)	94 (99%)	1 (1%)	73	78
1	E	96/100 (96%)	89 (93%)	7 (7%)	14	9
1	F	95/100 (95%)	89 (94%)	6 (6%)	18	13
All	All	571/600 (95%)	549 (96%)	22 (4%)	32	30

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	1	MSE
1	E	32	ARG
1	F	72	ASN
1	E	16	GLU
1	E	25	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	51	GLN
1	E	63	GLN
1	F	74	GLN
1	E	28	GLN
1	E	53	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#|Z| > 2$	Counts	RMSZ	$\#|Z| > 2$
2	PO4	C	115	-	4,4,4	1.52	0	6,6,6	0.41	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	106/114 (92%)	-0.17	0	100	100	10, 17, 31, 42	0
1	B	106/114 (92%)	0.04	1 (0%)	84	83	9, 19, 35, 40	0
1	C	106/114 (92%)	-0.06	6 (5%)	23	23	10, 18, 40, 51	0
1	D	106/114 (92%)	0.02	4 (3%)	40	39	12, 21, 40, 57	0
1	E	106/114 (92%)	0.38	8 (7%)	14	13	9, 20, 43, 56	1 (0%)
1	F	106/114 (92%)	0.63	13 (12%)	4	3	14, 32, 50, 56	0
All	All	636/684 (92%)	0.14	32 (5%)	28	28	9, 21, 43, 57	1 (0%)

The worst 5 of 32 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	16	GLU	5.3
1	E	16	GLU	5.2
1	F	108	GLU	4.8
1	E	108	GLU	4.3
1	D	108	GLU	4.1

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	PO4	C	115	5/5	0.68	0.26	29,33,38,39	0

6.5 Other polymers (i)

There are no such residues in this entry.