



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 23, 2024 – 04:10 AM EDT

PDB ID : 6FC0  
Title : Crystal structure of the eIF4E-eIF4G complex from *Chaetomium thermophilum*  
Authors : Gruener, S.; Valkov, E.  
Deposited on : 2017-12-20  
Resolution : 1.29 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
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)	:	2.37.1

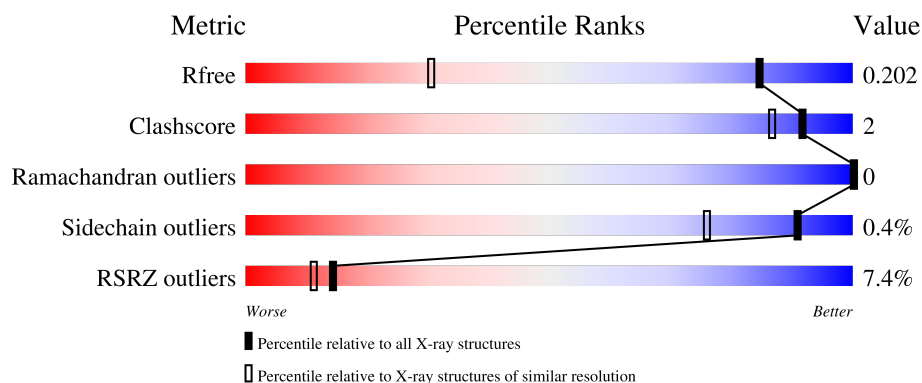
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.29 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1058 (1.30-1.30)
Clashscore	141614	1101 (1.30-1.30)
Ramachandran outliers	138981	1058 (1.30-1.30)
Sidechain outliers	138945	1058 (1.30-1.30)
RSRZ outliers	127900	1029 (1.30-1.30)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ . 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	200	<div> <div>8%</div> <div> <div></div> <div>91%</div> <div>5%</div> <div></div> </div> </div>
2	B	81	<div> <div>4%</div> <div> <div></div> <div>93%</div> <div>5%</div> <div></div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4700 atoms, of which 2231 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 Eukaryotic translation initiation factor 4E-like protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	192	Total	C	H	N	O	S	0	11	0
			3210	1039	1592	274	295	10			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	31	GLY	-	expression tag	UNP G0SCU4
A	32	PRO	-	expression tag	UNP G0SCU4
A	33	HIS	-	expression tag	UNP G0SCU4
A	34	MET	-	expression tag	UNP G0SCU4
A	?	-	GLY	deletion	UNP G0SCU4
A	?	-	ARG	deletion	UNP G0SCU4
A	?	-	HIS	deletion	UNP G0SCU4
A	?	-	ILE	deletion	UNP G0SCU4
A	?	-	ALA	deletion	UNP G0SCU4
A	?	-	SER	deletion	UNP G0SCU4
A	?	-	ARG	deletion	UNP G0SCU4
A	?	-	GLY	deletion	UNP G0SCU4
A	?	-	ASP	deletion	UNP G0SCU4
A	?	-	GLY	deletion	UNP G0SCU4
A	?	-	ASP	deletion	UNP G0SCU4
A	?	-	VAL	deletion	UNP G0SCU4
A	?	-	ALA	deletion	UNP G0SCU4
A	?	-	GLY	deletion	UNP G0SCU4
A	?	-	GLY	deletion	UNP G0SCU4
A	?	-	LYS	deletion	UNP G0SCU4
A	?	-	GLY	deletion	UNP G0SCU4
A	?	-	ARG	deletion	UNP G0SCU4
A	?	-	SER	deletion	UNP G0SCU4
A	?	-	LEU	deletion	UNP G0SCU4

- Molecule 2 is a protein called Eukaryotic translation initiation factor 4G.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	77	Total	C	H	N	O	0	3	0
			1260	404	639	105	112			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	950	GLY	-	expression tag	UNP G0SFP0
B	951	PRO	-	expression tag	UNP G0SFP0
B	952	HIS	-	expression tag	UNP G0SFP0
B	953	MET	-	expression tag	UNP G0SFP0

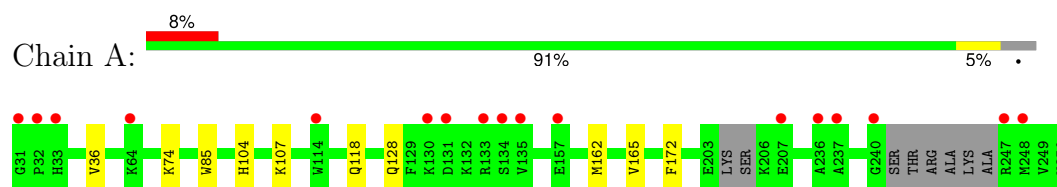
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	157	Total	O	0	0
			157	157		
3	B	73	Total	O	0	0
			73	73		

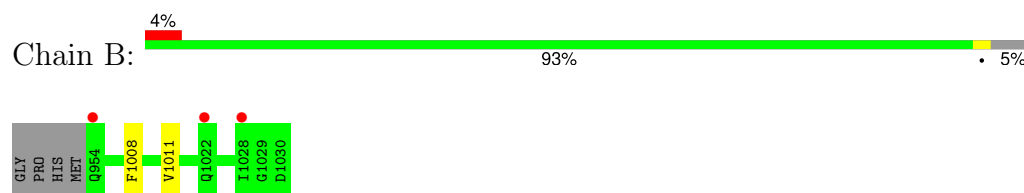
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Eukaryotic translation initiation factor 4E-like protein



- Molecule 2: Eukaryotic translation initiation factor 4G



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	63.59Å 75.17Å 48.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.71 – 1.29 40.71 – 1.29	Depositor EDS
% Data completeness (in resolution range)	93.4 (40.71-1.29) 93.4 (40.71-1.29)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.21 (at 1.29Å)	Xtriage
Refinement program	PHENIX (1.11_2567: ???)	Depositor
R, $R_{free}$	0.163 , 0.201 0.165 , 0.202	Depositor DCC
$R_{free}$ test set	2744 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	15.5	Xtriage
Anisotropy	0.158	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 45.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	4700	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.46% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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	0.44	0/1703	0.61	0/2297
2	B	0.39	0/648	0.55	0/877
All	All	0.43	0/2351	0.60	0/3174

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

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	1618	1592	1573	7	0
2	B	621	639	634	2	0
3	A	157	0	0	3	2
3	B	73	0	0	0	1
All	All	2469	2231	2207	7	2

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 2.

The worst 5 of 7 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:36:VAL:HG22	2:B:1011:VAL:HG12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128[B]:GLN:HG3	1:A:172:PHE:CD2	2.51	0.45
1:A:165[A]:VAL:HG13	3:A:382:HOH:O	2.17	0.45
1:A:107:LYS:NZ	3:A:307:HOH:O	2.45	0.45
1:A:85:TRP:CD1	2:B:1008:PHE:HB2	2.53	0.43

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:438:HOH:O	3:A:438:HOH:O[2_575]	1.79	0.41
3:A:311:HOH:O	3:B:1166:HOH:O[4_576]	1.99	0.21

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	197/200 (98%)	193 (98%)	4 (2%)	0	100	100
2	B	78/81 (96%)	77 (99%)	1 (1%)	0	100	100
All	All	275/281 (98%)	270 (98%)	5 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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	179/174 (103%)	178 (99%)	1 (1%)	86	65
2	B	70/70 (100%)	70 (100%)	0	100	100
All	All	249/244 (102%)	248 (100%)	1 (0%)	91	76

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	104	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	192/200 (96%)	0.09	17 (8%) 9 6	10, 19, 53, 68	0
2	B	77/81 (95%)	0.03	3 (3%) 39 36	12, 22, 40, 53	0
All	All	269/281 (95%)	0.07	20 (7%) 14 11	10, 20, 48, 68	0

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	247	ARG	6.3
1	A	130	LYS	6.3
1	A	135	VAL	4.7
2	B	954	GLN	4.4
1	A	133	ARG	4.2

### 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 monosaccharides in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.