



wwPDB X-ray Structure Validation Summary Report i

Feb 27, 2014 – 06:25 AM GMT

PDB ID : 4AXG
Title : Structure of eIF4E-Cup complex
Authors : Kinkelin, K.; Veith, K.; Gruenwald, M.; Bono, F.
Deposited on : 2012-06-12
Resolution : 2.80 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

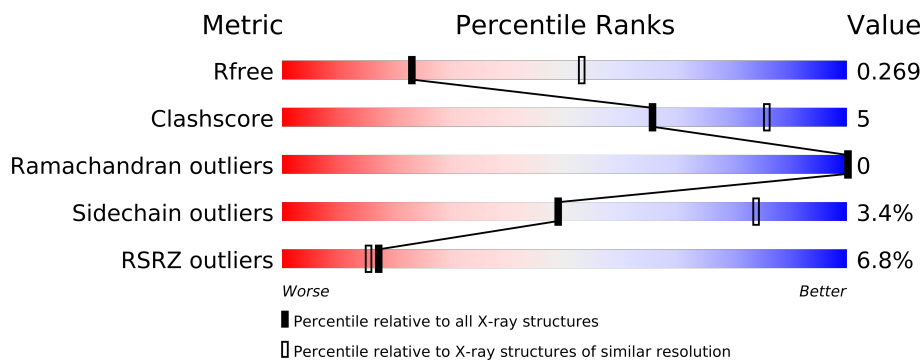
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.80 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}	66092	1799 (2.80-2.80)
Clashscore	79885	2295 (2.80-2.80)
Ramachandran outliers	78287	2252 (2.80-2.80)
Sidechain outliers	78261	2254 (2.80-2.80)
RSRZ outliers	66119	1802 (2.80-2.80)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	248	
1	B	248	
2	C	130	
2	D	130	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3047 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	181	Total	C	N	O	S	0	0	0
			1439	912	245	276	6			
1	B	167	Total	C	N	O	S	0	0	0
			1205	769	204	230	2			

- Molecule 2 is a protein called PROTEIN CUP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	37	Total	C	N	O	S	0	0	0
			288	176	59	50	3			
2	D	15	Total	C	N	O	S	0	0	0
			101	63	18	19	1			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	13	Total	O	0	0
			13	13		
3	B	1	Total	O	0	0
			1	1		

GLN	LEU
PRO	GLY
	ARG
	LEU
	ARG
	ARG
	MET
	ASN
	ILE
	TRP
	ARG
	THR
	THR
	SER
	ASP
	GLY
	THR
	ARG
	PHE
	ARG
	THR
	ARG
	SER
	THR
	THR
	ALA
	ASN
	LEU
	ASN
	MET
	ASN
	ASN
	ASN
	ASN
	ASN
	GLU
	CYS
	MET
	PRO
	ALA
	PHE
	PHE
	LYS
	ASN
	LYS
	ASN
	LYS
	PRO
	ASN
	LEU
	ILE
	SER
	ASP
	GLU
	SER
	ILE
	ILE
	GLN
	SER

4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	142.58Å 142.58Å 108.05Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	81.31 – 2.80 81.31 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (81.31-2.80) 100.0 (81.31-2.80)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.01 (at 2.82Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.228 , 0.244 0.254 , 0.269	Depositor DCC
R_{free} test set	824 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	67.1	Xtriage
Anisotropy	0.409	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 55.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 16494 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	3047	wwPDB-VP
Average B, all atoms (Å ²)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.27% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	0.30	0/1472	0.41	0/2002
1	B	0.28	0/1230	0.41	0/1686
2	C	0.24	0/290	0.41	0/386
2	D	0.22	0/101	0.32	0/136
All	All	0.29	0/3093	0.41	0/4210

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1439	0	9	11	0
1	B	1205	0	12	5	0
2	C	288	0	2	2	0
2	D	101	0	0	1	0
3	A	13	0	0	0	0
3	B	1	0	0	0	0
All	All	3047	0	23	16	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

The worst 5 of 16 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:73:MET:CE	2:C:324:VAL:CA	2.28	1.11
1:A:132:ARG:NH1	1:A:134:MET:SD	2.56	0.78
1:A:236:VAL:CG1	1:A:238:GLN:O	2.36	0.73
1:A:73:MET:CE	2:C:325:LYS:N	2.53	0.72
1:B:94:ASN:OD1	1:B:94:ASN:N	2.30	0.64

There are no symmetry-related clashes.

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	177/248 (71%)	173 (98%)	4 (2%)	0	100	100
1	B	161/248 (65%)	160 (99%)	1 (1%)	0	100	100
2	C	33/130 (25%)	33 (100%)	0	0	100	100
2	D	13/130 (10%)	13 (100%)	0	0	100	100
All	All	384/756 (51%)	379 (99%)	5 (1%)	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	152/215 (71%)	147 (97%)	5 (3%)	50	85
1	B	108/215 (50%)	104 (96%)	4 (4%)	45	81
2	C	29/118 (25%)	28 (97%)	1 (3%)	49	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	7/118 (6%)	7 (100%)	0	100	100
All	All	296/666 (44%)	286 (97%)	10 (3%)	49	84

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	225	SER
1	B	77	THR
1	B	124	TYR
1	A	222	ARG
1	B	94	ASN

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

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	181/248 (72%)	0.19	2 (1%) 77 78	31, 55, 106, 155	0
1	B	167/248 (67%)	0.58	21 (12%) 4 3	44, 95, 140, 154	0
2	C	37/130 (28%)	0.21	2 (5%) 25 25	36, 82, 116, 127	0
2	D	15/130 (11%)	0.04	2 (13%) 4 3	86, 111, 133, 133	0
All	All	400/756 (52%)	0.35	27 (6%) 17 15	31, 75, 134, 155	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	208	LEU	4.6
1	B	246	TYR	4.2
2	D	326	SER	4.1
1	B	203	ASN	4.0
1	B	102	VAL	3.6

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.