



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 08:57 PM GMT

PDB ID : 4UEA
Title : Complex of D. melanogaster eIF4E with a designed 4E-binding protein (Form I)
Authors : Peter, D.; Weichenrieder, O.
Deposited on : 2014-12-16
Resolution : 2.62 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

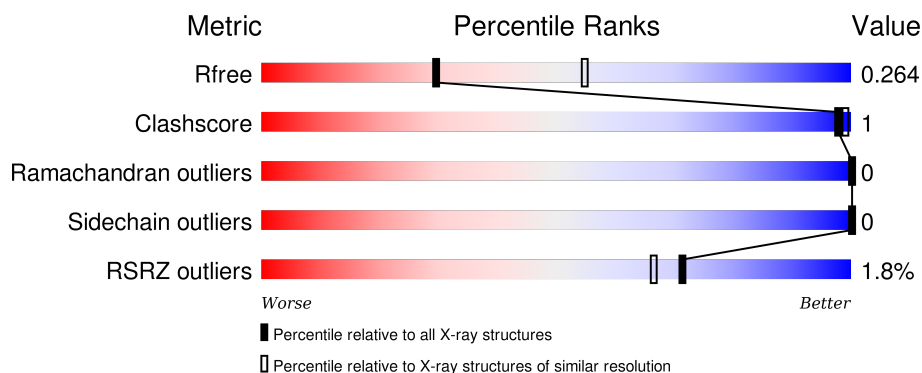
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.62 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}	91344	2700 (2.64-2.60)
Clashscore	102246	3065 (2.64-2.60)
Ramachandran outliers	100387	3015 (2.64-2.60)
Sidechain outliers	100360	3015 (2.64-2.60)
RSRZ outliers	91569	2706 (2.64-2.60)

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. 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	184	<div> <div>2%</div> <div>89%</div> <div>8%</div> </div>
1	C	184	<div> <div>%</div> <div>87%</div> <div>9%</div> </div>
1	E	184	<div> <div>3%</div> <div>88%</div> <div>9%</div> </div>
2	B	44	<div> <div></div> <div>86%</div> <div>11%</div> </div>
2	D	44	<div> <div>2%</div> <div>86%</div> <div>14%</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	44	 A horizontal bar chart showing the quality of the chain. The bar is divided into two segments: a green segment representing 84% and a yellow segment representing 14%. The total length of the bar represents 100%.

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 9875 atoms, of which 4874 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.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	169	Total	C	H	N	O	S	0	0	0
			2634	855	1283	232	258	6			
1	C	167	Total	C	H	N	O	S	0	0	0
			2652	855	1299	235	257	6			
1	E	167	Total	C	H	N	O	S	0	0	0
			2668	859	1312	234	257	6			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	65	GLY	-	EXPRESSION TAG	UNP P48598
A	66	PRO	-	EXPRESSION TAG	UNP P48598
A	67	HIS	-	EXPRESSION TAG	UNP P48598
A	68	MET	-	EXPRESSION TAG	UNP P48598
C	65	GLY	-	EXPRESSION TAG	UNP P48598
C	66	PRO	-	EXPRESSION TAG	UNP P48598
C	67	HIS	-	EXPRESSION TAG	UNP P48598
C	68	MET	-	EXPRESSION TAG	UNP P48598
E	65	GLY	-	EXPRESSION TAG	UNP P48598
E	66	PRO	-	EXPRESSION TAG	UNP P48598
E	67	HIS	-	EXPRESSION TAG	UNP P48598
E	68	MET	-	EXPRESSION TAG	UNP P48598

- Molecule 2 is a protein called DESIGNED 4E-BP.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	39	Total	C	H	N	O	S	0	0	0
			645	199	328	61	56	1			
2	D	38	Total	C	H	N	O	S	0	0	0
			638	196	326	60	55	1			
2	F	38	Total	C	H	N	O	S	0	0	0
			638	196	326	60	55	1			

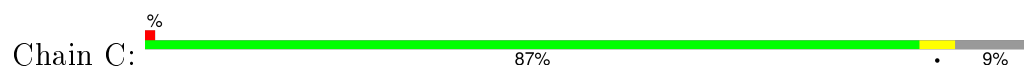
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

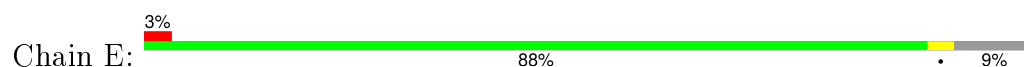
- Molecule 1: EUKARYOTIC TRANSLATION INITIATION FACTOR 4E



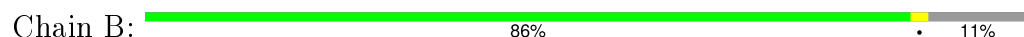
- Molecule 1: EUKARYOTIC TRANSLATION INITIATION FACTOR 4E



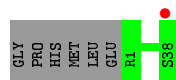
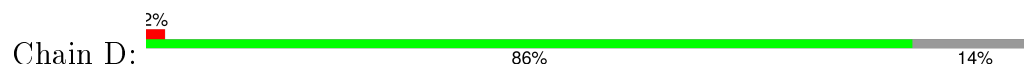
- Molecule 1: EUKARYOTIC TRANSLATION INITIATION FACTOR 4E



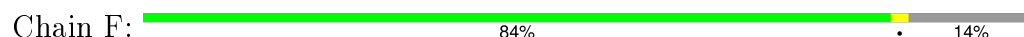
- Molecule 2: DESIGNED 4E-BP



- Molecule 2: DESIGNED 4E-BP



- Molecule 2: DESIGNED 4E-BP



GLY	PRO	HIS	MET	LEU	GLU	RS	RS7	RS8
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4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	94.54Å 94.54Å 131.96Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.27 – 2.62 47.27 – 2.62	Depositor EDS
% Data completeness (in resolution range)	99.5 (47.27-2.62) 99.6 (47.27-2.62)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.00 (at 2.61Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.9_1692)	Depositor
R, R_{free}	0.205 , 0.262 0.206 , 0.264	Depositor DCC
R_{free} test set	1013 reflections (5.07%)	DCC
Wilson B-factor (Å ²)	63.5	Xtriage
Anisotropy	0.443	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 45.6	EDS
Estimated twinning fraction	0.062 for h,-h-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 20025 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9875	wwPDB-VP
Average B, all atoms (Å ²)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 26.01 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.8526e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.22	0/1383	0.38	0/1875
1	C	0.21	0/1385	0.37	0/1878
1	E	0.23	0/1388	0.39	0/1880
2	B	0.24	0/323	0.38	0/434
2	D	0.24	0/318	0.39	0/427
2	F	0.24	0/318	0.37	0/427
All	All	0.22	0/5115	0.38	0/6921

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	1351	1283	1283	3	0
1	C	1353	1299	1299	4	0
1	E	1356	1312	1312	4	0
2	B	317	328	328	1	0
2	D	312	326	326	0	0
2	F	312	326	326	1	0
All	All	5001	4874	4874	11	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 1.

The worst 5 of 11 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:90:GLU:OE1	1:A:90:GLU:N	2.42	0.52
1:A:221:GLY:O	1:A:223:ASN:N	2.45	0.49
1:E:96:ILE:O	2:F:27:ARG:NH1	2.46	0.46
1:C:161:LEU:HD11	1:C:218:LEU:HD23	1.97	0.46
1:E:101:THR:OG1	1:E:104:ASP:OD2	2.35	0.43

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	167/184 (91%)	162 (97%)	5 (3%)	0	100	100
1	C	165/184 (90%)	160 (97%)	5 (3%)	0	100	100
1	E	165/184 (90%)	162 (98%)	3 (2%)	0	100	100
2	B	37/44 (84%)	37 (100%)	0	0	100	100
2	D	36/44 (82%)	36 (100%)	0	0	100	100
2	F	36/44 (82%)	36 (100%)	0	0	100	100
All	All	606/684 (89%)	593 (98%)	13 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	144/165 (87%)	144 (100%)	0	100	100
1	C	147/165 (89%)	147 (100%)	0	100	100
1	E	148/165 (90%)	148 (100%)	0	100	100
2	B	34/39 (87%)	34 (100%)	0	100	100
2	D	34/39 (87%)	34 (100%)	0	100	100
2	F	34/39 (87%)	34 (100%)	0	100	100
All	All	541/612 (88%)	541 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some 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 carbohydrates 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, 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	169/184 (91%)	0.11	3 (1%) 71 66	45, 65, 90, 104	0
1	C	167/184 (90%)	0.12	2 (1%) 81 77	56, 74, 100, 112	0
1	E	167/184 (90%)	0.19	5 (2%) 54 47	44, 66, 102, 118	0
2	B	39/44 (88%)	0.11	0 100 100	44, 63, 77, 82	0
2	D	38/44 (86%)	0.29	1 (2%) 59 53	59, 75, 82, 96	0
2	F	38/44 (86%)	0.09	0 100 100	54, 69, 80, 86	0
All	All	618/684 (90%)	0.14	11 (1%) 71 66	44, 69, 98, 118	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	220	LEU	10.7
2	D	38	SER	3.2
1	E	220	LEU	2.8
1	E	219	ARG	2.8
1	E	218	LEU	2.8

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.