



wwPDB X-ray Structure Validation Summary Report ⓘ

May 26, 2020 – 02:44 am BST

PDB ID : 3EIQ
Title : Crystal structure of Pdcd4-eIF4A
Authors : Loh, P.G.; Cheng, Z.; Song, H.
Deposited on : 2008-09-17
Resolution : 3.50 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

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

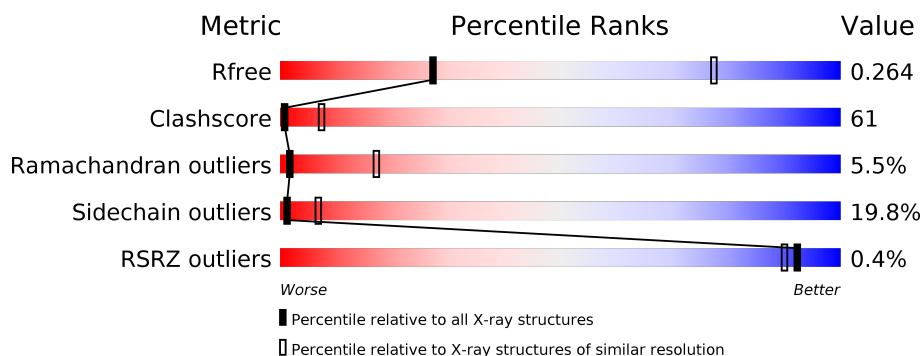
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

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 $\leq 5\%$. 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	414	<div> <div></div> <div>35% 37% 14% • 12%</div> </div>
1	D	414	<div> <div>%</div> <div>35% 38% 14% • 10%</div> </div>
2	C	358	<div> <div></div> <div>25% 42% 9% • 22%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8080 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 Eukaryotic initiation factor 4A-I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	364	Total	C	N	O	S	0	0	0
			2923	1853	497	554	19			
1	D	371	Total	C	N	O	S	0	0	0
			2979	1887	511	562	19			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	GLY	-	EXPRESSION TAG	UNP P60842
A	-6	PRO	-	EXPRESSION TAG	UNP P60842
A	-5	LEU	-	EXPRESSION TAG	UNP P60842
A	-4	GLY	-	EXPRESSION TAG	UNP P60842
A	-3	SER	-	EXPRESSION TAG	UNP P60842
A	-2	PRO	-	EXPRESSION TAG	UNP P60842
A	-1	GLU	-	EXPRESSION TAG	UNP P60842
A	0	PHE	-	EXPRESSION TAG	UNP P60842
D	-7	GLY	-	EXPRESSION TAG	UNP P60842
D	-6	PRO	-	EXPRESSION TAG	UNP P60842
D	-5	LEU	-	EXPRESSION TAG	UNP P60842
D	-4	GLY	-	EXPRESSION TAG	UNP P60842
D	-3	SER	-	EXPRESSION TAG	UNP P60842
D	-2	PRO	-	EXPRESSION TAG	UNP P60842
D	-1	GLU	-	EXPRESSION TAG	UNP P60842
D	0	PHE	-	EXPRESSION TAG	UNP P60842

- Molecule 2 is a protein called Programmed cell death protein 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	278	Total	C	N	O	S	0	0	0
			2178	1380	359	424	15			

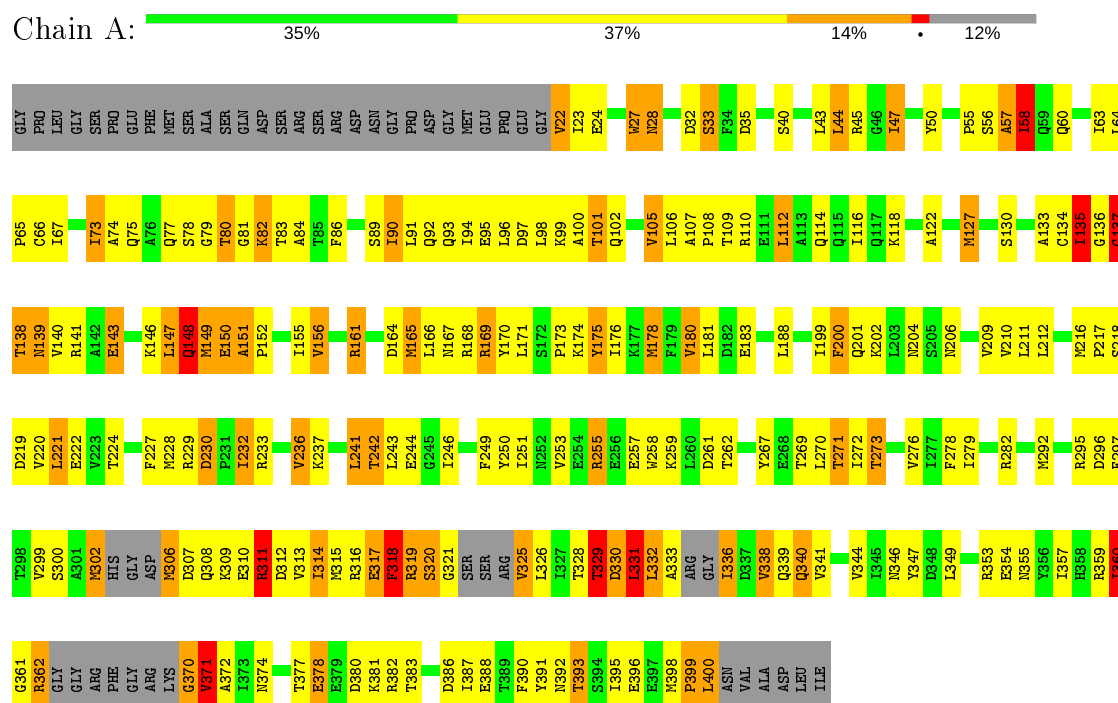
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	112	GLY	-	EXPRESSION TAG	UNP Q61823
C	113	PRO	-	EXPRESSION TAG	UNP Q61823
C	114	LEU	-	EXPRESSION TAG	UNP Q61823
C	115	GLY	-	EXPRESSION TAG	UNP Q61823
C	116	SER	-	EXPRESSION TAG	UNP Q61823
C	117	PRO	-	EXPRESSION TAG	UNP Q61823
C	118	GLU	-	EXPRESSION TAG	UNP Q61823
C	119	PHE	-	EXPRESSION TAG	UNP Q61823

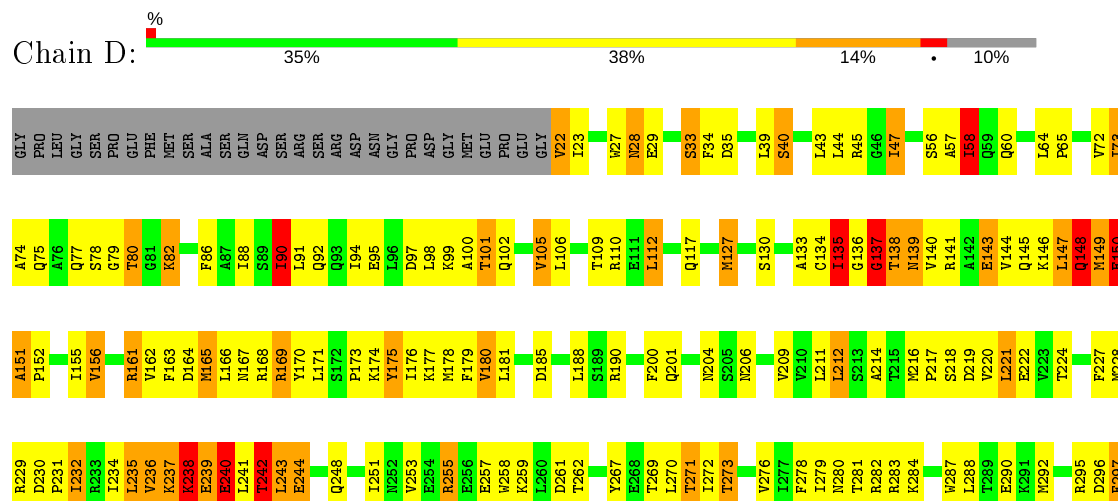
3 Residue-property plots

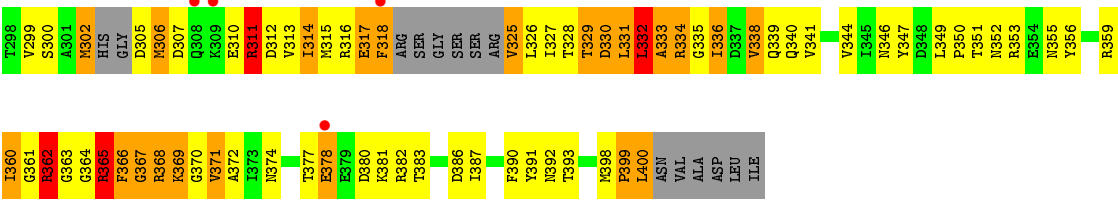
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: Eukaryotic initiation factor 4A-I

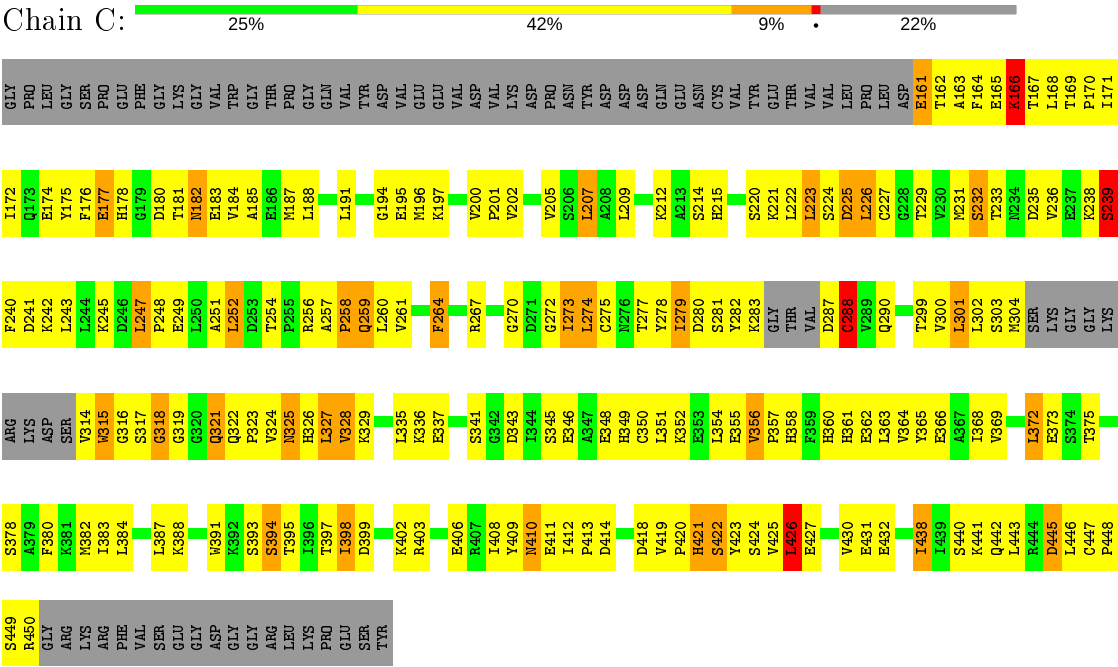


• Molecule 1: Eukaryotic initiation factor 4A-I





● Molecule 2: Programmed cell death protein 4



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	198.36 Å 198.36 Å 198.36 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.91 – 3.50 29.90 – 3.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.91-3.50) 100.0 (29.90-3.50)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.44 (at 3.47 Å)	Xtriage
Refinement program	REFMAC 5.4.0077	Depositor
R, R_{free}	0.220 , 0.269 0.217 , 0.264	Depositor DCC
R_{free} test set	1670 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	93.8	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 61.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.029 for l,-k,h	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8080	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.07% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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	0.95	3/2963 (0.1%)	1.01	8/3998 (0.2%)
1	D	0.96	1/3022 (0.0%)	1.07	11/4077 (0.3%)
2	C	0.72	0/2213	0.91	4/2989 (0.1%)
All	All	0.90	4/8198 (0.0%)	1.01	23/11064 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	D	0	1
All	All	0	3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	80	THR	CA-CB	5.42	1.67	1.53
1	A	200	PHE	CE1-CZ	5.40	1.47	1.37
1	A	66	CYS	CB-SG	-5.35	1.73	1.81
1	A	200	PHE	CG-CD2	5.04	1.46	1.38

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	365	ARG	NE-CZ-NH1	-13.21	113.69	120.30
1	D	365	ARG	NE-CZ-NH2	10.91	125.75	120.30
1	A	137	GLY	N-CA-C	-8.85	90.99	113.10
2	C	351	LEU	CA-CB-CG	-8.29	96.23	115.30
1	A	58	ILE	CG1-CB-CG2	-7.30	95.34	111.40

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	329	THR	Peptide
1	A	370	GLY	Peptide
1	D	150	GLU	Peptide

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	2923	0	2962	368	1
1	D	2979	0	3020	380	1
2	C	2178	0	2183	267	0
All	All	8080	0	8165	985	1

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 61.

The worst 5 of 985 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:D:367:GLY:HA2	1:D:368:ARG:CG	1.27	1.62
1:D:338:VAL:CG2	1:D:362:ARG:HH22	1.19	1.54
1:D:135:ILE:CG2	1:D:136:GLY:HA3	1.34	1.54
1:A:135:ILE:CG2	1:A:136:GLY:HA3	1.40	1.51
1:A:338:VAL:CG2	1:A:362:ARG:HH22	1.19	1.51

All (1) 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)
1:A:316:ARG:CD	1:D:99:LYS:CE[12_455]	1.94	0.26

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	354/414 (86%)	297 (84%)	38 (11%)	19 (5%)	2	17
1	D	365/414 (88%)	299 (82%)	45 (12%)	21 (6%)	1	16
2	C	272/358 (76%)	213 (78%)	44 (16%)	15 (6%)	2	17
All	All	991/1186 (84%)	809 (82%)	127 (13%)	55 (6%)	2	17

5 of 55 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	147	LEU
1	A	151	ALA
1	A	271	THR
1	A	320	SER
1	A	329	THR

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	325/363 (90%)	260 (80%)	65 (20%)	1	7
1	D	329/363 (91%)	257 (78%)	72 (22%)	1	5
2	C	245/312 (78%)	204 (83%)	41 (17%)	2	12
All	All	899/1038 (87%)	721 (80%)	178 (20%)	1	7

5 of 178 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	259	GLN
2	C	382	MET
1	D	318	PHE
2	C	273	ILE
2	C	325	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	178	HIS
2	C	358	HIS
1	D	340	GLN
2	C	215	HIS
2	C	325	ASN

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	364/414 (87%)	-0.38	0 100 100	46, 54, 74, 102	0
1	D	371/414 (89%)	-0.30	4 (1%) 80 75	35, 54, 73, 107	0
2	C	278/358 (77%)	-0.59	0 100 100	33, 56, 72, 80	4 (1%)
All	All	1013/1186 (85%)	-0.41	4 (0%) 92 90	33, 54, 73, 107	4 (0%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	318	PHE	3.3
1	D	309	LYS	3.0
1	D	378	GLU	2.9
1	D	308	GLN	2.2

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 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.