



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 04:25 PM UTC

PDB ID : 6IPA / pdb_00006ipa
Title : C-terminal EMAP II-like domain of p43 refined against twinned data
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Deposited on : 2018-11-02
Resolution : 2.47 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 types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Xtrriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

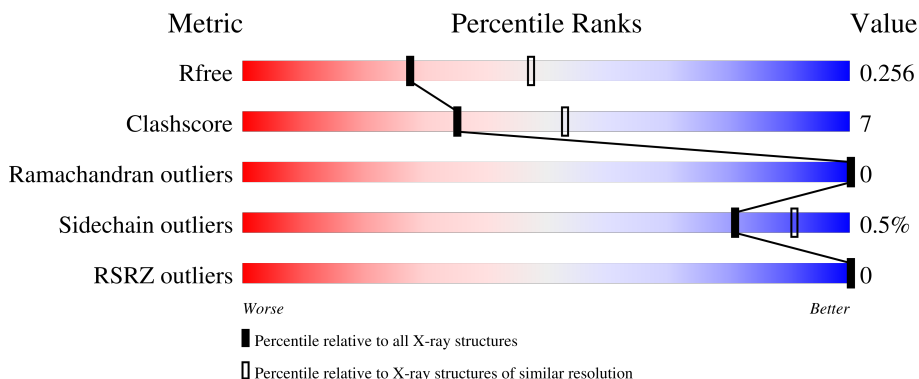
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.47 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}	180053	7589 (2.50-2.46)
Clashscore	190562	8295 (2.50-2.46)
Ramachandran outliers	187476	8164 (2.50-2.46)
Sidechain outliers	187428	8166 (2.50-2.46)
RSRZ outliers	180081	7593 (2.50-2.46)

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 ≥ 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	204	 68% 13% 19%
1	B	204	 64% 15% 19%
1	C	204	 64% 17% 19%
1	D	204	 64% 17% 19%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5342 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 aminoacyl-tRNA synthetase-interacting multifunctional protein p43.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	165	1295	820	221	247	7	0	0	0
1	B	165	1301	823	224	247	7	0	0	0
1	C	165	1301	823	224	247	7	0	0	0
1	D	165	1301	823	224	247	7	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	202	GLY	-	expression tag	UNP A0A1G4HHT8
A	203	ALA	-	expression tag	UNP A0A1G4HHT8
A	204	MET	-	expression tag	UNP A0A1G4HHT8
A	205	ALA	-	expression tag	UNP A0A1G4HHT8
B	202	GLY	-	expression tag	UNP A0A1G4HHT8
B	203	ALA	-	expression tag	UNP A0A1G4HHT8
B	204	MET	-	expression tag	UNP A0A1G4HHT8
B	205	ALA	-	expression tag	UNP A0A1G4HHT8
C	202	GLY	-	expression tag	UNP A0A1G4HHT8
C	203	ALA	-	expression tag	UNP A0A1G4HHT8
C	204	MET	-	expression tag	UNP A0A1G4HHT8
C	205	ALA	-	expression tag	UNP A0A1G4HHT8
D	202	GLY	-	expression tag	UNP A0A1G4HHT8
D	203	ALA	-	expression tag	UNP A0A1G4HHT8
D	204	MET	-	expression tag	UNP A0A1G4HHT8
D	205	ALA	-	expression tag	UNP A0A1G4HHT8

- Molecule 2 is water.

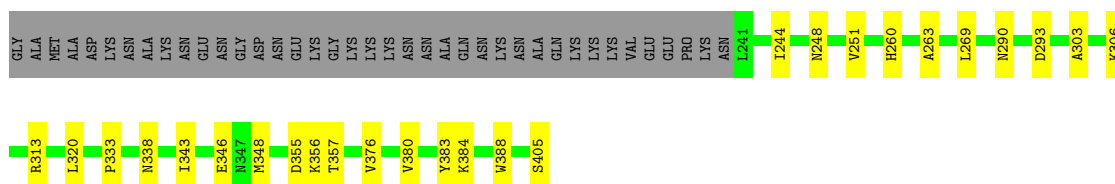
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	45	Total 45	O 45	0	0
2	B	18	Total 18	O 18	0	0
2	C	41	Total 41	O 41	0	0
2	D	40	Total 40	O 40	0	0

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.

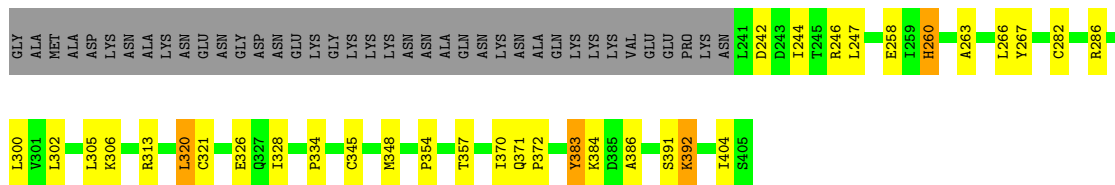
- Molecule 1: aminoacyl-tRNA synthetase-interacting multifunctional protein p43

Chain A: 



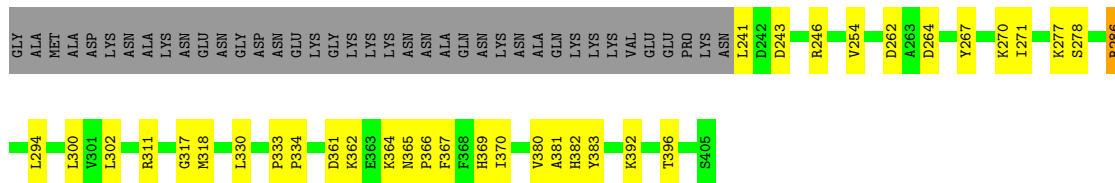
- Molecule 1: aminoacyl-tRNA synthetase-interacting multifunctional protein p43

Chain B: 



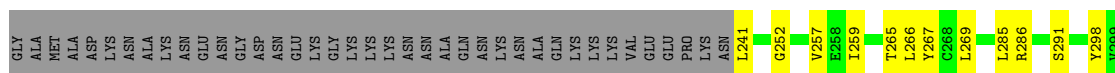
- Molecule 1: aminoacyl-tRNA synthetase-interacting multifunctional protein p43

Chain C: 



- Molecule 1: aminoacyl-tRNA synthetase-interacting multifunctional protein p43

Chain D: 



L300	L305	K306	G317	M318	C321	P333	P334	I343	I344	C345	E346	F360	H369	H373	L374	Y383	K384	D385	A386	K387	K392	G393	E394	I404	S405
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4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	37.17Å 146.90Å 146.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.73 – 2.47 36.73 – 2.47	Depositor EDS
% Data completeness (in resolution range)	99.7 (36.73-2.47) 99.7 (36.73-2.47)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.95 (at 2.48Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.202 , 0.261 0.202 , 0.256	Depositor DCC
R_{free} test set	1995 reflections (6.69%)	wwPDB-VP
Wilson B-factor (Å ²)	44.9	Xtriage
Anisotropy	0.271	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 20.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.366 for -h,l,k	Xtriage
Reported twinning fraction	0.646 for H, K, L 0.354 for -H, L, K	Depositor
Outliers	1 of 29839 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5342	wwPDB-VP
Average B, all atoms (Å ²)	50.0	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 27.95 % 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 2.0096e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 [i](#)

5.1 Standard geometry [i](#)

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	1.06	4/1317 (0.3%)	1.08	2/1775 (0.1%)
1	B	1.11	7/1323 (0.5%)	1.10	3/1782 (0.2%)
1	C	1.19	6/1323 (0.5%)	1.17	5/1782 (0.3%)
1	D	1.09	2/1323 (0.2%)	1.16	4/1782 (0.2%)
All	All	1.11	19/5286 (0.4%)	1.13	14/7121 (0.2%)

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	381	ALA	C-O	-6.73	1.15	1.23
1	C	380	VAL	C-O	-6.10	1.18	1.24
1	A	333	PRO	CA-C	-6.07	1.46	1.52
1	A	384	LYS	C-O	-5.95	1.19	1.24
1	B	383	TYR	C-O	-5.84	1.17	1.24

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	383	TYR	N-CA-C	-6.90	97.16	108.41
1	A	313	ARG	N-CA-C	6.56	119.64	109.07
1	B	260	HIS	CA-C-N	6.54	126.31	119.05
1	B	260	HIS	C-N-CA	6.54	126.31	119.05
1	D	383	TYR	N-CA-C	-6.33	98.10	108.41

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	1295	0	1313	18	0
1	B	1301	0	1324	20	0
1	C	1301	0	1324	17	0
1	D	1301	0	1324	24	0
2	A	45	0	0	0	0
2	B	18	0	0	0	0
2	C	41	0	0	1	0
2	D	40	0	0	0	0
All	All	5342	0	5285	78	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 7.

The worst 5 of 78 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:265:THR:HG23	1:D:266:LEU:HG	1.48	0.93
1:B:244:ILE:HG23	1:B:348:MET:HE2	1.60	0.81
1:D:373:HIS:HB3	1:D:384:LYS:HG2	1.65	0.79
1:B:267:TYR:CE2	1:B:286:ARG:HA	2.18	0.78
1:A:306:LYS:HG2	1:A:357:THR:CG2	2.19	0.73

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	163/204 (80%)	159 (98%)	4 (2%)	0	100	100
1	B	163/204 (80%)	160 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	163/204 (80%)	157 (96%)	6 (4%)	0	100	100
1	D	163/204 (80%)	161 (99%)	2 (1%)	0	100	100
All	All	652/816 (80%)	637 (98%)	15 (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	147/179 (82%)	146 (99%)	1 (1%)	76	88
1	B	148/179 (83%)	146 (99%)	2 (1%)	59	79
1	C	148/179 (83%)	148 (100%)	0	100	100
1	D	148/179 (83%)	148 (100%)	0	100	100
All	All	591/716 (82%)	588 (100%)	3 (0%)	81	91

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	346	GLU
1	B	313	ARG
1	B	320	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	338	ASN
1	A	401	GLN
1	C	290	ASN
1	C	327	GLN
1	C	371	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 oligosaccharides 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	165/204 (80%)	-0.87	0 100 100	34, 49, 71, 82	0
1	B	165/204 (80%)	-0.87	0 100 100	34, 47, 72, 89	0
1	C	165/204 (80%)	-0.89	0 100 100	31, 46, 68, 83	0
1	D	165/204 (80%)	-0.81	0 100 100	35, 51, 75, 95	0
All	All	660/816 (80%)	-0.86	0 100 100	31, 48, 72, 95	0

There are no RSRZ outliers to report.

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 oligosaccharides 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.