



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 3LNU / pdb_00003lnu
Title : Crystal structure of ParE subunit
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Deposited on : 2010-02-03
Resolution : 2.20 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
Xtriage (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

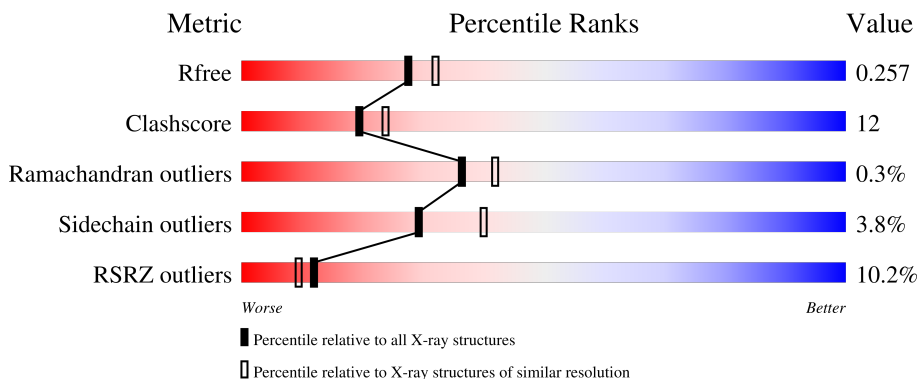
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	408	9% 66% 15% • 16%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2890 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 Topoisomerase IV subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	344	Total	C	N	O	S	0	0	0
			2696	1695	480	512	9			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	26	MET	-	expression tag	UNP Q5GYJ8
A	27	GLY	-	expression tag	UNP Q5GYJ8
A	28	SER	-	expression tag	UNP Q5GYJ8
A	29	SER	-	expression tag	UNP Q5GYJ8
A	30	HIS	-	expression tag	UNP Q5GYJ8
A	31	HIS	-	expression tag	UNP Q5GYJ8
A	32	HIS	-	expression tag	UNP Q5GYJ8
A	33	HIS	-	expression tag	UNP Q5GYJ8
A	34	HIS	-	expression tag	UNP Q5GYJ8
A	35	HIS	-	expression tag	UNP Q5GYJ8
A	36	SER	-	expression tag	UNP Q5GYJ8
A	37	SER	-	expression tag	UNP Q5GYJ8
A	38	GLY	-	expression tag	UNP Q5GYJ8
A	39	LEU	-	expression tag	UNP Q5GYJ8
A	40	VAL	-	expression tag	UNP Q5GYJ8
A	41	PRO	-	expression tag	UNP Q5GYJ8
A	42	ARG	-	expression tag	UNP Q5GYJ8
A	43	GLY	-	expression tag	UNP Q5GYJ8
A	44	SER	-	expression tag	UNP Q5GYJ8
A	45	HIS	-	expression tag	UNP Q5GYJ8

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	194	Total	O	0	0
			194	194		

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.

Chain A:

9% 66% 15% 16%

MET GLY SER SER HIS HIS HIS HIS HIS HIS HIS HIS SER SER SER GLY LEU VAL VAL PRO ARG ARG GLY SER SER HIS HIS ASN THR ARG TYR ASN ALA ASP ILE GLU VAL LEU SER G59 G65 M69 Y70 Y71 H78 Q81 H95 Q98 S108 G115 R116 H123 P124 E125 E126 K127 Y128 Y129 L133 L134 L135 T136 R137 L138 HIS ALA GLY GLY LYS PHE ASN ASN ARG ASN TYR THR PHE SER SER GLY GLY LEU HIS VAL G159 M164 L172 F173 H181 R182 M183 E184 L194 V197 K202 R208 L209 W212 L238 R261 G282 L263 R264 D265 K271 Y272 E273 H274 E275 M276 D280 L281 F282 K288 D289 T290 E291 D294 V300 F301 E302 G303 E304 L305 V306 S309 N312 L313 Q318 H319 G320 T321 K322 V323 L330 R335 D339 F340 R341 N342 L343 L350 A351 P352 E353 W356 D357 D369 P370 Q371 F372 S373 C374

4 Data and refinement statistics

Property	Value	Source
Space group	P 4 ₂ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	105.30Å 105.30Å 133.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.30 – 2.20 33.30 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.3 (33.30-2.20) 96.2 (33.30-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.93 (at 2.00Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.236 , 0.257 0.236 , 0.257	Depositor DCC
R_{free} test set	1871 reflections (3.64%)	wwPDB-VP
Wilson B-factor (Å ²)	36.7	Xtriage
Anisotropy	0.153	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 25.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2890	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.25% 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	0.38	0/2749	0.93	7/3718 (0.2%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	290	THR	N-CA-C	-21.55	90.05	114.62
1	A	289	ASP	N-CA-C	13.03	138.56	110.80
1	A	290	THR	N-CA-CB	-8.12	98.35	111.18
1	A	282	PHE	N-CA-C	-6.19	98.31	108.41
1	A	288	LYS	N-CA-C	-5.82	104.85	112.41

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	2696	0	2667	62	0
2	A	194	0	0	14	0
All	All	2890	0	2667	62	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 12.

The worst 5 of 62 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:135:LEU:HG	2:A:558:HOH:O	1.61	0.97
1:A:135:LEU:HD22	1:A:164:ASN:HB2	1.57	0.84
1:A:276:MET:HE2	1:A:300:VAL:HG22	1.66	0.78
1:A:98:GLN:HG3	2:A:593:HOH:O	1.90	0.71
1:A:339:ASP:HB3	2:A:533:HOH:O	1.90	0.71

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	340/408 (83%)	329 (97%)	10 (3%)	1 (0%)	36	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	382	SER

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	287/340 (84%)	276 (96%)	11 (4%)	29	40

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	322	HIS
1	A	357	ASP
1	A	418	ARG
1	A	377	LYS
1	A	290	THR

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	78	HIS
1	A	274	HIS
1	A	319	HIS
1	A	342	ASN
1	A	403	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	344/408 (84%)	0.53	35 (10%) 12 9	26, 37, 58, 76	0

The worst 5 of 35 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	138	LEU	6.8
1	A	422	ARG	5.8
1	A	375	GLN	5.6
1	A	288	LYS	5.4
1	A	289	ASP	4.6

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.