



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 8, 2023 – 04:37 AM EDT

PDB ID : 1QD7
Title : PARTIAL MODEL FOR 30S RIBOSOMAL SUBUNIT
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Deposited on : 1999-07-09
Resolution : 5.50 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 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 : 4.02b-467
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35

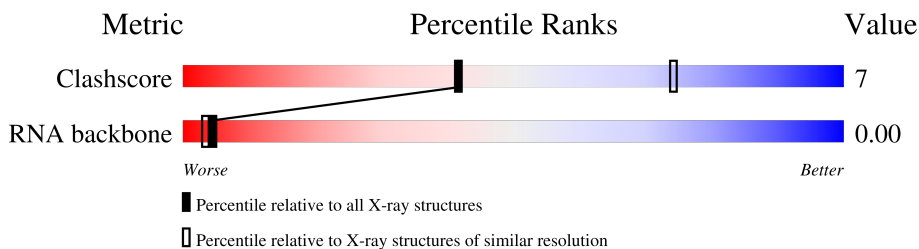
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 5.50 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))
Clashscore	141614	1010 (7.10-3.90)
RNA backbone	3102	1074 (7.80-3.00)

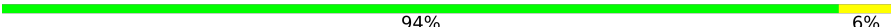
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	271	100%
2	B	88	93% 7%
3	C	159	100%
4	D	145	100%
5	E	97	100%
6	F	135	100%
7	G	136	100%
8	H	85	96% .
9	I	89	98% .

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Mol	Chain	Length	Quality of chain
10	J	100	 94% 6%

2 Entry composition i

There are 10 unique types of molecules in this entry. The entry contains 1305 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 RNA chain called CENTRAL FRAGMENT OF 16 S RNA.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
1	A	271	Total P 271 271	8	0	271

- Molecule 2 is a RNA chain called END FRAGMENT OF 16 S RNA.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	B	88	Total P 88 88	0	0	88

- Molecule 3 is a protein called S4 RIBOSOMAL PROTEIN.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
3	C	159	Total C 159 159	0	0	159

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	120	LEU	ILE	conflict	UNP P81288

- Molecule 4 is a protein called S5 RIBOSOMAL PROTEIN.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
4	D	145	Total C 145 145	0	0	145

- Molecule 5 is a protein called S6 RIBOSOMAL PROTEIN.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
5	E	97	Total C 97 97	0	0	97

- Molecule 6 is a protein called S7 RIBOSOMAL PROTEIN.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
6	F	135	Total C 135 135	0	0	135

- Molecule 7 is a protein called S8 RIBOSOMAL PROTEIN.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
7	G	136	Total C 136 136	0	0	136

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	25	ASP	GLU	conflict	UNP P24319
G	37	ARG	LYS	conflict	UNP P24319
G	52	ASP	GLU	conflict	UNP P24319
G	61	VAL	ILE	conflict	UNP P24319
G	62	TYR	HIS	conflict	UNP P24319
G	81	HIS	LYS	conflict	UNP P24319
G	88	LYS	ARG	conflict	UNP P24319
G	115	SER	PRO	conflict	UNP P24319

- Molecule 8 is a protein called S15 RIBOSOMAL PROTEIN.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
8	H	85	Total C 85 85	13	0	85

- Molecule 9 is a protein called S17 RIBOSOMAL PROTEIN.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
9	I	89	Total C 89 89	0	0	89

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	85	ARG	VAL	conflict	UNP P23828
I	86	ALA	LEU	conflict	UNP P23828

- Molecule 10 is a protein called S20 RIBOSOMAL PROTEIN.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
10	J	100	Total 100	C 100	0	0	100

3 Residue-property plots

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. 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. 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.

Note EDS was not executed.

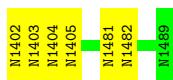
- Molecule 1: CENTRAL FRAGMENT OF 16 S RNA

Chain A:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: END FRAGMENT OF 16 S RNA

Chain B:  93% 7%



- Molecule 3: S4 RIBOSOMAL PROTEIN

Chain C:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: S5 RIBOSOMAL PROTEIN

Chain D:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: S6 RIBOSOMAL PROTEIN

Chain E:  100%

There are no outlier residues recorded for this chain.

- Molecule 6: S7 RIBOSOMAL PROTEIN

Chain F:  100%

There are no outlier residues recorded for this chain.

- Molecule 7: S8 RIBOSOMAL PROTEIN

Chain G:  100%

There are no outlier residues recorded for this chain.

- Molecule 8: S15 RIBOSOMAL PROTEIN

Chain H:  96%



- Molecule 9: S17 RIBOSOMAL PROTEIN

Chain I:  98%



- Molecule 10: S20 RIBOSOMAL PROTEIN

Chain J:  94% 6%



4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	401.60Å 401.60Å 174.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 5.50	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-5.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program		Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	1305	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

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 [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	271	0	0	0	0
2	B	88	0	0	3	0
3	C	159	0	0	0	0
4	D	145	0	0	0	0
5	E	97	0	0	0	0
6	F	135	0	0	0	0
7	G	136	0	0	0	0
8	H	85	0	0	2	0
9	I	89	0	0	1	0
10	J	100	0	0	3	0
All	All	1305	0	0	9	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 9 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)
8:H:22:GLY:CA	8:H:24:PRO:CA	2.30	1.10
9:I:82:LYS:CA	9:I:83:ALA:CA	2.50	0.90
10:J:58:UNK:CA	10:J:62:UNK:CA	2.56	0.83
2:B:1404:N:P	2:B:1405:N:P	2.78	0.82
8:H:22:GLY:CA	8:H:23:SER:CA	2.74	0.66

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	0/271	-	-
2	B	0/88	-	-
All	All	0/359	-	-

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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 monosaccharides 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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.