Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 09:44 PM GMT

PDB ID	:	1QD7
Title	:	PARTIAL MODEL FOR 30S RIBOSOMAL SUBUNIT
Authors	:	Clemons Jr., W.M.; May, J.L.C.; Wimberly, B.T.; McCutcheon, J.P.; Capel, M.S.; Ramakrishnan, V.
Deposited on	:	1999-07-09
Resolution	:	5.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 (i) symbol.

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

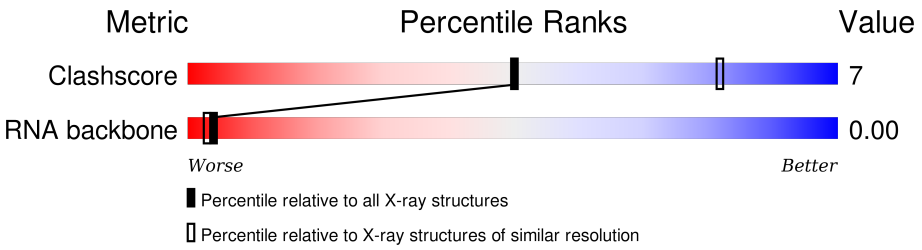
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

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	102246	1020 (7.10-3.70)
RNA backbone	2183	1101 (7.80-2.80)

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 <=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.

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% .

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Mol	Chain	Length	Quality of chain
9	I	89	98%
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
			Total	P			
1	A	271	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
			Total	P			
2	B	88	88	88	0	0	88

- Molecule 3 is a protein called S4 RIBOSOMAL PROTEIN.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
			Total	C			
3	C	159	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
			Total	C			
4	D	145	145	145	0	0	145

- Molecule 5 is a protein called S6 RIBOSOMAL PROTEIN.

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

- Molecule 6 is a protein called S7 RIBOSOMAL PROTEIN.

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

- Molecule 7 is a protein called S8 RIBOSOMAL PROTEIN.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
			Total	C			
7	G	136	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
			Total	C			
8	H	85	85	85	13	0	85

- Molecule 9 is a protein called S17 RIBOSOMAL PROTEIN.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
			Total	C			
9	I	89	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
			Total	C			
10	J	100	100	100	0	0	100

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.

Note EDS was not executed.

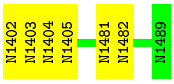
- Molecule 1: CENTRAL FRAGMENT OF 16 S RNA

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.

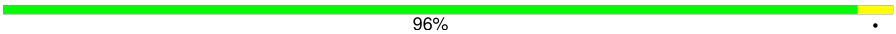
- Molecule 7: S8 RIBOSOMAL PROTEIN

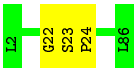
Chain G: 100%

There are no outlier residues recorded for this chain.

- Molecule 8: S15 RIBOSOMAL PROTEIN

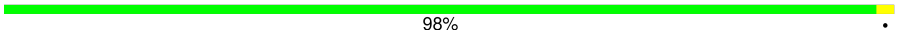
Chain H:





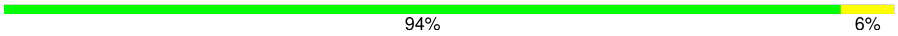
- Molecule 9: S17 RIBOSOMAL PROTEIN

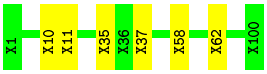
Chain I:



- Molecule 10: S20 RIBOSOMAL PROTEIN

Chain J:





4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section will therefore be 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	O	Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
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.

All (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
2:B:1402:N:P	2:B:1482:N:P	3.03	0.56
2:B:1403:N:P	2:B:1481:N:P	3.06	0.53
10:J:10:UNK:CA	10:J:11:UNK:CA	2.88	0.52
10:J:35:UNK:CA	10:J:37:UNK:CA	2.99	0.41

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 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)

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates (i)

EDS was not executed - this section will therefore be empty.

6.4 Ligands (i)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers (i)

EDS was not executed - this section will therefore be empty.