



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 01:37 PM BST

PDB ID : 1EG0
EMDB ID: : EMD-1003
Title : FITTING OF COMPONENTS WITH KNOWN STRUCTURE INTO AN
11.5 Å CRYO-EM MAP OF THE E.COLI 70S RIBOSOME
Authors : Gabashvili, I.S.; Agrawal, R.K.; Spahn, C.M.T.; Grassucci, R.A.; Svergun,
D.I.; Frank, J.; Penczek, P.
Deposited on : 2000-02-11
Resolution : 11.50 Å (reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could
stem from errors in the original structure(s) used in the fitting.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : unknown
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) : trunk27241

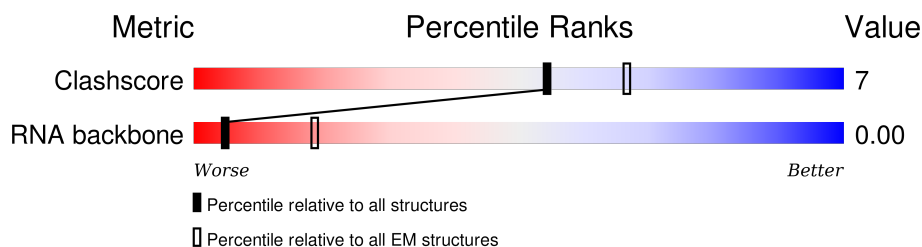
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 11.50 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)	EM structures (#Entries)
Clashescore	114402	924
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	I	33	 100%
2	L	57	 100%
3	M	26	 100%
4	O	76	 100%
5	A	159	 100%
6	B	148	 98% .
7	C	97	 100%
8	D	146	 92% 8%
9	E	138	 98% ..
10	F	89	 99% .

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Mol	Chain	Length	Quality of chain
11	G	93	<div><div style="width: 92%;">92%</div><div style="width: 6%;"></div></div>
12	H	100	<div><div style="width: 94%;">94%</div><div style="width: 6%;">6%</div></div>
13	N	229	<div><div style="width: 92%;">92%</div><div style="width: 6%;"></div></div>
14	J	171	<div><div style="width: 96%;">96%</div><div style="width: 4%;"></div></div>
15	K	140	<div><div style="width: 95%;">95%</div><div style="width: 5%;">5%</div></div>

2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 1658 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 FRAGMENT OF 16S RRNA HELIX 23.

Mol	Chain	Residues	Atoms		AltConf	Trace
1	I	33	Total	P	0	33
			33	33		

- Molecule 2 is a RNA chain called FRAGMENT OF 23S RRNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
2	L	57	Total	P	0	57
			57	57		

- Molecule 3 is a RNA chain called HELIX 95 OF 23S RRNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
3	M	26	Total	P	0	26
			26	26		

- Molecule 4 is a RNA chain called FORMYL-METHIONYL-TRNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
4	O	76	Total	P	0	76
			76	76		

- Molecule 5 is a protein called PROTEIN (S4 RIBOSOMAL PROTEIN).

Mol	Chain	Residues	Atoms		AltConf	Trace
5	A	159	Total	C	0	159
			159	159		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	ARG	EXPRESSION TAG	UNP P81288

- Molecule 6 is a protein called PROTEIN (S5 RIBOSOMAL PROTEIN).

Mol	Chain	Residues	Atoms		AltConf	Trace
6	B	145	Total	C	0	145
			145	145		

- Molecule 7 is a protein called PROTEIN (S6 RIBOSOMAL PROTEIN).

Mol	Chain	Residues	Atoms		AltConf	Trace
7	C	97	Total	C	0	97
			97	97		

- Molecule 8 is a protein called PROTEIN (S7 RIBOSOMAL PROTEIN).

Mol	Chain	Residues	Atoms		AltConf	Trace
8	D	135	Total	C	0	135
			135	135		

- Molecule 9 is a protein called PROTEIN (S8 RIBOSOMAL PROTEIN).

Mol	Chain	Residues	Atoms		AltConf	Trace
9	E	136	Total	C	0	136
			136	136		

- Molecule 10 is a protein called PROTEIN (S15 RIBOSOMAL PROTEIN).

Mol	Chain	Residues	Atoms		AltConf	Trace
10	F	88	Total	C	0	88
			88	88		

- Molecule 11 is a protein called PROTEIN (S17 RIBOSOMAL PROTEIN).

Mol	Chain	Residues	Atoms		AltConf	Trace
11	G	89	Total	C	0	89
			89	89		

- Molecule 12 is a protein called PROTEIN (S20 RIBOSOMAL PROTEIN).

Mol	Chain	Residues	Atoms		AltConf	Trace
12	H	100	Total	C	0	100
			100	100		

- Molecule 13 is a protein called PROTEIN (RIBOSOMAL PROTEIN L1).

Mol	Chain	Residues	Atoms		AltConf	Trace
13	N	220	Total 220	C 220	0	220

- Molecule 14 is a protein called PROTEIN (RIBOSOMAL PROTEIN L6).

Mol	Chain	Residues	Atoms		AltConf	Trace
14	J	164	Total 164	C 164	0	164

- Molecule 15 is a protein called PROTEIN (RIBOSOMAL PROTEIN L11).

Mol	Chain	Residues	Atoms		AltConf	Trace
15	K	133	Total 133	C 133	0	133

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 errors 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.

- Molecule 1: FRAGMENT OF 16S RRNA HELIX 23

Chain I:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: FRAGMENT OF 23S RRNA

Chain L:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: HELIX 95 OF 23S RRNA

Chain M:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: FORMYL-METHIONYL-TRNA

Chain O:  100%

There are no outlier residues recorded for this chain.

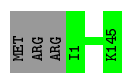
- Molecule 5: PROTEIN (S4 RIBOSOMAL PROTEIN)

Chain A:  100%

There are no outlier residues recorded for this chain.

- Molecule 6: PROTEIN (S5 RIBOSOMAL PROTEIN)

Chain B:  98%



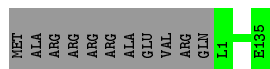
- Molecule 7: PROTEIN (S6 RIBOSOMAL PROTEIN)

Chain C:  100%

There are no outlier residues recorded for this chain.

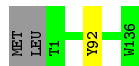
- Molecule 8: PROTEIN (S7 RIBOSOMAL PROTEIN)

Chain D:  92% 8%



- Molecule 9: PROTEIN (S8 RIBOSOMAL PROTEIN)

Chain E:  98% ..



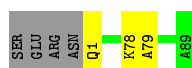
- Molecule 10: PROTEIN (S15 RIBOSOMAL PROTEIN)

Chain F:  99% .



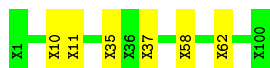
- Molecule 11: PROTEIN (S17 RIBOSOMAL PROTEIN)

Chain G:  92% . .



- Molecule 12: PROTEIN (S20 RIBOSOMAL PROTEIN)

Chain H:  94% 6%



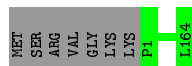
- Molecule 13: PROTEIN (RIBOSOMAL PROTEIN L1)

Chain N:  92% . .



- Molecule 14: PROTEIN (RIBOSOMAL PROTEIN L6)

Chain J:  96% .



- Molecule 15: PROTEIN (RIBOSOMAL PROTEIN L11)

Chain K: 

MET	ALA	LYS	LYS	VAL	ALA	ALA	Q1	V133
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4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Not provided	Depositor
Microscope	Not provided	Depositor
Voltage (kV)	Not provided	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	730.	Depositor
Maximum defocus (nm)	4340.	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, OMC, 4SU, H2U, PSU

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	I	33	0	0	0	0
2	L	57	0	0	0	0
3	M	26	0	0	0	0
4	O	76	0	0	0	0
5	A	159	0	0	0	0
6	B	145	0	0	0	0
7	C	97	0	0	0	0
8	D	135	0	0	0	0
9	E	136	0	0	1	0
10	F	88	0	0	0	0
11	G	89	0	0	2	0
12	H	100	0	0	3	0
13	N	220	0	0	6	0
14	J	164	0	0	0	0
15	K	133	0	0	0	0
All	All	1658	0	0	11	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 11 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)
13:N:152:ARG:CA	13:N:153:ILE:CA	1.94	1.46
13:N:150:ALA:CA	13:N:165:ALA:CA	2.46	0.92
9:E:92:TYR:CA	11:G:1:GLN:CA	2.48	0.92
11:G:78:LYS:CA	11:G:79:ALA:CA	2.50	0.89
13:N:149:LYS:CA	13:N:151:GLY:CA	2.53	0.87

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	I	0/33	-	-
2	L	0/57	-	-
3	M	0/26	-	-
4	O	0/76	-	-
All	All	0/192	-	-

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](#)

Of 5 non-standard protein/DNA/RNA residues modelled in this entry, 5 are modelled with single atom - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.