Full wwPDB EM Validation Report (i)

Feb 6, 2024 – 10:11 AM EST

PDB ID	:	2FTC
Title	:	Structural Model for the Large Subunit of the Mammalian Mitochondrial Ribosome
Authors	:	Mears, J.A.; Sharma, M.R.; Gutell, R.R.; Richardson, P.E.; Agrawal, R.K.; Harvey, S.C.
Deposited on	:	2006-01-24
Resolution	:	12.10 Å(reported)
Based on initial models	:	1NKW, 1JJ2, 1PNU, 1GIY

This is a Full wwPDB EM Validation Report for a publicly released PDB/EMDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

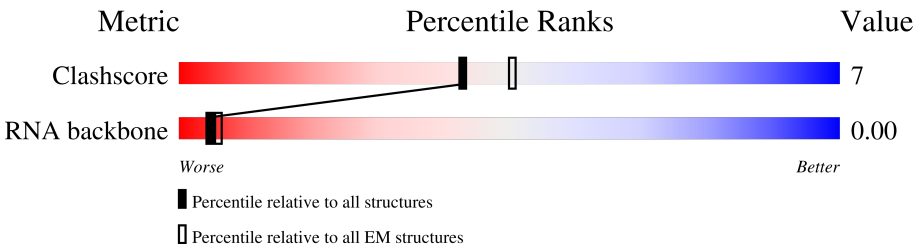
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 12.10 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)
Clashscore	158937	4297
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 <=5%

Mol	Chain	Length	Quality of chain
1	R	1568	91% · 8%
2	A	189	99% ·
3	B	136	100%
4	C	211	97% ·
5	D	175	97% ·
6	E	137	99% ·
6	F	137	97% ·
7	G	145	99% ·
8	H	148	99% ·
9	I	118	100%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
10	J	116	100%
11	K	98	96%
12	L	118	100%
13	M	110	99%
14	N	96	97%
15	O	69	94% 6%
16	P	52	98%
17	Q	38	100%

2 Entry composition (i)

There are 17 unique types of molecules in this entry. The entry contains 3536 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 Mitochondrial 16S ribosomal RNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	P		
1	R	1443	1443	1443	0	1443

- Molecule 2 is a protein called Mitochondrial ribosomal protein L1.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
2	A	189	189	189	0	189

- Molecule 3 is a protein called mitochondrial ribosomal protein L2.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
3	B	136	136	136	0	136

- Molecule 4 is a protein called Mitochondrial 39S ribosomal protein L3.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
4	C	211	211	211	0	211

- Molecule 5 is a protein called mitochondrial ribosomal protein L4 isoform a.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
5	D	175	175	175	0	175

- Molecule 6 is a protein called 39S ribosomal protein L12, mitochondrial.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
6	E	137	137	137	0	137

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
6	F	137	137	137	0	137

- Molecule 7 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
7	G	145	145	145	0	145

- Molecule 8 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
8	H	148	148	148	0	148

- Molecule 9 is a protein called Mitochondrial ribosomal protein L16.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
9	I	118	118	118	0	118

- Molecule 10 is a protein called Mitochondrial ribosomal protein L17.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
10	J	116	116	116	0	116

- Molecule 11 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
11	K	98	98	98	0	98

- Molecule 12 is a protein called MRPL20 protein.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
12	L	118	118	118	0	118

- Molecule 13 is a protein called mitochondrial ribosomal protein L22 isoform a.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
13	M	110	110	110	0	110

- Molecule 14 is a protein called mitochondrial ribosomal protein L24.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
14	N	96	96	96	0	96

- Molecule 15 is a protein called Mitochondrial 39S ribosomal protein L27.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
15	O	69	69	69	0	69

- Molecule 16 is a protein called mitochondrial ribosomal protein L33 isoform a.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
16	P	52	52	52	0	52

- Molecule 17 is a protein called 39S ribosomal protein L34, mitochondrial.

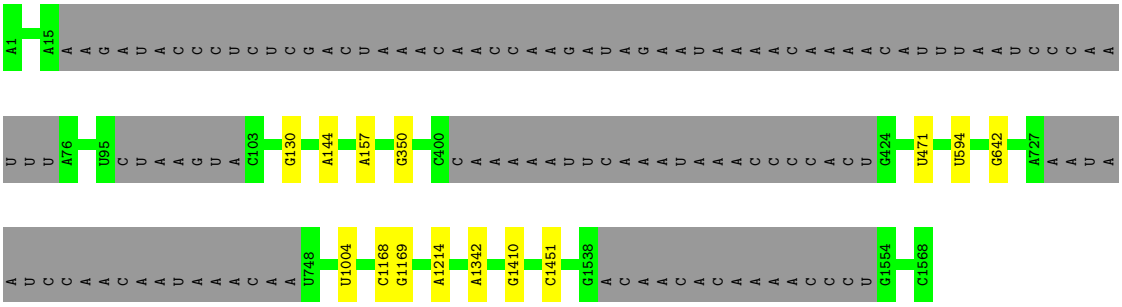
Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
17	Q	38	38	38	0	38

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. 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.

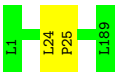
• Molecule 1: Mitochondrial 16S ribosomal RNA

Chain R: 91% 8%



• Molecule 2: Mitochondrial ribosomal protein L1

Chain A: 99%



• Molecule 3: mitochondrial ribosomal protein L2

Chain B: 100%

There are no outlier residues recorded for this chain.

• Molecule 4: Mitochondrial 39S ribosomal protein L3

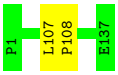
Chain C: 97%

• Molecule 5: mitochondrial ribosomal protein L4 isoform a

Chain D: 97%

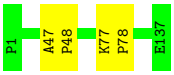
• Molecule 6: 39S ribosomal protein L12, mitochondrial

Chain E: 99%



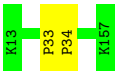
• Molecule 6: 39S ribosomal protein L12, mitochondrial

Chain F: 97%



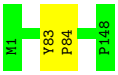
• Molecule 7: 39S ribosomal protein L11, mitochondrial

Chain G: 99%



• Molecule 8: 39S ribosomal protein L13, mitochondrial

Chain H: 99%



• Molecule 9: Mitochondrial ribosomal protein L16

Chain I: 100%

There are no outlier residues recorded for this chain.

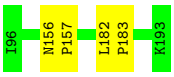
• Molecule 10: Mitochondrial ribosomal protein L17

Chain J: 100%

There are no outlier residues recorded for this chain.

• Molecule 11: 39S ribosomal protein L19, mitochondrial

Chain K: 96%



• Molecule 12: MRPL20 protein

Chain L: 100%

There are no outlier residues recorded for this chain.

• Molecule 13: mitochondrial ribosomal protein L22 isoform a

Chain M: 99%

H1 D11 P110

• Molecule 14: mitochondrial ribosomal protein L24

Chain N: 97%

G59 Y97 D124 P125 I154

• Molecule 15: Mitochondrial 39S ribosomal protein L27

Chain O: 94% 6%

A31 L42 G43 H76 P77 Y99

• Molecule 16: mitochondrial ribosomal protein L33 isoform a

Chain P: 98%

A9 K51 K60

• Molecule 17: 39S ribosomal protein L34, mitochondrial

Chain Q: 100%

There are no outlier residues recorded for this chain.

GLOBAL-STATISTICS INFOmissingINFO

4 Model quality (i)

4.1 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.

4.2 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	R	1443	0	0	13	0
2	A	189	0	0	1	0
3	B	136	0	0	0	0
4	C	211	0	0	5	0
5	D	175	0	0	4	0
6	E	137	0	0	1	0
6	F	137	0	0	2	0
7	G	145	0	0	1	0
8	H	148	0	0	1	0
9	I	118	0	0	0	0
10	J	116	0	0	0	0
11	K	98	0	0	2	0
12	L	118	0	0	0	0
13	M	110	0	0	1	0
14	N	96	0	0	2	0
15	O	69	0	0	3	0
16	P	52	0	0	1	0
17	Q	38	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	3536	0	0	25	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 (25) 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:R:1451:C:P	4:C:254:GLY:CA	2.08	1.40
1:R:1169:G:P	15:O:42:LEU:CA	2.10	1.37
1:R:1168:C:P	15:O:43:GLY:CA	2.56	0.94
1:R:1004:U:P	4:C:219:MET:CA	2.66	0.83
1:R:144:A:P	14:N:97:TYR:CA	2.78	0.72
1:R:471:U:P	1:R:594:U:P	2.89	0.71
1:R:642:G:P	5:D:135:ARG:CA	2.82	0.67
1:R:1214:A:P	16:P:51:LYS:CA	2.84	0.65
1:R:1342:A:P	4:C:255:THR:CA	2.87	0.63
1:R:157:A:P	13:M:11:ASP:CA	2.89	0.60
11:K:156:ASN:CA	11:K:157:PRO:CA	2.87	0.53
6:F:77:LYS:CA	6:F:78:PRO:CA	2.89	0.50
6:F:47:ALA:CA	6:F:48:PRO:CA	2.91	0.48
4:C:199:ARG:CA	4:C:200:PRO:CA	2.91	0.48
5:D:263:LEU:CA	5:D:264:PRO:CA	2.93	0.47
2:A:24:LEU:CA	2:A:25:PRO:CA	2.94	0.45
11:K:182:LEU:CA	11:K:183:PRO:CA	2.95	0.45
1:R:130:G:P	5:D:117:ARG:CA	3.04	0.44
8:H:83:TYR:CA	8:H:84:PRO:CA	2.96	0.44
15:O:76:HIS:CA	15:O:77:PRO:CA	2.96	0.44
1:R:350:G:P	5:D:154:GLY:CA	3.05	0.44
6:E:107:LEU:CA	6:E:108:PRO:CA	2.98	0.42
14:N:124:ASP:CA	14:N:125:PRO:CA	2.97	0.42
1:R:1410:G:P	4:C:234:THR:CA	3.08	0.42
7:G:33:PRO:CA	7:G:34:PRO:CA	2.99	0.41

There are no symmetry-related clashes.

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

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

4.3.2 Protein sidechains (i)

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

4.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	R	0/1568	-	-

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

4.6 Ligand geometry (i)

There are no ligands in this entry.

4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.