



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 01:39 PM BST

PDB ID : 2FTC
EMDB ID: : unknown
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 PDB ID : 1GIY, 1JJ2, 1NKW, 1PNU

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

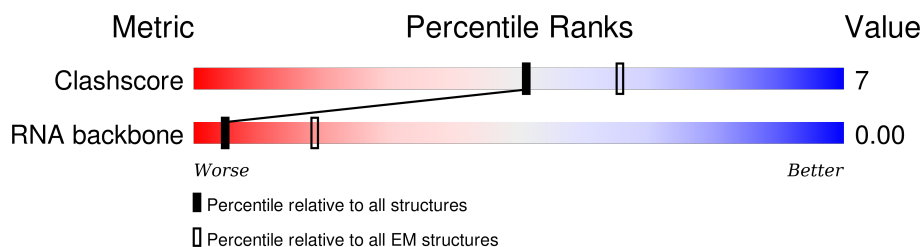
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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	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	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%

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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

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
1	R	1443	Total	P	0	1443
			1443	1443		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 12 is a protein called MRPL20 protein.

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

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

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

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

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

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

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

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

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

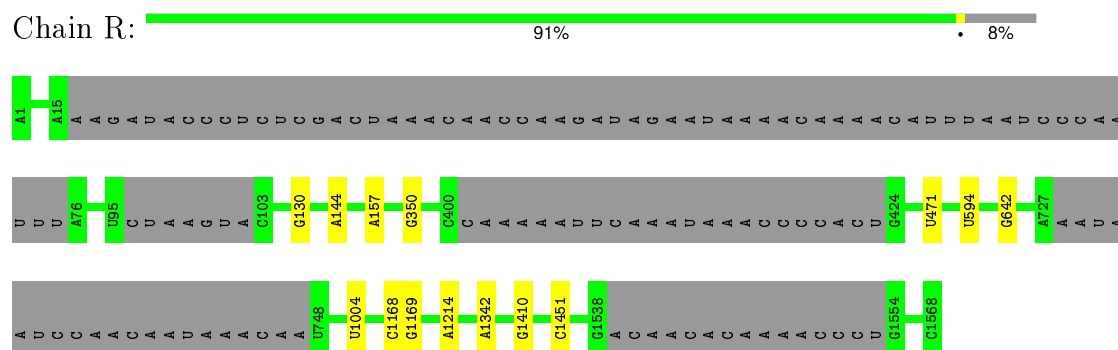
- Molecule 17 is a protein called 39S ribosomal protein L34, mitochondrial.

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

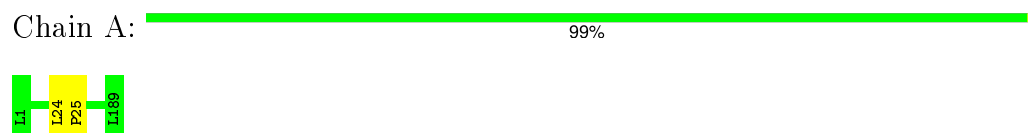
3 Residue-property plots [i](#)

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. 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



- Molecule 2: Mitochondrial ribosomal protein L1

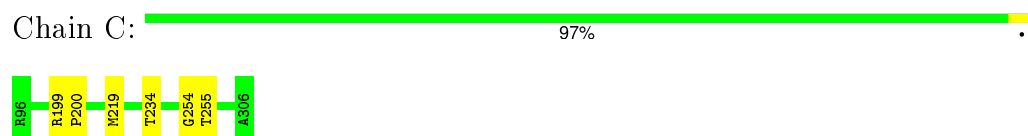


- Molecule 3: mitochondrial ribosomal protein L2

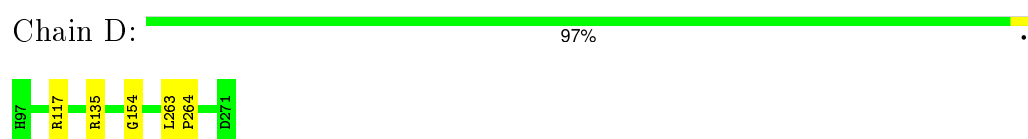


There are no outlier residues recorded for this chain.

- Molecule 4: Mitochondrial 39S ribosomal protein L3



- Molecule 5: mitochondrial ribosomal protein L4 isoform a



- Molecule 6: 39S ribosomal protein L12, mitochondrial

Chain E:  99%



- Molecule 6: 39S ribosomal protein L12, mitochondrial

Chain F:  97%



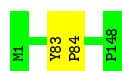
- Molecule 7: 39S ribosomal protein L11, mitochondrial

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.

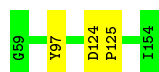
- Molecule 13: mitochondrial ribosomal protein L22 isoform a

Chain M:  99% .



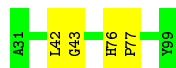
- Molecule 14: mitochondrial ribosomal protein L24

Chain N:  97% .



- Molecule 15: Mitochondrial 39S ribosomal protein L27

Chain O:  94%  6% .



- Molecule 16: mitochondrial ribosomal protein L33 isoform a

Chain P:  98% .



- Molecule 17: 39S ribosomal protein L34, mitochondrial

Chain Q:  100% .

There are no outlier residues recorded for this chain.

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	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4600	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	Depositor

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	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

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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.

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	R	0/1568	-	-

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.