



## wwPDB EM Validation Summary Report ⓘ

Jun 23, 2021 – 06:24 AM BST

PDB ID : 7OF0  
EMDB ID : EMD-12865  
Title : Structure of a human mitochondrial ribosome large subunit assembly intermediate in complex with MTERF4-NSUN4 (dataset1).  
Authors : Hillen, H.S.; Lavdovskaia, E.; Nadler, F.; Hanitsch, E.; Linden, A.; Bohnsack, K.E.; Urlaub, H.; Richter-Dennerlein, R.  
Deposited on : 2021-05-04  
Resolution : 2.20 Å (reported)  
Based on initial model : 5OOL

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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 ⓘ symbol.

---

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

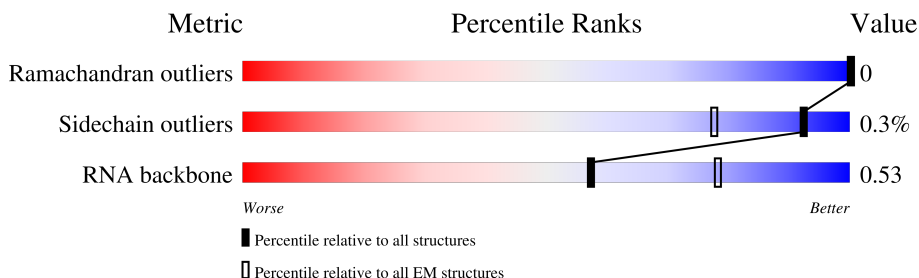
EMDB validation analysis : 0.0.0.dev75  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.20

# 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 2.20 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.














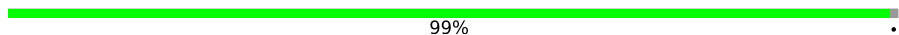

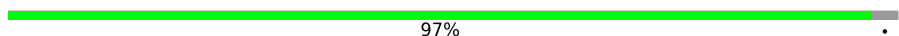










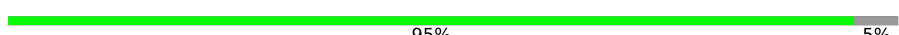
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	0	188	57% (Green), 43% (Grey)
2	1	65	80% (Green), 20% (Grey)
3	2	92	49% (Green), 51% (Grey)
4	3	188	51% (Green), 49% (Grey)
5	4	103	36% (Green), 64% (Grey)
6	5	423	92% (Green), 7% (Grey)
7	6	380	85% (Green), 15% (Grey)
8	7	338	83% (Green), 15% (Grey)
9	8	206	37% (Green), 63% (Grey)

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
10	9	137	 85% 15%
11	A	1559	 67% 21% 12%
12	B	69	 58% 23% 19%
13	C	384	 85% 15%
14	D	305	 78% 21%
15	E	348	 89% 11%
16	F	311	 80% 20%
17	G	381	 62% 38%
18	H	267	 35% 64%
19	I	261	 58% 42%
20	J	192	 73% 27%
21	K	178	 99%
22	L	145	 79% 21%
23	M	296	 97%
24	N	251	 73% 27%
25	O	175	 87% 13%
26	P	180	 78% 22%
27	Q	292	 74% 26%
28	R	149	 78% 22%
29	S	205	 76% 24%
30	T	206	 81% 19%
31	U	153	 91% 9%
32	V	216	 22% 78%
33	W	148	 68% 32%
34	X	256	 95% 5%

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain	
35	Y	250	70%	30%
36	Z	161	71%	29%
37	a	142	50%	50%
38	b	215	69%	31%
39	c	332	83%	17%
40	d	306	64%	35%
41	e	279	71%	29%
42	f	212	51%	49%
43	g	166	77%	22%
44	h	158	66%	34%
45	i	128	76%	24%
46	j	123	69%	31%
47	k	112	71%	29%
48	m	128	23%	77%
49	o	102	78%	22%
50	p	206	62%	38%
51	q	222	58%	42%
52	r	196	74%	26%
53	s	439	84%	16%
54	u	234	47%	53%
55	v	70	96%	..
56	w	156	50%	49%

## 2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 99476 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 protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	108	880	545	172	157	6	0	0

- Molecule 2 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	52	433	278	83	70	2	0	0

- Molecule 3 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	45	367	227	81	58	1	0	0

- Molecule 4 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	3	95	831	539	162	127	3	0	0

- Molecule 5 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	4	37	333	212	71	47	3	0	0

- Molecule 6 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	5	392	3199	2067	558	563	11	0	0

- Molecule 7 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	6	324	Total	C	N	O	S	0	0
			2723	1743	488	484	8		

- Molecule 8 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	7	287	Total	C	N	O	S	0	0
			2334	1495	397	425	17		

- Molecule 9 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	8	77	Total	C	N	O	S	0	0
			651	413	113	123	2		

- Molecule 10 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	9	117	Total	C	N	O	S	0	0
			947	614	163	168	2		

- Molecule 11 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
11	A	1376	Total	C	N	O	P	0	0
			29219	13111	5277	9455	1376		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3107	U	UNK	conflict	GB 1025814679

- Molecule 12 is a RNA chain called mitochondrial tRNAVal.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
12	B	56	Total	C	N	O	P	0	0
			1191	534	214	387	56		

- Molecule 13 is a protein called 5-methylcytosine rRNA methyltransferase NSUN4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	C	327	2595	1651	454	474	16	1	0

- Molecule 14 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	D	240	1872	1165	378	320	9	0	0

- Molecule 15 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	E	308	2427	1559	423	434	11	0	0

- Molecule 16 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	F	250	2013	1294	365	348	6	0	0

- Molecule 17 is a protein called Transcription termination factor 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	G	238	1943	1243	336	352	12	0	0

- Molecule 18 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
18	H	95	784	498	152	134	0	0

- Molecule 19 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	I	151	1228	795	222	201	10	0	0

- Molecule 20 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	J	140	Total	C	N	O	S	0	0
			1061	680	192	187	2		

- Molecule 21 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	K	177	Total	C	N	O	S	0	0
			1451	934	259	251	7		

- Molecule 22 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	L	115	Total	C	N	O	S	0	0
			889	559	171	154	5		

- Molecule 23 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	M	287	Total	C	N	O	S	0	0
			2305	1472	425	402	6		

- Molecule 24 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	N	183	Total	C	N	O	S	0	0
			1494	960	274	251	9		

- Molecule 25 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	O	152	Total	C	N	O	S	0	0
			1245	784	239	215	7		

- Molecule 26 is a protein called 39S ribosomal protein L18, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	P	141	Total	C	N	O	S	0	0
			1148	719	221	203	5		

- Molecule 27 is a protein called 39S ribosomal protein L19, mitochondrial.



Mol	Chain	Residues	Atoms					AltConf	Trace
27	Q	217	Total	C	N	O	S	0	0
			1805	1159	317	320	9		

- Molecule 28 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	R	116	Total	C	N	O	S	0	0
			971	616	200	151	4		

- Molecule 29 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	S	156	Total	C	N	O	S	0	0
			1251	806	222	219	4		

- Molecule 30 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	T	166	Total	C	N	O	S	0	0
			1368	875	254	232	7		

- Molecule 31 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	U	139	Total	C	N	O	S	0	0
			1154	734	220	197	3		

- Molecule 32 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	V	47	Total	C	N	O	S	0	0
			395	255	62	75	3		

- Molecule 33 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	W	100	Total	C	N	O	S	0	0
			801	518	150	130	3		

- Molecule 34 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	X	243	Total	C	N	O	S	0	0
			2035	1317	351	362	5		

- Molecule 35 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Y	176	Total	C	N	O	S	0	0
			1517	970	291	252	4		

- Molecule 36 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Z	115	Total	C	N	O	S	0	0
			937	598	175	161	3		

- Molecule 37 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	a	71	Total	C	N	O	S	0	0
			597	378	112	103	4		

- Molecule 38 is a protein called 39S ribosomal protein L43, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	b	148	Total	C	N	O	S	0	0
			1178	733	229	213	3		

- Molecule 39 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	c	275	Total	C	N	O	S	0	0
			2217	1415	383	410	9		

- Molecule 40 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	d	199	Total	C	N	O	S	0	0
			1653	1075	276	293	9		

- Molecule 41 is a protein called 39S ribosomal protein L46, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	e	197	Total	C	N	O	S	0	0
			1599	1027	277	290	5		

- Molecule 42 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	f	108	Total	C	N	O	S	0	0
			857	549	140	165	3		

- Molecule 43 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	g	129	Total	C	N	O	S	0	0
			1067	690	185	190	2		

- Molecule 44 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	h	105	Total	C	N	O	S	0	0
			862	548	151	160	3		

- Molecule 45 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	i	97	Total	C	N	O	S	0	0
			827	532	165	126	4		

- Molecule 46 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	j	85	Total	C	N	O	S	0	0
			684	423	133	126	2		

- Molecule 47 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	k	80	Total	C	N	O	S	0	0
			627	392	116	114	5		

- Molecule 48 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	m	29	245	157	48	38	2	0	0

- Molecule 49 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	o	80	676	426	134	113	3	0	0

- Molecule 50 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	p	127	1058	661	201	192	4	0	0

- Molecule 51 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	q	128	1076	671	208	192	5	0	0

- Molecule 52 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	r	146	1203	764	232	199	8	0	0

- Molecule 53 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	s	370	3036	1946	542	534	14	0	0

- Molecule 54 is a protein called Mitochondrial assembly of ribosomal large subunit protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	u	111	927	595	155	167	10	0	0

- Molecule 55 is a protein called MIEF1 upstream open reading frame protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
55	v	69	588	372	116	100	0	0

- Molecule 56 is a protein called Acyl carrier protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	w	79	638	410	95	128	5	0	0

- Molecule 57 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
57	0	1	1	1	0
57	4	1	1	1	0
57	r	1	1	1	0

- Molecule 58 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
58	A	59	59	59	0
58	E	1	1	1	0
58	g	1	1	1	0



LEU  
PRO  
ALA  
LEU  
GLY  
F66  
Q102  
MET

- Molecule 6: 39S ribosomal protein L37, mitochondrial

Chain 5: 92% 7%

MET  
ALA  
LEU  
ALA  
PRO  
SER  
GLY  
PRO  
ALA  
ARG  
ALA  
ARG  
ALA  
LEU  
ALA  
LEU  
ALA  
LEU  
GLY  
SER  
GLN  
LEU  
GLY  
LEU  
PHE  
GLY  
LEU  
ALA  
PRO  
ARG  
ARG  
GLY  
ALA  
Y31  
Q384  
R412  
A422  
ALA

- Molecule 7: 39S ribosomal protein L38, mitochondrial

Chain 6: 85% 15%

MET  
ALA  
ALA  
PRO  
TRP  
TRP  
ARG  
ALA  
LEU  
CYS  
GLY  
CYS  
ARG  
TRP  
VAL  
TRP  
ARG  
GLY  
PHE  
SER  
SER  
ILE  
LYS  
ALA  
VAL  
LEU  
ARG  
GLY  
R27  
R52  
G79  
GLU  
LYS  
THR  
ASP  
PRO  
LYS  
GLU  
LYS  
ILE  
ASP  
ILE  
GLY  
LEU  
PRO  
PRO  
LYS  
VAL  
SER  
R99  
E209  
GLU  
GLY  
SER  
L213  
S282  
GLU

ASP  
ALA  
ARG  
PRO  
SER  
PRO  
CYS  
Y291  
Y380

- Molecule 8: 39S ribosomal protein L39, mitochondrial

Chain 7: 83% 15%

MET  
GLU  
ALA  
LEU  
ALA  
MET  
GLY  
SER  
ARG  
ALA  
LEU  
LEU  
TRP  
VAL  
VAL  
ALA  
PRO  
GLY  
GLY  
LYS  
LYS  
TRP  
PHE  
ILE  
THR  
SER  
SER  
ALA  
SER  
GLN  
LEU  
S36  
R54  
D114  
W143  
K234  
L293  
K322  
MET  
VAL  
THR  
GLU  
ASP  
GLN  
SER  
LYS  
ALA  
THR  
GLU

CYS  
THR  
SER  
THR

- Molecule 9: 39S ribosomal protein L40, mitochondrial

Chain 8: 37% 63%

MET  
THR  
ALA  
SER  
VAL  
LEU  
ARG  
SER  
ILE  
SER  
SER  
LYS  
ILE  
ALA  
LEU  
ARG  
PRO  
THR  
SER  
GLY  
LEU  
LEU  
GLY  
TRP  
GLN  
THR  
GLN  
LEU  
ARG  
GLU  
PHE  
THR  
PRO  
LEU  
LEU  
PHE  
LEU  
ASP  
LYS  
ALA  
PHE  
TRP  
GLU  
PRO  
LEU  
VAL  
E105  
P181  
ILE  
PRO  
ASN  
TYR  
GLN  
PRO  
PRO  
LYS  
LYS  
VAL  
ASP  
LYS  
LYS  
ASP

ASP  
GLN  
GLU  
ALA  
LYS  
GLU  
ARG  
LEU  
LYS  
ARG  
LYS  
ILE  
ARG  
LYS  
LEU  
THR  
GLN  
GLU  
ALA  
THR  
GLN  
LEU  
ILE  
PRO  
GLU  
ASP  
PHE  
ILE  
THR  
PRO  
LEU  
PHE  
LEU  
ASP  
LYS  
ALA  
ARG  
GLU  
PRO  
GLN  
VAL  
E105  
P181  
ILE  
PRO  
ASN  
TYR  
GLN  
PRO  
PRO  
LYS  
LYS  
VAL  
ASP  
LYS  
LYS  
ASP

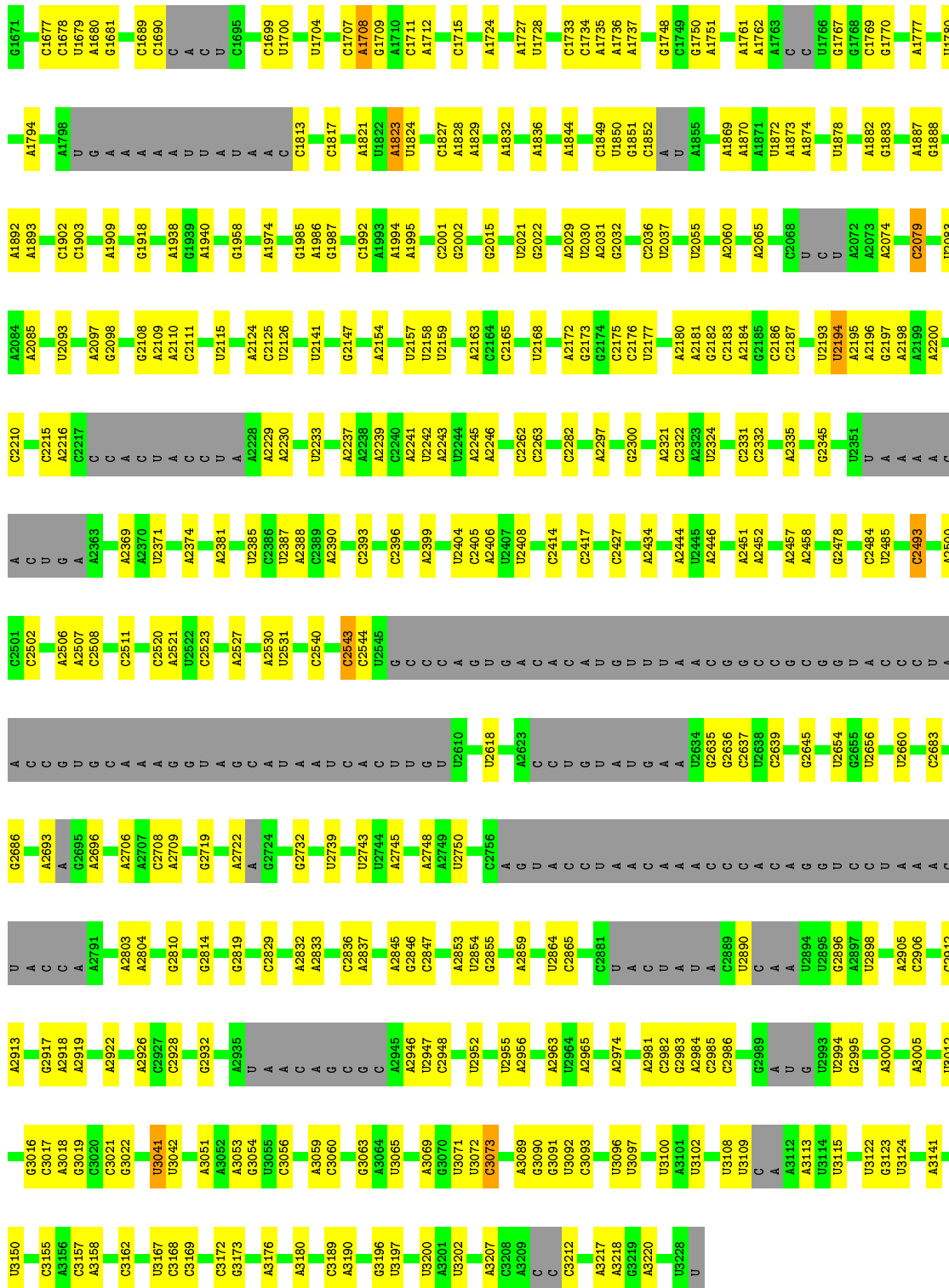
ILE  
THR  
LYS  
VAL  
TYR  
THR  
GLN  
VAL  
GLU  
PHE  
LYS  
ARG

- Molecule 10: 39S ribosomal protein L41, mitochondrial

Chain 9: 85% 15%

MET  
GLY  
VAL  
LEU  
ALA  
ALA  
ALA  
CYS  
LEU  
VAL  
ARG  
GLY  
A15  
D106  
GLY  
THR  
PHE  
ASP  
PRO  
ASP  
H143  
H137

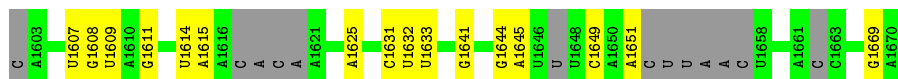
- Molecule 11: 16S ribosomal RNA



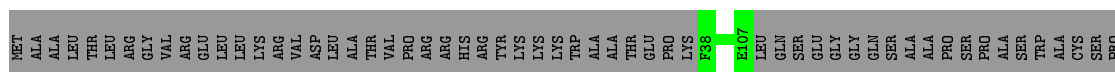
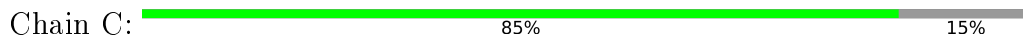
• Molecule 12: mitochondrial tRNA<sup>Val</sup>



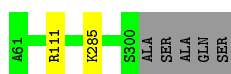
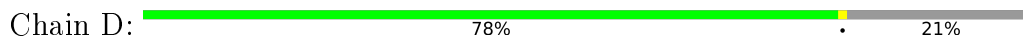




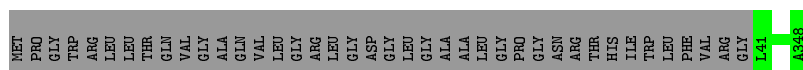
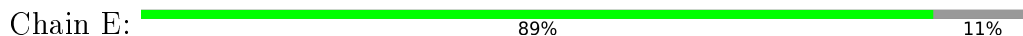
- Molecule 13: 5-methylcytosine rRNA methyltransferase NSUN4



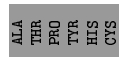
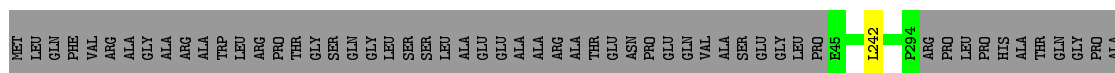
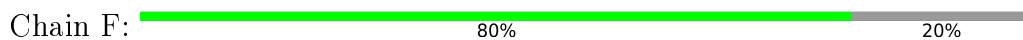
- Molecule 14: 39S ribosomal protein L2, mitochondrial



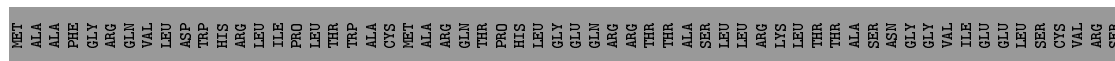
- Molecule 15: 39S ribosomal protein L3, mitochondrial



- Molecule 16: 39S ribosomal protein L4, mitochondrial



- Molecule 17: Transcription termination factor 4, mitochondrial

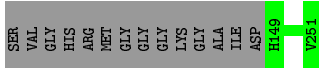







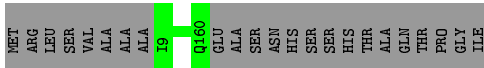
- Molecule 24: 39S ribosomal protein L16, mitochondrial

Chain N:  73% 27%




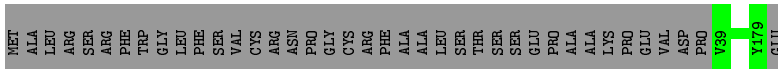
- Molecule 25: 39S ribosomal protein L17, mitochondrial

Chain O:  87% 13%



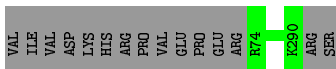
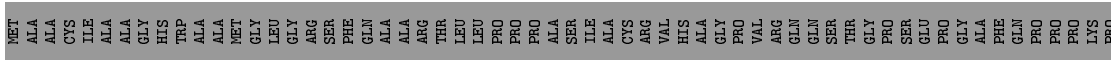
- Molecule 26: 39S ribosomal protein L18, mitochondrial

Chain P:  78% 22%




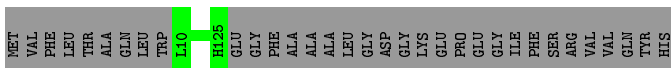
- Molecule 27: 39S ribosomal protein L19, mitochondrial

Chain Q:  74% 26%




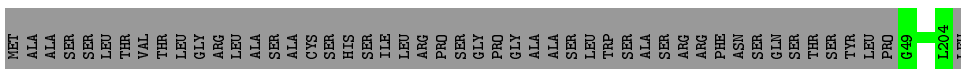
- Molecule 28: 39S ribosomal protein L20, mitochondrial

Chain R:  78% 22%



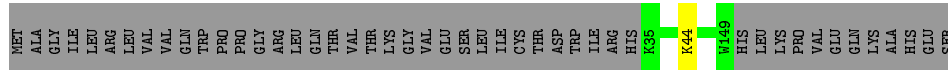
- Molecule 29: 39S ribosomal protein L21, mitochondrial

Chain S:  76% 24%



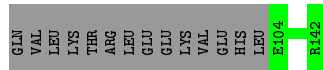


Chain Z:  71% 29%



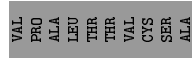
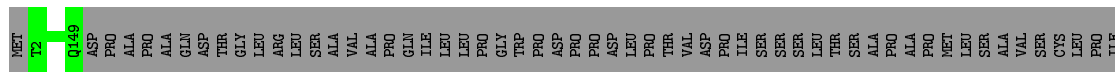
- Molecule 37: 39S ribosomal protein L42, mitochondrial

Chain a:  50% 50%




- Molecule 38: 39S ribosomal protein L43, mitochondrial

Chain b:  69% 31%



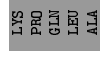
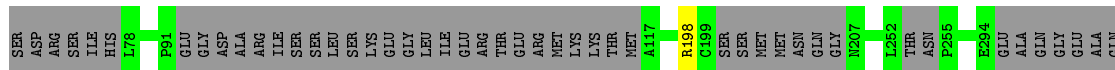
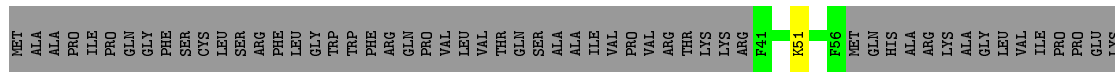
- Molecule 39: 39S ribosomal protein L44, mitochondrial

Chain c:  83% 17%



- Molecule 40: 39S ribosomal protein L45, mitochondrial

Chain d:  64% 35%



- Molecule 41: 39S ribosomal protein L46, mitochondrial

Chain e:  71% 29%



MET ALA ALA ALA ALA LEU LEU ALA ARG LEU LEU ARG ARG ARG PRO V43 R56 HIS ASP GLY SER E51 R73 ARG ARG ASP ALA ALA GLY SER SER GLY ASP PRO GLY ALA ASP THR ARG


- Molecule 48: 39S ribosomal protein L55, mitochondrial

Chain m:  23% 77%

MET ALA ALA VAL ARG SER LEU LEU LEU LYS LEU ARG ARG GLN SER THR R56 HIS VAL LYS ASP GLY THR R73 ARG ARG ARG LEU HIS THR SER SER TRP ARG ALA LYS ASP THR R50 F78 ILE ASP LEU ASP THR LEU SER PRO

GLU ARG ALA ARG LEU ARG LYS LEU ALA GLN LEU LYS THR TYR GLU ALA GLN LEU ARG ASP LEU ASP HIS THR SER VAL GLU ARG TYR ARG ALA SER PHE THR ARG THR LYS

- Molecule 49: Ribosomal protein 63, mitochondrial

Chain o:  78% 22%

MET PHE LEU THR ALA LEU TRP ARG GLY ARG ILE PRO GLY ARG GLN TRP ILE ILE GLY HIS R23 R23 S102

- Molecule 50: Peptidyl-tRNA hydrolase ICT1, mitochondrial

Chain p:  62% 38%

MET ALA THR ARG CYS LEU TRP GLY SER ARG ALA VAL TRP LEU LEU PRO PRO PRO ALA ARG CYS PRO ARG ARG ALA LEU HIS LYS LYS ASP GLY THR E38 V61 PRO ASN GLY ALA LYS GLN ALA ASP SER I70 S83 SER GLY PRO GLY GLN ASN VAL

ASN LYS V95 G163 THR PRO LYS PRO THR LYS ASP VAL R174 I193 HIS SER ALA VAL LYS THR SER ARG ARG ASP MET ASP

- Molecule 51: Growth arrest and DNA damage-inducible proteins-interacting protein 1

Chain q:  58% 42%

MET ALA SER VAL ARG GLN ALA ARG ARG LEU LEU VAL VAL ALA THR LEU ALA PRO GLY SER VAL Y25 R152 ARG ALA ARG ARG LEU GLN ALA GLU GLN LEU LEU TYR GLN VAL ASP PRO ARG SER ALA ARG ARG PHE GLN LEU LEU GLN ASP LEU LEU LYS LYS THR T47 T47 R134 LEU PRO GLY VAL VAL GLN PRO LYS SER LYS ASP G146 H196


GLU ARG LYS ARG LEU LYS GLU GLU LYS LYS LYS ARG GLY VAL ALA THR LEU ALA PRO GLY SER ALA VAL LYS VAL VAL GLN ASP PRO ALA ALA SER

- Molecule 52: 39S ribosomal protein S18a, mitochondrial

Chain r:  74% 26%

MET ALA LEU LYS ALA LEU VAL SER GLY ARG LEU LEU ARG GLY LEU ALA LEU ALA PRO GLY PRO ARG LEU PRO ALA ARG GLY F35 T41 T41 GLN GLY LYS THR T47 T47 R134 LEU PRO GLY VAL VAL PRO LYS SER LYS ASP G146 H196

- Molecule 53: 39S ribosomal protein S30, mitochondrial

Chain s:  84% 16%





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	1060638	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	36	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	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: MG, ZN

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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	0	0.33	0/895	0.53	0/1201
2	1	0.24	0/438	0.54	0/583
3	2	0.37	0/373	0.57	0/496
4	3	0.39	0/852	0.53	0/1136
5	4	0.36	0/341	0.57	0/451
6	5	0.32	0/3294	0.50	0/4488
7	6	0.31	0/2809	0.53	0/3818
8	7	0.30	0/2391	0.47	0/3234
9	8	0.25	0/665	0.49	0/894
10	9	0.34	0/972	0.49	0/1306
11	A	0.65	0/32679	0.83	23/50833 (0.0%)
12	B	0.22	0/1328	0.76	0/2056
13	C	0.25	0/2655	0.49	0/3601
14	D	0.34	0/1910	0.57	0/2569
15	E	0.38	0/2497	0.49	0/3386
16	F	0.37	0/2071	0.52	0/2817
17	G	0.27	0/1974	0.47	0/2652
18	H	0.31	0/798	0.53	0/1073
19	I	0.26	0/1252	0.50	0/1686
20	J	0.24	0/1077	0.50	0/1452
21	K	0.38	0/1495	0.49	0/2029
22	L	0.33	0/904	0.55	0/1218
23	M	0.37	0/2359	0.53	0/3185
24	N	0.28	0/1533	0.52	0/2061
25	O	0.34	0/1269	0.54	0/1708
26	P	0.30	0/1173	0.53	0/1588
27	Q	0.34	0/1846	0.51	0/2487
28	R	0.40	0/987	0.56	0/1320
29	S	0.36	0/1276	0.54	0/1729
30	T	0.40	0/1402	0.51	0/1886
31	U	0.37	0/1183	0.55	0/1600
32	V	0.33	0/404	0.44	0/545

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	W	0.38	0/823	0.50	0/1113
34	X	0.34	0/2090	0.47	0/2825
35	Y	0.34	0/1552	0.50	0/2079
36	Z	0.32	0/960	0.49	0/1295
37	a	0.36	0/616	0.50	0/833
38	b	0.36	0/1202	0.57	0/1626
39	c	0.33	0/2264	0.48	0/3059
40	d	0.26	0/1702	0.47	0/2307
41	e	0.24	0/1633	0.50	0/2204
42	f	0.27	0/873	0.44	0/1180
43	g	0.38	0/1102	0.51	0/1503
44	h	0.27	0/884	0.47	0/1203
45	i	0.39	0/849	0.54	0/1135
46	j	0.31	0/698	0.50	0/940
47	k	0.25	0/635	0.54	0/855
48	m	0.23	0/250	0.64	0/336
49	o	0.33	0/693	0.52	0/931
50	p	0.27	0/1071	0.52	0/1433
51	q	0.28	0/1107	0.50	0/1498
52	r	0.33	0/1238	0.52	0/1676
53	s	0.37	0/3114	0.52	0/4225
54	u	0.29	0/949	0.51	0/1281
55	v	0.26	0/597	0.60	0/796
56	w	0.25	0/647	0.46	0/871
All	All	0.45	0/104651	0.64	23/148292 (0.0%)

There are no bond length outliers.

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	A	2523	C	C2-N1-C1'	8.72	128.40	118.80
11	A	2523	C	N1-C2-O2	7.99	123.70	118.90
11	A	2523	C	N3-C2-O2	-6.47	117.37	121.90
11	A	2543	C	C2'-C3'-O3'	6.43	123.99	113.70
11	A	2523	C	C6-N1-C1'	-6.22	113.33	120.80

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	106/188 (56%)	104 (98%)	2 (2%)	0	100	100
2	1	50/65 (77%)	48 (96%)	2 (4%)	0	100	100
3	2	43/92 (47%)	42 (98%)	1 (2%)	0	100	100
4	3	93/188 (50%)	91 (98%)	2 (2%)	0	100	100
5	4	35/103 (34%)	34 (97%)	1 (3%)	0	100	100
6	5	390/423 (92%)	382 (98%)	8 (2%)	0	100	100
7	6	316/380 (83%)	305 (96%)	11 (4%)	0	100	100
8	7	285/338 (84%)	271 (95%)	14 (5%)	0	100	100
9	8	75/206 (36%)	73 (97%)	2 (3%)	0	100	100
10	9	113/137 (82%)	111 (98%)	2 (2%)	0	100	100
13	C	324/384 (84%)	312 (96%)	12 (4%)	0	100	100
14	D	238/305 (78%)	230 (97%)	8 (3%)	0	100	100
15	E	306/348 (88%)	300 (98%)	6 (2%)	0	100	100
16	F	248/311 (80%)	245 (99%)	3 (1%)	0	100	100
17	G	236/381 (62%)	227 (96%)	9 (4%)	0	100	100
18	H	93/267 (35%)	88 (95%)	5 (5%)	0	100	100
19	I	147/261 (56%)	140 (95%)	7 (5%)	0	100	100
20	J	138/192 (72%)	132 (96%)	6 (4%)	0	100	100
21	K	175/178 (98%)	172 (98%)	3 (2%)	0	100	100
22	L	113/145 (78%)	112 (99%)	1 (1%)	0	100	100
23	M	285/296 (96%)	282 (99%)	3 (1%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	N	177/251 (70%)	174 (98%)	3 (2%)	0	100	100
25	O	150/175 (86%)	146 (97%)	4 (3%)	0	100	100
26	P	139/180 (77%)	132 (95%)	7 (5%)	0	100	100
27	Q	215/292 (74%)	211 (98%)	4 (2%)	0	100	100
28	R	114/149 (76%)	113 (99%)	1 (1%)	0	100	100
29	S	154/205 (75%)	151 (98%)	3 (2%)	0	100	100
30	T	164/206 (80%)	162 (99%)	2 (1%)	0	100	100
31	U	135/153 (88%)	134 (99%)	1 (1%)	0	100	100
32	V	45/216 (21%)	44 (98%)	1 (2%)	0	100	100
33	W	98/148 (66%)	98 (100%)	0	0	100	100
34	X	241/256 (94%)	238 (99%)	3 (1%)	0	100	100
35	Y	174/250 (70%)	171 (98%)	3 (2%)	0	100	100
36	Z	113/161 (70%)	111 (98%)	2 (2%)	0	100	100
37	a	67/142 (47%)	67 (100%)	0	0	100	100
38	b	146/215 (68%)	141 (97%)	5 (3%)	0	100	100
39	c	271/332 (82%)	268 (99%)	3 (1%)	0	100	100
40	d	189/306 (62%)	186 (98%)	3 (2%)	0	100	100
41	e	191/279 (68%)	175 (92%)	16 (8%)	0	100	100
42	f	102/212 (48%)	92 (90%)	10 (10%)	0	100	100
43	g	127/166 (76%)	121 (95%)	6 (5%)	0	100	100
44	h	101/158 (64%)	98 (97%)	3 (3%)	0	100	100
45	i	95/128 (74%)	94 (99%)	1 (1%)	0	100	100
46	j	83/123 (68%)	82 (99%)	1 (1%)	0	100	100
47	k	76/112 (68%)	71 (93%)	5 (7%)	0	100	100
48	m	27/128 (21%)	19 (70%)	8 (30%)	0	100	100
49	o	78/102 (76%)	78 (100%)	0	0	100	100
50	p	119/206 (58%)	116 (98%)	3 (2%)	0	100	100
51	q	126/222 (57%)	126 (100%)	0	0	100	100
52	r	140/196 (71%)	136 (97%)	4 (3%)	0	100	100
53	s	366/439 (83%)	363 (99%)	3 (1%)	0	100	100
54	u	109/234 (47%)	103 (94%)	6 (6%)	0	100	100

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
55	v	67/70 (96%)	66 (98%)	1 (2%)	0	100	100
56	w	77/156 (49%)	70 (91%)	7 (9%)	0	100	100
All	All	8285/11756 (70%)	8058 (97%)	227 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	97/164 (59%)	97 (100%)	0	100	100
2	1	49/60 (82%)	49 (100%)	0	100	100
3	2	39/72 (54%)	39 (100%)	0	100	100
4	3	88/166 (53%)	88 (100%)	0	100	100
5	4	36/89 (40%)	36 (100%)	0	100	100
6	5	353/368 (96%)	351 (99%)	2 (1%)	86	93
7	6	286/332 (86%)	285 (100%)	1 (0%)	92	97
8	7	263/303 (87%)	258 (98%)	5 (2%)	57	71
9	8	70/190 (37%)	70 (100%)	0	100	100
10	9	99/112 (88%)	99 (100%)	0	100	100
13	C	284/328 (87%)	284 (100%)	0	100	100
14	D	194/245 (79%)	192 (99%)	2 (1%)	76	86
15	E	262/290 (90%)	262 (100%)	0	100	100
16	F	217/262 (83%)	216 (100%)	1 (0%)	88	94
17	G	221/350 (63%)	221 (100%)	0	100	100
18	H	86/228 (38%)	85 (99%)	1 (1%)	71	83
19	I	139/232 (60%)	139 (100%)	0	100	100
20	J	113/150 (75%)	113 (100%)	0	100	100
21	K	155/156 (99%)	155 (100%)	0	100	100

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	L	98/124 (79%)	97 (99%)	1 (1%)	76	86
23	M	245/249 (98%)	244 (100%)	1 (0%)	91	96
24	N	156/211 (74%)	156 (100%)	0	100	100
25	O	133/150 (89%)	133 (100%)	0	100	100
26	P	123/155 (79%)	123 (100%)	0	100	100
27	Q	199/256 (78%)	199 (100%)	0	100	100
28	R	101/126 (80%)	101 (100%)	0	100	100
29	S	141/180 (78%)	141 (100%)	0	100	100
30	T	146/176 (83%)	146 (100%)	0	100	100
31	U	124/135 (92%)	124 (100%)	0	100	100
32	V	43/191 (22%)	43 (100%)	0	100	100
33	W	83/119 (70%)	83 (100%)	0	100	100
34	X	219/229 (96%)	218 (100%)	1 (0%)	88	94
35	Y	159/223 (71%)	159 (100%)	0	100	100
36	Z	106/147 (72%)	105 (99%)	1 (1%)	78	88
37	a	67/133 (50%)	67 (100%)	0	100	100
38	b	130/186 (70%)	130 (100%)	0	100	100
39	c	241/288 (84%)	241 (100%)	0	100	100
40	d	184/274 (67%)	182 (99%)	2 (1%)	73	85
41	e	171/236 (72%)	171 (100%)	0	100	100
42	f	95/188 (50%)	95 (100%)	0	100	100
43	g	119/148 (80%)	118 (99%)	1 (1%)	81	90
44	h	100/148 (68%)	100 (100%)	0	100	100
45	i	86/110 (78%)	86 (100%)	0	100	100
46	j	68/97 (70%)	68 (100%)	0	100	100
47	k	71/90 (79%)	70 (99%)	1 (1%)	67	80
48	m	27/113 (24%)	27 (100%)	0	100	100
49	o	69/87 (79%)	69 (100%)	0	100	100
50	p	117/181 (65%)	117 (100%)	0	100	100
51	q	110/178 (62%)	110 (100%)	0	100	100
52	r	133/169 (79%)	133 (100%)	0	100	100

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	s	326/381 (86%)	325 (100%)	1 (0%)	92	97
54	u	105/200 (52%)	105 (100%)	0	100	100
55	v	59/60 (98%)	57 (97%)	2 (3%)	37	47
56	w	73/136 (54%)	72 (99%)	1 (1%)	67	80
All	All	7478/10171 (74%)	7454 (100%)	24 (0%)	92	97

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
34	X	23	ARG
40	d	198	ARG
40	d	51	LYS
43	g	91	MET
8	7	234	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
41	e	212	HIS
38	b	58	ASN
16	F	241	ASN
14	D	271	ASN
29	S	118	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	A	1357/1559 (87%)	323 (23%)	17 (1%)
12	B	51/69 (73%)	16 (31%)	1 (1%)
All	All	1408/1628 (86%)	339 (24%)	18 (1%)

5 of 339 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	A	1677	C
11	A	1678	C
11	A	1679	U
11	A	1680	A
11	A	1681	G



5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	A	3072	U
12	B	1607	U
11	A	3196	G
11	A	2530	A
11	A	3041	U

#### 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](#)

Of 64 ligands modelled in this entry, 64 are monoatomic - 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.

#### 5.7 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 Map visualisation

This section contains visualisations of the EMDB entry EMD-12865. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections

This section was not generated.

### 6.2 Central slices

This section was not generated.

### 6.3 Largest variance slices

This section was not generated.

### 6.4 Orthogonal surface views

This section was not generated.

### 6.5 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

## 7 Map analysis

This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution

This section was not generated.

### 7.2 Volume estimate versus contour level

This section was not generated.

### 7.3 Rotationally averaged power spectrum

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

## 9 Map-model fit

This section was not generated.