

wwPDB EM Validation Summary Report (i)

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EMDB ID	:	EMD-2566
Title	:	Structure of the yeast mitochondrial large ribosomal subunit
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Deposited on	:	2014-01-22
Resolution	:	3.20 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB 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 (1)) were used in the production of this report:

:	0.0.1.dev70
:	4.02b-467
:	20191225.v01 (using entries in the PDB archive December 25th 2019)
:	1.9.9
:	Engh & Huber (2001)
:	Parkinson et al. (1996)
:	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 3.20 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	EM structures		
	(# Entries)	(#Entries)		
Clashscore	158937	4297		
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 $\leq=5\%$ The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain									
1	А	3296	48% 26%	8% 18%								
2	В	393	• 55% 18	• 25%								
3	С	269	74%	16% • 7%								
4	D	286	62%	18% • 16%								
5	Е	292	78%	15% • 6%								
6	F	214	66%	17% • 14%								
7	G	139	35% 5%	60%								



Mol	Chain	Length	Quality of chain							
8	Н	163	74% 14% •• 9%							
9	Ι	138	80% 10% • 9%							
10	J	322	57% 9% • 32%							
11	K	232	66% 15% • 16%							
12	L	238	81% 13% • •							
13	М	169	73% 13% •• 11%							
14	Ν	161	65% 9% 27%							
15	О	309	57% 14% • 28%							
16	Р	263	60% 17% • 21%							
17	Q	297	• 79% 13% • 6%							
18	R	371	68% 16% · 14%							
19	S	258	46% 10% • 43%							
20	Т	319	5 3% 11% • 34%							
21	U	86	84% 12% 5%							
22	V	177	34% • 64%							
23	W	183	48% 12% • 39%							
24	X	70	79% 11% • 9%							
25	Y	105	35% 6% • 57%							
26	Z	115	45% 7% • 46%							
27	0	93	38% • 59%							
28	1	367	74% 15% · 10%							
29	2	147	61% 14% · 23%							
30	3	146	75% 11% 14%							
31	4	140	77%							
32	5	390	69% 13% · 16%							

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Mol	Chain	Length	Quality of c	hain
33	6	281	62%	11% · 26%
34	7	146	53%	19% • 27%
35	8	264	58%	10% • 31%
36	9	253	62%	13% · 23%
37	a	195	77%	12% • 10%
38	b	157	84%	14% •••
39	с	131	84%	6% 10%
40	d	226	78%	12% 10%
41	е	20	70% 	35%

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The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
44	ZN	0	100	-	-	Х	-



2 Entry composition (i)

There are 44 unique types of molecules in this entry. The entry contains 195137 atoms, of which 83818 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 21S ribosomal RNA.

Mol	Chain	Residues				AltConf	Trace			
1	А	2713	Total 86569	C 25948	H 28898	N 10265	0 18752	Р 2706	0	0

• Molecule 2 is a protein called 54S ribosomal protein RML2, mitochondrial.

Mol	Chain	Residues			AltConf	Trace				
2	В	295	Total 4603	C 1405	Н 2343	N 459	0 387	S 9	0	0

• Molecule 3 is a protein called 54S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues			AltConf	Trace				
3	С	249	Total 3906	C 1217	Н 1976	N 360	0 343	S 10	0	0

• Molecule 4 is a protein called 54S ribosomal protein YmL6, mitochondrial.

Mol	Chain	Residues			AltConf	Trace				
4	D	239	Total 3780	C 1187	Н 1914	N 337	O 339	${ m S} { m 3}$	0	0

• Molecule 5 is a protein called 54S ribosomal protein L7, mitochondrial.

Mol	Chain	Residues			AltConf	Trace				
5	Е	274	Total 4294	C 1363	Н 2169	N 387	O 369	S 6	0	0

• Molecule 6 is a protein called 54S ribosomal protein L6, mitochondrial.

Mol	Chain	Residues			Atom	S			AltConf	Trace
6	F	185	Total 2747	C 870	Н 1392	N 236	0 246	${ m S} { m 3}$	0	0



• Molecule 7 is a protein called 54S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues		A	Atoms	5			AltConf	Trace
7	G	55	Total 929	C 293	Н 471	N 86	O 78	S 1	0	0

• Molecule 8 is a protein called 54S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues			Atom	.s			AltConf	Trace
8	Н	148	Total 2394	С 742	Н 1218	N 225	O 205	${S \over 4}$	0	0

• Molecule 9 is a protein called 54S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues			Aton	ıs			AltConf	Trace
9	Ι	125	Total 1952	C 583	Н 1015	N 175	O 168	S 11	0	0

• Molecule 10 is a protein called 54S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues			Atoms	5			AltConf	Trace
10	J	220	$\begin{array}{c} \text{Total} \\ 3555 \end{array}$	C 1109	H 1828	N 325	O 290	${ m S} { m 3}$	0	0

• Molecule 11 is a protein called 54S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues			Atom	5			AltConf	Trace
11	K	195	Total 3208	C 1001	Н 1635	N 297	O 270	${f S}{5}$	0	0

• Molecule 12 is a protein called 54S ribosomal protein L8, mitochondrial.

Mol	Chain	Residues			Atoms	5			AltConf	Trace
12	L	229	Total	C	H	N	0	S	0	0
			3698	1139	1883	333	335	8		

• Molecule 13 is a protein called 54S ribosomal protein IMG1, mitochondrial.

Mol	Chain	Residues			Atom	S			AltConf	Trace
13	М	151	Total 2492	C 766	Н 1286	N 220	0 217	${ m S} { m 3}$	0	0

• Molecule 14 is a protein called 54S ribosomal protein L49, mitochondrial.



Mol	Chain	Residues			Atom	S			AltConf	Trace
14	Ν	118	Total 1958	C 598	Н 1010	N 177	0 171	${ m S} { m 2}$	0	0

• Molecule 15 is a protein called 54S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues			Atom	s			AltConf	Trace
15	0	223	Total 3684	C 1147	Н 1895	N 328	O 309	${ m S}{ m 5}$	0	0

• Molecule 16 is a protein called 54S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues			Atoms	5			AltConf	Trace
16	Р	207	Total 3450	C 1101	Н 1728	N 310	O 305	${ m S}{ m 6}$	0	0

• Molecule 17 is a protein called 54S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues			Atoms	5			AltConf	Trace
17	Q	279	Total 4287	C 1368	Н 2161	N 375	O 375	S 8	0	0

• Molecule 18 is a protein called 54S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues			Atoms	5			AltConf	Trace
18	R	318	Total 4981	C 1571	Н 2500	N 452	0 454	${S \atop 4}$	0	0

• Molecule 19 is a protein called 54S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues			Atom	.s			AltConf	Trace
19	S	146	Total 2440	C 763	Н 1249	N 220	O 207	S 1	0	0

• Molecule 20 is a protein called 54S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues			AltConf	Trace				
20	Т	209	Total 3264	C 1044	Н 1618	N 307	O 292	${ m S} { m 3}$	0	0

• Molecule 21 is a protein called 54S ribosomal protein L33, mitochondrial.



Mol	Chain	Residues		Α	toms			AltConf	Trace
21	U	82	Total 1341	C 410	Н 702	N 116	0 113	0	0

• Molecule 22 is a protein called 54S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues			AltConf	Trace				
22	V	64	Total 1083	C 332	Н 555	N 105	O 90	S 1	0	0

• Molecule 23 is a protein called 54S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues			AltConf	Trace				
23	W	112	Total 1922	C 587	Н 985	N 181	O 163	S 6	0	0

• Molecule 24 is a protein called 54S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
24	Х	64	Total 1077	C 330	Н 565	N 96	O 86	0	0

• Molecule 25 is a protein called 54S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
25	Y	45	Total 788	C 239	Н 412	N 80	O 57	0	0

• Molecule 26 is a protein called mitochondrial ribosomal protein YNL122C.

Mol	Chain	Residues		_	Atom	S			AltConf	Trace
26	Z	62	Total 1054	C 322	Н 546	N 111	0 74	S 1	0	0

• Molecule 27 is a protein called 54S ribosomal protein RTC6, mitochondrial.

Mol	Chain	Residues		A	AltConf	Trace				
27	0	38	Total 673	C 205	Н 349	N 66	O 50	${ m S} { m 3}$	0	0

• Molecule 28 is a protein called 54S ribosomal protein L35, mitochondrial.



Mol	Chain	Residues			Atom	5			AltConf	Trace
28	1	332	Total 5397	C 1744	Н 2690	N 467	O 490	S 6	0	0

• Molecule 29 is a protein called 54S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues			AltConf	Trace				
29	2	113	Total 1858	C 583	Н 939	N 169	0 162	${ m S}{ m 5}$	0	0

• Molecule 30 is a protein called 54S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues			AltConf	Trace				
30	3	126	Total 2025	C 643	Н 1030	N 181	0 168	${ m S} { m 3}$	0	0

• Molecule 31 is a protein called 54S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues			Atom	S			AltConf	Trace
31	4	138	Total 2263	C 700	Н 1146	N 219	0 193	${ m S}{ m 5}$	0	0

• Molecule 32 is a protein called 54S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues			Atom	S			AltConf	Trace
32	5	326	Total 5026	C 1596	Н 2541	N 425	O 453	S 11	0	0

• Molecule 33 is a protein called 54S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues			Atom	S			AltConf	Trace
33	6	209	Total 3187	C 1046	H 1595	N 273	0 271	${ m S} { m 2}$	0	0

• Molecule 34 is a protein called 54S ribosomal protein IMG2, mitochondrial.

Mol	Chain	Residues			ns		AltConf	Trace		
34	7	106	Total 1755	C 550	Н 901	N 150	0 152	${S \over 2}$	0	0

• Molecule 35 is a protein called 54S ribosomal protein L13, mitochondrial.



Mol	Chain	Residues			Atom	S			AltConf	Trace
35	8	182	Total 2829	C 898	Н 1416	N 241	0 271	${ m S} { m 3}$	0	0

• Molecule 36 is a protein called 54S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues			AltConf	Trace				
36	9	195	Total 2865	C 919	Н 1437	N 250	O 254	${ m S}{ m 5}$	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
9	169	GLY	ASP	conflict	UNP P36523

• Molecule 37 is a protein called 54S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues			Atom	.s			AltConf	Trace
37	a	176	Total 2882	C 898	Н 1455	N 264	O 259	S 6	0	0

• Molecule 38 is a protein called 54S ribosomal protein L25, mitochondrial.

Mol	Chain	Residues			Atom	.s			AltConf	Trace
38	h	155	Total	С	Η	Ν	Ο	\mathbf{S}	0	0
00	U	100	2671	850	1372	225	221	3	0	0

• Molecule 39 is a protein called 54S ribosomal protein L31, mitochondrial.

Mol	Chain	Residues			Atom	.s			AltConf	Trace
39	С	118	Total 2066	C 643	H 1066	N 190	0 163	$\frac{S}{4}$	0	0

• Molecule 40 is a protein called Mitochondrial homologous recombination protein 1.

Mol	Chain	Residues			Atom	5			AltConf	Trace
40	d	204	Total	C	H 1706	N 212	0	S	0	0
			3423	1099	1700	313	299	0		

• Molecule 41 is a RNA chain called E-site tRNA.



Mol	Chain	Residues	Atoms			AltConf	Trace			
41	е	20	Total 648	C 191	Н 221	N 81	0 136	Р 19	0	0

• Molecule 42 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
42	А	109	Total Mg 109 109	0
42	Ν	1	Total Mg 1 1	0

• Molecule 43 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	AltConf
43	В	1	Total Na 1 1	0

• Molecule 44 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
44	W	1	Total Zn 1 1	0
44	0	1	Total Zn 1 1	0



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 and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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: 21S ribosomal RNA















LIEU LIEU LITE LITE LITE PILE PILE ASP ASP CIU LITS CIU CIU CIU CIU CIU CIU CIU CIU CIU CIU	101 105 105 105 105 105 110 110 110 110	Cl 45 Rl 49 Rl 49 Rl 51 Rl 53 Rl 55 Rl 55 Rl 55 Rl 55 Rl 56 Rl 57 Rl 56 Rl 57 Rl 56 Rl 57 Rl 56 Rl 56
1180 1183 1193 1194 1195 1195 1197 1197 1197 1197 1197 1197	LEU LEU ASN GLY GLY GLY GLY CLY GLY CLY ASP ASP ASP ASP ASP ASP ASP CLY CLY CLY CLY CLY CLY CLY CLY CLY CLY	1246 1250 1253 1255 1255 1255 1255 1255 1255 1255
1286 H294 H294 1295 1299 1296 1290 1311 1311 1311 1311 1311 1311 1311 13	R330 R330 R334 R334 R339 R339 R339 R336 R351 R351 R355 R355 R355 R355 R355 R355	K375 K376 Q377 N378 N378 K381 K381 K382 K383 R385 R385 R385 R385 R385 R385 R385 R
• Molecule 3: 54S ribosoma	l protein L9, mitochondrial	
Chain C:	74%	16% • 7%
MET SER SER FHE FHE LFU CLU CLU CLU CLU CLU CLU CLU CLU CLU CL	444 H44 K53 K53 K53 K53 K53 C59 C59 C59 C59 C59 C59 C59 C50 C59 C50 C59 C50 C59 C50 C59 C50 C59 C50 C59 C50 C50 C50 C50 C50 C50 C50 C50 C50 C50	873 873 865 V87 V865 V87 N88 N894 M94 M94 M94 C106 C106 C106 C106 C116 C116 C116 C116
R120 M221 M222 M123 K134 K134 K138 F153 F153 F153 F153 F156 F160 F166 R169	K175 H193 H197 1197 207 N206 0209 0209 0210 0211 2211 7213 R213 R213 R213 R213 R213	1239 1240 A253 1268
• Molecule 4: 54S ribosoma	l protein YmL6, mitochond	lrial
Chain D:	62%	18% · 16%
MET THR THR LYS LYS ARG ASN ASN ASN ASN CLU CLU CLU CLU CLU CLU CLU CLU CLU CLU	THR THR ALA ALA ALA ALA CLU CLU CLU CLU CLU ASN T45 F50 F50 F50 F50	V65 V65 R70 L74 W75 W175 M106 M106 M106 A119 A119
1133 1134 1135 1136 1136 1136 1143 1143 1168 1168 1168 1168 1168 1168 1168 116	L182 L184 L184 L184 L184 L189 L189 L189 L189 L189 L189 L189 L189 L189 L189 L189 L186 L186 L186 L186 L184 L186 L	P204 P205 P210 P211 P215 P216 P216 P220 P238
V245 1246 7247 8247 8247 8247 8247 8247 8253 V253 1257 1257 8264 8264 8264 8264 8264 1257 8264 8264 8264 8264 8264 8264 8264 8264	E279 ILE HEU HES SER SER ASN	
• Molecule 5: 54S ribosoma	l protein L7, mitochondrial	
Chain E:	78%	15% • 6%
MET AGC AGC AGC AGC AGC AGC AGC AGC AGC AGC	221 H30 135 135 135 135 135 135 135 135 135 135	134 188 188 198 196 196 196 196 10 10 10 11 10 11 10 11 14 11 14 11 14
L161 L163 L163 L163 L163 L163 K170 V180 V183 H189 H189 H189 H189 K198 K198 K198 K198 K198 K198 K198 K	204 201 2211 1217 1217 2220 6222 6222 7269 7274 7274 7278	1279 1280 1288
• Molecule 6: 54S ribosoma	l protein L6, mitochondrial	
Chain F:	66%	17% • 14%
MET PHEE PHEE TLE CLE ARG ARG ARG CLN ARG CLEU HEE LEU ARC CLEA ARC CLEA ARC CLEA ARC	125 827 827 828 829 828 829 828 833 134 154 154 157 157 157 157 166	866 167 167 167 173 173 174 174 174 174 174 174 174 174 174 174



• Molecule 7: 54S ribosomal protein L50, mitochondrial

Chain G:	35%	5%	60%	
MET LEU HIS HIS CYS CYS CYS CYS CYS CYS CYS CYS CYS CY	K34 L44 M45 L49 Y57	ILE ASN THR GLU CLU LEU LEU LEU CLN GLN THR THR	GLU ALA LYS LYS LEU GLU GLU ASP HIS GLN GLN	LEU LEU SER SER SER ARG HIS HIS CLU CLU CLU CLU CLU CLU CLU CLU CLU
LEU ARG LYS GLU SER VAL PHE CLV CLV GLV GLU GLU	PRD PRD LYS GLU GLU GLU CYS GLY LEU LEU LEU LEU	SER SER GLY THR ILE CLU GLU GLU CLU CLU CLU CLV	ASP ILEU	
• Molecule 8: 54S	ribosomal pro	otein L23, mitoch	nondrial	
Chain H:		74%		14% •• 9%
MET S2 L15 115 127 127 138 137 138	L58 R42 G54 G55 Y56 V59	T60 463 463 463 468 83 883 883	F101 6102 M112 K117 L123	D124 N128 V128 N128 S149 TLE FLC FLU FLC FLU
LYS GLU SER TLE PHE ASN GLN LYS LYS				
• Molecule 9: 54S	ribosomal pro	tein L38, mitoch	nondrial	
Chain I:		80%		10% • 9%
M1 12 13 14 14 11 11 11 11 12 11 11 11	A04 K48 THR LEU GLN ASN ILE THR THR	THR THR ALA ASN ASN ASN ASN V74 V74 K79	1115 1115 1129 1138 1138	
• Molecule 10: 545	S ribosomal pr	otein L10, mitoo	chondrial	
Chain J:	57%		9% •	32%
MET LYS LYS ALA GLU ALC GLV CLN CLN CLN CLN SER SER SER SER	THR VAL THR VAL ILE GLY GLY CAS LYS LEU LEU ASN ASN	PHE VAL PRO SER MET MET LEU THR SER VAL VAL	ALI ASP TLE PHE PHE ARG GLY LEU	LYS PRO VAL VAL LEU ALA GLN SER TYR TYR TYR TYR TYR TGO
P66 K72 R79 899 891 891 892 892 892 892	485 A98 R103 E107 Y114	E132 L133 L133 R146 R146 E153 E153 W156	R161 L165 F182 N185	L190 1216 N225 R233 R238 R238 R238 R245 R245 R245 R245
E263 K266 Q269 Q269 CLY SER ARG H1S FHE	LEU LYS GLN ASN VAL LYS SER SER SER SER CIU	111 CLU CLU CLU CLU CLU CLU CLU SER SER SER SER SER CLU CLU CLU CLU CLU CLU CLU CLU CLU CLU	VAL PRO VAL VAL SER ASN SER LYS VAL	ASN ILLE LLEU LEU HLS HLS
• Molecule 11: 54	5 ribosomal pr	otein L16, mitoo	chondrial	
Chain K:	669	6	15%	• 16%
MET PHE PRO TYR TYR LEU ASN MET ASN LEU SER LLF	ML I GLY GLY THR LEU LYS GLU SER SER SER	ALA ALA ALA ALA LEU LEU ASN ASN ALA ALA ALA	PHE K33 R33 R44 R55 R55 R59	S63 164 169 171 175 175 175 175 175 175 175 175 176 170 170 170



• Molecule 12: 54S ribosomal protein L8, mitochondrial

Chain L:	81%		13% • •
MET 12 12 12 15 15 15 15 15 15 15 15 15 15 15 15 15	L69 476 893 893 893 893 8102 8111 8111 8111 8112 8123 8125 8125	L126 127 128 132 132 137 136 136	M163 P164 L165 L170 A174 A174 L188 L188 L188 K190
L194 N307 N507 N507 L213 L213 L213 L213 L213 L213 L213 L213			
• Molecule 13: 54S ribosoma	al protein IMG1, mito	chondrial	
Chain M:	73%	13%	•• 11%
MET TRP SER ARG ASI ASI ASI ASI CU LEU LEU LEU THR ARG SER ARG SER ARG V16 V16 V29 V29 V29	P30 R34 R34 R34 R35 R39 R39 R39 R46 R51 R65 R65 R65	V76 194 195 196 196 110 110 1121	L1.25 11.42 11.44 11.61 11.61 11.64 11.64 11.64 11.64 11.64 11.64
ARG LYS LYS			
• Molecule 14: 54S ribosoma	al protein L49, mitoch	ondrial	
Chain N:	65%	9%	27%
MET LLEU LEU LEU LEU LYS PHE PHC PRO PRO PRO PRO PRO PRO PRO PRO	SER PHC PHC PHC ASN ASN ASN ASN ASN ASN TLEU SER SER SER SER SER SER THR	LYS ALA LYS LYS LYS K50 K50	P108 K117 K126 K123 K126 R126 R131 T134
V141 R142 F145 D149 L150 T151 R154 N161			
• Molecule 15: 54S ribosoma	al protein L22, mitoch	ondrial	
Chain O: 57	7%	14% •	28%
MET ANSN PHES PHES PHES PHES PHES ALA ALA ALA ALA ALA ALA SER SER SER SER SER SER	VAL SER ARG ARG ARG TRP ARG TLE TLE TLE TLE SER ASN SER	GLY GLY SER LEU PHE GLY SER THR THR GLU	ASN PRO CLYS CLY GLU GLY ASN ARG GLV ASP GLU ASP
ALA GLY SER PHE SER SER ASP ASP ALA ALA ALA ALA ALA ALA ALA ALA ALA AL	ASN ARG ARG ASP E89 ASN B91 C10 C10 C10 C10 C110 C110 C110 C111 C1	L112 E122 1127 K133 K133 D135	4156 E145 E155 E155 E159 E160 E160 E160 A165
K171 K177 A177 A177 L1183 L1184 L1183 L1285 L121 L121 L221 L221 L221 L222 L222 L22	629 629 7260 7260 7260 7260 7260 7260 7260 7260	V272 R275 R276 R276 R276 E285 L294	1299 R300 K309 W309
• Molecule 16: 54S ribosoma	al protein L41, mitoche	ondrial	
Chain P:	50%	17% •	21%





MET TRP LYS ARG SER PHE PHE HHE HHE CLN CLN CLY GLY	PRO LIEU AIS AIS 117 120 K26 K26	P27 V28 P30 K31 K31 H43 N46	T57 S58 N59 L60 S73 N74 H39	195 196 896 8102 8102	N104 D105 E116 V119 L120	A121 R122 L127
V131 8144 8144 7147 7148 M149 M149 0151 1152	R153 H154 V155 M57 M57 L166 L161 L161 R176	Y187 F188 LEU LEU ASN LYS ASP TLE PRO	N201 ♦ N204 ♦ 7205 0 1207 1 1207	F210 G211 TLE SER GLU THR TLE TLE GLN	ASP ASN VAL D222 1229	A233
LYS ASP SER ASN ASN ASN ASP LLEU ILE SER GLU SER SER	GLN GLU THR THR ASP VAL CLY GLU SER PHE	ILE LEU PHE SER ASP PHE GLU PRO	HLS ALA VAL GLU GLU ALA CYS VAL ALA ILE	LYS ASP LEU ARG LYS SER PRO ASP	ASM LYS VAL PRO LYS LEU ASP	GLU LEU PRO THR
VAL ARG LYS TYR LEU LEU CLN GLN TLE HIS ALA	SER VAL GLU GLU GLU ALA ALA ALA					
• Molecule 21:	54S ribosomal	protein L33,	mitochondria	al		
Chain U:		84%			12% 5%	
MET V2 F3 F3 F4 S11 S11 113 113 113	L26 Y36 A42 143 L47 R72	R83 THR ILE ASP				
• Molecule 22:	54S ribosomal	protein L36,	mitochondria	al		
Chain V:	34%	·	64%			
MET LEU LYS LYS SER TLE PHE ALA ALA ALA	SER THR GLY SER FRO FRO GLY SER SER SER	H43 V57 ARG ASP ASP	VAL VAL VAL VAL AAL ASP ASN SER GLY GLY	SER LEU ASP ARG PHE ASN LYS ARG	ITA SER SER LEU PHE SER VAL	ASP SER THR THR
PRO ASN SER SER SER GLU THR VAL GLU LEU SER	GLU GLU ASN LYS LYS LYS THR GLN THR CVS LYS	GLU GLU GLU GLU ASP VAL SER GLU GLU	ALA PHE GLY MET ASP ASP TYR LEU SER LEU	LEU ASP ASP SER GLU GLU GLN ILE	LTS SER GLY LYS LEU ALA SER	LYS LYS ARG ASP
LYS						
• Molecule 23:	54S ribosomal	protein L32,	mitochondria	al		
Chain W:	48%		12% •	39%		
MET ASN SER LEU LLEU PLHE GLY CYS GLN ALA	PHE HIS LYS LYS ILF VAL PRO THR THR ALA ALA ALA GLY	TRP LEU VAL PRO LEU GLY ASN PRO SER	LEU GLN GLN GLY GLN CLY GLN CLY GLY GLY	SER ILE HIS ARG TRP LEU GLU	LIS LEU GLN GLN ASP HIS HIS	ASP THR GLU ASP
LYS ASP PHE PHE SER SER ASN GLY ILEU LEU	A72 K82 K84 R84 R84 R85 M97 M97	L101 N102 K103 K103 K111 M118	q123 1124 1127 1127 1137 1137 1137	R140 Q141 L148 R157	1163 K169 R178 D183	
• Molecule 24:	54S ribosomal	protein L39,	mitochondria	al		
Chain X:		79%		11%	• 9%	
MET VAL LYS LYS S6 K29 K29 K29 K29 V34	T35 036 137 145 145 146 148 148 148 148 168 168 168	T68 A69 LYS				

• Molecule 25: 54S ribosomal protein L34, mitochondrial



Chain Y:	35%	6% •	57%
MET PRO LLEU LLEU ARG CYS CYS CYS SER SER ARG SER	MET PHE SER SER ILE SER PHE SER SER	LEU SER VAL VAL LEU ARG ALN CLY MET CLY MET LEU SER SER SER	PRO LEU LEU THR PRO SER PRO SER PRO CLY CLY CLY CLY CLY CLY CLY CLY CLY CLY
861 171 171 171 175 175 180 180 180 180 180	L103 S104 H105		
• Molecule 26: mit	tochondrial rib	bosomal protein YNL	122C
Chain Z:	45%	7% •	46%
MET LYS LYS SER SER SER ARG ARG ARG GLY ARP ARP CLY	ASN ASN ASN MET SER VAL PHE ASN VAL	LLEU PRO LEU LEU LYS GLY SER ASN SER ASN VAL LYS LYS ASN ASN	GLY PHE PHE ASN ASN ASN ASN ASN ASN THR THR THR THR THR THR THR THR THR THR
W65 R74 R74 A100 A100 L111 L111			
• Molecule 27: 54\$	5 ribosomal pr	rotein RTC6, mitocho	ondrial
Chain 0:	38%	·	59%
MET PHE LEU LEU GLN GLN HR HR MET MET MET	LEU HIS MET LYS PRO SER PRO TLE THR	THLE ARG ALA ALA CYS CYS PRO PRO PRO SER SER SER SER ALA ALA PRO	CLN PRO ALA LEU VAL LEU VAL ASN ASN ASN ASN ASN ASN CLY CLY CLY CSO CSO CSO CSO CSO CSO CSO CSO CSO CSO
• Molecule 28: 545	5 ribosomal pr	cotein L35, mitochono	drial
Chain 1:		74%	15% • 10%
MET LEU ARG ARG ARG ARG ARG HIS THR THR THR THR THR THR TEU	PRO ASN ALA ALA ALA ASER H20 Q45 C45 LYS	LLS ALA SER ALEU ASP PRO PS3 SS4 SS5 SS5 IS5 IS5 IS5 IS5 IS5 IS5 IS5 IS5	173 173 173 174 174 120 127 178 178 178 178 178 178 178 100 100 100 110 110 110
F121 N122 K123 K124 L126 V126 V128 V138 V138 V139 V139 V139	L142 L142 G143 K144 L155 M156 M156 L165	7106 1171 1171 1172 1172 1172 1172 1176 1176	V229 N229 N229 D231 D233 V233 V233 V233 T243 T243 L249 L249 D262 7263 N264 V291
1299 GLU ASP LYS LYS 1208 1303 14 1321 1331 1331 1331	Lozz (1324 (1324 (1334 (1334 (1335 (1335 (1335 (1335 (1335 (1335) (1335) (1335) (1335) (1335) (1335) (1336) (1336) (1336) (1336) (1336) (1336) (1336) (1336) (1336) (1336) (1326)	D344 K346 K346 K346 V361 V361 K366 K367	
• Molecule 29: 545	5 ribosomal pr	rotein L28, mitochono	drial
Chain 2:	61%	1	.4% · 23%
MET LEU LEU ALA GLN GLN FHE LYS LYS HE HIS ALA ALA VAL	GLU GLU VAL SER SER GLY THR THR YAL PHE	ALLE ARN ARN ARN ARN ARN ARN LYS SER SER SER R41 V42 V42 V43 V42 V43 V42 V43	q 45 V 48 L 59 L 59 K 60 R 65 L 66 L 66 R 63 R 63 R 63 R 63 R 63 R 63 R 111





• Molecule 30: 54S ribosomal protein L27, mitochondrial

Chain 3:	75%	11%	14%	
MET LYS CLY GLY SER PRO TLE SER SER SER SER	LYS THR SER ALA ALA ALA L43 C43 C43 C43 C43 C43 C43 C43 C43 C43 C	L113 L119 T122	N128	Y142 K143 E144 R145 GLY
• Molecule 31:	: 54S ribosomal protein L51, mitochondrial			
Chain 4:	77%	18	3% • •	
MET V2 R13 I26 I26 I27 I27	C31 N32 N33 N33 N33 N33 N33 N33 N42 N42 N42 N42 N42 O50 O54 O54 O54 O54 O54 O54 O54 O56 O56 S67 N43 N66 N52 N43 N40 N33 N40 N33 N42 N42 N42 N42 N42 N42 N42 N42 N42 N42	L98 K99 K102	L121 128 L132 K136	R139 ILE
• Molecule 32:	: 54S ribosomal protein L3, mitochondrial			
Chain 5:	69% 1	L3% •	16%	
MET GLY CLY CLEU VAL LEU LEU ARG ALA ALA ALA	ALA ALA MET PRO PRO PRO ASN ASN ASN ASN ASN ASN ASN ASN ASN ASN	SER SER PHE THR SER	LYS ARG TYR LEU HIS LEU SER	THR LEU THR GLN GLN
CLU LYS PHE FG6 E67 E67 E67	Y73 Y73 L98 L98 L101 L101 L101 L103 L163 S115 X148 X148 X148 X148 X148 X148 X158 X158 X158 X158 X158 X158 X158 X15	A200 W203 M219	G227 L236 N237 D240	L244 S251 V260
W268 T271 V279 V280 F281 T281 T283	1287 1287 1286 1286 1286 1297 1231 1310 1311 1310 1311 1311 1311 1311	N370 N370 P381	V390	
• Molecule 33:	: 54S ribosomal protein L17, mitochondrial			
Chain 6:	62% 11% ·	•	26%	
MET LYS VAL ASN ASN LEU LEU LYS ARG GLY	LEU THR ALA ALA ALA ALA ALA ALA ALA ALA ALA AL	Q83 R97 K103	H104 G105 R106 K111 Q112 E113	V114 K115 L116 SER ASP
ASP THR VAL ALA PHE SER ASN ASN GLN	LYS GLN SER LYS ASP ASP ASP ASP ASP ASP ASP ASP ASP CIS CIS SER CIS SER CIS SER CIS SER CIS CIS CIS CIS CIS CIS CIS CIS CIS CIS	SER ASP E187 H192 V193	H194 E196 E196 E198 E198	4204 ASP GLN I207 V219
LEU GLN ASP ASP GLU GLU ARG ASN ALA GLU GLU	C239 173 175 175 175 175 175 175 175 175 175 175			
• Molecule 34:	: 54S ribosomal protein IMG2, mitochondria	al		

Chain 7: 53% 19% 27%



MET SER NET SE

• Molecule 35: 54S ribosomal protein L13, mitochondrial

Chain 8:	58%	10% •	31%	I
	LE RRC EU RRC EU RRC RRC ER RRC RRC RRC RRC RRC RRC RRC	E E E S L N	RP RC RC RC RC RC RC RC RC RC RC RC RC RC	L X H R S L



• Molecule 36: 54S ribosomal protein L15, mitochondrial

Chain 9:	62%	13% •	23%
MET AGLU AGLU AGLU AET MET MET MET AEC AEC AEC AEC AEC AEC AEC AEC AEC AEC	ASIA LEU GLN SER VAL ARG ARG H33 H33 H33 H33 H33 H33 H33 H33 H33 H3	N51 P52 L56 E59 V60 ASN ALA K63	E64 C655 C655 C75 C74 C77 F77 K77 R77 R77 R77 R77 R77 R77
182 188 198 198 198 198 198 198 103 110 1121 1121 1121 1121 1121 1121 1	ctur SER Cty Cty Cty Cty Cty Cty Cty Cty Cty Cty	H166 N167 N176 K181 K181 ASP G183 H184	L196 F199 1200 1203 R211 K211
9217 2224 2524 2524 257 258 150 150 157 158 258 258 258 258 258 258 258 258 258 2			
• Molecule 37: 54S ribosom	al protein L20, mitochor	ıdrial	
Chain a:	77%	12%	• 10%
MET 11.E 11.E ARG 0.1.Y 0.1.Y 0.1.Y 0.1.Y ALA ALA ALA ALA ALA ALA ALA ALA ALA AL	V28 129 130 130 135 135 135 135 135 135 135 135 137 170 170 170 170 170	L101 G109 L114 G115 P116 P116	K132 8150 9158 0158 0158 1162 K175 K175 R182
A187 191 1191 1192 A195			
• Molecule 38: 54S ribosom	al protein L25, mitochor	ıdrial	
Chain b:	84%		14% ••
MET SER 7 3 7 4 7 3 6 4 7 3 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6	E117 E83 E83 E83 E105 E117 E117 E117 E117 E123 E123 E123 E123 E123	E131 L132 K136 K137 E146 E146 N151	F157



• Molecule 39: 54S ribosomal protein L31, mitochondrial

Chain c:	84%	
MET PHE GLY CLEU PHE LEU PRO PRO PRO PRO PRO PRO PRO PRO PRO FRO FRO FRO FRO FRO FRO FRO FRO FRO F	K70 L78 1101 1117 1124 117 1124	

• Molecule 40: Mitochondrial homologous recombination protein 1

Chain d:	78%	12%	10%
MET NG 122 123 123 123 123 123 123 123 123 123	K72 K73 K83 K83 K94 K96 K96 K96 K101 L110 L111	1142 1442 1448 1448 1448 1448 1448 1448	D173 H177 K191 Q194 Q194 R195 V196
E203 1207 1207 1210 1210 1210 1210 1210 1210	GLN		
• Molecule 41: E-site tR	NA		
	70%		
Chain e:	65%	35%	
**********	•		
61 62 62 63 65 66 66 66 66 66 66 66 66 66	A76 A73 A76 A76 A76		



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	47124	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	25	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4700	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	1.687	Depositor
Minimum map value	-0.940	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.039	Depositor
Recommended contour level	0.0681	Depositor
Map size (Å)	482.40002, 482.40002, 482.40002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles $(^{\circ})$	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.34, 1.34, 1.34	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: NA, ZN, MG

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).

Mal	Chain	Bond	lengths	Bond angles	
	Ullaili	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.24	0/64599	0.70	13/100487~(0.0%)
2	В	0.32	0/2305	0.66	0/3102
3	С	0.32	0/1973	0.59	0/2654
4	D	0.33	0/1904	0.65	0/2579
5	Е	0.31	0/2181	0.54	0/2955
6	F	0.31	0/1376	0.58	0/1869
7	G	0.32	0/468	0.57	0/628
8	Н	0.36	0/1200	0.63	1/1610~(0.1%)
9	Ι	0.30	0/943	0.58	0/1260
10	J	0.33	0/1764	0.66	2/2360~(0.1%)
11	Κ	0.33	0/1606	0.65	0/2148
12	L	0.35	0/1843	0.64	0/2486
13	М	0.30	0/1224	0.64	0/1651
14	Ν	0.30	0/961	0.61	0/1295
15	0	0.35	0/1821	0.68	0/2444
16	Р	0.34	0/1766	0.63	0/2381
17	Q	0.31	0/2174	0.57	0/2946
18	R	0.36	0/2522	0.68	0/3392
19	S	0.34	0/1216	0.58	0/1626
20	Т	0.36	0/1689	0.69	0/2297
21	U	0.38	0/648	0.67	0/870
22	V	0.28	0/539	0.54	0/726
23	W	0.33	0/955	0.65	0/1273
24	Х	0.33	0/520	0.62	0/696
25	Y	0.44	0/383	0.69	0/504
26	Z	0.38	0/522	0.71	0/695
27	0	0.32	0/329	0.56	0/432
28	1	0.32	0/2777	0.61	0/3772
29	2	0.37	0/938	0.70	0/1264
30	3	0.31	0/1018	0.57	0/1368
31	4	0.33	0/1138	0.65	0/1526
32	5	0.34	0/2538	0.66	$1/3451 \ (0.0\%)$



Mal	Chain	Bond	lengths	E	Bond angles
1VIOI	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5
33	6	0.30	0/1631	0.54	0/2214
34	7	0.31	0/869	0.57	0/1166
35	8	0.35	0/1438	0.61	0/1945
36	9	0.34	0/1453	0.61	0/1969
37	a	0.33	0/1458	0.63	0/1961
38	b	0.34	0/1333	0.63	0/1783
39	с	0.35	0/1024	0.63	0/1367
40	d	0.34	0/1762	0.65	0/2381
41	е	0.21	0/476	0.73	2/739~(0.3%)
All	All	0.29	0/119284	0.67	19/174272~(0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	А	1	0
3	С	0	1
4	D	0	1
10	J	0	1
20	Т	0	1
37	а	0	1
All	All	1	5

There are no bond length outliers.

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	2897	A	C2'-C3'-O3'	7.88	126.83	109.50
1	А	1892	G	C2'-C3'-O3'	7.84	126.75	109.50
1	А	733	А	C2'-C3'-O3'	7.69	126.42	109.50
10	J	76	ARG	NE-CZ-NH1	7.44	124.02	120.30
8	Н	125	ARG	NE-CZ-NH1	7.28	123.94	120.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	А	1665	G	C1'

All (5) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
3	С	210	ASP	Peptide
4	D	49	PHE	Peptide
10	J	93	GLN	Peptide
20	Т	43	HIS	Peptide
37	a	87	MET	Peptide

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	А	57671	28898	28934	625	0
2	В	2260	2343	2303	47	0
3	С	1930	1976	1964	21	0
4	D	1866	1914	1898	30	0
5	Е	2125	2169	2125	23	0
6	F	1355	1392	1338	22	0
7	G	458	471	467	2	0
8	Н	1176	1218	1210	19	0
9	Ι	937	1015	1013	10	0
10	J	1727	1828	1812	12	0
11	Κ	1573	1635	1629	9	0
12	L	1815	1883	1873	21	0
13	М	1206	1286	1283	13	0
14	Ν	948	1010	1006	2	0
15	0	1789	1895	1877	21	0
16	Р	1722	1728	1718	22	0
17	Q	2126	2161	2092	19	0
18	R	2481	2500	2413	25	0
19	S	1191	1249	1234	16	0
20	Т	1646	1618	1557	22	0
21	U	639	702	699	11	0
22	V	528	555	553	3	0
23	W	937	985	974	9	0
24	Х	512	565	563	3	0
25	Y	376	412	410	4	0
26	Ζ	508	546	539	6	0
27	0	324	349	345	4	0
28	1	2707	2690	2661	24	0
29	2	919	939	923	14	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	3	995	1030	1012	10	0
31	4	1117	1146	1142	18	0
32	5	2485	2541	2488	26	0
33	6	1592	1595	1511	13	0
34	7	854	901	897	10	0
35	8	1413	1416	1381	14	0
36	9	1428	1437	1368	19	0
37	a	1427	1455	1449	0	0
38	b	1299	1372	1367	0	0
39	с	1000	1066	1062	0	0
40	d	1717	1706	1691	0	0
41	е	427	221	222	0	0
42	А	109	0	0	0	0
42	N	1	0	0	0	0
43	В	1	0	0	0	0
44	0	1	0	0	2	0
44	W	1	0	0	0	0
All	All	111319	83818	83003	1022	0

Continued from previous page...

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 6.

The worst 5 of 1022 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:A:45:U:O4	1:A:2895:A:N1	1.58	1.36
1:A:114:U:O4	1:A:118:A:N1	1.68	1.25
1:A:1913:A:N1	1:A:2880:U:O4	1.73	1.21
1:A:122:A:N6	1:A:139:U:N3	1.91	1.19
1:A:274:U:O4	1:A:367:A:N1	1.78	1.15

There are no symmetry-related clashes.

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.



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	В	291/393~(74%)	272~(94%)	16 (6%)	3~(1%)	15 54
3	С	247/269~(92%)	226 (92%)	15 (6%)	6(2%)	6 34
4	D	235/286~(82%)	211 (90%)	15 (6%)	9~(4%)	3 22
5	Е	272/292~(93%)	246 (90%)	22 (8%)	4 (2%)	10 44
6	F	173/214 (81%)	163 (94%)	7 (4%)	3(2%)	9 42
7	G	53/139~(38%)	50 (94%)	3 (6%)	0	100 100
8	Н	146/163~(90%)	138 (94%)	8 (6%)	0	100 100
9	Ι	121/138 (88%)	110 (91%)	10 (8%)	1 (1%)	19 58
10	J	218/322~(68%)	202 (93%)	14 (6%)	2 (1%)	17 56
11	K	193/232~(83%)	182 (94%)	7 (4%)	4 (2%)	7 37
12	L	225/238~(94%)	208 (92%)	14 (6%)	3 (1%)	12 47
13	М	149/169~(88%)	138 (93%)	9 (6%)	2 (1%)	12 47
14	N	116/161~(72%)	109 (94%)	6 (5%)	1 (1%)	17 56
15	Ο	219/309~(71%)	199 (91%)	18 (8%)	2 (1%)	17 56
16	Р	205/263~(78%)	189 (92%)	14 (7%)	2 (1%)	15 54
17	Q	269/297~(91%)	243 (90%)	22 (8%)	4 (2%)	10 44
18	R	310/371~(84%)	288 (93%)	17 (6%)	5 (2%)	9 43
19	S	142/258~(55%)	136 (96%)	6 (4%)	0	100 100
20	Т	203/319~(64%)	184 (91%)	13 (6%)	6(3%)	4 28
21	U	80/86~(93%)	77 (96%)	3 (4%)	0	100 100
22	V	62/177~(35%)	57 (92%)	5 (8%)	0	100 100
23	W	110/183~(60%)	100 (91%)	6 (6%)	4 (4%)	3 23
24	Х	62/70~(89%)	55 (89%)	6 (10%)	1 (2%)	9 43
25	Y	43/105 (41%)	41 (95%)	1 (2%)	1 (2%)	6 34
26	Z	60/115~(52%)	57 (95%)	3 (5%)	0	100 100
27	0	36/93~(39%)	34 (94%)	2 (6%)	0	100 100
28	1	324/367~(88%)	293 (90%)	26 (8%)	5 (2%)	10 44
29	2	111/147~(76%)	103 (93%)	5 (4%)	3(3%)	5 30
30	3	120/146~(82%)	103 (86%)	16 (13%)	1 (1%)	19 58
31	4	136/140~(97%)	128 (94%)	8 (6%)	0	100 100

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	Perce	entiles
32	5	324/390~(83%)	299~(92%)	23 (7%)	2 (1%)	25	64
33	6	195/281~(69%)	179 (92%)	12 (6%)	4 (2%)	7	37
34	7	104/146~(71%)	99~(95%)	5 (5%)	0	100	100
35	8	178/264~(67%)	168 (94%)	10 (6%)	0	100	100
36	9	185/253~(73%)	163 (88%)	14 (8%)	8 (4%)	2	20
37	a	174/195~(89%)	161 (92%)	7 (4%)	6 (3%)	3	24
38	b	153/157~(98%)	139 (91%)	12 (8%)	2(1%)	12	47
39	с	116/131~(88%)	108 (93%)	5 (4%)	3(3%)	5	31
40	d	200/226~(88%)	179 (90%)	16 (8%)	5 (2%)	5	32
All	All	6560/8505~(77%)	6037 (92%)	421 (6%)	102 (2%)	13	43

Continued from previous page...

5 of 102 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	В	382	VAL
3	С	211	PRO
4	D	49	PHE
4	D	50	PRO
4	D	135	ALA

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	Percent	tiles
2	В	233/337~(69%)	210 (90%)	23~(10%)	8 3	80
3	С	209/229~(91%)	190 (91%)	19 (9%)	9 3	84
4	D	200/248~(81%)	173 (86%)	27~(14%)	4 1	8
5	Ε	225/260~(86%)	201 (89%)	24 (11%)	6 2	27
6	F	141/190~(74%)	120 (85%)	21 (15%)	3 1	4
7	G	50/129~(39%)	47 (94%)	3 (6%)	19	54
8	Η	126/141~(89%)	117~(93%)	9~(7%)	14	47



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Mol	Chain	Analysed	Rotameric	Outliers	Perce	entiles
9	Ι	106/117~(91%)	101 (95%)	5~(5%)	26	62
10	J	175/274~(64%)	147 (84%)	28~(16%)	2	11
11	Κ	167/200~(84%)	138 (83%)	29~(17%)	2	10
12	L	202/212~(95%)	188 (93%)	14 (7%)	15	49
13	М	136/153~(89%)	124 (91%)	12 (9%)	10	36
14	Ν	107/147~(73%)	98 (92%)	9~(8%)	11	39
15	О	191/270~(71%)	169 (88%)	22 (12%)	5	24
16	Р	183/236~(78%)	155 (85%)	28 (15%)	2	13
17	Q	219/268~(82%)	198 (90%)	21 (10%)	8	32
18	R	250/337~(74%)	218 (87%)	32 (13%)	4	20
19	S	126/231~(54%)	116 (92%)	10 (8%)	12	43
20	Т	171/298~(57%)	156 (91%)	15 (9%)	10	36
21	U	73/77~(95%)	71 (97%)	2(3%)	44	75
22	V	59/161~(37%)	58 (98%)	1 (2%)	60	83
23	W	104/167~(62%)	90 (86%)	14 (14%)	4	18
24	Х	56/62~(90%)	52 (93%)	4 (7%)	14	47
25	Y	39/93~(42%)	37 (95%)	2(5%)	24	60
26	Z	50/100~(50%)	45 (90%)	5 (10%)	7	30
27	0	36/84~(43%)	36 (100%)	0	100	100
28	1	299/341~(88%)	269 (90%)	30 (10%)	7	30
29	2	99/137~(72%)	90 (91%)	9 (9%)	9	34
30	3	102/126~(81%)	97~(95%)	5 (5%)	25	61
31	4	121/123~(98%)	107 (88%)	14 (12%)	5	24
32	5	263/345~(76%)	234 (89%)	29 (11%)	6	26
33	6	153/252~(61%)	134 (88%)	19 (12%)	4	21
34	7	94/128~(73%)	81 (86%)	13 (14%)	3	16
35	8	149/240~(62%)	134 (90%)	15 (10%)	7	29
36	9	140/221~(63%)	127 (91%)	13 (9%)	9	33
37	a	156/171 (91%)	136 (87%)	20 (13%)	4	20
38	b	144/146~(99%)	122 (85%)	22 (15%)	2	13
39	с	110/120~(92%)	105 (96%)	5 (4%)	27	63



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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
40	d	185/210~(88%)	162 (88%)	23~(12%)	4 21
All	All	5649/7581~(74%)	5053 (89%)	596 (11%)	10 27

 $5~{\rm of}~596$ residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
32	5	368	MET
40	d	9	ARG
33	6	111	LYS
32	5	339	HIS
36	9	160	CYS

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such side chains are listed below:

Mol	Chain	Res	Type
19	S	84	ASN
22	V	81	ASN
35	8	235	GLN
3	С	207	GLN
2	В	378	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	А	2682/3296~(81%)	692~(25%)	132 (4%)
41	е	18/20~(90%)	6 (33%)	0
All	All	2700/3316~(81%)	698~(25%)	132 (4%)

5 of 698 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	А	22	U
1	А	26	А
1	А	27	А
1	А	28	U
1	А	29	А

 $5~{\rm of}~132$ RNA pucker outliers are listed below:



Mol	Chain	Res	Type
1	А	2906	U
1	А	3036	U
1	А	3252	U
1	А	840	С
1	А	781	G

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 113 ligands modelled in this entry, 113 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	А	5
41	е	1

The worst 5 of 6 chain breaks are listed below:



Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	2226:A	O3'	2227:U	Р	17.43
1	A	2197:A	O3'	2198:U	Р	17.36
1	е	6:G	O3'	63:G	Р	15.82
1	А	2344:A	O3'	2345:A	Р	15.67
1	А	1374:U	O3'	1375:A	Р	11.56



6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-2566. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

6.1.1 Primary map



The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

6.2.1 Primary map



X Index: 180

Y Index: 180





The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 212

Y Index: 145

Z Index: 182

The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map



The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.



6.5 Orthogonal surface views (i)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0681. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.6 Mask visualisation (i)

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



7 Map analysis (i)

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

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.



7.2 Volume estimate (i)



The volume at the recommended contour level is 1704 $\rm nm^3;$ this corresponds to an approximate mass of 1539 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.



7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.312 ${\rm \AA^{-1}}$



8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.312 \AA^{-1}



8.2 Resolution estimates (i)

$\begin{array}{ c c c c c c c c c c c c c c c c c c c$	Estimation criterion (FSC cut-off)		
Resolution estimate (A)	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.15	3.68	3.19
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.



9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-2566 and PDB model 3J6B. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.0681 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.



9.2 Q-score mapped to coordinate model (i)



The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0681).



9.4 Atom inclusion (i)



At the recommended contour level, 94% of all backbone atoms, 95% of all non-hydrogen atoms, are inside the map.



1.0

0.0 <0.0

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.0681) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9460	0.5070
0	0.9550	0.5600
1	0.9440	0.5060
2	0.9420	0.4870
3	0.9400	0.5180
4	0.9500	0.5420
5	0.9400	0.5190
6	0.9260	0.4600
7	0.9420	0.5170
8	0.8880	0.4180
9	0.9420	0.4650
А	0.9600	0.5070
В	0.9490	0.5350
С	0.9580	0.5580
D	0.9310	0.5210
E	0.9350	0.5150
F	0.9140	0.4500
G	0.9580	0.5080
Н	0.9470	0.5580
Ι	0.9150	0.5150
J	0.9570	0.5360
K	0.9390	0.5240
L	0.9380	0.5230
M	0.9380	0.5120
N	0.9520	0.5500
0	0.9350	0.5230
<u>Р</u>	0.9280	0.5110
Q	0.8950	0.4610
R	0.9300	0.4700
<u> </u>	0.9430	0.5270
<u>'1'</u>	0.8780	0.4520
U	0.9490	0.5350
V	0.9330	0.5010
W	0.9440	0.5330
Х	0.9260	0.5300



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Chain	Atom inclusion	Q-score
Y	0.9190	0.5590
Z	0.9610	0.5640
a	0.9390	0.5060
b	0.9180	0.4930
С	0.9370	0.5390
d	0.9390	0.5240
е	0.2880	0.1130

